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Genetics of Restless Legs Syndrome

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Abbreviations

a	year [1]
AAGAB	alpha- and gamma-adaptin binding protein [2]
ABCA10	ATP binding cassette subfamily A member 10 [2]
ADAM22	ADAM metallopeptidase domain 22 [2]
AG	Aktiengesellschaft [3] (public limited company)
ALLC	allantoicase [2]
ANOVA	analysis of variance [4]
approx	approximately, approximate [5]
aqua dest.	aqua destillata [6] (distilled water)
ARFRP1	ADP ribosylation factor related protein 1 [2]
ASRS	Augmentation Severity Rating Scale [7]
ASTN2	astrotactin 2 [2]
aSum	adaptive sum test [8]
ATP	adenosine 5-triphosphate [9]
ATP2C1	ATPase secretory pathway Ca^{2+} transporting 1 [2]
BAF	B allele frequency [10]
BBS7	Bardet-Biedl syndrome 7 [2]
BLK	B lymphoid tyrosine kinase, now: BLK proto-oncogene, Src family tyrosine kinase [2]
BMP	bone morphogenetic proteins [2]
bp	base pair [11]
BRV	burden of rare variants [12]
BTBD9	BTB domain containing 9 [2]
BVBA	besloten vennootschap met beperkte aansprakelijkheid (private limited liability company) [13]
CA	California [14]
CACNG8	calcium voltage-gated channel auxiliary subunit gamma 8 [2]
CADD	Combined Annotation-Dependent Depletion [15]
CADM1	cell adhesion molecule 1 [2]
CALML4	calmodulin like 4 [2]
CASC16	cancer susceptibility 16 [2]
CAST	cohort allelic sums test [16]
CBP	CREB binding protein [2]
CCDC148	coiled-coil domain containing 148 [2]
CDCV	common disease – common variant hypothesis [17]
cDNA	complementary deoxyribonucleic acid [18]
CDRV	common disease – rare variant hypothesis [19]
chr	chromosome
CI	confidence interval [20]
CLDN23	claudin 23 [2]
CLOCK	clock circadian regulator [2]
CMC	combined multivariate and collapsing [21]
cMorgan	centiMorgan
CNNM3	cyclin and CBS domain divalent metal cation transport mediator 3 [2]
CNS	central nervous system [9]
CNTN4	contactin 4 [2]

CNV	copy number variation [10]
COL20A1	collagen type XX alpha 1 chain [2]
COL6A6	collagen type VI alpha 6 chain [2]
COLEC11	collectin subfamily member 11 [2]
COPD	chronic obstructive pulmonary disease [22]
CORO6	coronin 6 [2]
CRBN	cereblon [2]
CREB**(1/5)**	cAMP responsive element binding protein (1/5) [2]
C-score	CADD score [15]
CTNNA2	catenin alpha 2 [2]
dATP	2’-deoxyadenosine-5’-triphosphate [23]
DCLK2	doublecortin like kinase 2 [2]
dCTP	2’-deoxycytidine-5’-triphosphate [23]
DDCI	dopa decarboxylase inhibitor [24]
dGTP	2’-deoxyguanosine-5’-triphosphate [23]
DHS	Dortmund Health Study [25]
DMPK	dystrophia myotonica protein kinase [2]
DMSO	dimethyl sulfoxide [23]
DMT1	divalent metal transporter 1 [26] (also: *SLC11A2* = solute carrier family 11 member 2 [2])
DNA	deoxyribonucleic acid [18]
dNTP	deoxynucleoside triphosphate [23]
dsDNA	double-stranded DNA [27]
dTTP	2’-thymidine-5’-triphosphate [23]
DZ	dizygotic (twins) [28]
E. coli	*Escherichia coli* [9]
e.g.	exempli gratia [29]
EB	elution buffer [30]
EBF3	early B-cell factor 3 [2]
EC	exponential-combination (test) [31]
EDTA	ethylenediamine tetraacetic acid [23]
EMSA	electrophoretic mobility shift assay [32]
eQTL	expression quantitative trait loci [20]
EREC	estimated regression coefficient [33]
ESRD	end-stage renal disease [34]
et al.	et alii/alia [35]
EURLSSG	European Restless Legs Syndrome Study Group [36]
EYA2	EYA transcriptional coactivator and phosphatase 2 [2]
FAM114A1	family with sequence similarity 114 member A1 [2]
FAM171A1	family with sequence similarity 171 member A1 [2]
FaST-LMM	factored spectrally transformed linear mixed models [37]
FCM	ferric carboxymaltose [38]
FDA	US Food & Drug Administration [39]
FDR	false discovery rate [20]
FFPE	formalin-fixed, paraffin-embedded [40]
FTSJ2	FtsJ RNA methyltransferase homolog 2 (*E. coli*) (new name: *MRM2*, mitochondrial

	rRNA methyltransferase 2) [2]
FWER	family-wise error rate [20]
GAC	Genome Analysis Center, Helmholtz Zentrum München [41]
GALNT12	polypeptide N-acetylgalactosaminyltransferase 12 [2]
GB	gigabyte [42]
gDNA	genomic deoxyribonucleic acid [43]
GEMMA	genome-wide efficient mixed model association algorithm [44]
GLM	generalized linear model [4]
GLMM	generalized linear mixed model [20]
GLO1	glyoxalase I [2]
GmbH	Gesellschaft mit beschränkter Haftung [45] (limited company)
GmbH & Co. KG	GmbH & Compagnie [46] Kommanditgesellschaft [47] (limited company & limited partnership)
GMMAT	generalized linear mixed model association test [48]
grammar	genome-wide rapid association using mixed model and regression [49]
GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B [2]
GRR	genotype relative risk [50]
GWAS	genome-wide association study [51]
HA	high availability [52]
HCl	hydrochloric acid
HF	high fidelity [53]
HMOX1	heme oxygenase 1 [2]
HNR	Heinz Nixdorf RECALL (Risk Factors, Evaluation of Coronary Calcium and Lifestyle) study [54, 55]
HPC	high performance computing [52]
HRM	high resolution melting [56]
HS	high sensitivity [57]
HWE	Hardy-Weinberg equilibrium [51]
IBD	identity/identical by descent [58, 59]
IBS	identity/identical by state [58, 59]
ICD-10	International Statistical Classification of Diseases and Related Health Problems 10th revision [60]
IDA	iron deficiency anemia [61]
IHG	Institute of Human Genetics, Helmholtz Zentrum München [62]
IL	interleukin [2]
Inc.	Incorporated [63]
IQCH	IQ motif containing H [2]
iRLS	idiopathic RLS [64]
IRLS	IRLSSG rating scale [65]
IRLSSG	International Restless Legs Syndrome Study Group [66]
IRP2	iron regulatory protein-2 [67]
JHRLSS	Johns Hopkins restless legs severity scale [68]
KBAC	kernel-based adaptive cluster [69]
KCNA4	potassium voltage-gated channel subfamily A member 4 [2]
KCNK13	potassium two pore domain channel subfamily K member 13 [2]
KCTD18	potassium channel tetramerization domain containing 18 [2]
KORA	Kooperative Gesundheitsforschung in der Region Augsburg (cooperative health

	study in the region of Augsburg) [41]
***KRTAP19*-5**	keratin associated protein 19-5 [2]
LAMA1	laminin subunit alpha 1 [2]
LC	liquid chromatography [20]
LCAT	lecithin-cholesterol acyltransferase [2]
LCL	lymphoblastoid cell line [70]
LD	linkage disequilibrium [59]
L-dopa	Levodopa [71]
LEO1	LEO1 homolog, Paf1/RNA polymerase II complex component [2]
LLC	limited liability company [72]
LM	linear model [4]
LRR	log-R ratio [10]
LRRN1	leucine rich repeat neuronal 1 [10]
LRT	likelihood ratio test [73]
MA	Massachusetts [14]
MAC	minor allele count [74]
MAF	minor allele frequency [59]
MALDI-TOF	matrix-assisted laser desorption ionization - time of flight mass spectrometry [75]
MAOA	monoamine oxidase A [2]
MAP2K5	mitogen-activated protein kinase kinase 5 [2]
Mb	mega base
MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1 [2]
MDS	multidimensional scaling [59]
MEIS(1/2)	Meis homeobox 1/2 [2]
meta-GWAS	meta-analysis of GWAS summary statistics [76]
MICAL	Molecule Interacting with CasL [77]
MICALL2	MICAL like 2 [2]
MIP	molecular inversion probe [78]
MIPseq	molecular inversion probe based sequencing
MN	Minnesota [14]
MPI	Max-Planck Institute
MPPED2	metallophosphoesterase domain containing 2 [2]
MQ	root mean square of the mapping quality of reads across all samples [79]
mRNA	messenger ribonucleic acid [80]
MS	multiple sclerosis [22]
MS	mass spectrometry [20]
mut	mutation
MYT1	myelin transcription factor 1 [2]
MZ	monozygotic (twins) [28]
NA	not available (= missing value) [4]
Na$_2$EDTA	disodium ethylenediaminetetraacetate [23]
NaOH	sodium hydroxide
NCBI	National Center for Biotechnology Information [81]
NECAP	adaptin-ear-binding coat-associated-protein [82]
NECAP1	NECAP endocytosis associated 1 [2]
NENF	neudesin neurotrophic factor [2]

NGS	next generation sequencing [83]
NH	New Hampshire [14]
NHGRI	National Human Genome Research Institute [84]
NJ	New Jersey [14]
No.	number [85]
NOS1	nitric oxide synthase 1 [2]
NPAS2	neuronal PAS domain protein 2 [2]
NPBWR2	neuropeptides B and W receptor 2 [2]
NRG3	neuregulin 3 [2]
NRSN2	neurensin 2 [2]
nt	nucleotide [43]
NTNG1	netrin G1 [2]
NY	New York [14]
OLFML2B	olfactomedin like 2B [2]
OPRL1	opioid related nociceptin receptor 1 [2]
OR	odds ratio [20]
OSBP	oxysterol binding protein [2]
OSGIN1	oxidative stress induced growth inhibitor 1 [2]
p	*p* value
PA	Pennsylvania [14]
PAR	pseudoautosomal region [80]
PC	principal component [20]
PCA	principal components analysis [20]
PCDHB5	protocadherin beta 5 [2]
PCR	polymerase chain reaction [18]
PD	Parkinson disease [22]
PDE11A	phosphodiesterase 11A [2]
PIAS1	protein inhibitor of activated STAT 1 [2]
PIK3R4	phosphoinositide-3-kinase regulatory subunit 4 [2]
PKP4	plakophilin 4 [2]
PLINK	population based linkage analysis [59]
PLM	periodic limb movement [86]
PLMD	periodic limb movement disorder [87]
PLMS	periodic leg movements in sleep [87]
PLXNA2	plexin A2 [2]
PolyPhen	polymorphism phenotyping [88]
PP	polypropylene [89]
PPTA	preprotachykinin [90]
PTPRD	protein tyrosine phosphatase, receptor type D [2]
PTPRM	protein tyrosine phosphatase, receptor type M [2]
QC	quality control [83]
qPCR	quantitative PCR [83]
QQ plot	quantile-quantile [20] plot
RAM	random-access memory [42]
RASGRP4	RAS guanyl releasing protein 4 [2]
RIMS2	regulating synaptic membrane exocytosis 2 [2]

RLS	restless legs syndrome [22]
RMPC	individual relative MIPs’ performance curve
RT	room temperature
sd	standard deviation [4]
SEMA6D	semaphorin 6D [2]
SETBP1	SET binding protein 1 [2]
SGCZ	sarcoglycan zeta [2]
SHIP	Study of Health in Pomerania [25]
SIFT	sorts intolerant from tolerant substitutions [91]
SKAT	sequence kernel association test [92]
SKAT-O	sequence kernel association test - optimal unified [93]
SKOR1	SKI family transcriptional corepressor 1 [2]
SLC14A2	solute carrier family 14 member 2 [2]
SLC39A7/8/11	solute carrier family 39 member 7/8/11 [2]
SNCA	synuclein alpha [2]
SNP	single nucleotide polymorphism [51]
SNV	single nucleotide variant [94]
SP	substance P [90]
SPATS2L	spermatogenesis associated serine rich 2 like [2]
SSU	sum of squared score test [95]
STEAP4	STEAP4 (six transmembrane epithelial antigen of prostate) metalloreductase [2]
SUN1	Sad1 and UNC84 domain containing 1 [2]
SYT5	synaptotagmin 5 [2]
T2D	type 2 diabetes [22]
TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [2]
TDT	transmission/disequilibrium test (transmission test for linkage disequilibrium) [96]
TH	tyrosine hydroxylase [2]
TOX3	TOX high mobility group box family member 3 [2]
TREM1	triggering receptor expressed on myeloid cells 1 [2]
Tris	tris(hydroxymethly)-amino-methane [23]
TUBB3	tubulin beta 3 class III [2]
TX	Texas [14]
UBL4B	ubiquitin like 4B [2]
UCSC	University of California, Santa Cruz [97]
unc	uncoordinated (in *Caenorhabditis elegans*) [98]
UNCX	UNC homeobox [2]
USA	United States of America
UTR	untranslated region [80]
VAV3	vav guanine nucleotide exchange factor 3 [2]
vcf	variant call format [99]
VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor [2]
vs	versus [100]
VT	variable threshold test [101]
WED	Willis-Ekbom Disease [102]
WHO	World Health Organization [103]
WI	Wisconsin [14]

WST	weighted-sum test [104]
XK	X-linked Kx blood group [2]
XKR6	XK related 6 [2]
ZNF175	zinc finger protein 175 [2]
ZNF804B	zinc finger protein 804B [2]

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Abstract

Background: The restless legs syndrome (RLS) is classified as a disease of the nervous system. It presents with an urge to move the legs, especially at rest in the evening or at night. Its prevalence is age dependent and high with approx 5% in Caucasian populations but lower in Asian populations. Multimorbidity is a risk factor for RLS. Pregnancy, female sex, uremic disease and iron deficiency are associated with RLS. The syndrome affects the quality of life of the patients and is currently treated with dopamine agonists (non-ergot-derived), opioids, α2δ ligands and iron supplements. As an adverse effect of dopaminergic treatment, a worsening of symptoms (augmentation) can appear. Many RLS cases are familial (approx 50%). They also appear to have a younger age of onset. These familial cases seem to follow an autosomal dominant inheritance pattern. Extensive linkage studies were performed in the past that resulted in the identification of 10 linkage loci. Many attempts were made to identify the causal sequence variant, but the yield was very low. In contrast, genome-wide association studies with the aim to identify common single nucleotide polymorphisms identified the *MEIS1* locus (chromosome 2p) and *BTBD9* locus (chromosome 6p), *MAP2K5*/*SKOR1* locus (chromosome 15q), *PTPRD* locus (chromosome 9p) and the *TOX3*/*CASC16* locus (chromosome 16q) as being associated with RLS. The major proportion of the heritability remains still unexplained. Parts of the missing heritability might be explained by rare genetic variants. It was already shown that rare single nucleotide polymorphisms in the *MEIS1* locus were associated with RLS. Until now, a systematic screening of rare genetic variation aside the known RLS associated loci has been missing. Furthermore, the analysis of RLS pedigrees had limited success in the search of causative variants and only little is known about the contribution of common RLS associated variants to familial RLS.

Methods: In this work, Illumina HumanExome Bead Chip genotype data was used to screen for associations between rare variants and the binary RLS phenotype in a cohort of 5,407 population based German controls and 3,785 German/Austrian primary RLS cases. Association tests were conducted for single variants and for sets of variants in gene-level tests. Mixed models were applied to address the problem of potential confounding population stratification and cryptic relatedness among the RLS cases. The statistical significance was empirically assessed for the gene-level tests. The resulting candidate genes were sequenced in their exonic and promotor regions together with further RLS candidate genes from a meta-GWAS of common variants using the MIPseq technology and 11,214 project specific molecular inversion probes (MIPs). Therefore, the technology had to be established and the MIPs were designed with a custom approach, which iteratively filled design gaps. Then a cohort of 704 German RLS cases and 752 population based controls was sequenced. The resulting rare single nucleotide polymorphisms were used in a gene-level and single variant association analysis using principal components and generalized linear mixed models to correct for confounding population stratification, respectively. Furthermore, in this work, also the contribution of common genetic variants was examined for the RLS phenotype. Previously published RLS GWAS loci were genotyped in 79 European families with familial RLS cases (843 individuals) using the Affimetrix Axiom Chip to answer the question whether an aggregation of common risk alleles might explain the phenotypes in the pedigrees. Therefore, association tests were applied, which used generalized linear mixed models, as well as a correlation analysis.

Results: After the quality control of the ExomeChip dataset, 3,652 cases, 5,360 controls and 137,011 markers were remaining. The analysis did not reveal new genome-wide or exome-wide significant signals. However, a list of 19 genes was obtained to be further sequenced in cases and controls using the MIPseq technology: *CORO6*, *DMPK*, *EYA2*, *FAM171A1*, *GALNT12*, *GRIN2B*, *KRTAP19-5*, *LEO1*,

NECAP1, *NENF*, *OLFML2B*, *OSBP*, *OSGIN1*, *PCDHB5*, *PDE11A*, *RASGRP4*, *TREM1*, *UBL4B* and *ZNF175*. Further 65 genes were added to the list for MIPseq from the annotation of an unpublished RLS meta-GWAS with 23&me. The MIPseq analysis revealed the genes *DMPK*, *MYT1*, *AAGAB*, *RASGRP4*, *COL20A1* and *PTPRD* as putative RLS causing genes. The single variant association test added *MYT1*, *ATP2C1*, *CADM1* and *OLFML2B* to this list. In the third part of this thesis, the RLS pedigree dataset consisted of 829 individuals in 79 families after the quality control. The analysis showed that single RLS risk variants could significantly explain 55% to 100% of the phenotypic variance in 8 families, which were enriched for Finnish origin. The burden of common variants significantly explained 10% to 100% of the phenotypic variance in 10 families.

Discussion: The analysis of the ExomeChip data might have suffered from a lack of power, but the success of the MIPseq showed that the ExomeChip could be used as an efficient screening technology to reduce the search space in association analyses. The MIPseq technology was established as a cost-efficient technology for a broad scale of project setups, which performance mainly depended on the balancing of the single molecular inversion probes and the quantification and preparation of the template DNA. The association analysis resulted in a list of genes that might be causal for RLS as rare mainly exonic variants were tested. The findings of the analysis have to be validated as well as replicated in a larger sample set. A power analysis showed that many more genes' association tests were to be expected to reach statistical significance. The third part of this thesis suggested that a genetic or environmental background might interact with RLS risk SNPs in RLS pedigrees to trigger RLS. More RLS associated variants might add to the explanation of the families' phenotypes.

Zusammenfassung

Hintergrund: Das Restless Legs Syndrom (RLS) ist eine Erkrankung des Nervensystems. Es äußert sich durch einen Bewegungsdrang in Ruhe in den Beinen, hauptsächlich am Abend oder in der Nacht. Aufstehen und Umhergehen bessert die Symptome. Die Prävalenz ist altersabhängig und mit 5 % in Populationen mit kaukasischer Abstammung hoch, jedoch niedriger in asiatischen Populationen. Multimorbidität ist ein Risikofaktor für RLS. Schwangerschaft, weibliches Geschlecht, Nierenerkrankung und Eisenmangel sind mit RLS assoziiert. Das Syndrom schränkt die Lebensqualität der Patienten ein und wird aktuell mit Dopamin-Agonisten (Nicht-Mutterkorn-Derivate), Opioiden, α2δ-Liganden und Eisenpräparaten behandelt. Als Nebenwirkung kann eine Verschlechterung der Symptome (Augmentation) eintreten, besonders nach der Behandlung mit Dopamin-Agonisten. Viele der RLS-Fälle sind familiär (ca. 50 %). Diese weisen zudem ein früheres Erkrankungsalter auf. Diese familiären Fälle scheinen einem autosomal-dominanten Erbgang zu folgen. Umfassende Linkage-Studien wurden in der Vergangenheit durchgeführt, welche zur Identifikation von 10 Linkage-Regionen führten. Viele Versuche wurden unternommen, um die kausale Sequenzvariante zu finden, doch die Ausbeute blieb gering. Im Gegensatz dazu konnten genomweite Assoziationsstudien, mit dem Ziel häufige Einzelnukleotidpolymorphismen zu identifizieren, die Regionen um *MEIS1* (Chromosom 2p) und *BTBD9* (Chromosom 6p), *MAP2K5*/*SKOR1* (Chromosom 15q), *PTPRD* (Chromosom 9p) und *TOX3*/*CASC16* (Chromosom 16q) als mit RLS assoziiert identifizieren. Weiterhin blieb ein Großteil der Vererbbarkeit jedoch unerklärt. Teile davon könnten durch seltene genetische Varianten erklärt werden. Es wurde bereits gezeigt, dass seltene genetische Varianten in der *MEIS1* Region mit RLS assoziiert sind. Aktuell fehlt aber eine systematische Suche nach seltenen genetischen Varianten neben den bisher bekannten Regionen. Außerdem hatten die Analysen von RLS-Stammbäumen nur wenig Erfolg bei der Suche nach kausalen Varianten. Es ist auch nur wenig über den Beitrag der häufigen RLS-assoziierten Varianten zum familiären RLS bekannt.

Methoden: In dieser Arbeit wurden Genotypdaten vom Illumina-HumanExome-Bead-Chip verwendet, um Assoziationen zwischen seltenen Varianten und dem binären RLS-Phänotyp in einer Kohorte von 5.407 populationsbasierten deutschen Kontrollen und 3.785 deutsch-österreichischen primären RLS-Fällen zu überprüfen. Die Assoziationstests wurden für einzelne Varianten und mittels genbasierter Tests für Gruppen von Varianten durchgeführt. Um das Problem von möglicherweise störender Populationsstratifikation und kryptischer Verwandtschaft zu beheben, wurden lineare gemischte Modelle verwendet. In den genbasierten Tests musste die statistische Signifikanz empirisch ermittelt werden. Die daraus resultierenden Kandidatengene wurden zusammen mit weiteren RLS-Kandidatengenen, aus einer nicht publizierten Meta-GWAS an häufigen Varianten, in deren Exons und Promotorregionen mit der MIPseq Technologie und dazu gehörigen 11.214 projekteigenen Molecular Inversion Probes (MIPs) sequenziert. Dazu musste die Technologie etabliert und die MIPs mit einer maßgeschneiderten iterativen Methode entworfen werden, welche Lücken im Design auffüllen konnte. Dann wurde eine Kohorte von 704 deutschen RLS Fällen und 752 populationsbasierten Kontrollen sequenziert. Mit den ermittelten Einzelnukleotidpolymorphismen wurde eine genbasierte und Einzelvariantenassoziationsanalyse durchgeführt, unter der Verwendung von Hauptkomponenten und generalisierter linearer gemischter Modellen, welche störende Populationsstratifikationen korrigieren. Des Weiteren wurde in dieser Arbeit auch der Beitrag von häufigen genetischen Varianten zum RLS-Phänotyp untersucht. Zuvor veröffentlichte RLS-GWAS-Loci wurden mit dem Affimetrix-Axiom-Chip in 79 europäischen Familien mit familiärem

RLS (843 Individuen) genotypisiert, um die Frage zu beantworten, ob die Phänotypen in jenen Stammbäumen durch eine Anreicherung der häufigen Varianten erklärt werden könnten. Dazu wurden generalisierte lineare gemischte Assoziationsmodelle und Korrelationsanalysen verwendet.

Ergebnis: Nach der Qualitätskontrolle des ExomeChip-Datensatzes verblieben 3.652 Fälle, 5.360 Kontrollen und 137.011 Marker. Die Analyse konnte keine neuen genomweit oder exomweit signifikanten Signale aufweisen, jedoch die 19 am besten assoziierten Genen sollten in Fällen und Kontrollen mit der MIPseq-Technologie sequenziert werden: *CORO6*, *DMPK*, *EYA2*, *FAM171A1*, *GALNT12*, *GRIN2B*, *KRTAP19-5*, *LEO1*, *NECAP1*, *NENF*, *OLFML2B*, *OSBP*, *OSGIN1*, *PCDHB5*, *PDE11A*, *RASGRP4*, *TREM1*, *UBL4B* und *ZNF175*. Weitere 65 Gene kamen aus der Annotation einer unveröffentlichten Meta-GWAS mit 23&me hinzu. Die MIPseq-Analyse zeigte mit genbasierten Tests, dass *DMPK*, *MYT1*, *AAGAB*, *RASGRP4*, *COL20A1* und *PTPRD* kausale RLS Gene sein könnten. Der Assoziationstest mit einzelnen Varianten fügte *MYT1*, *ATP2C1*, *CADM1* und *OLFML2B* zur Liste dieser Gene hinzu. Im zweiten Teil dieser Promotionsarbeit bestand der RLS-Familien-Datensatz nach der Qualitätskontrolle aus 829 Individuen aus 79 Familien. Die Analyse zeigte, dass einzelne RLS-Risikovarianten in 8 Familien, hauptsächlich finnischer Herkunft, 55 % bis 100 % der phänotypischen Varianz erklären konnten. Die Summe häufiger Varianten erklärte in 10 Familien signifikant einen Anteil von 10 % bis 100 % der phänotypischen Varianz.

Diskussion: Der Analyse der ExomeChip-Daten könnte es an statistischer Teststärke gemangelt haben, doch die Erfolge des MIPseq zeigten, dass der ExomeChip als eine effiziente Sichtmethode verwendet werden konnte, um den Suchraum in der Assoziationsanalyse einzugrenzen. Die MIPseq-Technologie wurde als eine kosteneffiziente Methode etabliert, deren Leistungsvermögen hauptsächlich von der Balance der einzelnen MIPs und der Quantifizierung sowie Präparation der Template-DNA abhing. Aus der Assoziationsanalyse resultierte eine Liste an Genen, welche für RLS kausal sein könnten, da hauptsächlich exonische Varianten getestet wurden. Die Ergebnisse der Analyse müssen validiert und in einer größeren Stichprobe repliziert werden. Eine Auswertung der statistischen Teststärke ließ erwarten, dass mehr Gene statistisch signifikant assoziiert sein könnten. Aus dem zweiten Teil dieser Arbeit folgt, dass möglicherweise in den RLS-Familien ein gemeinsamer genetischer oder umweltbedingter Hintergrund existiert, welcher durch eine Interaktion mit RLS-Risiko-SNPs RLS auslöst. Weitere RLS assoziierte Varianten könnten zudem zur Erklärung der Phänotypen beitragen.

1 Introduction

1.1 Restless Legs Syndrome

The restless legs syndrome (RLS) was already described by Thomas Willis in 1685 [105]. More than 150 years later, in 1944/1945, Karl-Axel Ekbom gave a detailed description of the disease, which he called “Irritable Legs” or “Restless Legs” [106-116]. Today, the terms “restless legs syndrome” (RLS) and “Willis-Ekbom Disease” (WED) are used. According to the WHO “International Classification of Diseases and Related Health Problems“ (ICD-10), RLS belongs to the group of “other specified extrapyramidal and movement disorders” (G25.8) of the “diseases of the nervous system” [60].

1.2 Diagnosis of Restless Legs Syndrome

Up to date, diagnosis is based on a diagnostic interview. Accordingly, the symptoms must fulfill essential criteria: an urge to move the legs, a worsening during rest, a relief during activity of the legs, an increase of symptoms at night/in the evening, and an absence of RLS mimicking physical/behavioral conditions [117]. The IRLSSG (International Restless Legs Study Group) defined international diagnostic criteria already in 1995 [118], which were revised in 2003 [119]. Some clinical features support the diagnosis of RLS, e.g. (family history, response to dopaminergic therapy, periodic limb movements during wakefulness or sleep [119].

RLS severity is scored by 10 IRLS-questions, which screen the scale of the first four diagnostic criteria as well as the occurrence of RLS and its impact on sleep and daily life [65]. Other scales exist [102], e.g. the RLS-6 or the Johns Hopkins restless legs severity scale (JHRLSS), but they were not validated for some issues concerning RLS [120].

RLS symptoms can worsen during treatment (with dopaminergic substances), which is called augmentation [121]. The level of augmentation is quantified by the “Augmentation Severity Rating Scale” (ASRS). It has to be applied from the beginning of dopaminergic therapies to create a baseline measurement, and it was not designed as a diagnostic tool [7]. But the diagnostic standards were defined as the “MPI diagnostic criteria for augmentation”, which evaluate the day time of RLS onset, number of body parts involved in RLS symptoms, latency to symptoms at rest, severity and effect of dopamine agonists [122].

The clinical course of RLS is differentiated between chronic persistent RLS and intermittent RLS. In chronic persistent RLS, the frequency of symptomatic days equals to/is greater than twice per week within the past year without treatment. Intermittent RLS without treatment has a lower frequency, but occurs at least 5 times per life [117].

As RLS can be diagnosed with a questionnaire, the phenotype is often treated as a binary trait. As an alternative, the age of onset or RLS severity scores might serve as quantitative traits.

1.3 Epidemiology of Restless Legs Syndrome

More than 50 studies were conducted to assess the prevalence of RLS in 5 of 6 continents and it was shown that the prevalence is higher in North America and Europe compared to Asia and that these differences might be also partially explained by culture, genetics and environment [123].

The prevalence in the general Caucasian population is approximately 2% to 5% [124]. The prevalence of RLS is negatively correlated with the strictness of the applied diagnostic criteria and positively with age in Caucasian general populations but not in Asian general populations [124]. And RLS affects twice as often women as men [124].

Of note, in some situation, the prevalence of RLS might depend on the term itself. A study showed that the prevalence of RLS depended on the term WED or RLS when random groups of newly graduated physicians had to perform a self-diagnosis according to the diagnostic criteria [125]. This result could influence the interpretation of study results where RLS was not diagnosed by an experienced physician.

As an example of an epidemiological study, the REST study estimated the RLS prevalence from 15,391 adults (aged ≥ 18 years) from the general population in Europe (2,082 UK; 2,010 France; 2,040 Germany; 2,020 Spain; 2,036 Italy) and the US (6,014) by a questionnaire according to the four diagnostic criteria [126]. The mean prevalence was 2.7% (range 1.3% to 4.2%) and 7.2% (range 4.1% to 10.8%) for frequent distressful RLS (≥ 2/week, "RLS sufferers") or "ever RLS", respectively [126]. RLS was more prevalent in women (3.7% v. 17% ("RLS sufferers") and 9.0% vs 5.4% (ever RLS)) for all age groups [126]. The peak of RLS prevalence was at age 79 years (prevalence ≈ 5% for "RLS sufferers"); however, 36.1% of "RLS sufferers" were aged below 49 years [126]. Other studies reported similar estimates for populations of Caucasian descent (e.g. 5.5% [127]).

Other studies reported a lower prevalence for RLS in Asia: 0.1% in the primary care population in Singapore and up to 0.6% in the elderly general population (aged > 55 years) [128], 15.4% in female and 8.5% in male Korean adults aged 40 years to 69 years [129], 2.1% in an Indian urban population based on an door-to-door survey [130]. In two elderly populations in Japan (aged > 65 years), very low prevalence values were observed (0.46% to 0.60% (males) and 1.18% to 1.46% (females)) [131, 132], and 1.8% in a rural population [133].

Two prospective cohorts were evaluated for the incidence of RLS in Germany (DHS = Dortmund Health Study, SHIP = Study of Health in Pomerania) [25], which resulted in an age-standardized cumulative incidence of 7.0% to 9.0%, and an increase was observed depending on age and female sex [25]. The persistence was 42% to 47% [25].

It was shown that multimorbidity was a strong risk factor for RLS in the DHS and SHIP cohort (e.g. diabetes, hypertension, myocardial infarction, obesity, stroke, cancer, renal disease, anemia, depression, thyroid disease, and migraine) [134]. In another study, further associations were reported with obesity, hypertension, loud snoring, alcoholic consumption, and smoking cigarettes [127].

1.4 Secondary Restless Legs Syndrome

In the past, many studies were published with an association of RLS with diverse disease comorbidities. When RLS accompanies another condition, then the term "secondary RLS" is used [135], in contrast to the term "primary/idiopathic RLS" (iRLS/iWED) [64]. A recent study reviewed these publications on a systematical basis and found convincing evidence of an increased occurrence of RLS only in iron deficiency and kidney disease [136]. An association might be possible with cardiovascular disease, arterial hypertension, diabetes, migraine and Parkinson disease [136]. No convincing associations were reported with MS (multiple sclerosis), stroke, and anemia without iron deficiency, COPD (chronic obstructive pulmonary disease), headache, narcolepsy or ataxia [136]. The authors hinted that the differentiation into "primary" and "secondary RLS" might be too stringent and that gene environment interactions might have led to the phenotype of RLS [136]. Compared to primary RLS, secondary RLS showed fewer PLMS (periodic leg movements in sleep) but no difference in age of onset in an Italian study [64].

A US study examined 251 patients with iron deficiency anemia (IDA) who were not treated for RLS [61]. Clinically significant RLS was found in 23.9% (total RLS 31%) of the study participants and was enriched compared to the general population (clinically significant RLS 2.7% and total RLS 7%) [61, 126]. However, the blood parameters did not differ between IDA patients with and without RLS, i.e. ferritin [61]. (Ferritin is the major iron storage protein [137].)

Different numbers were reported for the prevalence of RLS in end-stage renal disease (ESRD, kidney disease) patients. E.g. an Italian study reported a prevalence of 21.5% [138]. Other studies reported a similar prevalence for populations of European descent that were evaluated with the minimal diagnostic criteria from 1995 (and were of a larger sample size) (e.g. 20% [34] to 23% [139]), but prevalence values were higher when no diagnostic criteria were applied [140].

RLS was also reported to be increased in pregnant women, and it was associated with low ferritin levels during preconception as well as with low folate levels in general [141]. Of note, it was reported that giving birth might explain the differences in the prevalence of (familial) RLS between female and males [142].

1.5 Conditions Mimicking Restless Legs Syndrome

Conditions mimicking RLS can be: positional discomfort, cramps, positional ischemia, arthritic pain or leg injuries, hypnic jerks, leg shaking and jitters, neuropathies (e.g. in diabetes), sciatic pain, nervousness [143]. If these are taken into account for the diagnosis of RLS, then the specificity of the diagnostic criteria increases, e.g. from 84% [143] to 94.4% [144]. It is also possible that some substances might induce RLS (e.g. escitalopram, fluoxetine) [145].

1.6 Impact of Restless Legs Syndrome on Patients' Life

In the REST study, 85% of RLS sufferers reported disturbed daytime functioning and especially mood (51%), lack of energy (48%) and disturbance of normal daytime activities (40%) were most often mentioned to be affected [126], and, compared to the general (US) population, RLS sufferers had a lower quality of life [126], comparable to T2D (type 2 diabetes), osteoarthritis with hypertension or (to some extend) with depression [126]. A German study could also show an increased occurrence of anxiety and depression in RLS patients [146]. However, a large study could not detect an increased mortality related to RLS in the general population based on four prospective cohorts from Germany and the US [147]. The results were similar for ESRD patients with RLS [148].

1.7 Periodic Limb Movement in Sleep in Restless Legs Syndrome and Similarities to Periodic Limb Movement Disease

Periodic leg movements in sleep (PLMS) are common in RLS patients (e.g. 80%), but not all RLS patients present PLMS [149, 150]. In contrast, the periodic limb movement disorder (PLMD) exists without RLS symptoms but just with PLMS [151]. The two diseases differ in their presentation of PLMS [152]. Furthermore, both diseases seem to differ in their response to the same treatment, e.g. PLMD and RLS had different augmentation rates during treatment with levodopa (82% RLS, 31% PLMD) [121], which might indicate differences in the molecular pathophysiology. Interestingly, periodic limb movements were associated with low ferritin in an elderly cross-sectional cohort of 801 individuals from Wisconsin state employee agencies (after correcting for RLS associated genetic risk factors and inflammation status by C-reactive protein levels) [153]. In a study on RLS, some symptoms of RLS were also negatively correlated with ferritin levels (below 50 µg/L), e.g. PLMS, RLS severity and sleep efficiency [154].

1.8 Treatment for Restless Legs Syndrome

Several treatment options for RLS were evaluated in the past decades. Of note, patients with chronic persistent RLS require more often treatment than patients with intermittent RLS [24].

1.8.1 Dopamine and Dopamine Agonists

RLS was linked to dopamine by early pharmacological observations [155], and the effects of its D2-like receptor agonists were discussed to be linked to a A11 dopaminergic neuronal circuit in the hypothalamus [156].

Dopamine agonists are grouped into ergoline and non-ergoline derivatives [157]. A portfolio of these substances is or was used for RLS treatment: Ergot-derived agonists [157], e.g. pergolide [158], cabergoline [159], bromocriptine [155, 160], or non-ergot-derived agonists [157], e.g. pramipexole [161], ropinirole [162, 163], rotigotine [164]. The substances have different binding preferences for D2-like dopamine receptors (subtypes D_2, D_3, D_4) [165]. In contrast, dopamine antagonist could worsen RLS symptoms, e.g. pimozide did in one study [155].

Levodopa (L-dopa) is an inactive prodrug of dopamine, and it can enter the blood brain barrier, in contrast to dopamine itself, and it will be metabolized into active dopamine by a decarboxylase in the striatum [71]. It was also administered for RLS treatment [155], often in combination with dopa decarboxylase inhibitors (DDCI) as benserazide [155] or carbidopa [121] to prevent premature decarboxylation to dopamine in the periphery [71]. But levodopa has a short half-life and thus treated patients may wake up early in the morning due to RLS symptoms, which is called “rebound effect” [166]. Especially severe RLS cases tended to show morning rebound effects during treatment with levodopa in one study (13%) [121]. Therefore, levodopa can be administered in regular release (RR) or in combination with sustained release (SR) preparations [167, 168]. SR capsules provide levodopa for a longer period of time but with a reduced bioavailability (approx 60% of RR preparation) [169]. Thus, a combination therapy might help to maintain sleep during the night [168].

However, levodopa and dopamine agonists have adverse events, especially augmentation, which “is defined as the usual daily onset of [RLS] symptoms starting earlier than they did before treatment” [121]. Augmentation was associated with low ferritin levels [170], but augmentation rates also differ between substances (and thus seem to be associated with the choice of treatment): levodopa 82% augmentation (dose and severity dependent) [121], rotigotine 13% (dose dependent) [164], pramipexole 9.2% [161], and ropinirole low/neglectable [162, 163] (3% to 3.5% [171]). Ropinirole’s major adverse effect seemed to be nausea (approx 40% to 55%) and vomiting (12% to 20%) [162, 163]. Augmentation was also described for pergolide (15% [158]) and cabergoline (4% [172]). But more serious, they might also lead to cardiac valvulopathy [173-177] as well as pleuropulmonary disease (pergolide) [178]. But these adverse effects might not be unique to ergot-derived substances. One study showed that treatment with pramipexole, similar to cabergoline, might be associated with a higher risk of heart failure, however Parkinson’s disease was studied here [177]. In contrast to those “internal” adverse effects, rotigotine shows a unique effect due to its administration form of transdermal patches: Application site reactions (56% in rotigotine treated RLS patients) [164]. In a study, without confounding for the actual treated disease, treatment with dopamine agonists was also in association with impulse control disorders (e.g. compulsive shopping, hypersexuality, gambling addiction, binge eating), especially pramipexole and ropinirole [179]. These adverse effects might also affect RLS patients [180].

Due to adverse effects, the substances pergolide and cabergoline should not be used as a general RLS treatment [181]. Levodopa is not the first choice treatment due to rebound and augmentation effects, but it might be applied to intermittent RLS cases [166]. However, one expected adverse effect might be missing in RLS patients treated with levodopa: dyskineasia. It could not be observed in a 1-year treatment study of RLS, but it is a known adverse event during the treatment of Parkinson disease with levodopa [167].

The typical daily dose ranges are substance specific: 0.5 mg to 4.0 mg rotigotine [164], 0.25 mg to 4.00 mg ropinirole [162, 163], 0.125 mg to 0.750 mg pramipexole [161], and 150 mg to 600 mg RR-levodopa [167]. DDCI doses range from 25 mg (carbidopa, benserazide, 40% of L-dopa dose) [182] to 50 mg (carbidopa) [121].

The time point of treatment is comparable between the substances, except for rotigotine. Its transdermal patches may be applied daily in the morning (by avoiding the same application sites for a period of 2 weeks) [164]. Levodopa may be applied daily at bedtime/in the evening [167], ropinirole 1 h to 3 h before bedtime [162], and pramipexole 2 h to 3 h before bedtime [161].

The treatment durations in clinical studies differed: E.g. 1 year to 5 years rotigotine [164], levodopa 1 year without observing symptoms of dyskinesia [167], 0.5 year pramipexole [161], and 1 year and 3.5 months ropinirole [171]. One study reviewed clinical studies and as a conclusion, for long-term treatment of RLS, rotigotine, pramipexole and ropinirole should be effective for up to 0.5 year, and the latter two might even be effective for up to 1 year, whereas treatment with levodopa or rotigotine might even be prolonged to 2 years or 5 years, respectively [181].

In the past, bromocriptine mesylate was also successfully used against RLS symptoms [155]. However, the ergoline-derived dopamine agonist preferentially binds to subtype D_2 receptors [165] and was less effective than a D_3 binding agonist in the treatment of RLS patients [183].

1.8.2 Other Effective Treatments for Restless Legs Syndrome

1.8.2.1 α2δ Ligands

Calcium channels consist of five subunits: a transmembrane α1 subunit, an intracellular β subunit, a transmembrane γ subunit and an α2δ dimer [184]. The α2δ dimer originates from the same propetide by posttranslational processing and is covalently connected by a disulfide bond [185, 186]. The α2 subunit is mainly extracellular and in voltage gated calcium channels, and the dimer functions in current stimulation and subunit interaction [187], and in animal brain tissue, it was found to bind gabapentin [188] and pregabalin [189]. Neuronal circuits were discussed as potential target of the α2δ ligands [156].

Several studies showed the effective treatment of RLS using pregabalin [86, 190] and gabapentin [191-193].

For gabapentin, a dose of 300 mg was shown to be effective to decrease PLM (periodic leg movement) in RLS patients [194]. Higher doses were needed from the prodrug gabapentin encarbil (at least 600 mg to up to 1,800 mg) to lead to an effective treatment of RLS achieving more stable plasma levels after oral administration than gabapentin, and its main adverse effects were somnolence (19.7% to 30.6%) and dizziness (11% to 28%) with a probable dependence on the dose [195-198]. The treatment might be continued for up to 1 year and 3 months [198]. The FDA approved only a dose of 600 mg due to a potential risk of pancreas carcinogenicity [199].

As an alternative, pregabalin may be used in doses of up to 300 mg daily for up to 1 year with a lower rate of augmentation than an effective dose of pramipexole [200]. Doses of 124 mg daily were highly efficient as well [201]. Pregabalin seemed to mainly improve PLM and sleep architecture [86]. Again, the most frequent adverse effects were dizziness and somnolence [201]. Other adverse effects were reported, e.g. suicidal ideation [201] and addiction [202].

1.8.2.2 Opioids

The opioid oxycodone in combination with naloxone might be used for severe RLS patients whose alternative treatments failed or led to severe adverse effects [203]. The dose might be 10 mg oxycodone and 5 mg naloxone (up to 40 mg oxycodone and 20 mg naloxone twice daily) [203]. The substances could be administered for up to 1 year without addiction, withdrawal, augmentation or loss of efficacy [203]. Adverse effects were observed in 73% participants treated with the opioids (43% in the placebo group), and the most common side effect were constipation, somnolence and nausea, but also some cases of vomiting and duodenal ulcer were reported (2%) [203]. Other opioids were tested for RLS treatment like methadone [204], which was also shown to be effective and without augmentation in the first year of treatment [205].

1.8.2.3 Iron

A connection was shown between brain iron levels and RLS [206]. But the treatment of RLS with iron supplements did not lead to clear results. The oral administration of iron sucrose (1,000 mg daily) might not be efficient in RLS patients with low ferritin levels (≤ 45 µg/L) [207]. However, RLS symptoms could be improved in general RLS patients with IV ferric carboxymaltose (FCM, 500 mg) [38]. Other studies could observed an improvement of RLS symptoms in many patients (68% to 76%) after weekly intravenous administration of 250 mg iron dextran or a single intravenous administration of 1,000 mg iron dextran, but placebo controls were missing [208, 209].

1.8.3 Current Guideline

A guideline was recently published as a treatment scheme for RLS [210]: Initially, α2δ ligands should be used to prevent augmentation [210]. Iron supplements might be an option for RLS cases with low iron stores [210]. If the treatment was started with dopamine agonists, then the doses should be kept low [210]. In the case of mild or severe augmentation, the patient should respectively be treated by dividing the dose or with alternative substances like α2δ ligands or rotigotine [210]. As an alternative for severe cases of augmentation, opioids might be administered bypassing other mentioned treatment options [210].

1.9 Genetics of Restless Legs Syndrome

Many studies have contributed to show that RLS is a genetically complex disease.

1.9.1 Heritability and Genetic Model of Restless Legs Syndrome

Different definitions of heritability exist: The broad-sense heritability measures the proportion of genetic variance as a sum of additive genetic effects (breeding values), dominance genetic effects (interaction of alleles at the same locus) and epistatic effects (interaction of alleles at different loci) on the phenotypic variance of a trait, whereas the narrow-sense heritability measures the proportion of additive genetic variance on the variance of the trait [211].

Many studies suggested that a large proportion of idiopathic RLS cases are familial cases, e.g. 92% in a small scale study on 54 patients (29 women) [212]. Another study examined 300 patients according to the IRLS criteria using a personal questionnaire, and RLS was assigned as familial when a 1st degree relative was affected [213]. As a result, 42.3% to 54.9% of the idiopathic RLS cases (n = 232) where familial, but only 11.7% to 17.5% of the secondary (uremic) RLS patients (n = 68) [213]. The familial cases were also of younger age compared to non-familial cases (average 35.45 years vs 47.17 years) [213]. The study also demonstrated a worsening of symptoms during pregnancy, but the overall symptoms were similar between the groups [213]. Clinical and polysomnographic characteristics were also similar between familial and sporadic RLS in an Italian study [64]. Another study in the UK asked to female monozygotic (MZ, 911 pairs) and dizygotic twins (DZ, 983 pairs) (overall age = 20 years to 76 years, average = 51 years) the simple RLS related questions of whether the probands had “ever [experienced] an urge to move (their) legs during the night to relieve tingling or numbness” or had “ever [found] (their) legs jerk involuntarily during the night” [28]. As a result, a high prevalence was detected (39% in MZ and 36% in DZ) [28]. Despite the limitations of the study (only female probands, low quality questionnaire, high RLS prevalence), the heritability was estimated to be 54% (95% CI: 44% to 63%) due to additive genetic factors [28]. Furthermore, the best genetic model was using additive genetic effects and unique environmental effects to explain the liability to RLS [28].

A complex segregation analysis showed that familial RLS with an early age of onset (< 30 years) might be due to a single major gene with an autosomal dominant inheritance or RLS (phenocopy rate of 0.005), with a disease allele frequency of 0.003 and a complete penetrance, and further multifactorial components (additional genetic influences) [214]. In contrast, one major causal gene was unlikely in familial RLS with a late age of onset [214]. The study was conducted with 196 RLS index patients [214]. They were confirmed according to the four diagnostic criteria and 537 1st degree relatives and 133 spouses could be interviewed. The proportion of definite familial RLS was high (54.4%) [214]. The dominant model could be confirmed with a US study on 77 families and 570 phenotyped individuals (allele frequency = 0.077, phenocopy rate = 0.14) [215]. However, the model was independent of the age of onset [215]. An autosomal dominant mode of inheritance was also proposed in a study on 12 identical twin pairs, of which 83.33% showed concordant RLS [216]. Another study was conducted on 5 RLS pedigrees with a low mean age of onset (11.7 to 24 years), which had at least 4 generations available and which were phenotyped according to the diagnostic criteria from 1995 [118, 217]. All the pedigrees showed an autosomal dominant pattern and a high penetrance (4x 100%, 1x 86%) and also some signs of anticipation [217].

The RLS prevalence was often higher in females, but a study could show with 1,019 probands (527 male) affected by familial RLS that pregnancy might explain most of the differences between the sexes, which might rather relate to alterations in the iron/hormone balance than to genetic factors [142].

1.9.2 Linkage Studies on Families Affected by Restless Legs Syndrome

In the past, many loci were linked to RLS in pedigrees. Only one was found to show an autosomal recessive mode of inheritance on 12q [218]. However, most of them showed an autosomal dominant mode of inheritance and were located on different chromosomal arms: 14q, 9p, 2q, 20p, 19p, 16p, 13q, 4q and 17p [219-225]. The results from the linkage studies suggested that RLS is a genetically heterogeneous disease.

RLS1 was the first identified RLS linked locus, and it was found with an autosomal recessive mode of inheritance in a French-Canadian family with 25 individuals (14 affected) with a linkage haplotype on chromosome 12 (D12S1044 to D12S78, 14.71 cMorgan) [218]. The locus could be confirmed in 6 of 19 (mostly) French Canadian RLS families and was fine mapped to D12S326 to D12S304 [226]. The study also observed increased PLMS in the RLS1 families compared to other families, and it suggested a pseudodominant mode of inheritance for RLS families with an autosomal dominant pattern that could be caused by a highly frequent recessive allele [226]. Another confirmation was achieved in 12 families (70 affected individuals) by a transmission test of linkage disequilibrium (TDT) [227].

The first locus with an autosomal dominant mode of inheritance was RLS2. It was discovered in an Italian family with a linkage analysis on 24 members (9 affected) and three generations and a low mean age of onset (26 a ± 5.87 a) [219]. The locus could be mapped on the chromosomal cytogenetic band 14q13-21 (9.1 cMorgan, D14S70 to D14S1068) [219]. RLS2 was supported in one of 14 large French-Canadian pedigrees [228], and it replicated with 159 European trios using the TDT (D9S1846 to D9S171) [229].

The third locus was found by a non-parametric linkage analysis on 15 pedigrees of Northern America in the cytogenetic bands 9p24-22 [220], but there was some controversy about the analysis [230]. However, the locus could be replicated. E.g. in a large Bavarian family (9p24-22, D9S1810, 11.1 cMorgan, 16.6 Mb) using the TDT and a linkage analysis only of affected individuals [231]. Marginal significance was also found for this locus in a replication study with 159 European trios and the TDT (D9S1846 to D9S171 in South European trios, D9S156 to D9S157 in Central European trios) [229]. A large German family could confirm the locus in the cytogenetic band 9p21 (D9S974 to D9S1118, 9.9 Mb) using an autosomal dominant mode of inheritance [232].

RLS4 was identified with an isolate village from South Tyrol, of which 6 informative families (one large family with 12 affected members) were analyzed with an autosomal dominant mode of inheritance [221]. As a result, a shared haplotype was found on the chromosomal cytogenetic band 2q33 (18.2 cMorgan, D2S311 to D2S2208), and it was partially shared (1.6 cMorgan) by a more distantly related and affected individual from another family [221]. A fine mapping could shrink the locus to 46.9 Kb using 32 (partially small) families from South Tyrol [233].

The locus RLS5 was detected in a large French-Canadian pedigree by an autosomal dominant mode of inheritance on the chromosomal cytogenetic band 20p13 (D20S849) [222]. A replication was successful in a Dutch family (4.5 Mb, CGR490 to rs2065704) [234].

The 6th locus was linked to RLS in an Italian family (12 affected, 3 generations) by an autosomal dominant mode of inheritance with an assumed full penetrance [223]. The locus mapped to 19p13.11 (rs754292 to rs273265) and could be replicated using the transmission test of linkage disequilibrium in 159 trios (D19S930 to D19S410 and D19S410 to D19S89) [223]. An Irish family (11 members) showed a linkage to a nearby locus with an autosomal dominant mode (19p13.3, 2.5 Mb) [235].

The 7th locus could be found and fine mapped with an autosomal dominant mode of inheritance in a French Canadian family with 26 members (16p12.1, 1.18 Mb, D16S3130) [224].

In a Turkish family (9 affected, 2 unaffected members), a linkage analysis resulted in the detection of a locus on chromosome 13q (13q32.3 to 33.2, 5.2 Mb, rs2182885 to rs7333498) with an autosomal dominant mode of inheritance [236].

Two more loci on 4q and 17p were shown to be linked to RLS in a large German family (D4S406 to D4S402 and D17S1857 to D17S1294, respectively) using an autosomal dominant mode of inheritance [225].

But linkage studies were not always successful in finding a linked locus, as demonstrated by one study on a large US family of English descent (7 generation, 88 living members, 30 RLS cases) that showed an autosomal dominant mode of inheritance [237].

Furthermore, the yield was low in the search for the causal genes or variants in the loci that were detected by linkage studies, either on the protein [26] or sequence level [224, 233, 238, 239]. A regional association study screened 1,536 SNPs in 21 Mb of the RLS locus on chromosome 12 and found a common intronic variant (rs7977109) in *NOS1*, which was significantly associated with RLS after adjusting for multiple testing on a regional scale [240]. Another study also did whole exome sequencing in a pedigree with familial RLS cases. Two affected cousins were sequenced and the variants were filtered for replicating in the RLS linkage regions of three affected members of the same family (19 regions), and for having been shared in the cousins, and for having been protein altering and novel [241]. The resulting variants were analysed for segregation in the whole pedigree as well as in an unrelated set of 64 RLS patients and 250 controls [241]. The most promising variants were rare and found in *PCDHA3*, *WWC2*, *FAT2*, and *ATRN*, as they segregated with the phenotype in the family (four affected and two possibly affected and one healthy individual), and they could not be observed in the healthy control sample [241]. More variants in *PCDHA3* could be found in two cases from the case-control samples, but also in one healthy control [241]. The author stated that a non-coding regulatory variant might have been missed [241].

1.9.3 Genetic Association Studies and the Search for Causal Variants

1.9.3.1 Genome-Wide Association Studies with Restless Legs Syndrome

The first genome-wide association study (GWAS) was conducted with 306 RLS cases (with PLMS) and 15,664 controls from Iceland [242]: The study found a genome-wide significant intronic single nucleotide polymorphism (SNP) at the *BTBD9* locus (*OR* = 1.8, rs3923809, chromosome 6), which could be replicated in 123 cases (with PLMS) and 1,233 controls from Iceland and in 188 cases (with PLMS) and 662 controls from the US (*OR* = 1.5), and the population attributable risk was estimated to be 57% with a multiplicative model in the combined Icelandic cohort [242]. The study also demonstrated a significant decrease of serum ferritin levels in RLS cases by the identified risk allele [242].

The second GWAS was done with 401 familial German RLS cases and 1,644 population based controls [243]. Using an Armitage test of trend, an association of rs2300478 was genome-wide significant, which mapped to an intronic region of *MEIS1*, and subsignificant signals were observed on chromosome 6 (*BTBD9* locus), chromosome 9, chromosome 15, and chromosome 16 [243]. A replication study could partially confirm four associated loci in 903 familial and sporadic RLS cases and 891 population based controls from Germany as well as in 255 RLS cases and 287 controls from Canada, and the LD blocks of the associated SNPs were in proximity to four genes: *MEIS1* (containing exon 9, chromosome 2), *BTBD9* (in intron 5, chromosome 6), *MAP2K5* (3’ end, chromosome 15) to *SKOR1* and also *PTPRD* (linkage region RLS3, chromosome 9, nominally significant) [243]. Of note, a risk haplotype could be found for *MEIS1* (allele A of rs6710341 to allele G of rs12469063), which gave a stronger association signal in both the German and the Canadian samples (*OR* = 2.75 and 2.36, respectively) [243]. Furthermore, estimations hinted to a recessive model for the *MAP2K5*/SKOR1 related signal [243]. The three loci at *MEIS1*, *BTBD9* and *MAP2K5*/*SKOR1* had a population attributable risk of 68.6% in the German and 74.2% in the Canadian population [243]. The odds ratio for the *MEIS1* region was higher in familial RLS compared to sporadic RLS (1.82 vs 1.59, respectively) [243].

The next GWAS could confirm the previously observed *PTPRD* locus by a significant association [244]. Using 2,458 RLS cases and 4,749 controls (from Germany, Czech, Canada, Austria), two independent SNPs were associated with RLS: rs4626664 (*OR* = 1.44) and rs1975197 (*OR* = 1.31) [244]. Both SNPs were located in the 5’ UTR of *PTPRD* and were splice variants, but an interaction between the two SNPs (epistasis) could not be observed [244]. Of note, this genomic locus was observed before in the linkage studies, but sequencing could not detect obviously causal mutations in the *PTPRD* exons of affected family members from a pedigree linked to RLS3 [244].

The last genome-wide association study on common variants revealed two more loci using 954 German/Austrian RLS cases and 1,814 German controls [245]. The replication was conducted with 3,935 cases and 5,754 controls (of European origin and from the US of European origin) [245]. The new loci were found in an intergenic region on chromosome 2 (rs6747972, *OR* = 1.23, approx 1.3 Mb downstream of *MEIS1*) and in a LD block of chromosome 16 that intersects the 5' end of *TOX3* and is in proximity to the non-coding RNA *CASC16* (LOC643714, chromosome 16, rs3104767, *OR* = 1.35) [245]. All previously observed loci could be replicated: *MEIS1* locus (rs2300478, *OR* = 1.68), *BTBD9* locus (r29357271), *PTPRD* locus (rs1975197, *OR* = 1.29) and *MAP2K5*/*SKOR1* locus (rs12593812, *OR* = 1.41) [245]. Additionally, the genome-wide data could explain 6.8% of the genetic variance [245].

1.9.3.2 Examination of GWAS SNPs in Diverse Populations and Phenotypes

Many regional association studies were conducted to replicate or examine the findings from the different GWAS in different populations or diverse RLS associated conditions. The *BTBD9* locus was confirmed in a Korean population, and an attempt to show an association with serum iron levels failed [246]. The *PTPRD* locus could be validated in a Taiwanese study with RLS in ESRD patients but not the *BTBD9*, *MAP2K5*/*SKOR1*, *PTPRD* or *TOX3*/*CASC16* locus [247]. In contrast, a study on Greek/German ESRD patients could confirm the *BTBD9* locus, but it observed only a trend for the *MEIS1* (German subset) and *MAP2K5* (Greek subset) locus, and the other loci were not tested [248]. Only the *MAP2K5*/*SKOR1* locus could be confirmed in Czechian MS patients stratified by RLS but not the *MEIS1*, *BTBD9* and *PTPRD* locus [249]. A US study tested the *MEIS1*, *BTBD9* and *MAP2K5* locus with a family-based and a case-control based association study with participants of European descent, and all loci were significantly associated with RLS [250]. The *PTRPD* locus could also be confirmed in the US with Caucasian individuals, but no coding variant segregated in an RLS3 family [251]. Another project was conducted with the Wisconsin Sleep Cohort, where PLM was used as a quantitative trait and tested successfully for association with the *BTBD9* (top signal), *TOX3*/*CASC16*, *MEIS1*, *MAP2K5*/*SKOR1* and *PTRPD* locus [252]. Another study could confirm the *BTBD9* locus as being associated with both familial and sporadic RLS, and the other tested loci of the *MEIS1*, *BTBD9* and *MAP2K5* locus were also associated with RLS in familial RLS cases [253].

A study asked the question whether the RLS GWAS loci could be associated with comorbidity in RLS patients (or the general population) from German population surveys as multimorbidity was shown to be a risk factor of RLS, but no such association could be found [254]. Similarly, another study asked whether the GWAS loci might be associated with the serum iron levels in the general population as iron deficiency was shown to be a RLS risk factor, but no association could be found in a general German population [255]. But the first GWAS did find such an association in Icelandic RLS cases [242].

1.9.3.3 Regional Association Studies Based on Pathophysiological and Epidemiological Considerations

Many regional association tests were performed based on hypothesis mainly driven by epidemiological observations and pathophysiological considerations. Often only a small set of selected genetic variants was tested and some studies could report associations, but none would have been genome-wide significant. Some examples were the following genes: *VDR* (vitamin D (1,25-dihydroxyvitamin D3 receptor [2]), Spanish Caucasian population, 2 common SNPs, $p < 0.001$ and $p < 0.01$) [256], *CLOCK* (Korean schizophrenia patients, haplotypes in *CLOCK* and *NPAS2*, $p = 0.021$ for the *CLOCK* haplotype) [257], *HMOX1* (heme-oxygenase 1 [2] for iron metabolism, case-control cohort of Spanish descent, also tested *HMOX2*) [258], *IL1B* and *IL17A* (HIV cohort stratified by RLS, tested SNPs in *NOS1* and *NOS2* for dopamine metabolism, in *HFE* for iron metabolism, in *IFN*, *IL*, *NFKB* and *TNFA* for inflammation related genes) [259], *SNCA* (synuclein alpha [2], German RLS case-control cohort) [260], *NOS1* (screening of more than 1,500 SNPs in RLS1 locus, RLS case-control cohort of European descent) [240] (a replication failed [261]), *TH* (tyrosine hydroxylase [2], Val81Met polymorphism, study of antipsychotic-induced RLS in Korean female schizophrenic patients) [262], and *MAOA* (dopamine metabolism, RLS case-control cohort of European descent) [263]. Many more studies were done that could not find an association at all. One of those studies focused on 111 iron related genes, e.g. *HFE*, which common SNPs were regressed against the phenotypes of a case-control cohort (in total 2,425 German Austrian cases and 3,285 German controls) but with negative results, and the authors discussed that an intermediate phenotype might exist that underlies the RLS phenotype and rendered the study powerless, and that this putative intermediate phenotype might be influenced by additional factors [255]. As another example, a recent study could not show an association of the *BTBD9* locus with ferritin levels in 14,126 blood donors [264].

1.9.3.4 Search for Causal Variants in GWAS Loci

Some studies were done to find obviously causal variants in the GWAS loci. A recent study sequenced the exomes of 4 to up to 8 RLS patients from 7 French-Canadian families with an autosomal dominant pattern of RLS inheritance [265]. It analyzed the published RLS associated loci and identified common *GLO1* variants in putative functional regions (E111A and in the promotor region) that co-segregated with the phenotype in 4 families and that were associated with RLS in a case-control cohort (191 French-Canadian cases, 191 French-Canadian controls, 255 US cases, 291 US controls) [265]. But a conditional haplotype analysis could not confirm the association after correcting for the published *BTBD9* GWAS lead SNP rs9357271 [265]. Other putative functional variants were found in the GWAS loci, but none segregated with the phenotype in the families [265]. As another example, a pedigree showed a co-segregation of the phenotype with a *MEIS1* coding variant (R272H) (3 affected members, 3 unaffected family members) [266]. In another project, *PTPRD* was sequenced in an RLS3 family, but no variant could be found that segregated with the phenotype [251].

Another study used a multistage approach: Initial sets of 188 cases and 182 controls were selected for each GWAS locus separately and screened for variation using a high resolution melting curve genotyping method (HRM) [267]. Then the resulting candidate variants were genotyped in 3,262 German cases and 2,944 German controls using the Sequenom MALDI-TOF technology [267]. Furthermore, the *MEIS1* exons were screened in 3,760 German cases and 3,542 German controls using the HRM technology [267]. As a result, a significant excess of rare variants was found in *MEIS1* exons, especially non-synonymous coding variants of the transcript ENST00000398506, in the 5’ UTR and in the 3’ UTR (minimal empirical $p = 0.0001$, obtained by 10,000 permutations) [267]. The strongest signal was mainly driven by the rare SNP rs11693221 [267]. The observed rare nonsynonymous variants were screened in an *in vivo* complementation assay with zebrafish embryos, which showed a knock out phenotype in the neuronal development (optic tectum) mainly with variants that surrounded the TALE box region of *MEIS1* [267]. Of note, the R272H variant, which was formerly reported as segregating in an RLS family [266], showed a neurological phenotype in the *in vivo* assay [267]. A further study asked a similar question with a focus on *MEIS1*: Long range PCRs were used to screen the region of *MEIS1* where the risk haplotype was located (3 RLS cases homozygous for the *MEIS1* RLS risk haplotype and 2 RLS cases homozygous for the *MEIS1* RLS non-risk haplotype) [70]. No insertions/deletions were detected being larger than 250 bp [70]. A sequencing approach could not find structural variants in the *MEIS1* exons or in some conserved intronic regions between exon 8 and exon 9 in 570 French-Canadian cases/controls, and no loss of heterozygosity was detected for carriers of the *MEIS1* RLS risk haplotype [70]. Furthermore, only one coding variant was found, but it was non-synonymous and not associated with the phenotype [70]. But a non-coding variant was found (rs113851554) in a conserved region and this marker was significantly associated with RLS [70]. The SNP was in high LD with rs11693221 (r^2 = 0.83) that was observed in the previously described study [267].

1.10 Discussions on the Pathophysiology of Restless Legs Syndrome

Based on the contributions of many experiments, some hypothesis could be framed on the pathophysiology of RLS. First of all, RLS was observed in amputees [268-270], which implicated that the pathophysiological mechanisms of RLS were not (only) located in the limbs. In theory, *MEIS1* and *BTBD9* might positively regulate ferritin levels, which would positively regulate iron and thus dopamine levels and these dopamine levels could influence the RLS phenotype/PLMS phenotype [271].

1.10.1 Link between Iron and Dopamine in Restless Legs Syndrome

Iron is involved in the synthesis pathway of dopamine by the thyrosine hydroxylase (TH) [272], which is expressed in human brain [273] as well as in mouse adrenal glands and brain [274]. In rats, it is also related to the density of dopamine type 2 receptors in the striatum and the nucleus accumbens [275] as well as to the functioning and synthesis of the dopamine transporter [276]. An autopsy study showed decreased dopamine type 2 receptor levels in RLS cases but not in controls [277]. In addition, active and inactive TH levels were increased in RLS cases, and animal models of iron deficiency showed the same increase [277] as well as motor symptoms dependent on the D3 receptor [278]. Furthermore, the interaction of dopamine with serotonin or endorphin may be involved in RLS [155].

1.10.2 *MEIS1* in the Nervous System and the Link to Iron

The *MEIS1* RLS risk haplotype was associated with a reduced *MEIS1* expression in human brain and LCL (lymphoblastoid cell lines) samples [70]. Parts of the RLS risk haplotype are in a highly conserved non-coding region, and it was shown to have an enhancer activity only for the non-risk allele of the haplotype SNP rs12469063 in the developing embryonic CNS (central nervous system) of zebra fish (spinal cord, forebrain, midbrain, hindbrain and retina) and mouse (ganglionic eminences) by using a reporter assay and EMSA (electrophoretic mobility shift assay) [32]. And the putative enhancer bound the transcription factor CREB1 in an affinity chromatography experiment [32]. As a next step, the authors compared the transcriptome from ganglionic eminences of wildtype mice and mice with reduced *Meis1* expression [32]. A differential expression was detected in the Ingenuity pathways of “neurological disease”, “nervous system development” and “cardiovascular disease” [32]. And also hyperactivity and increased oxygen consumption could be demonstrated in mice that had a reduced *Meis1* expression [32]. The authors concluded that RLS is a developmental disorder [32]. Other studies have shown that the *MEIS1* orthologue in *Drosophila* acts on the development of limb [279] and motor neurons [280]. The orthologue in *Xenopus* is important for specifying the neural crest cell fate in embryos [281]. Despite the hints of neuronal development, Meis1 was found to function in vascular patterning, hematopoietic clusters in the aorta, vitelline and umbilical arteries in embryos of mice [282]. Similar observations were made in zebrafish [283].

The *MEIS1* RLS risk haplotype was also shown to be associated with an increased expression of light and heavy ferritin in the thalamus of RLS patients [284]. The study also screened the expression of further iron related genes and could find an association with *DMT1* (divalent metal transporter 1 [26]) expression [284]. As a next step, the authors could also demonstrate a reduction of the *MEIS1* expression upon iron depletion *in vitro* as well as an increased expression of the ferritin orthologue *in vivo* in *C. elegans* after the knockdown of the *MEIS1* orthologue [284].

It was also suggested that MEIS1 might act on the regulation of the expression of *PPTA* (preprotachykinin) to substance P (SP) in the amygdala and thus on the regulation of anxiety and depression [90]. And many hints were found that MEIS1 is important for the hematopoiesis and leukemogenesis [285].

1.10.3 *BTBD9* in the Nervous System and the Link to Iron

Two animal models were established that had an altered functioning of the *BTBD9* homologues: First, a knock-down model in *Drosophila melanogaster* could lead to an increased walking, sleep fragmentation and decreased dopamine levels [67]. Furthermore, the authors showed that cullin-3 might bind to dBTBD9, and they observed that the BTBD9 protein reduced the expression of IRP2 protein (iron regulatory protein-2) under basal and low iron conditions in HEK cells [67]. And IRP2 was known to regulate ferritin expression by an iron dependent positive feedback loop [286]. Cullin-3 was linked to the regulation of circadian rhythms and sleep [271].

A second model was established in mice by a knockout of *Btbd9* [287]. The serum iron level was increased as well as motor activity and sleep disturbances [287]. Furthermore, sensory alterations were demonstrated and rescued using ropinirole [287]. Of note, it was hypothesized that BTBD9 might be involved in the synaptic vesicle transport [288].

Taken together, BTBD9 might regulate the iron homeostasis, which influences the dopamine levels and thus the RLS phenotype [271]. Dopamine agonists would suppress the phenotype by inhibitory autoreceptors [271].

1.10.4 Functions of *PTPRD*, *MAP2K5*, *SKOR1* and *TOX3*

The *PTPRD* expression was associated with RLS associated GWAS SNPs in human post mortem brain tissues [289]. Experiments in *Drosophila* and mice suggested a role of *PTPRD* orthologues in the development of the motor neuron axon targets [290]. In rat, the expression of the *PTPRD* orthologue was down regulated by high doses of an estradiol derivative [291]. A knock-down mouse model was recently established that showed an altered locomotion, sleep and drug addiction behavior [289].

Both *MAP2K5*, also known as *MEK5* [2], and *SKOR1* might be of importance for the pathophysiology of RLS. In mice, the MAP2K5 orthologue was suggested to act on muscle cell differentiation [292] and on the negative regulation of 6-hydroxydopamine activated cell death of MN9D cells [293]. The MN9D cells might be used a model for dopamine neurons but with some limitations [294]. *SKOR1* is mainly expressed in the cerebellum [295] and in the spinal cord [296], it and might suppress BMP signaling [295].

The TOX3 orthologue was shown to interact with CREB and CBP, and it positively regulates Ca^{2+} dependent CRE-mediated transcription in neuronal rat cells [297]. It also acts on neuronal survival [298]. A recent study demonstrated that *Tox3* is expressed in the ganglionic eminences of mouse embryos and could regulate the neural progenitor identity [299].

1.11 Theory and Some Pitfalls of Genetic Association Analysis

A naïve genetic association study can easily lead to false positive and false negative results. Thus, very often, association analyses have to be modified and corrected according to the aims and the setup of a study.

1.11.1 Rare and Common Variants in Complex Traits

In contrast to Mendelian traits, the effects of many genes could sum up to a complex trait [300]. Two hypothesis try to explain complex diseases [19]: the "common disease – common variant" (CDCV) [17] and the "common disease – rare variant" (CDRV) [19, 301] hypothesis. They argue that common complex diseases might be explained by either genetic variants with high allele frequencies [17] or low allele frequencies [301], respectively. In particular, the "common disease – rare variant" theory assumes that complex diseases might be mainly caused by loci that show a rather high rate of mutations into susceptibility alleles but with mildly deleterious effects and large allelic heterogeneity, and as a consequence, these alleles might be quite common in a locus as a sum [301]. Association studies were shown to be superior to linkage studies for mapping disease susceptibility loci in complex diseases [302]. Interestingly, many complex diseases were tested successfully for associations with common genetic variants [303, 304]. However, most of these studies could only explain a small proportion the diseases' heritability with common genetic variants, which raised the problem of the "missing heritability" [305]. But interestingly, genetic studies on lipid levels showed an overlap of genes that were detected by common variant association mapping in the complex trait of lipid levels and in Mendelian dyslipidemia [306-308]. So it is possible that a complex disease/trait could be explained by both common variants of low effect and rarer variant of moderate effect [309]. This could be confirmed already [310]. As one extreme, very rare variants could cause a Mendelian disease variant when the variant's effect size is high [309].

1.11.2 Bias in Association Analysis

A genetic association can be tested between disease status and a genetic marker using the χ^2 test (with 2 degrees of freedom), which compares the distributions of categorical counts between cases and controls [311]. The categories can be e.g. the number of minor alleles of a genotype (0, 1, or 2) in the case of biallelic markers.

These genetic association studies face the problem of biases between cases and controls (or biases in the samples that contribute to a quantitative trait association study), which can introduce false positive results [312]. The main biases are population stratification/structure [312], cryptic relatedness [313], and technical genotyping artifacts [312]. Population stratification is a mismatch of cases and controls due to different proportions of ethnic groups or different fractions of ancestry from distinct ancestral populations [314]. Cryptic relatedness is a likely higher relatedness within the case group, compared to the control group, as the cases share a genetic disease [313].

Many methods were developed to address these problems in genome-wide association studies. One method was genomic control (GC) for case-control setups, which proposed λ_{GC} as a measure of population heterogeneity (cryptic relatedness, different proportions of subpopulations in cases and controls) [313]. The value of λ_{GC} can be estimated as the median of the χ^2 statistics divided by 0.675^2 [313]. (An approach based on the mean of the statistics was also proposed [315]). In particular, λ_{GC} is approximately the variance of the distribution of the absolute χ statistics that is approximately normally distributed under the null hypothesis [313]. This variance is greater 1 in the case of population heterogeneity [313]. A couple of assumptions are made to estimate λ_{GC} from SNP data:

The markers should be biallelic [313], independent from each other [313], and maybe from group of markers that are to be tested for association [314]. The resulting λ_{GC} can correct the observed χ^2 statistics and thus corrects for the detected population heterogeneity [313]. However, if samples are not independent, e.g. in case of relatedness, then the correction leads to a loss of power [313]. Of note, λ_{GC} can be locus specific when loci differ in mutation rate or selection [313]. The λ_{GC} can also be rescaled to be comparable between studies of different sample size [316].

As an alternative, the association analysis might be stratified by the population structure (if detected) [317-320].

A GWAS genotype dataset is a multidimensional dataset with each marker being a dimension. The principal components analysis (PCA) tries to transform these dimensions of interrelated variables into a set of much fewer dimensions that retain most of the variation of the dataset [321]. These principal components can be used to explain a large proportion (ideally most) of the genotypic variance of the GWAS dataset. As the genotypes can reflect population stratification, the principal components can capture (parts) of the stratification and can be used as covariates in an association analysis to correct for (parts) of the stratification [322]. However, the principal components will be calculated based on all sources of genotypic variance in the dataset and thus might also reflect technical biases [312], familial relationships [322] or LD structures [323]. Of note, PCA is applicable for sample sizes that are below the number of markers, and it can also be applied to multi allelic markers [322]. But it is not suitable for correcting for population structure in presence of closely related individuals [322]. A similar approach is multidimensional scaling (MDS). In principal, it transforms a (genetic) similarity (dissimilarity) matrix of the individuals into a coordinate system where each individual has a set of coordinates, and there the distances between the individuals reflect the distances from the similarity matrix [321].

Some tests do not need these corrections. E.g. the transmission test for linkage disequilibrium (TDT) is a family based test that tests for linkage and association, and it is resistant to population structure [96]. However tests like the TDT have disadvantages with respect to their statistical power [324].

Recently, methods were developed to use mixed models with case-control data (e.g. GMMAT [48]). The principals were established in the field of animal breeding research [325]. In the mixed models, fixed and random effects are implemented in a statistical model where the random effects can be modeled from genetic markers [326]. The inclusion of random effects was shown to correct for population structure, cryptic and familial relatedness [326], and it is now computational feasible [327].

1.11.3 Hardy Weinberg Equilibrium

The ratio of genotypes remains constant for a locus without selection and in a large population with random mating [328] (Hardy Weinberg Equilibrium, HWE). Thus the transmission of any allele is equally probable. In that case, the distribution of genotypes can be inferred from the allele frequencies [328]. If the inferred (expected) genotypes differ from the observed genotypes, then the assumption does not hold that the transmission of the genotypes is equally probable. This deviation from HWE might hint to an allele selection, e.g. a disease association [329] or a genotyping artifact [330]. Thus, the HWE should be carefully examined in genetic association datasets.

1.11.4 Genetic Association Tests

In a traditional case-control study, the samples can be stratified by genotype and disease status in a 2x3 contingency table [50]. The proportion of cases differs between the genotype categories in case of a real association (alternative hypothesis, H_I), or it is constant in the case of no association (null hypothesis, H_0) [50]. The proportions are genotype specific disease penetrances [50]. Their ratios are specific for a genetic mode of inheritance and are termed genotype relative risks (GRR) [50]. E.g. the denominator can be the penetrance of the homozygous AA genotype category, and GRRs are obtained for the two other genotype categories AB and BB: γ_{AB} and γ_{BB}, respectively [50]. The two GRRs have the following relations in the different genetic modes of inheritance: in a dominant model $\gamma_{AB} = \gamma_{BB}$ and $\gamma_{AB} > 1$; in a recessive model $\gamma_{AB} < \gamma_{BB}$ and $\gamma_{AB} = 1$; in an additive model $2\gamma_{AB} - 1 = \gamma_{BB}$ (which can be inferred from a linear increase of the GRR) and $\gamma_{BB} > 1$; in an multiplicative (codominant) model $\gamma_{AB}^2 = \gamma_{BB}$ and $\gamma_{BB} > 1$; in an overdominant model $\gamma_{AB} > \gamma_{BB}$ and $\gamma_{BB} = 1$ [50].

A genotype contingency table may be directly used for a χ^2 test or Fisher test, and it has an appropriate power for different genetic models [311]. However, it is more powerful to count and test alleles of cases and controls (instead of the individual genotypes) in a 2x2 contingency table, which assumes independent alleles (thus HWE) [331]. As an alternative to the χ^2 test, scores can be assigned to the genotype categories, and then a Cochran-Armitage trend test (CATT) can be performed [331-333]. This test has a superior power to the χ^2 test, even for different genetic models (additive, multiplicative, dominant, recessive) [334]. The additive model is asymptotically equivalent to the multiplicative model and does not suffer from a substantial loss of power in case of another true underlying genetic model [334]. But if the inheritance is overdominant, then the Armitage trend test will fail [311]. Furthermore, the CATT is resistant to HWE departure [334].

The logistic regression is another approach to the genetic association analysis of binary traits as RLS. In a logistic regression, the binary phenotypes are transformed using the logit function, which calculates the logarithm of the odds of being diseased for each genotype category [311]. These values are regressed against a linear model with regression parameters for each genotype category (general form) [311]. After fitting the model, a likelihood ratio test is performed of the full, alternative model, which that is determined by the regression parameters, against the reduced, null model, which has equal regression parameters of the genotype categories, with 2 degrees of freedom, which is equivalent to the Pearson χ^2 test [311]. If a genetic model is specified, than the power can be increased to detect an association due to this genetic model, e.g. by the specification of an additive model, which can be for example tested with an score test equivalent to the CATT with 1 degree of freedom [50, 311]. This approach also just requires fitting the null model and thus saves computation time [48]. If the alternative model is fitted as well, which has to done for each genetic locus separately, then a Wald test can be performed [48], which can approximate the score test [50]. The logistic regression has the advantage that it can incorporate covariates and interactions into the model [311]. Random effects can also be incorporated, which turns the regression framework into a generalized linear mixed model [48]. Of note, the significance of association can also approximately be tested using a linear mixed model instead of a generalized linear mixed model [327].

In a genome-wide association study (GWAS), many SNPs are tests against the same phenotype. Each test has a prespecified alpha level that is the probability of a false positive association (type-1 error, decision for the alternative hypothesis in case of a true null hypothesis) [311]. The alpha level is often set at 5% [311]. However, if many tests are performed of the same family at the alpha level 5%, then the probability of observing at least one false positive is higher than 5% [311]. Thus a new alpha level has to be defined, which can be approximated by the Bonferroni correction of dividing the alpha level by the number of (independent) tests [311]. However, the method is conservative and can be replaced by empirically estimating the type-1 error rate (with the cost of computational time) [311]. Other alternatives are adaptive approaches that sort *p* values and the null hypothesis are rejected in a step down procedure with less stringent criteria based on the number of already rejected null hypothesis [335]. Another method is the exact correction for multiple testing using Sidak's method, which is the basis of the Bonferroni approximation [336]. In a GWAS, the genome-wide significance threshold should be set below 1E-07 to keep the alpha level at 0.05, as found in a study with focus on European origin [337], and another study suggested a threshold of 7.2E-08 [338]. In contrast to this correction of the family wise error rate (FWER), the approach of the false discovery rate (FDR) enriches a list of associations with true positives and accepts a proportion of false positives [339].

1.11.5 Genetic Association Tests for Rare Variants

A typical individual genome has 4.1 million to 5 million variants and almost all of them are SNPs (single nucleotide polymorphisms) [340]. Most of these variants (90%) are rare thus there are only few observations of alternative alleles in the population [340]. In contrast, only for a small proportion of SNPs (10%), variants are commonly observed (in more than 5% of haploid genomes, MAF > 5%, MAF = minor allele frequency) [340].

But the association testing is underpowered for single rare variants [341] and might also be conservative, e.g. when the Wald test is applied [342]. Thus a variety of tests was designed to combine information from multiple variants of interest into one association test. They can be grouped into 5 classes: burden tests, adaptive burden tests, variance-components test, omnibus tests and EC tests [343].

The burden test can be performed in a simple way: The minor alleles of interest are counted for each individual and regressed against the phenotype (burden of rare variants, BRV) [12]. Of the same spirit, other tests are e.g. CAST (cohort allelic sum test) [16], CMC (combined multivariate and collapsing) [21] and WST (weighted-sum test) [104]. All burden like tests have high power when all variants are causal and their effects have the same direction [344].

Variance-component gene level tests can be much more powerful than burden like tests when the variants have different directions of effect and only a subset of markers is causal [92]. A widely used test is the SKAT (sequence kernel association test) [92]. SKAT performs a score test for each variant and collapses the squared score for a region of interest [92]. Thus SKAT is computational efficient because it has to fit the null model (including the covariates) once [92]. Other tests are special cases of the SKAT [92], e.g. the SSU [95] or C-alpha [344].

Adaptive burden tests are two step tests that select or weight variants based on initial tests prior to the actual association test [343], e.g. aSum (adaptive sum test) [8], EREC (estimated regression coefficient) [33], VT (variable threshold test) [101] and KBAC (kernel-based adaptive cluster) [69]. Most of the tests calculate empirical *p* values and need considerable computational time [343]. As an advantage, their power can be comparable to variance-component and omnibus tests [345].

Variance-component tests and burden test can be combined in an omnibus test, e.g. by the Fisher method [346]. This approach needs an empirical evaluation of the significance and thus computational time [346]. But it can be superior in means of power compared to another omnibus test, the SKAT-O [346]. The SKAT-O test sums the test statistics from its burden like test and its SKAT, and it does not require permutations [93, 347].

The EC test sums in principal the exponentials of quadratic variant scores for a region of interest, and it is powerful in case of a very small proportion of causal variants but requires permutations to evaluate the significance [31].

1.12 High Throughput Methods for Detection of Genetic Variation

High throughput methods can process many samples in a short period of time. For the detection of genetic variants, these methods are e.g. high resolution melting curve analysis (HRM), genotyping arrays and (multiplex) next generation sequencing (NGS) applications.

The Human Exome BeadChip from Illumina is an example of a genotyping array, and it uses the Infinium technology [348]. As a brief description of its method, genomic DNA is amplified, fragmented using an enzymatic step, purified, hybridized to probes that were covalently linked for each locus separately to immobilized beads, and assayed using a single nucleotide extension reaction with fluorescently labeled nucleotides [348, 349]. The ExomeChip (version 12v1_A) covers 247,870 markers that are mainly non-synonymous variants and thus putative functional. By the design, these non-synonymous variants were expected to cover 97% to 98% of the non-synonymous variants observed by average exome sequencing [350]. Other markers cover splice variants, stop altering variants, tags for previously described GWAS hits, ancestry informative markers, scaffold markers for identity by descent calculations, some functionally interesting variants, a random set of synonymous variants, fingerprint SNPs for sample tracking, coding mitochondrial SNPs, SNPs from chromosome Y, and HLA tag SNPs [350]. The markers were mainly selected based on exome sequences of more than 12,000 individuals with mainly metabolic and cardiovascular diseases, and they were included when a variant was observed at least twice [350].

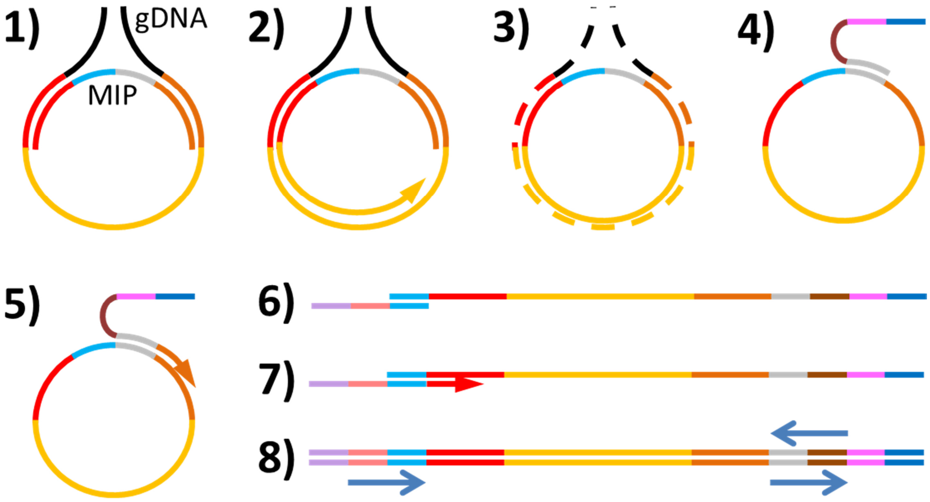


Figure 1: Working principle of molecular inversion probes: 1) A molecular inversion probe (MIP) hybridizes to single-stranded gDNA at two loci by an extension (red) and a ligation probe (light brown). 2) A polymerase reaction copies the sequence of interest (yellow). A ligase closes the DNA ring. 3) Exonucleases digest the linear gDNA. 4) The circular DNA hybridizes to one end (gray) of a PCR primer. The primer also contains an individual tag sequence for multiplex experiments. 5) The primer is elongated in a polymerase reaction at the beginning of a PCR. 6) The second primer of the PCR hybridizes to the product's end (light blue). 7) The next polymerase reaction elongates the primer. The ongoing PCR results in an amplification of the sequence of interest (yellow). 8) The final product contains the sequence of interest (yellow), the MIP's extension (red) and ligation probe (light brown), the PCR primer binding sites (gray/light blue), which serve as hybridization sites for the sequencing primers (blue arrows) in conjunction with neighboring sequences (light red/dark brown). The PCR primers also introduced sequences (dark blue/light violet) for the hybridization of the PCR product to the sequencing flow cell. Steps 1) to 7) can be carried out for one sample of gDNA. Step 8) can include a pool from different preparations if different tags were used for all step 4) reactions. [78]

Several next generation sequencing technologies were developed in the last decade. In the current Illumina systems, the DNA of interest is linked to two sequencing adapters (e.g. by a PCR) on each end, respectively. They allow the hybridization onto a flow cell with two types of immobilized oligonucleotide primers. Then each DNA fragment can be amplified into a clonal cluster of the two strands by a bridge amplification [351, 352]. Afterwards three PCRs are carried out to read the sequence, and the PCRs use reversible terminator nucleotides labeled with different fluorescent dyes and three different primers, respectively: two different primers in a sequence to assay the sequence of the one and the other strand (paired-end sequencing), and optional a third (and even forth) primer to assay an internal barcode for multiplex sequencing at the end of the strands distal to the sequencing primer binding sites [351-353]. NGS enables the sequencing of specific loci of the gDNA. As an example, Figure 1 illustrates the working principle of molecular inversion probes (MIPs), which can be used to create a multiplex sequencing library suitable for modern sequencers [78].

1.13 Aim of This Work

First, the aim of this work was to find putative causal genes for RLS by detecting rare genetic variation in exonic regions. As a first step, a large case-control cohort was to be screened using the Illumina HumanExome Bead Chip (ExomeChip) with the Illumina Infinium technology, and putative RLS associated genes were to be detected using single variant and gene level association analysis (with additive genetic models). Of note, the markers of the ExomeChip originated from cases of mainly metabolic and cardiovascular diseases [350]. This might introduce a bias. However, the ExomeChip could work as a cost efficient screening technology in the search of putative causal genes and was applied to reduce the search space for a targeted sequencing strategy. The targeted sequencing was to be based on the molecular inversion probes (MIPs) [78]. It was expected to detect further supportive variants in the set of putative RLS associated genes. And their associations to RLS could be detected using additive models, gene level and single variant analysis.

Second, it was shown in a study that a set of 3 out of 20 variants might explain familial aggregation of diabetes when the variants have a MAF of 1% (minor allele = risk allele) and an allelic OR of 3 [309]. To extend this consideration in an experiment for RLS, this thesis should show whether an aggregation of common RLS associated variant might account for familial aggregation of RLS. Thus the published RLS GWAS loci were to be typed and associated with the phenotype in multigenerational RLS affected pedigrees. The analysis was to shed some light into the (so far) negative search for putative causal variants in RLS affected pedigrees.

The over goal was to obtain new insights into the genetics of the Restless Legs Syndrome and thus set the path for future improvements in diagnosis/phenotyping and treatment of the disease.

2 Materials

2.1 Primers and Oligonucleotides

Primes and oligonucleotides were ordered at IDT (Integrated DNA Technologies, BVBA, Leuven, Belgium) at 100 µM in IDTE Buffer pH 8.0 and with standard desalting purification. All primers [78] and oligonucleotides are listed in the appendix.

2.2 Chemicals

The chemicals that were used in this work are listed in Table 1.

Table 1: Chemicals

Chemical (product name)	Source
Agencourt AMPure XP Beads	Beckman Coulter, Brea, CA, USA
Axiom water	Affimetrix/Thermo Fisher Scientific, Santa Clara, CA, USA
Buffer EB	Qiagen GmbH, Hilden, Germany
dNTP Set 100 mM Solutions (dATP, dGTP, dCTP, dTTP)	ThermoFisher Scientific, Waltham, MA, USA
EDTA disodium salt 2-hydrate	AppliChem GmbH, Darmstadt, Germany
ethanol absolute, p. A. A1613	AppliChem GmbH, Darmstadt, Germany
Hydrochloric Acid 0.5 M/37% p.A.	Carl Roth GmbH & Co. KG, Karlsruhe, Germany
LiChrosolv Water For Chromatography, LC-MS Grade	Merck Chemicals GmbH, Darmstadt, Germany
Sodium hydroxide p. A. (pellets)	Carl Roth GmbH & Co. KG, Karlsruhe, Germany
SYBR Green I (10,000X, in DMSO)	ThermoFisher Scientific, Waltham, MA, USA
Tris(hydroxymethyl)aminomethane p.A.	Merck Chemicals GmbH, Darmstadt, Germany

2.3 In-House Buffers and Solutions

Custom buffers and their components are listed in Table 2.

Table 2: Components of custom buffers and solutions

Buffer/solution	Components/recipe	Amount
0.5 M Na_2EDTA	EDTA disodium salt 2-hydrate	93 g
	aqua dest	ad 350 mL
	NaOH	50 pellets to 80 pellets
	aqua dest	ad 500 mL
	adjust pH 8.0 (HCl)	
1 M Tris/HCl pH 8.0	Tris	121.14 g
	aqua dest	ad 1 L
	adjust pH 8.0 (HCl)	
1X TE	1 M Tris/HCl pH 8.0	5.0 mL
	0.5 M Na_2EDTA	1.0 mL
	aqua dest	ad 500 mL
low TE buffer	Tris	1.214 g
	EDTA disodium salt 2-hydrate	36.8 mg
	aqua dest	ad 1 L
	adjust pH 8.0 (HCl)	

2.4 Enzymes and Enzyme Reaction Buffers

Commercial enzymes and components for enzymatic reactions are listed in Table 3.

Table 3: Commercial enzymes and enzyme reaction buffers

Enzyme/reaction buffer (product name)	Source
10X Ampligase Reaction Buffer	Epicentre, Madison, WI, USA
Ampligase DNA Ligase (100 U/µL)	Epicentre, Madison, WI, USA
Exonuclease I (*E. coli*) 20,000 U/mL	New England Biolabs Inc., Ipswich, MA, USA
Exonuclease III (*E. coli*) 100,000 U/mL	New England Biolabs Inc., Ipswich, MA, USA
Hemo KlenTaq	New England Biolabs Inc., Ipswich, MA, USA
iProof HF Master Mix	Bio-Rad Laboratories, Hercules, CA, USA
T4 DNA Ligase Reaction Buffer	New England Biolabs Inc., Ipswich, MA, USA
T4 Polynucleotide Kinase (10,000 Units/mL)	New England Biolabs Inc., Ipswich, MA, USA

2.5 Consumables

The consumables that were used in this work are listed in Table 4.

Table 4: Consumables

Consumables (product name)	Source
12.5 µL Matrix Tips	Matrix/ThermoFisher Scientific, Hudson, NH, USA
25 mL Disposable Multichannel Pipette Reservoirs	Integra Biosciences AG, Zizers, Switzerland
3M™ Empore™ Sealing Tape Pad	3M, St. Paul, MN, USA
ABgene Storage Plate, 96-well (AB-0932)	ABgene/ThermoFisher Scientific, Waltham, MA, USA
Adhesive PCR Plate Seals (AB-0558)	ThermoFisher Scientific, Waltham, MA, USA
CELLSTAR Serological Pipettes 2 mL, 5 mL, 10 mL, 25 mL	Greiner Bio-One GmbH, Frickenhausen, Germany
DNA LoBind Tubes, 1.5 mL/2.0 mL/5.0 mL, PCR clean	Eppendorf AG, Hamburg, Germany
Falcon 15 mL/50 mL High Clarity PP Centrifuge Tube, Conical Tube	Corning Incorporated (USA), Corning, NY, USA
KIMTECH SCIENCE Purple Nitrile (gloves)	Kimberly-Clark Worldwide, Inc., Dallas, TX, USA
Kimwipes Lite	Kimberly-Clark Worldwide, Inc., Dallas, TX, USA
Millipak-20 Filter Unit 0.22 µm	Merck Chemicals GmbH, Darmstadt, Germany
SR-L10F, SR-L200F, SR-L1000F, SS-L10, SS-L250, SS-L1000 pipette tips	Rainin Instruments, LLC/Mettler Toledo, Oakland, CA, USA
Stripe Tubes and Caps, 0.1 mL (qPCR)	Qiagen GmbH, Hilden, Germany
Thermo-Fast 96 PCR Plate Non-Skirted (AB-0600)	ABgene/ThermoFisher Scientific, Waltham, MA, USA

2.6 DNA Quantification and Analysis Kits

Commercial DNA quantification and analysis kits are listed in Table 5.

Table 5: Commercial DNA quantification and analysis kits

Kit (product name)	Source
Agilent DNA 1000 Kit	Agilent Technologies, Inc., Santa Clara, CA, USA
Qubit dsDNA HS Assay Kit	ThermoFisher Scientific, Waltham, MA, USA

2.7 Equipment and Machines

The equipment and machines that were used in this work are listed in Table 6.

Table 6: Equipment and machines

Item (product name)	Source
6 tube magnetic stand	AB Sciex LLC, Foster City, CA, USA
accu-jet pro pipette controller	Brand GmbH & Co. KG, Wertheim Main, Germany
Agilent 2100 Bioanalyzer	Agilent Technologies, Inc., Santa Clara, CA, USA
Centrifuge 5424	Eppendorf AG, Hamburg, Germany
DURAN laboratory flask 1 L, 5 L	DURAN Group GmbH, Wertheim Main, Germany
EF 103 easy-fit	Scotsman Ice Systems, Vernon Hills, IL, USA
Freezer (-20°C)	Liebherr-International Deutschland GmbH, Biberach an der Riß, Germany
Freezer (-20°C)	Privileg/OTTO GmbH & Co. KG, Hamburg, Germany
Linux Cluster (4 Dell PowerEdge R815 à 48 Cores, 256 GB RAM, Sun Grid Engine)	Max-Plank-Institut für Psychiatrie – Deutsche Forschungsanstalt für Psychiatrie, München, Germany
LKexv 2600 MediLine & FKS 2600 (fridge)	Liebherr-International Deutschland GmbH, Biberach an der Riß, Germany
macro pipette controller	Brand GmbH & Co. KG, Wertheim, Germany
Matrix Electronic Multichannel Pipette Impact 2	Matrix/ThermoFisher Scientific, Hudson, NH, USA
Mikro 20 (centrifuge)	Andreas Hettich GmbH & Co. KG, Tuttlingen, Germany
Milli-Q Synthesis (water purification system)	Merck Chemicals GmbH, Darmstadt, Germany
MS1, MS2, MS3, VF2 (vortexer)	IKA-Werke GmbH & Co. KG, Staufen im Breisgau, Germany
peqSTAR 96 Universal Gradient, 96 HPL & 96X (thermocycler)	VWR International, LLC, Radnor, PA, USA
PerfectSpin P (plate centrifuge)	VWR International, LLC, Radnor, PA, USA
Qubit 2.0 Fluorometer	Invitrogen, Carlsbad, CA, USA
Rainin Classic Pipette PR-2, PR-10, PR-20, PR-100, PR-200, PR-1000	Mettler-Toledo Rainin, LLC, Oakland, CA, USA
Rainin Pipet-Lite XLS+ LTS L-2XLS, L-10XLS, L-20XLS, L-200XLS, L-1000XLS, L12-10XLS, L12-20XLS & L12-200XLS	Mettler-Toledo Rainin, LLC, Oakland, CA, USA
Reax top & Reax 2 (vortexer)	Heidolph Instruments GmbH & Co. KG, Schwabach, Germany
Refrigerated Centrifuge 4K15	Sigma Laborzentrifugen GmbH, Osterode am Harz, Germany

continued table…

Item (product name)	**Source**
Rotana 46 RS (centrifuge)	Andreas Hettich GmbH & Co. KG, Tuttlingen, Germany
Rotator 2-1175	neoLab Migge GmbH, Heidelberg, Germany
Rotofix 32 A (centrifuge)	Andreas Hettich GmbH & Co. KG, Tuttlingen, Germany
Rotor-Gene Q (qPCR thermocycler)	QIAGEN GmbH, Hilden, Germany
Scientific Computing Matrix (HPC-HA-Cluster, Linux)	Helmholtz Zentrum München – Deutsches Forschungszentrum für Gesundheit und Umwelt, Neuherberg, Germany
Sigma 2-16 (centrifuge)	Sigma Laborzentrifugen GmbH, Osterode am Harz, Germany
Spectrafuge™ Mini Centrifuge	Labnet International, Inc., Woodbridge, NJ, USA
Sprout Mini Centrifuge 12V	Heathrow Scientific LLC, Vernon Hills, IL, USA
Titramax 100 (orbital shaker)	Heidolph Instruments GmbH & Co. KG, Schwabach, Germany

3 Methods

3.1 Screening for RLS Associated Rare Variants and Genes Using the Human Exome BeadChip

To gain new insights into the contribution of rare genetic variants to RLS, rare SNP genotype data was used from the Human Exome BeadChip genotyping array of a German/Austrian case-control cohort. The data was subject to a quality control, a single variant and gene level association analyses.

3.1.1 Quality Control of the Genotyping Data

Raw genotype data was obtained from the Illumina Human Exome BeadChip 12v1_A ("ExomeChip") from Prof. Winkelmann for RLS cases (unpublished data, of German/Austrian descent) and from KORA [354, 355] and HNR [55, 356] for population based German controls. All participants provided informed written consent.

PLINK [59] v1.07 and R [4] 2.15 and 3.0 were used to perform the quality control.

HNR [55, 356] samples' (2,486 individuals) initial 247,870 markers were called using the CHARGE cluster file 1.0 [357] and the Illumina GenomeStudio V2011.1V ("Genotyping" GenomeStudio Module 1.9.4 and "Illumina Genome Viewer" GenomeStudio Module 1.9.0). Low quality markers were removed [357]. Call rate filters were applied sequentially (individuals' genotyping rate < 80%, markers' genotyping rate < 80%, individuals' genotyping rate < 98%, markers' genotyping rate < 98%). A sex check was done based on 126 markers on the Y chromosome (non-PAR) and the respective genotype call rate; a call rate ≥ 50% was defined as a male property.

For RLS samples, a raw genotype dataset was obtained for 3,758 individuals (primary RLS cases) and 80 HapMap [358-363] controls. The CHARGE cluster file [357] version 1.0 was used as before to perform the calling on initial 247,870 markers. Samples and markers were filtered at call rates of 80% and 98%, as before. A sex check was performed based on 126 markers on the Y chromosome at a call rate threshold of 50%, as before.

The genotypes provided by KORA [354, 355] were called as before for initial 2,921 individuals and 237,982 markers, which had been subject to a KORA [354, 355] internal primary QC. Samples and markers were filtered at call rates 80% and 98%, as before. A sex check was provided by the collaborator.

The post-QC datasets were merged. Call rate filters were applied (individuals' genotyping rate < 98%, markers' genotyping rate < 98%). An autosomal dataset was obtained.

To check for putative sample contaminations, the data was split at MAF 1%, and a call rate QC was repeated as done before, and the sample-wise heterozygosity was calculated as a ratio of the number of observed heterozygous genotypes and the total number of observed genotypes. Samples were removed that showed an excess heterozygosity (with being more extreme than the mean ± 4 sd) in at least one of the two datasets.

A relatedness check was done: The autosomal dataset was cleaned for suspicious samples from the heterozygosity check, and markers were removed that were not on the Human Exome BeadChip v1.1 [357]. Markers were removed with MAF < 1%, HWE violation in controls ($p \leq$ 1E-06) and in long range LD regions [364]. The data was pruned for LD (PLINK [59] command "--indep-pairwise 100 5 0.2"). *PI_HAT* was calculated using PLINK [59], which estimates the pairwise proportion of alleles shared by IBD [59]. Samples were removed, which were overrepresented in all pairs with *PI_HAT* > 0.075. HapMap [358-363] samples were removed as well as duplicates (*PI_HAT* > 0.8, the better genotyped duplicate was kept). Related individuals were determined (*PI_HAT* > 0.09375, between third and fourth degree relatives) and those were flagged that would lead to a maximum of unrelated individuals after a putative removal and that had a lower genotype call rate (as a secondary criteria).

The genome-wide dataset was cleaned from suspicious samples of the heterozygosity check. Markers were removed that violated the HWE in controls ($p \leq$ 1E-07). Samples were removed that showed over-relatedness, were duplicated or were HapMap [358-363] samples (80 HapMap samples). Duplicated markers were removed based on the better respective call-rate. Four markers were removed that were known for having bad variant callings. Samples were removed with missing age, and only polymorphic autosomal markers were kept. This dataset was suitable for further downstream association analyses.

To enable genetic similarity estimations, the dataset was further pruned: Markers were removed with MAF < 0.1%, markers in long range LD regions [364] and markers in LD (PLINK [59] command "-indep-pairwise 100 5 0.2"). Two MDS coordinates were calculated for visual inspection of population structures using PLINK v1.90b3.32 [42, 59, 365] and only unrelated individuals.

3.1.2 Single Variant Association Analysis

A fast genome-wide mixed model single variant association analysis was done with the association analysis dataset from the quality control section using FaST-LMM v2.06 [37]. To estimate genetic similarities, the dataset for genetic similarity estimations was used during the analysis. The analysis options were set to not normalizing genotypes and to excluding variants in a range 2 Mb around the test SNP from genetic similarity estimations (to avoid proximal contamination [366, 367]). Age and sex were included as covariates. The association signals were validated for $p \leq 0.001$ using the same dataset and GMMAT v0.07 [48], and odds ratios were obtained. The genotype calling cluster plots were inspected to exclude false positive association signals.

The FaST-LMM [37, 366, 367] analysis was repeated with conditioning on the lead SNPs from the unconditioned analysis for the published RLS associated genomic regions [245] but only for individuals with non-missing genotypes in the conditioning SNPs.

3.1.3 Gene Level Association Analysis

The disease trait was transformed using GRAMMAR [49]. Therefore, polygenic residuals were obtained from a linear mixed model (R [4] package GenABEL [368] v.1.8-0) that random effects were based on an IBS matrix [49] from the dataset for genetic similarity estimations, and the fixed effects were age and sex. Additional covariates were added for a conditional analysis on the RLS associated genome-wide significant lead SNPs from the single variant analysis, and missing genotype covariates were mean imputed.

For gene level analysis, markers were kept with MAF < 5% in cases or controls from the association analysis dataset. Only genes were considered with more than two markers (based on the Illumina's annotation file v1 [369, 370]).

The associations were evaluated between the polygenic residuals and the groups of rare variants (gene based grouping) based on empirical *p* values of SKAT [92], burden [371] and combination tests [92, 346, 372] (10,000, 110,000 or 1,110,000 permutations) using R [4]. To obtain these *p* values, the SKAT [92] and burden tests (BRV [12], a sum of rare alleles for each individual) were applied to permutations of the polygenic residuals and two respective *p* values were obtained for each permutation. (A genotype imputation was applied to the test to address differential missingness between cases and controls [12].) Thus, for each gene, two (correlated) vectors of test statistics were obtained (*t* statistic for the burden test via a linear model [371] and *Q* statistic for the SKAT [92]). For each type of gene level test, an empirical *p* value was obtained (Equation 1, Equation 2).

Equation 1

$$p_{SKAT} = \frac{\sum_{k=1}^{K} I(Q_k \geq Q_o) + 1}{K + 1}$$

p_{SKAT} = empirical p value for SKAT
$I(Q_k \geq Q_o)$ = function assessing SKAT statistics from k^{th} permuted polygenic residuals equal/larger than the SKAT test statistic from the original vector of polygenic residuals (returning 1 or 0)
K = number of permutations

Equation 2

$$p_{BURDEN} = \frac{\sum_{k=1}^{K} I\left(t_k^2 \geq t_o^2\right) + 1}{K + 1}$$

p_{BURDEN} = empirical p value for burden of rare variants
$I(t_k^2 \geq t_o^2)$ = function assessing squared burden test statistics from k^{th} permuted polygenic residuals equal/larger than the squared burden test statistic from the original vector of polygenic residuals (returning 1 or 0)
K = number of permutations

To obtain empirical *p* values for combinations of SKAT and burden tests, the minimum-*p* and Fisher method was applied [346]. The empirical test statistics were used to calculate their rank-based *p* values, which were combined to a new test statistic using the minimum-*p* or Fisher method for each permutation, respectively (Equation 3, Equation 4, Equation 5, Equation 6) [346].

Equation 3

$$p_{SKAT,k} = \frac{rank(Q_k)}{K}$$

$rank(Q_k)$ = rank of SKAT statistic Q from the k^{th} permutation

Equation 4

$$p_{BURDEN,k} = \frac{rank(|t_k|)}{K}$$

$rank(|t_k|)$ = rank of absolute burden test statistic t from the k^{th} permutation

Equation 5

$$W_{FISHER,k} = -2\log\left(p_{BURDEN,k}\right) - 2\log(p_{SKAT,k})$$

Equation 6

$$W_{min,k} = \min(p_{BURDEN,k}, p_{SKAT,k})$$

A test statistic was also obtained for the original observed *p* values from the SKAT and burden test using the Fisher and minimum-*p* method (Equation 7, Equation 8,) and its statistical significance was assessed using themselves and the results from Equation 5 and Equation 6 as realizations of the null hypothesis, respectively (Equation 9, Equation 10) [346]:

Equation 7

$$W_{FISHER} = -2\log(p_{BURDEN}) - 2\log(p_{SKAT})$$

Equation 8

$$W_{min} = \min(p_{BURDEN}, p_{SKAT})$$

Equation 9

$$p_{FISHER} = \frac{\sum_{k=1}^{K} I\left(W_{FISHER,k} \geq W_{FISHER}\right) + 1}{K + 1}$$

Equation 10

$$p_{min} = \frac{\sum_{k=1}^{K} I\left(W_{min,k} \geq W_{min}\right) + 1}{K + 1}$$

In analysis “A” and on a genome-wide scale, the analysis was performed without weights or with CADD score (v1.0) [15] based weighting. Therefore, the raw scores from CADD 1.0 [15] were extracted for all variants of the association analysis dataset and transformed to range from 0 to 1: the minimum was subtracted from the raw scores and the resulting values were divided by their maximum. Only genes were included in the analysis that had at least two annotated different variants. Primary candidate genes were selected by a *p* value threshold that was based on the effective number of null hypothesis: For each gene, the smallest *p* value was obtained from the burden test results of the first 10,000 permutations of the polygenic residuals. The result was a vector of *p* values. This vector of *p* values was corrected for multiple testing using the Sidak approach [336] and a range of independent null hypothesis from 1 to the total number of genes (Equation 11).

Equation 11

$$\overrightarrow{p_m} = 1 - (1 - \overrightarrow{p_r})^n$$

$\overrightarrow{p_m}$ = *vector of p values corrected for multiple testing*
$\overrightarrow{p_r}$ = *vector of p values not corrected for multiple testing*
n = *number of independent null hypothesis*

For each vector of the corrected *p* values, the uniformity was tested using the Kolmogorov-Smirnov test in R [4]. The test with the highest *p* value showed the weakest evidence of deviation from uniformity and hinted to the effective number of independent null hypothesis. Using the number of independent null hypothesis, a *p* value candidate threshold was defined that was two orders of magnitude lower than the respective Bonferroni threshold for the independent number of null hypothesis. The threshold was applied to all empirical *p* values (from the burden [371], SKAT [92], minimum-*p* or Fisher method [346]) from the CADD [15] weighted or unweighted analysis, respectively, and primary candidate genes were selected.

In a refined analysis “B”, the analysis was repeated with and without CADD [15] based weighting of variants with primary candidate genes only. Now the analysis was conditioned on published RLS associated GWAS loci [245]. Based on the resulting empirical *p* values from analysis A and B, genes were determined for targeted sequencing from the group of candidate genes based on any *p* value that was below the inverse of the maximum number of independent null hypothesis from the analysis “A”. All cluster plots were inspected for the involved markers, and suspicious genes were removed.

3.2 Targeted Sequencing of RLS Candidate Genes

Putative RLS candidate genes were defined based on the previous analysis and another, unpublished study. The genes’ regions of interest were sequenced and analyzed for association with RLS.

3.2.1 Definition of RLS Candidate Genes

A targeted resequencing approach was established to screen candidate genes from the gene level association analysis of the ExomeChip data. The screening was complemented with additional genes that might be related to SNPs that showed significant signals in a parallel unpublished RLS meta-GWAS [373] project. The meta-GWAS [373] was based on AxiomChip data and summary statistics from 23&me. (Details of the analysis will be published elsewhere). To identify those additional genes, published and novel significant and sub-significant candidate meta-GWAS [373] loci were annotated using eQTL data. First, braineac eQTL data [374] was screened using three different approaches. Approach “A” was a screening for GWAS catalog [304] hits. Therefore, the GWAS catalog was downloaded [303], which contained information about significant braineac cis-eQTL signals ($FDR \leq 0.01$) [374] between published GWAS SNPs and gene transcripts. For targeted sequencing, those genes were extracted that showed an eQTL association with RLS associated GWAS SNPs. This approach was only possible for known published RLS loci and would have missed significant or sub-significant eQTL signals for novel RLS associated SNPs and for SNPs that were tagged by RLS associated SNPs and that might give a stronger eQTL signal. Therefore, approach “B” was applied: The supplementary data [374] was downloaded, which contained cis-eQTL signals with $FDR \leq 0.01$ but only for the “sentinel marker” [374] of each LD region. From this data, for targeted sequencing, genes were extracted that were associated to the meta-GWAS [373] lead SNPs or their proxy SNPs (down to $r^2 \geq 0.2$). These proxy SNPs were determined in flanking regions of ± 1 Mb using the R package snpStats (v1.12.0, [375]) and genotype probabilities of 4,065 RLS cases from the meta-GWAS [373] project. However, this approach would have missed putative interesting eQTL signals that might have an $FDR > 0.01$ and might be associated to a better proxy SNP. Approach “C” solved this problem: The meta-GWAS [373] lead SNPs or their respective proxy SNPs were queried in the online braineac form in decreasing order of r^2 until a match for which the eQTL summary data was downloaded and collected. These eQTL signal summaries were missing an FDR annotation. Thus the FDR values were estimated using the given p values and a linear model for each tissue separately. The linear model was obtained from the fully published significant eQTL signals, which showed a linear correlation between the $\log_{10}$ of the low p values and the $\log_{10}$ of low FDR values. After the application of this model, eQTL signals were kept from the collected summary that had an estimated $FDR \leq 0.2$. The respective genes were chosen for targeted sequencing.

Second, GTEx [376-378] portal (13 body tissues with sample size > 60) provided significant eQTL signals, which were queried with a highest available LD-proxy of the meta-GWAS lead SNPs. The LD-proxy SNPs were determined with SNAP [379] on the basis of HapMap (v2.1, v2.2, v3) [358, 361, 362] and 1000 Genomes (pilot 1) [380] data. The search for proxy SNPs was limited to a flanking region of ± 500 kb from the pool of markers of the Illumina Human ExomeChip or Illumina Omni 5M genotyping chip because the GTEx eQTL data was obtained with these markers that were enriched for low MAF. (LD measures based on imputed data were not applicable here.) The three best proxy-SNPs were queried at GTEx portal for each meta-GWAS [373] lead SNP. The respective eQTL genes were object of targeted sequencing.

Third, blood eQTL summary statistics [381] (samples size > 5,300) were downloaded for cis and trans-eQTL signals at $FDR \leq 0.2$. These signals were filtered for proxy SNPs of the meta-GWAS lead SNPs, and the proxy-SNPs were obtained as before (in the review of the braineac data [374]) but with an $r^2 \geq 0.5$ from imputed meta-GWAS [373] genotype probabilities of RLS cases. The resulting eQTL signals were filtered for the proxy SNPs with the highest correlation to the respective meta-GWAS [373] lead SNP. The eQTL genes were objects of targeted sequencing.

Fourth, the NCBI eQTL browser was used to screen further eQTL data sources [382-385]. The same proxy and lead SNPs were queried as before, and the most significant eQTL gene was chosen for targeted sequencing as no FDR or significance threshold was available or assessable.

Further candidate genes for targeted sequencing were defined elsewhere. In brief, the meta-GWAS [373] lead SNP regions were screened for coding genes being proximal, in the same LD block or of putative functional relevance. For target sequencing, genes were also chosen that were discussed in the literature with respect to GWAS results [245]. A summary is given in Table 7.

Table 7: Summary of the candidate gene selection scheme for the meta-GWAS lead SNP regions : Screening of subsignificant meta-GWAS [373] lead SNP regions was limited to putative functionally relevant genes. (RLS genes = genes discussed in the RLS GWAS literature [245], LD block genes = genes in the LD block of the lead SNP, eQTL genes = genes from this review of eQTL signals, proximal genes = closest gene to the meta-GWAS [373] lead SNP, known loci = previously published RLS GWAS signals, new signif. loci = meta-GWAS [373] locus with p ≤ 5E-08, new subsignif. loci = meta-GWAS [373] locus with 2 SNPs' p ≤ 1E-05)

meta-GWAS signal category	Prefilter for gene functionality	Gene screening criteria for meta-GWAS loci (any match for selection for targeted NGS)			
			Protein coding genes		
		I) RLS genes	II) LD block genes	III) eQTL genes	IV) Proximal genes (if I-III negative)
known loci	✗	✓	✓	✓	✓
new signif. loci	✗	✗	✓	✓	✓
new subsignif. loci	✓	✗	✓	✓	✓

3.2.2 Definition of RLS Candidate Genes’ Target Regions

For the RLS candidate genes, all genes and gene predictions were downloaded from the UCSC genome table browser (hg19) [97, 386, 387] (accessed on 10th November 2014) using different tracks. The tracks were: RefSeqGenes [388, 389], UCSC genes and old UCSC genes [390], AceView [391], Ensemble [392], comprehensive GenCode V7/V14/V17 [393], Vega [393]. Based on these sources, all exons were obtained for the genes of interest. The exons’ 5’ and 3’ ends were extended by 20 bp to cover splice sites [394-396], and promotor regions were defined as 500 bp upstream of any transcription start site [397]. The special inclusion of intron branch sites [398] was skipped.

3.2.3 Calibration of a Pool of Molecular Inversion Probes for MIPseq

3.2.3.1 Primary Design of Molecular Inversion Probes for MIPseq

The target regions were merged when overlapping or being close to each other (distance ≤ 100 bp) using self-written R functions (see appendix) to avoid overlapping designs of molecular inversion probes (MIPs).

MIPs were designed by an iterative approach to complete the coverage of the regions of interest with designed MIPs: In a loop, MIPs were designed for non-MIP-populated regions of interest (uniform captures size = 152 bp, uniform target capture insert size = 112 bp, uniform PCR product size = 266 bp) requesting the MIP design platform at Radbound University (Nijmegen) (A. Hoischen, personal communication, 2015) that was based on the original MIP software publication [78] and including alternative designs for probe binding regions affected by common SNPs. A self-written bundle of R [4] functions was used to perform a quality control (see appendix scripts): MIPs were removed that which extension or ligation probes were predicted to bind to more than 100 genomic regions or for which both probes were predicted to bind to more than 5 genomic regions. (Further MIPs were removed that had logistic quality scores ≤ 0.7, which was only applicable to later mipgen-derived MIPs [399], as described below). The resulting MIPs were added to the list of MIPs. Potential complementary probe overlaps between MIPs were determined, which resulted in sets of problematic MIPs. For each set, all subsets of MIPs were determined that did not show the problem of complementary probe overlaps, and one subset was chosen to be kept based on hierarchical criteria: highest coverage for the region of interest (most important criterion), shortest complementary probe overlaps, and lowest number of MIPs (least important criterion). After filtering, uncovered regions of interest were determined, and an additional design of MIPs was done for those regions, and the QC loop was repeated. If no improvement was observed in the coverage with MIPs for the regions of interest, then the design loop was continued using the alternative MIP design software mipgen [399] (v1.1) and the 1000 Genomes Project hs37d5 reference genome (a version of GRCh37 for mapping of reads for improved variant calling [400, 401]). Common SNP information was supplied (dbSNP [402, 403]) to enable alternative MIP design for regions where SNPs infer with probe binding regions (see appendix). Finally, MIPs were removed that were too far intronic or too distant to the regions of interest. Then regions were determined that were covered redundantly by MIPs (see appendix). For these regions, all possible subsets of MIPs were determined and one subset of MIPs was kept, respectively, based on hierarchical criteria: highest coverage for the region of interest (most important criterion), lowest number of predicted low performance MIPs from the Nijmegen designs, lowest number of MIPs, mean performance of MIPs from mipgen [399] and Nijmegen designs (lowest criterion). The MIPs were ordered at IDT in IDTE buffer (100 µM, 25 nmol).

3.2.3.2 Preparation of a Naïve MIPs Pool for Capturing of Target Regions

MIPs were pooled in equimolar amounts in a naïve pool and phosphorylated (Table 8, Table 9), followed by a 1/30 dilution in EB (QIAGEN) for a MIPs pool working dilution. Equation 12 [78] (definition of a standard MIP) and Equation 13 were used to determine the amount of MIPs pool for one sample of 100 ng gDNA [78], which could be used to estimate the amount of MIPs pool for a project of a specific sample size.

Equation 12

$$n(MIP_s) = 800 * n(1nDNA)$$

$n(MIP_s)$ = molar amount of standard MIP
$n(1nDNA)$ = molar amount of haploid genomes

Equation 13

$$V(MIP_s) = \frac{n(MIP_s)}{c(MIP_s)} = 800 * \frac{\frac{m(1nDNA)}{M(1nDNA)}}{c(MIP_s)} \approx \frac{4.38 * 10^{-17} mol}{c(MIP_s)}$$

$V(MIP_s)$ = volume of post-phosphorylation MIPs pool solution
$n(MIP_s)$ = molar amount of standard MIP
$c(MIP_s)$ = concentration of a standard MIP in post-phosphorylation MIPs pool solution
$m(1nDNA)$ = mass of human haploid genome
$M(1nDNA)$ = molar mass of human haploid genome

Table 8: Components for the phosphorylation of MIPs in the naïve MIPs pool: MIP prephosph. pool = pool of unphosphorylated MIPs, MIP_s = standard MIP (see Equation 12).

Component	**Naïve pool volume [µL] (4,000 samples)**
MIP prephosph. pool ($c(MIP_s)$ = 9.2 nM)	600.0
T4 Polynucleotide Kinase (10,000 Units/mL)	24.0
H_2O	24.0
10X T4 DNA Ligase Reaction Buffer (c(ATP) = 10 mM)	72.0

Table 9: MIP phosphorylation program for PeqLab PCR cyclers

T	**t**
37°C	45 min
65°C	20 min

3.2.3.3 Evaluation of the Naïve MIPs Pool

Equation 14 was used to determine the setup of a MIPseq library and its sequencing without further information on the variance of the MIPs’ performances.

Equation 14

$$l \geq c \cdot p \cdot m$$

$$l = \text{capacity of the flow cell's lane [cluster]}$$
$$c = \text{mean MIP target coverage [cluster/MIP/individual]}$$
$$m = \text{number of MIP targets [MIP]}$$
$$p = \text{multiplex level [individual]}$$

As a starting point for the next generation sequencing (NGS) setup consideration, each MIPs' target should have a mean NGS coverage of 400X (400 flow cell clusters) for each individual (A. Hoischen, personal communication, 2014). Thus, according to Equation 14, the multiplex level was set to 3 for the MIPseq library that should be used for the evaluation of the naïve MIPs pool on a MiSeq sequencer (2x 150 bp paired-end reads, v2 chemistry, 15E06 clusters [404]). Therefore, three DNA samples were selected that were of high quality.

3.2.3.3.1 Preparation of Individuals' MIPseq Libraries

The post-phosphorylation MIPs pool solution was used for capturing of target regions (Table 10). Equation 12 and Equation 13 were used to calculate the amount of the MIPs pool working dilution. Denaturation and enzymatic reaction were carried out in PeqLab PCR cyclers (Table 11).
After capturing, reaction solutions were cooled down to 4°C on ice, and genomic DNA content was digested using exonuclease reactions: 2 µL of exonuclease reaction mix (Table 12) were added to the post-capturing solution, and the enzymatic reaction was performed in a PeqLab cycler, followed by a nuclease inactivation (Table 13).

Table 10: Components for the capturing of MIP targets : The volumes refer to one DNA sample. V(MIP_s) = volume of post-phosphorylation MIPs pool solution (see Equation 13). The components were assembled on ice.

Component	**V [µL] (1 reaction = 1 DNA sample)**
10X Ampligase Reaction Buffer	2.500
MIP working pool dilution	V(MIP_s)
fresh dNTP à 250 µM in EB buffer	0.032
Hemo KlenTaq (10 U/µL)	0.320
Ampligase DNA Ligase (100 U/µL)	0.010
gDNA (20 ng/µL in 0.1X TE)	5.000
H_2O	ad 20.000

Table 11: MIPseq capture protocol for PeqLab PCR cyclers

T	**t**
95°C	10 min
60°C	22 h

Table 12: MIPseq master mix components of the exonuclease solution for digesting genomic DNA in post-capturing samples: The components were assembled on ice.

Component	V [µL] (for 1 reaction)
Exonuclease I (*E. coli*) 20,000 U/mL	0.5
Exonuclease III (*E. coli*) 100,000 U/mL	0.5
10X Ampligase Reaction Buffer	0.2
H_2O	0.8

Table 13: MIPseq exonuclease reaction and inactivation protocol for PeqLab cyclers

T	t
37°C	45 min
95°C	2 min

After exonuclease treatment, the captured targets had to be amplified using PCRs that also introduced the molecular tags for each sample to enable multiplex sequencing later. In general, the number of PCR cycles is MIPs pool dependent and requires a calibration, e.g. by qPCR (Table 14, Table 15, primers see appendix or [78]). A qPCR was always done using the QIAGEN Rotor-Gene Q system for a subset of samples for each original DNA source that was subject to sequencing (3 samples for MIPs pool balancing procedures and 8 samples for the large scale production phase of the whole project cohort).

Table 14: Components of the qPCR for the calibration of the MIPseq PCR : SLXA_PE_MIPBC2_REV_X = 1 of 384 reverse PCR primers with different molecular tags for multiplex sequencing. The components were assembled on ice.

Component	V [µL] (for 1 reaction)
iProof HF Master Mix	12.500
SLXA_PE_MIPBC_FOR (forward PCR primer) (100 µM)	0.125
SLXA_PE_MIPBC2_REV_X (reverse PCR primer) (10 µM in 0.1X TE)	1.250
SYBR Green I (1:100 dilution)	0.125
H_2O	6.000
post-exonuclease treatment sample	5.000

Table 15: MIPseq qPCR protocol for QIAGEN Rotor-Gene Q

Incubation	Cycles
98°C, 30 s	1
98°C, 10 s 60°C, 30 s 72°C, 30 s	35
72°C, 2 min	1

According to the qPCRs, the number of PCR cycles was set to 14 for all DNA sources, which corresponded to half of the PCR yield relative to the qPCR plateau.

PCRs were done using an individual reverse primer for each sample to introduce individual molecular tags to the PCR products (Table 16, Table 17, primers see appendix and [78]).

Table 16: Components of the PCR for MIPseq : SLXA_PE_MIPBC2_REV_X = 1 of 384 reverse PCR primers with different molecular tags for multiplex sequencing. The components were assembled on ice.

Component	V [µL] (for 1 reaction)
iProof HF Master Mix	12.500
SLXA_PE_MIPBC_FOR (forward PCR primer) (100 µM)	0.125
SLXA_PE_MIPBC2_REV_X (reverse PCR primer) (10 µM in 0.1X TE)	1.250
H_2O	6.125
post-exonuclease treatment sample	5.000

Table 17: MIPseq PCR protocol for PeqLab PCR cyclers

Incubation	Cycles
98°C, 30 s	1
98°C, 10 s 60°C, 30 s 72°C, 30 s	14
72°C, 2 min	1

3.2.3.3.2 Preparation, Purification and Quality Control of the MIPseq Multiplex Library

Post-PCR samples were quantified using the Bioanalyzer and a High Sensitivity Assay Chip and then pooled in equimolar amounts (c(266 bp product) = 9.2 nM). The pools contained impurities (e.g. primers, by-products). They were removed using a protocol that was based on a double purification with AMPure XP beads: The PCR pool (17.2 µL) was mixed by vortexing with prewarmed (RT) AMPure XP beads suspension of 0.9x PCR product volume to select for DNA fragments of size 266 bp [405]. The mixture was incubated to bind the DNA to the magnetic beads (RT, 10 min). Then the beads were attached to the wall of the reaction tube using a magnetic rack (RT, 5 min). The liquid phase was discarded. The bound beads were washed twice with 700 µL of fresh 80% ethanol by gently inverting the reaction tube in the magnetic rack (RT, 30 s). The ethanol was removed completely. The attached beads with DNA were dried by leaving the lid open (4 min to 6 min, RT). Twelve µL low-TE buffer were added, and the DNA was eluted by vortexing, followed by incubation on a magnetic rack (1 min, RT). The supernatant was the eluate and the purified pool. A sample was examined on the Bioanalyzer with Agilent DNA High Sensitivity chip for QC and quantification.

3.2.3.3.3 Sequencing of MIPseq Multiplex Library on the MiSeq

The MIPseq multiplex library pool was submitted to the IHG NGS facility (GAC) (Helmholtz Zentrum München) for sequencing on a MiSeq sequencer using custom sequencing primers (see appendix, [78]).

3.2.3.3.4 Evaluation of the Naïve MIPs Pool's Performance for Balancing of MIPs

First, the on-target performance of MIPs was evaluated: Reads mapping to targets of interest were counted for each MIP using the Nijmegen pipeline (A. Hoischen, personal communication, 2015) and the un-demultiplexed reads. The counts per MIP were ordered and based on visual inspection; MIPs were identified as bad performers (lowest on-target read coverages), low performers and over-performers. The other MIPs were kept as standard MIPs.

Second, the off-target performance of the MIPs was evaluated: The raw reads were counted per MIP (see script in appendix) and compared to the counts of on-target reads per MIP, respectively. MIPs were ranked according to their amount of off-target reads. The worst off-target MIPs were flagged, which accounted for 95% of the overall off-target reads. To visualize the mapping of off-target reads for the flagged MIPs, all paired reads were merged using pear v0.9.6 [406] and aligned to the 1000 Genomes Project hs37d5 reference genome for improved read mapping [400, 401] using bwa [407] (v0.7.10-r789, option "mem"). The aligned reads were sorted and indexed using samtools (v1.2, using htslib 1.2.1) [408, 409]. The mapping of reads was read out for each of the worst off-target MIPs using a custom script (see script in appendix).

3.2.3.4 Preparation of a Balanced MIPs Pool for Capturing of Target Regions

The MIPs were repooled, and individual MIP concentrations were adjusted according to the flags from the coverage evaluation: Standard (normal performing) MIPs were pooled in equimolar amounts. Each bad performing or low performing MIP was added to the pool with a final 20-fold or 10-fold concentration of a standard MIP's concentration, respectively. Over-performing MIPs were added to a final individual concentration of 0.5-fold of the standard MIP concentration. Off-target MIPs (and their SNP-binding alternative) were not added to the MIPs pool. The MIPs pool was phosphorylated (Table 18, Table 9, Equation 12, Equation 13) and diluted 1/30 in EB (QIAGEN).

Table 18: Components for the phosphorylation of MIPs in the balanced MIPs pool: MIP prephosph. pool = pool of unphosphorylated MIPs, MIP_s = standard MIP (see Equation 12).

Component	**V [µL] (for 40,000 samples)**
MIP prephosph. pool ($c(MIP_s)$ = 2.35 nM)	745.7
T4 Polynucleotide Kinase (10,000 Units/mL)	29.8
H_2O	7.5
10X T4 DNA Ligase Reaction Buffer (c(ATP) = 10 mM)	87.0

3.2.3.5 Evaluation of the Balanced MIPs Pool

A MIPseq multiplex library was prepared as described before, but the purification of the pooled PCR products was followed by a concentration step due to a low MIPseq multiplex library concentration after the pooling of PCR products (c(266 bp) = 3.22 nM) (similar to purification protocol: input = 16 µL, bead volume = 1.0x, elution in 5 µL).

As before, the pool was submitted to the IHG NGS facility (GAC) for sequencing on a MiSeq using the custom sequencing primers (see appendix).

The performance of the MIPs was examined and a rebalancing scheme created: First, bad performing MIPs were identified that did not improve in the balanced pool and were still classified as bad performers. Their target regions were selected for a secondary rescue MIP design. Second, low performing MIPs were identified that were at 1-fold or 10-fold concentration of a standard MIP in the balanced pool. For rebalancing, their concentration were to be increased to 10-fold or 20-fold of the concentration of a standard MIP, respectively, as no MIP should have a concentration higher than 20-fold of the concentration of a standard MIP (A. Hoischen, personal communication, 2015). Over-performing MIPs were flagged for inhibition. Second, the top off-target MIPs were determined as before but for 90% of the off-target effects. The MIPs were grouped by mapping to coding or non-coding targets. Of the latter, the top 14 were flagged to be inhibited in a rebalanced MIPs pool using a 3-fold standard MIP amount of the unphosphorylated MIP. Of the remaining off-target MIPs, low or bad performers were selected based on the on-target performance. If their concentrations were below the 20-fold of the standard MIP concentration, then they were selected to have an increased concentration.

In addition, the off-target MIPs of the previous naïve MIPs pool were also grouped by mapping to non-coding or coding targets. The latter were chosen to be reintroduced in the rebalanced pool to rescue the capturing of their coding targets.

3.2.3.6 Secondary MIP Design for Rescuing the Capture of MIPseq Targets

During the balancing of MIPs, 768 MIPs were found with non-improvable low performances. Their target regions were extended by 20 bp up- and downstream and merged. These regions were subject to an iterative redesign (see section of primary MIP design) using mipgen [399] and self-written R [4] functions (see appendix with scripts) using more stringent QC conditions: Neither MIP ligation nor extension probes were allowed to bind to more than 5 genomic regions. Newly designed MIPs were removed when they showed a complementary overlap of more than 6 bp with probes of the already used MIPs (using the self-written functions in the appendix).

3.2.3.7 Preparation of a Rebalanced MIPs Pool for Capturing of Target Regions

The unphosphorylated balanced MIPs pool was the basis for the rebalanced MIPs pool. MIPs were added based on the evaluation of the balanced pool after its MiSeq sequencing to increase the concentration by the 2-, 10- or 20-fold of the concentration of a standard MIP, respectively, and to introduce previous off-target MIPs and newly designed MIPs. The phosphorylation was done as before (Table 19, Table 9, Equation 12, Equation 13).

Table 19: Components for the phosphorylation of MIPs in the rebalanced MIPs pool: MIP prephosph. pool = pool of unphosphorylated MIPs, MIP_S = standard MIP (see Equation 12).

Component	**V [µL] (30,000 samples)**
MIP prephosph. pool ($c(MIP_S)$ = 2.3 nM)	581.2
T4 Polynucleotide Kinase (10,000 Units/mL)	23.2
H_2O	7.5
10X T4 DNA Ligase Reaction Buffer (c(ATP) = 10 mM)	68.0

After phosphorylation of MIPs, further unphosphorylated MIPs were added that were flagged for inhibition before. They were added to a final concentration of 1- or 3-fold of the concentration of a standard MIP to inhibit over-performing MIPs as well as the worst off-target MIPs of non-coding regions (0.46 µL of 2.86 µM MIPs pool for 1-fold inhibition concentration, 0.59 µL of 6.67 µM MIPs pool for 3-fold inhibition concentration).

The rebalanced MIPs pool was diluted 1/4 using EB buffer (QIAGEN) to a final MIP standard concentration of 0.48 nM.

3.2.3.8 Evaluation of the Rebalanced MIPs Pool

MIPseq libraries were created for 46 samples (24 KORA [354, 355] controls, 22 RLS cases) using the balanced and the rebalanced MIPs pool as done before. The individuals' MIPseq libraries were pooled (10 µL/sample) into MIPseq multiplex libraries and purified twice with 0.9-fold AMPure bead volumes as described before (1st purification: 200 µL input was purified and eluted in 50 µL low-TE buffer, 2nd purification: 31.2 µL input from the 1st purification was diluted with 18.8 µL low-TE buffer, purified and eluted in 20 µL low-TE buffer), respectively.

The two purified MIPseq multiplex libraries were submitted to the Helmholtz Zentrum München IHG NGS facility for sequencing, each on one lane of a HiSeq 2500 machine, using custom primers (see appendix and [78]). The output was preprocessed with the facility's pipeline tailed to the MIPseq specifications. In brief: The HiSeq output was demultiplexed using standard Illumina applications (CASAVA) to group reads for each individual. The reads were aligned on the 1000 Genomes Project reference hs37d5 (a version of GRCh37, including decoy sequences, which improves later variant calling) [400] using bwa (option "-mem", [407]). The reads contained the MIP probe sequences, which could lead to a variant calling bias. Thus the MIP probe sequences were masked in the reads by soft clipping. The unmasked part of the reads were used for variant calling using the GATK [410] haplotype caller (QC parameter ≥ 30, coverage ≥ 10X), which was restricted to the target sequences of the project. Variant calls were summarized by a multi-sample calling (GATK [410]). Furthermore, for QC purposes, sequencing summary statistics were generated: The total reads were counted for each individual and further tabled for being on or off target. Then the on-target counts were separated by MIP.

Based on the output of the IHG NGS pipeline, the proportion of off-targets was obtained for each person and MIPseq library, and they were compared between MIPseq libraries.

The MIPs pool had to be determined that gave the highest amount of usable output based on a comparable use of resources. Therefore, the HiSeq 2500 output was rescaled for the MIPseq library of the rebalanced MIPs pool to be comparable to the other pool. For both pools, the targets were counted that exceeded 10X coverage. These target counts were compared and the rebalanced MIPs pool was selected for further experiments.

3.2.4 MIPseq of a Case-Control Cohort Using the Rebalanced MIPs Pool

3.2.4.1 Power Analysis

Seqpower [411] and a European population model [412, 413] were used to evaluate the power of gene level association tests with MIPseq data. A variety of scenarios was set up for an analytical power estimation that compared the cumulative MAF between cases and controls (sample size of 1,500 or 10,000). The parameters were chosen as follows: The prevalence of RLS, 5% to 10% [87], was set as baseline effect. The proportion of causal detrimental variants was set to 75% or 100% as a *MEIS1* study observed 75% of 13 non-synonymous variants causing a phenotype in zebra fish [267]. The results from the same study and Manolio et al. [309] hinted to an OR of 3 to 4 as an upper bound for the effect size of detrimental variants. The lower bound was set to 1. The proportion of missing (non-sequenced and non-callable) sites was set to 25%. The proportion of missing genotypes was set to 1%. This was estimated by the application of a SNP call rate QC [59] (violation of HWE at $p \leq 0.001$, missingness ≥ 20%, 10X coverage) using the HiSeq 2500 data of the rebalanced MIPs pool. The proportion of non-causal variants was set to 25% (randomly assigned, 100 replications). The power analysis was based on variants with MAF ≤ 5% and genes having at least 2 variants. The proportion of false genotype calls was set to 1%, which was based on general concordance observations in Illumina NGS applications (IHG NGS facility, personal communication, 2015). No protective variants were considered and all other parameters were used with standard settings [414].

3.2.4.2 Capacity Estimation for HiSeq 4000 Sequencers

The HiSeq 2500 data from the rebalancing was used to simulate a 372-plex MIPseq library of cases and controls on a HiSeq 4000 sequencer for a whole range of sequencing lane numbers (see appendix with R [4] functions) (clusters per lane on a HiSeq 4000 = 3,125,000 [415], average proportion of off-target reads = 0.22, 25X coverage as threshold for calling variants). The average number of MIPs' targets suitable for calling was calculated and the optimum number of lanes determined to fulfill a cost-efficient well powered MIPseq experiment.

3.2.4.3 Preparation and Sequencing of MIPseq Multiplex Libraries

MIPseq libraries were created for a cohort of 704 German RLS cases and 752 KORA [354, 355] controls. The gDNA was stored in 96-well plates with 88 or 94 samples, respectively. In addition, two QC-control DNA samples (1 male, 1 female) were replicated on each plate. MIP target capture, exonuclease treatment and PCR/qPCR were done as before using the rebalanced MIPs pool, and one case and KORA control plate were processed simultaneously. All participants provided informed written consent.

Post-PCR solutions were pooled by PCR plate with 10 µL per sample, which contained impurities (e.g. primers, by-products). They were removed using a protocol that was based on a double purification with AMPure XP beads: 400 µL PCR pool were mixed by vortexing with 360 µL of warm (RT) AMPure XP beads suspension (0.9 fold of the PCR product volume) and incubated to bind the DNA to the magnetic beads (RT, 10 min). Then the beads were attached to the wall of the reaction tube using a magnetic rack (RT, 5 min). The liquid phase was discarded. The attached beads were washed twice with 700 µL of fresh 80% ethanol by gently inverting the reaction tube in the magnetic rack (RT, 30 s). The ethanol was removed completely. The attached beads with DNA were dried by leaving the lid open (4 min to 6 min, RT). Then 100 µL low-TE buffer were added and the DNA was eluted by vortexing, followed by incubation on a magnetic rack (1 min, RT). The eluate was purified again by using a similar protocol, but with 90 µL of warm AMPure XP beads suspension for DNA binding and 40 µL of low-TE buffer for elution. (During the balancing of the MIPs pool, the post-PCR pools had a lower volume and the volume of AMPure XP bead suspension was kept at a ratio of 0.9, however, the elution volume was not scaled down accordingly, but was at least 20 µL, to keep the elution efficiency high [416]). The purified pools were run on a Bioanalyzer with Agilent DNA 1000 chips for QC, and they quantified using the QUBIT 2.0 system with the QUBIT dsDNA HS assay kit (1 µL sample) according to manufacturers' protocols. Four pools (2x RLS cases, 2x KORA [354, 355] controls) were pooled in equimolar amounts (with respect to the pools' sample size) into MIPseq libraries. MIPseq libraries were submitted to the Helmholtz Zentrum München IHG NGS facility for sequencing on Illumina HiSeq 4000 machines (6 lanes per MIPseq multiplex library), and the output was preprocessed as described before.

3.2.4.4 Analysis of MIPseq Data from a Large Case-Control Cohort

3.2.4.4.1 Technical Quality Control

If the output from different HiSeq 4000 runs was similar, then the output quantity between MIPseq libraries was to be similar as well. Therefore, demultiplexed reads were counted per MIPseq library and compared (χ^2 test, R[4]). Furthermore, the same reads were counted per individual and compared between MIPseq libraries (ANOVA, R [4]).

The called variants were filtered at coverage ≥ 25X, being bi-allelic SNVs and called at least once in the cases, controls or replicated quality control samples (vcftools 0.1.12 [99] and PLINK [59]). The individuals' missingness of genotypes was calculated for further QC purposes (using PLINK [59]).

For each individual, the MIP performance curve was determined (similar to the balancing and rebalancing curve): The on-target reads were stratified by MIP and counted, and the counts were sorted and then weighted by the total number of the individual's on-target read counts. The result was an individual, relative MIPs performance curve (*RMPC*). The lower and upper quartiles were determined as a comparable representation of its shape ($RMPC_{25}$ and $RMPC_{75}$, respectively).

Parameters were assessed that might explain the performance of MIPseq multiplex libraries and possible batch effects. Therefore, several individuals' parameters were regressed against each other (linear regression or logistic regression, respectively, using R [4]) to estimate the pairwise associations: total number of reads, total number of mapped reads, total number of on-target reads, ratio of on-target reads with respect to total number of reads, proportion of missing genotypes, upper/lower quartiles from the relative MIPs' performance curves ($RMPC_{25}$ and $RMPC_{75}$), and the case-control status. Furthermore, measures of R^2 were estimated (Spearman's or Nagelkerke's R^2, respectively, using R [4] and the package fmsb v0.5.2, [417]) to assess how much of the variance is explained by the respective factors.

To validate some of the associations, additional tests were performed: First, the RMPCs were further compared between cases and controls. Therefore, the upper/lower quartiles from the relative MIPs' performance curves ($RMPC_{25}$ and $RMPC_{75}$) were stratified by case-control status. Within these groups, the quantiles were classified as "high" or "low" based on the overall median of the respective quantiles, and χ^2 tests were applied (R [4]). Second, if the pooling of plates into MIPseq libraries was correct, then each individual should have been equally represented in a MIPseq library, most importantly when stratified by originating from either case or control plates. To test this, the contributions were calculated as proportions of each plate to its MIPseq multiplex library (adjusted for the plates' samples sizes and based on the demultiplexed reads). The proportions were summed for case and control plates for the respective MIPseq multiplex library, and differences in the resulting two distributions were assessed using a paired t-test. Third, the on-target ratios were compared between cases and controls by a Fligner-Killeen test of homogeneity of variances and a t-test (assuming non-equal variances) (as implemented in R [4]).

For qualitative visualization, for each individual, mean and median MIPs' targets' coverages were calculated as ½ of the read counts, based on the MIPs that worked at least once in a case or control sample. They were averaged for cases and controls. Furthermore, for each MIP, the 2.5%, 50% and 97.5% quantiles of target coverage were calculated and plotted for cases, controls, and combined cases and controls.

Pairwise concordances were calculated between replicated QC-control DNA samples using the SNV genotype data (after refiltering for called genotypes ≥ 25X coverage) and R [4].

3.2.4.4.2 Quality Control for Association Analysis of MIPseq Data

Quality control steps were performed using PLINK v1.07 [59], PLINK 2 [42] (v1.90b3.32, [365]), R [4] and vcftools (0.1.12, [99]).

The called SNVs of at least 25X coverage were used, and cases and controls were kept. A call rate filter of 50% was applied to samples and SNVs. SNVs were further filtered for HWE violation in controls (PLINK, $p \leq 1E\text{-}06$). The dataset was subset to polymorphic SNV with MAF ≤ 0.05 for analysis purposes (PLINK [59] & R [4]).

To correct for population stratification, genome-wide post-QC SNP data was obtained for cases and controls from Prof. Winkelmann (unpublished, Affimetrix AxiomChip, including 6,228 RLS cases and 10,992 controls) and KORA [354, 355] (cohort S3F3: Omni Express & Omni 2.5 chip with 4,086 controls, cohort S4F4: Affimetrix AxiomChip with 3,788 controls), respectively. The three datasets were subject to a secondary QC to minimize batch effects from genotyping and primary QC: SNVs with a call rate below 98% and HWE violation ($p < 0.001$) were removed. The datasets were pruned to consistent SNPs and merged. After merging, rare SNVs (MAF < 5%), non-autosomal SNVs and SNVs in long-range LD regions [364, 418] were removed and the remaining SNPs LD pruned (PLINK [59] command "—indep –pairwise 50 5 0.2").

The genotyping chip data and the MIPseq data were pruned to the sample intersection, for which age and sex covariates were available (the better genotyped sample was kept in case of genotyping duplicates).

The concordance was determined [419] between the MIPseq genotype data and the ExomeChip genotype data that was used for the gene level association analysis before (see section 3.1.3, page 26) from the markers and individuals that were shared between both datasets. The non-reference genotype concordance was calculated for each marker and plotted against the MQ value (mapping quality) of the markers reads in the MIPseq data.

Based on the genotyping chip data, pairs of related individuals were determined (PLINK 2 v1.90b3.32 [42, 365], "genome" command, $PI\_HAT \geq 0.09375$, between third and fourth degree relatives), and the worse genotyped individuals removed. Then the first two principal components were calculated (PC1, PC2) using PLINK 2 v1.90b3.32 [42, 365]. The principal components were used to filter population outliers (more extreme than the mean of PC1 or PC2 ± 3 sd of PC1 or PC2, respectively). After removal of population outliers and in an iterative loop, the principal components were recalculated and additional outliers were determined and removed until no outlier was left. The last set of principal components was used as a final set of PC covariates for the later association analysis with the remaining individuals.

3.2.4.4.3 Gene Level Association Analysis

For gene level association analysis, the SNV loci of the MIPseq data were assigned to gene sets: The target regions from the MIP design were used as a template (including any exon, 20 bp off any exon for exon-intron boundaries, and 500 bp upstream of any transcriptional start site), and all SNVs from the MIPseq dataset were mapped to the gene sets.

The MIPseq dataset's individuals were filtered for the worse genotyped related individuals and the population outliers. Monomorphic SNVs were removed. The analysis was restricted to variants with MQ > 10 and to genes with at least two variants.

A SKAT-O [93] analysis was performed on the MIPseq data including age, sex and the first two principal components as covariates. The default small sample size adjustment was applied to SKAT-O [347]. As implemented in the package, monomorphic SNVs and SNVs with high missingness rate (cut-off at 15%) were excluded from the analysis, and further missing genotypes were mean imputed to reduce the inflation of the alpha error due to differential missingness [12]. To weight SNVs in the analysis, a linear weighted kernel was applied. The SNV's weights were calculated based on the beta density distribution and the MAF ($\text{Beta}(\text{MAF}, 1, 25)^2$) [92].

3.2.4.4.4 Single Variant Association Analysis

A single variant association test was performed with the data before the removal of related individuals and the PCA-based outlier pruning. The software GMMAT (v.07, [48]) was used, which can adjust for population substructure and cryptic relatedness by a generalized linear mixed model. Therefore, a genetic relationship matrix was needed. It was calculated based on the SNPs that were used for PCA calculations using GEMMA (v0.94.1, [44]). Using GMMAT [48], a null model was fitted to the case-control status as the phenotype, and age and sex were used as fixed covariates and genetic relations as random effects. A score test was applied to all variants. SNVs with p below 1E-04 were further analyzed with a full regression using GMMAT's Wald test function [48], and effect size estimates were obtained. All variants were annotated using the CADD annotation [15] (database 1.3) and dbSNP [403, 420] (human 9606 GRCH37p13, build142). Further annotation was obtained from the Helmholtz Zentrum München NGS pipeline, which was based on dbNSFP3.0a [94].

3.3 Explaining RLS Affected Families with RLS Risk SNPs

RLS families were genotyped for common SNPs including known RLS risk SNPs. After a quality control and imputation step, an association analysis was used to determine the contribution of the known RLS risk SNPs to familial RLS.

3.3.1 Genotyping of RLS Affected Families

The DNA of 79 families (843 individuals, informed written consent provided) with familial RLS was diluted 1:2 in Affimetrix water to a final volume of 20 µL and an approximate concentration of 30 ng/µL. The DNA samples were submitted to the Helmholtz Zentrum München GAC for the Affimetrix Axiom assay (Axiom_Gw_Hu_SNP_96), and the raw imaging assay output was obtained. Genotypes were called using the AxiomAnalysisSuite (v2.4.0) and its annotation file Axiom_GW_Hu_SNP.na35.annot.db. SNPs were output to a PLINK format [59] that were of the SNP categories (“conversion type”) “Hemizygous” (SNPs on the Y chromosome and mitochondrial chromosomes), “MonoHighResolution” (monomorphic SNPs), “NoMinorHom” (SNPs without minor allele homozygotes) or “PolyHighResolution” (SNPs with at least 2 observed minor allele homozygotes) (standard setting).

3.3.2 Quality Control of the Genotyping Data

After the calling, a quality control was done for the dataset of 843 individuals and 576,761 markers using PLINK (v1.07 [59]), PLINK 2 (v1.90b3.32, [42, 365]) and R [4]: Markers were removed that had a call rate below 95% and indications of HWE violations ($p \leq 0.001$, based on index patients). Individuals were removed who showed an excess of heterozygosity of at least ± 4 standard deviations from the mean. A sex check was performed based on the individual heterozygosity of the common (MAF ≥ 5%) non-PAR X-chromosomal markers (14,817 markers). (Common markers were chosen to increase the resolution between male and female individuals). Individuals were excluded who differed between empirical and reported sex. To remove genetic duplicates, common autosomal variants were kept (MAF > 5%) and pruned for long range LD [364, 418] and LD (based on index individuals, PLINK [59] command “--indep-pairwise 50 5 0.2”). Genetic similarities were calculated for all pairs of individuals using PLINK 2 v1.90b3.32 [42, 365]. An IBD proportion ≥ 0.8 (PI_HAT) identified duplicates or monozygotic twins. Duplicates were removed; the individuals with the better variant call rate were kept. Based on the QC, a dataset of autosomal markers was created.

3.3.3 Imputation of RLS Risk Loci

Missing genotypes were imputed for the published RLS associated risk loci [70, 245] using chunks of ± 1 Mb flanking the RLS SNPs of interest. The imputation was done using the Michigan Imputation Server [421] and the 1000 Genomes Project phase 3 data [340] as the reference (and random IDs were used for each individuals and each chunk).The chunks included all autosomal markers and individuals after the QC. To create the dataset for imputation, PLINK (v1.07, [59]), R [4] and vcftools (v0.1.12b, [99]) was used.

3.3.4 RLS Risk SNP Association and Correlation Analysis

Individuals with missing phenotypes were removed from the imputed and genotyped datasets (e.g. no diagnosis of RLS, but age < 40 years).

A centered relatedness matrix was estimated using GEMMA (v0.94.1, [44]) using the genotyped common autosomal LD pruned variants. The matrix was used to model random effects in a generalized linear mixed model association analysis using GMMAT v 0.7 [48]. The fixed effects were the imputed dosages (posterior mean genotypes [422]) of the published RLS risk SNPs [70, 245], and the response variable was the RLS affection status. The association analysis was run with a score test to assess the significance of association and a Wald test to also obtain effects sizes.

The analysis was repeated for each family separately using the R [4] package pedigreemm [423] (v.0.3.3), which depended on the R [4] package lme4 [424] (v1.1.9). The random effects were modeled using a revised version of the pedigree structures. Fixed effects were either the SNP dosages or the sum (burden) of the published risk allele [70, 245] dosages. The analysis resulted in likelihoods of the full and reduced model (intercept only model for the fixed effects). First, they were used to assess the statistical significance of the model improvement by adding the (burden of) SNP dosages using the R [4] package lmtest (v0.9.34) [425]. Second, they were used to calculate a pseudo-R^2 measure, which can be interpreted as a proportion of explained phenotypic variance by the fixed dosage effects [426, 427].

The correlation was assessed between the family size and the proportion of phenotypic variance attributable to the burden measurements (Spearman, using R [4]). Its significance was evaluated by calculating an empirical *p* value (100,000 permutations of the pseudo-R^2 values) (Equation 15).

Equation 15

$$p_{emp} = \frac{1 + \sum_{i=1}^{n} I\left(R_i^2 \geq R^2\right)}{n+1}$$

p_{emp} = empirical p value
R^2 = squared correlation coefficient between familial pseudo-R^2 and family size values
R_i^2 = squared correlation coefficient between the i^{th} permuted familial pseudo-R^2 and family size values
n = number of permutations
$I(R_i^2 \geq R^2)$ = function assessing R^2 from i^{th} permuted vector of pseudo-R^2 measures equal/larger than the R^2 from the original vector of pseudo-R^2 measures (returning 1 or 0)

4 Results

4.1 Screening for RLS Associated Rare Variants and Genes Using the Human Exome BeadChip

More than 100,000 rare SNPs were analyzed for association with RLS. The SNPs were genotyped in a German/Austrian RLS case-control cohort of approximately 9,000 individuals using the Human Exome BeadChip. Association analyses were single variant association and gene-level tests. As a result, 19 candidate genes were obtained.

4.1.1 Quality Control of the Genotyping Data

Genotype data was obtained from the Human Exome BeadChip ("ExomeChip") for RLS cases, HNR [55, 356] population based controls, and KORA [354, 355] population based controls. An initial QC was performed for each cohort separately. The data of RLS cases consisted of 3,839 individuals (with 2x40 HapMap [358-363] control replicates) and 247,870 markers. A total of 8,994 low quality markers were removed [357]. The application of call rate filters resulted in 3,824 individuals and 238,617 markers. The sex check confirmed the sex of 3,804 individuals, who were kept. The initial dataset from KORA [354, 355] consisted of 2,921 individuals and 237,982 markers. After the call rate filters, 237,973 markers remained. The raw HNR [55, 356] dataset consisted of 247,870 markers and 2,486 individuals. After removing 8,994 low quality markers [357], the call rate filters removed 15 individuals and 27 markers (238,849 remaining). Ten individuals failed in the sex check (2,476 remaining).

The genotype data was merged to 3,804 cases and 5,382 controls, 3,779 males and 5,407 females, with 238,867 markers. The call rate filters removed 1,228 markers and 237,638 were remaining (= genome-wide dataset), of which 232,618 were autosomal.

The autosomal dataset was split at MAF = 1% (198,764 markers with MAF < 1% and 33,854 markers with MAF ≥ 1%), and a call-rate QC detected 13 individuals as outliers (in the dataset with common markers). In both datasets, 24 and 30 individuals were detected as outliers based on deviation from the mean heterozygosity in the dataset with rare and common variants, respectively (intersection of 7 individuals). All detected outliers were removed from the complete autosomal dataset. Markers were kept that were on the Human Exome BeadChip v1.1 [357] (228,263 markers). To detect problematic samples, the dataset was cleaned for 188,019 low frequency markers, 29 markers with HWE violations in controls, and 9,957 markers in long range LD regions [364]. The remaining 30,267 autosomal markers were pruned for LD, and the remaining 19,624 markers were used to calculate pairwise PI_HAT for the individuals [59]. A total of 31 duplicate pairs were detected (30 cases, 1 control) as well as one problematic individual who showed a high relatedness to a broad variety of individuals.

From the genome-wide dataset, 47 samples were removed with large deviations from mean heterozygosities as well as 35 markers with HWE violations in controls. Furthermore, 31 worse genotyped duplicates and one problematic sample as well as the 80 HapMap [358-363] controls were removed. Another 713 duplicated markers were removed as well as 4 markers that were known to have bad genotype callings. Two cases were missing the age phenotype and were removed (9,012 individuals remaining). Finally, only polymorphic autosomal markers were kept. The resulting dataset consisted of 3,652 cases and 5,360 controls (3,752 males and 5,260 females), and 137,011 markers, and it was used as the analysis dataset.

To obtain a dataset for genetic similarity estimations, the analysis dataset was pruned. Therefore, 6,807 markers in long range LD regions [364], then 76,700 markers with MAF < 1% and then 10,284 markers in high LD were removed. Finally, 43,220 markers were left. Based on this genotype data for 8,810 unrelated individuals, 2 MDS [59] coordinates were calculated (Figure 2). HNR [55, 356] and KORA [354, 355] samples could add to each other to fit to the RLS samples.

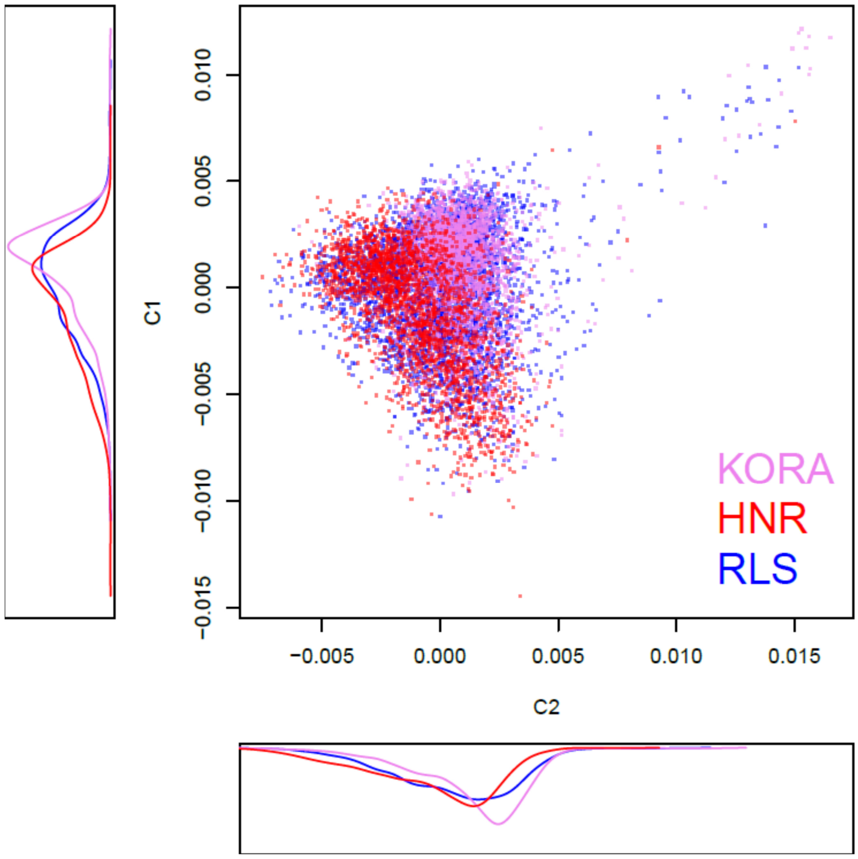


Figure 2: MDS plot of two coordinates of the combined unrelated ExomeChip dataset from RLS cases, KORA and HNR controls: Combined HNR [55, 356] and KORA [354, 355] controls populated the same area as RLS cases. The marginal plots represent the respective point densities.

4.1.2 Single Variant Association Analysis

A fast mixed model association analysis was done for single variants using FaST-LMM [37, 366, 367] and including age and sex as covariates (Figure 3, p. 47, Figure 4, p. 48): The QQ plot did not show a large deviation from the diagonal. However, λ_{GC} was 1.288 due to inflation in the lower tail. The association results were validated for $p \leq 0.0001$ using GMMAT [48]. No new RLS associated loci were found below a genome-wide significance threshold (Table 20, p. 49). One signal of the *PTRPD* locus could not be replicated (rs4626664), but it was published as an independent signal from the neighboring RLS associated SNP (rs1975197) [244] and was part of the dataset. The significant markers did not show differential missingness (minimal p = 5.8E-02 for rs9296249 at the *BTBD9* locus) or HWE violations (minimal p = 6.7E-02 for exm2267781 at the *MAP2K5* locus). In the range between $p \leq 0.0001$ and $p >$ 5E-08, 21 signals were observed, of which 10 came from coding variants (9 missense, 6 common variants with MAF > 5%). The genes were: *AAGAB*, *C7orf62*, *ABCA10*, *CLDN23*, *ABCA10*, *SLC39A7* (with common variants) and *RASGRP4*, *CNNM3*, *OSBP*, *SLC39A8* (with rare variants, MAF < 5%). However, the marker in *CNNM3* showed a significant evidence for differential missingness in cases and controls.

In the conditional analysis, SNPs were used as additional covariates: exm-rs2300478, exm-rs3923809, exm2267781, exm-rs3104767, exm-rs6747972, exm-rs1975197 and exm-rs4626664. They were the lead SNPs from the published RLS associated genomic regions (rs4626664 could not be replicated but was included as a covariate in the conditional analysis). The conditional analysis was done with 3,649 cases and 5,359 controls who did not miss the covariates (Table 21, p. 51). Exm-rs11897119 gave a signal at the *MEIS1* locus, and it was not entirely removed by conditioning on the lead SNPs including the un-replicated SNP rs4626664 of the *PTRPD* locus. Of note, many of the non-significant top markers had only slightly changed *p* values after conditioning on these SNPs. Only exm1171910 had a conditional *p* value greater 0.05 and this SNP was in proximity to the *BTBD9* locus. The SNP exm1462496 improved most from *p* = 3.12E-05 (unconditional analysis) to *p* = 7.69E-06 (conditional analysis), but did not reach genome-wide significance. The SNP was a missense variant in *RASGRP4*.

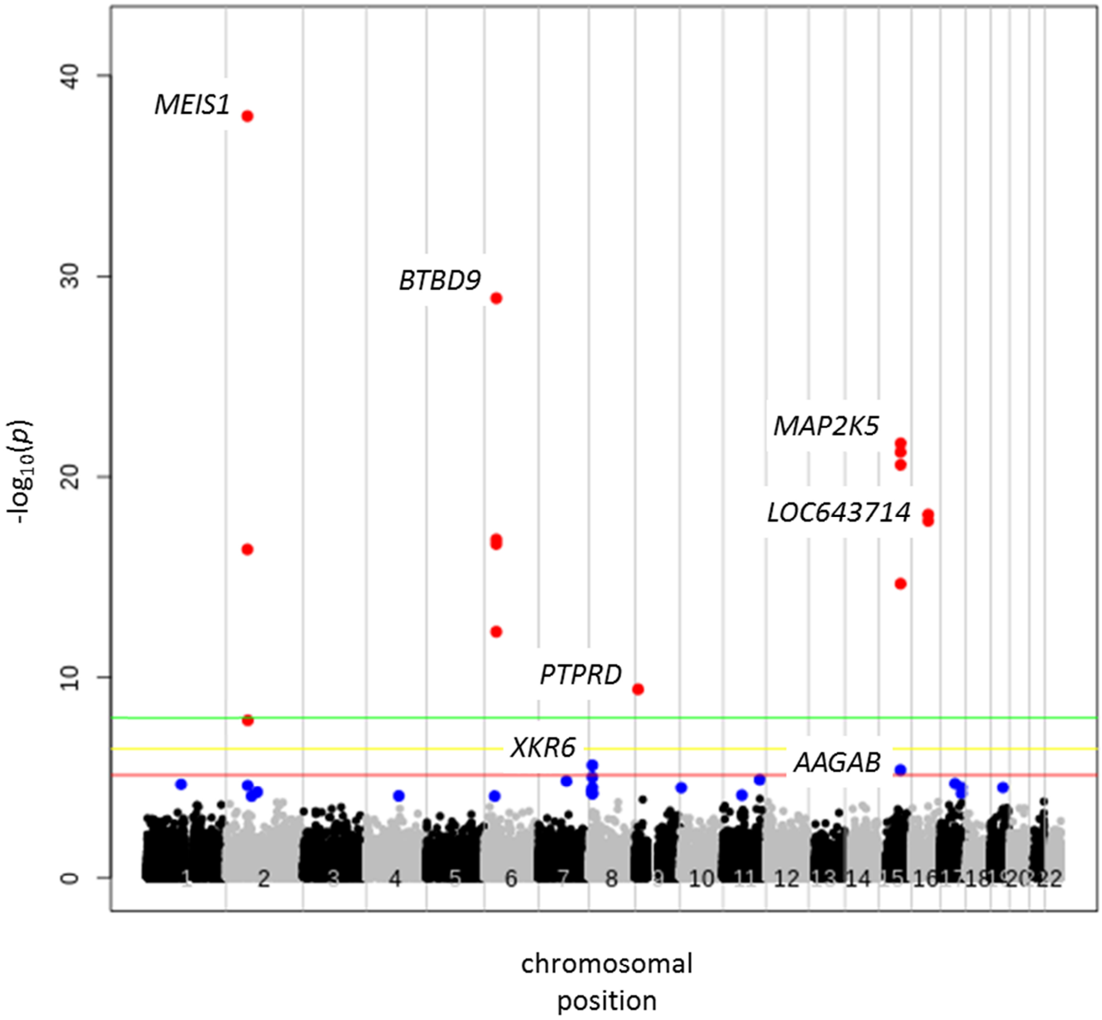


Figure 3: Manhattan plot of single variant association results using ExomeChip genotype data: Age and sex were included as covariates, and 137,011 polymorphic autosomal markers were analyzed using FaST-LMM [37, 366, 367]. Candidates were found on an intergenic region of chromosome 1, in CNNM3 (chromosome 2), in SLC39A8 (chromosome 4), in ZNF804B (chromosome 7), in XKR6/BLK/CLDN23 (chromosome 8), on chromosome 10, in OSBP (chromosome 11), on chromosome 11, in AAGAB (chromosome 15), on chromosome 17, in RASGRP4 (chromosome 19). (Horizontal lines: green = genome-wide significance threshold p < 5E-08, yellow = study's significance threshold p < 0.05/137,011, red = candidate threshold p < 1/137,011.)

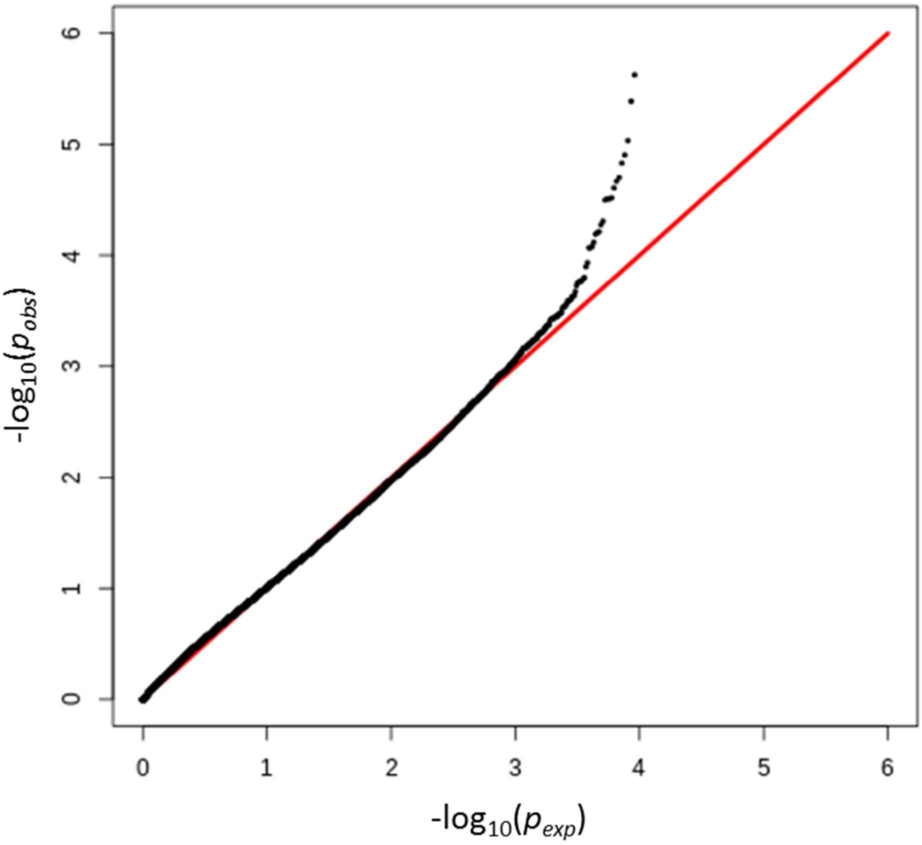


Figure 4: QQ plot of single variant association result using ExomeChip data: Age and sex were used as covariates. A total of 137,011 polymorphic autosomal markers were analyzed using FaST-LMM [37, 366, 367]. Lambda (λ_{GC}) was 1.288. (x-axis = -$\log_{10}$ of the expected p values under the null hypothesis, y-axis = -$\log_{10}$ of the observed p values, red = diagonal)

Table 20: Summary statistics from the single variant association analysis of ExomeChip data. No. = SNP rank, SNP = SNP identifier, Chr = chromosome, pos = physical position hg19, min = minor allele, maj = major allele = test allele, underscored allele = risk allele, p_F = association p value from FaST-LMM [37, 366, 367], p_s = association p value from GMMAT [48] score test, p_W = association p value from GMMAT [48] Wald test, OR_{risk} = odds ratio for risk allele (95% CI in brackets), Gene = SNP location in gene, Mut = mutations for minor allele (listed for all annotated transcripts [369, 370] from the respective gene), MAF = minor allele frequency based on all samples, p_{HWE} = p value from HWE test in controls, f_a = proportion of missing genotypes in cases, f_u = proportion of missing genotypes in controls, p_m = p value from the Fisher test for differential missingness between cases and controls. The alleles were listed according to Illumina top strand annotation.

No.	**SNP**	**Chr:pos[maj/min]**	p_F	p_s	p_W	OR_{risk}	**Gene**	**Mut**	**MAF**	p_{HWE}	f_a	f_u	p_m
1	exm-rs2300478	2:66,781,453[A/$\underline{C}$]	1.0E-38	1.4E-35	3.2E-35	1.60 [1.49; 1.73]	*MEIS1*		0.2871	4.9E-01	0.0E00	0.0E00	1.0E00
2	exm-rs3923809	6:38,440,970[$\underline{A}$/G]	1.2E-29	5.2E-28	9.5E-28	1.55 [1.43; 1.67]	*BTBD9*		0.2724	1.1E-01	0.0E00	0.0E00	1.0E00
3	exm2267781	15:68,095,085[$\underline{G}$/A]	2.2E-22	2.1E-19	2.3E-19	1.42 [1.32; 1.53]	*MAP2K5*		0.2925	9.3E-01	8.2E-04	0.0E00	6.7E-02
4	exm-rs12593813	15:68,036,852[$\underline{G}$/A]	5.9E-22	5.0E-19	5.3E-19	1.41 [1.31; 1.52]	*MAP2K5*		0.2968	6.4E-01	0.0E00	0.0E00	1.0E00
5	exm-rs4489954	15:68,072,075[$\underline{C}$/A]	2.5E-21	3.3E-18	3.5E-18	1.41 [1.31; 1.53]	*MAP2K5*		0.2757	4.4E-01	2.7E-04	0.0E00	4.1E-01
6	exm-rs3104767	16:52,624,738[$\underline{C}$/A]	7.5E-19	4.2E-16	4.4E-16	1.34 [1.25; 1.44]	*LOC643714*		0.3857	2.0E-01	0.0E00	0.0E00	1.0E00
7	exm-rs3112612	16:52,635,164[$\underline{G}$/A]	1.6E-18	7.6E-16	8.1E-16	1.34 [1.25; 1.44]	*LOC643714*		0.3857	2.4E-01	0.0E00	0.0E00	1.0E00
8	exm-rs9357271	6:38,365,873[$\underline{A}$/G]	1.4E-17	1.8E-16	2.2E-16	1.43 [1.31; 1.56]	*BTBD9*		0.2053	7.5E-02	0.0E00	0.0E00	1.0E00
9	exm-rs9296249	6:38,365,841[$\underline{A}$/G]	2.3E-17	2.6E-16	3.2E-16	1.43 [1.31; 1.56]	*BTBD9*		0.2044	5.8E-02	0.0E00	0.0E00	1.0E00
10	exm-rs11897119	2:66,772,000[$\underline{A}$/G]	4.2E-17	1.8E-15	1.8E-15	1.34 [1.25; 1.44]	*MEIS1*		0.3629	7.5E-01	0.0E00	0.0E00	1.0E00
11	exm-rs2241423	15:68,086,838[$\underline{G}$/A]	2.2E-15	2.9E-13	3.0E-13	1.38 [1.27; 1.50]	*MAP2K5*		0.2044	9.4E-01	0.0E00	0.0E00	1.0E00
12	exm2266182	6:38,389,301[A/$\underline{G}$]	5.4E-13	1.1E-12	1.0E-12	1.28 [1.20; 1.38]	*BTBD9*		0.4966	8.5E-01	0.0E00	0.0E00	1.0E00
13	exm-rs1975197	9:8,846,955[G/$\underline{A}$]	3.8E-10	1.9E-09	1.9E-09	1.31 [1.20; 1.44]	*PTPRD*		0.1746	6.8E-01	0.0E00	1.9E-04	1.0E00
14	exm-rs6747972	2:68,070,225[G/$\underline{A}$]	1.4E-08	2.4E-07	2.4E-07	1.20 [1.12; 1.29]			0.4674	7.6E-01	0.0E00	0.0E00	1.0E00
15	exm-rs7819412	8:11,045,161[A/$\underline{G}$]	2.4E-06	3.4E-06	3.4E-06	1.17 [1.10; 1.25]	*XKR6*		0.4804	8.3E-01	0.0E00	0.0E00	1.0E00
16	exm1171910	15:67,528,374[$\underline{A}$/C]	4.1E-06	1.3E-05	1.3E-05	1.18 [1.10; 1.27]	*AAGAB*	I132L	0.3129	2.8E-01	0.0E00	0.0E00	1.0E00
17	exm-rs7824557	8:11,104,111[A/$\underline{G}$]	9.3E-06	3.4E-05	3.4E-05	1.16 [1.08; 1.24]			0.3867	8.2E-01	0.0E00	0.0E00	1.0E00
18	exm2249584	11:115,685,475[G/$\underline{A}$]	1.2E-05	5.4E-05	5.4E-05	1.15 [1.08; 1.24]			0.4536	4.9E-01	2.7E-04	1.9E-04	1.0E00
19	exm632310	7:88,423,881[A/$\underline{G}$]	1.5E-05	6.0E-05	6.1E-05	1.27 [1.13; 1.43]	*ZNF804B* *C7orf62*	- I126V	0.0900	4.1E-01	8.2E-04	0.0E00	6.7E-02
20	exm2264631	17:46,791,801[A/$\underline{C}$]	2.0E-05	6.4E-05	6.4E-05	1.15 [1.08; 1.24]			0.4587	5.1E-01	0.0E00	0.0E00	1.0E00
21	exm2268922	1:107,163,979[$\underline{A}$/G]	2.2E-05	5.9E-05	6.0E-05	1.16 [1.08; 1.25]			0.3032	5.9E-01	0.0E00	0.0E00	1.0E00
22	exm2269076	2:67,729,255[C/$\underline{A}$]	2.5E-05	1.8E-04	1.8E-04	1.14 [1.07; 1.22]			0.4908	8.9E-01	2.7E-04	0.0E00	4.1E-01

continued table…

No.	SNP	Chr:pos[maj/min]	p_F	p_s	p_W	OR_{risk}	Gene	Mut	MAF	p_{HWE}	f_a	f_u	p_m
23	exm1349521	17:67,210,992[A/G]	3.1E-05	1.7E-04	1.7E-04	1.14 [1.07; 1.22]	*ABCA10*	I287V	0.4307	7.4E-01	3.6E-03	9.3E-04	7.7E-03
24	exm-rs13277113	8:11,349,186[G/A]	3.1E-05	1.8E-04	1.8E-04	1.16 [1.07; 1.25]			0.2474	5.7E-01	1.4E-03	0.0E00	1.1E-02
25	exm1462496	19:38,901,633[G/A]	3.1E-05	5.4E-05	5.8E-05	1.58 [1.26; 1.98]	*RASGRP4*	E551K E606K E528K E523K E431K E620K E586K	0.0230	4.7E-01	0.0E00	0.0E00	1.0E00
26	exm-rs2031577	10:4,050,003[G/A]	3.2E-05	8.4E-05	8.4E-05	1.15 [1.07; 1.24]			0.3854	6.8E-01	0.0E00	0.0E00	1.0E00
27	exm680383	8:8,560,602[G/A]	4.9E-05	1.9E-04	1.9E-04	1.16 [1.07; 1.26]	*CLDN23*	P232S	0.2329	8.8E-01	2.7E-04	1.9E-04	1.0E00
28	exm213626	2:97,482,906[G/A]	5.3E-05	9.6E-05	1.3E-04	2.58 [1.59; 4.18]	*CNNM3*	G298S	0.0050	1.0E00	1.4E-02	1.1E-03	6.4E-15
29	exm-rs2618476	8:11,352,541[A/G]	6.1E-05	2.9E-04	2.9E-04	1.15 [1.07; 1.24]	*BLK*		0.2564	5.8E-01	2.7E-04	0.0E00	4.1E-01
30	exm1349535	17:67,212,423[A/G]	6.3E-05	1.1E-03	1.1E-03	1.13 [1.05; 1.21]	*ABCA10*	P203S	0.3386	2.3E-01	0.0E00	0.0E00	1.0E00
31	exm-rs1600249	8:11,359,638[C/A]	6.5E-05	2.0E-04	2.0E-04	1.16 [1.07; 1.26]	*BLK*		0.2376	3.0E-01	0.0E00	0.0E00	1.0E00
32	exm913705	11:59,368,345[G/A]	7.6E-05	6.6E-04	2.3E-03	7.96 [2.09; 30.26]	*OSBP*	R376C	0.0009	1.0E00	0.0E00	0.0E00	1.0E00
33	exm415951	4:103,184,317[C/G]	8.3E-05	3.2E-04	8.6E-01	8.60E04 [0.00; 3.70E61]	*SLC39A8*	V356L V423L	0.0003	1.0E00	0.0E00	1.9E-04	1.0E00
34	exm-rs1547387	6:33,169,895[C/G]	8.6E-05	1.0E-04	1.0E-04	1.23 [1.11; 1.36]	*SLC39A7*	S209S	0.1185	5.3E-01	5.5E-04	0.0E00	1.6E-01
35	exm-rs6740609	2:79,855,622[A/G]	8.6E-05	2.0E-04	2.0E-04	1.18 [1.08; 1.28]	*CTNNA2*		0.2048	8.4E-01	1.9E-03	7.5E-04	1.3E-01

*Table 21: P values from conditional single variant association analysis using FaST-LMM and ExomeChip data: The covariates were the lead SNPs of the unconditional analysis for each published RLS locus and rs4626664. No. = order from unconditional FaST-LMM [37, 366, 367] analysis, SNP = SNP identifier, Chr = chromosome, pos = physical position hg19, p/p_{cond} = p value from unconditional or conditional analysis (shown for $p_{cond} \leq 1E-04$) with FaST-LMM [37, 366, 367], Magnitude = $\log_{10}(p/p_{cond})$, * = genome-wide significant in unconditional analysis*

No.	**SNP**	**Chr:pos**	**Gene**	***p***	***p_{cond}***	**Magnitude**
1	*exm-rs2300478	2:66,781,453	*MEIS1*	1.02E-38	NA	NA
2	*exm-rs3923809	6:38,440,970	*BTBD9*	1.19E-29	NA	NA
3	*exm2267781	15:68,095,085	*MAP2K5*	2.16E-22	NA	NA
4	*exm-rs12593813	15:68,036,852	*MAP2K5*	5.89E-22	7.22E-01	-21.09
5	*exm-rs4489954	15:68,072,075	*MAP2K5*	2.52E-21	6.09E-01	-20.38
6	*exm-rs3104767	16:52,624,738	*LOC643714*	7.47E-19	NA	NA
7	*exm-rs3112612	16:52,635,164	*LOC643714*	1.62E-18	5.30E-01	-17.51
8	*exm-rs9357271	6:38,365,873	*BTBD9*	1.35E-17	5.28E-01	-16.59
9	*exm-rs9296249	6:38,365,841	*BTBD9*	2.30E-17	6.28E-01	-16.44
10	*exm-rs11897119	2:66,772,000	*MEIS1*	4.24E-17	5.80E-03	-14.14
11	*exm-rs2241423	15:68,086,838	*MAP2K5*	2.15E-15	7.32E-01	-14.53
12	*exm2266182	6:38,389,301	*BTBD9*	5.45E-13	2.83E-02	-10.71
13	*exm-rs1975197	9:8,846,955	*PTPRD*	3.78E-10	NA	NA
14	*exm-rs6747972	2:68,070,225		1.39E-08	NA	NA
15	exm-rs7819412	8:11,045,161	*XKR6*	2.36E-06	5.05E-06	-0.33
16	exm1171910	15:67,528,374	*AAGAB*	4.11E-06	5.83E-01	-5.15
17	exm-rs7824557	8:11,104,111		9.26E-06	2.50E-05	-0.43
18	exm2249584	11:115,685,475		1.25E-05	2.35E-05	-0.27
19	exm632310	7:88,423,881	*ZNF804B* & *C7orf62*	1.47E-05	2.27E-05	-0.19
20	exm2264631	17:46,791,801		1.99E-05	6.03E-05	-0.48
21	exm2268922	1:107,163,979		2.16E-05	8.38E-05	-0.59
22	exm2269076	2:67,729,255		2.48E-05	1.10E-04	-0.64
23	exm1349521	17:67,210,992	*ABCA10*	3.06E-05	1.16E-04	-0.58
24	exm-rs13277113	8:11,349,186		3.10E-05	1.39E-05	0.35
25	exm1462496	19:38,901,633	*RASGRP4*	3.12E-05	7.69E-06	0.61
26	exm-rs2031577	10:4,050,003		3.19E-05	3.03E-05	0.02
27	exm680383	8:8,560,602	*CLDN23*	4.93E-05	5.61E-05	-0.06
28	exm213626	2:97,482,906	*CNNM3*	5.33E-05	5.61E-04	-1.02
29	exm-rs2618476	8:11,352,541	*BLK*	6.12E-05	4.18E-05	0.17
30	exm1349535	17:67,212,423	*ABCA10*	6.27E-05	2.18E-04	-0.54
31	exm-rs1600249	8:11,359,638	*BLK*	6.47E-05	5.80E-05	0.05
32	exm913705	11:59,368,345	*OSBP*	7.63E-05	1.64E-04	-0.33
33	exm415951	4:103,184,317	*SLC39A8*	8.31E-05	6.62E-05	0.10
34	exm-rs1547387	6:33,169,895	*SLC39A7*	8.55E-05	4.89E-04	-0.76
35	exm-rs6740609	2:79,855,622	*CTNNA2*	8.56E-05	5.45E-05	0.20
…	…	…	…	…	…	…
36	exm-rs638882	11:115,764,045	*LOC105369512*	1.16E-04	7.74E-05	0.18
…	…	…	…	…	…	…
42	exm234700	2:159,459,601	*PKP4*	1.75E-04	8.69E-05	0.30
…	…	…	…	…	…	…
63	exm417043	4:106,196,951	*TET2-AS1* & *TET2*	3.56E-04	7.76E-05	0.66
…	…	…	…	…	…	…
75	exm967062	11:124,740,559	*ROBO3*	4.30E-04	8.15E-05	0.72
76	exm-rs16965350	17:36,614,563	*ARHGAP23*	4.34E-04	7.17E-05	0.78

4.1.3 Gene Level Association Analysis

To perform a gene level association analysis, polygenic residuals were obtained (using an IBS-matrix and the method GRAMMAR [49], R [4] and GenABEL [368] v.1.8-0) that random effects were based on an IBS matrix [49]. The association analysis dataset consisted of 122,224 markers with MAF ≤ 5% in either cases or controls. Of these, 109,593 markers in 14,147 genes were used in the gene level association analysis.

The gene level association analysis was done with SKAT [92], burden test (BRV) [371], or combined tests (Fisher method, minimum-*p* method) [346]. The tests were performed without and with CADD [15] based weighting of variants. In a genome-wide scan, empirical *p* values were obtained. The number of independent null hypothesis was 11,833 and 11,799 for the 14,147 genes in the genome-wide burden tests without and with CADD [15] based weighting of variants, respectively. In the QQ plot (Figure 5, p. 53), large deviations were observed from the diagonal for *p* values from the Fisher method [346], but not for *p* values based on burden or SKAT [92] tests. A deflation was observed for the *p* values from the minimum-*p* method [346]. The genomic inflation factors λ_{GC} [313] were 0.996 and 1.029 from the burden [371], 1.056 and 1.069 from the SKAT [92], 0.739 and 0.929 from the Fisher method [346], and 0.575 and 0.96 from the minimum-*p* method [346], for unweighted and CADD [15] weighted gene level association tests, respectively. Neither exome-wide significant associations were observed nor significant associations after Bonferroni correction for 11,799 burden tests.

A total of 76 genes were selected for the refined association analysis by conditioning on the published RLS risk SNPs (with and without CADD [15] based weighting of variants), but no gene reached significance, neither exome-wide nor after Bonferroni correction for 11,799 tests (Figure 6, p. 54). Of those 76 genes, 20 genes were selected as genes for targeted sequencing, because at least one empirical *p* value was below 1/11,833. One gene was removed due to false genotype calling that were observed by the inspection of the respective cluster plots from the genotype calling. The final 19 genes were: *CORO6*, *DMPK*, *EYA2*, *FAM171A1*, *GALNT12*, *GRIN2B*, *KRTAP19-5*, *LEO1*, *NECAP1*, *NENF*, *OLFML2B*, *OSBP*, *OSGIN1*, *PCDHB5*, *PDE11A*, *RASGRP4*, *TREM1*, *UBL4B* and *ZNF175*.

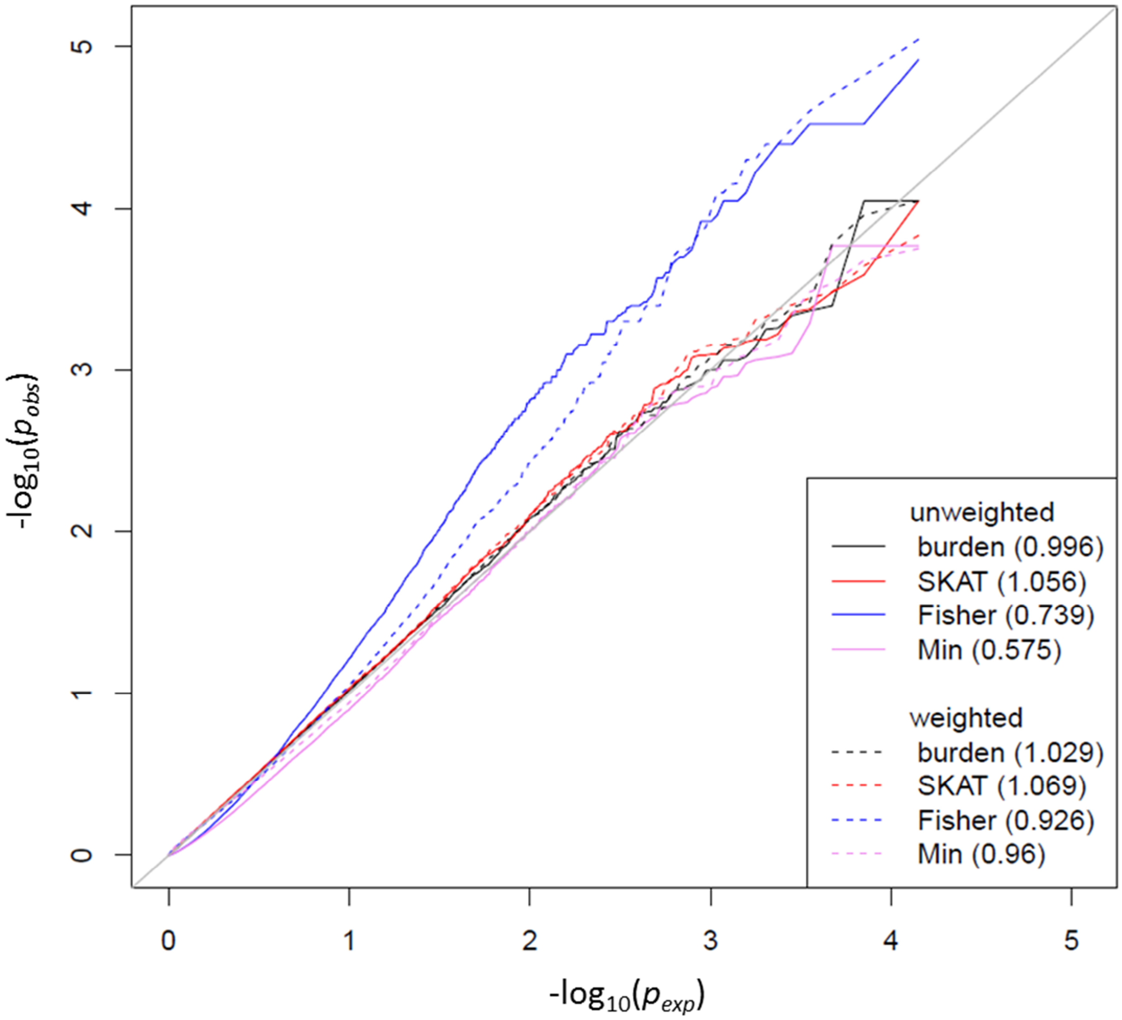


Figure 5: QQ plot of gene-level association analyses using ExomeChip data: The analysis was performed with and without CADD-based [15] weighting scores. SKAT = SKAT analysis [92], burden = burden [12] analysis, Fisher/Min = Fisher or minimum-p method [346] of combining burden [12] and SKAT [92] analysis. Genomic inflation factors λ_{GC} [313] are given in brackets. X-axis: -$\log_{10}$ of the expected association p values under the null hypothesis. Y-axis: -$\log_{10}$ of the observed association p values.

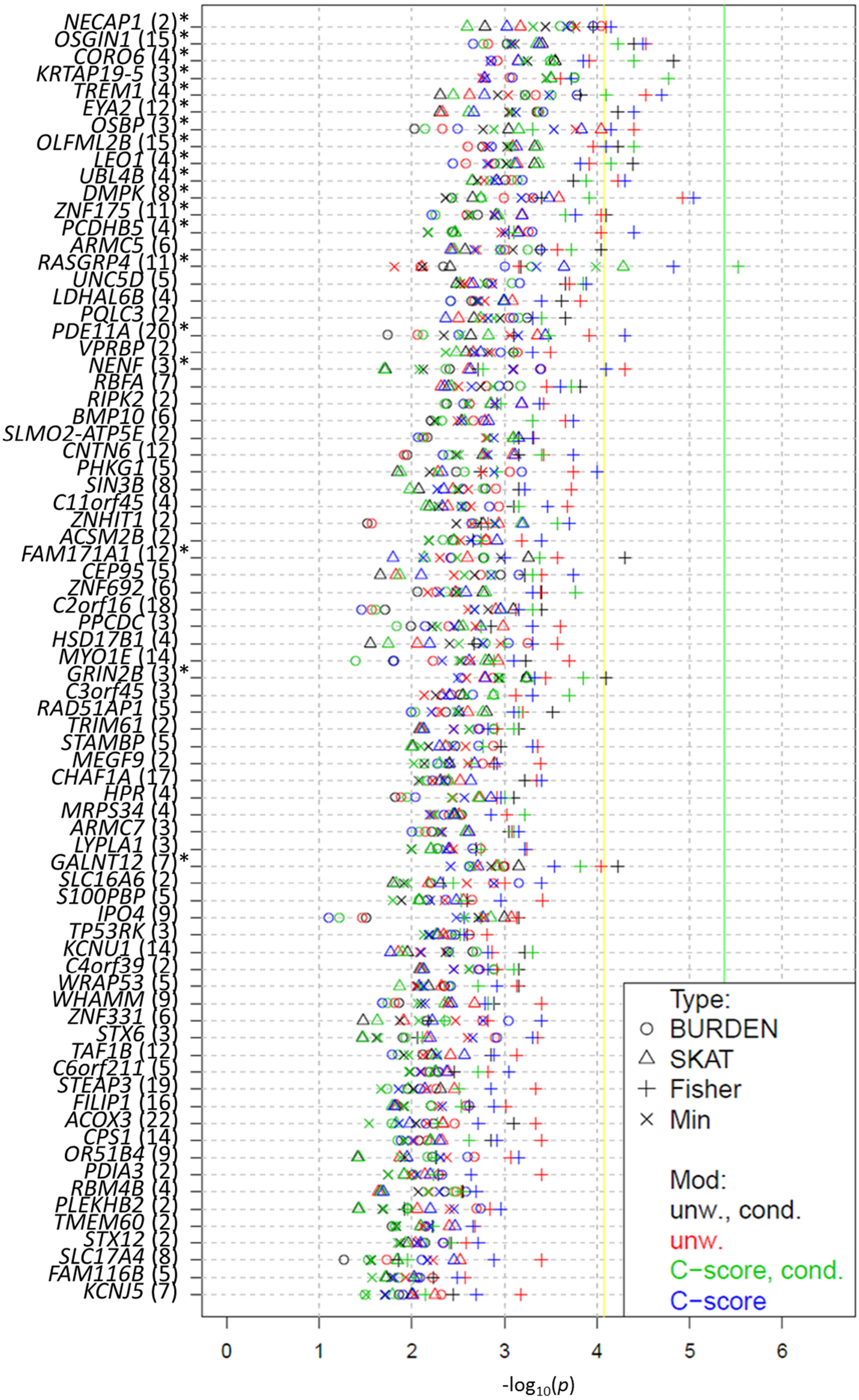


*Figure 6: Gene level association analysis using ExomeChip data: The shown top genes were determined by a screen of 14,147 genes (threshold = any –log$_{10}$(p) ≥ -log$_{10}$(0.05/11,833) – 2). Y-axis: genes (ordered by mean p value, number of markers in brackets, * = selected for MIPseq). Type = type of association test, BURDEN = burden test [12], SKAT = SKAT [92], Fisher or Min = Fisher's or minimum-p method of combining burden test and SKAT [346], Mod = gene level test modification, unw. = unweighted analysis, C-score = analysis with variants weighted based on CADD scores [15], cond. = analysis conditioned on RLS associated common variants, green line = significance threshold for 11,833 independent null hypothesis (Bonferroni), yellow line = MIPseq candidate selection threshold 1/11,833*

4.2 Targeted Sequencing of RLS Candidate Genes

Eighty-four RLS candidate genes were sequenced and analyzed for association in more than 1,200 individuals of a case-control cohort. The highest significant signals were detected for *COL20A1* and *MYT1*.

4.2.1 Definition of RLS Candidate Genes

A total of 84 genes were selected for targeted sequencing (see appendix p. 151, Table 32). Of those, 19 genes were ExomeChip candidate genes, and 65 were obtained from annotating meta-GWAS [373] lead SNPs, of which 10 genes were obtained from eQTL annotations (Figure 7).

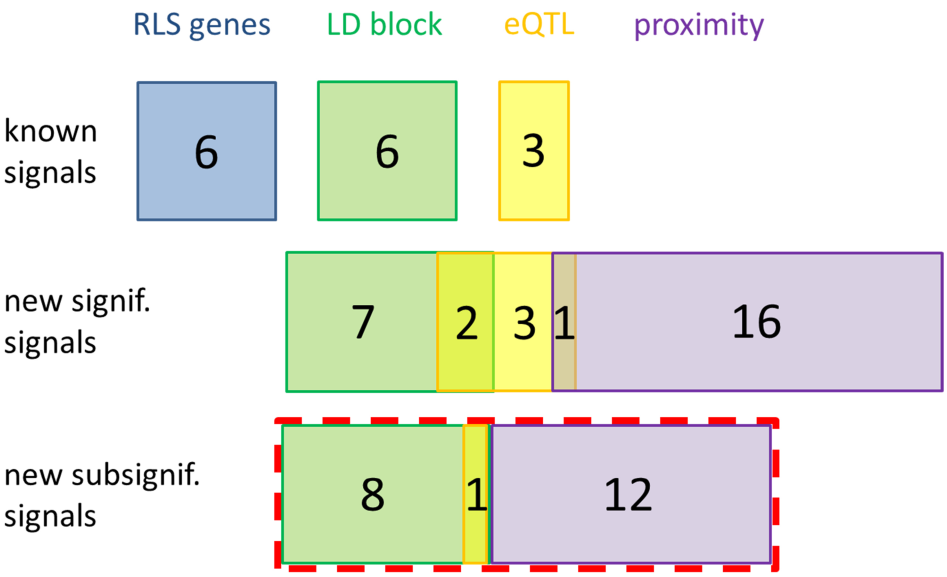


Figure 7: Count of selected RLS candidate genes from an unpublished meta-GWAS: Genes were selected based on annotating lead SNPs with genes of the respective LD block, from eQTL signals, in close proximity, or which were discussed in the literature, or which were of putative functional relevance. The independent annotation approaches led to partially overlapping results. Red dashed line = annotation of genes restricted to functional relevance, known signals = published genome-wide significant RLS associated loci, new signif. signals = unpublished genome-wide significant RLS associated loci from a meta-GWAS [373], new subsignif. signals = locus two SNPs with p ≤ 1E-05 in the RLS meta-GWAS [373]

4.2.2 Definition of RLS Candidate Genes' Target Regions

On average, 11,010 bp were defined as target regions for MIPseq for each gene (median = 9,475 bp, minimum = 1,002 bp for gene *KRTAP19-5*, maximum = 28,250 bp for *GRIN2B*). The average coding target size was 3,961 bp (median = 3,591 bp, minimum = 220 bp for *KRTAP19-5*, maximum = 11,445 bp for *LAMA1*). Table 32 summarizes the size of the target regions for each gene.

4.2.3 Calibration of a Pool of Molecular Inversion Probes for MIPseq

4.2.3.1 Primary Design of Molecular Inversion Probes for MIPseq

A total of 10,883 MIPs were designed, of which 75 mapped to intersecting genes. On average, 131 MIPs were designed for each genes' target regions (median = 113 MIPs, minimum = 13 MIPs for *KRTAP19-5*, maximum = 298 MIPs for *GRIN2B*). For 39 genes, the design could cover all target regions. On average, the design was successful for 99.2% of the genes' target regions (median = 100%, minimum = 93% for *ASTN2*, maximum = 100%). The genes' coding regions were populated with 46 MIPs on average (median = 40 MIPs, minimum = 3 MIPs for *KRTAP19-5*, maximum = 164 MIPs for *LAMA1*). The completeness of the MIP design was 99.9% on average for the genes' coding target regions (median = 100%, minimum = 96.0% for *FTSJ2*). For 77 genes, the coding targets were completely covered by the MIP design. Details are shown in the appendix (Table 32).

4.2.3.2 Evaluation of the Naïve MIPs Pool for the Balancing of MIPs

Three DNA samples were sequenced on the MiSeq using a naïve pool of the designed MIPs. Of these 10,883 MIPs, 1,322 MIPs were bad performers with having the lowest on-target coverages. Another 741 MIPs were low performers with rather low on-target coverages. The top 100 MIPs were flagged as over-performers. From the MiSeq output, only 23,835,175 reads were count to be on target, but a total of 52,727,012 reads were observed by grepping reads based on MIP probes. The discrepancy was due to off-target reads. Thus the proportion of off-target reads was 54.8%. The majority of the off-target reads (95%) originated from just 90 MIPs. Figure 8 (p. 58) shows two MIP examples for the distribution of off-target reads. These 90 MIPs were flagged for removal (94 MIPs, including their alternative MIP for probe regions with SNPs).

4.2.3.3 Evaluation of the Balanced MIPs Pool

The MIPs pool improved by balancing towards a more uniform coverage: The number of non-performing MIPs was reduced and the coverage of the MIPs' target regions was increased in the lower tail. The lower tail also contained a higher proportion of removed MIPs. After balancing, their target regions' coverage showed a drop to the baseline (Figure 9, p. 59).

After the balancing, 51,343,088 reads were observed by grepping reads based on MIP probes, and a total of 44,456,764 reads mapped on target, which indicated a reduction of the proportion of off-target reads to 13.4%.

In the balanced MIPs pool, 768 MIPs were bad performers, which target regions were selected for a secondary MIP design. Of the low performer MIPs, 127 MIPs were chosen to be enhanced by adding 10-fold of the standard MIP concentration, and 1 MIP was enhanced by adding 20-fold of the standard MIP concentration. The number of over-performing MIPs was 35.

Of the off-targets MIPs of the balanced MIPs pool, 14 were chosen for being inhibited. They caused 57% of all off-target reads. Of the remaining off-target MIPs, 6 MIPs were chosen to be enhanced by adding 1-fold concentration of the standard MIP concentration because their on-target performance was to be increased and the off-target effects were acceptable. Twenty-four off-target MIPs were reintroduced from the evaluation of the naïve MIPs pool to rescue the coding target regions for the MIPseq.

4.2.3.4 Secondary MIP design for Rescuing the Capture of MIPseq Targets

An iterative redesign was performed for target regions of non-improvable low performing MIPs (after balancing), which affected 80,726 bp of MIP target regions. After the secondary design, QC and filtering, 331 additional MIPs were obtained (see MIPs in appendix, p. 155), which covered 18,548 bp (23.0%), and added to the rebalanced MIPs pool at one standard MIP concentration.

4.2.3.5 Evaluation of the Rebalanced MIPs Pool

MIPseq libraries were prepared for 46 samples using either the balanced or rebalanced MIPs pool. The libraries were sequenced on HiSeq 2500 machines. The coverage distributions were compared for the MIPs' targets between the balanced and rebalanced MIPs pool (Figure 10, p. 60). By visual inspection, the shape did not differ (Figure 10, A and B2, p. 60). But, as expected, the off-target ratio was higher in the MIPseq data of the rebalanced MIPs pool (on average per individual 21.26% vs 17.43%, *p* = 3.752E-06, two sided t-test). To compare the performance of the two MIPs pools in more detail, the effect of the two distinct sequencer machine runs were removed. Therefore, the MIPs' targets' coverages were corrected to remove differences in the general sequencer output amount of the two machine runs. Then the MIPs' targets were counted that exceeded 10X coverage (as the lowest threshold for variant calling) and summed for all individuals. As a result, the rebalanced MIPs pool led to a slightly better performance compared to the balanced MIPs pool (412,750 targets vs 409,163 targets and 8,973 targets/person vs 8,895 targets/person, respectively). The odds were calculated of the MIPs' targets that were suitable and not suitable for the calling of genetic variants, respectively, and they were lower for the rebalanced MIPs pool compared to the balanced MIPs pool (4.00 vs 4.47, respectively). To sum up, the rebalanced MIPs pool enabled the acquisition of more data of interest with the same sequencer setup and it was selected for further experiments.

Figure 8: Exemplary bar plots of MIPs' reads distributed over hg19 decoy reference genome: A) MIP with many off-target reads and B) normal MIP. (The MIPs' names are indicated in grey.)

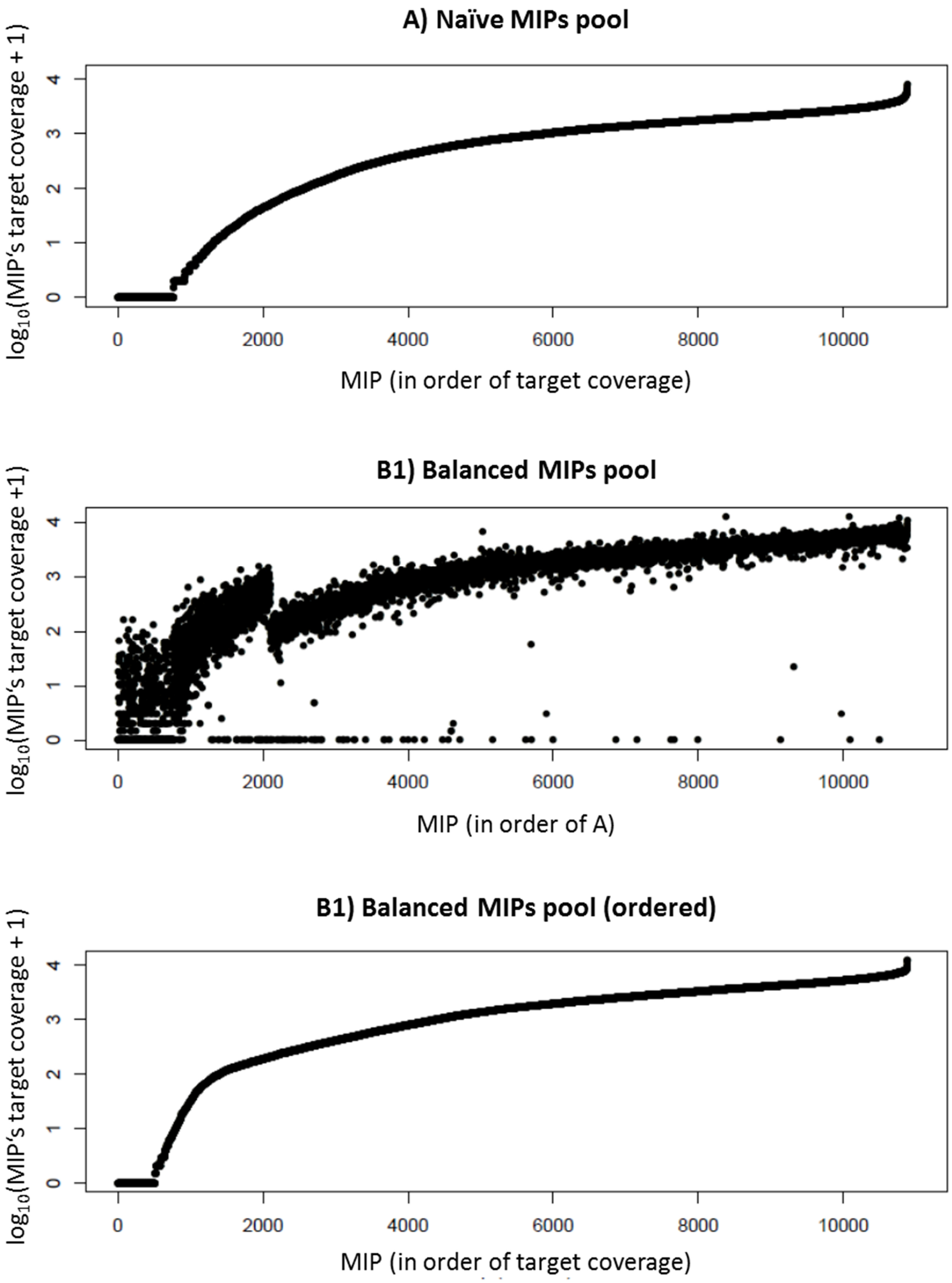


Figure 9: Total coverage distribution of MIPs' targets after balancing: Shown are the $\log_{10}$ of the minimum base coverages of the MIPs' targets, summed over all sequenced individuals. A) Naïve MIPs pool, B1) MIPs pool after balancing in order of A), B2) MIPs pool after balancing (reordered)

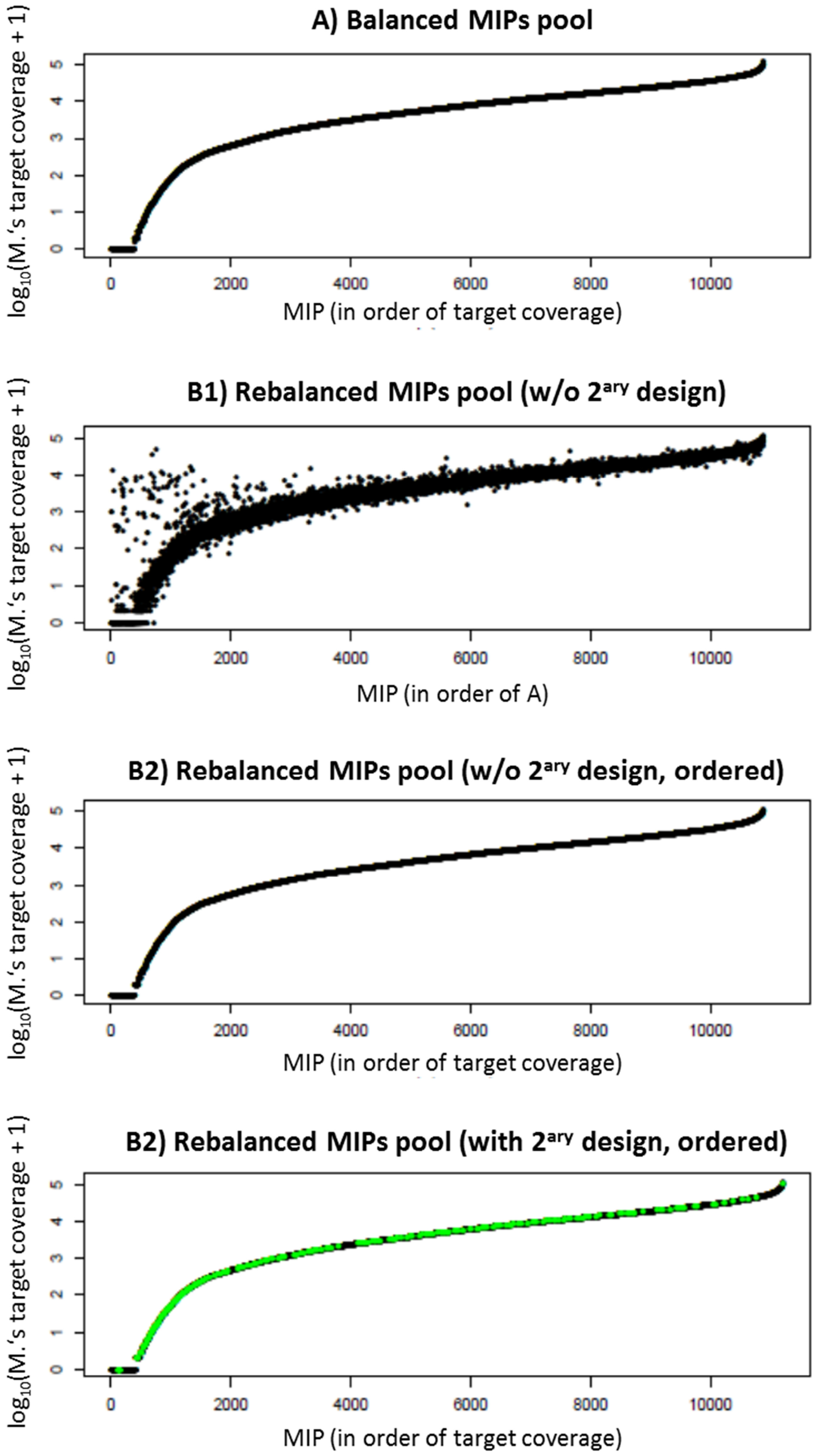


Figure 10: Total coverage distribution of MIPs' targets after rebalancing: Shown are the log$_{10}$ of the minimum base coverages of the MIPs' targets, summed over all sequenced individuals. A) balanced MIPs pool, B1) rebalanced MIPs pool (without MIPs' targets from the 2^{ary} design, in order of A), B2) as B1 (reordered), B3) as B2 (with MIPs' targets from the 2^{ary} design in green).

4.2.4 MIPseq of a Case-Control Cohort Using the Rebalanced MIPs Pool

4.2.4.1 Power Analysis

The median analytic power was calculated for comparing differences in cumulative MAF [411] between 750 RLS cases and 750 controls under a variety of scenarios (100 replicates, results in Table 22, p. 62). No power estimates were obtained for 2 of 84 genes (*CASC16* and *LAMA1*, which were not part of the population model used for the power analysis). Eight genes showed a power greater 80% in at least one scenario: *TANC1*, *SETBP1*, *COL6A6*, *PTPRM*, *MYT1*, *ASTN2*, *EYA2*, and *PLXNA2*. The power would be substantially higher with 5,000 cases and 5,000 controls, and 57 genes showed a power greater 80% in at least one scenario. Of those, 7 genes showed a power of at least 80% in all scenarios. Table 23 (p. 65) shows the respective results of this power analysis.

4.2.4.2 Capacity Estimation for HiSeq 4000 Sequencers

The optimal HiSeq 4000 setup was determined based on a simulated 372-plex MIPseq library (Figure 11). The optimum number of lanes was heuristically determined to be 6; a plateau was reached for the average number of targets exceeding a minimal coverage threshold suitable for calling variants.

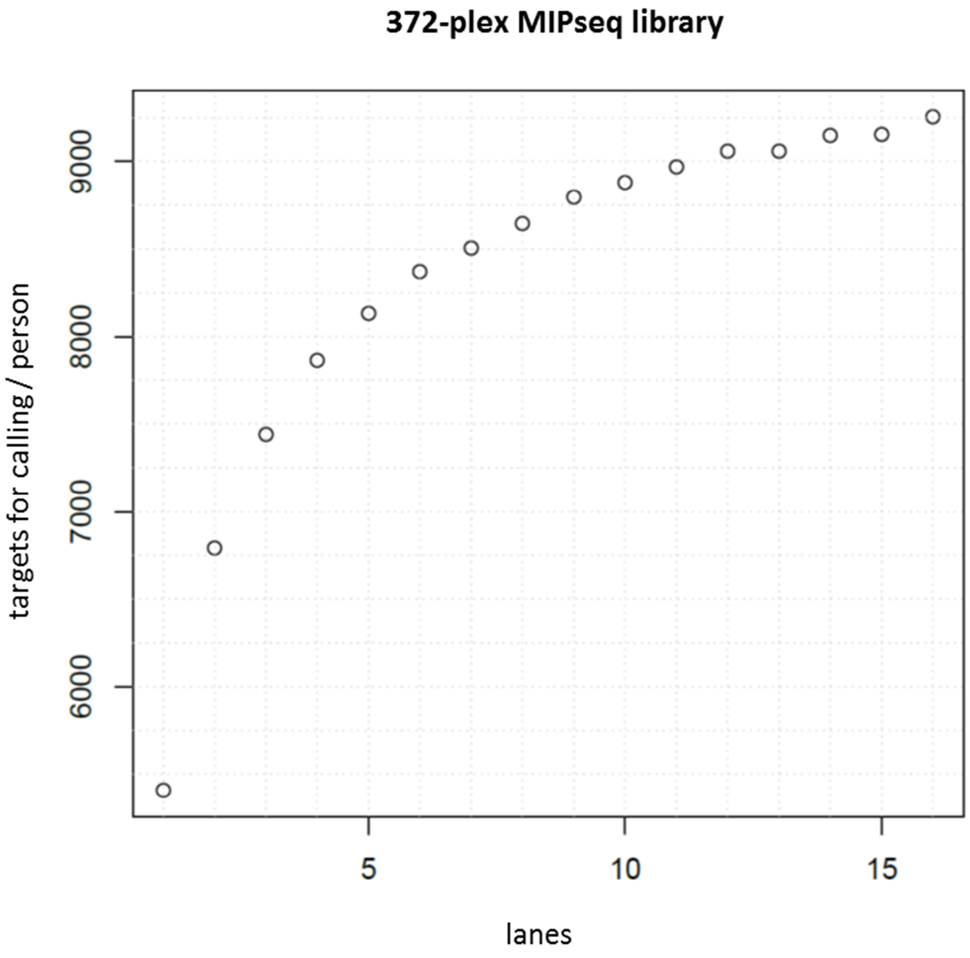


Figure 11: Average number of MIPseq targets per person with a coverage suitable for variant calling as a function of HiSeq 4000 lanes: A 372-plex MIPseq library was simulated to have been sequenced on an increasing number of HiSeq 4000 lanes, which was based on the MIPseq output of the HiSeq 2500 rebalancing run (sample size 46).

Table 22: Power analysis for gene-level tests of 82 genes and sample size 1,500: The median power is shown from 100 replicates (of gene models). CASC16 and LAMA1 were not included in the power analysis. The genes were ordered according to power over all scenarios. Green = genes with median power ≥ 0.8, OR = upper bound for OR of detrimental variants, causal = proportion of RLS causing variants in detrimental variants, α = type I error rate (for 100 and 20,000 independent null hypotheses, respectively).

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α = 2.5E-06		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**	
	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**
TANC1	0.62	0.29	0.97	0.50	0.95	0.81	1.00	0.99	0.75	0.04	0.49	0.33	0.98	0.54	1.00	0.77
SETBP1	0.30	0.02	0.85	0.19	0.93	0.26	0.98	0.77	0.25	0.10	0.86	0.23	0.80	0.28	0.99	0.77
COL6A6	0.03	0.09	0.33	0.20	0.78	0.08	0.98	0.71	0.10	0.02	0.69	0.09	0.74	0.66	0.93	0.47
PTPRM	0.05	0.01	0.32	0.27	0.68	0.29	0.96	0.44	0.27	0.03	0.41	0.15	0.40	0.08	0.85	0.35
MYT1	0.22	0.01	0.49	0.19	0.40	0.09	0.91	0.36	0.07	0.00	0.31	0.10	0.46	0.07	0.87	0.40
ASTN2	0.19	0.00	0.51	0.08	0.36	0.08	0.77	0.45	0.05	0.01	0.50	0.19	0.53	0.06	0.80	0.31
EYA2	0.07	0.01	0.75	0.14	0.43	0.04	0.77	0.29	0.11	0.01	0.15	0.28	0.39	0.04	0.66	0.22
PLXNA2	0.01	0.00	0.58	0.18	0.47	0.08	0.81	0.43	0.00	0.00	0.14	0.08	0.27	0.02	0.78	0.25
COL20A1	0.03	0.01	0.49	0.11	0.24	0.03	0.77	0.30	0.02	0.01	0.22	0.09	0.21	0.03	0.52	0.25
MDGA1	0.13	0.00	0.41	0.04	0.23	0.04	0.62	0.22	0.02	0.00	0.23	0.02	0.16	0.02	0.38	0.12
IQCH	0.01	0.00	0.17	0.08	0.18	0.04	0.65	0.11	0.02	0.00	0.12	0.05	0.14	0.01	0.64	0.21
TOX3	0.00	0.00	0.21	0.05	0.10	0.02	0.52	0.15	0.06	0.00	0.25	0.35	0.22	0.04	0.22	0.20
RIMS2	0.05	0.00	0.10	0.08	0.11	0.03	0.60	0.27	0.00	0.00	0.07	0.09	0.08	0.01	0.52	0.21
CORO6	0.00	0.01	0.15	0.15	0.04	0.02	0.67	0.26	0.00	0.00	0.12	0.02	0.13	0.02	0.52	0.05
ADAM22	0.01	0.02	0.12	0.05	0.12	0.02	0.39	0.26	0.03	0.00	0.12	0.05	0.15	0.03	0.58	0.18
OLFML2B	0.01	0.00	0.25	0.07	0.07	0.02	0.49	0.17	0.00	0.00	0.13	0.04	0.07	0.01	0.41	0.18
VAV3	0.03	0.00	0.34	0.02	0.04	0.02	0.51	0.16	0.01	0.00	0.05	0.03	0.06	0.00	0.39	0.11
GRIN2B	0.01	0.01	0.09	0.05	0.10	0.02	0.49	0.20	0.01	0.00	0.14	0.03	0.10	0.01	0.34	0.11
FAM171A1	0.00	0.00	0.27	0.08	0.06	0.01	0.33	0.12	0.01	0.00	0.01	0.06	0.21	0.00	0.21	0.08
CNTN4	0.03	0.00	0.01	0.07	0.07	0.00	0.38	0.09	0.00	0.00	0.19	0.05	0.05	0.02	0.21	0.10
ZNF804B	0.00	0.00	0.04	0.03	0.04	0.00	0.31	0.06	0.00	0.00	0.03	0.01	0.03	0.00	0.49	0.19
ZNF175	0.00	0.00	0.03	0.03	0.03	0.00	0.29	0.13	0.00	0.00	0.08	0.03	0.02	0.00	0.26	0.08
PTPRD	0.01	0.00	0.05	0.03	0.04	0.01	0.36	0.07	0.00	0.00	0.04	0.01	0.04	0.00	0.25	0.06
PIK3R4	0.01	0.00	0.05	0.01	0.02	0.00	0.41	0.20	0.00	0.00	0.03	0.03	0.01	0.00	0.11	0.09
PCDHB5	0.01	0.00	0.06	0.06	0.02	0.00	0.26	0.09	0.01	0.00	0.04	0.01	0.01	0.01	0.22	0.07
GALNT12	0.00	0.00	0.06	0.02	0.05	0.00	0.20	0.08	0.00	0.00	0.03	0.02	0.02	0.00	0.34	0.04
NRG3	0.00	0.00	0.09	0.00	0.01	0.00	0.14	0.41	0.00	0.00	0.00	0.01	0.01	0.00	0.09	0.03
ATP2C1	0.01	0.00	0.08	0.03	0.04	0.00	0.15	0.07	0.00	0.00	0.08	0.01	0.02	0.00	0.19	0.05

continued table…

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α **= 2.5E-06**		***α*** **= 5E-04**		***α*** **= 2.5E-06**		***α*** **= 5E-04**		***α*** **= 2.5E-06**		***α*** **= 5E-04**		***α*** **= 2.5E-06**		***α*** **= 5E-04**	
	OR **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**	***OR*** **= 4**	***OR*** **= 3**
DCLK2	0.00	0.00	0.10	0.03	0.03	0.00	0.23	0.05	0.00	0.00	0.14	0.02	0.02	0.00	0.06	0.07
SKOR1	0.00	0.00	0.06	0.03	0.03	0.00	0.21	0.07	0.00	0.00	0.06	0.01	0.01	0.00	0.19	0.05
DMPK	0.00	0.00	0.01	0.00	0.02	0.00	0.13	0.09	0.00	0.00	0.04	0.02	0.07	0.00	0.27	0.03
SLC14A2	0.00	0.00	0.04	0.02	0.02	0.00	0.20	0.05	0.00	0.00	0.07	0.02	0.00	0.00	0.15	0.10
LEO1	0.01	0.00	0.07	0.02	0.01	0.00	0.13	0.06	0.00	0.00	0.04	0.01	0.01	0.00	0.16	0.04
FAM114A1	0.00	0.00	0.03	0.02	0.01	0.00	0.13	0.05	0.00	0.00	0.09	0.00	0.01	0.00	0.15	0.03
CCDC148	0.00	0.00	0.09	0.01	0.00	0.00	0.15	0.02	0.00	0.00	0.07	0.01	0.00	0.00	0.09	0.04
SUN1	0.00	0.00	0.05	0.01	0.00	0.00	0.17	0.05	0.00	0.00	0.06	0.01	0.01	0.00	0.09	0.03
MAP2K5	0.00	0.00	0.14	0.00	0.00	0.00	0.04	0.05	0.00	0.00	0.08	0.00	0.01	0.00	0.13	0.03
ALLC	0.00	0.00	0.04	0.00	0.01	0.00	0.26	0.04	0.00	0.00	0.01	0.01	0.01	0.00	0.02	0.03
RASGRP4	0.00	0.00	0.03	0.02	0.01	0.00	0.11	0.04	0.00	0.00	0.04	0.01	0.01	0.00	0.10	0.04
PIAS1	0.00	0.00	0.01	0.00	0.01	0.00	0.12	0.03	0.00	0.00	0.06	0.03	0.00	0.00	0.10	0.03
PDE11A	0.00	0.00	0.08	0.01	0.01	0.00	0.09	0.06	0.00	0.00	0.02	0.01	0.00	0.00	0.07	0.02
EBF3	0.00	0.00	0.01	0.02	0.00	0.00	0.10	0.03	0.00	0.00	0.02	0.01	0.00	0.00	0.07	0.02
BBS7	0.00	0.00	0.03	0.01	0.00	0.00	0.08	0.03	0.00	0.00	0.01	0.01	0.00	0.00	0.07	0.02
SEMA6D	0.00	0.00	0.01	0.01	0.00	0.00	0.11	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.07	0.02
NTNG1	0.00	0.00	0.01	0.00	0.03	0.00	0.07	0.01	0.00	0.00	0.03	0.01	0.01	0.00	0.03	0.02
PKP4	0.00	0.00	0.03	0.01	0.00	0.00	0.07	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.04	0.01
ARFRP1	0.00	0.00	0.04	0.00	0.00	0.00	0.05	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.04	0.01
CACNG8	0.00	0.00	0.02	0.01	0.00	0.00	0.07	0.02	0.00	0.00	0.01	0.02	0.00	0.00	0.02	0.01
NECAP1	0.00	0.00	0.06	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02
UNCX	0.00	0.00	0.02	0.01	0.00	0.00	0.04	0.02	0.00	0.00	0.01	0.01	0.00	0.00	0.04	0.02
KCNK13	0.00	0.00	0.06	0.00	0.00	0.00	0.04	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.04	0.01
SLC39A11	0.00	0.00	0.01	0.01	0.00	0.00	0.06	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.04	0.01
CREB5	0.00	0.00	0.01	0.00	0.00	0.00	0.08	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.02
SYT5	0.00	0.00	0.02	0.00	0.00	0.00	0.04	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.04	0.01
SGCZ	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.01
BTBD9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00
OSBP	0.00	0.00	0.01	0.00	0.00	0.00	0.06	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01

continued table…

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α = 2.5E-06		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**	
	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**
MEIS1	0.00	0.00	0.02	0.01	0.00	0.00	0.04	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
NPBWR2	0.00	0.00	0.01	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.01
CRBN	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.01
AAGAB	0.00	0.00	0.01	0.00	0.00	0.00	0.06	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
KCNA4	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.04	0.01	0.00	0.00	0.01	0.01
MICALL2	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.01
TUBB3	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
MPPED2	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
STEAP4	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
NRSN2	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
C7orf62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
COLEC11	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
TREM1	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
MEIS2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
FTSJ2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CALML4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
UBL4B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
C15orf61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OSGIN1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NENF	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LRRN1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CADM1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OPRL1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GLO1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
KRTAP19-5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 23: Power analysis for gene-level tests of 82 genes and sample size 10,000 : The median power is shown from 100 replicates (of gene models). CASC16 and LAMA1 were not included in the power analysis. The genes were ordered according to power over all scenarios. Green = genes with median power ≥ 0.8, OR = upper bound for OR of detrimental variants, causal = proportion of RLS causing variants in detrimental variants, α = type I error rate (for 100 and 20,000 independent null hypotheses, respectively).

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α = 2.5E-06		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**	
	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**
TANC1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
SETBP1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00	1.00	1.00	1.00
COL6A6	1.00	0.92	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96	1.00	1.00	1.00	1.00	1.00	1.00
PTPRM	1.00	0.91	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96	1.00	1.00	1.00	1.00	1.00	1.00
MYT1	1.00	0.86	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96	1.00	0.99	1.00	1.00	1.00	1.00
COL20A1	0.99	0.81	1.00	0.99	1.00	1.00	1.00	1.00	0.95	0.82	1.00	0.99	1.00	1.00	1.00	1.00
ADAM22	1.00	0.87	1.00	0.96	1.00	0.99	1.00	1.00	1.00	0.93	0.87	0.92	1.00	0.99	1.00	1.00
MDGA1	1.00	0.81	1.00	1.00	1.00	0.99	1.00	1.00	1.00	0.42	0.99	0.98	1.00	0.97	1.00	1.00
EYA2	1.00	1.00	1.00	0.98	1.00	1.00	1.00	1.00	1.00	0.26	0.99	0.91	1.00	1.00	1.00	1.00
TOX3	1.00	0.97	1.00	0.95	1.00	1.00	1.00	1.00	0.90	0.84	1.00	0.44	1.00	0.99	1.00	1.00
ASTN2	1.00	0.90	1.00	0.46	1.00	1.00	1.00	1.00	0.93	0.70	1.00	0.99	1.00	1.00	1.00	1.00
IQCH	1.00	0.52	1.00	0.98	1.00	1.00	1.00	1.00	0.97	0.61	0.98	0.78	1.00	0.96	1.00	1.00
PLXNA2	1.00	0.32	1.00	0.98	1.00	1.00	1.00	1.00	0.98	0.46	1.00	1.00	1.00	1.00	1.00	1.00
GRIN2B	0.84	0.63	1.00	0.94	1.00	0.95	1.00	1.00	0.99	0.23	0.99	0.96	1.00	0.88	1.00	0.99
OLFML2B	0.35	0.74	1.00	0.99	1.00	0.99	1.00	1.00	0.96	0.70	0.86	0.86	1.00	0.75	1.00	1.00
VAV3	0.99	0.74	1.00	0.64	1.00	0.85	1.00	1.00	0.96	0.34	1.00	0.71	1.00	0.88	1.00	1.00
RIMS2	0.89	0.29	1.00	0.99	1.00	0.99	1.00	1.00	0.45	0.13	1.00	0.99	1.00	0.98	1.00	1.00
DCLK2	0.54	0.32	0.90	0.86	1.00	0.80	1.00	0.97	0.68	0.05	1.00	0.85	0.99	0.72	1.00	0.97
PCDHB5	0.61	0.17	1.00	0.94	0.98	0.80	1.00	1.00	0.99	0.01	1.00	0.37	0.99	0.75	1.00	0.97
GALNT12	0.54	0.03	0.99	0.48	0.99	0.77	1.00	0.96	0.94	0.29	0.99	0.58	1.00	0.76	1.00	0.94
ZNF175	0.47	0.43	0.99	0.86	0.92	0.78	1.00	0.99	0.83	0.43	0.84	0.06	0.91	0.36	1.00	0.97
CORO6	0.00	0.39	1.00	0.85	1.00	0.99	1.00	1.00	0.00	0.11	0.85	1.00	1.00	0.66	1.00	0.94
ATP2C1	0.59	0.18	0.98	0.64	0.99	0.77	1.00	0.98	0.63	0.22	0.89	0.58	0.91	0.56	1.00	0.88
PTPRD	0.63	0.16	0.99	0.27	1.00	0.74	1.00	0.90	0.66	0.13	0.86	0.70	0.99	0.78	1.00	0.94
SLC14A2	0.39	0.19	0.98	0.45	0.98	0.47	1.00	0.94	0.65	0.28	0.98	0.61	0.95	0.93	1.00	0.87
ZNF804B	0.75	0.54	0.99	0.17	1.00	0.63	1.00	0.87	0.50	0.08	0.75	0.70	1.00	0.70	1.00	0.92
DMPK	0.26	0.02	0.91	0.73	1.00	0.76	1.00	0.98	0.81	0.16	0.93	0.36	0.67	0.76	1.00	0.96
FAM171A1	0.99	0.57	0.78	0.12	1.00	0.72	1.00	0.99	0.03	0.29	1.00	0.07	1.00	0.68	1.00	0.96

continued table…

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α = 2.5E-06		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**	
	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**
PIK3R4	0.99	0.07	0.94	0.65	1.00	0.70	1.00	0.87	0.47	0.05	0.83	0.34	0.75	0.41	1.00	0.95
LEO1	0.56	0.04	0.99	0.53	0.97	0.64	1.00	0.85	0.44	0.10	0.84	0.57	0.95	0.53	1.00	0.89
SKOR1	0.53	0.01	0.99	0.71	0.99	0.51	1.00	0.96	0.14	0.09	0.95	0.68	0.75	0.54	0.99	0.90
CNTN4	0.22	0.04	0.67	0.95	1.00	0.89	1.00	0.99	0.04	0.00	0.24	0.09	1.00	0.84	1.00	0.97
SUN1	0.46	0.27	0.98	0.67	0.95	0.30	0.99	0.83	0.30	0.13	0.85	0.16	0.71	0.40	0.99	0.76
FAM114A1	0.05	0.26	0.97	0.48	0.95	0.34	1.00	0.88	0.63	0.13	0.95	0.03	0.84	0.44	1.00	0.81
CCDC148	0.85	0.02	0.95	0.72	0.99	0.20	1.00	0.80	0.01	0.00	0.72	0.52	0.89	0.18	0.68	0.76
RASGRP4	0.31	0.07	0.83	0.43	0.91	0.30	0.98	0.80	0.47	0.10	0.58	0.42	0.77	0.36	0.97	0.75
NRG3	0.72	0.12	0.95	0.02	0.88	0.30	1.00	0.80	0.06	0.12	0.97	0.05	0.79	0.23	1.00	0.82
SEMA6D	0.53	0.01	0.92	0.47	0.86	0.18	0.98	0.96	0.01	0.00	0.74	0.29	0.34	0.13	0.94	0.84
PDE11A	0.41	0.03	0.82	0.19	0.82	0.31	0.97	0.61	0.04	0.00	0.60	0.26	0.69	0.59	0.92	0.53
ALLC	0.00	0.05	0.34	0.44	0.84	0.30	0.98	0.74	0.04	0.05	0.71	0.25	0.81	0.65	0.99	0.47
EBF3	0.24	0.03	0.65	0.39	0.73	0.35	0.98	0.59	0.14	0.04	0.66	0.10	0.71	0.20	0.91	0.83
PKP4	0.11	0.05	0.60	0.76	0.56	0.95	0.94	0.56	0.12	0.03	0.50	0.19	0.48	0.14	1.00	0.44
BBS7	0.23	0.05	0.48	0.25	0.71	0.19	0.98	0.73	0.27	0.03	0.68	0.25	0.68	0.12	0.95	0.72
MAP2K5	0.04	0.00	0.02	0.52	0.96	0.57	1.00	1.00	0.00	0.00	0.01	0.01	0.86	0.30	1.00	0.87
NECAP1	0.22	0.05	0.97	0.03	0.46	0.50	0.92	0.65	0.12	0.04	0.06	0.57	0.63	0.15	1.00	0.60
PIAS1	0.00	0.07	0.97	0.02	0.87	0.22	0.97	0.80	0.00	0.13	0.13	0.02	0.73	0.24	0.98	0.71
MICALL2	0.04	0.01	0.56	0.01	0.33	0.90	0.82	0.17	0.02	0.01	0.33	0.04	1.00	0.92	0.60	0.98
CACNG8	0.00	0.11	0.49	0.07	0.65	0.02	0.94	0.62	0.00	0.08	0.87	0.03	0.67	0.15	0.90	0.55
CREB5	0.01	0.06	0.25	0.43	0.79	0.06	0.96	0.70	0.31	0.05	0.07	0.04	0.48	0.18	0.94	0.58
KCNK13	0.00	0.07	0.81	0.03	0.86	0.09	0.84	0.82	0.31	0.03	0.37	0.03	0.40	0.05	0.83	0.34
UNCX	0.13	0.04	0.51	0.28	0.56	0.14	0.89	0.50	0.11	0.01	0.42	0.13	0.28	0.07	0.86	0.43
SLC39A11	0.21	0.02	0.53	0.09	0.53	0.10	0.84	0.46	0.09	0.01	0.44	0.25	0.38	0.05	0.84	0.37
NTNG1	0.29	0.00	0.24	0.16	0.67	0.12	0.97	0.43	0.05	0.01	0.12	0.11	0.55	0.02	0.76	0.43
ARFRP1	0.00	0.00	0.87	0.08	0.48	0.00	0.88	0.45	0.34	0.00	0.00	0.00	0.37	0.06	0.82	0.35
SYT5	0.12	0.00	0.63	0.16	0.33	0.11	0.69	0.43	0.09	0.01	0.26	0.09	0.23	0.06	0.73	0.42
SGCZ	0.01	0.00	0.75	0.01	0.76	0.06	0.81	0.36	0.00	0.01	0.03	0.00	0.32	0.03	0.74	0.14
NPBWR2	0.01	0.01	0.51	0.12	0.30	0.05	0.68	0.27	0.03	0.02	0.40	0.01	0.29	0.03	0.64	0.36

continued table…

Gene	**Prevalence = 5%**								**Prevalence = 10%**							
	75% causal				**100% causal**				**75% causal**				**100% causal**			
	α = 2.5E-06		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**		**α = 2.5E-06**		**α = 5E-04**	
	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**	***OR* = 4**	***OR* = 3**
OSBP	0.05	0.05	0.26	0.18	0.36	0.03	0.38	0.65	0.21	0.00	0.01	0.16	0.31	0.00	0.68	0.22
CRBN	0.04	0.00	0.33	0.04	0.26	0.04	0.76	0.27	0.04	0.01	0.11	0.04	0.21	0.02	0.52	0.25
MEIS1	0.03	0.00	0.16	0.03	0.22	0.04	0.68	0.22	0.04	0.00	0.35	0.11	0.06	0.02	0.63	0.25
MPPED2	0.04	0.01	0.57	0.07	0.10	0.01	0.69	0.26	0.00	0.00	0.04	0.02	0.06	0.01	0.58	0.17
KCNA4	0.03	0.00	0.07	0.38	0.08	0.01	0.44	0.11	0.27	0.00	0.67	0.03	0.04	0.01	0.14	0.03
TUBB3	0.01	0.00	0.14	0.11	0.11	0.02	0.44	0.18	0.01	0.00	0.11	0.16	0.07	0.03	0.39	0.13
AAGAB	0.02	0.00	0.55	0.02	0.12	0.02	0.36	0.11	0.00	0.00	0.08	0.01	0.06	0.01	0.33	0.17
STEAP4	0.02	0.00	0.20	0.05	0.06	0.01	0.45	0.15	0.02	0.00	0.09	0.06	0.04	0.01	0.34	0.14
MEIS2	0.00	0.00	0.01	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.51	0.00	0.00	0.10	0.87	0.01
BTBD9	0.75	0.00	0.06	0.01	0.03	0.00	0.25	0.07	0.00	0.00	0.03	0.01	0.02	0.00	0.21	0.06
FTSJ2	0.00	0.02	0.05	0.01	0.00	0.10	0.03	0.03	0.14	0.00	0.00	0.00	0.00	0.00	0.95	0.01
NRSN2	0.01	0.00	0.05	0.01	0.03	0.00	0.22	0.05	0.01	0.00	0.04	0.04	0.01	0.00	0.19	0.06
COLEC11	0.00	0.00	0.09	0.02	0.02	0.00	0.19	0.07	0.00	0.00	0.03	0.01	0.01	0.00	0.18	0.06
OPRL1	0.04	0.00	0.00	0.00	0.00	0.00	0.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
TREM1	0.01	0.00	0.08	0.03	0.01	0.00	0.16	0.06	0.00	0.00	0.02	0.01	0.01	0.00	0.15	0.05
C7orf62	0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.28	0.00	0.00	0.00	0.03	0.23
CALML4	0.00	0.00	0.01	0.00	0.00	0.00	0.06	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.34	0.01
C15orf61	0.00	0.00	0.01	0.01	0.00	0.00	0.05	0.02	0.00	0.00	0.03	0.00	0.00	0.00	0.05	0.01
UBL4B	0.00	0.00	0.01	0.01	0.00	0.00	0.05	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.03	0.01
OSGIN1	0.03	0.00	0.03	0.00	0.00	0.00	0.04	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.01
LRRN1	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.04	0.00
NENF	0.00	0.00	0.01	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
GLO1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
CADM1	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
KRTAP19-5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

4.2.4.3 Analysis of MIPseq Data from the Case-Control Cohort

4.2.4.3.1 Technical Quality Control

First, the total output of demultiplexed reads significantly differed between the multiplex MIPseq libraries (p < 2.2E-16, χ^2 test) with a maximum difference of 147,133,922 reads (4,529,164,503 reads in library #782 (= NGS pipeline ID) vs 4,676,298,425 reads in library #776). Thus, the sequencing log files were reviewed and showed technical issues in 2 of 6 lanes for library #782. But, in a more differentiated analysis, the individuals' number of total reads did not differ between MIPseq libraries (ANOVA, p = 0.7148), which indicated a higher variance within MIPseq libraries than between MIPseq libraries.

The precalled variants were obtained from the Helmholtz Zentrum München NGS pipeline (coverage threshold ≥ 10X) and were filtered at a threshold of 25X and pruned to biallelic SNVs, resulting in 44,089 SNVs for 1,474 individuals.

Table 24 (p. 69) summarizes the results of the pairwise comparison of individual quality parameters and the case-control status. The case-control status was significantly associated with genotype missingness (p = 2.3E-15), $RMPC_{25}$ and $RMPC_{75}$ (p = 7.1E-23 and 8.3E-04), and on-target ratio of the reads (p = 1.9E-18), but the status was not associated with any parameter reflecting the total number of reads (e.g. p = 0.51 for association with total number of reads). However, the case-control status explained a very small proportion of the variances of these significantly associated quality measurements. The highest measures of R^2 were 6.09% (status vs proportion of missing genotypes), 7.57% (status vs on-target ratio) and 10.13% (status vs $RMPC_{25}$). Of note, the case-control status was the worst predictor of genotype missingness. Much better predictors were the number of on-target reads (R^2 = 54.80%, p = 3.8E-231) and the $RMPC_{25}$ (R^2 = 67.70%, p = 6.4E-244).

Some comparisons were validated using alternative methods with mainly positive results: First, the upper/lower quartiles from the individual relative MIPs' performance curves ($RMPC_{25}$ and $RMPC_{75}$) were compared between cases and controls and a difference could be detected (χ^2 test on lower quartiles $RMPC_{25}$: p = 8.5E-23, on upper quartiles $RMPC_{75}$: p = 1.3E-03, Figure 12, p. 70), which validated the observation of a different shape of the RMPC in cases and controls. Second, as the samples of a multiplex library were processed in two case and two control plates, the on-target reads of each multiplex-library were binned according to originating from a case or control plate. The counts in those bins were divided by the total number of on-target reads of their respective multiplex library as a measurement of contribution to the respective multiplex library. The means of these contributions were compared between the case and control bins. No differences could be observed (paired t-test, p = 0.64). Third, the individuals' proportions of on-target reads were determined with respect to the individuals' total number of reads. They differed between cases and controls in the variance (cases: 0.0041, controls: 0.0047, p = 0.001) and the mean (cases: 0.71, controls: 0.68, p < 2.2E-16).

Median and mean MIPs' target coverages were obtained per person (for MIPs that worked at least once in cases or controls: 10,940 of 11,214 MIPs). The averages of the medians were 238X (cases) and 220X (controls) and averages of the means were 393X (cases) and 383X (controls) (Figure 13, p. 70).

Figure 14 (p. 71) shows the quantiles of MIPs' read counts for cases, controls and combined cases and controls: The controls seemed to have lower MIPs' on-target read counts compared to cases. In contrast, however, the variance was substantial within the groups of cases or controls.

Median pairwise concordance was 0.997 (minimum: 0.993, maximum: 0.998) for QC-control samples, based on SNVs called at 25X coverage.

*Table 24: Pairwise correlation of the individuals' MIPseq quality measurements and with the case-control status : Results of pairwise R^2 (Spearman's R^2 or Nagelkerke's R^2) are in %. n(reads) = number of reads, n(mapped) = number of mapped reads, n(on target) = number of mapped reads on the MIPseq targets of interest, $RMPC_{25}/RMPC_{75}$ = lower/upper quartile of the individual relative MIPs' performance curve, f = per individual call rate, status = case-control status, * = LRT p value from GLM/LM regression neither nominal significant nor significant after correction for multiple testing of 56 comparisons)*

***n*(reads)**	***n*(mapped)**	***n*(on target)**	***n*(on target)/*n*(reads)**	$RMPC_{25}$	$RMPC_{75}$	***f***	**Status**	
	100	93	1	7	30	50	0*	***n*(reads)**
		94	1	7	30	50	0*	***n*(mapped)**
			10	8	32	55	0*	***n*(on target)**
				3	5	8	8	***n*(on target)/*n*(reads)**
					25	68	10	$RMPC_{25}$
						41	1	$RMPC_{75}$
							6	***f***
								Status

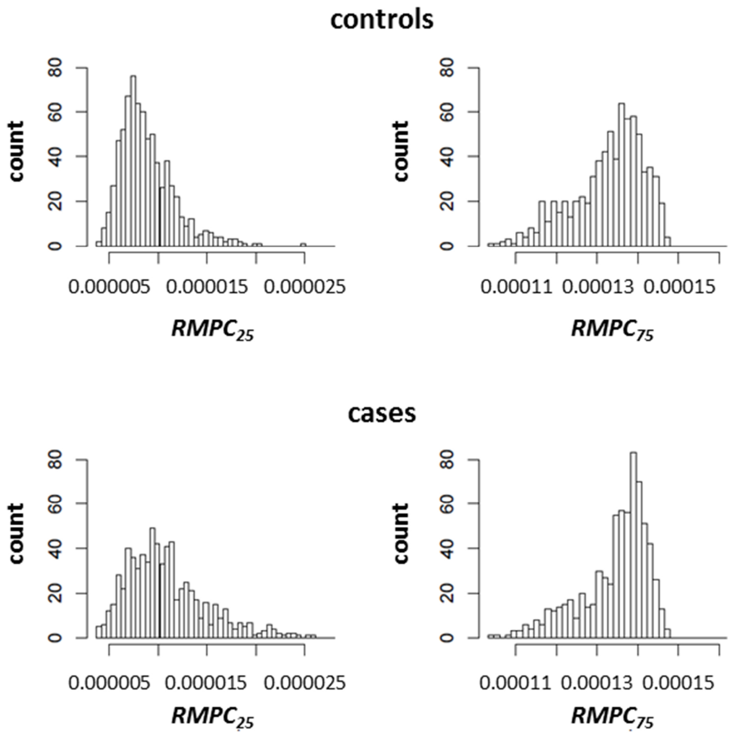


Figure 12: Histograms of the quartiles from the individual relative MIPs' performance curves: $RMPC_{25}$ = lower quartile, $RMPC_{75}$, = upper quartile. The Individual relative MIPs' performance curves were obtained from the on-target read counts.

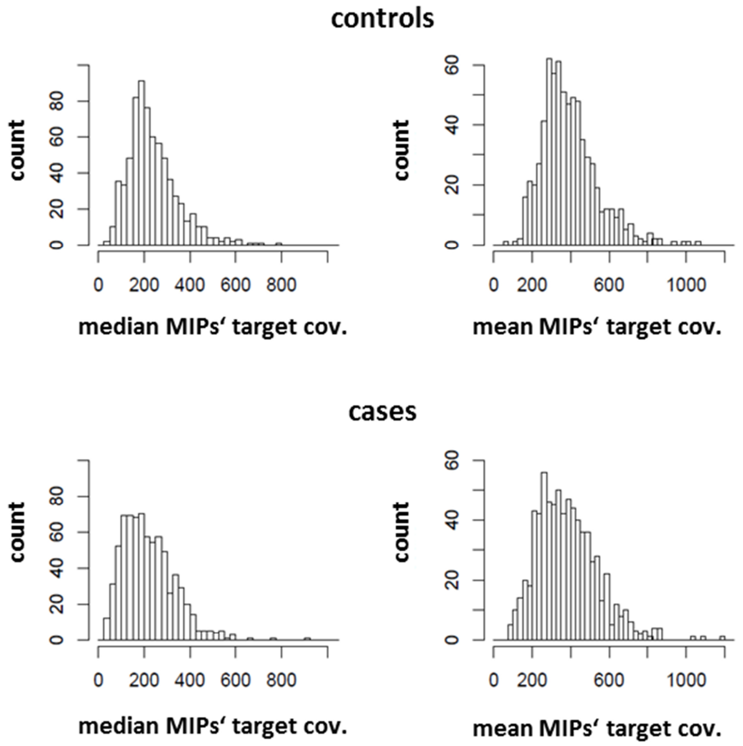


Figure 13: Distributions of the individuals' median and mean MIPs' target coverages: Median and mean were calculated for MIPs that worked at least once in cases or controls.

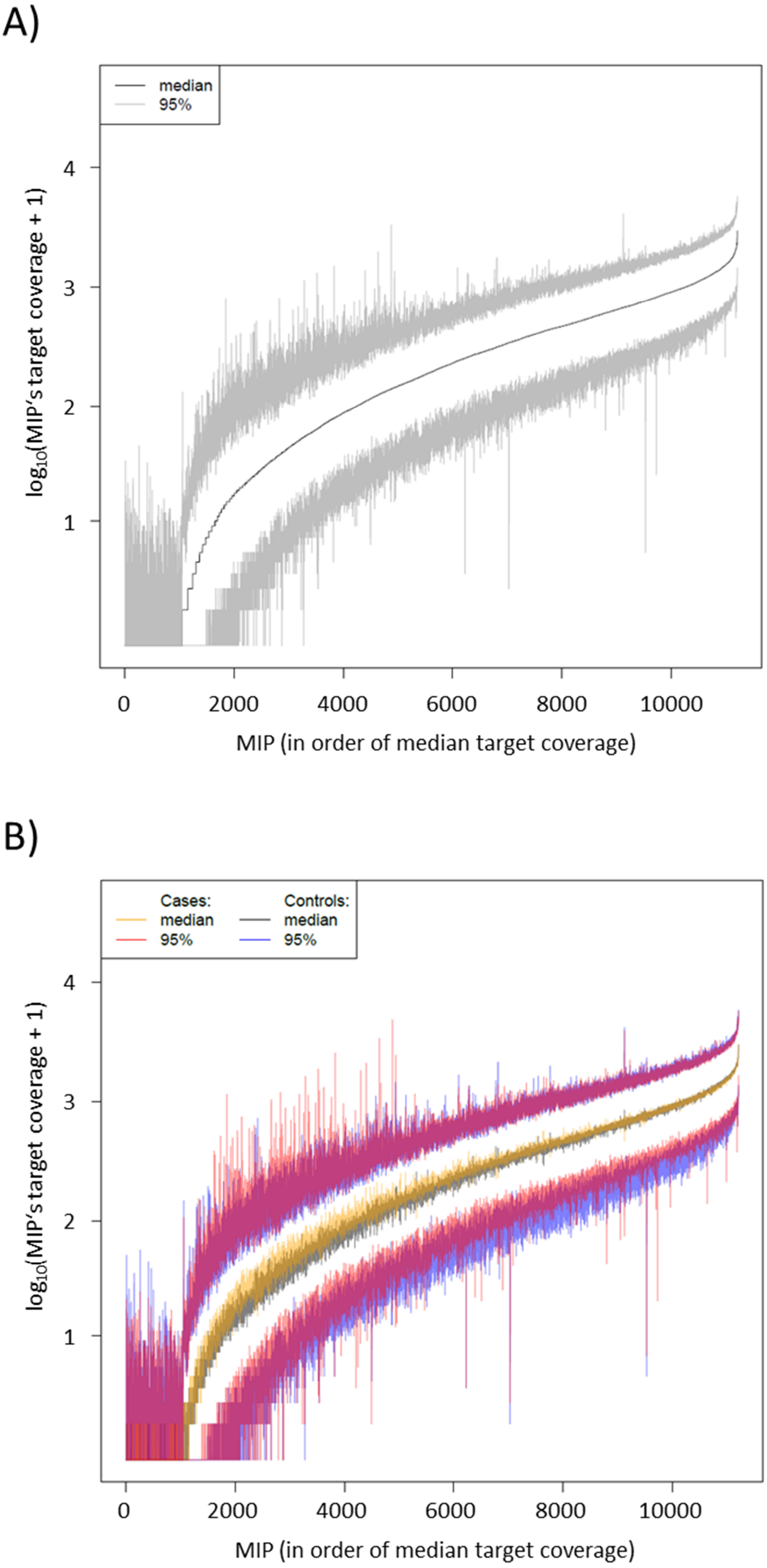


Figure 14: Quantiles of MIPs' target coverages: 2.5%, median and 97.5% quantiles per MIP target were calculated for combined (A)/separated (B) cases and controls and were plotted in increasing order according to the median of (A).

4.2.4.3.2 Quality Control for Association Analysis of MIPseq Data

A QC was done for the MIPseq SNV genotype data: A genotype call rate filter resulted in 35,183 remaining SNV loci (1,387 individuals, 682 cases, 705 controls). A set of 135 SNVs violated the HWE in controls ($p \leq$ 1E-06) and were removed. A total of 26,630 SNV loci had a MAF ≤ 0.05 and were kept for further association analysis.

Genome-wide SNP datasets were prepared to enable correction for population substructure in association analysis. After call-rate and HWE filtering, 448,153 markers (AG Winkelmann dataset), 554,596 markers (KORA [354, 355] F4) and 669,918 markers (KORA [354, 355] F3) were remaining. After merging and pruning for consistent markers, 144,857 markers were remaining (25,094 individuals). After pruning the markers for common autosomal variants in low LD, 62,278 markers were left.

The genotyping chip data and the MIPseq data were pruned to the sample intersection of 1,336 individuals (631 cases, 438 female cases = 69.4%, male cases median/mean/sd age = 64 a/62 a/14 a, female cases 64 a/61 a/13 a, respectively; 705 controls, 352 female controls = 50.0%, male controls median/mean/sd age = 58 a/58 a/13 a, female controls 58 a/58 a/12 a, respectively, details see appendix Figure 18, p. 313).

The genotype concordances were calculated between the sample and marker intersection of the MIPseq data and the ExomeChip data that was used for the gene level association analysis (577 individuals, 286 SNPs). The concordances were 0.9998 (all genotypes), 0.9999 (homozygous reference genotypes), and 0.9941 (non-reference genotypes). Lower non-reference genotype concordances were observed for variants that had MQ < 10.

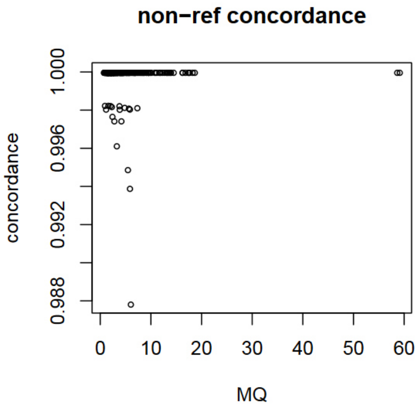


Figure 15: Concordances of MIPseq and ExomeChip SNP genotypes: The non-reference genotype concordances were calculated for each SNP separately and plotted against the root mean square mapping quality of the respective reads (MQ).

Nine individuals (2 cases, 7 controls) were removed due to relatedness (*PI_HAT* ≥ 0.0975 [42, 365]). PCA based filtering removed 60 individuals as population outliers (Figure 16) (1,267 individuals remaining; 601 cases, 417 female cases = 69.4%, male cases median/mean/sd age = 64 a/62 a/14 a, female cases = 63 a/61 a/13 a, respectively; 666 controls, 335 female controls = 50.3%, male controls median/mean/sd age = 58 a/58 a/13 a, female controls 57 a/58 a/12 a, respectively, see appendix Figure 18, p. 313).

4.2.4.3.3 Gene Level Association Analysis with Variants from MIPseq

A SKAT-O [347] analysis was done with 601 cases and 666 controls (515 males and 752 females) and 708 SNVs in 79 genes. Table 25 (p. 75) shows the results. Two genes reached exome-wide significance in the gene level tests: *MYT1* (*p* = 4.84E-07, myelin transcription factor 1 [2], chromosome 20) and *PTPRD* (*p* = 2.14E-06; chromosome 9; protein tyrosine phosphatase, receptor type D [2]). *MYT1* was selected for MIPseq due to an eQTL annotation of an unpublished RLS meta-GWAS [373] signal. Another four genes reached significance after Bonferroni correction for multiple testing of 61 genes: *COL20A1* (*p* = 2.11E-05, chromosome 20, collagen type XX alpha 1 chain [2]), *DMPK* (*p* = 3.40E-05, dystrophia myotonica protein kinase [2], chromosome 19), *RASGRP4* (*p* = 1.99E-04, RAS guanyl releasing protein 4 [2], chromosome 19), and *AAGAB* (*p* = 4.17E-04, chromosome 15, alpha- and gamma-adaptin binding protein [2]). *DMPK* and *RASGRP4* were selected for MIPseq due to ExomeChip association signals, and *COL20A1* and *AAGAB* were selected due to an eQTL and LD-block annotation of the unpublished RLS meta-GWAS [373], respectively.

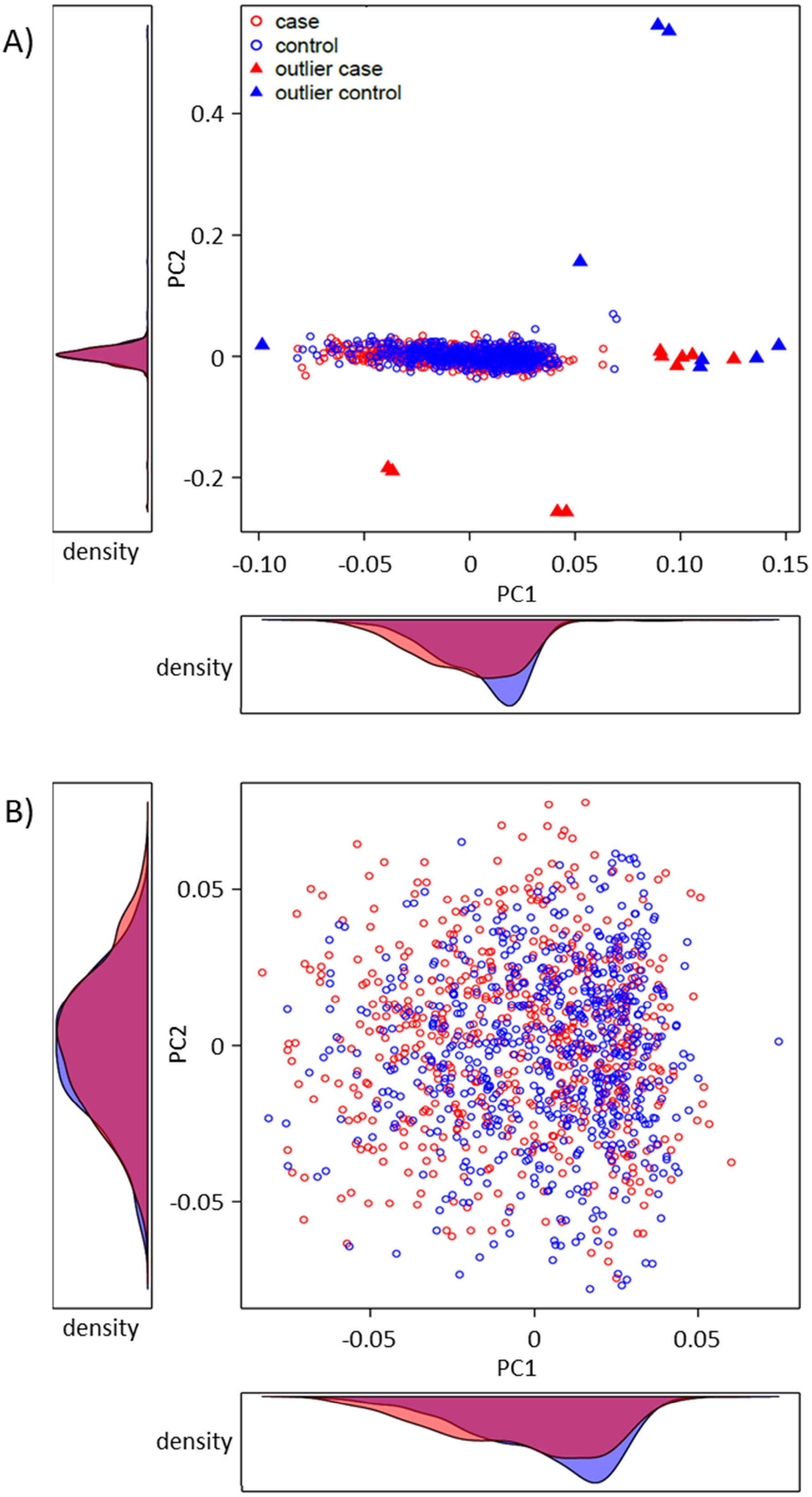


Figure 16: First two principal components of the MIPseq samples based on common SNPs: The plots illustrate the PCs of the sample set before and after removal of related individuals and population outliers (based on deviating ± 3sd from the mean of any of the two principal components PC1 and PC2). Density plots are indicated at the x- and y-axis for cases (red) and controls (blue) (violet = overlap).

continued table…

*Table 25: Results from the gene-level association test with SKAT-O and variants from MIPseq : Asterisks indicate p values below significance thresholds (** ≤ exome-wide significance threshold = 2.50E-06, * p value ≤ threshold for multiple testing of 84 genes = 5.95E-04). p = p value, n_{SNP} = initial number of SNPs, $n_{SNP|tested}$ = number of SNPs used for SKAT-O [92, 93, 347], MAC = total minor allele count, m = number of individuals with minor alleles.*

Gene	***p***	n_{SNP}	$n_{SNP\|tested}$	**MAC**	***m***
MYT1	4.84E-07	11	9	726	509
PTPRD	2.14E-06	8	7	520	415
COL20A1	2.11E-05	15	9	446	386
DMPK	3.40E-05	7	6	260	231
RASGRP4	1.99E-04	9	9	601	341
AAGAB	4.17E-04	7	7	277	256
OSBP	1.66E-03	11	11	532	286
MEIS2	1.81E-03	24	18	941	629
ATP2C1	2.64E-03	11	11	979	512
PTPRM	3.18E-03	18	17	973	632
CCDC148	7.56E-03	5	4	318	298
ADAM22	1.17E-02	12	11	667	372
COLEC11	1.35E-02	5	5	309	229
TUBB3	2.04E-02	9	6	233	214
ZNF804B	2.28E-02	2	2	82	81
OSGIN1	2.95E-02	7	5	322	295
PIK3R4	3.19E-02	3	3	117	112
SEMA6D	3.37E-02	9	8	447	387
ARFRP1	6.67E-02	3	2	40	39
NRG3	7.20E-02	5	4	268	249
CNTN4	7.27E-02	8	8	609	487
COL6A6	8.56E-02	6	6	397	156
FAM171A1	8.58E-02	8	6	306	285
NRSN2	9.33E-02	7	6	378	314
GRIN2B	9.41E-02	41	40	3032	694
KCNA4	1.31E-01	2	2	107	56
BBS7	1.34E-01	4	3	223	214
IQCH	1.36E-01	6	6	339	243
TANC1	1.67E-01	35	34	1823	696
MPPED2	1.72E-01	14	13	777	480
KRTAP19-5	1.92E-01	3	3	146	92
SUN1	2.02E-01	25	20	1289	651
STEAP4	2.23E-01	5	5	179	167
DCLK2	2.53E-01	9	8	435	292
SLC39A11	2.74E-01	13	12	602	495
FAM114A1	2.90E-01	3	3	196	180
MICALL2	2.91E-01	22	6	297	236
RIMS2	3.01E-01	10	10	703	453
SYT5	3.10E-01	29	24	1164	368
LRRN1	3.37E-01	11	7	357	330
CRBN	3.60E-01	15	15	539	322
NENF	3.77E-01	2	2	65	64
VAV3	4.24E-01	8	6	367	324

Gene	***p***	n_{SNP}	$n_{SNP\|tested}$	**MAC**	***m***
MDGA1	4.72E-01	23	20	1279	619
CREB5	4.85E-01	17	17	892	546
EBF3	4.91E-01	3	3	70	69
FTSJ2	5.18E-01	5	3	216	209
TOX3	5.24E-01	2	2	123	114
SLC14A2	5.43E-01	2	2	212	208
CORO6	5.57E-01	4	3	201	195
SETBP1	5.62E-01	9	4	164	158
OLFML2B	5.82E-01	5	5	303	243
LAMA1	6.20E-01	14	13	893	566
KCNK13	6.33E-01	3	2	230	220
GALNT12	6.35E-01	6	5	238	227
PLXNA2	6.53E-01	28	26	1121	642
MAP2K5	6.71E-01	3	3	361	341
BTBD9	6.77E-01	8	6	474	372
MEIS1	6.82E-01	19	18	1083	506
CADM1	6.92E-01	11	11	684	464
CALML4	7.01E-01	2	2	72	71
NTNG1	7.56E-01	14	12	470	411
ASTN2	7.58E-01	13	11	459	383
EYA2	7.85E-01	6	4	262	185
PKP4	7.87E-01	12	10	519	297
PDE11A	8.33E-01	12	12	717	397
CACNG8	8.53E-01	5	5	359	328
NECAP1	8.59E-01	3	3	222	208
SGCZ	8.84E-01	5	4	212	193
C7orf62	1.00E+00	2	2	138	137
OPRL1	1.00E+00	5	2	114	111

4.2.4.3.4 Single Variant Association Analysis with Variants from MIPseq

Table 26 (p. 78) shows the results from the single variant association analysis using GMMAT [48] ($p \leq$ 1E-04 for score tests). One variant reached genome-wide significance: The SNP at chr20:62,872,612 (hg19) (p = 1.34E-11) was significant in the score test. The respective Wald test was invalid due to convergence issues when fitting the model. The SNP had a minor allele frequency of 3.6%, but was not observed in controls. The variant was in the 3’ UTR of *MYT1*. A second SNP was near genome-wide significance: chr1:161,967,710 (score test p = 5.65E-08, Wald test invalid due to convergence failure during model fitting) in the gene *OLFML2B*. The minor allele’s frequency was 2.4% in cases and the minor allele was absent in controls. It coded for an amino acid exchange: aspartate 460/461 to glycine, depending on the transcript. Of note, none of these variants had a dbSNP rsID. Two other SNPs reached significance after correcting for multiple testing (Bonferroni correction for 26,192 tests): chr3:130,613,210 (score test p = 1.24E-07, Wald test p = 1.06E-6, intronic in *ATP2C1* locus) and rs111818736 (chr11:115,088,501) (score test p = 1.78E-06, Wald test p = 8.42E-05, intronic in *CADM1* locus). The minor alleles were more frequent in controls (MAF was 4.3% and 2.6%, respectively) than in cases (MAF was 1.0% and 0.2%, respectively). The ORs were high for the risk alleles (5.23 and 11.08, respectively). However, the differential missingness of variant calls was nominal significant for the SNP of *ATP2C1*. Both SNPs were intronic variants in the UCSC transcripts of *ATP2C1* and *CADM1*, respectively.

*Table 26: Top association signals of the SNPs from MIPseq: A generalized linear mixed model was applied. Results are shown for the score and Wald test. ** = Genome-wide significant p value, * = significant p value after correction for multiple testing (Bonferroni, 26,192 valid score tests), rsID = dbSNP [403, 420] identifier, Chr:pos[ref/alt] = chromosome, position, reference (= test allele) and alternative allele (hg19) (underscore = risk allele from score test), MQ = root mean mapping quality, n = sample size, MAF_a/MAF_u = minor allele frequency in cases/controls, Missingness = test for differentially missing calls in cases and controls (f_a/f_u = proportion of missingness in cases/controls, p_m = p value from Fisher test for differential missingness), C-score Raw/Phr = raw/Phred-like C-score [15], Gene = gene or gene locus, effect = variant location/amino acid changes in case of missense/nonsense variants for UCSC [390] transcripts (from the IHG NGS pipeline), Pph = PolyPhen 2 score [428], SIFT = SIFT score [91, 429-432], Score test = summary of score test (s_s = score, V_s = variance of score, p_s = p value from score statistic), Wald test = summary of Wald test (p_W = p value, OR_{risk} = odds ratio of the risk allele with 95% confidence interval). "Gene", "effect", "Pph" and "SIFT" were obtained from the IHG (see methods).*

Chr:pos[ref/alt] (rsID)	***MQ***	***n***	**MAF_a MAF_u**	**Missingness**		**C-score**		**Gene & effect**	**Pph**	**SIFT**	**Score test**			**Wald test**	
				f_a f_u	**p_m**	**Raw**	**Phr**				**s_s**	**V_s**	**p_s**	**p_W**	**OR_{risk} (95% CI)**
**20:62,872,612[G/$\underline{A}$]	10.02	1336	0.0365 0.0000	0.000 0.000	1.00	-0.57	0.15	*MYT1* 3' UTR	NA	NA	-21.4	10.0	1.4E-11	NA	NA
*1:161,967,710[T/$\underline{C}$]	9.08	1336	0.0238 0.0000	0.000 0.000	1.00	1.04	10.87	*OLFML2B* Asp460Gly Asp461Gly	benign	0.04	-14.1	6.7	5.7E-08	NA	NA
*3:130,613,210[$\underline{A}$/G]	26.09	1241	0.0101 0.0434	0.066 0.086	0.05	1.87	15.38	*ATP2C1* intron	NA	NA	20.1	14.5	1.2E-07	1.1E-06	5.23 [2.75; 9.95]
*11:115,088,501[$\underline{A}$/C] (rs111818736)	10.97	1336	0.0024 0.0262	0.000 0.000	1.00	-0.31	0.64	*CADM1* intron	NA	NA	14.1	8.7	1.8E-06	8.4E-05	11.08 [3.47; 35.43]
11:59,341,913[$\underline{G}$/T]	10.19	1325	0.0064 0.0338	0.003 0.014	0.07	0.78	9.35	*OSBP* 3' UTR	NA	NA	15.2	11.7	8.5E-06	4.3E-05	5.11 [2.39; 10.90]
9:8,504,141[$\underline{A}$/G]	16.67	1336	0.0159 0.0461	0.000 0.000	1.00	0.10	3.61	*PTPRD* intron	NA	NA	18.6	17.7	9.5E-06	2.0E-05	3.21 [1.91; 5.39]
20:61,962,063[$\underline{T}$/C]	12.62	1298	0.0008 0.0184	0.015 0.039	0.01	0.73	9.00	*COL20A1* near splice	NA	NA	10.2	5.6	1.5E-05	2.6E-03	26.77 [3.37; 212.62]
18:8,069,846[$\underline{A}$/T]	15.58	1336	0.0119 0.0418	0.000 0.000	1.00	4.61	24.4	*PTPRM* Glu432Val Glu219Val	probably damaging	0.26	16.8	15.3	1.7E-05	4.0E-05	3.51 [1.96; 6.28]
15:67,494,024[$\underline{A}$/G]	14.96	1336	0.0103 0.0376	0.000 0.000	1.00	0.43	6.87	*AAGAB* 3' UTR	NA	NA	14.6	13.5	7.2E-05	1.5E-04	3.47 [1.86; 6.46]
2:159,145,304[C/$\underline{G}$] (rs140922308)	10.47	1328	0.0494 0.0193	0.005 0.008	0.73	0.12	3.87	*CCDC148* Gln299His Gln332His Gln233His intronic	benign	0.01	-17.0	18.6	8.2E-05	1.2E-04	2.61 [4.19; 1.62]

4.3 Explaining RLS Families with RLS Risk SNPs

Common RLS risk SNPs were analyzed in RLS families. Especially Finnish families could be well explained by the RLS risk SNPs.

4.3.1 Genotyping of RLS Families and Quality Control

A total of 843 individuals (79 families) were genotyped and called for 576,761 markers using the Affimetrix Axiom assay. The 95% call rate filter removed 13,637 markers, and 840 markers failed in the HWE test. One individual was removed due to an excess of heterozygosity. Six individuals failed the sex check, and 6 individuals were identified as duplicates based on 91,485 common variants in low LD. The final dataset consisted of 91,485 markers and 829 individuals (325 male, 504 female). Of these, 105 individuals were of uncertain phenotype or not related to the families. Thus724 individuals (78 families) were left for the analysis (see appendix, Table 34, p. 315).

4.3.2 RLS Risk SNP Association and Correlation Analysis

A generalized linear mixed model was used to test for associations between RLS disease status and the dosages of published RLS risk SNPs in the combined families (without correcting for age and sex) (fixed effects) and correcting for relatedness using a genetic similarity matrix (random effects). Table 27 shows the results from the analysis. Only SNPs rs113851554 and rs2300478 were significantly associated after correcting for multiple testing of 9 SNPs. The variants are located in introns of *MEIS1* [420]. For all SNPs, the OR intervals were wider and completely overlapping with previous GWAS results [245]. The OR estimates for the nominal significant associations were also comparable with published OR estimates [245].

In the analysis of the individual families, eight families showed significant associations of at least one RLS risk SNP with the RLS disease phenotype: b006, k5332, t006, t007, t017, t026, t033 and t040 (Table 28, Table 29). The lowest pseudo-R^2 was 55% for those families, which were enriched for Finnish origin (pedigree ID with prefix “t”, empirical $p = 0.03$, based on 100 replicates of selecting 10 random family IDs and counting the number of Finnish families). The associated SNPs were located on chromosomes 2, 6, 9 and 15, but not on chromosome 16. Multiple SNPs were associated in 4 families (b006, t007, t017 and t040). The highest number of SNPs was associated in family t017 with pseudo-R^2 values of 1 for each SNP (all at/in proximity to the *MEIS1* locus). Of note, the set of test SNPs was not completely independent as some SNPs were in proximity.

The burden of risk alleles explained a significant proportion of the phenotypic variance in 10 families (Table 30): i001, t009, b006, p002, t007, t026, b015, i004, k5301, and rls0002. These proportions ranged from 0.10 to 1. Of note, for those 10 families, the degree of correlation, the values of the pseudo-R^2, could be mainly explained by a negative correlation with the size of the families ($R = -0.87$, $R^2 = 0.76$, $p = 0.0017$). Only three of these families had significant single variant associations as well: b006, t007, and t026.

Table 27: Summary statistics from the association analysis between RLS disease status and SNP dosages of RLS risk SNPs using a logistic regression with a generalized linear mixed model in combined RLS families: SNP = dbSNP [403, 420] identifier, Gene locus = genes mapping to the SNP or near the SNP (in brackets), Chr:pos[ref/alt] (hg19) = chromosome and physical position of the SNP in hg 19 (ref = reference/test allele, alt = alternative allele, underscore = risk allele), OR_{risk} *(95% CI) = odds ratio for the risk allele with 95% confidence interval,* p_W *= p value from the Wald statistic [48],* s_s *= score from the score test [48],* V_s *= variance of the score,* p_s *= p value from the score statistic, OR Winkelmann et al. 2011 = published odds ratios for the risk alleles from the latest published RLS GWAS [245].*

SNP	**Gene locus**	**Chr:pos[ref/alt]**	OR_{risk} **(95% CI)**	p_W	s_s	V_s	p_s	***OR*** **Winkelmann et al. 2011**
rs113851554	*MEIS1*	2:66,750,564[G/T]	2.59 [1.74; 3.87]	2.89E-06	-27.01	32.06	1.83E-06	NA
rs2300478	*MEIS1*	2:66,781,453[T/G]	1.80 [1.37; 2.38]	3.22E-05	-30.94	55.23	3.14E-05	1.68 [1.57; 1.81]
rs9357271	*BTBD9*	6:38,365,873[T/C]	1.51 [1.12; 2.02]	6.48E-03	17.70	41.99	6.31E-03	1.47 [1.35; 1.47]
rs12593813	*MAP2K5*/(*SKOR1*)	15:68,036,852[A/G]	1.34 [1.04; 1.72]	2.24E-02	-17.46	59.09	2.31E-02	1.41 [1.32; 1.52]
rs3104788	*CASC16*/(*TOX3*)	16:52,638,503[T/C]	1.35 [1.04; 1.75]	2.33E-02	17.09	56.35	2.28E-02	1.33 [1.25; 1.43]
rs3104767	*CASC16*/(*TOX3*)	16:52,624,738[G/T]	1.32 [1.02; 1.71]	3.73E-02	15.66	56.29	3.69E-02	1.35 [1.27; 1.43]
rs6747972	-	2:68,070,225[A/G]	1.09 [0.85; 1.40]	4.97E-01	5.36	62.39	4.97E-01	1.23 [1.16; 1.31]
rs1975197	*PTPRD*	9:8,846,955[G/A]	1.06 [0.76; 1.49]	7.17E-01	2.11	33.99	7.18E-01	1.29 [1.19; 1.40]
rs2116050	-	2:68,072,763[G/A]	1.05 [0.81; 1.34]	7.27E-01	2.72	61.10	7.28E-01	1.22 [1.15; 1.30]

Table 28: LRT p values from the GLMM association analysis between RLS risk SNP dosages and RLS disease status in RLS families: The results are shown for 62 families. The other 18 families failed in the test due to uniform phenotypes (only cases or controls available). Sample sizes are given in brackets after the pedigree ID. Green = significant after Bonferroni correction for 9 SNPs, yellow = nominal significant, Pedigree = pedigree ID, Gene locus = genes mapping to the SNP or near the SNP (in brackets), SNP = dbSNP [403, 420] identifier, Chr:pos = chromosome and physical position of the SNP in hg19.

Pedigree	**Gene locus** **SNP** **Chr:pos**								
	MEIS1 **rs113851554** **2:66,750,564**	***MEIS1*** **rs2300478** **2:66,781,453**	**-** **rs6747972** **2:68,070,225**	**-** **rs2116050** **2:68,072,763**	***BTBD9*** **rs9357271** **6:38,365,873**	***PTPRD*** **rs1975197** **9:8,846,955**	***MAP2K5* (& *SKOR1*)** **rs12593813** **15:68,036,852**	***CASC16* (& *TOX3*)** **rs3104767** **16:52,624,738**	***CASC16* (& *TOX3*)** **rs3104788** **16:52,638,503**
b002 (9)	0.8580	0.3406	0.0946	0.2872	0.0907	0.8580	0.7642	0.1183	0.1418
b005 (9)	NA	0.3406	0.0458	0.4761	0.0067	0.2864	0.0176	0.3562	0.2969
b006 (14)	0.0013	0.0018	0.1756	0.1593	0.0042	0.1777	0.6486	0.5255	0.4534
b008 (16)	0.3178	0.9680	0.1110	0.1111	NA	0.4537	0.3196	0.2811	0.2816
b010 (6)	NA	0.1046	0.1046	0.1046	0.7913	NA	0.2077	NA	0.9893
b015 (6)	0.0201	0.5257	0.2077	0.2093	0.2011	0.0201	0.3406	NA	0.2100
b020 (6)	0.0057	0.0764	1.0000	0.9949	NA	0.5447	NA	0.0512	0.0309
b027 (8)	0.2437	0.0457	0.0457	0.0457	NA	0.1321	0.2437	0.3787	0.6360
b029 (7)	0.1996	0.0925	0.4389	0.4393	0.8097	0.8097	0.4389	0.8055	0.8113
b030 (8)	0.0712	0.0712	1.0000	0.9997	0.6764	0.4305	NA	0.6179	0.2536
d006 (3)	NA	NA	0.0507	0.0507	0.0507	0.3063	NA	0.0507	0.0507
d010 (5)	0.1352	0.1352	0.4772	0.4772	NA	NA	NA	NA	0.7740
i001 (9)	0.9985	0.0298	0.0297	0.0303	NA	0.0453	0.2864	0.1481	0.2200
i002 (22)	0.0144	0.9538	0.9601	0.9984	0.7450	0.5321	0.1841	0.9088	0.9047
i004 (4)	0.1889	0.1889	0.1889	0.1889	0.4097	0.1889	0.1889	0.8216	0.4018
i014 (2)	0.0959	0.0959	NA	0.0959	0.0959	NA	0.0959	0.0959	0.0959
k5006 (17)	0.0472	0.5134	0.8301	0.8201	0.1385	0.9414	0.2558	0.6597	0.6398
k5301 (9)	0.0297	0.0297	0.0507	0.1356	0.0083	0.3503	0.5784	0.1338	0.1339
k5332 (22)	0.0181	0.9885	0.5275	0.5408	0.4116	0.0011	0.6477	0.7587	0.7161
k7150 (45)	0.8299	0.1168	0.1786	0.1617	0.7175	0.6023	0.1610	0.2113	0.3615
p001 (8)	0.5302	0.6890	0.5923	0.4305	1.0000	NA	NA	NA	0.9355
p002 (5)	0.2764	0.7098	0.7098	0.0880	0.2764	NA	0.4521	0.0095	0.0095
p004 (7)	0.6682	0.3321	0.8097	0.8081	0.4389	0.8097	0.8097	0.8524	0.8896
p015 (6)	0.0057	0.1046	0.0507	NA	0.1480	0.5447	0.5502	0.4490	0.4437

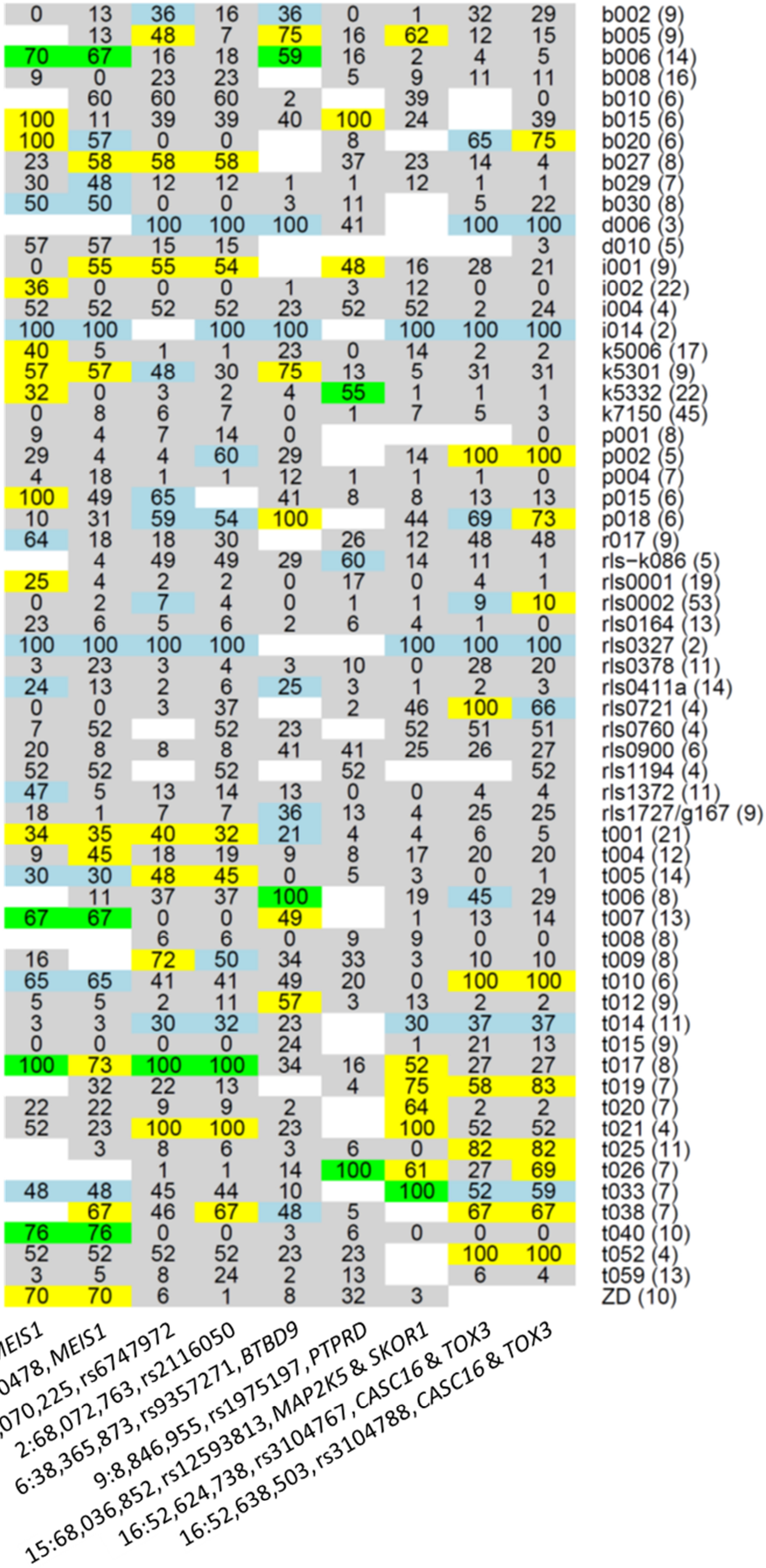
continued table…

Pedigree	**Gene locus SNP Chr:pos**								
	MEIS1 **rs113851554** **2:66,750,564**	***MEIS1*** **rs2300478** **2:66,781,453**	**-** **rs6747972** **2:68,070,225**	**-** **rs2116050** **2:68,072,763**	***BTBD9*** **rs9357271** **6:38,365,873**	***PTPRD*** **rs1975197** **9:8,846,955**	***MAP2K5* (& *SKOR1*)** **rs12593813** **15:68,036,852**	***CASC16* (& *TOX3*)** **rs3104767** **16:52,624,738**	***CASC16* (& *TOX3*)** **rs3104788** **16:52,638,503**
p018 (6)	0.5179	0.2337	0.0779	0.0955	0.0085	NA	0.1424	0.0501	0.0418
r017 (9)	0.0611	0.3503	0.3503	0.2262	NA	0.2588	0.4635	0.1168	0.1168
rls-k086 (5)	NA	0.7098	0.1352	0.1352	0.2764	0.0880	0.4521	0.5235	0.8295
rls0001 (19)	0.0470	0.4471	0.6090	0.6087	0.9831	0.1103	0.9529	0.4418	0.6734
rls0002 (53)	0.7053	0.3714	0.0970	0.2136	0.8744	0.6171	0.6310	0.0594	0.0450
rls0164 (13)	0.1399	0.4586	0.4892	0.4822	0.6480	0.4841	0.5600	0.7811	0.9237
rls0327 (2)	0.0959	0.0959	0.0959	0.0959	NA	NA	0.0959	0.0959	0.0959
rls0378 (11)	0.6179	0.1717	0.6179	0.5978	0.6179	0.3852	0.9239	0.1251	0.1956
rls0411a (14)	0.0981	0.2264	0.6291	0.4224	0.0860	0.5760	0.6911	0.6494	0.5629
rls0721 (4)	0.9280	0.9280	0.7698	0.2571	NA	0.8160	0.1951	0.0190	0.0988
rls0760 (4)	0.6557	0.1889	NA	0.1889	0.4097	NA	0.1889	0.1912	0.1930
rls0900 (6)	0.3406	0.5447	0.5447	0.5444	0.1480	0.1480	0.2730	0.2617	0.2534
rls1194 (4)	0.1889	0.1889	NA	0.1889	NA	0.1889	NA	NA	0.1889
rls1372 (11)	0.0548	0.5563	0.3438	0.3285	0.3438	0.8867	0.8867	0.6221	0.5885
rls1727/g167 (9)	0.2588	0.8272	0.4960	0.4987	0.0940	0.3406	0.5958	0.1732	0.1750
t001 (21)	0.0187	0.0165	0.0097	0.0236	0.0718	0.4406	0.4502	0.3558	0.3714
t004 (12)	0.3578	0.0293	0.1914	0.1881	0.3836	0.3916	0.2129	0.1756	0.1732
t005 (14)	0.0712	0.0702	0.0173	0.0217	0.8520	0.4768	0.5812	0.8425	0.7980
t006 (8)	NA	0.4305	0.1321	0.1321	0.0027	NA	0.2904	0.0878	0.1840
t007 (13)	0.0037	0.0037	0.9131	0.9065	0.0189	NA	0.7612	0.2553	0.2516
t008 (8)	NA	NA	0.5513	0.5513	1.0000	0.4620	0.4620	0.9994	0.9644
t009 (8)	0.3108	NA	0.0141	0.0551	0.1324	0.1372	0.6764	0.4363	0.4326
t010 (6)	0.0507	0.0507	0.1480	0.1480	0.1046	0.3406	1.0000	0.0057	0.0057
t012 (9)	0.5784	0.5784	0.7492	0.3820	0.0297	0.6327	0.3406	0.7246	0.7094
t014 (11)	0.6083	0.6050	0.0947	0.0822	0.1451	NA	0.0923	0.0603	0.0599
t015 (9)	0.8971	0.9055	0.9055	0.9065	0.1821	NA	0.8271	0.2193	0.3396

continued table…

Pedigree	**Gene locus** **SNP** **Chr:pos**								
	MEIS1 **rs113851554** **2:66,750,564**	***MEIS1*** **rs2300478** **2:66,781,453**	**-** **rs6747972** **2:68,070,225**	**-** **rs2116050** **2:68,072,763**	***BTBD9*** **rs9357271** **6:38,365,873**	***PTPRD*** **rs1975197** **9:8,846,955**	***MAP2K5* (& *SKOR1*)** **rs12593813** **15:68,036,852**	***CASC16* (& *TOX3*)** **rs3104767** **16:52,624,738**	***CASC16* (& *TOX3*)** **rs3104788** **16:52,638,503**
t017 (8)	0.0011	0.0136	0.0011	0.0011	0.1321	0.3115	0.0496	0.1847	0.1830
t019 (7)	NA	0.1656	0.2649	0.3892	NA	0.6576	0.0166	0.0475	0.0092
t020 (7)	0.2649	0.2649	0.4878	0.4882	0.7650	NA	0.0328	0.7620	0.7673
t021 (4)	0.1889	0.4097	0.0339	0.0339	0.4097	NA	0.0339	0.1889	0.1889
t025 (11)	NA	0.6623	0.4449	0.5154	0.6623	0.5154	0.9130	0.0057	0.0057
t026 (7)	NA	NA	0.8097	0.8097	0.3904	0.0038	0.0489	0.2232	0.0328
t033 (7)	0.0938	0.0937	0.1092	0.1121	0.4776	NA	0.0044	0.0782	0.0574
t038 (7)	NA	0.0362	0.1028	0.0362	0.0943	0.6366	NA	0.0374	0.0377
t040 (10)	0.0036	0.0036	1.0000	0.9985	0.6356	0.4870	1.0000	0.8996	0.9985
t052 (4)	0.1889	0.1889	0.1889	0.1889	0.4097	0.4097	NA	0.0339	0.0339
t059 (13)	0.6133	0.5151	0.4056	0.1356	0.6807	0.2735	NA	0.4631	0.5430
ZD (10)	0.0190	0.0190	0.5273	0.8206	0.4768	0.1390	0.6638	NA	NA

Table 29: Correlation of RLS disease status and dosage of RLS risk SNPs in RLS families: The results are shown for 62 families. The other 16 families failed due to uniform phenotypes (only cases or controls). Nagelkerke's pseudo-R² values were based on a GLMM (pedigree structures = random effects). Colors represent LRT p values (green p ≤ 0.05/9, yellow p ≤ 0.05, blue p ≤ 0.10, gray p > 0.10, white NA). Families are in alphabetical order (and brackets indicate the sample size in the analysis). Columns/SNPs are ordered by genomic position (hg19), dbSNP [403, 420] identifier and gene locus.



2:66,750,564, rs113851554, MEIS1	2:66,781,453, rs2300478, MEIS1	2:68,070,225, rs6747972	2:68,072,763, rs2116050	6:38,365,873, rs9357271, BTBD9	9:8,846,955, rs1975197, PTPRD	15:68,036,852, rs12593813, MAP2K5 & SKOR1	16:52,624,738, rs3104767, CASC16 & TOX3	16:52,638,503, rs3104788, CASC16 & TOX3	
0	13	36	16	36	0	1	32	29	b002 (9)
	13	48	7	75	16	62	12	15	b005 (9)
70	67	16	18	59	16	2	4	5	b006 (14)
9	0	23	23		5	9	11	11	b008 (16)
	60	60	60	2		39		0	b010 (6)
100	11	39	39	40	100	24		39	b015 (6)
100	57	0	0		8		65	75	b020 (6)
23	58	58	58		37	23	14	4	b027 (8)
30	48	12	12	1	1	12	1	1	b029 (7)
50	50	0	0	3	11		5	22	b030 (8)
		100	100	100	41		100	100	d006 (3)
57	57	15	15					3	d010 (5)
0	55	55	54		48	16	28	21	i001 (9)
36	0	0	0	1	3	12	0	0	i002 (22)
52	52	52	52	23	52	52	2	24	i004 (4)
100	100		100	100		100	100	100	i014 (2)
40	5	1	1	23	0	14	2	2	k5006 (17)
57	57	48	30	75	13	5	31	31	k5301 (9)
32	0	3	2	4	55	1	1	1	k5332 (22)
0	8	6	7	0	1	7	5	3	k7150 (45)
9	4	7	14	0				0	p001 (8)
29	4	4	60	29		14	100	100	p002 (5)
4	18	1	1	12	1	1	1	0	p004 (7)
100	49	65		41	8	8	13	13	p015 (6)
10	31	59	54	100		44	69	73	p018 (6)
64	18	18	30		26	12	48	48	r017 (9)
	4	49	49	29	60	14	11	1	rls−k086 (5)
25	4	2	2	0	17	0	4	1	rls0001 (19)
0	2	7	4	0	1	1	9	10	rls0002 (53)
23	6	5	6	2	6	4	1	0	rls0164 (13)
100	100	100	100			100	100	100	rls0327 (2)
3	23	3	4	3	10	0	28	20	rls0378 (11)
24	13	2	6	25	3	1	2	3	rls0411a (14)
0	0	3	37		2	46	100	66	rls0721 (4)
7	52		52	23		52	51	51	rls0760 (4)
20	8	8	8	41	41	25	26	27	rls0900 (6)
52	52		52		52			52	rls1194 (4)
47	5	13	14	13	0	0	4	4	rls1372 (11)
18	1	7	7	36	13	4	25	25	rls1727/g167 (9)
34	35	40	32	21	4	4	6	5	t001 (21)
9	45	18	19	9	8	17	20	20	t004 (12)
30	30	48	45	0	5	3	0	1	t005 (14)
	11	37	37	100		19	45	29	t006 (8)
67	67	0	0	49		1	13	14	t007 (13)
		6	6	0	9	9	0	0	t008 (8)
16		72	50	34	33	3	10	10	t009 (8)
65	65	41	41	49	20	0	100	100	t010 (6)
5	5	2	11	57	3	13	2	2	t012 (9)
3	3	30	32	23		30	37	37	t014 (11)
0	0	0	0	24		1	21	13	t015 (9)
100	73	100	100	34	16	52	27	27	t017 (8)
	32	22	13		4	75	58	83	t019 (7)
22	22	9	9	2		64	2	2	t020 (7)
52	23	100	100	23		100	52	52	t021 (4)
	3	8	6	3	6	0	82	82	t025 (11)
		1	1	14	100	61	27	69	t026 (7)
48	48	45	44	10		100	52	59	t033 (7)
	67	46	67	48	5		67	67	t038 (7)
76	76	0	0	3	6	0	0	0	t040 (10)
52	52	52	52	23	23		100	100	t052 (4)
3	5	8	24	2	13		6	4	t059 (13)
70	70	6	1	8	32	3			ZD (10)

*Table 30: Association and correlation between burden of RLS risk alleles and RLS disease status in RLS families: The results are shown for 59 families. The other 20 families failed in the analysis. Pedigree = pedigree ID (sample size in brackets), R^2 = Nagelkerke's pseudo-R^2 measure, p = p value from association using a GLMM approach and LRT, * = significant association between burden of RLS risk alleles and disease status (p value < 0.05).*

Pedigree	***R^2***	***p***	**Pedigree**	***R^2***	***p***
*i001 (9)	0.878	0.002	rls0760 (4)	0.202	0.444
*t009 (8)	0.850	0.005	b029 (7)	0.114	0.446
*b006 (14)	0.553	0.006	b010 (6	0.145	0.462
*p002 (5)	1.000	0.009	t004 (12)	0.058	0.475
*t007 (13)	0.515	0.015	t001 (21)	0.032	0.496
*t026 (7)	0.789	0.018	rls-k086 (5)	0.097	0.542
*b015 (6)	1.000	0.020	b030 (8)	0.067	0.542
*i004 (4)	1.000	0.034	t038 (7)	0.075	0.542
*k5301 (9)	0.493	0.047	t019 (7)	0.067	0.551
*rls0002 (53)	0.097	0.047	t012 (9)	0.049	0.570
d006 (3)	1.000	0.051	t025 (11)	0.047	0.573
t010 (6)	0.649	0.052	rls1194 (4)	0.098	0.601
t020 (7)	0.551	0.054	t006 (8)	0.046	0.617
i014 (2)	1.000	0.096	p001 (8)	0.056	0.625
rls0327 (2)	1.000	0.096	b008 (16)	0.022	0.634
r017 (9)	0.476	0.117	t008 (8)	0.034	0.651
k5006 (17)	0.244	0.131	t040 (10)	0.026	0.654
k7150 (45)	0.065	0.163	rls0001 (19)	0.011	0.698
t059 (13)	0.202	0.172	b005 (9)	0.021	0.704
t021 (4)	0.519	0.189	rls1372 (11)	0.018	0.728
t017 (8)	0.261	0.192	p015 (6)	0.027	0.729
b020 (6)	0.335	0.198	d010 (5)	0.024	0.784
rls0164 (13)	0.172	0.209	t005 (14)	0.006	0.814
rls1727/g167 (9)	0.172	0.266	rls0721 (4)	0.018	0.815
k5332 (22)	0.062	0.326	ZD (19)	0.007	0.833
rls0900 (6)	0.194	0.342	p004 (7)	0.009	0.834
t015 (9)	0.111	0.378	t014 (11)	0.002	0.898
b027 (8)	0.121	0.408	b002 (9)	0.002	0.917
rls0378 (11)	0.081	0.427	rls0411a (14)	0.000	0.991
i002 (22)	0.041	0.439	i001 (9)	0.878	0.002

5 Discussions

5.1 Screening for RLS Associated Rare Variants and Genes Using the Human Exome BeadChip

Rare variant genotype data was obtained from the Human Exome BeadChip for a German/Austrian case-control cohort. It was controlled for quality and analyzed for association with RLS, which resulted in a list of putative RLS candidate genes.

5.1.1 Quality Control of the Genotyping Data

Genotype calling was a challenge for the ExomeChip that mainly included low frequency variants. Those variants might lack clear intensity clusters for the genotype calling procedures, especially for low frequency genotypes due to a low number of observations. This could lead to false positive calls and no calls if the standard Illumina calling procedures are used. A number of alternative calling methods were developed like optiCALL [433], zCALL [434] and iCALL [435]. ZCALL [434] was applied during initial calling attempts with RLS and KORA [354, 355] raw data, but seemed to call too many homozygous variants and the application of the cluster file from CHARGE [357] was superior (data not shown). This cluster file was manually curated and was shown before to be superior to zCALL or the Illumina cluster file [357]. However, in general, if cluster positions are applied to genotyping intensity data from a different source, then some markers might show drops in the call rate (or calling accuracy) due to technical artifacts. In this study, the three initial ExomeChip datasets were genotyped at different time points. The KORA [354, 355] and RLS genotypes were obtained from the same genotyping facility, and they were genotyped in a sequence. However, the HNR [55, 356] samples were genotyped elsewhere. But the same cluster file was applied to all cohorts. Thus a potential technical artifact could introduce a bias. Therefore, each dataset was separately controlled for its quality, and then the datasets were combined and subjects of another QC. As a consequence, only markers were left that had high call rates in all cohorts. But, markers might still have been left that had false calls. Therefore, any marker was reviewed that was part of an association signal and removed in case of false genotype calls.

During the combined quality control, the heterozygosity was checked based on rare and common variants. This approach would detect potentially contaminated samples, which would show up with an increased heterozygosity, and maybe also potential population outliers. Their MAF spectrum might be different and so would be their heterozygosity. Furthermore, contaminated samples might have been better detected with high frequency markers and samples of low quality maybe with low frequency markers.

5.1.2 Single Variant Association Analysis

The single variant association analysis could not detect new genome-wide significant associations. However, most of the published associations could be reproduced (except for the *PTPRD* locus) [244, 245]. The genomic control value λ_{GC} [313] was high, which could have been an artifact of the analysis using FaST-LMM [37, 366, 367]. During the analysis, markers were removed from the estimation of genetic similarities that were in proximity to the test SNPs. This approach should reduce the proximal contamination, where real association signals might be masked by indirectly using them as a covariate by the genetic similarity estimations [367]. However, FaST-LMM [37] was not directly designed for binary traits and used a linear mixed model. Therefore, the top signals were replicated using the recently published alternative method GMMAT [48], which used a generalized linear mixed model, which was suitable for binary traits [48]. Of note, the p values were approximately one order of magnitude higher, especially for the common variants (Table 20, p. 49). Thus GMMAT [48] should be used in single variant association analysis of binary traits with mixed models. However, a polygenic inheritance was shown to lead to inflated test statistics [436], and further work has to been done to dissect the source of inflation using the recently published method of LD score regression [437].

Of note, recent publications used less stringent significance thresholds, e.g. a Bonferroni correction for the conducted number of tests (with variable success) [438, 439]. However, this approach would not have rendered new genomic loci being significantly associated with RLS.

5.1.3 Gene Level Association Analysis

The gene level association analysis showed one significant gene with rare variant ExomeChip data after Bonferroni correction for multiple testing of 11,833 independent burden null hypothesis: *RASGRP4* (RAS guanyl releasing protein 4 [2]). But, the signal would not have been significant after correction for 4x4x11,833 null hypothesis as not only burden tests [12] were done, but also SKAT [92] and combined tests(Fisher's method, minimum-*p* method) [346] as well as conditional tests and weighted tests, although these tests were not independent from each other. Furthermore, the signal came from Fisher's method of combining gene level tests [346]. But the QQ plot showed a high inflation for Fisher's method of meta-analysis [346] compared to the minimum-*p* meta-analysis method [346] or particular burden [12] and SKAT [92] tests (Figure 5, p. 53). But its inflation was lower after weighting variants based on CADD [15] scores. Thus CADD [15] score based weighting might have reduced the contribution of functionally irrelevant, putatively stratified rare variants, which might have been enriched in different sub populations due to genetic drift and lack of selection. As a simplified description of the tests, Fisher's method [346] combines signals from to different statistical tests, whereas the minimum-*p* method [346] rather picks one of them. Thus Fisher's method might enhance the inflation that might be present for the gene-level association test. Of note, the minimum-*p* method might have shown a lack of power.

The screen on the ExomeChip might have lacked power in general. The outcome was also low in other recent studies of comparable sample sizes (e.g. [438, 440]). Even large samples sizes showed only a few significant associations. E.g. a study was recently published about an ExomeChip analysis on fasting glucose and type 2 diabetes, and just one significant gene could be identified with a sample size of 60,564 [439]. Other examples showed that larger samples sizes could lead to significant results (e.g. [441-444]).

5.2 Targeted Sequencing of RLS Candidate Genes Using MIPseq

The previous ExomeChip data analysis resulted in a list of candidate genes for RLS. These genes were sequenced together with a number of genes from an unpublished RLS meta-GWAS [373] annotation.

5.2.1 Definition of RLS Candidate Genes

As a main hypothesis, RLS is a neurological disorder. Therefore, brain related eQTL data had a high impact on the selection of RLS candidate genes for targeted sequencing: Rather tolerant eQTL FDR thresholds (and FDR estimates) were used to obtain a comprehensive list of genes. The focus was to not miss a putative RLS gene (high sensitivity) instead of avoiding false positives. However, the eQTL review as a whole might have been biased and thus not exhaustive due to the chosen inclusion thresholds and criteria. Due to this bias, putative pathway inferences might be problematic. However, some connections were observed between the selected candidate genes: In blood eQTL [381] data, *BBS7* is a trans eQTL of the association signal at chromosome 16 proximal to *TOX3* (via

SNP rs3104767, rs3112612). But *BBS7* is also a trans eQTL of rs8102476. This SNP gave a cis eQTL signal for *RASGRP4*, which emerged as a candidate in the analysis of the ExomeChip data. Furthermore, the two top associated genes, *MYT1* and *COL20A1*, emerged from the same RLS associated locus at chromosome 20 (from the meta-GWAS [373]). The significance of these observed connections was not assessed. Thus further research has to be done to link RLS associated markers and candidate genes to a network on a systematic basis. Furthermore, gene level association signals might also partially be explained by proximal RLS associated common variants.

5.2.2 MIP Design and Scale of the MIPseq Project

MIPs were designed for the exons and promotor regions of the candidate genes. The scale of the MIP design was comparable with other large scale MIP projects [78, 445-447]. The MIPs of this project were obtained from two design programs [78, 399]. A mixing of designs was shown before to be applicable [445], and a complete design could be achieved for almost all target regions of interest by a custom iterative design framework.

A power analysis showed that the putative future sequencing of 5,000 cases and 5,000 controls might reveal a considerable large number of associated genes (Table 23, p. 65). The power analysis was not specifically done with the SKAT [92] test because an inflation was shown for those types of power analyses [448]. Sequencing these numbers of individuals would also make the MIPseq project more cost efficient (Figure 17, p. 90). In detail: The costs of a MIP project can be separated into four items: MIPs order/pooling, MIPs pool balancing, multiplex library generation, multiplex library quality control/sequencing. IDT synthesized a MIP oligonucleotide at a lowest amount of 25 nmol. Such an amount is sufficient to sequence at least 1,650,000 individuals. Thus, any nowadays typical study's sample size does not affect the MIP order itself and the costs only depend on the actual number of different MIPs. The more MIPs, the higher would be the costs. However, the relative costs per person go down if the MIPs are used for studies with high sample numbers. After the ordering, MIPs would be pooled and the pool would be balanced. The balancing costs do not depend on the sample size and should be constant over a broad range of MIP numbers: According to Equation 14 (p. 33), up to 10,883 MIPs could be balanced on a MiSeq with 3 exemplary individuals and 400x mean MIPs' target coverage. Higher MIP numbers would require either lower mean coverages or more sequencing, which would increase the sequencing costs. However, the contribution to the total project costs will decrease with study size and so will the costs per person. After the balancing of the MIPs pool, the actual MIPseq multiplex NGS libraries would be prepared. The individuals' NGS libraries are approximately independently prepared of the number of MIPs. So, the preparations' costs per individual would remain constant. After the preparation of the libraries, the quality control and sequencing would be done. The sequencing costs per individual would be constant over a broad range of MIP numbers, for example, in this setup, for up to 3,255 MIPs: According to Equation 14 (p. 33), these numbers of MIPs will generate NGS multiplex libraries that cannot exhaust the sequencing capacity of one sequencing lane at the desired mean coverage, even at the highest multiplex level. But, if more MIPs are used, then the sequencing costs per person are increasing. Because of Equation 14 (p. 33), the MIP number now leads to NGS multiplex libraries that exceed the capacity of one sequencing lane, and the desired mean coverage is not reached. So either each multiplex NGS library needs more sequencing lanes, or the multiplex level has to be reduced. The latter solution increases the total number of sequencing batches, and thus both solutions will increase the sequencing costs of the project and the sequencing costs per person. Thus, the sequencing costs per person depend on the number of MIPs and not on the number of individuals, with one exception: Studies sizes may be below 384 individuals. And according to Equation 14 (p. 33), such a study will completely fit into one sequencing lane for a broad range of MIP numbers. If two studies are compared, e.g. studies with 100 vs 200 individuals, their total sequencing costs are the same, but the costs per person are higher in the study with the lower sample size. So, for low number of MIPs and low number of study participants, the sequencing costs per person decrease with study size. As a summary, the costs per person get expansive with a very high number of MIPs and/or a low number of samples (Figure 17). Of note, to cover the human exome [449], approximately 320,000 MIPs would be needed. The MIPseq technology was a cost efficient method to perform the targeted resequencing of this study. And the RLS MIPseq setup gets more cost efficient when further samples would be sequenced and therefore might be a useful product for further studies on RLS genetics, e.g. in replication studies, clinical applications, and family studies.

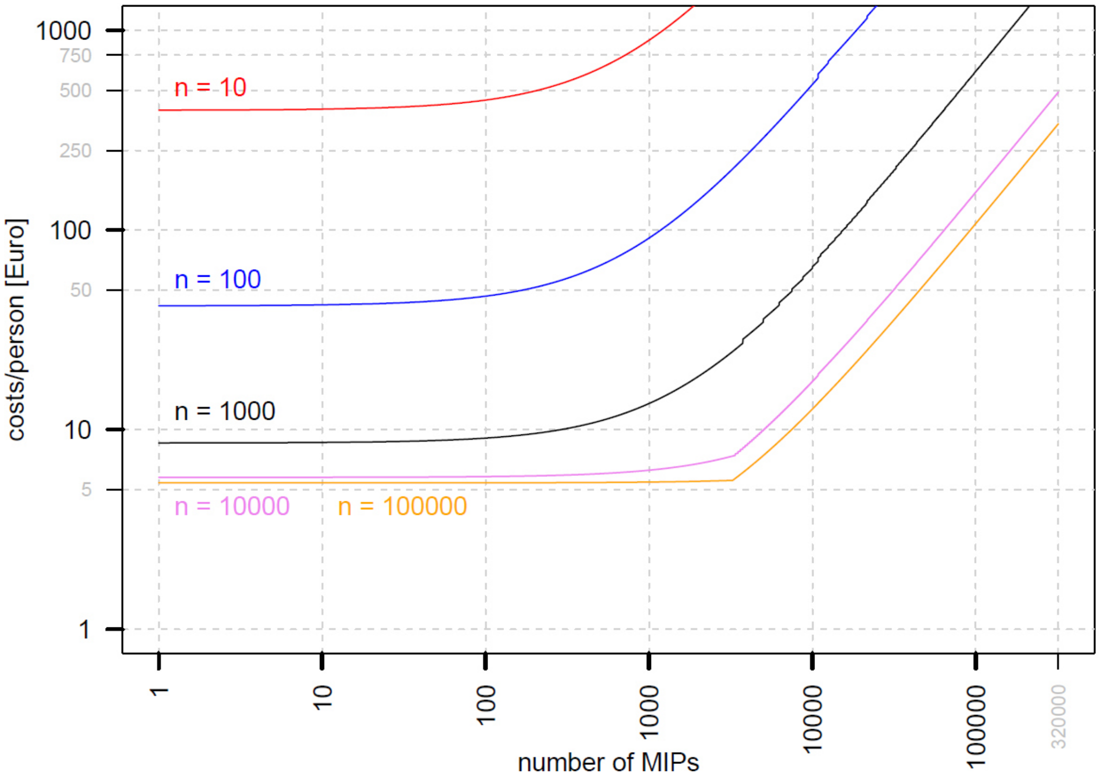


Figure 17: MIPseq costs per person depending on MIPs pool size and study size: Calculations were based on three rounds of calibrating the MIPs pool (naïve, balanced and rebalanced MIPs pool) including three DNA samples each, balancing on a MiSeq (150 nt paired end reads & index read), mean MIP length of 70 nt, mean target size of 110 nt and sequencing on a HiSeq 2500 (100 nt paired end & index read). The costs were calculated without taxes, personal, discounts or package sizes of materials, despite for the usage of sequencers. (number of MIPs = number of different MIPs, n = sample size of the study)

5.2.3 Balancing and Rebalancing of the MIPs Pool

For an ideal MIPs pool, a balancing plot would show a uniform coverage of the MIPs' targets, thus a horizontal row of dots (or a horizontal line in case of many MIPs). In reality, the lower tail would show a drop and the upper tail a rise for the coverages of some MIPs' targets. The vast majority of dots would show a slightly increasing coverage for the vast majority of MIPs' targets in the center of the graph. This shape of the graph visualizes a buffering capability of a MIPs pool: If the coverage threshold for calling variants is very much below the median MIPs’ target coverage, thus in the range of the dropping lower tail of the balancing plot, then the balancing curve could be vertically translated to some extent, but the number of a MIPs’ targets above the variant calling threshold would not change much. For example, a vertical translation could be realized by a random variation of the total flow cell capacity, or similar, by increased off-target effects of the MIPs: If more off-target sequences are covered with reads, then the available capacity is reduced for the on-target sequences. The total off-target effects can be increased for a MIPs pool by adding some MIPs with strong off-target effects. But the vertical translation can also be achieved for the balancing plot by just adding more MIPs to the MIPs pool. Thus, it is possible that MIPs and MIPs with strong off-target effects can be added to a MIPs pool and this pool will result in more targets suitable for calling variants because more new additional targets are suitable for calling than targets that were lost for calling variants due to a drop in the coverage caused by additional MIPs and more off-target sequences. This was the case in this study. During the calibration of the MIPs, a balanced and a rebalanced MIPs pool was obtained. The rebalanced MIPs pool contained more different MIPs than the balanced pool as additional MIPs were added from a secondary design as well as some more MIPs that targeted coding regions and that were absent in the balanced pool due to off-target considerations. As a consequence, the proportion of off-target reads was increased for the MIPseq library from the rebalanced MIPs pool. Thus more sequencing capacity was wasted for covering off-target sequences with reads, and less capacity remained to cover the targets of interest. Compared to the sequencing results of the balanced MIPs pool, the odds dropped between targets of interest suitable and targets of interest not suitable for variant calling, e.g. targets covered more than/equal to 10X and targets below that coverage. However, the absolute number of targets of interest covered ≥ 10X was higher, although the difference was small (on average 78 targets/person). As the rebalanced pool led to a slightly higher amount of data for variant calling (when using 10X coverage as a calling threshold), the rebalanced pool was used for further experiments.

5.2.4 Technical Quality Control of the MIPseq Data

The technical quality control had the major task to check for biases between cases and controls. No serious biases were introduced due to pooling and sequencing of the MIPseq libraries: First, the sequencing runs varied, e.g. due to technical issues with some lanes or maybe also library quantification errors, but the effect was negligible with respect to the intra-library variation of sample coverages. Second, plates were shown to be pooled in equimolar amounts into MIPseq libraries with respect to the plates’ sample sizes. But the performance of the MIPs pool was different between cases and controls. The later had a lower and broader distribution of the on-target ratio of the reads. And controls seemed to have a different shape/width of the relative MIPs’ performance curve. As a consequence, the case-control status was associated with a missingness of genotypes. However, only little of its variance was explained by the case-control status. Much better predictors were the total number of on-target reads and the width of the relative MIPs’ performance curve. This indicated that the variation between the samples in general was higher than the variation between cases and controls. Several sources of these variations might be possible. The number of on-target reads might mainly depend on the input amount of gDNA and also DNA quality as MIPs might hybridize worse to degraded DNA. The DNA quality could also determine the width of the relative MIPs’ performance curves, but also genetic variation that might interfere with MIP binding on some target sites. It could also depend on the GC content of the targets, which could determine the discrepancy of the PCR efficiency for the different targets, which could result in a broader distribution of PCR yields for the different target sites. Of note, a genetic difference between cases and controls was expected in the target sites. Thus, a different performance of the MIPs between cases and controls might have been expected as MIP binding and PCR depend on genetic variation. To sum up, the missingness of genotypes between cases and controls was present, but small with respect to other sources of genotype missingness. However, a differential missingness between cases and controls could introduce an inflated type I error in downstream gene-level association analyses, and thus a correction was used in the gene-level association tests [12].

Of note, for some MIP targets, the 2.5% quantile of the individuals' read counts (Figure 14, p. 71) showed extreme drops by some orders of magnitude compared to the quantiles of the other MIPs. This might be a hint to deletions in cases and controls at those loci (or other genetic variation that strongly interfered with the binding of MIPs to gDNA). Some 97.5% quantiles were ranging up some orders of magnitude, which might hint to loci of duplications.

Sample replicates were used on each sample plate of the MIPseq libraries. The high pairwise genotype concordances could rule out plate rotations. The basis of the concordance calculations, the genotype calls, might have been affected by PCR artifacts and sequencing errors in the multiplex tags, which might have led to false genotype calls, which could explain that the concordances were not 100%.

Of note, the binding of MIPs to gDNA can be affected by SNPs, and thus the standard MIP design tries to design multiple MIPs for SNPs in the probe binding regions. These SNPs were common SNVs. The rare SNVs were neglected. If the rare SNVs would have been taken into account, then a substantial number of alternative MIPs would have been expected to be designed as rare variation is common in the human genome [340]. But this would have led to increased project costs. However, the disease model expects more rare variants in cases compared to controls, especially in the selected target regions for MIPseq. Thus in the DNA from cases, the following situation might appear more often: A MIP could show a lower or higher binding affinity to the strand that probe binding region contains the rare allele of a heterozygous variant, compared to the DNA strand of the sister chromatid that contains the allele that was considered in the MIP design. This would result in unbalanced read counts for the respective two DNA strands, and if then the target region of the MIP also contains a heterozygous variant, then the calling of this variant might be biased. In the worst case, an excess of false homozygous genotypes would be expected in the cases for the regions of interest. And if only a subset of the regions of interest would be affected by this putative problem (e.g. only a subset of the genes or exons might be relevant for RLS), then the MIPs' performance curve might show a higher variance in the cases. This would be a less uniform MIPs' performance in cases, and this would result in a lower coverage of those regions because libraries were quantified and pooled with respect to the total library content and not with respect to RLS relevant DNA amplicons. This lower coverage of RLS relevant regions might also lead to differential missingness in cases compared to controls. Even if some regions of interest harbor more rare variants in controls, the overall problem might remain. To address this question, future studies might have to be considered. E.g. alternative data, e.g. WES or WGS data, for a random subset of cases and controls might be used to calculate concordances with respect to the MIPseq data. Or Sanger sequencing could confirm the rare variants' genotypes in exons that might be highly associated with the phenotype, for a random subset of RLS cases and controls. However, an early publication on MIPs showed [78], that the applied calling parameters led to a precision > 97% and sensitivity > 98% in 121 Joubert syndrome patients with available high quality Sanger sequencing data, which were sequenced in causal genes of the Joubert syndrome (supplemental material of [78]). Thus the described putative problem might be of minor importance. But interestingly, the detection of the described problem, and hints were already found in this study, might then already hint to a genetic difference between cases and controls, which would already shade more light into the genetics of RLS. However, a differential MIPs performance might also hint to different DNA quality.

5.2.5 Variant Calling

The variant calling was rather strict to obtain high confidence calls, and the chosen calling thresholds were comparable to the optimum determined in a previous publication [78]. Less stringent calling parameters were also used in the literature [446], especially for nonsense and splice variants [78]. However, the demultiplexing of reads to samples after the sequencing had an approximate false negative rate of 5% (data not show), which might compromise variant callings at lower coverage thresholds. Thus a higher threshold was applied to this study. But still, only further experiments can exclude false positive calls, e.g. Sanger sequencing, which might have to be applied to validate positive association signals. However, the concordances with ExomeChip genotypes were high, especially for variants with a MQ value greater than 10.

In principal, the MIP technology is also suitable for CNV calling [78] as similar applications were established in the field of cancer research on FFPE samples [40]. Thus the data of this project might be suitable for further research on CNVs in restless legs syndrome.

5.2.6 Association Analysis

The SKAT-O test [93] was used with SNVs that were called from the MIPseq of the cases and controls, and should identify genes that are associated with the RLS status. This test method was shown to achieve a high power over a broad range of scenarios [93]. Due to the small sample size, a correction had to be applied based on resampling [347]. This disabled the application of a generalized linear mixed model [74]. Thus principal components had to be used to correct for population stratification, but a correction for cryptic relatedness was missed [327]. However, highly related individuals were removed from the dataset and the impact of the cryptic relatedness might have been low [450] as the case-control cohort was likely an outbred population [355, 451]. However, the SKAT tests are more susceptible to population stratification [452], and the application of principal components or mixed models might fail to correct for the stratification if the disease risk is also stratified [453]. However, this stratification might be low in the German population [25].

In the SKAT-O tests [93], differential missingness was corrected [12, 74]. As a note, inflated test statistics are even expected after a successful correction for population substructure in traits with a polygenic inheritance [436, 437], which could be the case for RLS [214]. Thus further studies have to be performed to dissect the confounding from polygenicity using LD-score regression analysis [437].

Besides *PTPRD*, *MYT1* (myelin transcription factor 1, also *KIAA0835*, *KIAA1050*, *MTF1*, *MYTI* or *PLPB1 [2]*) was significantly associated with RLS. *MYT1* is widely expressed in developing vertebrate neuronal tissues [454], and it is involved in the proliferation and differentiation of oligodendrocytes [455]. *MYT1* interacts with *STEAP3* [456], which was a candidate gene for RLS association in the analysis of the ExomeChip data and it is involved in iron homeostasis [457]. Of note, *COL20A1* (collagen type XX alpha 1 chain, also *KIAA1510* [2]) was significant after correcting for testing 61 genes. The gene is transcribed in the brain [458]. It is in close proximity to *MYT1*. The genes *DMPK* (dystrophia myotonica protein kinase [2]), *RASGRP4* (RAS guanyl releasing protein 4 [2]) and *AAGAB* (alpha- and gamma-adaptin binding protein [2]) were also significantly associated with RLS after correcting for multiple testing of 61 genes. *DMPK* was related to the pathophysiology of myotonic dystrophy [459]. *RASGRP4* functions in the mast cell development [460]. And *AAGAB* is mainly known for its involvement in punctate palmoplantar keratoderma [461, 462]. However, the samples of the MIPseq experiment and the ExomeChip experiment were partially overlapping and not independent. Thus a Bonferroni correction for 61 tests might not be stringent enough to avoid false positive associations. Further functional studies are needed to assess its function in the pathophysiology of RLS and to validate the variants that were observed in this study.

In the single variant association test, one SNP reached genome-wide significance and another one almost genome-wide significance. The variants were located in *MYT1* (3' UTR) and *OLFML2B* (Aps60/61Gly) and were unlikely to be detrimental. Of note, the rare allele was unique to cases. Further analysis has to be considered to validate these SNPs and to exclude the possibility of sequencing artefacts as the mapping qualities of the respective reads were near 10. Two other SNPs were significant after correcting for multiple testing of 26,192 score tests. For both SNPs, the common allele was the risk allele, and they were located in introns of *ATP2C1* and *CADM1*. They might be regulatory variants of high impact. These SNPs have to be validated as well.

The findings from the MIPseq data have to be replicated in a larger samples set. Furthermore, a correction for population substructure might have been less effective than expected, and thus another replication might be performed based on family data.

5.3 Explaining RLS Families with RLS Risk SNPs

This work did not only address the rare variant-common disease hypothesis for RLS, but also the common variant-common disease hypothesis: The question was raised whether the published RLS associated risk loci might explain families enriched with RLS cases. Therefore, 79 families were genotyped using the Affimetrix Axiom technology, and the RLS risk SNPs were imputed in case of missing genotype calls. After the QC, 78 families were remaining (see appendix, Table 34, p. 315).

The leading SNPs from the latest published RLS GWAS [245] were used for the analysis and also rs113851554, which was shown to be associated with RLS [70]. Only little is known about the causality of these SNPs (e.g. see [32]), and thus these variants might tag the real causal variants. So a slightly different set of SNPs could have been chosen as well to address the general question, e.g. rs11693221 instead of rs113851554 [32]. However, the overall message should not change.

The variants rs113851554 and rs2300478 of the *MEIS1* locus were associated with the RLS phenotype in the cohort of the combined families. The *p* values differed between Wald test and score test (Table 27, p. 80) of the rare variant rs113851554. This was expected. Especially the Wald test gives deflated *p* values in case of analyzing rarer variants [342, 463], but the score test is inflated [464]. Thus the Wald test is conservative in single rare variant association tests. The typical GWAS significance threshold might not have to be applied here because the different SNPs throughout the pedigrees might be more correlated than in GWAS studies and thus a GWAS significance threshold might be too conservative.

For each individual family, the correlation was examined between RLS phenotypes and dosages of RLS associated risk alleles [70, 245] or their burden (only independent SNPs). Eight families showed at least one significant alternative model including an RLS risk SNP as a predictor for the disease status. These families were enriched for Finnish families. Their population is a founder population [465, 466], and a common genetic background might exist. Its setup might lead to an increased susceptibility to RLS. This background (or a common environmental component in Finland) might trigger RLS already with one RLS risk allele being present. As this background might be quite common, the inheritance of a SNP allele might already lead to inherited RLS. It might be interesting to examine the interaction of the linkage loci and the (burden of) disease risk SNPs in families that were subject to a linkage analysis in the past. The common risk allele burden significantly explained the familial phenotypic variance in 10 families. And two observations were made: First, only three families did also show significant associations of single SNP dosages with the disease status. Thus for some families, some RLS risk SNPs might have been less relevant than others, and adding less relevant SNPs to a burden calculation might have added noise to the model and reduced the significance. The relevance of a SNP might be correlated with its effect size in GWAS, and adding these effect sizes as a weighting scheme in the burden analysis might help to improve the burden model. However, the relevance of a SNP might also depend on the environmental or genetic background of a family. Second, the familial pseudo-R^2 depended on the size of the families: The larger the family, the lower the pseudo-R^2 value, the less phenotypic variance could be explained by the burden of risk alleles. The identification of new risk variants might then add to the explainable proportion of phenotypic variance in the larger families.

6 Concluding Remarks

6.1 Conclusion

This work added to the knowledge about the association of rare variants with RLS. It screened RLS cases and population based controls exome-wide for rare genetic variations using the ExomeChip. Single and gene-level association analyses were performed, and a set of RLS candidate genes was obtained. These genes were sequenced in their exonic and promotor regions using MIPseq in a large scale RLS NGS project, which had to be established as a technique. Further RLS candidate genes were added to the sequencing based on eQTL, functional and physical annotations of lead SNPs from an unpublished RLS meta-GWAS [373] with 23&me. The sequence data was used for a gene-level and single variant association analysis for rare SNPs.

Second, this work also explored whether families with multiple cases of RLS could be explained by common published RLS GWAS SNPs. Therefore, RLS families were selected and the individuals genotyped using the Affimetrix Axiom technology followed by genotype imputation. Then, the families' members' phenotypes were explained using logistic regression and correlation measurements.

6.1.1 Rare Variant Screening Using the ExomeChip

The ExomeChip genotype data enabled a screening of mainly rare and putative functional variants. Although the design of the ExomeChip itself was hypothesis driven and could not cover all functionally interesting rare variants of the human genome [350], the analysis could result in a list of genes that might contribute to RLS. Two types of analysis were performed: Single variant and gene-level association analysis with a generalized linear mixed model to correct for population structures and cryptic relatedness. The best associated gene was *RASGRP4* based on the Fisher method of combining gene level association analyses [346] and a strong single variant signal. But no unpublished gene or variant association reached genome-wide or exome wide significance.

6.1.2 Sequencing of RLS Candidate Genes Using MIPseq

The ExomeChip screen defined RLS candidate genes and further genes were added to this list based on annotations of an unpublished RLS meta-GWAS [373] with 23&me, summing up to 84 genes. Of these 84 genes, the exonic and promotor regions were then sequenced using the NGS technology MIPseq with 11,214 molecular inversion probes, which had to be established first. Then, 704 RLS cases and 752 population based controls could be sequenced and controlled for quality. Unrelated individuals were subject to a gene-level association analysis and all individuals to a single variant association analysis with SNPs. Population stratification was controlled in the gene-level tests using the first two principal components from external common variant genotype data. As a result, *RASGRP4*, *AAGAB*, *DMPK*, *COL20A1* as well as *MYT1* and *PTPRD* showed very low p values of association with RLS using the SKAT-O test for rare SNPs. The latter two new genes were eQTL of a meta-GWAS [373] signal, which showed that common and rare genetic variants might contribute to RLS. This gene-level association analysis on MIPseq data revealed a list of putative causal genes as the analysis was mainly based on exonic variants. These variants are assumed to be of functional relevance, e.g. in the case of nonsense or missense variants. But even synonymous variants can have an impact based on codon preferences [467, 468], mRNA splicing [469] and mRNA stability [470]. The single variant analysis was performed using a generalized linear mixed model and showed a genome-wide association for a variant in *MYT1* and also an almost genome-wide significant signal in *OLFM2B*. The rare alleles were exclusively found in RLS patients. Further rare variants were significant on a dataset-wide scale in *ATP2C* and *CADM1*, which were intronic, and the common alleles were the risk alleles. The association signals and genotypes have to be validated independently.

6.1.3 Explaining RLS Families with RLS Risk SNPs

In this work, individuals were genotyped from pedigrees with familial RLS on a genome-wide scale for common variants, followed by genotype imputation. The genotyped data was used to model the reported pedigree structure in single and gene-level association analysis with published RLS risk SNPs using generalized linear mixed models. These SNPs could significantly explain the majority of the phenotypes in 8 families that were enriched for Finnish origin. In another 7 families, the phenotypes were significantly explained by the burden of risk alleles.

6.2 Future Perspectives

The data, technologies and results of this work may promote future studies.

6.2.1 Future Research

The data of the ExomeChip might be used for further analyses. First, CNVs might be called using the ExomeChip probe intensity data as the method was already demonstrated to be successful [10]. Thus the probe intensities could be clustered by batch (RLS cases, KORA controls [354, 355], HNR controls [356]) for each marker, and the cluster positions could be used to call B allele frequencies (BAF) and log-R-ratios (LRR) for each marker and individual, and then CNVs could be called [10]. A preliminary analysis showed that a combined calling of BAF and LRR would lead to artefactual CNV calls.

The ExomeChip data could also be used in a pathway analysis. There are two options. First, the MAGENTA software could be applied, which takes association summary statistics [471], but the software was developed for common variants and would have to be adopted to rare variants; e.g. it assumes that 50% of all supplied variants are in high LD [471]. Thus either the existing gene-level association *p* values could be supplied to MAGENTA instead of single variant level summary statistics or a second approach could be applied. In this approach, the performed gene-level association analysis could be repeated. But instead of assigning variants to genes, the variants could be assigned to whole pathways. As pathways are overlapping by genes, the number of independent null hypothesis could be assed empirically as done before in this work. This would increase the study power, as the number of published human pathways is much lower than the number of human genes, and each pathway would combine more variants than the respective genes alone.

A recent publication on LD score regression showed that the inflation of test statistics could be dissected into sources of confounding and into an effect from the polygenicity of a trait [437]. It might be interesting to apply that technique to the RLS ExomeChip dataset, and for example to examine the performance of (different approaches and marker sets for) the correction for population stratification.

It might also be interesting to examine the epistasis in the ExomeChip data, e.g. for the variants of the candidate genes.

The MIPseq project should be expanded to a larger sample size so that more genes reach the significance threshold in the gene-level association analysis. Then the genes' signals might be dissected into gene regions (e.g. UTRs, exons, splice sites) to localize the signal origin. Furthermore, the association analysis might be conditioned on the local RLS associated common variants, and maybe then the strength of association could be enhanced. One might also consider the inclusion of weighting schemes for the variants in the gene level tests, but an overweighting of highly detrimental variants might mask signals, because RLS might not be a disease with a high potential for purifying selection or a severe impact on health. Of note, the MIPs were designed to populate each region of interest with at least three MIPs. This might enable the calling of larger structural variations, which might add to the understanding of the genetics of the restless legs syndrome.

Based on the results of this work, functional studies should be done on *COL20A1*, *MYT1*, *DMPK*, *RASGRP4*, *AAGAB* and *PTPRD*. For example, the orthologue could be knocked down/out in a mouse model, and the phenotype could be studied for overlaps with RLS symptoms.

The MIPseq setup could also be applied to the families of this work, and maybe an analysis could add to the explanation of the phenotypes in the pedigrees.

As a next step in the family study, the analysis could also be done with other RLS associated variants that are to be published in the future, or with an alternative phenotype readout, e.g. age of onset or RLS severity. Under the assumption of causality for the RLS associated test SNP (or a tagged variant), it might be interesting to find the underlying genetic or environmental background that enabled RLS in some pedigrees with a specific marker but not in others. An interaction analysis might be a method to address this question.

6.2.2 Vision

This work contributed to the dissection of the RLS genetics. In the future, it might add to the definition of a genetic RLS pathway and as a consequence to the definition of putative genetic RLS subtypes. This might enhance the diagnosis and the treatment of the restless legs syndrome.

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Appendix A – MIPseq Primers

The MIPseq primer sequences [78] are listed in the following table:

Table 31: MIPseq PCR and sequencing primers

Primer	Sequence	Usage
MIPBC_SEQ_FOR	CATACGAGATCCGTAATCGGGAAGCTGAAG	sequencing
MIPBC_SEQ_REV	ACACGCACGATCCGACGGTAGTGT	sequencing
MIPBC_SEQ_INDX	ACACTACCGTCGGATCGTGCGTGT	sequencing
SLXA_PE_MIPBC_FOR	AATGATACGGCGACCACCGAGATCTACACATACGAGATCCGTAATCGGGAAGCTGAAG	PCR
SLXA_PE_MIPBC2_REV_001	CAAGCAGAAGACGGCATACGAGATGTTAAGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_002	CAAGCAGAAGACGGCATACGAGATTCTAAGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_003	CAAGCAGAAGACGGCATACGAGATTGTACATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_004	CAAGCAGAAGACGGCATACGAGATAATACCGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_005	CAAGCAGAAGACGGCATACGAGATTGTCTATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_006	CAAGCAGAAGACGGCATACGAGATTCACTGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_007	CAAGCAGAAGACGGCATACGAGATTTGTATTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_008	CAAGCAGAAGACGGCATACGAGATAGACTAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_009	CAAGCAGAAGACGGCATACGAGATATTGTCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_010	CAAGCAGAAGACGGCATACGAGATGTTCTACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_011	CAAGCAGAAGACGGCATACGAGATTTCATTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_012	CAAGCAGAAGACGGCATACGAGATAAGCGTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_013	CAAGCAGAAGACGGCATACGAGATCGTAGGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_014	CAAGCAGAAGACGGCATACGAGATAGTTAGCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_015	CAAGCAGAAGACGGCATACGAGATGAACGTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_016	CAAGCAGAAGACGGCATACGAGATAGAACACTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_017	CAAGCAGAAGACGGCATACGAGATTGTTGGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_018	CAAGCAGAAGACGGCATACGAGATGGCTAATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_019	CAAGCAGAAGACGGCATACGAGATGCTAGAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_020	CAAGCAGAAGACGGCATACGAGATTGTACTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_021	CAAGCAGAAGACGGCATACGAGATAGTTACACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_022	CAAGCAGAAGACGGCATACGAGATGTACACGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_023	CAAGCAGAAGACGGCATACGAGATACTGTAAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_024	CAAGCAGAAGACGGCATACGAGATGATCATGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_025	CAAGCAGAAGACGGCATACGAGATTGCTAACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_026	CAAGCAGAAGACGGCATACGAGATTAATGCTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_027	CAAGCAGAAGACGGCATACGAGATCTTGTTGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_028	CAAGCAGAAGACGGCATACGAGATGATACAAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_029	CAAGCAGAAGACGGCATACGAGATATACAGCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_030	CAAGCAGAAGACGGCATACGAGATCTGGATAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_031	CAAGCAGAAGACGGCATACGAGATTCATCAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_032	CAAGCAGAAGACGGCATACGAGATTTATACCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_033	CAAGCAGAAGACGGCATACGAGATGCTGATTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_034	CAAGCAGAAGACGGCATACGAGATATAAGGCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_035	CAAGCAGAAGACGGCATACGAGATAAGACTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_036	CAAGCAGAAGACGGCATACGAGATTAGCAACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_037	CAAGCAGAAGACGGCATACGAGATCAAGTAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_038	CAAGCAGAAGACGGCATACGAGATTCATGATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_039	CAAGCAGAAGACGGCATACGAGATTAGCTCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_040	CAAGCAGAAGACGGCATACGAGATACTACATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_041	CAAGCAGAAGACGGCATACGAGATTGTGCCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_042	CAAGCAGAAGACGGCATACGAGATGACTTCCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_043	CAAGCAGAAGACGGCATACGAGATTATTCTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_044	CAAGCAGAAGACGGCATACGAGATCACTAGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_045	CAAGCAGAAGACGGCATACGAGATCTTCGCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_046	CAAGCAGAAGACGGCATACGAGATCTAGCGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_047	CAAGCAGAAGACGGCATACGAGATTACGTTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_048	CAAGCAGAAGACGGCATACGAGATAAGTAGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_049	CAAGCAGAAGACGGCATACGAGATGACGTATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_050	CAAGCAGAAGACGGCATACGAGATACGTTCAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_051	CAAGCAGAAGACGGCATACGAGATAGCTATATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_052	CAAGCAGAAGACGGCATACGAGATAGTGCGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_053	CAAGCAGAAGACGGCATACGAGATCAATGGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_054	CAAGCAGAAGACGGCATACGAGATATTCCGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_055	CAAGCAGAAGACGGCATACGAGATAGCTGTTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_056	CAAGCAGAAGACGGCATACGAGATTTCGACTCACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	**Sequence**	**Usage**
SLXA_PE_MIPBC2_REV_057	CAAGCAGAAGACGGCATACGAGATCGAATGGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_058	CAAGCAGAAGACGGCATACGAGATTAGTGTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_059	CAAGCAGAAGACGGCATACGAGATACGCATGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_060	CAAGCAGAAGACGGCATACGAGATTTCGTACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_061	CAAGCAGAAGACGGCATACGAGATTTCTGCTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_062	CAAGCAGAAGACGGCATACGAGATTGGAAGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_063	CAAGCAGAAGACGGCATACGAGATGATGCTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_064	CAAGCAGAAGACGGCATACGAGATAGCCTGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_065	CAAGCAGAAGACGGCATACGAGATCACCAGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_066	CAAGCAGAAGACGGCATACGAGATGTTACACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_067	CAAGCAGAAGACGGCATACGAGATGCGTTAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_068	CAAGCAGAAGACGGCATACGAGATTGACGTTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_069	CAAGCAGAAGACGGCATACGAGATTAGGCGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_070	CAAGCAGAAGACGGCATACGAGATAAGTGAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_071	CAAGCAGAAGACGGCATACGAGATCCGGAATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_072	CAAGCAGAAGACGGCATACGAGATAATAGGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_073	CAAGCAGAAGACGGCATACGAGATTTCAGGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_074	CAAGCAGAAGACGGCATACGAGATTAATCGCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_075	CAAGCAGAAGACGGCATACGAGATCTTAGGTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_076	CAAGCAGAAGACGGCATACGAGATTTGATCTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_077	CAAGCAGAAGACGGCATACGAGATTCTTACTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_078	CAAGCAGAAGACGGCATACGAGATGAGTACACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_079	CAAGCAGAAGACGGCATACGAGATACGTTACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_080	CAAGCAGAAGACGGCATACGAGATTGGTAAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_081	CAAGCAGAAGACGGCATACGAGATGATAGCACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_082	CAAGCAGAAGACGGCATACGAGATGACTTAGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_083	CAAGCAGAAGACGGCATACGAGATAGTCGTTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_084	CAAGCAGAAGACGGCATACGAGATCGTGATTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_085	CAAGCAGAAGACGGCATACGAGATTCAGTAGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_086	CAAGCAGAAGACGGCATACGAGATATGTGTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_087	CAAGCAGAAGACGGCATACGAGATCAGAATATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_088	CAAGCAGAAGACGGCATACGAGATTAAGTCTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_089	CAAGCAGAAGACGGCATACGAGATATCGACATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_090	CAAGCAGAAGACGGCATACGAGATACAGCTGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_091	CAAGCAGAAGACGGCATACGAGATATCACAAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_092	CAAGCAGAAGACGGCATACGAGATGTCGAATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_093	CAAGCAGAAGACGGCATACGAGATTGCCGATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_094	CAAGCAGAAGACGGCATACGAGATACTAATGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_095	CAAGCAGAAGACGGCATACGAGATCTAGTAGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_096	CAAGCAGAAGACGGCATACGAGATTTAAGCCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_097	CAAGCAGAAGACGGCATACGAGATGCATAACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_098	CAAGCAGAAGACGGCATACGAGATTTCTCGGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_099	CAAGCAGAAGACGGCATACGAGATAGATCCAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_100	CAAGCAGAAGACGGCATACGAGATACACGTTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_101	CAAGCAGAAGACGGCATACGAGATCGATCTGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_102	CAAGCAGAAGACGGCATACGAGATGTACCTATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_103	CAAGCAGAAGACGGCATACGAGATCGTATCTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_104	CAAGCAGAAGACGGCATACGAGATCATGATCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_105	CAAGCAGAAGACGGCATACGAGATTGCAACACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_106	CAAGCAGAAGACGGCATACGAGATCCAAGCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_107	CAAGCAGAAGACGGCATACGAGATGGAACCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_108	CAAGCAGAAGACGGCATACGAGATCACGTCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_109	CAAGCAGAAGACGGCATACGAGATAGGTCAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_110	CAAGCAGAAGACGGCATACGAGATCAAGATGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_111	CAAGCAGAAGACGGCATACGAGATTTGCTGGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_112	CAAGCAGAAGACGGCATACGAGATGAATCGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_113	CAAGCAGAAGACGGCATACGAGATAATGACAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_114	CAAGCAGAAGACGGCATACGAGATGTGGTCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_115	CAAGCAGAAGACGGCATACGAGATCAGTCTTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_116	CAAGCAGAAGACGGCATACGAGATACAGTTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_117	CAAGCAGAAGACGGCATACGAGATCATTGAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_118	CAAGCAGAAGACGGCATACGAGATGCATCTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_119	CAAGCAGAAGACGGCATACGAGATCTGCCTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_120	CAAGCAGAAGACGGCATACGAGATCTCAATGAACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	Sequence	Usage
SLXA_PE_MIPBC2_REV_121	CAAGCAGAAGACGGCATACGAGATCCGATTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_122	CAAGCAGAAGACGGCATACGAGATCAATTCAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_123	CAAGCAGAAGACGGCATACGAGATGTTGTAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_124	CAAGCAGAAGACGGCATACGAGATGACAATAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_125	CAAGCAGAAGACGGCATACGAGATAAGGCATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_126	CAAGCAGAAGACGGCATACGAGATTCTATTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_127	CAAGCAGAAGACGGCATACGAGATGGATCGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_128	CAAGCAGAAGACGGCATACGAGATTTAAGTGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_129	CAAGCAGAAGACGGCATACGAGATACAGGCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_130	CAAGCAGAAGACGGCATACGAGATATCGGTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_131	CAAGCAGAAGACGGCATACGAGATGACCACATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_132	CAAGCAGAAGACGGCATACGAGATAACTTGGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_133	CAAGCAGAAGACGGCATACGAGATTATTCGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_134	CAAGCAGAAGACGGCATACGAGATGGAGACTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_135	CAAGCAGAAGACGGCATACGAGATAGTCATGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_136	CAAGCAGAAGACGGCATACGAGATAGGTACGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_137	CAAGCAGAAGACGGCATACGAGATACGATCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_138	CAAGCAGAAGACGGCATACGAGATAGCAACTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_139	CAAGCAGAAGACGGCATACGAGATTACTGACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_140	CAAGCAGAAGACGGCATACGAGATCTACGAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_141	CAAGCAGAAGACGGCATACGAGATATCTAGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_142	CAAGCAGAAGACGGCATACGAGATATCCTTGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_143	CAAGCAGAAGACGGCATACGAGATTTAATGCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_144	CAAGCAGAAGACGGCATACGAGATTTAACCTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_145	CAAGCAGAAGACGGCATACGAGATTAGACACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_146	CAAGCAGAAGACGGCATACGAGATCCACAAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_147	CAAGCAGAAGACGGCATACGAGATGCTAATCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_148	CAAGCAGAAGACGGCATACGAGATGTTGCTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_149	CAAGCAGAAGACGGCATACGAGATGTTGGCTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_150	CAAGCAGAAGACGGCATACGAGATCATGTGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_151	CAAGCAGAAGACGGCATACGAGATAACGAAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_152	CAAGCAGAAGACGGCATACGAGATATTATCGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_153	CAAGCAGAAGACGGCATACGAGATGTATTGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_154	CAAGCAGAAGACGGCATACGAGATAGACTTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_155	CAAGCAGAAGACGGCATACGAGATACCATGCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_156	CAAGCAGAAGACGGCATACGAGATTGAGCATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_157	CAAGCAGAAGACGGCATACGAGATTAAGGCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_158	CAAGCAGAAGACGGCATACGAGATTCAATGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_159	CAAGCAGAAGACGGCATACGAGATGTCAGACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_160	CAAGCAGAAGACGGCATACGAGATCATCTGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_161	CAAGCAGAAGACGGCATACGAGATCGTGGATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_162	CAAGCAGAAGACGGCATACGAGATTCATGTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_163	CAAGCAGAAGACGGCATACGAGATATCTCGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_164	CAAGCAGAAGACGGCATACGAGATAGTACTCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_165	CAAGCAGAAGACGGCATACGAGATTCGGAACTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_166	CAAGCAGAAGACGGCATACGAGATAAGCAATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_167	CAAGCAGAAGACGGCATACGAGATGTCTTGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_168	CAAGCAGAAGACGGCATACGAGATACTTCGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_169	CAAGCAGAAGACGGCATACGAGATTGCAGTTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_170	CAAGCAGAAGACGGCATACGAGATCGTAACGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_171	CAAGCAGAAGACGGCATACGAGATTTAGCACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_172	CAAGCAGAAGACGGCATACGAGATGCGATCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_173	CAAGCAGAAGACGGCATACGAGATCGCATATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_174	CAAGCAGAAGACGGCATACGAGATACCAGGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_175	CAAGCAGAAGACGGCATACGAGATTCATAGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_176	CAAGCAGAAGACGGCATACGAGATTACAATGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_177	CAAGCAGAAGACGGCATACGAGATATAAGCAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_178	CAAGCAGAAGACGGCATACGAGATTGAACGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_179	CAAGCAGAAGACGGCATACGAGATGATTCCTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_180	CAAGCAGAAGACGGCATACGAGATCAGAGTGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_181	CAAGCAGAAGACGGCATACGAGATAGATAACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_182	CAAGCAGAAGACGGCATACGAGATGAGTAACTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_183	CAAGCAGAAGACGGCATACGAGATATACCTGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_184	CAAGCAGAAGACGGCATACGAGATGCTAGTTGACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	**Sequence**	**Usage**
SLXA_PE_MIPBC2_REV_185	CAAGCAGAAGACGGCATACGAGATTAGTGCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_186	CAAGCAGAAGACGGCATACGAGATACTCTGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_187	CAAGCAGAAGACGGCATACGAGATCTCTAATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_188	CAAGCAGAAGACGGCATACGAGATCATAGACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_189	CAAGCAGAAGACGGCATACGAGATACCACTGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_190	CAAGCAGAAGACGGCATACGAGATCATCAATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_191	CAAGCAGAAGACGGCATACGAGATAACGCTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_192	CAAGCAGAAGACGGCATACGAGATATACGCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_193	CAAGCAGAAGACGGCATACGAGATCTCTAGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_194	CAAGCAGAAGACGGCATACGAGATGGTGAACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_195	CAAGCAGAAGACGGCATACGAGATAGCTCTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_196	CAAGCAGAAGACGGCATACGAGATTGAGTGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_197	CAAGCAGAAGACGGCATACGAGATACGCTTATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_198	CAAGCAGAAGACGGCATACGAGATCAGATAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_199	CAAGCAGAAGACGGCATACGAGATGTCACCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_200	CAAGCAGAAGACGGCATACGAGATTGGTCGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_201	CAAGCAGAAGACGGCATACGAGATGCAATATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_202	CAAGCAGAAGACGGCATACGAGATCACATGCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_203	CAAGCAGAAGACGGCATACGAGATTCCTTCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_204	CAAGCAGAAGACGGCATACGAGATCTGATGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_205	CAAGCAGAAGACGGCATACGAGATCACTGCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_206	CAAGCAGAAGACGGCATACGAGATTCGGAGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_207	CAAGCAGAAGACGGCATACGAGATCGGTATGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_208	CAAGCAGAAGACGGCATACGAGATCTGAGCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_209	CAAGCAGAAGACGGCATACGAGATCTTGGTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_210	CAAGCAGAAGACGGCATACGAGATCTGACAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_211	CAAGCAGAAGACGGCATACGAGATTGGTACAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_212	CAAGCAGAAGACGGCATACGAGATGGTCTCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_213	CAAGCAGAAGACGGCATACGAGATTGGCTAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_214	CAAGCAGAAGACGGCATACGAGATAGAGGATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_215	CAAGCAGAAGACGGCATACGAGATCGAATACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_216	CAAGCAGAAGACGGCATACGAGATAGCGTTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_217	CAAGCAGAAGACGGCATACGAGATTGACCTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_218	CAAGCAGAAGACGGCATACGAGATTAGTTGCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_219	CAAGCAGAAGACGGCATACGAGATGTTGCAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_220	CAAGCAGAAGACGGCATACGAGATATAGAGGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_221	CAAGCAGAAGACGGCATACGAGATCTTGACTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_222	CAAGCAGAAGACGGCATACGAGATAACCTCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_223	CAAGCAGAAGACGGCATACGAGATTCAACCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_224	CAAGCAGAAGACGGCATACGAGATGCTATGGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_225	CAAGCAGAAGACGGCATACGAGATTCTTGACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_226	CAAGCAGAAGACGGCATACGAGATACATGGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_227	CAAGCAGAAGACGGCATACGAGATATGACAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_228	CAAGCAGAAGACGGCATACGAGATAACTCCTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_229	CAAGCAGAAGACGGCATACGAGATACTTAAGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_230	CAAGCAGAAGACGGCATACGAGATTCTTGCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_231	CAAGCAGAAGACGGCATACGAGATGACTGTTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_232	CAAGCAGAAGACGGCATACGAGATACTGACCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_233	CAAGCAGAAGACGGCATACGAGATTGTGTCCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_234	CAAGCAGAAGACGGCATACGAGATCCTGTCATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_235	CAAGCAGAAGACGGCATACGAGATATGTACTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_236	CAAGCAGAAGACGGCATACGAGATGAATAATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_237	CAAGCAGAAGACGGCATACGAGATGTCTATGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_238	CAAGCAGAAGACGGCATACGAGATCCTTAGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_239	CAAGCAGAAGACGGCATACGAGATGAATTCGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_240	CAAGCAGAAGACGGCATACGAGATCTAGTCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_241	CAAGCAGAAGACGGCATACGAGATTCAGAGGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_242	CAAGCAGAAGACGGCATACGAGATGACATTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_243	CAAGCAGAAGACGGCATACGAGATCTAACACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_244	CAAGCAGAAGACGGCATACGAGATGTGTGATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_245	CAAGCAGAAGACGGCATACGAGATCTGTTCACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_246	CAAGCAGAAGACGGCATACGAGATGGTCAGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_247	CAAGCAGAAGACGGCATACGAGATAACCGATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_248	CAAGCAGAAGACGGCATACGAGATCAGCTAAGACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	**Sequence**	**Usage**
SLXA_PE_MIPBC2_REV_249	CAAGCAGAAGACGGCATACGAGATGATCCATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_250	CAAGCAGAAGACGGCATACGAGATCACGATACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_251	CAAGCAGAAGACGGCATACGAGATACATGCGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_252	CAAGCAGAAGACGGCATACGAGATGCTTATGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_253	CAAGCAGAAGACGGCATACGAGATTGACAGGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_254	CAAGCAGAAGACGGCATACGAGATAAGATACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_255	CAAGCAGAAGACGGCATACGAGATGATGGACTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_256	CAAGCAGAAGACGGCATACGAGATGAAGTTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_257	CAAGCAGAAGACGGCATACGAGATCGATCAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_258	CAAGCAGAAGACGGCATACGAGATGCCTACAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_259	CAAGCAGAAGACGGCATACGAGATATTAGATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_260	CAAGCAGAAGACGGCATACGAGATACTTGTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_261	CAAGCAGAAGACGGCATACGAGATTACATGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_262	CAAGCAGAAGACGGCATACGAGATCTAGAATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_263	CAAGCAGAAGACGGCATACGAGATATGGTTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_264	CAAGCAGAAGACGGCATACGAGATGGCATCTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_265	CAAGCAGAAGACGGCATACGAGATCATTACGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_266	CAAGCAGAAGACGGCATACGAGATGTTACGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_267	CAAGCAGAAGACGGCATACGAGATGGATTCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_268	CAAGCAGAAGACGGCATACGAGATTCGATTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_269	CAAGCAGAAGACGGCATACGAGATTTGCACACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_270	CAAGCAGAAGACGGCATACGAGATATACGTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_271	CAAGCAGAAGACGGCATACGAGATACGAAGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_272	CAAGCAGAAGACGGCATACGAGATGCGTCATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_273	CAAGCAGAAGACGGCATACGAGATGTTCGGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_274	CAAGCAGAAGACGGCATACGAGATATTGTGCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_275	CAAGCAGAAGACGGCATACGAGATTGGATCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_276	CAAGCAGAAGACGGCATACGAGATTACAACTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_277	CAAGCAGAAGACGGCATACGAGATGAAGACGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_278	CAAGCAGAAGACGGCATACGAGATCGACGATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_279	CAAGCAGAAGACGGCATACGAGATATCTTCCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_280	CAAGCAGAAGACGGCATACGAGATTACTGGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_281	CAAGCAGAAGACGGCATACGAGATTGAATTCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_282	CAAGCAGAAGACGGCATACGAGATATCGCTTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_283	CAAGCAGAAGACGGCATACGAGATGCAATTGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_284	CAAGCAGAAGACGGCATACGAGATATCTGCGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_285	CAAGCAGAAGACGGCATACGAGATAAGCTTGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_286	CAAGCAGAAGACGGCATACGAGATGAGAATCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_287	CAAGCAGAAGACGGCATACGAGATTACAGAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_288	CAAGCAGAAGACGGCATACGAGATTCGAGATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_289	CAAGCAGAAGACGGCATACGAGATTATCAGCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_290	CAAGCAGAAGACGGCATACGAGATTGCGTGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_291	CAAGCAGAAGACGGCATACGAGATCGTTATCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_292	CAAGCAGAAGACGGCATACGAGATTCAGATACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_293	CAAGCAGAAGACGGCATACGAGATTAGCCGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_294	CAAGCAGAAGACGGCATACGAGATATCCGAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_295	CAAGCAGAAGACGGCATACGAGATTGCTATGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_296	CAAGCAGAAGACGGCATACGAGATGAACTACCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_297	CAAGCAGAAGACGGCATACGAGATGGTATTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_298	CAAGCAGAAGACGGCATACGAGATTACGAGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_299	CAAGCAGAAGACGGCATACGAGATGCACATAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_300	CAAGCAGAAGACGGCATACGAGATGAGCGATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_301	CAAGCAGAAGACGGCATACGAGATACGTGTTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_302	CAAGCAGAAGACGGCATACGAGATTATCCAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_303	CAAGCAGAAGACGGCATACGAGATTATCGGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_304	CAAGCAGAAGACGGCATACGAGATCTTGCGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_305	CAAGCAGAAGACGGCATACGAGATCTATTGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_306	CAAGCAGAAGACGGCATACGAGATTGCGATCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_307	CAAGCAGAAGACGGCATACGAGATTGACGAAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_308	CAAGCAGAAGACGGCATACGAGATATTGGACGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_309	CAAGCAGAAGACGGCATACGAGATACATTGCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_310	CAAGCAGAAGACGGCATACGAGATTCACTTGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_311	CAAGCAGAAGACGGCATACGAGATTTACCGACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_312	CAAGCAGAAGACGGCATACGAGATCATGTACCACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	Sequence	Usage
SLXA_PE_MIPBC2_REV_313	CAAGCAGAAGACGGCATACGAGATTTGTTCCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_314	CAAGCAGAAGACGGCATACGAGATTGATTATCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_315	CAAGCAGAAGACGGCATACGAGATCTCCTGATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_316	CAAGCAGAAGACGGCATACGAGATTCCTCTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_317	CAAGCAGAAGACGGCATACGAGATGTACTCAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_318	CAAGCAGAAGACGGCATACGAGATCAATGAGGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_319	CAAGCAGAAGACGGCATACGAGATCACGCATAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_320	CAAGCAGAAGACGGCATACGAGATCAATAGCCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_321	CAAGCAGAAGACGGCATACGAGATCCTACAGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_322	CAAGCAGAAGACGGCATACGAGATCACAGTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_323	CAAGCAGAAGACGGCATACGAGATTAACGAGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_324	CAAGCAGAAGACGGCATACGAGATTCTGCTTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_325	CAAGCAGAAGACGGCATACGAGATTGTATAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_326	CAAGCAGAAGACGGCATACGAGATGTATACATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_327	CAAGCAGAAGACGGCATACGAGATATGGCACAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_328	CAAGCAGAAGACGGCATACGAGATAACTCGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_329	CAAGCAGAAGACGGCATACGAGATGATCTGGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_330	CAAGCAGAAGACGGCATACGAGATACAAGTCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_331	CAAGCAGAAGACGGCATACGAGATACGAGACTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_332	CAAGCAGAAGACGGCATACGAGATATGAGTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_333	CAAGCAGAAGACGGCATACGAGATATTCAAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_334	CAAGCAGAAGACGGCATACGAGATCGGAATTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_335	CAAGCAGAAGACGGCATACGAGATCTGGAGTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_336	CAAGCAGAAGACGGCATACGAGATGTCCATCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_337	CAAGCAGAAGACGGCATACGAGATTAACAGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_338	CAAGCAGAAGACGGCATACGAGATCATTGTGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_339	CAAGCAGAAGACGGCATACGAGATACTTGATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_340	CAAGCAGAAGACGGCATACGAGATTTGACCGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_341	CAAGCAGAAGACGGCATACGAGATACAATGTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_342	CAAGCAGAAGACGGCATACGAGATAAGTTCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_343	CAAGCAGAAGACGGCATACGAGATCGCCATAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_344	CAAGCAGAAGACGGCATACGAGATAGACGAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_345	CAAGCAGAAGACGGCATACGAGATACCGTATTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_346	CAAGCAGAAGACGGCATACGAGATGCTAACAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_347	CAAGCAGAAGACGGCATACGAGATCTATGCTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_348	CAAGCAGAAGACGGCATACGAGATTCAACTCGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_349	CAAGCAGAAGACGGCATACGAGATTTCAAGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_350	CAAGCAGAAGACGGCATACGAGATACGGTGTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_351	CAAGCAGAAGACGGCATACGAGATACCAGTATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_352	CAAGCAGAAGACGGCATACGAGATCCATGTACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_353	CAAGCAGAAGACGGCATACGAGATTACGCAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_354	CAAGCAGAAGACGGCATACGAGATTCTATAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_355	CAAGCAGAAGACGGCATACGAGATTTCAGAGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_356	CAAGCAGAAGACGGCATACGAGATATCCTGTCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_357	CAAGCAGAAGACGGCATACGAGATTTCCACGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_358	CAAGCAGAAGACGGCATACGAGATTAACTTAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_359	CAAGCAGAAGACGGCATACGAGATATCTTAGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_360	CAAGCAGAAGACGGCATACGAGATCATACCTGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_361	CAAGCAGAAGACGGCATACGAGATTAGAGTCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_362	CAAGCAGAAGACGGCATACGAGATATGACCAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_363	CAAGCAGAAGACGGCATACGAGATTATACGGTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_364	CAAGCAGAAGACGGCATACGAGATCGTTCTATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_365	CAAGCAGAAGACGGCATACGAGATGGAATAGCACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_366	CAAGCAGAAGACGGCATACGAGATTCAGACCAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_367	CAAGCAGAAGACGGCATACGAGATCCTCGTAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_368	CAAGCAGAAGACGGCATACGAGATCATTCGGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_369	CAAGCAGAAGACGGCATACGAGATACGGCAATACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_370	CAAGCAGAAGACGGCATACGAGATTAACCATGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_371	CAAGCAGAAGACGGCATACGAGATTTGTCAACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_372	CAAGCAGAAGACGGCATACGAGATCAGTTGAAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_373	CAAGCAGAAGACGGCATACGAGATAGAAGCTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_374	CAAGCAGAAGACGGCATACGAGATTGCATCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_375	CAAGCAGAAGACGGCATACGAGATACTGGAGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_376	CAAGCAGAAGACGGCATACGAGATCCATAGTTACACGCACGATCCGACGGTAGTGT	PCR

continued table…

Primer	**Sequence**	**Usage**
SLXA_PE_MIPBC2_REV_377	CAAGCAGAAGACGGCATACGAGATCTAAGTTAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_378	CAAGCAGAAGACGGCATACGAGATGTTAGCCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_379	CAAGCAGAAGACGGCATACGAGATTTCGTGAGACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_380	CAAGCAGAAGACGGCATACGAGATAGTCTCTTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_381	CAAGCAGAAGACGGCATACGAGATGGATATACACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_382	CAAGCAGAAGACGGCATACGAGATAAGACGCTACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_383	CAAGCAGAAGACGGCATACGAGATGTGTCTGAACACGCACGATCCGACGGTAGTGT	PCR
SLXA_PE_MIPBC2_REV_384	CAAGCAGAAGACGGCATACGAGATAGAGTGCAACACGCACGATCCGACGGTAGTGT	PCR

Appendix B – R Functions for Processing MIP Designs and Setting Up MIPseq

The following functions were written in R [4]. They were used to process mipgen [399] output and MIP design outputs from the Nijmegen platform. In detail, they enable the combination of different MIP designs, their quality control as well as annotation and automated iterative MIP designs. The function “iterative_redesign.fct” needs to specify the path to the mipgen [399] design software, the path to a wrapper (shell script, see appendix) for the mipgen [399] design software, an indexed reference genome and a compressed vcf file of the SNPs to be considered in the MIP design.

```
# function to check for factors//////////////////////////////////////

data_contains_factor.fct <- function(data.x) {
  if (nrow(data.x) == 0) {
    return(0)
  }
  is_factor.v <- apply(as.matrix(1:ncol(data.x)), 1, function(index.s) {
    is.factor(data.x[, index.s])
  })
  if (any(is_factor.v)) {
    warning("Data contains factors!", immediate. = TRUE)
    return(1)
  } else {
    return(0)
  }
}

# function to collapse a bed matrix/df///////////////////////////////

collapse_bed.fct <- function(bed.df, integer.merge.mode = TRUE,
  buffer.region = 0, verbose = T, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[collapse_bed.fct]: beginning")
  }
  # DESCRIPTION: bed.df should be a df with at least three
  # columns (col 1 = chr..., col 2 & 3 = positions, col 4 =
  # annotation)
  # if integer merge mode, than merging of
  # neighbouring integer positions sould be done e.g range 1 to
  # 4 and 5 to 6 will be merged to 1 to 6
  # DATA CHECK:
  data_contains_factor.fct(bed.df)
  if (nrow(bed.df) == 0) {
    return(NULL)
  }
  # prepare the bed.df
  if (nrow(bed.df) < 1) {
    return(NULL)
  }
  if (ncol(bed.df) == 3) {
    bed.df$anno <- NA
  }
  colnames(bed.df) <- c("chr", "start", "stop", "anno")
  bed.df$chr <- as.character(bed.df$chr)
  bed.df$start <- as.numeric(bed.df$start)
  bed.df$stop <- as.numeric(bed.df$stop)
  bed.df$anno <- as.character(bed.df$anno)
  # perform region merging
  # order the entries according to positions
  if (verbose) {
    cat(feed, "[collapse_bed.fct]: sorting positions")
  }
  for (index in 1:nrow(bed.df)) {
    positions.v <- bed.df[index, c("start", "stop")]
    bed.df[index, c("start", "stop")] <-
```

```
      positions.v[order(positions.v)]
  }
  bed.df <- bed.df[order(bed.df$chr, bed.df$start, bed.df$stop),
    ]
  # if just one line is supplied, than return the bed.df
  if (nrow(bed.df) == 1) {
    return(bed.df)
  }
  # asign overlaps, get vector hinting to overlapping regions
  if (verbose) {
    cat(feed, "[collapse_bed.fct]: searching overlaps for region ",
      feed)
  }
  region.v <- c(1, rep(NA, nrow(bed.df) - 1))
  zaehler.region.s <- 1
  nrow.bed.df <- nrow(bed.df)
  for (index in 2:nrow.bed.df) {
    if (verbose) {
      cat("\r")
      cat(index)
      cat("/")
      cat(nrow.bed.df)
    }
    # NOTE: as regions might be surrounded by a previous region,
    # the stop of a collapsed region sould always be the maximum
    # stop of the collapsed region’s members. NOTE: This is
    # important, because a subsequent querried region might
    # intersect with the maximum extend, but not with the
    # previously querried member and a new region might be opened
    max.stop.current_region.s <- max(bed.df[region.v %in%
      zaehler.region.s, "stop"])
    if (!integer.merge.mode) {
      if (bed.df[index, "start"] - buffer.region <=
        max.stop.current_region.s +
        buffer.region & bed.df[index, "stop"] + buffer.region >=
        bed.df[index - 1, "start"] - buffer.region &
        bed.df[index, "chr"] == bed.df[index - 1, "chr"]) {
        region.v[index] <- zaehler.region.s
      } else {
        zaehler.region.s <- zaehler.region.s + 1
        region.v[index] <- zaehler.region.s
      }
    } else {
      if (bed.df[index, "start"] - 1 - buffer.region <=
        max.stop.current_region.s + buffer.region & bed.df[index,
        "stop"] + buffer.region >= bed.df[index - 1,
        "start"] - 1 - buffer.region & bed.df[index,
        "chr"] == bed.df[index - 1, "chr"]) {
        region.v[index] <- zaehler.region.s
      } else {
        zaehler.region.s <- zaehler.region.s + 1
        region.v[index] <- zaehler.region.s
      }
    }
  }
  # create overlap
  if (verbose) {
    cat(feed, "[collapse_bed.fct]: collapsing regions ")
  }
  new.bed.df <- as.data.frame(t(apply(matrix(1:zaehler.region.s),
    1, function(region.s) {
      auswahl.v <- region.v %in% region.s
      minimal.start <- min(bed.df[auswahl.v, "start"],
        na.rm = T)
      maximal.stop <- max(bed.df[auswahl.v, "stop"], na.rm = T)
      collapsed.chr <- unique(bed.df[auswahl.v, "chr"])
      collapsed.anno <- paste(unique(bed.df[auswahl.v,
        "anno"]), collapse = ",")
      # NOTE: Here just characters are returned!!!
```

```
      return(c(collapsed.chr, minimal.start, maximal.stop,
        collapsed.anno))
    })), stringsAsFactors = F)
  colnames(new.bed.df) <- c("chr", "start", "stop", "anno")
  # return result
  new.bed.df$start <- as.numeric(new.bed.df$start)
  new.bed.df$stop <- as.numeric(new.bed.df$stop)
  if (verbose) {
    cat(feed, "[collapse_bed.fct]: done", feed)
  }
  return(new.bed.df)
}

# function to compare the coverage of one bed df with another////////

uncovered_regions_of_bed1_by_bed2.fct <- function(bed1.df, bed2.df,
  verbose = T, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[uncovered_regions_of_bed1_by_bed2.fct]: beginning")
  }
  # DATA CHECK:
  data_contains_factor.fct(bed1.df)
  data_contains_factor.fct(bed2.df)
  if (nrow(bed1.df) == 0) {
    warning("bed1.df has no rows", immediate. = TRUE)
    return(NULL)
  }
  if (nrow(bed2.df) == 0) {
    warning("bed2.df has no rows", immediate. = TRUE)
    return(NULL)
  }
  # DESCRIPTION: bed.df should be a df with at least three
  # columns (col 1 = chr..., col 2 & 3 = positions, col 4 =
  # annotation) NOTE: This function checks whether regions from
  # bed1 are completely covered by regions from bed2 and return
  # a report for each region NOTE: Start and STOP positions
  # should be ordered
  if (verbose) {
    cat(feed, "[uncovered_regions_of_bed1_by_bed2.fct]: preparing")
  }
  if (ncol(bed1.df) == 3) {
    bed1.df$anno <- NA
  }
  colnames(bed1.df) <- c("chr", "start", "stop", "anno")
  bed1.df$chr <- as.character(bed1.df$chr)
  bed1.df$start <- as.numeric(bed1.df$start)
  bed1.df$stop <- as.numeric(bed1.df$stop)
  bed1.df$anno <- as.character(bed1.df$anno)
  #
  if (ncol(bed2.df) == 3) {
    bed2.df$anno <- NA
  }
  colnames(bed2.df) <- c("chr", "start", "stop", "anno")
  bed2.df$chr <- as.character(bed2.df$chr)
  bed2.df$start <- as.numeric(bed2.df$start)
  bed2.df$stop <- as.numeric(bed2.df$stop)
  bed2.df$anno <- as.character(bed2.df$anno)
  # calculatins
  if (verbose) {
    cat(feed, "[uncovered_regions_of_bed1_by_bed2.fct]:",
    "calculating ")
  }
  result.uncovered <- apply(as.matrix(1:nrow(bed1.df)), 1,
    function(index.s) {
      data.bed.df <- bed1.df[index.s, ]
      # get all regions of bed2 overlapping with region of interest
      # in bed1
      auswahl.v <- (bed2.df$chr %in% data.bed.df$chr) &
        (bed2.df$start <= data.bed.df$stop) & (bed2.df$stop >=
```

```
      data.bed.df$start)
    if (!any(auswahl.v)) {
      return(data.bed.df)
    }
    # get the un-targeted region size. NOTE: These procedures
    # assume that the single regions are non-overlaping
    # get targeting bed2 regions
    sub.bed2.df <- bed2.df[auswahl.v, ]
    # merge if possible or needed
    if (nrow(sub.bed2.df) > 1) {
      sub.bed2.df <- collapse_bed.fct(sub.bed2.df,
        feed = feed)
    }
    # order by start position
    sub.bed2.df <- sub.bed2.df[order(sub.bed2.df$start),
      ]
    # get uncovered regions surounded by covered regions
    if (nrow(sub.bed2.df) < 2) {
      uncovered.between.df <- data.frame(chr = NULL,
        start = NULL, stop = NULL, anno = NULL,
        stringsAsFactors = FALSE)
    } else {
      uncovered.between <- apply(matrix(c(2:nrow(sub.bed2.df))),
        1, function(index.s) {
        new.chr.s <- sub.bed2.df[index.s, "chr"]
        new.start.s <- sub.bed2.df[index.s - 1, "stop"] +
          1
        new.stop.s <- sub.bed2.df[index.s, "start"] -
          1
        if (new.start.s <= new.stop.s) {
          return(data.frame(chr = new.chr.s, start = new.start.s,
          stop = new.stop.s, stringsAsFactors = F))
        } else {
          return(NULL)
        }
        })
      uncovered.between.df <- do.call(rbind, uncovered.between)
      if (nrow(uncovered.between.df) != 0) {
        uncovered.between.df$anno <- "between"
      } else {
        uncovered.between.df <- data.frame(chr = NULL,
        start = NULL, stop = NULL, anno = NULL,
        stringsAsFactors = FALSE)
      }
    }
    # get uncovered region at the ends of the target region at
    # the start
    if (sub.bed2.df[1, "start"] > data.bed.df$start) {
      uncovered.start.df <- data.frame(chr = data.bed.df$chr,
        start = data.bed.df$start, stop = sub.bed2.df[1,
        "start"] - 1, anno = "start", stringsAsFactors = FALSE)
    } else {
      uncovered.start.df <- data.frame(chr = NULL,
        start = NULL, stop = NULL, anno = NULL,
        stringsAsFactors = FALSE)
    }
    # at the end
    if (sub.bed2.df[nrow(sub.bed2.df), "stop"] <
      data.bed.df$stop) {
      uncovered.end.df <- data.frame(chr = data.bed.df$chr,
        start = sub.bed2.df[nrow(sub.bed2.df), "stop"] +
        1, stop = data.bed.df$stop, anno = "end",
        stringsAsFactors = FALSE)
    } else {
      uncovered.end.df <- data.frame(chr = NULL, start = NULL,
        stop = NULL, anno = NULL, stringsAsFactors = FALSE)
    }
    # get a dataframe of uncovered regions
    uncovered.df <- rbind(rbind(uncovered.start.df,
```

```
        uncovered.between.df), uncovered.end.df)
      # if regions are uncovered, than add the target’s annotation
      if (!(nrow(uncovered.df) == 0)) {
        uncovered.df$anno <- data.bed.df$anno
      }
      # return the uncovered regions
      return(uncovered.df)
    })
  if (verbose) {
    cat(feed, "[uncovered_regions_of_bed1_by_bed2.fct]: done ")
  }
  return(result.uncovered)
}

# function for missingness stats for a specific bed /////////////////

coverage_stats.fct <- function(bed.df, uncovered_regions.bed.df,
  verbose = TRUE, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[coverage_stats.fct]: beginning")
  }
  bed1.df <- bed.df
  bed2.df <- uncovered_regions.bed.df
  # DATA CHECK:
  data_contains_factor.fct(bed1.df)
  if (nrow(bed1.df) == 0) {
    warning("[coverage_stats.fct]: bed.df is null")
    return(NULL)
  }
  if (ncol(bed1.df) == 3) {
    warning("[coverage_stats.fct]: no annotation supplied...",
      "treating supplied regions of interest as one gene",
      immediate. = TRUE)
    bed1.df$anno <- NA
  }
  colnames(bed1.df) <- c("chr", "start", "stop", "anno")
  bed1.df$chr <- as.character(bed1.df$chr)
  bed1.df$start <- as.numeric(bed1.df$start)
  bed1.df$stop <- as.numeric(bed1.df$stop)
  bed1.df$anno <- as.character(bed1.df$anno)
  #
  if (nrow(bed2.df) == 0) {
    missingness.df <- as.data.frame(t(apply(
      as.matrix(unique(bed1.df$anno)), 1, function(anno.s) {
        total.target.s <- sum(apply(
          as.matrix(bed1.df[bed1.df$anno %in%
          anno.s, c("start", "stop")]), 1, function(x) {
          return(x[2] - x[1] + 1)
        }))
        total.missing.s <- 0
        return(c(anno.s, total.target.s, total.missing.s,
          total.missing.s/total.target.s))
      })), stringsAsFactors = FALSE)
  } else {
    data_contains_factor.fct(bed2.df)
    if (ncol(bed2.df) == 3) {
      warning("[coverage_stats.fct]: no annotation supplied...",
      "treating supplied uncovered regions of interest as one gene",
        immediate. = TRUE)
      bed2.df$anno <- NA
    }
    colnames(bed2.df) <- c("chr", "start", "stop", "anno")
    bed2.df$chr <- as.character(bed2.df$chr)
    bed2.df$start <- as.numeric(bed2.df$start)
    bed2.df$stop <- as.numeric(bed2.df$stop)
    bed2.df$anno <- as.character(bed2.df$anno)
    # the input df should contain 4 columns: 1 = chr, 2 = start,
    # 3 = stop, 4 = anno, data merging is based on anno!!! bed1
    # is the desired target, bed2 the missing regions
```

```
    missingness.df <- as.data.frame(t(apply(
      as.matrix(unique(bed1.df$anno)), 1, function(anno.s) {
        total.target.s <- sum(apply(
          as.matrix(bed1.df[bed1.df$anno %in%
          anno.s, c("start", "stop")]), 1, function(x) {
          return(x[2] - x[1] + 1)
        }))
        total.missing.s <- sum(apply(
          as.matrix(bed2.df[bed2.df$anno %in%
          anno.s, c("start", "stop")]), 1, function(x) {
          return(x[2] - x[1] + 1)
        }))
        return(c(anno.s, total.target.s, total.missing.s,
          total.missing.s/total.target.s))
      })), stringsAsFactors = FALSE)
  }
  #
  colnames(missingness.df) <- c("anno", "target_size",
    "missing_size", "missing_percent")
  missingness.df$target_size <- as.numeric(
    missingness.df$target_size)
  missingness.df$missing_size <- as.numeric(
    missingness.df$missing_size)
  missingness.df$missing_percent <- as.numeric(
  missingness.df$missing_percent)
  if (verbose) {
    cat(feed, "[coverage_stats.fct]: done")
  }
  return(missingness.df)
}

# Function for redundancy check for a bed file //////////////////////

redundancy_check.fct <- function(bed.df, verbose = T, feed = "\n",
  verbose_output_information = FALSE, ...) {
  if (verbose) {
    cat(feed, "[redundancy_check.fct]: beginning")
  }
  # DATA CHECK:
  data_contains_factor.fct(bed.df)
  # DESCRIPTION: bed.df should be a df with at least three
  # columns (col 1 = chr..., col 2 & 3 = positions, col 4 =
  # annotation) if integer merge mode, than merging
  # neighbouring integer positions sould be done e.g range 1 to
  # 4 and 5 to 6 will be merged to 1 to 6 prepare the bed.df
  if (nrow(bed.df) < 1) {
    return(NULL)
  }
  if (ncol(bed.df) == 3) {
    bed.df$anno <- NA
  }
  colnames(bed.df) <- c("chr", "start", "stop", "anno")
  bed.df$chr <- as.character(bed.df$chr)
  bed.df$start <- as.numeric(bed.df$start)
  bed.df$stop <- as.numeric(bed.df$stop)
  bed.df$anno <- as.character(bed.df$anno)
  # order the bed file according to chromosome and start
  # position
  bed.df <- bed.df[order(bed.df$chr, bed.df$start, bed.df$stop),
    ]
  # check the number of overlaps up and downstream of a region
  nrow.bed.df <- nrow(bed.df)
  number.overlaps.x <- apply(
    matrix(1:nrow.bed.df), 1, function(index) {
    if (verbose) {
      cat("\r")
      cat(index)
      cat("/")
      cat(nrow.bed.df)
```

```
    }
    # check, how many regions unequal the index region share a
    # region with the index region. NOTE: just check the
    # surrounding 5 regions to speed up the analysis
    auswahl.v <- bed.df[-index, "chr"] %in% bed.df[index,
      "chr"] & bed.df[-index, "start"] <= bed.df[index,
      "stop"] & bed.df[-index, "stop"] >= bed.df[index,
      "start"]
    if (verbose_output_information) {
      # get a vector of whether the overlap is up- or downstream
      downstream_overlap.v <- bed.df[-index, "start"] >=
        bed.df[index, "start"]
      upstream_overlap.v <- bed.df[-index, "stop"] <= bed.df[index,
        "stop"]
      # create a dataframe as output
      if (any(auswahl.v)) {
        output.df <- data.frame(chr = (bed.df[-index,
          "chr"])[auswahl.v], start = (bed.df[-index,
          "start"])[auswahl.v], stop = (bed.df[-index,
          "stop"])[auswahl.v], anno = (bed.df[-index,
          "anno"])[auswahl.v], querry = bed.df[index,
          "anno"], overlaping = (bed.df[-index, "anno"])[auswahl.v],
          overlaps_querry_upstream = upstream_overlap.v[auswahl.v],
          overlaps_querry_downstream =
          downstream_overlap.v[auswahl.v],
          stringsAsFactors = FALSE)
        return(output.df)
      } else {
        return(NULL)
      }
    } else {
      return(c(sum(auswahl.v), paste(
        c(bed.df[-index, "anno"])[auswahl.v], collapse = ",")))
    }
  })
  if (verbose) {
    cat(feed = feed)
  }
  if (verbose_output_information) {
    if (verbose) {
      cat(feed, "[redundancy_check.fct]: done")
    }
    return(number.overlaps.x)
  } else {
    number.overlaps.m <- t(number.overlaps.x)
    # create an output dataframe with the input data.frame
    new.bed.df <- bed.df
    new.bed.df$further_overlap_count <- as.numeric(
      number.overlaps.m[, 1])
    new.bed.df$further_overlap_anno <- as.character(
      number.overlaps.m[, 2])
    if (verbose) {
      cat(feed, "[redundancy_check.fct]: done")
    }
    return(new.bed.df)
  }
}

# Function for check for steric interaction of MIPs ////////////////

steric_check.fct <- function(mip.df,
  skip.SNP.based.duplicates.s = TRUE,
  verbose = TRUE, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[steric_check.fct]: beginning")
  }
  # DATE CHECK:
  data_contains_factor.fct(bed.df)
  if (nrow(mip.df) == 0) {
```

```
    return(0)
  }
  # DESCRIPTION: NOTE: This function returns the MIPs, which
  # show steric (thus physical strand) overlap with other MIPs.
  # create the maximal extend of a MIP
  start_stop.mip.m <- t(apply(as.matrix(mip.df[, c("lig_probe_start",
    "lig_probe_stop", "ext_probe_start", "ext_probe_stop")]),
    1, function(x) {
      return(c(min(as.numeric(x)), max(as.numeric(x))))
    }))
  # for each mip, check overlaps from the same strand
  resultat.steric_analysis.list <- apply(as.matrix(1:nrow(mip.df)),
    1, function(index.mip.s) {
      # select the strand
      auswahl.strand.v <- mip.df[, "probe_strand"] %in%
        mip.df[index.mip.s, "probe_strand"]
      # select the chromosome
      auswahl.chr.v <- mip.df[, "chr"] %in% mip.df[index.mip.s,
        "chr"]
      # get the overlapping mips
      auswahl.overlap.v <- start_stop.mip.m[, 1] <=
        start_stop.mip.m[index.mip.s, 2] &
        start_stop.mip.m[, 2] >= start_stop.mip.m[index.mip.s, 1]
      # select the intersecting MIPs
      auswahl.steric.v <- auswahl.strand.v & auswahl.chr.v &
        auswahl.overlap.v
      # if desired, skip MIPs with duplicates for SNP purposes
      if (skip.SNP.based.duplicates.s) {
        # do not select mips, which share the ‘notes’ column, if a
        # ‘snp’ is mentioned there and have the same target region
        if (grepl("snp", mip.df[index.mip.s, "notes"])) {
          same.target.v <- mip.df[, "mip_target_start_position"] %in%
          mip.df[index.mip.s, "mip_target_start_position"] &
          mip.df[, "mip_target_stop_position"] %in%
            mip.df[index.mip.s, "mip_target_stop_position"]
          same.notes.v <- mip.df[, "notes"] %in% mip.df[index.mip.s,
          "notes"]
          # create an identity vector to still select the querry mip
          identity.v <- rep(FALSE, nrow(mip.df))
          identity.v[index.mip.s] <- TRUE
          auswahl.steric.v <- auswahl.steric.v & (!(same.target.v &
          same.notes.v) | identity.v)
        }
      }
      # count and return the numbers
      output.df <- data.frame(steric_count = sum(auswahl.steric.v),
        steric_mips_index = paste(mip.df[auswahl.steric.v,
          "X.mip_pick_count"], collapse = ","),
          stringsAsFactors = FALSE)
      return(output.df)
    })
  if (is.list(resultat.steric_analysis.list)) {
    resultat.steric_analysis.list <- do.call(rbind,
      resultat.steric_analysis.list)
  }
  if (verbose) {
    cat(feed, "[steric_check.fct]: done")
  }
  return(resultat.steric_analysis.list)
}

# Function for removal of far intronic MIPs ////////////////////////

remove_far_intronic_MIPs.fct <- function(mip.df, CNV.mode = FALSE,
  verbose = TRUE, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[remove_far_intronic_MIPs.fct]: beginning")
  }
  # DATA CHECK:
```

```
data_contains_factor.fct(mip.df)
if (nrow(mip.df) == 0) {
  return(NULL)
}
# DESCRIPTION: input is the MIP design output df
# create a internal feature (= region of interest) identifier
ident.feature.v <- apply(
  as.matrix(1:nrow(mip.df)), 1, function(index.s) {
  paste(mip.df[index.s, c("chr", "feature_start_position",
    "feature_stop_position")], collapse = "_")
})
# for each feature, check whether its MIPs target region is
# overlapping
if (verbose) {
  cat(feed, "[remove_far_intronic_MIPs.fct]: filtering feature")
}
length.unique.ident.feature.v <- length(unique(ident.feature.v))
selected.mips <- apply(as.matrix(unique(ident.feature.v)),
  1, function(feature.s) {
    if (verbose) {
      cat("\r")
      cat(feature.s, "/", length.unique.ident.feature.v,
        ": ")
    }
    # select the mips of the particular feature
    auswahl.v <- ident.feature.v %in% feature.s
    sub.mip.df <- mip.df[auswahl.v, ]
    # according to position
    sub.mip.df <- sub.mip.df[order(
      sub.mip.df$mip_target_start_position,
      sub.mip.df$mip_target_stop_position), ]
    mip.is.upstream.of.feature.logic <- as.numeric(
      sub.mip.df$mip_target_start_position) <
      as.numeric(sub.mip.df$feature_start_position) &
      as.numeric(sub.mip.df$mip_target_stop_position) <
        as.numeric(sub.mip.df$feature_stop_position)
    if (any(mip.is.upstream.of.feature.logic)) {
      start.index.s <- max(
      c(1:nrow(sub.mip.df))[mip.is.upstream.of.feature.logic])
      # check for same targeting mips
      # and resize the selection (because those might be SNP mips)
      start.index.s <- (c(1:nrow(sub.mip.df))[
        (sub.mip.df$mip_target_start_position ==
        sub.mip.df[start.index.s, "mip_target_start_position"]) &
        (sub.mip.df$mip_target_stop_position ==
        sub.mip.df[start.index.s, "mip_target_stop_position"])])
    } else {
      start.index.s <- NULL
    }
    mip.is.downstream.of.feature.logic <- as.numeric(
      sub.mip.df$mip_target_start_position) >
      as.numeric(sub.mip.df$feature_start_position) &
      as.numeric(sub.mip.df$mip_target_stop_position) >
        as.numeric(sub.mip.df$feature_stop_position)
    if (any(mip.is.downstream.of.feature.logic)) {
      stop.index.s <- min(
        c(1:nrow(sub.mip.df))[mip.is.downstream.of.feature.logic])
      # check for same targeting mips and
      # resize the selection (because those might be SNP mips)
      stop.index.s <- (c(1:nrow(sub.mip.df))[
        (sub.mip.df$mip_target_start_position ==
        sub.mip.df[stop.index.s, "mip_target_start_position"]) &
        (sub.mip.df$mip_target_stop_position ==
        sub.mip.df[stop.index.s, "mip_target_stop_position"])])
    } else {
      stop.index.s <- NULL
    }
    # get mips with target region totally in feature
    target.in.feature.logic <- (as.numeric(
```

```
        sub.mip.df$mip_target_start_position) >=
        as.numeric(sub.mip.df$feature_start_position) &
        as.numeric(sub.mip.df$mip_target_stop_position) <=
          as.numeric(sub.mip.df$feature_stop_position)) |
        (as.numeric(sub.mip.df$mip_target_start_position) <=
          as.numeric(sub.mip.df$feature_start_position) &
          as.numeric(sub.mip.df$mip_target_stop_position) >=
          as.numeric(sub.mip.df$feature_stop_position))
      index.target.in.feature.v <- c(
        1:nrow(sub.mip.df))[target.in.feature.logic]
      # select the mips within or just at the border of the feature
      auswahl.v <- unique(c(start.index.s, index.target.in.feature.v,
        stop.index.s))
      auswahl.v <- auswahl.v[order(auswahl.v)]
      if (!CNV.mode) {
        sub.mip.df <- sub.mip.df[auswahl.v, ]
      } else {
        if (length(auswahl.v) > 2) {
          return(sub.mip.df <- sub.mip.df[auswahl.v,
          ])
        } else {
          return(sub.mip.df)
        }
      }
      return(sub.mip.df)
    })
  if (verbose) {
    cat(feed = feed)
  }
  if (is.list(selected.mips)) {
    selected.mips <- do.call(rbind, selected.mips)
  }
  if (verbose) {
    cat(feed, "[remove_far_intronic_MIPs.fct]: done")
  }
  return(selected.mips)
}

# Function for getting estimates for MIPs sequencing approaches /////

setup.sequencing.fct <- function(number.mips.s, size.samples.s,
  gb_per_lane = 45, coverage.s = 400, read.s = 200,
  max.multiplex.s = 384,
  sequencing.time.s = 4, exact_values.s = FALSE) {
  # this function helps to estimate the experimental sequencing
  # setup after MIP design calculating the multiplex level
  level.multiplex.s <- floor((gb_per_lane * 1e+09)/(number.mips.s *
    coverage.s * read.s))
  if (level.multiplex.s > max.multiplex.s) {
    level.multiplex.s <- max.multiplex.s
  }
  # calc sequencing size
  seq_size.s <- level.multiplex.s * read.s * coverage.s *
  number.mips.s
  # calc required number of lanes and flow cells and sequencing
  # time
  number.lanes.s <- if (exact_values.s) {
    seq_size.s/(gb_per_lane * 1e+09)
    # (size.samples.s/level.multiplex.s)
  } else {
    ceiling(seq_size.s/(gb_per_lane * 1e+09))
  }
  number.flow_cells.s <- if (exact_values.s) {
    (number.lanes.s/8)
  } else {
    ceiling(number.lanes.s/8)
  }
  number.days.s <- sequencing.time.s * ceiling(number.flow_cells.s)
  # calc number of lanes with distributing maximal multiplex
```

```
  distributed_multiplex_lanes <- if (exact_values.s) {
    (((number.mips.s * coverage.s * read.s * max.multiplex.s)/
    (1e+09))/gb_per_lane)
  } else {
    ceiling(((number.mips.s * coverage.s * read.s * max.multiplex.s)/
    (1e+09))/gb_per_lane)
  }
  all_samples_distributed_multiplex_lanes <- if (exact_values.s) {
    distributed_multiplex_lanes * (size.samples.s/max.multiplex.s)
  } else {
    distributed_multiplex_lanes * ceiling(
      size.samples.s/max.multiplex.s)
  }
  return(data.frame(Multiplex_Level = level.multiplex.s,
    sequencing_output_bases = seq_size.s,
    Required_total_lanes_at_multiplex_level = number.lanes.s,
    Required_Total_Flow_Cells = number.flow_cells.s,
    Required_Sequencing_Days_at_multiplex_level = number.days.s,
    number_distributed_lanes_at_full384_multiplex_level =
      distributed_multiplex_lanes,
    all_samples_required_lanes_at_full384_multiplex_level =
     all_samples_distributed_multiplex_lanes,
    stringsAsFactors = FALSE))
}

# function to create ucsc tracks ///////////////////////////////////

create_feature_track_bed.fct <- function(mip.df = NULL,
  name.s = NULL,
  file.s = NULL, ...) {
  # DATA CHECK:
  data_contains_factor.fct(mip.df)
  # calc:
  if (is.null(name.s)) {
    stop("No general track name supplied!")
  }
  if (is.null(mip.df)) {
    stop("No MIP df supplied!")
  }
  if (is.null(file.s)) {
    stop("No destination file supplied!")
  }
  # try to detect a logistic score and output that score rather
  # than a nijmegen -1 to 5 score
  if (!is.null(mip.df$logistic_score)) {
    mip.df$rank_score <- mip.df$logistic_score
  }
  # This functon reformates the mip dataframe to an ucsc track
  # bed file
  # create an identfier for each mip including the mip
  # index, the quality and the feature, the strand & a note
  feature.v <- apply(
    as.matrix(as.numeric(as.factor(apply(as.matrix(mip.df[,
    c("chr", "feature_start_position", "feature_stop_position")]),
    1, function(x) {
      paste(x, collapse = "_")
    })))), 1, function(x) {
    paste(c("feat", "#", as.character(x)), collapse = "")
  })
  id.v <- apply(as.matrix(mip.df$X.mip_pick_count), 1, function(x) {
    paste(c("ID#", x), collapse = "")
  })
  rankscore.v <- apply(as.matrix(mip.df$rank_score), 1, function(x) {
    paste(c("RankScore:", x), collapse = "")
  })
  strand.v <- apply(as.matrix(mip.df$probe_strand), 1, function(x) {
    paste(c("Strand:", x), collapse = "")
  })
  notes.v <- apply(as.matrix(mip.df$notes), 1, function(x) {
```

```
    paste(c("Note:", x), collapse = "")
  })
  ident.v <- apply(matrix(c(feature.v, id.v, rankscore.v, strand.v,
    notes.v), ncol = 5), 1, function(x) {
    paste(x, collapse = "_")
  })
  # create a color for each feature
  unique.feature.v <- unique(feature.v)
  colors.unique.feature.v <- apply(
    as.matrix(1:length(unique.feature.v)),
    1, function(x) {
      paste(as.character(sample(1:200, 3, replace = TRUE)),
        collapse = ",")
    })
  colors.feature.v <- apply(as.matrix(feature.v), 1, function(feature.s) {
    return(colors.unique.feature.v[unique.feature.v %in%
      feature.s])
  })
  # create output df
  chr.v <- apply(as.matrix(mip.df$chr), 1, function(chr.s) {
    paste("chr", as.character(chr.s), sep = "")
  })
  start_stop.m <- t(apply(as.matrix(mip.df[, c("ext_probe_start",
    "ext_probe_stop", "lig_probe_start", "lig_probe_stop")]),
    1, function(x) {
      return(c(min(x), max(x)))
    }))
  # NOTE: coordinates have to be one-based and the ‘end’
  # coordinate always hints to the first base, NOT being of the
  # specific interest
  output.df <- data.frame(chr = chr.v, start = start_stop.m[,
    1] - 1, stop = start_stop.m[, 2], ident = ident.v, unknown = 100,
    strand = mip.df$probe_strand, target_start =
      mip.df$mip_target_start_position -
      1, target_stop = mip.df$mip_target_stop_position,
    color = colors.feature.v)
  # create the plus track
  auswahl.plus.v <- mip.df$probe_strand %in% "+"
  spec.track.s <- paste(c("track name=", name.s,
    "_plus itemRgb=on\n"),
    collapse = "")
  sink(file = file.s)
  cat(spec.track.s)
  sink()
  write.table(file = file.s, output.df[auswahl.plus.v, ],
    col.names = F,
    row.names = F, sep = "\t", quote = FALSE, append = T)
  # and for the minus track
  spec.track.s <- paste(c("track name=", name.s,
    "_minus itemRgb=on\n"),
    collapse = "")
  sink(file = file.s, append = TRUE)
  cat(spec.track.s)
  sink()
  write.table(file = file.s, output.df[!auswahl.plus.v, ],
    col.names = F, row.names = F, sep = "\t", quote = FALSE,
    append = T)
}

# function to map MIPs to regions of a bed df ///////////////////////

remap_mips_to_bed.fct <- function(mip.df, bed.df,
  reset.feature = TRUE,
  remap_based_on_mip_target = FALSE, verbose = TRUE, feed = "\n",
  ...) {
  if (verbose) {
    cat(feed, "[remap_mips_to_bed.fct]: beginning")
  }
  # DATA CHECK:
```

```
  data_contains_factor.fct(mip.df)
  data_contains_factor.fct(bed.df)
  if (nrow(bed.df) == 0) {
    return(NULL)
  }
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # NOTE: This function maps mips (from
  # nijmegen like mip dataframe) to the desired regions in a
  # bed file (col 1= chromosome, 2 = start, 3 = stop, 4 =
  # annotation). NOTE: bed regions should be collapsed together
  # before send to this function
  if (ncol(bed.df) < 4) {
    bed.df$anno <- NA
  }
  # CAUTION: Check whether both df are based on the same
  # coordinate’s start (either 1- or 0-based)
  # create a MIP
  # start and stop matrix
  if (remap_based_on_mip_target) {
    start_stop.mip.m <- as.matrix(mip.df[, c(
      "mip_target_start_position",
      "mip_target_stop_position")])
  } else {
    start_stop.mip.m <- t(apply(as.matrix(mip.df[, c(
      "lig_probe_start",
      "lig_probe_stop", "ext_probe_start", "ext_probe_stop")]),
      1, function(x) {
        return(c(min(as.numeric(x)), max(as.numeric(x))))
      }))
  }
  # go through each bed region
  total.index.s <- nrow(bed.df)
  if (verbose) {
    cat(feed, "[remap_mips_to_bed.fct]: mapping mips to feature",
      feed)
  }
  nrow.bed.df <- nrow(bed.df)
  filtered.mips.x <- apply(
    as.matrix(1:nrow.bed.df), 1, function(index.bed.s) {
      auswahl.v <- mip.df$chr %in% bed.df[index.bed.s, 1] &
      as.numeric(start_stop.mip.m[, 1]) <=
        as.numeric(bed.df[index.bed.s,
        3]) & as.numeric(start_stop.mip.m[, 2]) >=
        as.numeric(bed.df[index.bed.s,
      2])
    if (verbose) {
      cat("\r", index.bed.s, "/", nrow.bed.df)
    }
    sub.mip.df <- mip.df[auswahl.v, ]
    if (nrow(sub.mip.df) > 0) {
      sub.mip.df$anno <- bed.df[index.bed.s, 4]
      if (reset.feature) {
        # reset the feature name create a new feature identifier for
        # the sub.mip.df
        auswahl.same_anno.bed.df <- bed.df[, 4] %in%
          bed.df[index.bed.s, 4]
        # get identifiers for the entries
        ident.auswahl.bed.v <- apply(
          as.matrix(bed.df[auswahl.same_anno.bed.df,
          ]), 1, function(x) {
          paste(as.character(c(x[1], as.numeric(x[2:3]),
          as.character(x[-c(1:3)]))), collapse = "_")
        })
        ident.index.bed.s <- paste(as.character(bed.df[index.bed.s,
          ]), collapse = "_")
        # get the feature suffix
        suffix.feature.s <- which(ident.auswahl.bed.v ==
```

```
          ident.index.bed.s)
        # get the feature prefix
        prefix.feature.s <- which(unique(bed.df[, 4]) ==
          bed.df[index.bed.s, 4])
        # asign the feature
        feature.s <- (paste(as.character(c(prefix.feature.s,
          suffix.feature.s)), collapse = "_"))
        sub.mip.df$feature_mip_count <- feature.s
        # reset the feature start and stop positions
        sub.mip.df$feature_start_position <- bed.df[index.bed.s,
          2]
        sub.mip.df$feature_stop_position <- bed.df[index.bed.s,
          3]
      }
    }
    return(sub.mip.df)
    if (verbose) {
      cat(feed = feed)
    }
  })
  if (is.list(filtered.mips.x)) {
    filtered.mips.x <- do.call(rbind, filtered.mips.x)
  }
  if (verbose) {
    cat(feed, "[remap_mips_to_bed.fct]: done")
  }
  return(filtered.mips.x)
}

# Function to get MIPs with overlapping arms at different strands////

get_arm_overlaps.fct <- function(mip.df, threshold.filter.s = 0,
  verbose = TRUE, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[get_arm_overlaps.fct]: beginning")
  }
  # DATA CHECK:
  data_contains_factor.fct(mip.df)
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # DESCRIPTION: NOTE: This functions checks, whether MIP
  # ligation and extension arms show an overlap
  if (verbose) {
    cat(feed, "[get_arm_overlaps.fct]: determining complementary",
      "arms",
      feed)
  }
  nrow.mip.df <- nrow(mip.df)
  filtered.overlap.arms.x <- apply(as.matrix(1:nrow.mip.df),
    1, function(index.mip.s) {
      if (verbose) {
        cat("\r", index.mip.s, "/", nrow.mip.df)
      }
      # select MIPs of other strand and same chromosome and same
      # range
      auswahl.v <- !(mip.df$probe_strand %in% mip.df[index.mip.s,
        "probe_strand"]) & mip.df$chr %in% mip.df[index.mip.s,
        "chr"]
      red.mip.df <- mip.df[auswahl.v, ]
      #
      if (nrow(red.mip.df) == 0) {
        return(NULL)
      }
      #
      mip_start_stop.m <- t(apply(as.matrix(red.mip.df[,
        c("lig_probe_start", "lig_probe_stop", "ext_probe_start",
          "ext_probe_stop")]), 1, function(x) {
        return(c(min(as.numeric(x)), max(as.numeric(x))))
```

```
    }))
    start_stop.selected_mip.v <- mip.df[index.mip.s,
      c("lig_probe_start", "lig_probe_stop", "ext_probe_start",
        "ext_probe_stop")]
    start_stop.selected_mip.v <- c(min(as.numeric(
      start_stop.selected_mip.v)),
      max(as.numeric(start_stop.selected_mip.v)))
    auswahl.v <- (mip_start_stop.m[, 1] <=
      start_stop.selected_mip.v[2]) &
      (mip_start_stop.m[, 2] >= start_stop.selected_mip.v[1])
    red.mip.df <- red.mip.df[auswahl.v, ]
    # perform analysis of overlap
    if (nrow(red.mip.df) > 0) {
      # create a new dataframe with columns containing ligation and
      # extension arms
      start_stop.df <- data.frame(mip_arm_start = unlist(
        red.mip.df[,
        c("lig_probe_start", "ext_probe_start")]),
        mip_arm_stop = unlist(red.mip.df[, c("lig_probe_stop",
        "ext_probe_stop")]), mip_id = rep(red.mip.df[,
        "X.mip_pick_count"], 2), mip_arm_arm_type = c(rep("lig",
        nrow(red.mip.df)), rep("ext", nrow(red.mip.df))),
        querry_id = mip.df[index.mip.s, "X.mip_pick_count"],
        stringsAsFactors = FALSE)
      # check the overlap with the selected MIP and return the
      # number of bases overlapping
      overlap.lig_arm.v <- apply(as.matrix(start_stop.df[,
        c("mip_arm_start", "mip_arm_stop")]), 1, function(
        start_stop.v) {
        # determine number of overlaps by the minimum of the
        # start-stop-difference
        raw.overlap.v <- min(c(max(as.numeric(start_stop.v)) -
        min(as.numeric(mip.df[index.mip.s, c("lig_probe_start",
          "lig_probe_stop")])), max(as.numeric(mip.df[index.mip.s,
        c("lig_probe_start", "lig_probe_stop")])) -
        min(as.numeric(start_stop.v))))
        # return the number of overlapping bases...consider that
        # one base has to be added to the count, because
        # substration acts in an exclusive manner for coordinates
        if (raw.overlap.v >= 0) {
        return(raw.overlap.v + 1)
        } else {
        return(0)
        }
      })
      overlap.ext_arm.v <- apply(as.matrix(start_stop.df[,
        c("mip_arm_start", "mip_arm_stop")]), 1, function(
        start_stop.v) {
        # determine number of overlaps by the minimum of the
        # start-stop-difference
        raw.overlap.v <- min(c(max(as.numeric(start_stop.v)) -
        min(as.numeric(mip.df[index.mip.s, c("ext_probe_start",
          "ext_probe_stop")])), max(as.numeric(mip.df[index.mip.s,
        c("ext_probe_start", "ext_probe_stop")])) -
        min(as.numeric(start_stop.v))))
        # return the number of overlapping bases...consider that
        # one base has to be added to the count, because
        # substration acts in an exclusive manner for coordinates
        if (raw.overlap.v >= 0) {
        return(raw.overlap.v + 1)
        } else {
        return(0)
        }
      })
      # create an output
      start_stop.df$lig_overlap <- overlap.lig_arm.v
      start_stop.df$ext_overlap <- overlap.ext_arm.v
      start_stop.df$max_overlap <- apply(
        matrix(c(overlap.lig_arm.v,
```

```
          overlap.ext_arm.v), ncol = 2), 1, max)
        auswahl.v <- overlap.lig_arm.v >= threshold.filter.s |
          overlap.ext_arm.v >= threshold.filter.s
        rownames(start_stop.df) <- 1:nrow(start_stop.df)
        return(start_stop.df[auswahl.v, ])
      } else {
        return(NULL)
      }
    })
  if (verbose) {
    cat(feed = feed)
  }
  # prepare the output
  if (is.data.frame(filtered.overlap.arms.x)) {
    cat("[get_arm_overlaps.fct]: general output: list creation ")
    filtered.overlap.arms.x <- list(filtered.overlap.arms.x)
  }
  if (verbose) {
    cat(feed, "[get_arm_overlaps.fct]: done")
  }
  return(filtered.overlap.arms.x)
}

# function to create a nijmegen-like version of a MIPGEN
# output dataframe //////////////////////////////////////////////////

convert_mipgen_to_nijmegen_format.fct <- function(mip.df, ...) {
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # NOTE: This function reformates the MIPGEN output into a
  # datafraqme similar to nijmegen’s format
  notes.v <- apply(matrix(1:nrow(mip.df)), 1, function(index.s) {
    paste(mip.df[index.s, c("mip_name", "scan_target_sequence")],
      collapse = "_")
  })
  new.mip.df <- data.frame(X.mip_pick_count = c(1:nrow(mip.df)),
    rank_score = NA, chr = mip.df$chr,
    ext_probe_start = mip.df$ext_probe_start,
    ext_probe_stop = mip.df$ext_probe_stop,
    ext_probe_sequence = mip.df$ext_probe_sequence,
    ext_copy_count = mip.df$ext_probe_copy,
    lig_probe_start = mip.df$lig_probe_start,
    lig_probe_stop = mip.df$lig_probe_stop,
    lig_probe_sequence = mip.df$lig_probe_sequence,
    lig_copy_count = mip.df$lig_probe_copy,
    mip_target_start_position = mip.df$mip_scan_start_position,
    mip_target_stop_position = mip.df$mip_scan_stop_position,
    mip_target_sequence = mip.df$scan_target_sequence,
    feature_start_position = mip.df$feature_start_position,
    feature_stop_position = mip.df$feature_stop_position,
    feature_mip_count = NA, probe_strand = mip.df$probe_strand,
    notes = notes.v, X70mer = mip.df$mip_sequence,
    stringsAsFactors = F,
    logistic_score = mip.df$logistic_score)
  return(new.mip.df)
}

# Wrapper for complete missingness/coverage check between a
# desired bed df and a mip df ////////////////////////////////////////

# NOTE: returns a list
inspect_bed_by_mip_coverage.fct <- function(bed.df, mip.df,
  verbose = TRUE,
  feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[inspect_bed_by_mip_coverage.fct]: beginning ")
  }
  # DATA CHECK:
```

```
  data_contains_factor.fct(mip.df)
  data_contains_factor.fct(bed.df)
  # calc: collapse mip targets, supplied in bed format:
  collapsed_targets.mip.df <- collapse_bed.fct(mip.df[, c("chr",
    "mip_target_start_position", "mip_target_stop_position")],
    feed = feed)
  # get the bed’s regions, which are not covered by the MIP’s
  # targets
  uncovered_regions.bed.df <- do.call(rbind,
    uncovered_regions_of_bed1_by_bed2.fct(bed.df,
    collapsed_targets.mip.df, feed = feed))
  # use those regions to calc stats of degree of missingness
  missingness.uncovered_regions.bed.df <- coverage_stats.fct(bed.df,
    uncovered_regions.bed.df, feed = feed)
  missingness.uncovered_regions.bed.df <-
    missingness.uncovered_regions.bed.df[order(
    missingness.uncovered_regions.bed.df$missing_percent,
    missingness.uncovered_regions.bed.df$missing_size), ]
  # create an output
  if (verbose) {
    cat(feed, "[inspect_bed_by_mip_coverage.fct]: done ")
  }
  return(list(collapsed_mip_targets = collapsed_targets.mip.df,
    missing_target_regions = uncovered_regions.bed.df,
    missingness_stats = missingness.uncovered_regions.bed.df))
}

# Wrapper for calculations of arm overlaps for MIPs ////////////////

summary.arm_overlaps.fct <- function(mip.df, overlap_threshold.s,
  verbose = TRUE, feed = "\n", ...) {
  if (verbose) {
    cat(feed, "[summary.arm_overlaps.fct]: beginning ")
  }
  # DATA CHECK:
  data_contains_factor.fct(mip.df)
  # calc get arm overlaps for MIPs on opposite strands
  arm_overlaps.mip.l <- get_arm_overlaps.fct(mip.df,
    overlap_threshold.s,
    feed = feed)
  # get the MIP IDs (querry id and matching id)
  ids.mip.v <- apply(as.matrix(1:length(arm_overlaps.mip.l)),
    1, function(index.s) {
      if (!is.null(arm_overlaps.mip.l[[index.s]])) {
        return(unlist((arm_overlaps.mip.l[[index.s]])[,
          c("mip_id", "querry_id")]))
      } else {
        return(NULL)
      }
    })
  if (is.list(ids.mip.v)) {
    ids.mip.v <- unlist(ids.mip.v)
  }
  ids.mip.v <- c(ids.mip.v)
  # get the mip information for overlapping mips
  mip.df <- mip.df[mip.df$X.mip_pick_count %in% ids.mip.v,
    ]
  # return
  if (verbose) {
    cat(feed, "[summary.arm_overlaps.fct]: done")
  }
  return(mip.df)
}

# Function to convert a bed file ///////////////////////////////////

convert_bed_frame.fct <- function(bed.df, state_chr.s = FALSE,
  add_base.s = 0, verbose = TRUE, feed = "\n", ...) {
  # NOTE: Should contain 4 columns: chr, start, stop and anno
```

```
  # DATA CHECK:
  data_contains_factor.fct(bed.df)
  # calc: check chr format
  is_chr_format.v <- grepl("chr", as.character(bed.df[, 1]))
  if (state_chr.s) {
    bed.df[!is_chr_format.v, 1] <- apply(
      as.matrix(1:sum(!is_chr_format.v)), 1, function(index.s) {
        return(paste("chr", (bed.df[!is_chr_format.v,
          1])[index.s], sep = ""))
      })
  } else {
    bed.df[is_chr_format.v, 1] <- apply(
      as.matrix(1:sum(is_chr_format.v)), 1, function(index.s) {
        return(substr((bed.df[is_chr_format.v, 1])[index.s],
          4, nchar((bed.df[is_chr_format.v, 1])[index.s])))
      })
  }
  # adjust base
  bed.df[, 2] <- as.numeric(bed.df[, 2]) + add_base.s
  bed.df[, 3] <- as.numeric(bed.df[, 3]) + add_base.s
  return(bed.df)
}

# Function to run primary QC ////////////////////////////////////////
# NOTE: this function runs a primary QC for a mip dataframe
# and a given bed file NOTE: the bed file should be 1-based
# and should not contain ‘chr’ prefixes NOTE: runs QC for arm
# mapping as well as remapping to a given bed file

primary_mip_qc.fct <- function(path_to_mip.s, path_to_bed.s,
  output_prefix.s, convert_bed_to_mip.s = FALSE,
  convert_mip_to_nijmegen_format = F,
  overlap_threshold.s = 7, feed = "\n", make_stats = TRUE,
  stringent = TRUE, ...) {
  # DATA CHECK:
  if (is.null(path_to_mip.s)) {
    stop("No file for MIPs supplied!")
  }
  if (is.null(path_to_bed.s)) {
    stop("No file for desired target supplied!")
  }
  if (is.null(output_prefix.s)) {
    stop("No output prefix supplied!")
  }
  # run QC load data
  cat("Loading data...")
  data_mip.df <- read.table(file = path_to_mip.s, header = T,
    as.is = T, sep = "\t")
  data_bed.df <- read.table(file = path_to_bed.s, header = F,
    as.is = T, sep = "\t")
  cat("done.")
  # convert data
  if (convert_mip_to_nijmegen_format) {
    data_mip.df <- convert_mipgen_to_nijmegen_format.fct(data_mip.df,
      feed = feed)
    cat("Converted MIPs to Nijmegen format!")
  }
  if (convert_bed_to_mip.s) {
    data_bed.df <- convert_bed_frame.fct(data_bed.df, state_chr.s = FALSE,
      add_base.s = 1, feed = feed)
    cat("Converted bed for consistency with 1-based MIPs!")
  }
  # perform remapping:
  data_mip.df <- remap_mips_to_bed.fct(data_mip.df, data_bed.df,
    feed = feed)
  cat("Creating track and saving results...")
  create_feature_track_bed.fct(mip.df = data_mip.df,
    name.s = "remapped",
    file.s = paste(output_prefix.s, "remapped.bed", sep = ""),
```

```
    feed = feed)
  save(file = paste(output_prefix.s, ".mip.R", sep = ""), data_mip.df)
  cat("done!")
  # perform qc:
  cat("Removing bad MIPs...")
  if (stringent) {
    bad.qc.v <- as.numeric(data_mip.df$ext_copy_count) >
      100 | as.numeric(data_mip.df$lig_copy_count) > 100 |
      (as.numeric(data_mip.df$ext_copy_count > 5) | as.numeric(
      data_mip.df$lig_copy_count > 5))
  } else {
    bad.qc.v <- as.numeric(data_mip.df$ext_copy_count) >
      100 | as.numeric(data_mip.df$lig_copy_count) > 100 |
      (as.numeric(data_mip.df$ext_copy_count > 5) & as.numeric(
      data_mip.df$lig_copy_count > 5))
  }
  data_mip.df <- data_mip.df[!bad.qc.v, ]
  if (convert_mip_to_nijmegen_format) {
    cat("also based on logistic score...")
    bad.qc.v <- as.numeric(data_mip.df$logistic_score) <=
      0.7
    data_mip.df <- data_mip.df[!bad.qc.v, ]
  }
  cat("done.")
  cat("Creating track and saving results...")
  create_feature_track_bed.fct(mip.df = data_mip.df,
    name.s = "post qc",
    file.s = paste(output_prefix.s, "post_qc.bed", sep = ""),
    feed = feed)
  save(file = paste(output_prefix.s, ".qc.mip.R", sep = ""),
    data_mip.df)
  cat("done!")
  # create statistics
  if (make_stats) {
    # coverage
    cat("Checking coverage...")
    coverage.data_mips_bed.l <- inspect_bed_by_mip_coverage.fct(
      data_bed.df,
      data_mip.df, feed = feed)
    cat("done.")
    cat("Coverage summary:")
    print(coverage.data_mips_bed.l$missingness_stats)
    cat(feed = feed)
    save(file = paste(output_prefix.s,
      "summary_coverage_missingness.qc.mip.R",
      sep = ""), coverage.data_mips_bed.l)
    # arm overlaps
    cat("Filtering MIPs with complementary arm overlaps of",
      "equal/more than ")
    cat(overlap_threshold.s)
    cat(" bp...")
    data_mip.df <- summary.arm_overlaps.fct(data_mip.df,
      overlap_threshold.s, feed = feed)
    cat("done.")
    cat("Creating track and saving results...")
    if (nrow(data_mip.df) != 0) {
      create_feature_track_bed.fct(mip.df = data_mip.df,
        name.s = "complementary arms",
        file.s = paste(output_prefix.s,
          "complementary_arms.bed", sep = ""))
    }
    save(file = paste(output_prefix.s, "complementary_arms.qc.mip.R",
      sep = ""), data_mip.df)
  }
  cat("done.")
  #
  return(NULL)
}
```

```
# Function to run filter for problematic MIPs //////////////////////

filter_problem_mips.fct <- function(mip.df, problem_mips.v, bed.df,
  problem_threshold.s = 7, fast_screen.s = FALSE, verbose = TRUE,
  feed = "\n", ...) {
  # DATA CHECK:
  if (verbose) {
    cat(feed, "[filter_problem_mips.fct]: data check.")
  }
  data_contains_factor.fct(mip.df)
  data_contains_factor.fct(bed.df)
  if (is.null(problem_mips.v) | is.factor(problem_mips.v)) {
    stop(
    "[filter_problem_mips.fct]: No proper problem MIP-IDs supplied!")
  }
  if (length(problem_mips.v) == 0) {
    return(mip.df)
  }
  if (is.factor(problem_mips.v)) {
    problem_mips.v <- as.character(problem_mips.v)
  }
  if (any(duplicated(mip.df$X.mip_pick_count))) {
    warning("[filter_problem_mips.fct]: MIP dataframe contained",
      "redundnant MIP ids!!! If same IDs hint to different MIPs,",
      "than filtering might contain errors!!!")
  }
  # removal of duplicates: NOTE: some duplicates have to stay,
  # as those might bind to SNPs!!! So include the ligation and
  # extension probe sequnce as an idnetifier
  auswahl.v <- duplicated(apply(as.matrix(1:nrow(mip.df)),
    1, function(index.s) {
      return(paste(mip.df[index.s, c("chr",
        "mip_target_start_position",
        "mip_target_stop_position", "ext_probe_sequence",
        "lig_probe_sequence")], collapse = "_"))
    }))
  mip.df <- mip.df[!auswahl.v, ]
  # NOTE: DON’T FILTER OUT SNP-MIPS (binding to SNPs) later!!!
  # Thus create an identifier based on chr, position of target
  # start and stop (if they target the same region, but have
  # different arms, than asgin the same identifier) also add
  # the strand coding
  ident.v <- apply(as.matrix(1:nrow(mip.df)), 1, function(index.s) {
    return(paste(mip.df[index.s, c("chr",
      "mip_target_start_position",
      "mip_target_stop_position", "probe_strand")], collapse = "_"))
  })
  # collapse bed.df
  bed.df <- collapse_bed.fct(bed.df, feed = "\r")
  # flag mips:
  mips.df <- mip.df
  mips.df$ident <- ident.v
  mips.df$problem_mip <- FALSE
  mips.df[
    mips.df$X.mip_pick_count %in% problem_mips.v, "problem_mip"] <-
    TRUE
  # define groups of problematic MIPs
  # Note: use established functions
  # define collapsed binding regions of the
  # problematic mips
  ranges.problem_mips.m <- t(apply(
    as.matrix(1:sum(mips.df$problem_mip)),
    1, function(index.s) {
      probes.v <- as.numeric(unlist((mips.df[mips.df$problem_mip,
        ])[index.s, c("ext_probe_start", "ext_probe_stop",
        "lig_probe_start", "lig_probe_stop")]))
      return(c(min(probes.v), max(probes.v)))
    }))
  bed.ranges.problem_mips.df <- data.frame(
```

```
    chr = c(mips.df$chr)[mips.df$problem_mip],
    start = ranges.problem_mips.m[, 1],
    stop = ranges.problem_mips.m[, 2],
    anno = c(mips.df$anno)[mips.df$problem_mip],
    stringsAsFactors = F)
  collapsed.bed.ranges.problem_mips.df <- collapse_bed.fct(
    bed.ranges.problem_mips.df,
    feed = "\r")
  # remap all mips to those regions
  remapped.mips.df <- remap_mips_to_bed.fct(mips.df,
    collapsed.bed.ranges.problem_mips.df,
    feed = "\r")
  # NOTE: The ‘feature_mip_count’ columns defines now MIPs
  # which show overlapping arms and other overlaps with other
  # problematic neighbouring MIPs go through each feature
  unique.remapped.mips.df_feature_mip_count <- unique(
    remapped.mips.df$feature_mip_count)
  length.unique.unique.remapped.mips.df_feature_mip_count <- length(
    unique.remapped.mips.df_feature_mip_count)
  best.problem_mips.x <- apply(
    as.matrix(unique.remapped.mips.df_feature_mip_count),
    1, function(feature_mip_count.s) {
      if (verbose) {
        cat(feed, "[filter_problem_mips.fct]: MIP group",
          which(unique.remapped.mips.df_feature_mip_count ==
          feature_mip_count.s), "/",
          length.unique.unique.remapped.mips.df_feature_mip_count,
          ", size ")
      }
      # select the mips of the feature
      sub.remapped.mips.df <- remapped.mips.df[
        remapped.mips.df$feature_mip_count %in%
        feature_mip_count.s, ]
      ids.problem_mips.v <- sub.remapped.mips.df[
        sub.remapped.mips.df$problem_mip,
        "X.mip_pick_count"]
      ids.problem_mips.v <- unique(ids.problem_mips.v)
      length.ids.problem_mips.v <- length(ids.problem_mips.v)
      if (verbose) {
        cat(length.ids.problem_mips.v, "\n")
      }
      if ((length.ids.problem_mips.v) == 1) {
        return(ids.problem_mips.v)
      }
      #
      ident.problem_mips.v <- sub.remapped.mips.df[
        sub.remapped.mips.df$problem_mip, "ident"]
      ident.problem_mips.v <- unique(ident.problem_mips.v)
      length.ident.problem_mips.v <- length(ident.problem_mips.v)
      if (verbose) {
        cat(length.ident.problem_mips.v, "\n")
      }
      if ((length.ident.problem_mips.v) == 1) {
        sub.remapped.mips.df[sub.remapped.mips.df$ident %in%
          ident.problem_mips.v, "X.mip_pick_count"]
      }
      # define a
      # bed file of the feature NOTE: This section shrinks the
      # region of the feature to regions, which are of interest for
      # final coverage with mips, thus which are defined by the
      # supplied bed.df
      bed.sub.remapped.mips.df <- sub.remapped.mips.df[1,
        c("chr", "feature_start_position", "feature_stop_position",
          "anno")]
      # reduce the bed data to the actual regions of interest,
      # supplied by a bed file before by the user
      negative_of_roi_bed.sub.remapped.mips.df <- do.call(rbind,
        uncovered_regions_of_bed1_by_bed2.fct(
          bed.sub.remapped.mips.df,
```

```
          bed.df, feed = "\r"))
      if (nrow(negative_of_roi_bed.sub.remapped.mips.df) >
        0) {
        bed.sub.remapped.mips.df <- do.call(rbind,
          uncovered_regions_of_bed1_by_bed2.fct(
            bed.sub.remapped.mips.df,
            negative_of_roi_bed.sub.remapped.mips.df, feed = "\r"))
      } else {
        bed.sub.remapped.mips.df <- bed.sub.remapped.mips.df
      }
      if (verbose) {
        cat(feed, "[filter_problem_mips.fct]: creating group’s MIP",
          "combinations for size ", feed)
      }
      # option of fast screening
      if (fast_screen.s) {
        # cut the search space get the smallest possible targeting
        # size of MIPs as refernce for minimal tilling density
        smallest_targeting_size.s <- min(apply(
          as.matrix(sub.remapped.mips.df[,
          c("mip_target_start_position",
          "mip_target_stop_position")]),
          1, function(x) {
          return(as.numeric(x[2]) - as.numeric(x[1]) + 1)
          }))
        # get the size of the regions of interest, which belong to
        # the current mip subpopulation
        total_size.bed.sub.remapped.mips.s <- sum(apply(
          as.matrix(bed.sub.remapped.mips.df[,
          2:3]), 1, function(x) {
          return(as.numeric(x[2]) - as.numeric(x[1]) +
          1)
        }))
        # calc the needed number of MIPs for perfect tilling
        # (multiply with 2 like for perfect double-tilling, to ensure
        # that enough MIPs are available, taking some overlap into
        # account):
        maximum_number_of_needed_mips <- ceiling(
         (total_size.bed.sub.remapped.mips.s/
         smallest_targeting_size.s) * 2)
        # check the number, which should not be larger than the real
        # number of MIPs
        if (maximum_number_of_needed_mips >
          length.ident.problem_mips.v) {
          maximum_number_of_needed_mips <-
          length.ident.problem_mips.v
        }
        # create combination list
        if (verbose) {
          cat(feed, "[filter_problem_mips.fct]: restricting MIP",
          "combinations to maximum size",
          maximum_number_of_needed_mips, "of possible",
          length.ident.problem_mips.v, feed)
        }
        combinations_of_problem_ids.l <- do.call(c, apply(
          as.matrix(1:maximum_number_of_needed_mips),
          1, function(amount.s) {
          if (verbose) {
            cat("\r", amount.s, "/", length.ident.problem_mips.v)
          }
          sample.ident.l <- combn(x = ident.problem_mips.v,
            m = amount.s, FUN = NULL, simplify = FALSE)
          corresponding_ids.l <- lapply(sample.ident.l,
            function(ident.v) {
            return(sub.remapped.mips.df[
              sub.remapped.mips.df$ident %in%
              ident.v, "X.mip_pick_count"])
            })
          return(corresponding_ids.l)
```

```
        }))
    } else {
      combinations_of_problem_ids.l <- do.call(c, apply(
        as.matrix(1:length.ident.problem_mips.v),
        1, function(amount.s) {
        if (verbose) {
          cat("\r", amount.s, "/", length.ident.problem_mips.v)
        }
        sample.ident.l <- combn(x = ident.problem_mips.v,
          m = amount.s, FUN = NULL, simplify = FALSE)
        corresponding_ids.l <- lapply(sample.ident.l,
          function(ident.v) {
          return(sub.remapped.mips.df[
            sub.remapped.mips.df$ident %in%
            ident.v, "X.mip_pick_count"])
          })
        return(corresponding_ids.l)
        }))
    }
    if (verbose) {
      cat(feed)
    }
    # for each combination of MIPs, get a coverage value, maximal
    # overlap value
    if (verbose) {
      cat(feed, "[filter_problem_mips.fct]: creating",
        "combination’s evaluation statistics",
        feed)
    }
    length.combinations_of_problem_ids.l <- length(
      combinations_of_problem_ids.l)
    evaluation_stats.df <- do.call(rbind, apply(
      as.matrix(1:length.combinations_of_problem_ids.l),
      1, function(index.s) {
        if (verbose) {
        cat("\r", index.s, "/",
          length.combinations_of_problem_ids.l,
          feed)
        }
        subset_problem_ids.v <-
          combinations_of_problem_ids.l[[index.s]]
        # select good MIPs and subset of problematic MIPs
        sub.sub.remapped.mips.df <- sub.remapped.mips.df[
          sub.remapped.mips.df$X.mip_pick_count %in%
          subset_problem_ids.v | !sub.remapped.mips.df$problem_mip,
        ]
        # get coverage values
        coverage.bed.sub.remapped.mips.l <-
          inspect_bed_by_mip_coverage.fct(bed.sub.remapped.mips.df,
          sub.sub.remapped.mips.df, feed = "\r")
        missingness.s <- sum((
          coverage.bed.sub.remapped.mips.l[[3]])$missing_size)
        # get number of querried MIPs
        amount.problem_mips.s <- length(subset_problem_ids.v)
        # get overlap values for the remaining problematic MIPs
        if (amount.problem_mips.s > 1) {
        complementary_arm_overlaps.subset.problem_mips.x <-
          get_arm_overlaps.fct(
            sub.remapped.mips.df[
              sub.remapped.mips.df$X.mip_pick_count %in%
              subset_problem_ids.v, ], 0, feed = "\r")
          if (
            is.null(
              complementary_arm_overlaps.subset.problem_mips.x)) {
              max_complementary_overlap.s <- 0
          } else {
            complementary_arm_overlaps.subset.problem_mips.df <-
              do.call(rbind,
              complementary_arm_overlaps.subset.problem_mips.x)
```

```
              max_complementary_overlap.s <- max(
                complementary_arm_overlaps.subset.problem_mips.df$
                max_overlap)
            }
          } else {
            max_complementary_overlap.s <- 0
          }
          # create an output
          output.df <- data.frame(missingness = missingness.s,
          max_overlap = max_complementary_overlap.s,
          amount_problem_mips = amount.problem_mips.s)
          return(output.df)
        }))
      # asign a
      # number, corresponding to the subset of MIPs
      evaluation_stats.df$subset_id <- 1:nrow(evaluation_stats.df)
      # filter out subsets, which overcome the problem threshold
      evaluation_stats.df <- evaluation_stats.df[
        evaluation_stats.df$max_overlap <
        problem_threshold.s, ]
      # select based on highest coverage, lowest overlaps, lowest
      # number of MIPs,
      evaluation_stats.df <- evaluation_stats.df[
        order(evaluation_stats.df$missingness,
        evaluation_stats.df$max_overlap,
        evaluation_stats.df$amount_problem_mips),
        ]
      # return the best combination of MIP IDs
      return(combinations_of_problem_ids.l[[evaluation_stats.df[1,
        "subset_id"]]])
    })
  # reformate selected ids and filter
  if (is.list(best.problem_mips.x)) {
    best.problem_mips.v <- unlist(best.problem_mips.x)
  } else {
    best.problem_mips.v <- c(best.problem_mips.x)
  }
  auswahl.v <- !(mip.df$X.mip_pick_count %in% problem_mips.v) |
    (mip.df$X.mip_pick_count %in% best.problem_mips.v)
  if (verbose) {
    cat(feed, "[filter_problem_mips.fct]: done")
  }
  return(mip.df[auswahl.v, ])
}

# function to remove duplicate MIPs /////////////////////////////////

remove_mip_duplicates.fct <- function(mip.df, verbose = TRUE,
  feed = "\n") {
  if (verbose) {
    cat(feed, "[remove_mip_duplicates.fct]: beginning")
  }
  # DATA check
  data_contains_factor.fct(mip.df)
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  auswahl.v <- duplicated(apply(as.matrix(1:nrow(mip.df)),
    1, function(index.s) {
      return(paste(mip.df[index.s, c("chr",
        "mip_target_start_position",
        "mip_target_stop_position", "ext_probe_sequence",
        "lig_probe_sequence")], collapse = "_"))
    }))
  mip.df <- mip.df[!auswahl.v, ]
  if (verbose) {
    cat(feed, "[remove_mip_duplicates.fct]: done")
  }
  return(mip.df)
```

```
}

# function to check MIPs for their sequencing sizes ////////////////

check_sequencing_size.fct <- function(mip.df, verbose = TRUE,
  feed = "\n", ...) {
  # Peform data check:
  data_contains_factor.fct(mip.df)
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # definition:
  part.MIPBC_SEQ_REV <- "ATCCGACGGTAGTGT"
  part.MIPBC_SEQ_FOR <- "CTTCAGCTTCCCGAT"
  SLXA_PE_MIPBC2_REV_193 <-
    "CAAGCAGAAGACGGCATACGAGATCTCTAGCAACACGCACGATCCGACGGTAGTGT"
  SLXA_PE_MIPBC_FOR_reversed <-
    "GAAGTCGAAGGGCTAATGCCTAGAGCATACACATCTAGAGCCACCAGCGGCATAGTAA"
  # calcs: determine PCR size:
  output.df <- return(as.data.frame(t(apply(
    as.matrix(1:nrow(mip.df)),
    1, function(index.s) {
      mip_sequence.s <- mip.df[index.s, "X70mer"]
      amount_bases_1.s <- nchar(unlist(strsplit(mip_sequence.s,
        part.MIPBC_SEQ_FOR))[1])
      amount_bases_2.s <- nchar(unlist(strsplit(mip_sequence.s,
        part.MIPBC_SEQ_REV))[2])
      amount_bases_3.s <- nchar(mip.df[index.s,
        "mip_target_sequence"])
      target_size.s <- amount_bases_3.s
      # capture means length of targeted region, which
      # is included into the MIPs after polymerase action
      capture_size.s <- sum(c(amount_bases_1.s, amount_bases_2.s,
        amount_bases_3.s))
      pcr_size.s <- capture_size.s + nchar(SLXA_PE_MIPBC2_REV_193) +
        nchar(SLXA_PE_MIPBC_FOR_reversed)
      output.v <- c(target_size.s, capture_size.s, pcr_size.s)
      names(output.v) <- c("target_size", "capture_size",
        "pcr_size")
      return(output.v)
    })), stringsAsFactors = FALSE))
  return(output.df)
}

# function to filter for redundnancy ////////////////////////////////

filter_redundancy.fct <- function(mip.df, bed.df, verbose = TRUE,
  feed = "\n", ...) {
  # DATA CHECK:
  if (verbose) {
    cat(feed, "[filter_redundancy.fct]: data check.")
  }
  data_contains_factor.fct(mip.df)
  data_contains_factor.fct(bed.df)
  if (any(duplicated(mip.df$X.mip_pick_count))) {
    warning("[filter_problem_mips.fct]: MIP dataframe contained",
    "redundnant MIP ids!!! If same IDs hint to different MIPs, than",
    "filtering might contain errors!!!")
  }
  # removal of duplicates: NOTE: some duplicates have to stay,
  # as those might bind to SNPs!!! So include the ligation and
  # extension probe sequence as an identifier
  auswahl.v <- duplicated(apply(as.matrix(1:nrow(mip.df)),
    1, function(index.s) {
      return(paste(mip.df[index.s, c("chr",
      "mip_target_start_position",
        "mip_target_stop_position", "ext_probe_sequence",
        "lig_probe_sequence")], collapse = "_"))
    }))
```

```
  mip.df <- mip.df[!auswahl.v, ]
  # removal of duplicates NOTE: DON’T FILTER OUT SNP-MIPS
  # (binding to SNPs)!!! Thus create an identifier based on
  # chr, position of target start and stop(if they target the
  # same region, but have different arms, than asign the same
  # identifier)
  ident.v <- apply(as.matrix(1:nrow(mip.df)), 1, function(index.s) {
    return(paste(mip.df[index.s, c("chr",
      "mip_target_start_position",
      "mip_target_stop_position", "lig_probe_start",
      "lig_probe_stop",
      "ext_probe_start", "ext_probe_stop")], collapse = "_"))
  })
  # collapse bed.df
  bed.df <- collapse_bed.fct(bed.df, feed = "\r")
  # perform data check
  if (verbose) {
    cat(feed, "[filter_redundancy.fct] beginning...")
  }
  data_contains_factor.fct(mip.df)
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # determine groups of redundancy
  if (verbose) {
    cat(feed, "[filter_redundancy.fct] determining overlapping",
    "groups")
  }
  overlaping_mips.mip.l <- redundancy_check.fct(mip.df[, c("chr",
    "mip_target_start_position", "mip_target_stop_position",
    "X.mip_pick_count")], verbose_output_information = TRUE)
  # NOTE: overlaping_mips.mip.l was reordered and does not have
  # the sme order as the input mip.df!!!
  auswahl.unproblematic_mips.v <- unlist(lapply(
    overlaping_mips.mip.l,
    function(overlap_summary.df) {
      if (nrow(as.data.frame(overlap_summary.df)) == 0) {
        return(TRUE)
      }
      if ((nrow(overlap_summary.df) %in% c(1, 2)) & any(
        overlap_summary.df$overlaps_querry_downstream !=
        overlap_summary.df$overlaps_querry_upstream)) {
        return(TRUE)
      }
      return(FALSE)
    }))
  auswahl.problematic_mips_ids.v <- unlist(lapply(
    overlaping_mips.mip.l,
    function(overlap_summary.df) {
      if (nrow(as.data.frame(overlap_summary.df)) == 0) {
        return(NULL)
      }
      if ((nrow(overlap_summary.df) %in% c(1, 2)) & any(
        overlap_summary.df$overlaps_querry_downstream !=
        overlap_summary.df$overlaps_querry_upstream)) {
        return(NULL)
      }
      return(unique(unlist(overlap_summary.df[, c("querry",
         "overlaping")])))
    }))
  if (length(auswahl.problematic_mips_ids.v) != 0) {
    regions_of_overlaps.df <- collapse_bed.fct(mip.df[
      mip.df$X.mip_pick_count %in%
      auswahl.problematic_mips_ids.v, c("chr",
      "mip_target_start_position",
      "mip_target_stop_position", "X.mip_pick_count")])
  } else {
    return(mip.df)
  }
```

```
  mips.df$problem_mip <- FALSE
  mips.df[mips.df$X.mip_pick_count %in% problem_mips.v,
    "problem_mip"] <- TRUE
  mips.df$ident <- ident.v
  remapped.mips.df <- remap_mips_to_bed.fct(mips.df,
    regions_of_overlaps.df,
    remap_based_on_mip_target = TRUE)
  # filter based on best combination of MIPs to cover a region
  unique.remapped.mips.df_feature_mip_count <- unique(
    remapped.mips.df$feature_mip_count)
  length.unique.unique.remapped.mips.df_feature_mip_count <- length(
    unique.remapped.mips.df_feature_mip_count)
  best.problem_mips.x <- apply(as.matrix(
    unique.remapped.mips.df_feature_mip_count),
    1, function(feature_mip_count.s) {
      if (verbose) {
        cat(feed, "[filter_problem_mips.fct]: MIP group",
          which(unique.remapped.mips.df_feature_mip_count ==
          feature_mip_count.s), "/",
          length.unique.unique.remapped.mips.df_feature_mip_count,
          ", size ")
      }
      # select the mips of the feature
      sub.remapped.mips.df <- remapped.mips.df[
        remapped.mips.df$feature_mip_count %in%
        feature_mip_count.s, ]
      ids.problem_mips.v <- sub.remapped.mips.df[
        sub.remapped.mips.df$problem_mip,
        "X.mip_pick_count"]
      ids.problem_mips.v <- unique(ids.problem_mips.v)
      length.ids.problem_mips.v <- length(ids.problem_mips.v)
      if (verbose) {
        cat(length.ids.problem_mips.v, "\n")
      }
      if ((length.ids.problem_mips.v) == 1) {
        return(ids.problem_mips.v)
      }
      #
      ident.problem_mips.v <- sub.remapped.mips.df[
        sub.remapped.mips.df$problem_mip,
        "ident"]
      ident.problem_mips.v <- unique(ident.problem_mips.v)
      length.ident.problem_mips.v <- length(ident.problem_mips.v)
      if (verbose) {
        cat(length.ident.problem_mips.v, "\n")
      }
      if ((length.ident.problem_mips.v) == 1) {
        return(ids.problem_mips.v)
      }
      # define a bed file of the feature
      bed.sub.remapped.mips.df <- sub.remapped.mips.df[1,
        c("chr", "feature_start_position", "feature_stop_position",
          "anno")]
      # reduce the bed data to the actual regions of interest,
      # supplied by a bed file before by the user
      negative_of_roi_bed.sub.remapped.mips.df <- do.call(rbind,
        uncovered_regions_of_bed1_by_bed2.fct(
          bed.sub.remapped.mips.df,
          bed.df, feed = "\r"))
      if (nrow(negative_of_roi_bed.sub.remapped.mips.df) >
        0) {
        bed.sub.remapped.mips.df <- do.call(rbind,
          uncovered_regions_of_bed1_by_bed2.fct(
            bed.sub.remapped.mips.df,
            negative_of_roi_bed.sub.remapped.mips.df, feed = "\r"))
      } else {
        bed.sub.remapped.mips.df <- bed.sub.remapped.mips.df
      }
      # create a list of all
```

```
      # possible combinations of problematic ids
      if (verbose) {
        cat(feed, "[filter_problem_mips.fct]: creating group’s MIP",
          "combinations for size ",
          feed)
      }
      combinations_of_problem_ids.l <- do.call(c, apply(
        as.matrix(1:length.ident.problem_mips.v),
        1, function(amount.s) {
          if (verbose) {
          cat("\r", amount.s, "/", length.ident.problem_mips.v)
          }
          sample.ident.l <- combn(x = ident.problem_mips.v,
          m = amount.s, FUN = NULL, simplify = FALSE)
          corresponding_ids.l <- lapply(sample.ident.l,
          function(ident.v) {
            return(sub.remapped.mips.df[
              sub.remapped.mips.df$ident %in% ident.v,
              "X.mip_pick_count"])
          })
          return(corresponding_ids.l)
        }))
      if (verbose) {
        cat(feed)
      }
      # for each combination
      # of MIPs, get a coverage value, maximal overlap value
      if (verbose) {
        cat(feed, "[filter_problem_mips.fct]:",
          "creating combination’s evaluation statistics",
          feed)
      }
      length.combinations_of_problem_ids.l <- length(
        combinations_of_problem_ids.l)
      evaluation_stats.df <- do.call(rbind, apply(
        as.matrix(1:length.combinations_of_problem_ids.l),
        1, function(index.s) {
          if (verbose) {
          cat("\r", index.s, "/",
            length.combinations_of_problem_ids.l,
            feed)
          }
          subset_problem_ids.v <-
            combinations_of_problem_ids.l[[index.s]]
          # select good MIPs and subset of problematic MIPs
          sub.sub.remapped.mips.df <- sub.remapped.mips.df[
            sub.remapped.mips.df$X.mip_pick_count %in%
            subset_problem_ids.v | !sub.remapped.mips.df$problem_mip,
          ]
          # get coverage values
          coverage.bed.sub.remapped.mips.l <-
            inspect_bed_by_mip_coverage.fct(bed.sub.remapped.mips.df,
            sub.sub.remapped.mips.df, feed = "\r")
          # get number of querried MIPs
          amount.problem_mips.s <- length(subset_problem_ids.v)
          # bad rank_score
          amount.bad_rank_score.s <- sum(
            sub.sub.remapped.mips.df$rank_score %in% -1)
          # judge the mean performance
          mean_performance.logistic_score.s <- 1 - mean(as.numeric(
            sub.sub.remapped.mips.df$logistic_score),
            na.rm = TRUE)
          mean_performance.rank_score.s <- 5 - mean(as.numeric(
            sub.sub.remapped.mips.df$rank_score),
            na.rm = TRUE)
          # create an output
          output.df <- data.frame(missingness = missingness.s,
          bad_rank_score = amount.bad_rank_score.s,
          mean_performance.logistic_score =
```

```
          mean_performance.logistic_score.s,
          mean_performance.rank_score =
          mean_performance.rank_score.s,
          amount_problem_mips = amount.problem_mips.s)
          return(output.df)
        }))
      # asign a number, corresponding to
      # the subset of MIPs
      evaluation_stats.df$subset_id <- 1:nrow(evaluation_stats.df)
      # filter out subsets, which overcome the problem threshold
      # select based on highest coverage, lowest number of MIPs and
      # rank_score = -1 MIPs
      evaluation_stats.df <- evaluation_stats.df[order(
        evaluation_stats.df$missingness,
        evaluation_stats.df$bad_rank_score,
        evaluation_stats.df$amount_problem_mips,
        evaluation_stats.df$mean_performance.logistic_score,
        evaluation_stats.df$mean_performance.rank_score),
        ]
      return(combinations_of_problem_ids.l[[evaluation_stats.df[1,
        "subset_id"]]])
    })
  # reformate selected ids and filter
  if (is.list(best.problem_mips.x)) {
    best.problem_mips.v <- unlist(best.problem_mips.x)
  } else {
    best.problem_mips.v <- c(best.problem_mips.x)
  }
  auswahl.v <- !(mip.df$X.mip_pick_count %in% problem_mips.v) |
    (mip.df$X.mip_pick_count %in% best.problem_mips.v)
  if (verbose) {
    cat(feed, "[filter_problem_mips.fct]: done")
  }
  return(mip.df[auswahl.v, ])
}

# Function to check whether MIPs binding to SNPs are missing
# in a new mip df ///////////////////////////////////////////////////

SNP_binding_mips.fct <- function(mip.df, verbose = TRUE, feed = "\n",
  ...) {
  # check the data
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: data check.")
  }
  data_contains_factor.fct(mip.df)
  # create a vector of MIP idents, and state with ‘mult’
  # whether there are duplicates
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: creating identifiers.")
  }
  ident.v <- apply(as.matrix(1:nrow(mip.df)), 1, function(index.s) {
    paste(c(mip.df[index.s, c("chr", "ext_probe_start",
      "ext_probe_stop", "lig_probe_start", "lig_probe_stop",
      "mip_target_sequence")]), collapse = "_")
  })
  ident.v <- as.character(as.numeric(as.factor(ident.v)))
  auswahl.v <- ident.v %in% ident.v[duplicated(ident.v)]
  ident.v[auswahl.v] <- apply(as.matrix(ident.v[auswahl.v]),
    1, function(ident.s) {
      paste(ident.s, "mult", sep = "_")
    })
  # modify the notes for mipgen-derived SNP annotation
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: adjust notes")
  }
  mip.df[grepl("SNP", mip.df$notes), "notes"] <- apply(
    as.matrix(mip.df[grepl("SNP",
    mip.df$notes), "notes"]), 1, function(x) {
```

```
    return(paste(unlist(strsplit(x, split = "_"))[-4], collapse =
    "_"))
  })
  # check for each mip of same ident whether they bind to
  # different SNP versions
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: checking allele mip ratios.")
  }
  ext_lig_arm.allele_mip_ratio.m <- t(apply(as.matrix(ident.v),
    1, function(ident.s) {
      auswahl.v <- ident.v %in% ident.s
      ext_lig_arm.allele_mip_ratio.v <- apply(as.matrix(
        mip.df[auswahl.v,
        c("ext_probe_sequence", "lig_probe_sequence")]),
        2, function(arm_sequences.v) {
          # count the number of alleles (neglect the ‘haplotype’ of a
          # MIP)
          independant_allele_count.arm_sequences.v <- apply(
            as.matrix(as.data.frame((strsplit(arm_sequences.v,
            split = "")), stringsAsFactors = F)), 1,
            function(base.s) {
              length(unique(base.s))
            })
          # calc a allele-mip ratio allele_mip_ratio.s <-
          allele_mip_ratio.s <- max(
            independant_allele_count.arm_sequences.v)/
            length(arm_sequences.v)
          # return
          return(allele_mip_ratio.s)
        })
      # return
      return(ext_lig_arm.allele_mip_ratio.v)
    }))
  # count the ident
  ident.count.v <- apply(as.matrix(ident.v), 1, function(ident.s) {
    return(sum(ident.v %in% ident.s))
  })
  # check by notes whether a SNP binding mip is missing
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: checking snp binding MIPs by",
    "annotation.")
  }
  # nijmegen like notes: grep ‘snp’
  snp_binding_mip_count_by_notes.v <- apply(as.matrix(
    1:nrow(mip.df)),
    1, function(index.s) {
      note.s <- mip.df[index.s, "notes"]
      # check for nijmegen mip or modified mipgen-derived SNP
      # binding MIP annotation
      if (grepl("snp", note.s) | grepl("SNP", note.s)) {
        return(sum(mip.df$notes %in% note.s))
      } else {
        return(NA)
      }
    })
  # create an overall judgement
  SNP_binding_mip_issue.v <- rep(FALSE, nrow(mip.df))
  auswahl.v <- (snp_binding_mip_count_by_notes.v == 1) |
    (apply(ext_lig_arm.allele_mip_ratio.m,
    1, function(x) {
      max(x)
    }) != 1)
  SNP_binding_mip_issue.v[auswahl.v] <- TRUE
  # create an annotation output
  output.df <- data.frame(binding_class_ident = ident.v,
    count_binding_class_ident = ident.count.v,
    ext_arm_allele_mip_ratio = ext_lig_arm.allele_mip_ratio.m[,
      1], lig_arm_allele_mip_ratio = ext_lig_arm.allele_mip_ratio.m[,
      2], snp_binding_issue = SNP_binding_mip_issue.v,
```

```
    stringsAsFactors = F)
  if (verbose) {
    cat(feed, "[SNP_binding_mips.fct]: done.")
  }
  return(output.df)
}

# Function to add an ordering name to a MIP.df //////////////////////

add_ordering_name_to_mips.fct <- function(mip.df, project_name.s,
  verbose = TRUE, feed = "\n", ...) {
  # check the data
  if (verbose) {
    cat(feed, "[add_ordering_name_to_mips.fct]: data check.")
  }
  data_contains_factor.fct(mip.df)
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
  # create a ordering name
  mod.mip.x <- apply(as.matrix(unique(mip.df$anno)), 1, function(
    anno.s) {
    # select the MIPs of interest for that annotation
    auswahl.v <- mip.df$anno %in% anno.s
    sub.mip.df <- mip.df[auswahl.v, ]
    # order
    sub.mip.df <- sub.mip.df[order(
      sub.mip.df$mip_target_start_position),
      ]
    # create ordering name
    ordering_name.v <- apply(as.matrix(1:nrow(sub.mip.df)),
      1, function(index.s) {
        return(paste(c(project_name.s, "_", anno.s, "_MIP",
          as.character(index.s)), collapse = ""))
      })
    sub.mip.df$ordering_name <- ordering_name.v
    return(sub.mip.df)
  })
  if (is.list(mod.mip.x)) {
    mod.mip.x <- do.call(rbind, mod.mip.x)
  }
  if (verbose) {
    cat(feed, "[add_ordering_name_to_mips.fct]: done.")
  }
  return(mod.mip.x)
}

# Function to add mips to a existing panel by a redesign ///////////

iterative_redesign.fct <- function(mips.df = data.frame(NULL,
  stringsAsFactors = FALSE), path_to_mipgen.s, path_to_mipgen_script.s,
  out_folder.s, result_folder.s, start_bed_regions.s,
  desired_bed_regions.s, prefix.s, genome_index.s, snps_path.s,
  verbose = TRUE, feed = "\n", ...) {
  # check the data
  if (all(is.null(c(start_bed_regions.s, desired_bed_regions.s)))) {
    stop("[iterative_redesign.fct]: no regions supplied")
  }
  if (is.null(path_to_mipgen_script.s)) {
    stop("[iterative_redesign.fct]: no mipgen script supplied")
  }
  if (is.null(start_bed_regions.s)) {
    start_bed_regions.s <- desired_bed_regions.s
  }
  if (is.null(desired_bed_regions.s)) {
    desired_bed_regions.s <- start_bed_regions.s
  }
  # set parameters and variables
  iteration_step.s <- 1
```

```
  missingness_changes.s <- TRUE
  path.current_missing_regions_bed.s <- start_bed_regions.s
  desired_bed_regions.df <- convert_bed_frame.fct(bed.df =
    collapse_bed.fct(read.table(file = desired_bed_regions.s,
    header = FALSE, as.is = T, sep = "\t")), state_chr.s = FALSE)
  # iterate
  while (missingness_changes.s) {
    cat("[iterative_redesign.fct]: iteration", iteration_step.s,
      "\n")
    # launch a redesign for MIPGEN1.1
    cat("[iterative_redesign.fct]: launching MIPGEN1.1")
    befehl.s <- paste(c("bash ", " ",path_to_mipgen.s, " ",
      path_to_mipgen_script.s, " ", path.current_missing_regions_bed.s,
      out_folder.s, prefix.s, "iter", as.character(iteration_step.s),
      " ", prefix.s, "iter", as.character(iteration_step.s),
      genome_index.s, snps_path.s), collapse = "")
    print(befehl.s)
    system(befehl.s)
    # process the redesign
    cat("[iterative_redesign.fct]: primary qc\n")
    # define the path to the results of the redesign
    path_to_redesign_file.s <- paste(c(out_folder.s, prefix.s,
      "iter", as.character(iteration_step.s), "/", prefix.s,
      "iter", as.character(iteration_step.s),
      "_overview_pickedmips.txt"),
      collapse = "")
    # primary QC
    if (iteration_step.s == 1) {
      path_to_mipprocessing_output_folder.s <- paste(result_folder.s,
        prefix.s, sep = "")
      system(paste("mkdir", path_to_mipprocessing_output_folder.s,
        sep = " "))
    }
    path_to_mipprocessing_output_prefix.s <- paste(
      path_to_mipprocessing_output_folder.s,
      paste(c(prefix.s, "iter", iteration_step.s), collapse = ""),
      sep = "/")
    primary_mip_qc.fct(path_to_mip.s = path_to_redesign_file.s,
      path_to_bed.s = desired_bed_regions.s, output_prefix.s =
      path_to_mipprocessing_output_prefix.s,
      convert_bed_to_mip.s = TRUE, convert_mip_to_nijmegen_format =
      TRUE, overlap_threshold.s = 7, feed = "\n")
    # add the redesign to the current MIPs
    # load the redesign
    load_R_data.fct <- function(path.s) {
      get(load(path.s))
    }
    new.mips.df <- load_R_data.fct(paste(
      path_to_mipprocessing_output_prefix.s,
      ".qc.mip.R", sep = ""))
    # keep columns which are present in both MIP dfs, but make
    # sure, that no column is skipped!!!
    column_selection.v <- intersect(colnames(new.mips.df),
      colnames(mips.df))
    # add column names, which are missing so far in one of the
    # dataframes to the mips.df
    add_to_mips.df <- as.data.frame(matrix(NA, nrow = nrow(mips.df),
      ncol = sum(!(colnames(new.mips.df) %in% column_selection.v))),
      stringsAsFactors = F)
    colnames(add_to_mips.df) <- (colnames(new.mips.df))[!(colnames(
      new.mips.df) %in% column_selection.v)]
    mips.df <- cbind(mips.df, add_to_mips.df)
    # to the new.mips.df
    add_to_new.mips.df <- as.data.frame(
      matrix(NA, nrow = nrow(new.mips.df),
      ncol = sum(!(colnames(mips.df) %in% column_selection.v))),
      stringsAsFactors = F)
    colnames(add_to_new.mips.df) <- (colnames(mips.df))[
      !(colnames(mips.df) %in% column_selection.v)]
```

```
    new.mips.df <- cbind(new.mips.df, add_to_new.mips.df)
    # combine
    column_selection.v <- intersect(colnames(new.mips.df),
      colnames(mips.df))
    mips.df <- rbind(mips.df[, column_selection.v], new.mips.df[,
      column_selection.v])
    mips.df$X.mip_pick_count <- 1:nrow(mips.df)
    # perform filtering
    cat("[iterative_redesign.fct]: filtering\n")
    # complementary arms
    compl_7bp.mips.df <- summary.arm_overlaps.fct(mips.df,
      7)
    complementary_filtered.mips.df <- filter_problem_mips.fct(
      mips.df,
      compl_7bp.mips.df$X.mip_pick_count, desired_bed_regions.df,
      problem_threshold.s = 7)
    # remap for coverage check
    remap.complementary_filtered.mips.df <- remap_mips_to_bed.fct(
      complementary_filtered.mips.df,
      desired_bed_regions.df, remap_based_on_mip_target = TRUE)
    remap.complementary_filtered.mips.df$X.mip_pick_count <-
      1:nrow(remap.complementary_filtered.mips.df)
    # get coverage
    coverage.remap.complementary_filtered.mips.l <-
      inspect_bed_by_mip_coverage.fct(desired_bed_regions.df,
      remap.complementary_filtered.mips.df)
    # create new bed file of missing regions
    path.current_missing_regions_bed.s <- paste(
      path_to_mipprocessing_output_prefix.s,
      ".missing.bed", sep = "")
    write.table(file = path.current_missing_regions_bed.s,
      convert_bed_frame.fct(bed.df =
       (coverage.remap.complementary_filtered.mips.l[[2]]),
        state_chr.s = TRUE), col.names = F, row.names = F,
      sep = "\t", quote = F)
    # check difference: mind case of iteration step 1 and total
    # coverage reached!
    cat("[iterative_redesign.fct]: checking improvement\n")
    if (iteration_step.s == 1) {
      # check completeness of coverage:
      if (all((coverage.remap.complementary_filtered.mips.l[[3]])$
        missing_percent ==
        0)) {
        cat("[iterative_redesign.fct]: no improvement... stopping",
        "iteration\n")
        missingness_changes.s <- FALSE
      } else {
        # set new ‘previous coverage’ for the comparison of the next
        # iteration step
        previous_iter.coverage.remap.complementary_filtered.mips.l <-
          coverage.remap.complementary_filtered.mips.l
        iteration_step.s <- iteration_step.s + 1
      }
    } else {
      # compare with previous coverage
      compare_coverage.df <- merge(
        previous_iter.coverage.remap.complementary_filtered.mips.l[[
        3]], coverage.remap.complementary_filtered.mips.l[[3]],
        by = "anno")
      if (any(compare_coverage.df$missing_percent.x >
        compare_coverage.df$missing_percent.y) |
        all((coverage.remap.complementary_filtered.mips.l[[3]])$
          missing_percent == 0)) {
        # set new ‘previous coverage’ for the comparison of the next
        # iteration step
        previous_iter.coverage.remap.complementary_filtered.mips.l <-
          coverage.remap.complementary_filtered.mips.l
        iteration_step.s <- iteration_step.s + 1
      } else {
```

```
        cat("[iterative_redesign.fct]: no improvement...",
          "stopping iteration\n")
        missingness_changes.s <- FALSE
      }
    }
    # reset mips.df
    mips.df <- remap.complementary_filtered.mips.df
    # write to file
    path_to_final_mips.s <- paste(c(
      path_to_mipprocessing_output_folder.s,
      "/", prefix.s, "_intermediate_mips.csv"), collapse = "")
    write.table(file = path_to_final_mips.s, mips.df, col.names = T,
      row.names = F, quote = F, sep = "\t")
  }
  # perform ‘intron’ filtering (filtering of mips to far away
  # from the region of interest)
  cat("[iterative_redesign.fct]: removing to far mips\n")
  intron_filtered.mips.df <- remove_far_intronic_MIPs.fct(mips.df,
    CNV.mode = TRUE)
  # removal of duplicates
  cat("[iterative_redesign.fct]: removing duplicates\n")
  no_dup.intron_filtered.mips.df <- remove_mip_duplicates.fct(
    intron_filtered.mips.df)
  # filter redundancy
  cat("[iterative_redesign.fct]: removing redundancy\n")
  redundancy_filtered.no_dup.intron_filtered.mips.df <-
    filter_redundancy.fct(no_dup.intron_filtered.mips.df,
    bed.df = desired_bed_regions.df)
  # multi-annotate MIPs mapping to multiple regions
  cat("[iterative_redesign.fct]: reannotate mips\n")
  remap.redundancy_filtered.no_dup.intron_filtered.mips.df <-
    remap_mips_to_bed.fct(
      redundancy_filtered.no_dup.intron_filtered.mips.df,
      desired_bed_regions.df, remap_based_on_mip_target = TRUE)
  reanno.remap.redundancy_filtered.no_dup.intron_filtered.mips.df <-
    do.call(rbind, apply(as.matrix(unique(
      remap.redundancy_filtered.no_dup.intron_filtered.mips.df$
      X.mip_pick_count)),
      1, function(x.mip_pick_count) {
        auswahl.v <-
          remap.redundancy_filtered.no_dup.intron_filtered.mips.df$
          X.mip_pick_count %in% x.mip_pick_count
        sub.df <-
          remap.redundancy_filtered.no_dup.intron_filtered.mips.df[
          auswahl.v, ]
        anno.sub.v <- unique(sub.df$anno)
        anno.sub.v <- anno.sub.v[order(anno.sub.v)]
        sub.df$anno <- paste(anno.sub.v, collapse = "_")
        return(sub.df[1, ])
      }))
  # write to file
  mips.df <-
    reanno.remap.redundancy_filtered.no_dup.intron_filtered.mips.df
  path_to_final_mips.s <- paste(c(
    path_to_mipprocessing_output_folder.s,
    "/", prefix.s, "_final_mips.csv"), collapse = "")
  write.table(file = path_to_final_mips.s, mips.df, col.names = T,
    row.names = F, quote = F, sep = "\t")
  cat("[iterative_redesign.fct]: done\n")
  return(mips.df)
}

# Function to create a fasta file of the mips  //////////////////////

create_fasta_file.fct <- function(mip.df, ...) {
  # As done by the MIPGEN1.1 software check the data
  if (nrow(mip.df) == 0) {
    return(NULL)
  }
```

```
  # create a fasta file
  header.v <- apply(as.matrix(1:nrow(mip.df)), 1, function(index.s) {
    # create a header
    start_stop_capture.s <- c(min(as.numeric(mip.df[index.s,
      c("lig_probe_start", "lig_probe_stop", "ext_probe_start",
        "ext_probe_stop")])), max(as.numeric(mip.df[index.s,
      c("lig_probe_start", "lig_probe_stop", "ext_probe_start",
        "ext_probe_stop")])))
    header.s <- paste(c(">", mip.df[index.s, "chr"], ":",
      as.character(start_stop_capture.s[1]), "-", as.character(
      start_stop_capture.s[2]),
      "/", as.character(nchar(mip.df[index.s,
      "ext_probe_sequence"])),
      ",", as.character(nchar(mip.df[index.s,
      "lig_probe_sequence"])),
      "/", mip.df[index.s, "probe_strand"]), collapse = "")
    cat(header.s, "\n", sep = "")
    # create the sequence
    sequence.s <- paste(c(mip.df[index.s, c("ext_probe_sequence",
      "mip_target_sequence", "lig_probe_sequence")]), collapse = "")
    if (mip.df[index.s, "probe_strand"] == "-") {
      sequence.s <- reverse_complement.fct(sequence.s)
    }
    # cut the sequence into pieces of 80 nts
    anzahl.s <- ceiling(nchar(sequence.s)/80)
    for (index2.s in 1:anzahl.s) {
      if (index2.s < anzahl.s) {
        teil.sequence.s <- substr(sequence.s, 1 + ((index2.s -
          1) * 80), 80 + ((index2.s - 1) * 80))
      } else {
        teil.sequence.s <- substr(sequence.s, 1 + ((index2.s -
          1) * 80), nchar(sequence.s))
      }
      cat(teil.sequence.s, "\n", sep = "")
    }
    return(header.s)
  })
  # return the vector of names of the fasta sequences
  return(header.v)
}

# Function to create the reverse complement of a sequence //////////

reverse_complement.fct <- function(sequence) {
  return(paste(apply(
    as.matrix(unlist(strsplit(sequence, split = ""))[
    nchar(sequence):1]),
    1, function(base.s) {
      if (base.s == "A") {
        return("T")
      }
      if (base.s == "a") {
        return("t")
      }
      if (base.s == "C") {
        return("G")
      }
      if (base.s == "c") {
        return("g")
      }
      if (base.s == "T") {
        return("A")
      }
      if (base.s == "t") {
        return("a")
      }
      if (base.s == "G") {
        return("C")
      }
```

```
      if (base.s == "g") {
        return("c")
      }
      if (base.s == "N") {
        return("N")
      }
      if (base.s == "n") {
        return("n")
      }
      if (base.s == "S") {
        return("S")
      }
      if (base.s == "s") {
        return("s")
      }
      if (base.s == "W") {
        return("W")
      }
      if (base.s == "w") {
        return("w")
      }
      if (base.s == "K") {
        return("M")
      }
      if (base.s == "k") {
        return("m")
      }
      if (base.s == "M") {
        return("K")
      }
      if (base.s == "m") {
        return("k")
      }
      if (base.s == "R") {
        return("Y")
      }
      if (base.s == "r") {
        return("y")
      }
      if (base.s == "Y") {
        return("R")
      }
      if (base.s == "y") {
        return("r")
      }
      return("?")
    }), collapse = ""))
}
reverse.fct <- function(sequence) {
  return(paste(unlist(strsplit(sequence, split = ""))[nchar(sequence):1],
    collapse = ""))
}

# Function to simulate yield of sequencing /////////////////////////

simulate_seq.fct <- function(on_target_coverage_data,
  cluster.lane = 5e+09/16,
  off_target_proportion = 0.25, process_read_lost_proportion = 0.05,
  call_threshold = 25, level.multiplex = 372, lanes.v = 1:16) {
  set.seed(1)
  auswahl.v <- sample(1:nrow(on_target_coverage_data),
    level.multiplex, replace = T)
  sim.data.m <- on_target_coverage_data[auswahl.v, ]
  norm.sim.data.m <- sim.data.m/sum(sim.data.m)
  callable.v <- apply(as.matrix(lanes.v), 1, function(lanes.s) {
    reads.s <- (lanes.s * cluster.lane) * (1 -
      process_read_lost_proportion) * (1 - off_target_proportion)
    sum((norm.sim.data.m * reads.s) >= call_threshold)
  })
```

```
  plot(x = lanes.v, y = callable.v/level.multiplex, xlab = "lanes",
    ylab = "callable targets/person", main = paste(level.multiplex,
      "-plex", sep = ""))
  steigung.v <- callable.v/level.multiplex
  steigung.v <- steigung.v[2:length(steigung.v)] - steigung.v[1:
   (length(steigung.v) - 1)]
  names(steigung.v) <- paste(1:(length(steigung.v) - 1), 2:length(
    steigung.v), sep = "_")
  return(steigung.v)
}
```

Appendix C – Script for Automated MIP Design

The following Linux shell script is a wrapper for the mipgen design software [399] and was used to enable an iterative design of MIPs.

```
#!/bin/bash

#script for running MIPGEN with a given bed-file

#get command line arguments-----------------------------------------------
MIPGEN=$1
DATEI=$2
#DATEI is the path to the bed file, which should not contain a header
DATEILAENGE=$(wc -l ${DATEI} | awk ‘{print $1}’)
OUTPUTFOLDER=$3
OUTPUTPREFIX=$4
GENOMEINDEX=$5
#The GENOMEINDEX is the path to the indexes reference genome in fasta
#format (see mipgen publication for details). The files should be
#separated into chromosomes and the files’ prefixes should be the same as
#the chromosomal coding in the supplied bed file
SNPS=$6
#The SNPS ist the path to the gzipped vcf file containing the information
#about the SNPs to be considered in the MIP design.

#set parameters-----------------------------------------------------------
MAXCAPTURESIZE=152
MINCAPTURESIZE=152
mkdir ${OUTPUTFOLDER}
OUTPUTPFAD=${OUTPUTFOLDER}/${OUTPUTPREFIX}
LOGFILE=${OUTPUTPFAD}.mipdesign_shell.log

#iterate the design-------------------------------------------------------

for index in `seq 1 ${DATEILAENGE}`
do
echo ${index}----------------------------------------------------
echo
echo ${index}---------------------------------------------------- >> \
${LOGFILE} 2>&1
echo >> ${LOGFILE} 2>&1
head -n ${index} ${DATEI} | tail -1 > tmp.tmp
CHR=$(awk ‘{print $1}’ tmp.tmp)
GENE=$(awk ‘{print $4}’ tmp.tmp)
${MIPGEN} \
-arm_length_sums 40,41,42 \
-tag_sizes 0,0 \
-capture_increment 1 \
-double_tile_strands_separately off \
-max_mip_overlap 40 \
-logistic_priority_score 0.70 \
-logistic_optimal_score 0.92 \
-regions_to_scan tmp.tmp \
-project_name ${OUTPUTPFAD}.${GENE}.bed_index.${index} \
-min_capture_size ${MINCAPTURESIZE} \
-max_capture_size ${MAXCAPTURESIZE} \
-bwa_genome_index ${GENOMEINDEX}/${CHR}.fa \
-snp_file ${SNPS} \
>> ${LOGFILE} 2>&1
done

#collect data into one file-----------------------------------------------
FILESPICKEDMIPS=$(ls ${OUTPUTPFAD}*picked_mips.txt)
FIRSTFILESPICKEDMIPS=$(ls ${OUTPUTPFAD}*picked_mips.txt| head -1)
head -1 ${FIRSTFILESPICKEDMIPS} > ${OUTPUTPFAD}_overview_pickedmips.txt
for DATEI in ${FILESPICKEDMIPS}
do
echo ${DATEI}
```

```
awk ‘NR>1{print $0}’ ${DATEI} >> ${OUTPUTPFAD}_overview_pickedmips.txt
done
#add SNP binding MIPs from file
FILESSNPBINDINGMIPS=$(ls ${OUTPUTPFAD}*snp_mips.txt)
for DATEI in ${FILESSNPBINDINGMIPS}
do
echo ${DATEI}
awk ‘NR>1{print $0}’ ${DATEI} | grep -v Alternate >>
${OUTPUTPFAD}_overview_pickedmips.txt
done
echo done
```

Appendix D – Primary MIP Design Outcome

The following table lists a summary of the primary MIP design (Table 32). Numbers are shown for all target regions (“all”) and for the coding regions of any transcript (“coding regions”).

Table 32: Summary of primary MIP Design: The genes were ordered according to the signal category in alphabetical order. (Selection criteria = criteria of gene selection (LD-block = gene in LD block of an unpublished RLS meta-GWAS [373] lead SNP or proximal SNP, eQTL = eQTL gene of an unpublished RLS meta-GWAS [373] lead SNP or proximal SNP, proximity = gene near an unpublished meta-GWAS [373] lead SNP or proximal SNP, published = gene that is discussed as an RLS gene in the GWAS related literature, function = gene with putative RLS related function, ExomeChip = gene from the candidate list of the ExomeChip association analysis), Cat = signal category (1 = published RLS association signal, 2 = genome-wide significant RLS association signal from an unpublished RLS meta-GWAS [373], 3 = sub-significant RLS association signal from an unpublished RLS meta-GWAS [373] defined by a locus with at least two SNPs’ p values < 1E-05), l = size of the collapsed promotor regions and exons (in bp), f = size of the target regions that could not be covered by the primary MIPs design (in bp), f/l = proportion of the region of interest without successful primary MIPs design, n = number of MIPs). Some genes had overlapping transcripts.

Gene	**Selection criteria**	**Cat**	**All**				**Coding regions**			
			l **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**	***l*** **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**
AAGAB	LD-block	1	12973	92	0.01	145	1859	0	0.00	35
BBS7	eQTL	1	8895	142	0.02	112	3308	0	0.00	48
BTBD9	published	1	12119	1	0.00	144	3600	0	0.00	37
C15orf61	LD-block	1	4698	96	0.02	49	1480	0	0.00	10
CALML4	LD-block	1	6743	0	0.00	75	1104	0	0.00	11
CASC16	published	1	3464	0	0.00	43	NA	NA	NA	NA
GLO1	eQTL	1	6132	323	0.05	69	1638	0	0.00	18
IQCH	LD-block	1	12055	57	0.00	155	5119	0	0.00	63
MAP2K5	published	1	12505	18	0.00	161	2170	0	0.00	51
MDGA1	eQTL	1	21148	0	0.00	234	4710	0	0.00	50
MEIS1	published	1	22448	0	0.00	247	5091	0	0.00	56
PIAS1	LD-block	1	7450	0	0.00	133	2403	0	0.00	47
PTPRD	published	1	20401	0	0.00	265	7276	0	0.00	107
SKOR1	LD-block	1	6498	0	0.00	81	9351	0	0.00	56
TOX3	published	1	7083	0	0.00	78	3758	0	0.00	30
ADAM22	function proximity	2	17447	440	0.03	210	5185	0	0.00	77
ALLC	proximity	2	4038	0	0.00	54	1242	0	0.00	26
ARFRP1	eQTL	2	9731	0	0.00	101	2770	0	0.00	27
ATP2C1	LD-block	2	24568	396	0.02	285	4745	0	0.00	72
C7orf62	LD-block	2	2005	0	0.00	24	763	0	0.00	10
CCDC148	LD-block	2	7690	30	0.00	113	2803	9	0.00	39
CNTN4	function proximity	2	16736	322	0.02	207	4919	0	0.00	61
COL20A1	eQTL	2	16722	1	0.00	214	5944	0	0.00	93
COL6A6	proximity	2	12214	0	0.00	164	7634	0	0.00	115
COLEC11	proximity	2	4860	0	0.00	62	1476	0	0.00	27

continued table…

Gene	**Selection criteria**	**Cat**	**All**				**Coding regions**			
			l **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**	***l*** **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**
CRBN	function proximity	2	11022	176	0.02	125	3098	0	0.00	31
FTSJ2	function proximity eQTL	2	4078	36	0.01	44	4222	165	0.04	17
LRRN1	function proximity	2	6418	0	0.00	70	4232	0	0.00	30
MICALL2	LD-block	2	17616	172	0.01	203	9305	0	0.00	80
MYT1	LD-block eQTL	2	10419	5	0.00	135	5546	0	0.00	66
NPBWR2	LD-block	2	1893	0	0.00	20	1003	0	0.00	11
NTNG1	function proximity	2	14089	0	0.00	170	3591	0	0.00	45
OPRL1	eQTL	2	5461	0	0.00	65	2120	0	0.00	22
PIK3R4	proximity	2	11138	39	0.00	137	5830	0	0.00	65
PKP4	LD-block eQTL	2	24101	144	0.01	273	8328	74	0.01	74
SEMA6D	LD-block	2	16734	0	0.00	195	5827	0	0.00	51
SETBP1	proximity	2	14104	82	0.01	149	5738	0	0.00	61
SLC14A2	function proximity	2	8322	188	0.02	112	3174	0	0.00	48
STEAP4	function proximity	2	12059	280	0.02	128	3090	0	0.00	22
SUN1	function proximity	2	19759	485	0.02	235	5497	0	0.00	63
TANC1	function proximity	2	21149	10	0.00	241	8869	0	0.00	91
UNCX	function proximity	2	2671	0	0.00	28	1985	0	0.00	19
VAV3	function proximity	2	15203	0	0.00	196	4108	0	0.00	74
ZNF804B	LD-block	2	5350	0	0.00	59	4054	0	0.00	46
ASTN2	LD-block function	3	14736	999	0.07	172	7206	0	0.00	79
CACNG8	function proximity	3	9415	147	0.02	101	1668	0	0.00	18
CADM1	LD-block function	3	18199	0	0.00	202	2982	0	0.00	34
CREB5	LD-block function	3	21923	0	0.00	251	4146	0	0.00	56

continued table…

Gene	**Selection criteria**	**Cat**	**All**				**Coding regions**			
			***l* [bp]**	***f* [bp]**	***f/l***	***n* [MIP]**	***l* [bp]**	***f* [bp]**	***f/l***	***n* [MIP]**
DCLK2	function proximity	3	10323	279	0.03	123	4028	0	0.00	53
EBF3	LD-block function eQTL	3	8733	1	0.00	105	2553	0	0.00	37
FAM114A1	function proximity	3	8649	334	0.04	104	2147	0	0.00	31
KCNA4	function proximity	3	5098	0	0.00	53	1963	0	0.00	20
KCNK13	LD-block function	3	3105	0	0.00	33	1229	0	0.00	15
LAMA1	function proximity	3	21834	234	0.01	291	11445	0	0.00	164
MEIS2	function proximity	3	22874	0	0.00	249	4325	0	0.00	47
MPPED2	function proximity	3	15258	0	0.00	172	2135	0	0.00	26
NRG3	LD-block function	3	12485	132	0.01	153	3952	0	0.00	55
NRSN2	function proximity	3	6351	102	0.02	71	2222	0	0.00	22
PLXNA2	function proximity	3	18839	0	0.00	230	9191	0	0.00	97
PTPRM	function proximity	3	22025	1	0.00	274	8242	0	0.00	104
RIMS2	LD-block function	3	18314	191	0.01	223	8000	129	0.02	104
SGCZ	LD-block function	3	3562	0	0.00	44	947	0	0.00	18
SLC39A11	LD-block function	3	13295	287	0.02	160	3478	25	0.01	40
SYT5	function proximity	3	7509	2	0.00	91	3197	0	0.00	32
TUBB3	function proximity	3	10516	418	0.04	117	5024	55	0.01	47
CORO6	ExomeChip	NA	5737	0	0.00	65	4543	0	0.00	36
DMPK	ExomeChip	NA	9534	0	0.00	106	3931	0	0.00	42
EYA2	ExomeChip	NA	9648	64	0.01	122	3509	0	0.00	43
FAM171A1	ExomeChip	NA	9013	143	0.02	102	5812	0	0.00	43
GALNT12	ExomeChip	NA	8249	41	0.00	97	2757	0	0.00	36

continued table…

Gene	**Selection criteria**	**Cat**	**All**				**Coding regions**			
			l **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**	***l*** **[bp]**	***f*** **[bp]**	***f/l***	***n*** **[MIP]**
GRIN2B	ExomeChip	NA	28250	0	0.00	298	4467	0	0.00	62
KRTAP19-5	ExomeChip	NA	1002	0	0.00	13	220	0	0.00	3
LEO1	ExomeChip	NA	4677	138	0.03	62	3627	0	0.00	35
NECAP1	ExomeChip	NA	7758	389	0.05	84	2135	0	0.00	19
NENF	ExomeChip	NA	2526	20	0.01	32	904	0	0.00	11
OLFML2B	ExomeChip	NA	6116	0	0.00	72	3225	0	0.00	30
OSBP	ExomeChip	NA	8820	80	0.01	99	3324	0	0.00	37
OSGIN1	ExomeChip	NA	5793	0	0.00	73	2340	0	0.00	31
PCDHB5	ExomeChip	NA	3466	0	0.00	42	4742	0	0.00	31
PDE11A	ExomeChip	NA	18109	79	0.00	228	3465	0	0.00	62
RASGRP4	ExomeChip	NA	6254	44	0.01	79	3091	0	0.00	41
TREM1	ExomeChip	NA	5816	0	0.00	62	1857	0	0.00	16
UBL4B	ExomeChip	NA	2566	0	0.00	27	526	0	0.00	7
ZNF175	ExomeChip	NA	6224	0	0.00	66	4250	0	0.00	29

Appendix E – MIPs of This Study

The following table lists all MIPs used in this study.

Table 33: MIPs of this study: The MIPs from the primary and secondary design are listed in order of concentration in the rebalanced MIPs pool. ID = MIP name, MIP = MIP sequence, c = MIP concentration as the multiple of the standard MIP concentration.

ID	MIP	*c*
M00764_ADAM22_MIP28	CACTGACTTCCACAATGGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCACAATAAACATACAT	0
M00764_ADAM22_MIP29	TGCGAGGACAAAAAACCAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATAGACTGGATTAAGA	0
M00764_ARFRP1_MIP42	GAGGTGGGAGGATGGCTTGAGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGAGGCAGAAGCA	0
M00764_ASTN2_MIP119	CAACCTCCACCTCCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTCCAGCTCCTAACCGCGAG	0
M00764_ASTN2_MIP121	CAGCAGTACCGTCCAGCTTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCGAATCCCAGTCTCC	0
M00764_ASTN2_MIP69	TCAGAACACAGTGCAATCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACCCCAATCAACAG	0
M00764_ASTN2_MIP71	GAGATTTATAGCACTAAATGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGCTCCTGAATGACTA	0
M00764_ASTN2_MIP73	CTCCCTCTACACACTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTAGTTATTTCTTGCCTTCT	0
M00764_ATP2C1_MIP22	AGAGGGAGAGGGAGAGGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCGGCACTCGGCAGGC	0
M00764_ATP2C1_MIP23	AGAGGGAGAGGGAGAGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCGGCACTCGGCAGGC	0
M00764_ATP2C1_MIP239	ACCGAGATGGCGCCACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATGGTGAAACCCCGTCTCTA	0
M00764_ATP2C1_MIP24	GCCGAGATGGCAGCAGTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGGAGCTGGAGACCAGC	0
M00764_ATP2C1_MIP25	GCCGAGATGGCAGCAGTACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGGAGCTGGAGACCAGC	0
M00764_ATP2C1_MIP28	CCCCGCCGCCATCACATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGAGCGTCTCTGCTTGGCC	0
M00764_BBS7_MIP38	TGGGCGGATCACAAGGTCAGGAGATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGAGGGCAAGAGA	0
M00764_BTBD9_MIP144	GGTGTCGAACTCCTGAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTCCCCAGGTTCAAG	0
M00764_CACNG8_MIP64	GCATGAGCCACTGCGCCCGGCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACCCAGCTACTT	0
M00764_CACNG8_MIP66	CTGGGACTACAGGCACACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCATCCTTGCTCTGTCA	0
M00764_CACNG8_MIP83	GTGTGCACCACCGCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTTTGAGACAGAGTCTTGC	0
M00764_CCDC148_MIP36	CAAGCTGGCTGCAGAAATTTGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAAGAGGTGACCTG	0
M00764_DMPK_MIP42	CTGAACCTGGGAGGCGGAGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGATGGAGACCAG	0
M00764_EBF3_MIP53	CCTCAGATGATCCGCCTGCCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGATTCTCCTGCCTCAGG	0
M00764_EBF3_MIP54	TGCCAACACACCCGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTAGACAGGGTCTTGCTCTGT	0
M00764_FAM114A1_MIP32	GACAGGGTTTCACCATGTTGCCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTCGGCTCCCT	0
M00764_FAM114A1_MIP33	GACAGGGTTTCACCATGTTGCCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTCTGCTCCCT	0
M00764_FAM114A1_MIP87	CCTGGCGACAGAGTGAGACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAAATTGGCTGGGCG	0
M00764_GALNT12_MIP25	ACTCCTGACGTCAGGCGTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCCTCCTCAGCCTCC	0
M00764_GALNT12_MIP45	ATCGTGCCACTGCGCTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACCTCGTCTATACTAAAA	0
M00764_GALNT12_MIP46	GCCGGGCATGATGGCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTGCAGTGGCTCACACCTAT	0
M00764_GALNT12_MIP47	GCCAGGCATGATGGCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTGCAGTGGCTCACACCTAT	0
M00764_GALNT12_MIP75	GTTGCAGTGAGCTGAGATTGCACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACATGGCAAAACT	0
M00764_GALNT12_MIP76	AGTGATCCACCTGCCTCAGCCTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCAGTCTCCTGA	0
M00764_GLO1_MIP37	ATTAGCTGGGCGTAGTGGCGGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGTGGTGGGTCACG	0
M00764_IQCH_MIP2	CACACCATTGCATTCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGCCCGTCTCTACTAAAAAT	0
M00764_IQCH_MIP3	CACACCATTGCATTCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGCCTGTCTCTACTAAAAAT	0
M00764_LAMA1_MIP258	CAGATGTGAGCCACCACGCCTGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCACCACACCCAG	0
M00764_LAMA1_MIP259	CAGATGTGAGCCACCGCGCCTGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCACCACACCCAG	0
M00764_LAMA1_MIP93	GAGACAGGGTCTCACTATGTTGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTGCAGTGGAACA	0
M00764_MAP2K5_MIP78	ACCTTGAACATCAGACTCCAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAATCTGGGTGGG	0
M00764_MAP2K5_MIP79	GCACTGTTGGCTTCCCTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTTCTTCCATGCTGGA	0
M00764_MDGA1_MIP106	TGAACCCAGGAGGTGGAGGTTGCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATCAAGAGTTCGA	0
M00764_MEIS2_MIP212	GGGGAGAGAGAGAGAGAGAGAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGGGGGGTGGAA	0
M00764_MEIS2_MIP213	GGGGAGAGAGAGAGAGAGAGAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGGAGGGTGGAA	0
M00764_MEIS2_MIP65	GCTTTCACAAGGTATTGTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACAAGTAGGAATCTG	0
M00764_MICALL2_MIP25	GCCAGGATGGTCTCGATCTGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGCCTCCAGGGTT	0
M00764_MICALL2_MIP26	GCCAGGATGGTCTCCATCTGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGCCTCCAGGGTT	0
M00764_MICALL2_MIP28	GCCGGGCATGGTGGTGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTACGGTGGCTCATGCCTG	0
M00764_MICALL2_MIP29	GCCGGGCATGGTAGTGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTACGGTGGCTCATGCCTG	0
M00764_MPPED2_MIP4	ACCGCGCCTGGCCAGGATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTACCACGCCCAACTAAT	0
M00764_MYT1_MIP35	AAAAATGAGCTGGGCGTGGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGGGCTCGGTGGC	0
M00764_NECAP1_MIP7	GGCTGAGGCAGGAGAATTGCTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGACCAGCCTGAC	0
M00764_NRG3_MIP104	GTGGGGGAGCTTTTTGAGCCAGGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAAAGAGAGTTAG	0
M00764_NRSN2_MIP3	ACTGAGGTGGGAGGATCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGTGGATCACTTGAGCT	0
M00764_NRSN2_MIP4	GCCTGGACAACAGAGTGAGACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAAATTAGCTAGGCA	0
M00764_OSGIN1_MIP59	GAAGTACATTGGTTCGGTCTGGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAAGGTTGAGGA	0
M00764_OSGIN1_MIP8	GTGATCTGCCCGCCTCAGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTCCCTCAGACTCCT	0
M00764_PDE11A_MIP45	CGTCTGTAGTCCCAGCTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCCCAGCAATTTGGAAGG	0
M00764_PDE11A_MIP46	CGTCTGTAGTCCCAGCTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCCCAGAAATTTGGAAGG	0
M00764_PDE11A_MIP50	GACCTCAGGTGAGCCACCCACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATTCTCCAGCCTCA	0
M00764_PKP4_MIP127	GCCCATCTTGGCCTCCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGCCTTCCAAGTAGTT	0
M00764_PKP4_MIP128	ACCCATCTTGGCCTCCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGCCTTCCAAGTAGTT	0
M00764_PKP4_MIP201	AATTTACAAATTTGTGTTGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCGTCCTTGGGCC	0
M00764_RASGRP4_MIP6	GTTTCCCCATGTTGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAATCTCAGCTCACTGCAAC	0
M00764_RASGRP4_MIP7	GTTTCCCCATGTTGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAATCCCAGCTCACTGCAAC	0
M00764_SLC14A2_MIP36	GTTCTCGTGATAGTGAGTGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGATATGGTTTGGCTC	0

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ID	MIP	*c*
M00764_SLC39A11_MIP156	CGAGATCTGATGGTTTTATAAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAATCTCATCTTG	0
M00764_SLC39A11_MIP32	CTGCACTCCAGCCTGGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTTGAGGTCAGGAGTTGGA	0
M00764_SLC39A11_MIP59	GCACACCTGTAATCCCAGCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTAATGCCAGCACTC	0
M00764_SLC39A11_MIP60	GATGGGATTTCACCATGTTGGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACTCTTGGCTCCC	0
M00764_SLC39A11_MIP61	GATGGGATTTCACCATGTTGGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTCTTGGCTCCC	0
M00764_SLC39A11_MIP97	ACTTGGGAGGCTGAGATGGGAGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGCAGATGGCTT	0
M00764_STEAP4_MIP70	GCCTGCCTCCGCCTCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATCAGCCTCCCGAGTAG	0
M00764_STEAP4_MIP71	ACCTGGGAGGAGGAGGTTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCAAGACCAGCCTGA	0
M00764_SUN1_MIP114	CAGGATGGTCTCGATTTCCTGACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCTCCAGAGTTCA	0
M00764_SUN1_MIP2	GTCTGGCCAACATGGTGTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAACATAGTGAGACCCCC	0
M00764_SUN1_MIP3	TGATTCGCCTGCCTCGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTCCTGCCTCAGTCTCCCC	0
M00764_SUN1_MIP61	GGCGCCTGTAGTTTCAGCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTGGAATCCCAGTACTT	0
M00764_SUN1_MIP98	GCGGTGAGCCGAGATCACACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGAAACCCCATGTC	0
M00764_SUN1_MIP99	GCAGTGAGCCGAGATCACACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGAAACCCCATGTC	0
M00764_SYT5_MIP14	GAGGAGCTTGCAGTGAGCCGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCCTGGCTAACACGGTG	0
M00764_TANC1_MIP177	CACCACTGCACTCCAGCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATGGCAAAACCCCATCTT	0
M00764_TREM1_MIP61	CCTGGAAACATACAACCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAAAACACAATCAGAA	0
M00764_TUBB3_MIP52	CCTCTCGAGTAGCTGGGAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTTCCTTCCTTCCTTCC	0
M00764_TUBB3_MIP60	GCCTGGGCGACAGAGTGAGACACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAAATTAGCCGGGA	0
M00764_ADAM22_MIP26	GCCCCCCAAATCAACACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCTATGTATTCAGAGG	0.17
M00764_ATP2C1_MIP97	GGGTGGTGGTATTCTAGTTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACCCCTCTGCAGA	0.17
M00764_NTNG1_MIP91	GGTATCCCCAGTATTTCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGTGTGCTAATTTCTT	0.17
M00764_PDE11A_MIP155	GTGGGGTTCATGGGTCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTAAACGGCAATAAAGC	0.17
M00764_AAGAB_MIP53	GCCCCTGGTATGCCACTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAAGATTTAAGGCAAA	0.5
M00764_AAGAB_MIP84	CAACAGCAACCCCATTTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTCTTCTTTCTTTGCC	0.5
M00764_ADAM22_MIP100	GACCAGTAGCATAAGCCAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGCCCACCACTAAAA	0.5
M00764_ADAM22_MIP136	GCTTAGCAAGGATGTCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTCACATCTTCTACCC	0.5
M00764_ADAM22_MIP46	CAGTGGTGTGTCGTGTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATCTGACAAATGCAC	0.5
M00764_ADAM22_MIP76	GGTGGTGCCTGCCTTTTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGACATTCACAAATGA	0.5
M00764_ADAM22_MIP88	GTCAGGCGGACTTCTCAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGGGTATTTGCTTTTC	0.5
M00764_ASTN2_MIP30	GGATGGGCTATTTCCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCCAAATACTACATCA	0.5
M00764_ASTN2_MIP40	GTTGTGTTTGGTTTTCTGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTGGTGAAAAAAAG	0.5
M00764_ASTN2_MIP42	CACCCTCCTTCTATTTCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACAAAGCACTCAACACA	0.5
M00764_ASTN2_MIP44	GAAGGCATATTCTTCCAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTCTGATAGGTCCC	0.5
M00764_ASTN2_MIP81	GCTGAGGTCACACCTGCACCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGGCATGGGCTGGC	0.5
M00764_ATP2C1_MIP105	CCCCCAAAAAGAGTAAAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGCATCCATGAGATA	0.5
M00764_ATP2C1_MIP13	GTAGTAACAGTGGTGGTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTGCAGCAAGTGTT	0.5
M00764_ATP2C1_MIP162	GGACAGACCAGAGATTTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTCAAAACCTTAGG	0.5
M00764_ATP2C1_MIP179	AAACTCCTGGACTAGCCCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCAGACAAAATGGTG	0.5
M00764_ATP2C1_MIP230	GCCAGCTCCTTACACTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTAAGGTATGAGACATC	0.5
M00764_ATP2C1_MIP59	GTAAGTCTTGTGGCTGATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGATAGGCCCAGAGAAC	0.5
M00764_ATP2C1_MIP73	GGTATGGATTTCTGCCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATATATTCATGGGAG	0.5
M00764_BBS7_MIP74	GCCCTTAAAACAGTAACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGGCAAAAAAAATCC	0.5
M00764_CADM1_MIP100	CCACCAGCCATGAGTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAACAAAAACTTAGCCC	0.5
M00764_CADM1_MIP170	GTTGGGGCAGTGTGTGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATATGACGGTATATACA	0.5
M00764_CADM1_MIP72	GTTTGTTTGTTGCGTTCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTCTGCTGTTTGACA	0.5
M00764_CADM1_MIP87	CCCCAGCCAAACATGTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATAAATCTCAAATGCCAT	0.5
M00764_CASC16_MIP36	CCCTGTGTGATTGCATAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTACATAGGACCAGCTA	0.5
M00764_CCDC148_MIP16	ATTTTTAGGTTGCTGTTGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTCTTCTGCCCTTTC	0.5
M00764_CCDC148_MIP20	AGGTGGTGAATGGAGTCTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAACAGAAGTGGCAA	0.5
M00764_CCDC148_MIP90	ATGTATACATCCATCCTGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCATGATCTCTGCCTC	0.5
M00764_CNTN4_MIP105	ACCTTTGCCCCTTGCTCACTACTTCAGCTTCCCGATATCCGACGGTAGTGTACATTAATCAAATCGAGTC	0.5
M00764_CNTN4_MIP107	ATGGTCCGGCTTTTGCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAACTAGACAGATGTAGG	0.5
M00764_CNTN4_MIP154	GGCTTTTGAGAGGACTAAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCAGAGCAGTCACAA	0.5
M00764_CNTN4_MIP192	CATGCCGTTGTGATTTTGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATTACTCGTACAGT	0.5
M00764_CNTN4_MIP47	GGGCAGAGGGGAAAAATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATTAGTGTTCCTAATCA	0.5
M00764_CNTN4_MIP74	GGATAAGGGTGTGTGAAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGAAATGGAAAGCA	0.5
M00764_CNTN4_MIP84	GGCCCCAGGACCTTGTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATTTAGACAACAAAGC	0.5
M00764_CNTN4_MIP96	CCATGCATACAACTTTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTGCACAATTAATTCCT	0.5
M00764_COL6A6_MIP15	CATCAACTGCTCCCTCCTTGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAATGCAGCCCATT	0.5
M00764_CRBN_MIP19	GAAGGAAGGACCCACTAAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTCACTCCACCTTC	0.5
M00764_CRBN_MIP87	CCCGAATGTGTGTTGCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGGAAAATCTTGGTATT	0.5
M00764_CREB5_MIP138	GATGGTGTGCTGGGTGCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTACCTGTGCTTGGTTG	0.5
M00764_CREB5_MIP74	GGTGGTGGAAGAAAGAGGTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCTAAGATGAGGGC	0.5
M00764_CREB5_MIP80	GTGCCTGCCTTCTCTGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTATAACATACAGCTACGA	0.5
M00764_DCLK2_MIP40	AGCCTGGTAGACTTGACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGATTAAAGGTATGAAAT	0.5
M00764_DCLK2_MIP81	GTTGCTATTGCTGCTTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTAGTACTTTAACTTTG	0.5
M00764_EYA2_MIP35	GTCTGGGTTTAGGTAATCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGAAGGAGGGGAAT	0.5
M00764_EYA2_MIP45	GGGTGATGTTCTGCAGAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAGGTGGGCATGTGAG	0.5
M00764_GLO1_MIP52	ACTCTTTGCTAATTTGCGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACATACCTTCTACCCT	0.5
M00764_GRIN2B_MIP150	CCTCCTTTTGCTTAATGGTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCACTTTTAGCCCC	0.5
M00764_GRIN2B_MIP245	GTTCTCTCTACCTCACTGATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGGGTGGGTTGTC	0.5
M00764_GRIN2B_MIP281	GCCAGGGAAATAGGTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTGAGCTGATTCTGGA	0.5

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ID	**MIP**	***c***
M00764_IQCH_MIP25	ACTATGGCCAGAAATTTATTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTGGTCCCCCAGA	0.5
M00764_IQCH_MIP73	GCCCCTTGTTTTATTCAAATTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGCATCAGGACCTC	0.5
M00764_KRTAP19-5_MIP5	CCATAGTAGTTGCCGTAGTAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCGAAGCCAGAGCC	0.5
M00764_LAMA1_MIP152	GGGTTTGAGCAGAGATTCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATCCAGAGCCTGAT	0.5
M00764_LAMA1_MIP220	GGCTATGGTGAGAGGGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTCACTGGGCAAAATTC	0.5
M00764_LAMA1_MIP247	GCCAACCCCTGCTTTAAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAGCCATTTGCCTGTGT	0.5
M00764_LEO1_MIP41	GTGCCCTCTCCTCATCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATTAGCCTTTTCCTCC	0.5
M00764_MAP2K5_MIP70	AGCGAGCAAGTAAAGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATTAGAACTGTGTCCTC	0.5
M00764_MEIS1_MIP109	GTTTTTCCTAGAAGATAAACCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCACACGTCACAC	0.5
M00764_MEIS1_MIP126	GGAGTGAATGGAAATGCTAAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTTCAGAGCTGCT	0.5
M00764_MEIS2_MIP114	GGCCTCTTCAAATGTTAATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAACAACAAGTGC	0.5
M00764_MEIS2_MIP86	GCCCAAGTGAAAAAAGCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGGCCCATATGTTT	0.5
M00764_MPPED2_MIP53	CTCTGAGAGAATGTGTCAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAACTTGGGGTATTT	0.5
M00764_MPPED2_MIP86	GTCTGCCACAATCCCCTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGCAGTTTATTCTCCTC	0.5
M00764_NECAP1_MIP10	GTTGGGTGTTTTCAGCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTATAGTCTATTTAACA	0.5
M00764_NECAP1_MIP35	GGTCAGGTGGCCTCTGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTCGTGGTAGTTTTTG	0.5
M00764_NECAP1_MIP47	GTGTGCCACTCTTGTTACCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTATAGCCTGCAAT	0.5
M00764_NECAP1_MIP71	ATAGGGGTAGATATGGAGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGTGCCTCTTTGTG	0.5
M00764_NRG3_MIP112	ACTGAGAATTCTGTGCTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCATCTCCACCCCAC	0.5
M00764_NRG3_MIP90	GCTTATGTCCCCAGTAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCAGAAAACACAGGG	0.5
M00764_NRG3_MIP95	GCACAGAACATGCCCACGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCATTTCCACAGGTTC	0.5
M00764_NTNG1_MIP119	ATGCATGGATAGGGTGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGATGTAGATTATTGATGT	0.5
M00764_OSBP_MIP4	CCCAGCAGTCAAAGTCACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATTTAGTTGGGGAATT	0.5
M00764_PDE11A_MIP88	GCCTTATTTTTCCTCCTCCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGTTGCATACCCCT	0.5
M00764_PIAS1_MIP52	ACTGGAGCCTGTTGTGTAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAATAAGGAATCCGGA	0.5
M00764_PIAS1_MIP58	GGCTGGTTGTAGCTATTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACATATTTTAGAAGCA	0.5
M00764_PIAS1_MIP93	GGGCTTTTCTTTGTTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTTCATTTTTTTCTGGA	0.5
M00764_PIK3R4_MIP103	GAAGGTGTACCATTATTTGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTTTTGCATTTTGG	0.5
M00764_PIK3R4_MIP111	CCTGGGGAGTACTCGGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTAACCTTACTAAAGA	0.5
M00764_PIK3R4_MIP18	GGCCAGCAGTGCACCACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTGTTGTAATCTTCTCC	0.5
M00764_PIK3R4_MIP4	GGTTTTATTTCCACACCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCAGTCATGAAACAG	0.5
M00764_PIK3R4_MIP41	GTGGTGGTTTACTCTCCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTCCCAAATAACATTT	0.5
M00764_PIK3R4_MIP88	AGAGAACACACAAACGTTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAAGGCCTAAAGACA	0.5
M00764_PKP4_MIP16	GTGATCGGTGTCTCTGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTTTCTAATTATAAGGTG	0.5
M00764_PKP4_MIP203	GGGGTCCTGAAAACAAGGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGCATTATCAGCCCT	0.5
M00764_PKP4_MIP207	CAACAGCCCCCCAAACCTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTGTGGCACAGAAAG	0.5
M00764_PKP4_MIP240	GTCCCCATAGCACCACACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACAGTGGTTGGGCATT	0.5
M00764_PKP4_MIP63	GTCTTTTCCAGCTGTCTAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCAGCCTAACCATTC	0.5
M00764_PLXNA2_MIP122	GCTTGAGAGTGAGGTCATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCAGGGAGAAGGGC	0.5
M00764_PLXNA2_MIP158	GTGGGGTCATGAGTGCAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCAAGCCATTGGAC	0.5
M00764_PLXNA2_MIP43	GCGAAGTGTTTGGTGCATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAGATAAAGCTCAGTT	0.5
M00764_PTPRD_MIP104	GCTCGGCCATCCACTTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTACGTAATACATCTGG	0.5
M00764_PTPRD_MIP118	GTTCCAGGGAAACCTCGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTGTTTTGTTTTGTT	0.5
M00764_PTPRD_MIP120	GCACAGACATGATTACCTGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCTGAACTAAAAAC	0.5
M00764_PTPRD_MIP128	ATCCGGTATTCAGTCCATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGATCAAGACTGTG	0.5
M00764_PTPRD_MIP15	GTTCTGATGTAGGTTAGAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACCCCCTTTGTTTA	0.5
M00764_PTPRD_MIP161	GATGTCCATGCTTGTTCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTATTCTCAAAACTGGG	0.5
M00764_PTPRD_MIP162	GAACAATGCATTAACACCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACAAAAACAAAGAAGG	0.5
M00764_PTPRD_MIP165	CATTTGGCTCTTCAGGTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATATGTTTTCTGGGGC	0.5
M00764_PTPRD_MIP199	GCAGTTACGATCAGGTAGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAAGGTGGTTGAGC	0.5
M00764_PTPRD_MIP245	GGCCCGTGATATTCCAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGATAAATGAGTGTCTA	0.5
M00764_PTPRD_MIP81	GGCCTTTCTCAGTGTCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACACCATCATTTCCTTTGC	0.5
M00764_PTPRD_MIP91	GCAACCAGCCCTTACTCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCATCACACACTTATC	0.5
M00764_PTPRM_MIP105	GCCGAGATTTGACCTCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGTATCCCAGCTTACT	0.5
M00764_PTPRM_MIP143	ACTCCGAAACCAGTCCCAGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTCTGCTGGCTCTG	0.5
M00764_PTPRM_MIP185	CCTTTTCCTTTGCAGACGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGGGTGTGTACTATTT	0.5
M00764_PTPRM_MIP189	GCCCACTTCCTATCATTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGTTTATCGATTTTA	0.5
M00764_PTPRM_MIP201	GCCCACTCCTCCTAAAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTTAGGAAGTTTTGTTT	0.5
M00764_PTPRM_MIP24	GATGTTCCCTCCCTGCCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCTAGGTACTTGAAT	0.5
M00764_RIMS2_MIP42	GGCCACACAAATTCCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAATGTGCTCCATTAACT	0.5
M00764_SEMA6D_MIP145	AGTTTTTATGGCAGCACATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTTCAGCCCGTAAT	0.5
M00764_SGCZ_MIP43	ATTTGGGGAAAGGGCTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAGTGACAGATAAGAAT	0.5
M00764_SLC14A2_MIP4	GTTCTGTGGCTTTGTGTCATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTTTGGCTGGTCCT	0.5
M00764_SLC14A2_MIP7	AGACGGATGAACTCCCCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTAAGAGAAAATTGCA	0.5
M00764_SLC14A2_MIP84	CTCGACTGTGGGCTTCCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATACGAATGCAAGAAAA	0.5
M00764_SLC39A11_MIP148	AAGGGGTTGTGGTGTTTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGGTGATCATTAAACA	0.5
M00764_SLC39A11_MIP34	CAAGGGACAGGCCAAGGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGACCCTTAGTCAAA	0.5
M00764_TANC1_MIP223	ATCCACCCCAAAGAAAAAAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCTGGGCTGTC	0.5
M00764t_LRRN1_MIP52	CACTGCGAAGGCGGCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGAGTGGTGGTAGTTTT	0.5
M00764_TREM1_MIP44	GGGGGAAAGAAGGGCCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAATGGTCAACCTTCAAG	0.5
M00764t_ZNF804B_MIP17	CCACTTTGCCTTACCTGCTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAACCTTTCCAGGGG	0.5
M00764_VAV3_MIP168	CCTTAGGTGTCTGAAAATAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCATTTTTGGCTTCA	0.5
M00764_VAV3_MIP170	GGATACGGCCCAACAACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATCCATCATATTTACAA	0.5

continued table…

ID	**MIP**	***c***
M00764_VAV3_MIP33	GCTCGGTATGACTTCTGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTGCATTTGATAGCAT	0.5
M00764_VAV3_MIP63	GGCTTTTTACAATGCTTCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTAAGTGGGGACAAA	0.5
M00764_ZNF175_MIP20	GGGGGGGACCACTTGAAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTTAAAAGCCTCTTC	0.5
M00764_ZNF175_MIP25	GGTAGAATTTGCCTTTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTTTCCTACCTCTCTA	0.5
M00764_AAGAB_IQCH_MIP1	GAGAGAGTGTTTACTCTGAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCCACAGGTTTTT	1
M00764_AAGAB_IQCH_MIP10	ACTCTAAAACCGTTCACCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGACTCCCTCCAACTC	1
M00764_AAGAB_IQCH_MIP11	CCAGAGGCAGAAAGTCCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATTTGTCTCTCCTCCAC	1
M00764_AAGAB_IQCH_MIP12	GCTTTTCTTAAACACCCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTGAGGCATCATTTTT	1
M00764_AAGAB_IQCH_MIP13	CACATATTTCAATTTGTCTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAAAGGTCTTTCA	1
M00764_AAGAB_IQCH_MIP14	GTTTTCACATTTATGTGAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTGACATTTAAAAAC	1
M00764_AAGAB_IQCH_MIP15	AAATGCCATGATCATTTCAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGACAGAGTGACC	1
M00764_AAGAB_IQCH_MIP16	CATCTAGGAGAGACTTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTTGACTAAGTCTTG	1
M00764_AAGAB_IQCH_MIP2	ATTAAGAGATAGGGGCAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGGTTCATCTCAACG	1
M00764_AAGAB_IQCH_MIP3	GTTCCTTTCGGCTTCCTGTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTCTGGGCCTTGTC	1
M00764_AAGAB_MIP1	GGCACATAGTGTTTGGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTATCTAAAGTGACCTAT	1
M00764_AAGAB_MIP10	GTGTGCGGGCACCTTCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCAGTGCTTATAAGGT	1
M00764_AAGAB_MIP100	ATCCCGGAGGCACTTAAAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAAGGGGCTAATG	1
M00764_AAGAB_MIP101	AAATATACAGCCATGGTTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAAACGTGTTTGCAC	1
M00764_AAGAB_MIP102	ACGTATACTATCAGCTGCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAAGTTCCCAGGTGAT	1
M00764_AAGAB_MIP103	AGTTAGGCTCAGTGGAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAATGATGATAATAATGG	1
M00764_AAGAB_MIP104	CAGCCTTTTAAAAATGTATGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCCACTTCTCCCT	1
M00764_AAGAB_MIP105	AAAGAAAGAAAAGAAGGAAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGGTGAAAATGTT	1
M00764_AAGAB_MIP108	ACCAAGTAAGTTGTTCAGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCCTTTGAAGTATGA	1
M00764_AAGAB_MIP109	CCTTTAGTGTCTTCTTAAAAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTCCTTCCTGCC	1
M00764_AAGAB_MIP11	GCTGAGAACTGGTTCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACTGCAAATAAAAATCC	1
M00764_AAGAB_MIP110	CCTGAGTTAGATTTGTGTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATCCAATTTATCTGGG	1
M00764_AAGAB_MIP111	GCAGTTTCTTGGACATTGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTTTAAAAATATTTA	1
M00764_AAGAB_MIP112	GTTACTTACCATTCTTCATCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCCTTCAATCAGCG	1
M00764_AAGAB_MIP113	CCTCTTGTTCCTTGTAAGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCCTGATTAGATG	1
M00764_AAGAB_MIP114	CAAAAATGTGGCCAGGCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACCACACATTGGCATT	1
M00764_AAGAB_MIP115	CCATTCTTGAGCTTTTTGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTTCCCTGAATTAAAA	1
M00764_AAGAB_MIP116	GAACTTAGTCCAGAGGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAAGAATATTGCAGGA	1
M00764_AAGAB_MIP117	CCGATTTCTAGAGGGAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGCATGTACCAACTA	1
M00764_AAGAB_MIP118	GATAGTGTCTCCTCATGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTTTTCTATGAAGGC	1
M00764_AAGAB_MIP119	CACCACACATAGATTGATGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAGGCATGCAATAA	1
M00764_AAGAB_MIP12	CAAAAGATAGTCCTCCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTACAAAGTCTACAAA	1
M00764_AAGAB_MIP120	GTTACTGCAGAGATTGCAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTTGGAACAGAAGA	1
M00764_AAGAB_MIP121	GGTACTTTTGCTGTTTCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGGAAGTCACTTCCA	1
M00764_AAGAB_MIP122	GTATGGACTTGCTGAGGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGTTGACTTTACAGAC	1
M00764_AAGAB_MIP123	GACCTGTCATATAAACTGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACCCAGAATCTCTGT	1
M00764_AAGAB_MIP124	GGTTACACTCTAAATTCGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGCATAGACTTGCTG	1
M00764_AAGAB_MIP125	AGAAAAGGGGTGTGTCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGAAAGTAAACTTG	1
M00764_AAGAB_MIP126	GCTTTTAGAAGACCTTACAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGTCTTCCTCTTT	1
M00764_AAGAB_MIP127	AGCAGAGACCCCCCCACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAACTTAGAGGCTGATG	1
M00764_AAGAB_MIP128	GGCACTTCTCTGAATTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAGGGTTTTATAAAG	1
M00764_AAGAB_MIP129	GGTAGGAATTGTCCATCAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGGTGTTGACCTTTG	1
M00764_AAGAB_MIP13	CCTTTGTCTTGTTTGAGTGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGGGGTGGGTGGGGA	1
M00764_AAGAB_MIP15	CAGAGCTGTGTTGTTGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATATGTTGTATGTTAGA	1
M00764_AAGAB_MIP16	ATTCTTTCTAGCATGAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGGACTCCTTAAGGTT	1
M00764_AAGAB_MIP17	AAAAAGCCAGTGTGGATTTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCAGCTGCAGAATT	1
M00764_AAGAB_MIP18	GTGCAGTATCAAGTGTGAATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACATAGCTCACAT	1
M00764_AAGAB_MIP19	CCTGGGTGATTTGGGTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATAAATCTCAGAGGTC	1
M00764_AAGAB_MIP2	CCTAGAAGAGGCCAATATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACAACTTGTGGTAGCAT	1
M00764_AAGAB_MIP20	ACTCTCTTACAATATACTGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCTGGAGGTTGT	1
M00764_AAGAB_MIP21	CAGTGATAGTAATGAGTGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGCCAAAATTGCCCT	1
M00764_AAGAB_MIP22	GAAAGGCCTTCAATTTCATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGCAGCCAACATGAT	1
M00764_AAGAB_MIP23	CATACTAGGGTTTGACCAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGTAGCTGTTGCCT	1
M00764_AAGAB_MIP24	CCTTGAATACCATTTGACCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGAAGCATGCAACA	1
M00764_AAGAB_MIP25	CAGAGGACTGGAGGGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATAAATAACAAAGCTGT	1
M00764_AAGAB_MIP26	CCTGCCAATAGCATGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGATGATGTGTAAAGAC	1
M00764_AAGAB_MIP27	AACTTGTATGGTTGATGGTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTGGATGGTGAGT	1
M00764_AAGAB_MIP28	CTCACACTAAGACCCTTCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATCCTGAGTCTCAA	1
M00764_AAGAB_MIP29	GTTGCTGCAGTCAAACCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACCTATAAAAGGTCCAG	1
M00764_AAGAB_MIP3	AATCTACTAAAAGCCCATGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGAAGAGTCTGTCA	1
M00764_AAGAB_MIP31	GCGACGCTTCCTCATGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTACATGTAATGACTACATCA	1
M00764_AAGAB_MIP32	CATTGAAAGAAACAAGGCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTTTCAAAGACATGT	1
M00764_AAGAB_MIP33	GTTACATAAGGTGGAAACTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGCTGTCTTGAGAA	1
M00764_AAGAB_MIP34	GATCTGATTACCTTTCATTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGGAGTAGCTAAG	1
M00764_AAGAB_MIP35	GTTCCCATGTTGATGCTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCATGTTAGATCTGGA	1
M00764_AAGAB_MIP36	CACCAATGATCGAAGGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTGGCTAATTCTTGAAT	1
M00764_AAGAB_MIP37	CATCAAGGTTAGCATTTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTACCTCATGACGATG	1
M00764_AAGAB_MIP38	GTTTCCAACTCGGAAAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACTATTTTATCCTCACA	1
M00764_AAGAB_MIP39	CCTGCGTCTGAATCAACTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTTTATAGTGGTTGTC	1

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M00764_AAGAB_MIP4	CATACCCCCTAATAAAAAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATAGCTGAGGTCTTA	1
M00764_AAGAB_MIP42	CACAGGTCTCCTTCCTTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTACAAATCTTTTACTGTT	1
M00764_AAGAB_MIP43	ACATAGTGGGCCTGGAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTGGTGGAGAAATGTTA	1
M00764_AAGAB_MIP44	GCATCTTTGCAACAGCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTAGCACTTGCATATA	1
M00764_AAGAB_MIP45	GTGGAACCATGTAAGTTAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTCAAATCATGGCTT	1
M00764_AAGAB_MIP46	ACTAAGCTCCATGAAGATAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACAGAGGTTAATTTAT	1
M00764_AAGAB_MIP47	GGTTAAGGTCATAGTCATTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAACCAAGATGCGTTT	1
M00764_AAGAB_MIP48	GTAATTGAGCTGTTAATGTAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATATAGACAATTTGGT	1
M00764_AAGAB_MIP49	ATCACAAACTTTTATCTTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTTCTTTACCCAGC	1
M00764_AAGAB_MIP5	GTGAGGGAAGCCCTATATCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGACTAGAAAAAGCT	1
M00764_AAGAB_MIP50	GGCATGGGAAGAAAATGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGAAGAGTTTAAATGCA	1
M00764_AAGAB_MIP51	CGCCTGGTTTTCTTCCTACTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGACCTCCATGCCGC	1
M00764_AAGAB_MIP52	GGTGAGGAATGGAAACAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGATGAGGACTGGAAA	1
M00764_AAGAB_MIP54	CCCCTAGTGTTAACATCGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGGAAGATGTGGAA	1
M00764_AAGAB_MIP55	AACTCTGTGTACTATTTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAAAAACCGATGAAG	1
M00764_AAGAB_MIP56	CGACTTTAACACTTGTATGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTAACCATGCCATAG	1
M00764_AAGAB_MIP57	AAAGACTGAGGAACTGTCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAGGATGCAGTGAGA	1
M00764_AAGAB_MIP58	GAGTTTCTCCAGTGTAAAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTGCAGTTATGCATT	1
M00764_AAGAB_MIP59	CAGATGCCAGCCACTTTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATAGTTCTTGGTAGCA	1
M00764_AAGAB_MIP6	CAGAGCCAACTTCCCTAATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAAAATCAAATTCA	1
M00764_AAGAB_MIP60	GATGCTGTCCTTTCTTTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGATATACTACTTCTC	1
M00764_AAGAB_MIP61	CCTTCCAGAAGAATCCCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATTTGACCAGCAAAG	1
M00764_AAGAB_MIP62	CCCCATTCTTTTTTGAGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCATGGATACTTAGCT	1
M00764_AAGAB_MIP63	CTGGAACAATTTGACCAGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAAGAAAAAATACAGG	1
M00764_AAGAB_MIP64	GAAAGCAAGATCTGGCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTGAGAATTTTCTTAA	1
M00764_AAGAB_MIP65	CATTCTCCAATAAAAGGAACTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTGCGTGTTGGT	1
M00764_AAGAB_MIP66	GCACATGCCTGTAATCCCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAGCACTTTGGGAGGT	1
M00764_AAGAB_MIP67	GCACATGCCTGTAATCTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAGCACTTTGGGAGGT	1
M00764_AAGAB_MIP68	GTGCCACTGCACTCCACCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACTAAAAAACAACAC	1
M00764_AAGAB_MIP69	GCAATCTCGCTTCCTGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACTTAGCACTCAGATCT	1
M00764_AAGAB_MIP7	AAGATGGAAGGTTTTAGAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTGTTCTGAAAGACT	1
M00764_AAGAB_MIP70	CGCATATACACACACATCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAACAACACACACACA	1
M00764_AAGAB_MIP71	CCTAGTTCTGTCCACTGAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCCTTTGGTACTGGA	1
M00764_AAGAB_MIP73	GAGAGTTAGGTTTCTCACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATACTGAACTCTACT	1
M00764_AAGAB_MIP74	ACCCACTTCAGTGTGATTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTCCTATAAGAAACAA	1
M00764_AAGAB_MIP75	ACAGTAATTGGACTAGATACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTTAGCCTCTCAATT	1
M00764_AAGAB_MIP76	CACTTGAGTTTTCTACATGAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGAGACTCTGGCA	1
M00764_AAGAB_MIP78	ATTCCAGCTTCAGCTCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATTACTGCACATGAGC	1
M00764_AAGAB_MIP79	CAGTATGCTGTCCAAAAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGCCCTTCCATATGCT	1
M00764_AAGAB_MIP8	ATGCTCCAGTCACTGAGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGAAACACTGATGGGC	1
M00764_AAGAB_MIP80	GTTTCGCCACCTGGTTCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAAGGGGATATAAAATA	1
M00764_AAGAB_MIP81	GCTAGCTCTGTATCACGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGCTATCAGAAAAAGGA	1
M00764_AAGAB_MIP82	GAGAAGGGAAAAAAATTGGTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAACAGATGCCCAG	1
M00764_AAGAB_MIP83	GGAAAATACACATAAGCAACAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCAGCCAAAGGAG	1
M00764_AAGAB_MIP85	ATCTTGACACATTCACCATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCCTTCTCAACTCA	1
M00764_AAGAB_MIP86	ATGATGAAACAAAGGCTACTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACCCAATGCTATG	1
M00764_AAGAB_MIP87	GCTACAAACTCACTGTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCATGCAACTTAGGTAA	1
M00764_AAGAB_MIP88	ACGTGAGACCACATGATAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGAAAGCATTTAGAACA	1
M00764_AAGAB_MIP89	ACTCAGAGACATTCCCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGGGAATTGTCTAATAT	1
M00764_AAGAB_MIP9	GAAGAGGCTTTCCAGGGAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACACCCCTCCAGACA	1
M00764_AAGAB_MIP90	GGAAAAAGAGTCATCAAAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTTTGTCCACACTT	1
M00764_AAGAB_MIP91	GTCTCCCTAGGAGGTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGGAAAGGATATGTATT	1
M00764_AAGAB_MIP92	GCTTCTAGGACTGCTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCAGCATTATGACACAA	1
M00764_AAGAB_MIP93	AGAAATCCAAGAACTGTTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTAGTCTATTCATCC	1
M00764_AAGAB_MIP94	AGCCAGGCAATCAACGTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAGCCATTCCTGTAC	1
M00764_AAGAB_MIP95	GGTTGGTAGATGTGCCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCTAGTGATTCTCAACT	1
M00764_AAGAB_MIP96	ATATATAGACAACCATTCCAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATACCCCCCTGGGTC	1
M00764_AAGAB_MIP97	AGAGAAAGAAGACAGGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTTTAATTCAGAAGGC	1
M00764_AAGAB_MIP98	GCACCTGGCCAAAAGTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGCTAACTTTTGTATTT	1
M00764_AAGAB_MIP99	AAAATGCTGAATTTATTCCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTTGGCCTCCGAAA	1
M00764_ADAM22_MIP1	ATGATTTAGCTTAACTCTACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGCAGACAGACCACT	1
M00764_ADAM22_MIP101	CCTGTGGCTTCTTTCAACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCATTTTTTGCTCTCA	1
M00764_ADAM22_MIP102	AGACACCTGTGTTCTAAGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCTGTCTATTTCTGT	1
M00764_ADAM22_MIP103	CATTTTGCTTCCTAAAAAATGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCTGACCCTGACA	1
M00764_ADAM22_MIP104	GGGAGACCTGATGTTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTAAGCAGAAATATAAT	1
M00764_ADAM22_MIP105	ATTTCTCTGTTAAAATTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAACCTTTGTATTAGA	1
M00764_ADAM22_MIP107	GTTGACATTTACTCTAGCTTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTACTGGAGGGAGAA	1
M00764_ADAM22_MIP108	GGTACAGAAGCATGAAAAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCATCATCATTGTG	1
M00764_ADAM22_MIP109	GCTGCTCTCTGAAAACTTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTGGATAGGTTCTGA	1
M00764_ADAM22_MIP11	GCAAGAAGGGCACGGACACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCCTTTTCAATACGC	1
M00764_ADAM22_MIP110	GTTGCTGGCACCAATATCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTTGAAAAATACTCA	1
M00764_ADAM22_MIP111	AATCCTTTCAGAAACTTTATTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCCACGCAGTTAT	1
M00764_ADAM22_MIP112	CATTGGTTGAATATACTTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTGCTGGCCCTCAT	1

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M00764_ADAM22_MIP114	GACTCATATTAGCATTGTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTGATGTCCTTCC	1
M00764_ADAM22_MIP115	GGTGACTCTTTTTATAGCGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTCTTTTTCCTGAA	1
M00764_ADAM22_MIP116	CATAATCTCCCTGGGGTAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGATGGAACAGGTAGAA	1
M00764_ADAM22_MIP117	CCTTTGTTCTTTGATTACTCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTTCTGTCGCATT	1
M00764_ADAM22_MIP119	CGAAGTAACTCTTGGCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCATTTGGTTACATTTT	1
M00764_ADAM22_MIP12	ATATATGTGTGGAGGCGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATACCATTTCCCGGGAATC	1
M00764_ADAM22_MIP120	GGTCGCCCATTTTCACAGATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGAAGAGCTAAAG	1
M00764_ADAM22_MIP121	ACACTAGACACTTTGTGAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCCTGGTTGTAAAG	1
M00764_ADAM22_MIP122	GCTGCCGAATCCCATCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGCCCTATGTCTAATTA	1
M00764_ADAM22_MIP123	CCTCGGTCTAATTCAACTGAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCACTTGAAATGCC	1
M00764_ADAM22_MIP124	ATCTTTTGCCTCTGATTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGGAGACATGGTTTAC	1
M00764_ADAM22_MIP125	GCTTTTCTCTCTTACATAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTCCAAGGTCCT	1
M00764_ADAM22_MIP126	AAAGTTTTGACTGGAAAAACAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTGTCTGGGCGAG	1
M00764_ADAM22_MIP127	ATTCTGGGCTGCCACTTAATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCCCAAGCACCTGA	1
M00764_ADAM22_MIP128	GAGGTCTTCAGTTGTTGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTCTGACCATGAATTG	1
M00764_ADAM22_MIP129	ACTAAATTACTAAACCCAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGCAGTCATTCAC	1
M00764_ADAM22_MIP13	CCCCGCGCACTCGGGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATTCCTCTTCAGAAGGA	1
M00764_ADAM22_MIP130	GCAGCTGCAGTGTTCCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAAGTATGTTCCAGTT	1
M00764_ADAM22_MIP131	CCTTTTAATTGTTCTTAGGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACCCTATCTGCTCC	1
M00764_ADAM22_MIP132	ACAAAGTTCTCTTTCCAATATAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCAGGCCACCTC	1
M00764_ADAM22_MIP133	ACTTTGGGAAGCCACTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATTTTCAAAAAGCATCA	1
M00764_ADAM22_MIP134	AATTAGAAGCTCCCTTTCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGGGTGATTATGAGG	1
M00764_ADAM22_MIP135	GTGCTGTGTATTTTCAGATTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCCTTGTTGTAGCT	1
M00764_ADAM22_MIP137	ATACTGTAGTGTGACTGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGGTTCAAAAGAGAC	1
M00764_ADAM22_MIP138	GTATGTGCTGGGAGAGTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAGAACCAGACTTGC	1
M00764_ADAM22_MIP139	GCTTTCTCTTCATTTTATGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTGCCTTTTGACT	1
M00764_ADAM22_MIP14	GTCCTTCCCAGTTGGGTTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGGTCAAAGCCTGTTTT	1
M00764_ADAM22_MIP140	GCTTAAGATGGTGATAGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCATTATGAAACTGCT	1
M00764_ADAM22_MIP141	AAAAGTGTGTTCAGAACAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGGGTATTTTCTGCTG	1
M00764_ADAM22_MIP142	CGTACATGCTCAGTCATTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCTTCTTCATCAAC	1
M00764_ADAM22_MIP143	GTGCAGCTATGGGAGACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTAGACTTTGCAAGAG	1
M00764_ADAM22_MIP144	ACAGAAAAGAGCAAAATTGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTCTGAAGAGCAGAT	1
M00764_ADAM22_MIP145	ACTAACCATGAAAAGAACTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCATGGAATCACTGC	1
M00764_ADAM22_MIP146	ATGTGAAACTCCGCTTCCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTGTCATGCGGATTA	1
M00764_ADAM22_MIP147	GCACATCCTCACTGTAAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTGGTATGTTAATGG	1
M00764_ADAM22_MIP148	AGAACGTCAAGTTCTGAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAAAAATCCTATATGC	1
M00764_ADAM22_MIP15	AGAGCCTTGGACCAGCTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAAAAGGCGAAAATAA	1
M00764_ADAM22_MIP150	GCCTATGGGATATTGGCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACACTTGTGTGTAACAGC	1
M00764_ADAM22_MIP152	GAAGATCACTGGATGGATGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCAATAAAACTGCCT	1
M00764_ADAM22_MIP153	CCTGGAAATCATCTATCCCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTGTGCACAGTCTG	1
M00764_ADAM22_MIP154	GCAGAGTGGGCTCCTGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACGTTGTCTCATGTGTC	1
M00764_ADAM22_MIP155	GTCACCCTTATCTGTGAAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTGAGATTAAGCA	1
M00764_ADAM22_MIP156	AAGTTTTGCCAAGGAACAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTCAGAGTCAGTGC	1
M00764_ADAM22_MIP157	AGTTACACTAACAGCTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCCCAACAAGTCATTC	1
M00764_ADAM22_MIP158	CGCAGATGCTGCATCTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATTATAACAGCTATCA	1
M00764_ADAM22_MIP159	ATTTCCTCATTTGCTGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCTTTAAAACCAAAG	1
M00764_ADAM22_MIP16	GAAGAGGAAGGAAAACCGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCGTAGGGGAGACG	1
M00764_ADAM22_MIP160	CAGAGCAGACCATGTGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGATGATATGGATTTTGT	1
M00764_ADAM22_MIP161	AAGGCAGCATTTTATACTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACAGGTTTTCAGAT	1
M00764_ADAM22_MIP162	ACTCGGCCCTTCAGTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCATGAAAAATGCTGTT	1
M00764_ADAM22_MIP163	GTTGCCACATAGCTCAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGGAAAGCAATTTAATG	1
M00764_ADAM22_MIP164	GCCCAACACTCACCCAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTTTTGTACACTCAGTA	1
M00764_ADAM22_MIP165	AGGTACACAAACTCTAATTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAACGTGCACTGAAT	1
M00764_ADAM22_MIP167	GTAATAACCTTCCTGTGGAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTCTGTGTGTCTTTC	1
M00764_ADAM22_MIP168	AACCATGTCTCCCAAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGAATAGAACATTAAA	1
M00764_ADAM22_MIP17	GCTCCATCAATGAGGCGTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGTCGCCCCGCACC	1
M00764_ADAM22_MIP170	AATCCCACAAATGGCTCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTAATGCTACCTACCT	1
M00764_ADAM22_MIP171	CACAGTTTATATCATGCAACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTTCTAGAGGCATT	1
M00764_ADAM22_MIP172	CGGCCTCAAAGTTTCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAACTGGAAGAGGGGA	1
M00764_ADAM22_MIP173	GTAAACCCTGATTTAAAGGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGTTATTTGGCCTT	1
M00764_ADAM22_MIP174	CAATGACTATGGATAAATGGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGTGGCTGGAGG	1
M00764_ADAM22_MIP175	GCAACATGGTGAGGGCTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGGCCACATGAACTG	1
M00764_ADAM22_MIP176	CCACAGATTGCATGTGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACATTTTTTAAAGGAAC	1
M00764_ADAM22_MIP177	GTTTCTCTCTCTTTTCCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTCGATTAGGAATAA	1
M00764_ADAM22_MIP178	GGTATCACTTAATAAAGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTTCTGACAACTTC	1
M00764_ADAM22_MIP180	ATAGTCCTTCTCTGAAAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAATCCCAAAAAAGGTA	1
M00764_ADAM22_MIP183	CAGGAGCGAGGAGGGACAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAATAATAAATTCTTA	1
M00764_ADAM22_MIP184	ACTTGGCTCTCCCCTTCCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTTACCAACTGGTAG	1
M00764_ADAM22_MIP185	GCACCTAATTATATTTTTCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCTGCTGCCACT	1
M00764_ADAM22_MIP186	ATATGATGCTGCAAATGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGTAGAGCAAGAATGA	1
M00764_ADAM22_MIP187	CCTCCTGAGATGTTTTTGAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTTTCCACTCCGTT	1
M00764_ADAM22_MIP188	CACGGAAGTGTTTACTTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTATCAAAGTCCTTAG	1

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ID	**MIP**	***c***
M00764_ADAM22_MIP189	GTAGCCCCGCTGTTAAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCCTGGCATGGAAG	1
M00764_ADAM22_MIP190	GCCGCTCAGCCAATTTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGAAAAGCTCCTCTT	1
M00764_ADAM22_MIP191	GTGTTTCTACTGACATTTTATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGAATTGTTGGC	1
M00764_ADAM22_MIP192	CCTGTTTTCTAAAGTCCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATATAAAGGACAAAAG	1
M00764_ADAM22_MIP193	GGAGATGAGTCCTAAAAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAAACCAAAAACCTAA	1
M00764_ADAM22_MIP194	GTGACTTCCTAAGTTGCATAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGGAATCTTCCTGT	1
M00764_ADAM22_MIP195	GCTTGGCAGATTGACTGAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTCCTGGCATAGACA	1
M00764_ADAM22_MIP196	CAGAAGTCTGTCTTAGGCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAAGCTTCCCCATAT	1
M00764_ADAM22_MIP197	GTGTTTTTGGTTTTGTTTTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATCCCTGTTGCAC	1
M00764_ADAM22_MIP198	GCCTGGTTTTGATTTCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACAAGAAAGGAAAATAC	1
M00764_ADAM22_MIP199	CCTTAGGGCTTAGCCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAATGAGACGAATTCTTA	1
M00764_ADAM22_MIP2	CAACCGCTGGGTACATAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGGACTGAATTAATGG	1
M00764_ADAM22_MIP20	GGTCTTCTGGGATTCTGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAACTCCTTGCCCTT	1
M00764_ADAM22_MIP200	GAATGCAGATCAGAATATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGTGTTACTTGTTCAA	1
M00764_ADAM22_MIP201	GCCTGACTAGAAACCCCACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATGCAAATAGCCCCA	1
M00764_ADAM22_MIP202	GCAGGAACTTTTGTATTATTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAACAAAGGTGTTGA	1
M00764_ADAM22_MIP203	GGAAGACTTGCCCCTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTAAAGGGCAAAAATGA	1
M00764_ADAM22_MIP205	GTTAATAGCAGCATGGTTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGTTTTACCTAAAC	1
M00764_ADAM22_MIP206	GGCTTCCACTATCTATAGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAGCTTAACGAACCT	1
M00764_ADAM22_MIP207	ACTGCTTTCCTGAGCAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTAATCATGTGTATAT	1
M00764_ADAM22_MIP208	GCCATATACATTTCCATTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAGAAATTTGAACC	1
M00764_ADAM22_MIP209	GATTTATGTTATTTTGATGCACGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCACTGTAACTTA	1
M00764_ADAM22_MIP22	CCACTTGTAAAGTTTTTTCTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATGTTGACCAAGCA	1
M00764_ADAM22_MIP25	GCCGAATTCTACCAGAGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACATACACTCTCCCAAT	1
M00764_ADAM22_MIP3	CAACCGGAAGGACACGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGAGCTGTTCTGTTTAC	1
M00764_ADAM22_MIP30	ATCCATGTCCCTACAAAGGACATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTAAAGGTCCCCT	1
M00764_ADAM22_MIP31	AAGATTCATCATTGATGCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGAAAAAGCCTTAGT	1
M00764_ADAM22_MIP32	GCATTTGAGAAACATGCTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACTGTTACCAAGTAA	1
M00764_ADAM22_MIP33	ACTTTGGAAGAGAAATGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTACTGTCTAGGTGACT	1
M00764_ADAM22_MIP34	ATCTATTTATAGAAGTTGTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACTTCAGTAGCTTC	1
M00764_ADAM22_MIP35	AACATCATTTCTAAAGCCATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTTGGAAAGCAGCC	1
M00764_ADAM22_MIP36	GCCATGGTAATTGGAATTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTCCTTGGCTCTGT	1
M00764_ADAM22_MIP37	GCAGGAGACCTCCAATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACTGTTAAAGAATCTA	1
M00764_ADAM22_MIP38	CATTGTCAACATGCCACGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTCCTGTGAAATGAA	1
M00764_ADAM22_MIP39	AATGAGTCAGGGTTTCCTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTGACACAAAATAGG	1
M00764_ADAM22_MIP4	ATCTCTTTCTTTTGCCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCGGATAACTTAAGTA	1
M00764_ADAM22_MIP40	GGGATGTTCTATGACGGGAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGATGGGACTGGG	1
M00764_ADAM22_MIP41	AAAAAATAATTAGGCATGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTCTCAGCATAAACA	1
M00764_ADAM22_MIP42	CCTGGGTTTAGAGAGGTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGAAAATGGAAATCC	1
M00764_ADAM22_MIP43	CATCTGGTATGATGTTCATATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCCTAAGGCTGGA	1
M00764_ADAM22_MIP44	CAAACAGTCTGGATTTGTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGTGGGCTAATGAT	1
M00764_ADAM22_MIP45	ATCACACAAACCATTAAGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAAATTCTAAAAGG	1
M00764_ADAM22_MIP47	GCCGTTTACTCCTTTTTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGTTTATCACACCCTGA	1
M00764_ADAM22_MIP48	CCTGTGTTACAGCTTCGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCAAATTGATGAAAAAT	1
M00764_ADAM22_MIP49	AAGGAAACAGCACCTAATTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTAGGCACAAACAGG	1
M00764_ADAM22_MIP5	CCAGTATTCATCTGCATCGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACCTCGTGACTGTG	1
M00764_ADAM22_MIP50	ATCATCTCATCAGAGAAAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTTACTAAATCTGCC	1
M00764_ADAM22_MIP51	CACTTCAGCCAAGGTGTCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAATCTGTGGTGAACA	1
M00764_ADAM22_MIP53	CGTAACTTCTGTAATGATGTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGAAACCTGGGCGA	1
M00764_ADAM22_MIP54	AAAAAGGTGAACTGCATCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATCTATCTGCCATCTG	1
M00764_ADAM22_MIP58	CCAGAAATACTAAGCTCTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTCTTCAACAGCTC	1
M00764_ADAM22_MIP60	GCAACTTTTCTCTAAATTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAACTGAAGGATGGA	1
M00764_ADAM22_MIP61	GACACTTACTGGGGATTTATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCACATTTTCCCCAT	1
M00764_ADAM22_MIP62	CAACTTACTTTCAAGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTTACATAAAAGTATTA	1
M00764_ADAM22_MIP63	CATTTAATCATCATGTCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAAAATTTAACACAA	1
M00764_ADAM22_MIP64	ATCCTGGATTGGATTTGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAACAGTCAATAAAAT	1
M00764_ADAM22_MIP65	CAGAGAAGTGATTTTGTGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATTTCCTCAGCTTTC	1
M00764_ADAM22_MIP66	GCCAAAAATACATATCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAAGGTTTATGAGGGA	1
M00764_ADAM22_MIP67	GTAAACTAATAATGAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATTAATCTTGCAAGAAA	1
M00764_ADAM22_MIP68	GCAAGGGAAGAATGTGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTCCCCTTTTAGAAAA	1
M00764_ADAM22_MIP69	AGTAGGTGTGAACATCTGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGAACTGTGAACAGT	1
M00764_ADAM22_MIP70	CATTCACGCCTCCTCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCATACTGATTTGTAATA	1
M00764_ADAM22_MIP71	GAAGAGGCTGAACACACTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGTTTTCCCAAACTG	1
M00764_ADAM22_MIP73	AACTTACCACTTGCTAACTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCGCTGGATGTTTAT	1
M00764_ADAM22_MIP74	CCACTTTATTCCTTAAAATGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCCATTATGCACC	1
M00764_ADAM22_MIP75	CATGGAATCTAGCACTTATAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGACACGTGGTCC	1
M00764_ADAM22_MIP77	CCACTATTCAGGAAGTCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTCTCTAAGATTCAA	1
M00764_ADAM22_MIP78	GTGCCATACCCAAATATCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATCACACTCCTCTC	1
M00764_ADAM22_MIP79	GTGCCATACCCAAATATACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATCACACTCCTCTC	1
M00764_ADAM22_MIP8	GAAGCACAATGCAGCACTGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCGAGCTCTTGTCG	1
M00764_ADAM22_MIP80	GATGTATGGAGCAAATGTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTGAGTGTGGCAAT	1
M00764_ADAM22_MIP81	GTCTTTGCTGTAAAAAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTACTTTCAGGAAAGT	1
M00764_ADAM22_MIP82	CAACACTCTGCTCCTTCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCCTTAATGATTTAA	1

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ID	MIP	*c*
M00764_ADAM22_MIP84	ATAACTGCTCTAAAACTTATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACAGTTTCACACGT	1
M00764_ADAM22_MIP85	GGCTTGAATTTCCTGAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAATGGAGAAATGATG	1
M00764_ADAM22_MIP86	GTGCAAAATATAAGGCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCTGGTACATGTGAAA	1
M00764_ADAM22_MIP87	GTAGAGAGGCCTTTTATCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGTTTTGCATCTTCC	1
M00764_ADAM22_MIP89	AATTCCAAAAATGTTACCAACGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGATGCTGTCACCT	1
M00764_ADAM22_MIP90	GTGGAGACGTCAGCCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAATTTTTTTCTGCCTTA	1
M00764_ADAM22_MIP91	GTTGCACTGTATCCATGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATGAGGTTAAGGAGGC	1
M00764_ADAM22_MIP92	AATAATCTTCTCTCATTTTAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGTTCTCCAAGCC	1
M00764_ADAM22_MIP93	CATTCTGTAAGAATCTGAGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTTTGTGGTTACCT	1
M00764_ADAM22_MIP94	GCAGTTTAATGTTCTTCCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTCTCTATAGACTAGA	1
M00764_ADAM22_MIP95	GACATGGCCCCATATGAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGCTGGATGATGAAA	1
M00764_ADAM22_MIP96	ATGCTACTATAAAAGTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAATGACTAAACTATTG	1
M00764_ADAM22_MIP97	GCTTGGTAGCCCAGGTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGTTTGCTATATTGAAT	1
M00764_ADAM22_MIP98	GTTGGCTGACCCAAAAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATTGATAAAGTTTAGG	1
M00764_ADAM22_MIP99	AGGAAGCAATATTGCCTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAGTAATTACATTCAAA	1
M00764_ALLC_MIP1	CAAAGGCCCCACTGTCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCCAGAAAAAGTAAAT	1
M00764_ALLC_MIP10	GTCTAGATTTTATTTGCAACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGATTCTGTCGCTTC	1
M00764_ALLC_MIP11	ACCATAAATCTGATACCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTACATCAACCCTTT	1
M00764_ALLC_MIP12	ACTGGCAAATTAGCATATTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGCAGAAAACCTCA	1
M00764_ALLC_MIP13	GGATTCCAGGTAATAACAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAGATCACATGAATG	1
M00764_ALLC_MIP14	CCATCCATTTCCCAAACTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAAAGCTGACCCAAAAC	1
M00764_ALLC_MIP15	GTGGACGTTTCTTACTTCACGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCACTGCCTCGCAT	1
M00764_ALLC_MIP16	ATCCCCAGCCTGAGGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTATAATTCTCATTTTGGGGAC	1
M00764_ALLC_MIP17	GCTTGACTAAGGCTACTTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCAAACTTGGAAGAA	1
M00764_ALLC_MIP18	ACTCCTGAGGAGTTTGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCATACAAACCACCAAG	1
M00764_ALLC_MIP19	GGGATTTCTGGTAGTTTATCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAGCAGTTTCCC	1
M00764_ALLC_MIP2	GCTCAGTGTTTTCTGAGTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGTGGGCTTCTTTA	1
M00764_ALLC_MIP20	CGGCCACAACTATTTTCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAATAGGATGACAGAAT	1
M00764_ALLC_MIP21	CCTGGCTTAAGCTCAGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATAAAATAAAGAAGCCA	1
M00764_ALLC_MIP22	GTAATTTCTCCTTTTTATGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGGTAATCGTGACA	1
M00764_ALLC_MIP24	AGAAACTATTTTAGACCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACATGAAATCTGCATG	1
M00764_ALLC_MIP25	ATGTTACAGGGACACACTGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGAGAGATGGGCAA	1
M00764_ALLC_MIP26	CAGGTTTCCCCAGCTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTACAGAGTTAATATCCA	1
M00764_ALLC_MIP27	GAACTAGAATGGCAGTGATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGTGACTAAAAGCAA	1
M00764_ALLC_MIP28	GTCTGTTGAAAGTGAAGTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTGGCATAAAACCCT	1
M00764_ALLC_MIP29	ATCACTCATTTTCACTAAATTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCATAACCCGGCT	1
M00764_ALLC_MIP3	GTCCTGACCTACTAGAGAAGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGCCTGGGCCTGA	1
M00764_ALLC_MIP30	GGTAAAACAATGGAAGTCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGCTAGAAGGTGGAA	1
M00764_ALLC_MIP31	ATTTTGGTAGCTATTTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCATGTTTTAGTACAA	1
M00764_ALLC_MIP32	AACTCACAGCATCTGATTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTACAACACCACCCTG	1
M00764_ALLC_MIP33	CCCGAATGCTGTTTGACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTATTCTGAATCACATT	1
M00764_ALLC_MIP34	CCATACAGATAATGTTTCGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTGTTGTTCACTTC	1
M00764_ALLC_MIP35	AGCTCTGGAGTAAATAACAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACGATACAAGAGTGG	1
M00764_ALLC_MIP36	CACAGCCTGAAATTATCTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGGCCTCAGAAAA	1
M00764_ALLC_MIP37	GCTTGTTGTATTTGAGAAACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGCATGAGAGGGAA	1
M00764_ALLC_MIP38	CCTTTGCACTTGATATTACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGTAAAAATGGCTGC	1
M00764_ALLC_MIP39	AAGAACCTGCAGACCTAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTAGTGTATGATACACA	1
M00764_ALLC_MIP4	CGAGGGTCTTGCAGAGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAGTCAGGTTACTGGCC	1
M00764_ALLC_MIP40	GGGGTCAGTTGCAGTCCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTTCCTAAATAAGCCA	1
M00764_ALLC_MIP41	GCAGTGGATGAGATTAATCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCACCCAAACAATATA	1
M00764_ALLC_MIP43	GTGGCCGGTCCAGCCTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAGCATTTAGAACAATGC	1
M00764_ALLC_MIP44	GGAGTAATAACTCGAATTGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGACTGGTTTCTTG	1
M00764_ALLC_MIP45	CACAACCCGGAACCAAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGTCTTTAGAATAAAC	1
M00764_ALLC_MIP46	AGCCGTAAAGTGGATGGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGCAGGGACTTGTTTT	1
M00764_ALLC_MIP47	AGCTGTAAAGTGGATGGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGCAGGGACTTGTTTT	1
M00764_ALLC_MIP48	GCGTGATTTTCTGCCCGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGTGGTTTCCACTTG	1
M00764_ALLC_MIP49	GCTCCAAAGTTTCTGCTCAGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGATTCTCCCGGCC	1
M00764_ALLC_MIP5	ACAAGGCCCGAAGCCAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGTAGAGACAGAACTT	1
M00764_ALLC_MIP50	GCTTGCTTTTCAGTTGTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGCCCAATTATCATCA	1
M00764_ALLC_MIP51	CAGAGGTCCTAGTCTGTTAACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGGCGGCTCACTC	1
M00764_ALLC_MIP52	CAAACCCTTAACACACACAAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACGCCAGGCTCACC	1
M00764_ALLC_MIP53	GAAGCTCACCGAGAACTTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCAATTTGTGAGACG	1
M00764_ALLC_MIP54	GGTGGTCTCTACGGAACTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCATAGTCTTCTTTTCA	1
M00764_ALLC_MIP6	ATTTCTGACTGCTGGGTGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACAGCCAATCTCTG	1
M00764_ALLC_MIP7	CCCCAGAAGCCAGCCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGACTGAAATTCATCTCT	1
M00764_ALLC_MIP8	GACTTTCAAAAGTCAGGCAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCGGGTCAGTCTTC	1
M00764_ALLC_MIP9	ACAAGGGTTGAAGGCATCCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCCTTCCAGGAAGCA	1
M00764_ARFRP1_MIP1	GGGGTGCCAAGGATGTAGAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTGTCCCCGGCT	1
M00764_ARFRP1_MIP13	GCTGGGAGTGGCTGTTTTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGTGATGCAGCCTCG	1
M00764_ARFRP1_MIP38	GCTGCTCTGGGAGGGATGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTGAGCCCCAACTCC	1
M00764_ARFRP1_MIP41	ACGGCCAACCTGGGCAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCTGCCGGCAACCTTTG	1
M00764_ARFRP1_MIP45	AGCTCAGACCTCTGCAGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGGGAGTGCACCTGT	1
M00764_ARFRP1_MIP46	AGTGACTCTGGCCCTGTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAGGTGCACTCATCTG	1

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ID	MIP	*c*
M00764_ARFRP1_MIP47	ACAGCTCACATTTGCCACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCCTGGGCAAGACAG	1
M00764_ARFRP1_MIP48	ACGCGGAGTTTGCTGTGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGACCACCAGCTTGT	1
M00764_ARFRP1_MIP49	CAGACAACCCCATCCCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAACTGGATGCTGACCA	1
M00764_ARFRP1_MIP5	GGGAGTGGGAGGAATTCATAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGCTCTGGGTGCAT	1
M00764_ARFRP1_MIP50	GCTCAGACACCCTAAGGATTTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGGCCTGGCCTTG	1
M00764_ARFRP1_MIP53	AAGGTTCATGTGCAACCGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACACAAGGGAGCAGG	1
M00764_ARFRP1_MIP56	ACCCCACAATGACCACTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGGGGAGCTCCCATT	1
M00764_ARFRP1_MIP57	CATGCCACACATGTGGACACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCAGTCAGAGGGACT	1
M00764_ARFRP1_MIP58	GGTTCTTTGCTGTAACACTAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTATCCTGCATCCT	1
M00764_ARFRP1_MIP59	GAGCTCAGCAGGGTCAGGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCCCCTTTCTGTGGTG	1
M00764_ARFRP1_MIP61	GTCTGGAGAAGGGCTCAGACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCTGCCTCATGGG	1
M00764_ARFRP1_MIP63	GGAAGTGTGGGTCCACATAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAAGGAAGGGCTGTG	1
M00764_ARFRP1_MIP64	GTTGGAGAGGGGTTCCTCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTCCCACAGAAACCA	1
M00764_ARFRP1_MIP65	CAGGCCATGGTGTGAAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTTGCTTCATGTTGGAG	1
M00764_ARFRP1_MIP67	CGACCTGTCTCAGCATCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCCAGTTCTCCTCCAG	1
M00764_ARFRP1_MIP68	GGTACAGGATGCACACTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGAAGTCAGACAGGAC	1
M00764_ARFRP1_MIP69	GCTAGAAGTCACAGCAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATCTGTGTCACTCCCC	1
M00764_ARFRP1_MIP70	CATGGCCAAGTGATCTCTGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTGATGCCATCT	1
M00764_ARFRP1_MIP71	AGTGCTGGACTCAGTGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGAGATCAGGACCTGG	1
M00764_ARFRP1_MIP72	GGCAGAGCCTGTGGCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTCTCCTATTTTGACA	1
M00764_ARFRP1_MIP73	CATCCTGCCGTCCCCACATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCAGAAATGCCCAAAA	1
M00764_ARFRP1_MIP74	CCTCTCCCCTGATGAGGTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGTGGGGACCTGGG	1
M00764_ARFRP1_MIP75	AACATTCCCAGACACTTGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAGGAGTGCAGGGT	1
M00764_ARFRP1_MIP78	AGGCGATCAGATCAGAGCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTGTTTTGTCCCAG	1
M00764_ARFRP1_MIP79	AAAGAAGTGGCACTGGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTCAGCTAAGGGTTCA	1
M00764_ARFRP1_MIP80	GTCCCTCGGGTTTTCTCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGCTGCAGTCTTTG	1
M00764_ARFRP1_MIP81	GGTCCTCGACACACCCAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTCTTACCTTGTCCC	1
M00764_ARFRP1_MIP83	CCCCTTGTAGTTCTTGTTAAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGCTGTGGCCAC	1
M00764_ARFRP1_MIP84	GAGTCTATCCAAAATCACCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAACAGACCTGAGTA	1
M00764_ARFRP1_MIP85	GGCTTCCGTCTGGGTAGTGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGGGCTATACTGGC	1
M00764_ARFRP1_MIP87	GTGCAGCCAGAAAGCACCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCACCGTCTTCCCAG	1
M00764_ARFRP1_MIP9	AGAGTCCAGGCACTCCCTTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGAGTGTGGCTCTGT	1
M00764_ASTN2_MIP1	GCTTCTGGACATGCAGTGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACACAAGAGTGCTGAT	1
M00764_ASTN2_MIP10	CCTGCCATGGACCCCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTCTATCAAAAGTCTCT	1
M00764_ASTN2_MIP100	GCCCTAGACCTTGCTCCTATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCCTTCACACCTCA	1
M00764_ASTN2_MIP101	GCAGAAATCTGGGGTGAGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAGAAGGGAGCTGG	1
M00764_ASTN2_MIP103	AGAGGATTGAATCGTGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAAATAGGGATTAAAC	1
M00764_ASTN2_MIP104	CAGGTGAGCTCTGAGCCATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGTCTCCCCAGACCC	1
M00764_ASTN2_MIP105	CATCCACTTTCCCAGCAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCAGGCTTCACTAATG	1
M00764_ASTN2_MIP106	GTATTTTGTGCCTTACCCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCTCTCCTTGGTCA	1
M00764_ASTN2_MIP107	CACTGCTGCACCATGGGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACATGCTAGGTCCTT	1
M00764_ASTN2_MIP108	CGGGTCCGGAGCAACCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCAAGAGCTGCAGGGTG	1
M00764_ASTN2_MIP109	GTCTTACCAGTGAGCAGTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCCATACCCTTCCT	1
M00764_ASTN2_MIP11	GTTTGCTTTGGCCTTGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATAAGAAAAGGTTTAAAA	1
M00764_ASTN2_MIP110	CATGTGCCAGACCCTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAACAACTTCATCAAGGA	1
M00764_ASTN2_MIP111	GGACTACAGGGCAAGGAGGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGCTCCTCCACCGG	1
M00764_ASTN2_MIP112	AACAACCTGGGCACAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATACCCTCTTTGGAGAG	1
M00764_ASTN2_MIP113	CCTCCACGCAACTGTATGATACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTGTAACCATGTAGC	1
M00764_ASTN2_MIP114	GTACAAACTGGCTCCTGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTCTCCTTCCTAAACT	1
M00764_ASTN2_MIP115	AGGCTGAACCTTGACCTTCAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTACGATGCCAC	1
M00764_ASTN2_MIP116	CATCCTTCATGGGTTTCAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATGAAGATGGTGCTC	1
M00764_ASTN2_MIP117	CATTGACTGCTCTGATGGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGAGAGGGTGTGAT	1
M00764_ASTN2_MIP118	GGCGGCCAGGCGGAGAAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCCAGATGTGATGGTG	1
M00764_ASTN2_MIP12	CCTGTGGATAGTGGACAGAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACAGAGACTCTCCA	1
M00764_ASTN2_MIP120	GAAAATACGAAAACCAGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTGAGCACTGAATGA	1
M00764_ASTN2_MIP122	GGAGACTGACTCTAATTTTATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCGGCAAGCTGAG	1
M00764_ASTN2_MIP123	GACCTCCAGTGATCCTCCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGGCTCGGCATGAGAGGG	1
M00764_ASTN2_MIP124	AGCATAAGACTCCATATCTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTTATTTTCACCTC	1
M00764_ASTN2_MIP125	ATGAAGTCTGACTGAGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGAATTACAGGTATGA	1
M00764_ASTN2_MIP126	GCGAGGGAACGCTGGTAAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCACTCGCAACTTCA	1
M00764_ASTN2_MIP127	CAAAGTATGTGGACAGCATCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTTACCACACATCCC	1
M00764_ASTN2_MIP128	ACCATCAATGACCTGCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTAAGTTATGGTTTCAA	1
M00764_ASTN2_MIP129	GGTTGATGGACAGCTCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGTGGTTCTCCAACAG	1
M00764_ASTN2_MIP13	GTCCTTGAGGATGCTATACCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTGCTCCCCCTCC	1
M00764_ASTN2_MIP130	GATGTGCTCGTCACGGAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCCAATGGAAACTCTT	1
M00764_ASTN2_MIP131	CAGCATTATTTAAGGAACAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAAGTAGACCTGC	1
M00764_ASTN2_MIP132	GGAGAGGGGAGAGAAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCATTTCCCAGAATTA	1
M00764_ASTN2_MIP133	CCATAGACCTTGGCCCTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATATAAGTAGTCTTGCCC	1
M00764_ASTN2_MIP134	ACTCACCCTTCACTCTGTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGGTTTTGCAGGAAC	1
M00764_ASTN2_MIP135	CCAGGACAGTGCAGGACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTTTTTCTTTTCACTT	1
M00764_ASTN2_MIP136	CATGGAAAGAGGGTAATCTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCTGCACTCTCCTG	1
M00764_ASTN2_MIP137	CATCTGTCGTCCTTTGTCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCAGAATCCATGG	1
M00764_ASTN2_MIP138	GACCCAGAAACCGGTGAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCTACCTGGACATCTC	1

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ID	**MIP**	***c***
M00764_ASTN2_MIP139	ATTTTAAGGTCTTAGCTGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCATTGATCTGGTAA	1
M00764_ASTN2_MIP14	CCAAAATCACGTGTGAGGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGCCACTGCTCCAGC	1
M00764_ASTN2_MIP140	GCATCTAAAGACCTTGGAAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAAGAGCCGAGCAT	1
M00764_ASTN2_MIP141	ACTCACAGCAATCAGTGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGGTGTGGAGCATCT	1
M00764_ASTN2_MIP142	CCTGCATCCTGGCCATGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATTCCCAAACTTGATGC	1
M00764_ASTN2_MIP143	AGATTTTGTGTTCACTAGCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAGGCAGACGATGA	1
M00764_ASTN2_MIP144	ATTCCTCAACCATCCCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAGAATGTCAGCTGAG	1
M00764_ASTN2_MIP145	CAGCTGACCGATCTCGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATCTCCCTAGCATCTTT	1
M00764_ASTN2_MIP146	GGCAGGGAAGAGGAAGCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTACCTTATAGCAGCAG	1
M00764_ASTN2_MIP147	CAGCCCCTAGAGCACTAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGGGACTCCACTGTCT	1
M00764_ASTN2_MIP148	CCCCTGGATGTCCCAGACTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAAAACACTGCCTG	1
M00764_ASTN2_MIP149	AGAGAAGGTGGACTTTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCCATCCTGGATGACT	1
M00764_ASTN2_MIP15	ATTAAAGAAGTCCAGATCAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGGCACTGTTTCCA	1
M00764_ASTN2_MIP150	CAGCACAGATGGGATGTAGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGGCTCCTCATCCT	1
M00764_ASTN2_MIP151	ATCCCGGCTGCAAACCCACAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGCCCAGCGACGTT	1
M00764_ASTN2_MIP152	CCACTGTTCTTTGGAATCGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCTGGGGGATGCG	1
M00764_ASTN2_MIP153	CATTTGTGTGTCCTTCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATGTCTCTCTAGCTT	1
M00764_ASTN2_MIP154	ACTTCTTCACTTCTCTGAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTACACTCTGCCAGGA	1
M00764_ASTN2_MIP155	GCCTAGGGTCACATAGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATTGCTCTGACATGAC	1
M00764_ASTN2_MIP156	CATCCCAAGGACAGTTGCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATAGGAAGCAAATCAGA	1
M00764_ASTN2_MIP157	GGGAGATGGAGTCTAGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATCTTATATTTGCAGC	1
M00764_ASTN2_MIP158	ACTGGGACAAAGTAGGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTAGGCTGTCTTACATC	1
M00764_ASTN2_MIP16	ATGGCTGTCTCATCCTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTTGAATCAGTGTTTG	1
M00764_ASTN2_MIP160	GCAGATGCACATCCTCCACATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTGCACTGGAGAC	1
M00764_ASTN2_MIP161	CAGGGAGGAAAAGAGCCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTACAAGGTGCCATTC	1
M00764_ASTN2_MIP17	ACTTCTAGGATATGGGAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTATCTACTCCAGATT	1
M00764_ASTN2_MIP18	ATACTAGGTTAAAGGCTCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGCATATGGTGTCAA	1
M00764_ASTN2_MIP19	AGCTCAAGCAAGGCTCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAGAACAACCAAAAGTT	1
M00764_ASTN2_MIP2	AGCCACCAATTCATGAGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTAACTTACAGTGGG	1
M00764_ASTN2_MIP20	CACCCATTAAAAGGGGGTAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACACAGACAGTTAGA	1
M00764_ASTN2_MIP21	CCTTTGTGATTCCCTTTCATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCACTGGAGTTGGGA	1
M00764_ASTN2_MIP22	CCAGACTGAGAGAAAAGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGAGGATAAGACCATC	1
M00764_ASTN2_MIP23	CTACTCTTATAAGGGATTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCAGAACTTTTCTGTG	1
M00764_ASTN2_MIP24	CCAACACCTGTAAGTACAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAAGAGTTTGACGTG	1
M00764_ASTN2_MIP25	CATCACTCTCATTGTCATCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCACCTCATAAAGT	1
M00764_ASTN2_MIP26	GCAAGCATCAGGTGCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCCAAGGCTTAAACTAG	1
M00764_ASTN2_MIP27	CACTGGGTTGAGGAACACTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCATTAGGTGTATTTTGT	1
M00764_ASTN2_MIP28	GTTAATATTTCTGTCTGCCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTGTGGCGTCCTC	1
M00764_ASTN2_MIP29	CGGAGAGAACATAAACTACTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGTCATCAGTTTGGA	1
M00764_ASTN2_MIP3	CAGTTATCCTGCTGTTGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGACTCTTGGGCAGTAC	1
M00764_ASTN2_MIP31	CAAAATGAAGTTGGAAAAGACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGCTTGGCAGGGA	1
M00764_ASTN2_MIP32	ATGTGCAGGTTAGTTACATGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCAACCCTGGGCTC	1
M00764_ASTN2_MIP33	ATATCCTCCAGGAGACTAGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGGGCCAGAAAG	1
M00764_ASTN2_MIP34	GAGATTGCTCCAACATCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCAGTAATGGTTTGT	1
M00764_ASTN2_MIP35	GTCAGAAGTGGAGCTGTGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGGTTAGCGGGTTAT	1
M00764_ASTN2_MIP36	GTCTTTACAGCCTCCTGGAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGCTGTGTGAGTCAT	1
M00764_ASTN2_MIP38	CTATTTCTGAGAGGGCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATAGTGAGAGTTGTAG	1
M00764_ASTN2_MIP39	GACAAGATCTACAATCTGTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCAGAGCTTATGC	1
M00764_ASTN2_MIP4	GGCCAGTCTAGAGAGGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGGAGATCTATGTGTCA	1
M00764_ASTN2_MIP43	GTATGTAAAATCACAGGTACAATACTTCAGCTTCCCGATATCCGACGGTAGTGTATTATCTTTGAAAGGT	1
M00764_ASTN2_MIP45	AGAAGAAATTGAAGGCACTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAAGGCAGAAGGTAG	1
M00764_ASTN2_MIP46	GCATACAGAGTGAACCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAATATGGGAGTTACTT	1
M00764_ASTN2_MIP47	ACGAGGGAGGCACTCAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTTTCCTGTAGCCTCA	1
M00764_ASTN2_MIP48	GTGCAGGCCAGCCAAATGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTATCTACTCAGTCAT	1
M00764_ASTN2_MIP49	GGAGGGAGAAAAAGAAAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTCCAGACACTTGAA	1
M00764_ASTN2_MIP5	AGGAGCAAGACTAGACCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTCATCATCTGATATAA	1
M00764_ASTN2_MIP50	GAGAATTCCTGAGTTTTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTTGCTTTTTCTATCC	1
M00764_ASTN2_MIP51	GAAATGACCTTGCATATTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATTATGGACTTATTT	1
M00764_ASTN2_MIP53	AGTCTTCTGGAGCCTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTGAGACTAGTTTTTGG	1
M00764_ASTN2_MIP54	ATATTTGAAAACGAAGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATACAGCAATAGACCATC	1
M00764_ASTN2_MIP55	GGGAGTTTTTTCAGAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTATCTCAAAGATTGT	1
M00764_ASTN2_MIP56	GCCTCAGCTACCATTTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAAGTGAAATTGGAA	1
M00764_ASTN2_MIP57	GATTTGAGACCTTTCTTGTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTTTGCTTATTGT	1
M00764_ASTN2_MIP58	GCTATCTAGCCAAACTGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACTCAAAGTAAGCCA	1
M00764_ASTN2_MIP6	AAGTAGAGCTGCTATGTGACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGGTCTCAGGCAG	1
M00764_ASTN2_MIP60	AGCTGCCAAAGATCACTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATATCAAGATGAGACTAA	1
M00764_ASTN2_MIP61	GGAACTTGTTCATTCCATGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCATCTGGGCTTAG	1
M00764_ASTN2_MIP62	ACTGAAAAGGAGAAAATATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACCTTCTTGCAAGA	1
M00764_ASTN2_MIP63	GTCTTCTCAGAGAATCACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCTACTATGTGAGATT	1
M00764_ASTN2_MIP66	CTTACAAAGAGACTTAGACTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGGAAACAAAACA	1
M00764_ASTN2_MIP67	CTTACAAAGAGACTTAGACTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATGGAAACAAAACA	1
M00764_ASTN2_MIP68	CCCACTGTCAACATTAGATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTTCGAGCTAACTA	1
M00764_ASTN2_MIP7	GTAGCAGGAAGAGGCAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAATAAGTGAATAAACA	1

continued table…

ID	MIP	*c*
M00764_ASTN2_MIP70	GACAGTTTGTTATAATTTCTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGCTTTCATTTCG	1
M00764_ASTN2_MIP72	AAAGAACATCTTTATTTCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAGGGTGTCAGTTTCA	1
M00764_ASTN2_MIP74	GCTAGCTTTTGTGTGTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGTAGTCTATCAATTTTG	1
M00764_ASTN2_MIP76	GGTTTGCCAATATTTTATTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTGTCTTTGTTTCA	1
M00764_ASTN2_MIP77	GCCTTGGACAAAATTCAACAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATCAAGTTGGCT	1
M00764_ASTN2_MIP78	AGTGTCTGTGTATTCATCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAATCTTCCAATGCCT	1
M00764_ASTN2_MIP79	ACCTGTACACAGGTAGGTACATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCCAACAGTGGAG	1
M00764_ASTN2_MIP8	GCAGGCCTGTCCATGCATTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGCTCTGAGGATGGT	1
M00764_ASTN2_MIP80	GCATAGGTTTCAGTCTGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGACCACAGTACTG	1
M00764_ASTN2_MIP82	GATGCCAATGGGCTCCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTGTCATCATTGTCTAT	1
M00764_ASTN2_MIP83	ATTTCCAGCAGCACTGGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGACAAAGGGTCCACA	1
M00764_ASTN2_MIP84	AACCGTGTGGTGCCACTTTATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGATGACCAGCTCAT	1
M00764_ASTN2_MIP85	GCACAAGACAGGAAGAGCGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAATCTCCACACCTGA	1
M00764_ASTN2_MIP86	GAGCTGGGCAGCAAGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCATCTTTTTACTTCCTCA	1
M00764_ASTN2_MIP87	GCAAAACATTCCTTTACAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTCCACCTTCACC	1
M00764_ASTN2_MIP88	AGGCAGACTTGGGGAGTACACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGAAGGGCAGTGCTT	1
M00764_ASTN2_MIP89	GCCCATTTCTCAGATGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGTTCATGGATAAACT	1
M00764_ASTN2_MIP9	GAAAGCAGAGTGTGGCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCATGCTTCCTCACTG	1
M00764_ASTN2_MIP90	ACGGAAAAATCAAACTTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATAAGCCAGAATGCGTA	1
M00764_ASTN2_MIP91	ATTACGTGTCGCTAAGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTAGACATTGAGACTG	1
M00764_ASTN2_MIP97	CATGTGGGAGATGGGAGGGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGGGCTGAGGAGAT	1
M00764_ASTN2_MIP99	GTTTTCGGAGTGGGCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAATATGAAGGAACTG	1
M00764_ATP2C1_MIP1	GCCAAGAGGTCTGTGGTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAACATTAACTTTCCCT	1
M00764_ATP2C1_MIP10	CGAAGAACAGGTATCATTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGACAAGGACCCTC	1
M00764_ATP2C1_MIP101	CCTTAGAAAAATGAAAATGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTTTTGCCTCTTTT	1
M00764_ATP2C1_MIP102	GACTTCTGAACTATTTATGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAATCCTTAATTGTA	1
M00764_ATP2C1_MIP103	AGGAAAACGAAACATTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTAGATGTCTGGAATTAC	1
M00764_ATP2C1_MIP106	AGACCTCTTTGAATTTATATTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAAAATACTTGTGT	1
M00764_ATP2C1_MIP107	ATGGAAAAAACTTCAACCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAAATACCACTTGT	1
M00764_ATP2C1_MIP108	GCTTGGTATTTAGTGAATCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGGTAGAAACTGC	1
M00764_ATP2C1_MIP109	CAGCCTTCTCCTGAGAGTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGACTTCTCATTAGCAA	1
M00764_ATP2C1_MIP11	GGTTTCTCAGCGTCGATAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACCTGTACCTATAAA	1
M00764_ATP2C1_MIP110	GAAGTTACCCTGCTGTGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATACGTCTCTCATAGAAC	1
M00764_ATP2C1_MIP111	CAAAGCTATGATTTCCTATAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGTGAGTGTGGGA	1
M00764_ATP2C1_MIP112	GTAACTAGACATGTCCTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAGTATGCTGCTAGA	1
M00764_ATP2C1_MIP114	GCTGTGGATGAACAGTTAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTACTTGCCTACCT	1
M00764_ATP2C1_MIP115	GCAAGAACTTACTTAGGCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGGATTGGTCCAATT	1
M00764_ATP2C1_MIP117	GGGGGTGAAAATGCAATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAATATTAGAACAAAAGT	1
M00764_ATP2C1_MIP118	CCCTTGAGAAAAAAAAAAAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGGATAATATGTC	1
M00764_ATP2C1_MIP119	CAAGGTCTTCCAAAGGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAATAAGTTTGAGATAT	1
M00764_ATP2C1_MIP12	ACCACCAGAAAAAGCTACCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGGATTTGGCTTTG	1
M00764_ATP2C1_MIP120	AGAAAGAACAGAAGTTATGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCCATAATGTAGCT	1
M00764_ATP2C1_MIP121	ATTATTTGCAAGAGTGCTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTTTGCAGTATGGA	1
M00764_ATP2C1_MIP123	GGTTTGTTTGTTACAGCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGAGAAGGTTGATGT	1
M00764_ATP2C1_MIP124	GATTGTGCCTTTAGACTTCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCTGATTTGTCTA	1
M00764_ATP2C1_MIP125	ATGATACTCTAGATCTTCTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGACTTTTCACAATT	1
M00764_ATP2C1_MIP126	GACTCAGTCTTGAGATTTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGATAGAGTCCTTGC	1
M00764_ATP2C1_MIP127	AGCATTGACTTCATACTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTCCAGTTAATCATT	1
M00764_ATP2C1_MIP128	AATAGGGTCATGCATTCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTTTTCTACTTCTGC	1
M00764_ATP2C1_MIP129	AACACAATTGGGAGCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGATTAAAAGGAAATAGA	1
M00764_ATP2C1_MIP130	CCATGACTGCAAAACATTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATATTTCTAACAGGCGCT	1
M00764_ATP2C1_MIP131	GCATCCAAAAGATGTTACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAATGCAAGAAAGAAG	1
M00764_ATP2C1_MIP132	GCTCATCTACTGCTTTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGCAGAGGAATAATTAA	1
M00764_ATP2C1_MIP133	CGTTGTATCTAGATTGTAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCAAGTCCAGGAA	1
M00764_ATP2C1_MIP135	CAACTTTAAAATCAACCAGTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATTTGAACTAGG	1
M00764_ATP2C1_MIP136	AAGCACATAAGCAACAACATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGCTGCTTCTACT	1
M00764_ATP2C1_MIP138	GCCATTCCAAATACTATTTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACCATACTTAACTC	1
M00764_ATP2C1_MIP139	AAACCCTGTACACATTAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGATAAAATACGCATA	1
M00764_ATP2C1_MIP14	ATTCAGACTGGCGAGGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAAAATCTCTGTTCAA	1
M00764_ATP2C1_MIP140	GGTTAACAGTTGTAAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATCCATAGAGATAGC	1
M00764_ATP2C1_MIP141	GTTTATTCATGTTGTAGCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGGCAACCACTCA	1
M00764_ATP2C1_MIP142	GTGAAAAAAGACAGATACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAAATATTCATCAACT	1
M00764_ATP2C1_MIP143	GATGAGGACAGTAAACTACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACAATTTTACATTTAT	1
M00764_ATP2C1_MIP144	GAATGTTCACGGCAACACTATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTATCCCTGGCTTC	1
M00764_ATP2C1_MIP145	CCTTTTGAGAAGTTTATTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATCACACAAGTAAGAGA	1
M00764_ATP2C1_MIP146	GGATACCTAGTAGCTGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGTAGGTTAAACAGCAC	1
M00764_ATP2C1_MIP147	CGCTAGCTCTTGGTGTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTAAGTAACATCCAAT	1
M00764_ATP2C1_MIP148	CAGGAATTGCTGCTACAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATAAGAATGCTCTTAAC	1
M00764_ATP2C1_MIP149	CATAATGATGTTTGGCTTATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAAAAAGCTGCCTA	1
M00764_ATP2C1_MIP15	GCCCAGGGGGCATGTACTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACCAATGTCTCGCTCT	1
M00764_ATP2C1_MIP150	GACGAAGAATGAAATGACTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAGGATTCTAGTCTT	1
M00764_ATP2C1_MIP151	AACAAATCACATTACAGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTTTCTTAAAGGGATA	1
M00764_ATP2C1_MIP152	ATCTATATTTCTTTACTAAATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATATAAGTGTAAT	1

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M00764_ATP2C1_MIP153	ATCTATCTTTCTTTACTAAATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATATAAGTGTAAT	1
M00764_ATP2C1_MIP155	GTGATCTTTAGGTTACTGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTTCTAGGTGAACA	1
M00764_ATP2C1_MIP156	AACACTACAAACACTTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCTCAACAATTCTGCT	1
M00764_ATP2C1_MIP157	GTATTTTTCTTAGGCGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGTGATGTTGTTCAT	1
M00764_ATP2C1_MIP158	GAAGAAAGTCACCATCTTGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTAAGGCCCCTTCT	1
M00764_ATP2C1_MIP16	CACTCTCCTCATTTTAAGCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCGTTCCAACTAGA	1
M00764_ATP2C1_MIP160	GCAAAAGTGGATGGCTGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTTCTTTGTTAAAGGA	1
M00764_ATP2C1_MIP161	GTTGAAGTCCATCAAGACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATCTAAGCTAAACAGG	1
M00764_ATP2C1_MIP163	CAACTTGTACTTACCTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAGTGTCAAGGTCTGC	1
M00764_ATP2C1_MIP164	GGAAAGGTAGAGCCTTCTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACATACCAGAGCAAAG	1
M00764_ATP2C1_MIP165	GCCTTACCTCTGAGTCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAACACCTCAATACTGGC	1
M00764_ATP2C1_MIP166	GTATGTGCATGTTACAAGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGCTTTTAACCTTGA	1
M00764_ATP2C1_MIP168	AACCAACGTTACAAATAAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGAGCAAGCTAAA	1
M00764_ATP2C1_MIP169	CCCTGTCATCATCCTTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACCATTAATACCAACAA	1
M00764_ATP2C1_MIP17	GCTAACCTCAAAGTTGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTACAGAGTAGAATCAAA	1
M00764_ATP2C1_MIP170	GCCTTCTCTTCAGAGTGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGAAGGAGTAAAAGAA	1
M00764_ATP2C1_MIP171	GTACATGAAAACTCCTGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGGCAAACACCTTT	1
M00764_ATP2C1_MIP173	GGGTTTGTTAGGCTTTAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAACTGAAGGGCAGA	1
M00764_ATP2C1_MIP175	GGTTCTGGATAAGGGGTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGTCATGAAAACATCA	1
M00764_ATP2C1_MIP176	GTCCTGAACTGGGACAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTAAGTGATTTATTTAA	1
M00764_ATP2C1_MIP177	AGCCAAAGCAAGAACTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCCAGTAATCATTTTTA	1
M00764_ATP2C1_MIP178	GTGGTGCATAATTTTGTGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGTTACAACACTCAT	1
M00764_ATP2C1_MIP18	GAAACAGAGCAGCAAAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGTTCTTAATTTTTA	1
M00764_ATP2C1_MIP180	GCTAGCTTAAATAGTCAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACATGATTACCACAGA	1
M00764_ATP2C1_MIP181	GAATCGAAACTAGGCCAATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCACTTTGGGGCTAC	1
M00764_ATP2C1_MIP182	CAGAGATTACAAGCCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATTCTTAGGTATGCTAGC	1
M00764_ATP2C1_MIP183	GCTACAGGATCACTTGAGCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAACCTATCTGAATC	1
M00764_ATP2C1_MIP184	GAATTTTCAAGGCTGGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAATGCTCATTTAGTATG	1
M00764_ATP2C1_MIP185	CCAAAACTTCCCAGTCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGTAACAAAAGAGAACAG	1
M00764_ATP2C1_MIP186	ATACAATCCCAGACGACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAACACTTAGAATAAGG	1
M00764_ATP2C1_MIP189	GTCAGAAATACTGTGAAGCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAGCCCAAGGCACA	1
M00764_ATP2C1_MIP19	CCTTGGGCCTTCCTATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAATTTTTGATGTTACT	1
M00764_ATP2C1_MIP190	CCTTGGGAGACACAATTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTGTTGTGAAGGGCT	1
M00764_ATP2C1_MIP191	GGACTATCAGGATTTGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTGCTACTAATATTCCC	1
M00764_ATP2C1_MIP192	AAAATAGGGAGGATTTGTTTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATACAGTTCTCACAGA	1
M00764_ATP2C1_MIP193	ATAATATAGACCACCCATTGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTTCTTCTGTAGCG	1
M00764_ATP2C1_MIP194	GTTTGCAAAGAGGCAGCAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTCTGCTCCACTCTA	1
M00764_ATP2C1_MIP195	GGCCCATCGCAACTCCAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGACAGGAAAGGATA	1
M00764_ATP2C1_MIP196	ATTCCAGCTGAGCACGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTACAGTGTTTTAGTA	1
M00764_ATP2C1_MIP197	ATCCCTTTACCCTCTTCGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGAAGTTTCTAGGCAT	1
M00764_ATP2C1_MIP198	GTAAATGTAACAGTTAGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAAGTAGAACTTAAGC	1
M00764_ATP2C1_MIP199	ACCTATTTATCATGCCATTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACTACACAATACCC	1
M00764_ATP2C1_MIP20	GCTGGGGAAATCACTGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTGATTTAAAGAGAGG	1
M00764_ATP2C1_MIP202	ACTTTCCTAATCCTCTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGATTTTTAAATGCTAA	1
M00764_ATP2C1_MIP203	GTTAATGCTGCTATACTCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAGCTCATGCAATT	1
M00764_ATP2C1_MIP204	GTTATAAATTGTGTGATGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAGGTACGAGTTTTT	1
M00764_ATP2C1_MIP205	GGAAAGACAGCATTTTGACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTAGTGAGGTTGTGA	1
M00764_ATP2C1_MIP206	GTTGCGAGGAGGTTTACGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATGTTAATATAGCAGCT	1
M00764_ATP2C1_MIP207	GGGAAGTTAAGGGAGCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAATCATTGTTTGTGGGA	1
M00764_ATP2C1_MIP208	GTTCAATGCACTAAGTTCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCGATTTATCCATT	1
M00764_ATP2C1_MIP209	GCATGTGAAGGTCATTGTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCATAATCTTTGCCT	1
M00764_ATP2C1_MIP210	GTTATTTACTTTCCTCCGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTGACCAAGGAGTA	1
M00764_ATP2C1_MIP211	CAGAGTCCAATCTCAAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATAACGTTTTCTTTACC	1
M00764_ATP2C1_MIP212	ACTTGATTTGAAAAAGGAGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGAGCCTAAGCAT	1
M00764_ATP2C1_MIP213	CCAGAAGCATGTTAGTTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAAGTTTCAAAGAAATG	1
M00764_ATP2C1_MIP214	CCCTGCTCCTTTCAACCTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCTTGAACTTGCC	1
M00764_ATP2C1_MIP215	GCTGGCAGTCCCAAATGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAAACTAGGAATTGCAG	1
M00764_ATP2C1_MIP216	GGTTAAAGTCTTAAGTCTTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAGGTTTTGCCTTT	1
M00764_ATP2C1_MIP217	ACTATTTATGGTGGTGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAGCATATGGTCAGTT	1
M00764_ATP2C1_MIP218	ACTGTTAGACTTCTTTAAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCAAATAGAATGCCT	1
M00764_ATP2C1_MIP219	GTATCAAGTTTTTTGCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAAATTTAATCATTTC	1
M00764_ATP2C1_MIP220	ACATGGTATCTGAGCTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACACTTACTAAGAAAAACA	1
M00764_ATP2C1_MIP221	GGTGTTCTAGGGTAACAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGATTGAAAAGCCTATA	1
M00764_ATP2C1_MIP222	GCCCTGCATGAATTCTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTTTACCTCAAAAAGGA	1
M00764_ATP2C1_MIP225	ATTGGGCATGCTAGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTATATGTGGAAGATTC	1
M00764_ATP2C1_MIP226	GTTTGTGCTAAAATCTAGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTATACCTCATCAAGC	1
M00764_ATP2C1_MIP227	GTTTAATCCTTCTTGAAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATCAGTTTTTATGA	1
M00764_ATP2C1_MIP228	GTTAGAATTGGGACCAATTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCCCTATCAATGA	1
M00764_ATP2C1_MIP229	AAATGTACATTGTTCCATGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTGTTAGCACTGAAA	1
M00764_ATP2C1_MIP231	GCTTTGCATTTTAGGTTCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAACATGGAAGCCATT	1
M00764_ATP2C1_MIP232	ACGTGCATTTAATACGTATTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCCCACTGGGATG	1
M00764_ATP2C1_MIP233	GCTGGAGAATGCATAGTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTCATTTGCTTTGTAC	1
M00764_ATP2C1_MIP234	GGATAATTTTAATTTCTGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCATTTAACTCATCCA	1

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M00764_ATP2C1_MIP235	GTATTAGATGAGAGGTCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGTTCCTTTCTCTA	1
M00764_ATP2C1_MIP236	CAGGAAATGGGACAGTTATATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCCTGAGTGCCATG	1
M00764_ATP2C1_MIP237	GTTTTTCTTTCATTAAAAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATATCAAATCCTCCCT	1
M00764_ATP2C1_MIP238	ACTGCAGCCTCTGTCTCCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAATCAAGGTAGGGAG	1
M00764_ATP2C1_MIP240	ATTACAGGTGTGAGCCACTACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCCTCCATGATGC	1
M00764_ATP2C1_MIP241	AAGGCCAAGGCAGGCAGATCATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAGTCAAGTACA	1
M00764_ATP2C1_MIP242	ATAACCTTACTGAGGAACTCCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCTCATTAGATAC	1
M00764_ATP2C1_MIP245	GCCCAGCATCAGCCAGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATATTCCATCAGGAATAG	1
M00764_ATP2C1_MIP246	GCATTTATTCTACTTGGTTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCTTTAAAGCTACC	1
M00764_ATP2C1_MIP247	GGGCAAGATCTGAAAATATACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTACTGCTCTGGAA	1
M00764_ATP2C1_MIP248	ACTTTTTCATTAAAAAATGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCCTCTATTTGGC	1
M00764_ATP2C1_MIP250	CCTGGAGTGCACCTAAAGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTGGTATTGCTGCA	1
M00764_ATP2C1_MIP251	GGAGAAGTTGAAACTAATGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGTCTGGCCAATGA	1
M00764_ATP2C1_MIP252	CCAGCTGCTACTTAAAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTGACTAAGTACTTA	1
M00764_ATP2C1_MIP253	CATTTCAAAAAGTTTTAAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATGTTCCATTTCAG	1
M00764_ATP2C1_MIP255	GAAGCTTCTGTATTTCTAAATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCGTTACCACCC	1
M00764_ATP2C1_MIP256	ACTATGTTCCTCTAAGTTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAACAGGTCAGTCC	1
M00764_ATP2C1_MIP257	AACTCAGTTTGCATCAAACTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCAGCTGTTCTAAGAA	1
M00764_ATP2C1_MIP258	GACCTTGTGGCATTGAATAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATACCAACACTTGGT	1
M00764_ATP2C1_MIP259	GCCCCCGCTGAAATATTCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGTGGAAGCCTGGT	1
M00764_ATP2C1_MIP26	GTCTCATTCACTCAGTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACGCCTGACTGGTTTTCGTT	1
M00764_ATP2C1_MIP260	CATCTAAACAATGAGAGCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTGCTGGCATAGT	1
M00764_ATP2C1_MIP261	CAATGGTAGTTATCCTGTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGCAAAGAATCTTTG	1
M00764_ATP2C1_MIP262	ACACTTTAATTTTAAAGAAAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAACTGAGCTGG	1
M00764_ATP2C1_MIP263	CTGCAAAACCACTAAGCATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCAAATGATGCCAAT	1
M00764_ATP2C1_MIP264	CTGATAAACTGGTACCTTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGGCAGTTTGTTAGA	1
M00764_ATP2C1_MIP265	GTGGATTCCAATTAATCCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACAGCAGGATTGTTC	1
M00764_ATP2C1_MIP266	CAGTCAAGAATGGCCTTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGTAAAAAGCCTTG	1
M00764_ATP2C1_MIP267	CCTCTTTAGTTACCACAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTAAACAGTGTTGTT	1
M00764_ATP2C1_MIP268	GCTGCAACAGCAAATAAAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATATAAGGCCCAGAGAT	1
M00764_ATP2C1_MIP27	CGAGCCAAGATCACGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCATATCCCAGACGATGGGT	1
M00764_ATP2C1_MIP270	CCTACTGCTGCTGTCACTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGTGGAGAGACAAACA	1
M00764_ATP2C1_MIP271	GATCAATGGATTGGACATCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGACAATAAGGGAGT	1
M00764_ATP2C1_MIP272	GTTTTTGTCCCTACACCCTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGGCACATAGGCTC	1
M00764_ATP2C1_MIP273	GAATCTCAGCTCTAATGGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCCTCATTCACTCTA	1
M00764_ATP2C1_MIP274	GGAGAGAGTTGTATCCTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGTAAGAAATGCAATT	1
M00764_ATP2C1_MIP275	GAGCCTTTTTCTGATAACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCATGATTCAATCCAA	1
M00764_ATP2C1_MIP276	ACAGTGACTCAAAATCAATTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCTCCCACATATT	1
M00764_ATP2C1_MIP277	CAGCTGAAGAGCTGGAAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTCAGATGGAAGCACA	1
M00764_ATP2C1_MIP278	CCCCATCTGGAGACAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGCTTTAAATATAAGTGA	1
M00764_ATP2C1_MIP279	CCCCATGTGGAGACAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGCTTTAAATATAAGTGA	1
M00764_ATP2C1_MIP280	GTATCTCAACCAGCTGCTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGATGGTGCTAAGA	1
M00764_ATP2C1_MIP281	ACTGTAACAGCTTTTCATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCTTGTGCCCAGCC	1
M00764_ATP2C1_MIP282	GGGCTGTTTCTTTATTTAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGGCATTTATGAAGC	1
M00764_ATP2C1_MIP283	ATCTTTTCCACTGGTCTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAAGATGTTTTTCTCTTC	1
M00764_ATP2C1_MIP284	CAGGGAAAAAGTAAATTCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGAACAGTAAAGAGA	1
M00764_ATP2C1_MIP285	ACACATTTTGACCTCTGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTAAACCCTAAATCTGT	1
M00764_ATP2C1_MIP29	CCCTACCAGCCAAAATATTATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAGGAAGAGTCAA	1
M00764_ATP2C1_MIP3	GAGTTAAAAGCCTTCTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATTGTTATCAAGGAG	1
M00764_ATP2C1_MIP30	GGCTATTGACTGATCAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATAGCAAGTCTAAAAAAA	1
M00764_ATP2C1_MIP32	GTCCCTGGCAGGAGCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACTAAGCACACCCCTTA	1
M00764_ATP2C1_MIP33	CCTCCCGAGTCTCGCACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACAAAGTCTGTAGGGG	1
M00764_ATP2C1_MIP36	CAAACCCAAACATTGTCCATTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGAATCTCCGACC	1
M00764_ATP2C1_MIP37	AGGTCGCTCGGGGTTGGTGGCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACTTCCGCTGAG	1
M00764_ATP2C1_MIP4	ACTGAGCTGTGTGTCTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTTTTCAGTGCTGACAA	1
M00764_ATP2C1_MIP44	GGTGACAGCCTGGGATTCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCGAGATAGTGGCTGG	1
M00764_ATP2C1_MIP46	GTTGTCTTTGTTTTTCCACCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCCGTGGCTGACA	1
M00764_ATP2C1_MIP47	GAGTGGATGTGTGGCAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAGTTTTAGGGAAAT	1
M00764_ATP2C1_MIP48	CAAGTTTTTAAGCTGTCAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGAAAACAGAAGGG	1
M00764_ATP2C1_MIP49	GCTATAGATAATTACTTATGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCAGCTTTTGTC	1
M00764_ATP2C1_MIP5	GCGGTCTGAGCTGGAAAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTCGTGAGGCTTAATT	1
M00764_ATP2C1_MIP50	AAACTGTTTAACACAACTCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGGTTAGTGAAGG	1
M00764_ATP2C1_MIP51	AGTAGCCAGTTGTCTTTTCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTTCCCACCAGCTC	1
M00764_ATP2C1_MIP52	CAACGCACCATGACAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATAATCCTCTAAACTCA	1
M00764_ATP2C1_MIP53	AATAGCGTGCTTTTCATTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAAGCTTAGCTGTA	1
M00764_ATP2C1_MIP54	CCACCAACATAAGAGTAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTAATAGGAAAGACA	1
M00764_ATP2C1_MIP55	ACTGCATTACACTTGTTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTTGAGAAGTAGCAT	1
M00764_ATP2C1_MIP56	ATCCAAAAGTTCACAGCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAATACAGGAATCATT	1
M00764_ATP2C1_MIP57	AGGGACTAGATGGTGTAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACGTTTTCAAAAAAT	1
M00764_ATP2C1_MIP58	ACTTACTTGGAGAATGCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGGCTACTATGCTGAA	1
M00764_ATP2C1_MIP6	GACAGTCGCATCACTACCACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTGTTTAAGAACTAG	1
M00764_ATP2C1_MIP62	GCTCCCCCATGTCCCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAAAAAATCAATTTTGT	1
M00764_ATP2C1_MIP63	CAAAATGCAAATTGTACACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTATCAGTGGTTGCC	1

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M00764_ATP2C1_MIP64	GTTTTTCTTTTCTGTGCTAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCCCTCCCTCTCTAT	1
M00764_ATP2C1_MIP66	GTAATTTATTAATACATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTAAACAAATGTGAAGT	1
M00764_ATP2C1_MIP68	CGTCAGTATCACTGTGGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGAGAACTGTCATGTA	1
M00764_ATP2C1_MIP69	GCATTAAAACACTGATGACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCTGAGAGCACTTCT	1
M00764_ATP2C1_MIP7	GCAACAGTGTTCTGTTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGACAGCCAAGTATGA	1
M00764_ATP2C1_MIP70	GATCAGCTGGAAAAGAAATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAACGATAAGTATTGCC	1
M00764_ATP2C1_MIP71	CCTACCGTTATTGGGGGGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCCTGTTTCTTTTGT	1
M00764_ATP2C1_MIP72	GTGCTTATATTCTTACCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAACGATATTCCTATTC	1
M00764_ATP2C1_MIP74	GATCATACCAATGGCATTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGGAACTTTTTGTGT	1
M00764_ATP2C1_MIP75	CAGTGTGCGTGAAGGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTTAGAAACAGTCTTT	1
M00764_ATP2C1_MIP76	GGTTAAAAAAAAAAAAATTCATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCGTAAGTCAGCAG	1
M00764_ATP2C1_MIP77	GGATAAACATTACTAGTTTTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGACTTGGTTCCA	1
M00764_ATP2C1_MIP78	CATGCAGATCATAACTATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGGGGAAAAATGTTAC	1
M00764_ATP2C1_MIP79	CCATATTTCCAGAACTTTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACGGCATGTATAACAA	1
M00764_ATP2C1_MIP8	ATCTTTAGGCATCTGAGGAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGGACGCTTCTAG	1
M00764_ATP2C1_MIP80	GCAGATTAAAACCATCGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAAAATACAACTAGGAA	1
M00764_ATP2C1_MIP81	ACTGATTCTGGTCTTTTAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTTAGCTAGTGTCA	1
M00764_ATP2C1_MIP82	GACATGCAAAGTAGAATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCATCATCACTTCTTCC	1
M00764_ATP2C1_MIP83	GAGTCCAGCTTGACAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTAATCAATGGAAAAGGG	1
M00764_ATP2C1_MIP84	ATCCACAGCCTTAGGGAACATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCAGTGTTCCCATAA	1
M00764_ATP2C1_MIP85	CCTTTGTTTGAAACTATTTTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGCTCCTCAGCC	1
M00764_ATP2C1_MIP86	GTGTTGTCATTGGAACAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTAGGAGTGTGTATGT	1
M00764_ATP2C1_MIP87	GGGGAAAAACAGGAAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACAATGAAGAATTTCAG	1
M00764_ATP2C1_MIP88	GAATGGAAATCAGTTGTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGATGCAAGCAGAA	1
M00764_ATP2C1_MIP9	CAAAGCAAATGTTCTCCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCATAGTGAGGAAAGC	1
M00764_ATP2C1_MIP90	ACCTTGGAATATGTCTTCTATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAAGGATTTTGAGC	1
M00764_ATP2C1_MIP92	GGTAACCTGCCAAAACTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTAAAATAACCTACAAG	1
M00764_ATP2C1_MIP93	GAGAAATCCAGAGGATTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTAGTAACCCAGGTC	1
M00764_ATP2C1_MIP94	GATTTTTCCTCAAAAGGAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGAGGGAGGATTAAA	1
M00764_ATP2C1_MIP95	GTTCTCCCTCCTACCAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAACTGAGACTTAGATT	1
M00764_ATP2C1_MIP98	CATACTCACTCTTCTCTTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATGGCTACTAGTAGT	1
M00764_ATP2C1_MIP99	GGGAAAAGATATCCTGGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTTTTTTGTCAAGGG	1
M00764_BBS7_MIP1	GAGCTAAAGGCTGGGCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTAACAACCATATGACTG	1
M00764_BBS7_MIP10	GCAAAAGGAATATCAGTTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTACAGCATGTCTAA	1
M00764_BBS7_MIP100	CGTAACAACCTGCATGTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTCAGTCACAACTTTA	1
M00764_BBS7_MIP101	CCTAGTTTCAACAATTACCAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAACAGATTATCA	1
M00764_BBS7_MIP102	CCTTCTTTATTATTAAGTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGGAGTAACATCTCA	1
M00764_BBS7_MIP103	GTGAACCTTTTTGTTAAACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAGCTCTGTGTCTT	1
M00764_BBS7_MIP104	GACAAGAACAGGAGGGACAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAATCCTCTCCGGGT	1
M00764_BBS7_MIP107	CGCAGCAGCGTACTGACGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAAACCGCCCTGTAT	1
M00764_BBS7_MIP108	CCTTATCGCTGTAGAAAAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCAGAGGCGGAGAG	1
M00764_BBS7_MIP109	AAGAAGTCCAGTATTAGCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAGAACCGCTGCTGTA	1
M00764_BBS7_MIP11	GGTAGTGTTTTATGACTCTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGAACCCAAGTACT	1
M00764_BBS7_MIP110	GCTTTTTGTGGGTTTTCTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGGGTCCTACAAAG	1
M00764_BBS7_MIP111	GGTCTTTGTGCTCCTCAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACGGGTACACTAAAATC	1
M00764_BBS7_MIP112	CATTATATCGCTCTGTATGTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCTTGAGTGGCGA	1
M00764_BBS7_MIP12	CAGTTGTGAAGATCAAATAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCAGGACACAAAGC	1
M00764_BBS7_MIP16	AGACCACTTCTTTGGGACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAAAGAAATAGAAGCA	1
M00764_BBS7_MIP18	CATGCCTTTAAAGAAAAAACATAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCTGCATCGAAGA	1
M00764_BBS7_MIP2	GTCATCTTAACATTTAGGCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCGTTTTCTTATGTGT	1
M00764_BBS7_MIP21	ACAGAGTAAGGGAGGTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTATAAAAATGCAGCAT	1
M00764_BBS7_MIP23	AACCTGGTATAAAATGAATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAATTTATTGCACAGA	1
M00764_BBS7_MIP24	CCTTGGGAAATAGCCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTAAAAGTAGCTTGACA	1
M00764_BBS7_MIP25	CATGTAAGAGAAGCTGGGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGAAGAGGCAGATCA	1
M00764_BBS7_MIP26	CAGAAGCACCTTAATATTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGATGTGCAGGTTGC	1
M00764_BBS7_MIP27	ATGAGGGAAATACGAACTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTGGACTGGTGATTA	1
M00764_BBS7_MIP28	ACTGGTACTCCAGCTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATCCAATGTAATGTTAA	1
M00764_BBS7_MIP29	GCTTTTGGCTAAGAAAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTACATTATTAATGT	1
M00764_BBS7_MIP3	AGTACTGTATTACTATGTGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTAGTTCAAGGTGCC	1
M00764_BBS7_MIP30	CCTTTTTGTAGCTTCTTTAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGACCAGATGCAGTT	1
M00764_BBS7_MIP33	CAGAAGAAATCTACAGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATATAAATTGTCACAT	1
M00764_BBS7_MIP34	GCTTACTTACATAAGTATGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATATATGCCTCCTAAA	1
M00764_BBS7_MIP39	GTGGTACCCTAAAGAAAAATAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCATTGTTAAGCCA	1
M00764_BBS7_MIP4	GGCAACCAACAAAAAACACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCCTAATGAAGATGC	1
M00764_BBS7_MIP40	GGCCATAACACTGCATGGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATACCCCTGACCACAGTG	1
M00764_BBS7_MIP41	GTTAGGAGTTATTTGTGAGTAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGACATTTTACT	1
M00764_BBS7_MIP42	GTCAGTGTATTCATGGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTGTATCTAGAAAGGT	1
M00764_BBS7_MIP43	CACTCCTGGGTGGTTTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAATTCTGCTTATTAACG	1
M00764_BBS7_MIP44	GCTCTTTCCTTTGTCCTACCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAATATTAAATCTA	1
M00764_BBS7_MIP46	GCAACAAAACATATCTTTAGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTGGCGGACCTG	1
M00764_BBS7_MIP47	CCTCTTTTGTGTTGAATCAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAGCTGGACAGCT	1
M00764_BBS7_MIP48	CCTGCTGGTATGTCTTACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTATTCTTCCCAGTCA	1
M00764_BBS7_MIP49	CATTTGCTTAAGCACCTGTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTGCCTGGCACCGA	1

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M00764_BBS7_MIP5	CAGCTTGGGGAAAAATAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACGTATAGTTAAGAGAGTT	1
M00764_BBS7_MIP52	GTACCTCTAAGATAAGGCTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTGTCTAAAACTAAA	1
M00764_BBS7_MIP53	CAGGTAAGCAAAATGTCTAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAATCAAGCAAAGC	1
M00764_BBS7_MIP54	ACTCATTCCTGGAGAAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATCATCTTTATTTAGT	1
M00764_BBS7_MIP55	GCAGTATAAGGTATTGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCAATAAAAACCCATT	1
M00764_BBS7_MIP57	CAGACCTGTAACCCAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTCATGAGATTTTTAAA	1
M00764_BBS7_MIP58	GGAAAGTGGACCAGGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGTACATTGGAGTTTC	1
M00764_BBS7_MIP59	ACAGTTATAGTAGTCCCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGACAGCTATGATGAAA	1
M00764_BBS7_MIP6	ACTGTTTTCTAAAAAATTCGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGACCTTATTAAAATA	1
M00764_BBS7_MIP61	GATGTTGTCTGAAAGCGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGTCTGCACATAAACAT	1
M00764_BBS7_MIP64	GTGTATTGACAGCTTTGACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCAAAGTTTTTTTGC	1
M00764_BBS7_MIP65	CATAGCAGACTTAGCAATTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCAAGTGGGAAATTCA	1
M00764_BBS7_MIP66	GTCTTCTCCAGAGTCACCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGAATCTGAACTACA	1
M00764_BBS7_MIP68	ACTTACTATTAAAACACATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGCCCCCCAAAAAAGA	1
M00764_BBS7_MIP69	ACTAGAATTGAGACAGTTGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTTCCTGGACCCCC	1
M00764_BBS7_MIP70	GCATTCATGAATAACATCAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCATTTCCATTGT	1
M00764_BBS7_MIP71	CCTTATATTTCTGGTAAAAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTTGGAGGGAGG	1
M00764_BBS7_MIP72	GTTCTCTGTAGTCAAAGTACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCCATAAACACTGGA	1
M00764_BBS7_MIP73	CATCACCTTTATCTTCCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGAGAAGCATATTTGG	1
M00764_BBS7_MIP75	ACATGTGGAAACAATTTTTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTGCTCAGAGTTTT	1
M00764_BBS7_MIP76	GTTGGTCTTTGCAGTCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATACAAATAACAGCAACC	1
M00764_BBS7_MIP77	CCAGTGGAAAGATTATCTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATGTTCTCAGGCACAT	1
M00764_BBS7_MIP78	ACTTAGAGAACACAGTTTTTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGTCTGAGCCAGA	1
M00764_BBS7_MIP8	ACTATTTCTGCACTCTTCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTCAATATTCCCTTG	1
M00764_BBS7_MIP80	ACTTCTTTGTGTACTATGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGAAAATGAGGATG	1
M00764_BBS7_MIP82	ATCTCACATATCAGGCAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGACAAGGAATTGTTT	1
M00764_BBS7_MIP83	GAATCACAGGGAGCTGAAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCTGTCAAAGTTAG	1
M00764_BBS7_MIP84	GCCAAGGAACATAAAGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGGGAGCTATATTTCA	1
M00764_BBS7_MIP85	GATAGTTCTGGTTTTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTTTAAAGAACTTTAT	1
M00764_BBS7_MIP88	CCAGTTCCAGCCTTGCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATACATAGCTTTAATGCTT	1
M00764_BBS7_MIP9	GCCATCTTAGATTTTCCTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCAGTGCTATAAAT	1
M00764_BBS7_MIP90	CAGCAGGTCTTCAGGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAAAAAGTACACAAATT	1
M00764_BBS7_MIP92	CTGGTTCCTATGCCTACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGTCATTGAAATCTAAA	1
M00764_BBS7_MIP93	ATTCTCATTCAGTTGATCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATGTTCATTGGACCT	1
M00764_BBS7_MIP94	AAATGTGAATGTATGACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGGCAAATTCTTTAAT	1
M00764_BBS7_MIP95	CAAAGCTATACTTACTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCAGACTCATATCTCACA	1
M00764_BBS7_MIP96	GAAGGGGAAAAATGGTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGTCATAATATTAATAA	1
M00764_BBS7_MIP97	GACACCCCCACAAAAAATAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCTGTAATAGATGGA	1
M00764_BBS7_MIP98	CCTAGATTTTCTGATCTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATATATTGTGTTGTCC	1
M00764_BBS7_MIP99	GTTATGGACAGAAATGCCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCATAGATTTTGTTCC	1
M00764_BTBD9_MIP1	CGATGCCCAGGGACAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCGGGCAGATGTACAAA	1
M00764_BTBD9_MIP10	GCTGGAGGCCATGGGGTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCACAGCCCCTGATGG	1
M00764_BTBD9_MIP100	GTCTGAAAAGGATAAAAAGGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACGCACAGCCTGCAT	1
M00764_BTBD9_MIP101	GCACTTTTAAACATCGTGTTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGGGAAGGAGAGGGT	1
M00764_BTBD9_MIP102	AAAAATCATTGGTATCAAAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCTCTCAAGTGAAG	1
M00764_BTBD9_MIP103	GAATGTTAAGTATGGTGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAAAGGGAGAGGAAA	1
M00764_BTBD9_MIP104	GTCTGCATGACTTTTGATGTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAACGCTGACAGA	1
M00764_BTBD9_MIP105	CATTCCACCATATAATAATGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCAGCACCTCCT	1
M00764_BTBD9_MIP106	CCAAGACACCACTGCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATAACTGTTATTTCCAA	1
M00764_BTBD9_MIP107	CAGGACACAAGAGGAATGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCCTCAAATAGGATTT	1
M00764_BTBD9_MIP108	GAACCATTTTAAATGATTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGATCACTCTCATC	1
M00764_BTBD9_MIP11	CCTCGCCTTCCTGGGACATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACTCAGGACTAGCAG	1
M00764_BTBD9_MIP111	GTAATCTCTCTTTTAGGACTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCTGCAAAAGCAA	1
M00764_BTBD9_MIP112	ACCCCTGAAGGTTTCCATTAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTTGTCCCACCCTC	1
M00764_BTBD9_MIP113	ACCCAGTGAAGAGGTATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATACAGGATTGGGGATAAG	1
M00764_BTBD9_MIP114	CCCCAACTTCAACAAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAGAACTTCTCCTTCTC	1
M00764_BTBD9_MIP115	GTTCCAAGGGAGCCTCATCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGAGGCCTAAGTGCT	1
M00764_BTBD9_MIP116	ACTTAGAGGTAGAGCTTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAATTGATAGGCTATT	1
M00764_BTBD9_MIP117	GAGCTAAGCTCAATGCTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCTTATTGACCTTGTTC	1
M00764_BTBD9_MIP118	CCTCATAGAGTTGTTTCAAATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTACAAAGACATC	1
M00764_BTBD9_MIP119	GCTCTTGGCCAGGTGCAGTGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATATACTAATCAC	1
M00764_BTBD9_MIP12	GAATTGGGAGGGGACGGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCAGGGCAGGGACTG	1
M00764_BTBD9_MIP120	CAGACCATACTGGCTAACACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAACAATAAACACAGGC	1
M00764_BTBD9_MIP121	CCAGACCAAATAGTGCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATAATGACAAAGTCTTG	1
M00764_BTBD9_MIP122	AATATTGGCACCTGGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGATATTGAATTGAGAG	1
M00764_BTBD9_MIP123	GTAGAAAACACTGGTATTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAATATGGCGACG	1
M00764_BTBD9_MIP124	ATCTTGTGGAATAGACGATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCCACCACGAATGT	1
M00764_BTBD9_MIP125	CCTCTTCGCCCCTTTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATTTTTACTTAGCTGTG	1
M00764_BTBD9_MIP126	CCTGCTTCCCTTAACTGTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGTACACATAGAAAA	1
M00764_BTBD9_MIP127	GGATACCATTGATTAACTCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGACTGTGATGGCT	1
M00764_BTBD9_MIP128	ATATATTGAGCAAGGTTGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCCAAACACTAACAG	1
M00764_BTBD9_MIP129	ACTGTAAGGAATATGAGACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTGTAATTTAGGCC	1
M00764_BTBD9_MIP130	ATCTTCTGGGGCCAGGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATTATACCGAATAGAAA	1

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ID	**MIP**	***c***
M00764_BTBD9_MIP131	CAAGGTTTGCTCTCTTGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCCCACCCCCAAATC	1
M00764_BTBD9_MIP132	GCTGAAAATCAGCAGATAAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGGTAGCCACATG	1
M00764_BTBD9_MIP133	AAGACTTACTAAAAAAAGAAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTGTCCCTTTGG	1
M00764_BTBD9_MIP137	AGTCACCACACGTCACTGTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCAGGCCCAGAAAG	1
M00764_BTBD9_MIP138	GACTTACCCGGAGCCAGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTGCACCTCCAAGAA	1
M00764_BTBD9_MIP139	GCTAAGTGATGCTCGTTAATTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCCTGTGGAGTGAC	1
M00764_BTBD9_MIP140	CCTTCCTGCACCTCCAAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGAGAGGAAACTGAGA	1
M00764_BTBD9_MIP141	GTGAAAATGAAATAAGGTATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGGCTGCTAAGTG	1
M00764_BTBD9_MIP142	GAGAGTCAAGGCTGGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGAGCCACCAAGTCAAA	1
M00764_BTBD9_MIP143	CCCCGTCTCTACAAAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGTACTTTGTAAGTATA	1
M00764_BTBD9_MIP16	CCGTGAGTATTTATAGCCCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCAGCTTCGTGT	1
M00764_BTBD9_MIP17	CAGACTGGCCTGGGAGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATTGTGAGTCTTCAGG	1
M00764_BTBD9_MIP19	GTGATTTTCAAACAATGGTGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGACGTGGGCCCAG	1
M00764_BTBD9_MIP2	CGATGCCCAGGGACAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCAGGCAGATGTACAAA	1
M00764_BTBD9_MIP21	CCTCCCTGATGGAAGCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGAAAATCCTAGCTG	1
M00764_BTBD9_MIP22	GGAAAGAGGCTGTGCCCTTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAATGGTGAAGGGCG	1
M00764_BTBD9_MIP23	CATGCCATTTAAACCTTGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAAGCAAACCTTTTC	1
M00764_BTBD9_MIP24	CATCTCTCTCGCTGACACGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGCCACCGTGGCTTTT	1
M00764_BTBD9_MIP25	CAGCTGCCAAAACAAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGACAACTTCTAATTTA	1
M00764_BTBD9_MIP26	GCATATTTTTCCTGACAACAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATGTGGTGACCAGC	1
M00764_BTBD9_MIP27	GACACCTTTCTTCCCTGTCCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTGGGCATCGCTC	1
M00764_BTBD9_MIP28	ATTAAATTTGCTTCCTTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAATAAAAAGCGAGC	1
M00764_BTBD9_MIP29	GTTGACTGGGCTGGAGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCACCAAGTGGCCTCA	1
M00764_BTBD9_MIP3	CCTTTTGGGCATCTTTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTTCACACACATGGAC	1
M00764_BTBD9_MIP30	CACTTATCCTTTCCAGAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTTTTGAATTGTGC	1
M00764_BTBD9_MIP33	ACTGATTCCTTGGCAAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTTTAAATTGTCACTT	1
M00764_BTBD9_MIP34	AATGAAAGCAGAAAAAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAAAACACTTTTAATGTA	1
M00764_BTBD9_MIP35	GCACAAGCCATGATGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGCCCCCACCGTCTCTC	1
M00764_BTBD9_MIP36	ACGGCTCCTGTGAGACTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGAAAATGGTAAAACG	1
M00764_BTBD9_MIP37	AGCTGCCAGAAGGTGACTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCAAAGTGCTCACA	1
M00764_BTBD9_MIP38	GCAGCTGTGTCCATGCAGCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGTAGAAAGGCAA	1
M00764_BTBD9_MIP39	GCAGCTGTGTCCGTGCAGCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGTAGAAAGGCAA	1
M00764_BTBD9_MIP4	GTGCTGCTATGTGGAATGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCCTGTAAAGATGTGT	1
M00764_BTBD9_MIP40	ACTTCATTGGAGCTTTTGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCAGGCAAAGAAATG	1
M00764_BTBD9_MIP41	CCACCTGTCAGCCTCACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAAAAGTGAAGGGTGGG	1
M00764_BTBD9_MIP42	CAATGGTCCTCAGTAACCAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAAGCCCCTGGTC	1
M00764_BTBD9_MIP44	GAGGGCTCCTGGGCACCACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTGGAGTTCCCCAGA	1
M00764_BTBD9_MIP45	CCTGGAGATGAGGTCCTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCTTCAAGTGTTTAG	1
M00764_BTBD9_MIP47	CCTTTTGGAGTCCAGGGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGGTGTGACACACCTT	1
M00764_BTBD9_MIP49	CATGCCCCGAAGGAAAGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTGCCATCAGTCCTCA	1
M00764_BTBD9_MIP5	GGGCCGAGCTCCAGGCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCCCTGCCCTTGCATCA	1
M00764_BTBD9_MIP50	GATCTCTGTCCCTCCTGTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACGAGATAGCAGCTT	1
M00764_BTBD9_MIP52	GGCCCTGCATCTGCAACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAAATGAGCCATTCACA	1
M00764_BTBD9_MIP53	GGAGCTCTCTGGCTAATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCATGTTTAAAAAGAAGC	1
M00764_BTBD9_MIP54	GCACACACAGCACTTCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCATTTCATAATGGGA	1
M00764_BTBD9_MIP56	GAGAGTGGAACACTCCTGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGTGGACACGTTCC	1
M00764_BTBD9_MIP57	CAGTTTGATGCTACCCTACTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACCGGGGAGGATGG	1
M00764_BTBD9_MIP58	GTGATTAAATTGGAAGACTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTCAGGTGTGTCAA	1
M00764_BTBD9_MIP59	GGGAGACTCCCAGGCTGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCGCAGCTGATATGTC	1
M00764_BTBD9_MIP60	CATGGCACGTGAGCAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACTTAGTGATTTCCATT	1
M00764_BTBD9_MIP61	AGTCCCCAGTTGAGTACTGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCCAGGGCAGGCAG	1
M00764_BTBD9_MIP62	AAAAATAGCAGTTCCAAGAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCTTAGCTGCCCC	1
M00764_BTBD9_MIP63	ACTATTTCCTTGTCAGCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGCTTCGATAAACACA	1
M00764_BTBD9_MIP64	GCTGCTAATTCACTGTTCCGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAAGCAAATCAACCT	1
M00764_BTBD9_MIP65	CAAGCTGAACCGTTCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTATTAACTCCAGTGTCC	1
M00764_BTBD9_MIP66	GGGGACAGAGACCCATCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAGTTATTCTCCACTCA	1
M00764_BTBD9_MIP67	CAAAGGCCCAATGGCTTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGAACACCTATGATTCA	1
M00764_BTBD9_MIP68	GGAGGCACCCTTTAGGAATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACCCTACCTCTCTAA	1
M00764_BTBD9_MIP69	AAGCAGCCCCTTTCTGTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGACTTCCTCCTGTTCCC	1
M00764_BTBD9_MIP70	CAATTTATCCAAATCAGGCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGAGCAGGGGTCT	1
M00764_BTBD9_MIP71	GCTGCCTCCTTTATTGGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGCTTTTGCAGCTA	1
M00764_BTBD9_MIP73	AAGGAAAAGACCCCATGAGTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGAGTCGAGCTGC	1
M00764_BTBD9_MIP74	CAGGTGTTCCACTGTGTCCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGGGAAGGACCTCC	1
M00764_BTBD9_MIP75	AGGCAGGCTGCCTTTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAACAAACAATTCCACT	1
M00764_BTBD9_MIP76	CATCCGTATCGTTGGGACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTCAGTGGACATGA	1
M00764_BTBD9_MIP77	ACACAACTTACTTGCAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGAAGATCACTGGAGT	1
M00764_BTBD9_MIP78	CCTATTGAAAAGACAGTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTGGGATTGTGATGA	1
M00764_BTBD9_MIP79	CATATCCCTCCCACCCACCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTTGGTAGAAACCTC	1
M00764_BTBD9_MIP80	GTATCAAGAAAGGAGTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCAATACGGTAAGAAG	1
M00764_BTBD9_MIP81	CCCCATTCAGCAAGGCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTATGAATGAGGAGGAA	1
M00764_BTBD9_MIP82	AATTATGACTGGGATTCTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTGATGCCAAATCT	1
M00764_BTBD9_MIP83	GAACATCTGGATTATCTTCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCATGGGAACTGTGA	1
M00764_BTBD9_MIP84	CAAGAGTGAAGGTTTTGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATTTAAATCAACCAG	1

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ID	**MIP**	***c***
M00764_BTBD9_MIP85	GAAGGGGCTGATAGGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTCAACACATTTTCTT	1
M00764_BTBD9_MIP86	AGCTTGACTTCAGACTCTATATCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCTGACGGTAAAAAG	1
M00764_BTBD9_MIP87	GTTGCCTAATCTAAGGTTATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTATGGTGCCCACTCT	1
M00764_BTBD9_MIP88	CAGGTATTATAGGCATGAGCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCACACCACCAAAG	1
M00764_BTBD9_MIP89	GGGTAGTGGTAACATGAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACTGACAGTGACAGT	1
M00764_BTBD9_MIP90	GGCTTTGGGGGAAGTTATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTCTACTGAACTTTAG	1
M00764_BTBD9_MIP91	CAGACACGGGCTGGAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGATATGTTTAGTAGTT	1
M00764_BTBD9_MIP92	GGTTAGTTTTCAGTGGTTAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTCACAGGTCTTAC	1
M00764_BTBD9_MIP93	GGTTAGTTTTCAGTGATTAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTCACAGGTCTTAC	1
M00764_BTBD9_MIP95	GGAACGGCAGTCATCATCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGCTAAGTCATCTCA	1
M00764_BTBD9_MIP96	GCATCGAGATTAAGCTAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACTATGAAGTATGGA	1
M00764_BTBD9_MIP97	ATTCTAGCATTCCAGTTTATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCCCCCTTTACAA	1
M00764_BTBD9_MIP98	GGATGGCATCAGGAGACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCGGTTTTAATGGCATG	1
M00764_BTBD9_MIP99	GGATGCCATTAAAGTGCGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGTGTAAGCACAATT	1
M00764_C15orf61_MIP1	GGAGAGGCCATACATAAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACCCATTACCAATCC	1
M00764_C15orf61_MIP15	GGGCAGGACAGGAGGGCGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGATGTTCACGGGAA	1
M00764_C15orf61_MIP16	GTTTTACTAAAAGCACCAAAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCGTCCTACTGCA	1
M00764_C15orf61_MIP17	AACTTGCCGGGAATTCATACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGTAAACATCCTCA	1
M00764_C15orf61_MIP18	GCCTCAAGATGTTTTGAACTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCATGGAGACGCC	1
M00764_C15orf61_MIP19	CCTGGTTATTTGCCAGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACATTGTAATTTGTTAAC	1
M00764_C15orf61_MIP2	ACACGTGAGGTTTTTAAATAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCTTTTCCGAAAG	1
M00764_C15orf61_MIP20	GGAATACCTAGAAAACAAACGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCACACTTTCAATACAT	1
M00764_C15orf61_MIP23	ACTCTGAAGAGAAAATATAGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTAGCTGATGTG	1
M00764_C15orf61_MIP25	CATTTACCTGGAGGAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACATTAGGATGTATGATG	1
M00764_C15orf61_MIP26	CACAAGGCCTTTAAAACGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGTTTCATTCACCTTG	1
M00764_C15orf61_MIP28	AGATCTTAATTGTTCTTACAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAAGTGCCATTAGG	1
M00764_C15orf61_MIP3	CGTCCGAACACACAAAGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCGTTGTTTGGTAAG	1
M00764_C15orf61_MIP30	GGCTTTCAAAAATGCAATTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAACACCCATTGGTTT	1
M00764_C15orf61_MIP32	AAAATGTGTAAGTGTTGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCTTTAACGAAGCTA	1
M00764_C15orf61_MIP33	GTAACACTTTAATCAAAGAAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTGAAGGCACCAG	1
M00764_C15orf61_MIP34	GAAGAACAGTTCACTCTGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTGTGTAAGCCATTC	1
M00764_C15orf61_MIP35	CCTCTGTAATGGGCAAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGTCCAGAAGAATATAC	1
M00764_C15orf61_MIP36	AATCAGTTCTAGCCTTCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTTTATCAGCCTTGT	1
M00764_C15orf61_MIP37	CCTCTTTTCACACTGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGTCAAATACTGCTCAT	1
M00764_C15orf61_MIP39	ACTTTTAGTACAAAACCTTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGGCCCTTCTCTT	1
M00764_C15orf61_MIP4	ACCTTGCGGAGGTGGTTAGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAAAGTGCTCCCGG	1
M00764_C15orf61_MIP40	CACCTTTATTAAAACAGTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCTCACAACTTACA	1
M00764_C15orf61_MIP41	CCTAAAATGCCAAATTGTAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGCAAATTCCTAGGC	1
M00764_C15orf61_MIP42	CAGCCTCTCTCACGCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTTGAATTTTTACGGA	1
M00764_C15orf61_MIP43	ACGTTAGAAAAATATTAATGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGAGAATCGCTTGG	1
M00764_C15orf61_MIP45	AATGTTTCAGCTAGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATCATTCTTTAACAGAG	1
M00764_C15orf61_MIP46	CCTAAAGCTAGTGGATTAAGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATAGTTCTTCATGA	1
M00764_C15orf61_MIP47	GCATTAGCTTTTCAGTGCAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACTGTTGACCCAGG	1
M00764_C15orf61_MIP48	CACGATCAAATCTTGTTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAACAAGTACTTAGCA	1
M00764_C15orf61_MIP49	CAGCAAAGTGCAGTTACATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTAATTGAACTAGTAA	1
M00764_C15orf61_MIP5	CAGAACTCAAACCCAAGTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGGTGTGACCTCA	1
M00764_C15orf61_MIP6	GCTCACGCTTCCCATCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTCCTCAGGCCCAAAT	1
M00764_C7orf62_MIP1	GCAATATACACAGAGGTAATATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCTGCTCCTTCTC	1
M00764_C7orf62_MIP10	CAAGAAGAGAAACAACGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATCATCTGGAAAAATA	1
M00764_C7orf62_MIP11	GTAAATCACGGTTTGTCAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGACATGAGGAGTCTT	1
M00764_C7orf62_MIP12	CAGTAAAGAGGTACCCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTTCATTTCAAATACA	1
M00764_C7orf62_MIP13	GTCATGTAATGGTGATTACAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAGTTTTATCAGGA	1
M00764_C7orf62_MIP16	GTGACATGACTAAAGGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAGAAAACAAATAAAG	1
M00764_C7orf62_MIP18	GACCTGGAAAAAAAAATTGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGGCAGAACACAG	1
M00764_C7orf62_MIP19	GCAGAGGAAGTGTGAATGGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGTTCTCAGCTGT	1
M00764_C7orf62_MIP2	GCAATATACACAGAGGTAATATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCTGCTCCTTCAC	1
M00764_C7orf62_MIP20	AGTGTTTGTCGAGATACCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTATCAAACGGAAAAAAA	1
M00764_C7orf62_MIP21	ACTTCAGGAACACATATCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTCAGGTGCATTTGT	1
M00764_C7orf62_MIP24	GTTTTAAAATTACTGTTTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTACTTGGATAATT	1
M00764_C7orf62_MIP3	GTTGCCGGGTCCATGAATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAGTAGCACAAACTCC	1
M00764_C7orf62_MIP4	GACCCATACACATCACTCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACTAAAGGACCAGGC	1
M00764_C7orf62_MIP5	CCTTTAGGGACTGTGACTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTGGGAGGAGTAGG	1
M00764_C7orf62_MIP6	GTCATCACAGATTTTCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAACAAATGAAAATTAT	1
M00764_C7orf62_MIP7	GCAGAATGGAAGTGGGATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATTGGAATGTTATGA	1
M00764_C7orf62_MIP8	CCTCGAGTCCTCCAGCGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGATACAAGCAAATGTAGAAA	1
M00764_C7orf62_MIP9	GACTTGGAGAAAAAGAAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTCAGCAACATCTT	1
M00764_CACNG8_MIP100	GGGCCTGATCTTCAACCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGGCACAGAATGAAA	1
M00764_CACNG8_MIP11	CAGACGCCTCTTTTCAACCCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGACGCCTTCCAGGC	1
M00764_CACNG8_MIP14	ACATCATTCTGGGCGCAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTTTTCCTTTCCTTCC	1
M00764_CACNG8_MIP28	GCATTCATTCATTTTTTTCATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCAACTCCTGGA	1
M00764_CACNG8_MIP29	CGCGTCCAACCCTTCTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAGAAGGCCCTTTCTG	1
M00764_CACNG8_MIP3	GGAAGGAGTTTCTGGAGCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATGGTGGGATGACT	1
M00764_CACNG8_MIP30	GGAGGCAGGAAAACAGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACATAAGAAGGCATTGGA	1

continued table…

ID	**MIP**	***c***
M00764_CACNG8_MIP31	CCTAGCTTTTTAAGGCGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAACTGTAATTTATTGT	1
M00764_CACNG8_MIP34	GTAGGTCAGGAGTTCAGATTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCAGCACGTGCAA	1
M00764_CACNG8_MIP35	CACAATCTGGCCCTGTCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTACTCTTGCCTCC	1
M00764_CACNG8_MIP36	GTAATTACACAGATGCTGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAACGTGAATGGTGTA	1
M00764_CACNG8_MIP37	GCTTCCTCCCACAAGAGTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGGCCAAAAATGGC	1
M00764_CACNG8_MIP38	ATCAAACACCGCCATCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACTCGTTCATTCAGC	1
M00764_CACNG8_MIP40	GGTGAAAACGGGAGGAAGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGTGAGCAGCACTTG	1
M00764_CACNG8_MIP46	GCAGCCTCGAACTCTTGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTCTCACCATCCTTAG	1
M00764_CACNG8_MIP47	GCTTCCCTTCCATATTTGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGGGACTGAGGCTC	1
M00764_CACNG8_MIP48	GCCTTCTCAGTGAACTTCAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAGCAGGGCAAGAT	1
M00764_CACNG8_MIP49	GCTCTGCGTGCCCTTCTCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCGGTGCTGGGAGTG	1
M00764_CACNG8_MIP50	CCACGTCCTCCTCAAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTTCAGTCTCTCTCTTC	1
M00764_CACNG8_MIP51	AAGGAATACAAATCAGTGAGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGAGCTGGGTGTT	1
M00764_CACNG8_MIP52	CCTACATTTCCCAGCATCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGATTAGGAGCCAC	1
M00764_CACNG8_MIP53	CAACATATTGAAATCTTGTCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACGTGGAGAGAAGAGG	1
M00764_CACNG8_MIP54	GTCTGGAACTCCTGAGCTCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCCTCCCAGGCCCA	1
M00764_CACNG8_MIP57	CCAAACTAGTAGAGTCACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGAATGGATTCTA	1
M00764_CACNG8_MIP59	ACAAAAAGCAACGTGGAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGAGAGAGAAGAGGAA	1
M00764_CACNG8_MIP60	GAATCTCTGAGTCTGTCTCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGAGATTGGGTCTAG	1
M00764_CACNG8_MIP67	GCATTCCACCCACCAGAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGTGAGTGGTAACAGA	1
M00764_CACNG8_MIP68	GGCCCCCAGACTTTCTCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAGGCCCTAACTGAT	1
M00764_CACNG8_MIP69	AGTGCTTGGAGGGTTTTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCAGGTCTTCGAGGAG	1
M00764_CACNG8_MIP72	GAATTACATTGCTGTGCTGAGCATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGCCAGGCCAATC	1
M00764_CACNG8_MIP73	GTTAGTGGGATGGAGGAAGTGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAACAAGAACAGCA	1
M00764_CACNG8_MIP74	AATTGGGCACGCACATCTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTGGAGTTAGTGGGA	1
M00764_CACNG8_MIP75	AGAGAGTTCTTCTCTTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATCTATCTTGACACAT	1
M00764_CACNG8_MIP76	GCTCAAAAACGTAAGTTTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGGAGGAACCAA	1
M00764_CACNG8_MIP78	CAGGAGGGTTACAGAGGGCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGACGTGGCCTAGCAG	1
M00764_CACNG8_MIP79	CAGCCTACCTCGAGATCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCATCAGACCTAATGGTC	1
M00764_CACNG8_MIP80	ATTTGGGGGGAAGACAGAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGATGCAGAGAGCAG	1
M00764_CACNG8_MIP85	GTCAGCTAGGCTCTGGCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATAGGGAGATGGGAGG	1
M00764_CACNG8_MIP86	CATCCTCTCTTCCCTGCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCACCTCAATAGGTCT	1
M00764_CACNG8_MIP87	AGTTCTTGGAAATACTTTCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGTCTCTTGCTGC	1
M00764_CACNG8_MIP88	AATGAATGATGAAAACGTGTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCTCAAACGCCAA	1
M00764_CACNG8_MIP91	AGAGAGACTGACAGGTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGATTGCACCATTGCAC	1
M00764_CACNG8_MIP92	CCTTTTCTGTCTTCTCTGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTCCACGTTGCTTT	1
M00764_CACNG8_MIP93	ACTTCTGTCCCATCTCTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCCAGAGATTCGCAT	1
M00764_CACNG8_MIP95	CCTTTGCCCATTCATCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCAGACAATTAGAATACA	1
M00764_CACNG8_MIP97	GTGCTCCATCGGAAAAGTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGACTGCCTGTGACCT	1
M00764_CADM1_MIP1	AGTCCCTGGCTATGGCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAATTTTCTCTCTATC	1
M00764_CADM1_MIP10	ACTGTGAGCCTGTGCACGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGATGCAATCGTAACATT	1
M00764_CADM1_MIP101	CCATAATATGGCCAAGTGATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCTAATGGGAAGAA	1
M00764_CADM1_MIP102	CCTCTTGAGCTTTGCTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTTGTGGAGAGTTTTC	1
M00764_CADM1_MIP103	CGAATGGCTGCAGGACCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGTGTATGTGCCTCT	1
M00764_CADM1_MIP104	GAATTTCCCCACAACTGAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGCCTTTGAATGC	1
M00764_CADM1_MIP105	GCCAGCAGTGCGCATTACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTCTTCCTTTTCCTGAC	1
M00764_CADM1_MIP106	GGCCAAACATTCTGAAACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAATTGTACGTGCTT	1
M00764_CADM1_MIP107	GCTACATGCTCGTACCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCATATCCCCAATGAGTT	1
M00764_CADM1_MIP108	AGAGAAGGGGCACAGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATACTGAATTAAGAACAA	1
M00764_CADM1_MIP11	ATATTTCAGACGTGACCGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTTTACTCCCTCCTAA	1
M00764_CADM1_MIP110	CCGTCTGTAGACACAACGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTATTATTGCTTGTCA	1
M00764_CADM1_MIP111	ATTCTTTGGTTCTGGGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGAGCAAGCTTTCAAAGA	1
M00764_CADM1_MIP112	GTTTTCCTCACTGGCTCGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATGCTTTAAGAGCCAT	1
M00764_CADM1_MIP113	CCTTTGTTTTAACCCAACCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGATGAGAAACACCAG	1
M00764_CADM1_MIP114	ATGTTTGAATGTTATGAATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCTATTCATCTACA	1
M00764_CADM1_MIP115	CCTGCGCACAAAATACATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATCAAAGGTACCTCTA	1
M00764_CADM1_MIP116	GTGGTGGTGGTGGTTGTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATTTAAAGGGAACTTT	1
M00764_CADM1_MIP117	CACCACCACCACCACCATCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATGCCTTTGTTTTG	1
M00764_CADM1_MIP118	GCTTCTTTAAGTTCTAGAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCTGAGGACACAGC	1
M00764_CADM1_MIP119	GGCCTGAGGTGGACCCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTGAGAAGATAAAATGCT	1
M00764_CADM1_MIP12	GGCTCGAGTTGTATTTCCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCAACACTTCGAAGG	1
M00764_CADM1_MIP121	GAAGCTTCAAACATAGTGGGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCTGCAGGCCTGT	1
M00764_CADM1_MIP122	GGAGATATTTTAAGTTCACAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACTCTCACCCAAGT	1
M00764_CADM1_MIP123	GTGTCACCCTGCATGTGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTCTGTTCAAAGTTTT	1
M00764_CADM1_MIP124	CAACTCAGGCAGGACAGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACACGATCAGGTGTTG	1
M00764_CADM1_MIP125	GTGAAACCACACAGCGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTTCTAAACAAGTCT	1
M00764_CADM1_MIP126	CCACCTTTGATTCTGGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGATGGTTACTAACAC	1
M00764_CADM1_MIP127	GGGGCTTCCCGATGGCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTCCTGAAAAACCATCC	1
M00764_CADM1_MIP128	GAAGGCCAAAGTTGGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTTGTGTTTTTGTCACA	1
M00764_CADM1_MIP129	CCTTCAGTAACACCCTTCTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACTTGAGGCTTATCT	1
M00764_CADM1_MIP13	GCCTATTGAAATGCAGAATGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGCCTCTTCAGTA	1
M00764_CADM1_MIP130	GGATGGGAGAGAGTAAGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGATGTGGCGCAGTT	1
M00764_CADM1_MIP131	AGGTGAAGCCATAGATATCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAAATAGATAAGAGA	1

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M00764_CADM1_MIP132	AGGCAAATGAGTTTCCTTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAACATAGAAGAGGC	1
M00764_CADM1_MIP134	GAGATGTCAGAGTTTTCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCTACTTCAATCTGT	1
M00764_CADM1_MIP135	CAATCCATAATTAAAGCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTAGTTTTAGGGATG	1
M00764_CADM1_MIP136	GCAGGTTTCCAGTGACCGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTATACTATATAAA	1
M00764_CADM1_MIP137	GACCCAGCGGTATCTAGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCGGAGGTGGAAGAGT	1
M00764_CADM1_MIP138	CCCTCTGTCCTCTAACCCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGCATCAGCTGACTG	1
M00764_CADM1_MIP139	CAGTTACTAAATATGTCTGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAAGCTGCAGATTG	1
M00764_CADM1_MIP140	CAGTGTCTTTCTGGATATCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACTACTTCAGTGTGTG	1
M00764_CADM1_MIP141	ATTGAAGTCAACTGCACTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCCTTTTTGATAGC	1
M00764_CADM1_MIP142	GCCCATCTTGCTGAATTTTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTCCTGGGTAAGA	1
M00764_CADM1_MIP143	AGTTCACTGCTAGAAAAATTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGCCCCACATGCG	1
M00764_CADM1_MIP144	GATGAAGGAAGATACTTTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTCCGTCCACCTTCT	1
M00764_CADM1_MIP145	AGTAGCTGAATCACAGAGTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAAAGGTGGCCTT	1
M00764_CADM1_MIP146	AATCCCAACAGGCAGACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTTTTCTTCCCTTTTT	1
M00764_CADM1_MIP147	CATTTAGCATGGCTCTAATACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATTCTGCCCATCAC	1
M00764_CADM1_MIP148	GCCTAGTTCCCACTTTAATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGATGATTCCAGGCTT	1
M00764_CADM1_MIP149	CAGCTTTTGTGAATGCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAGGGACAAAATACAA	1
M00764_CADM1_MIP150	ACTCTGACCTTTCCAATACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTAAGTGGCTCCTTG	1
M00764_CADM1_MIP151	GTGAGTGAGTGACTCTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAAGCTATTTGGTCAG	1
M00764_CADM1_MIP152	CACGATGAACTGCCTATACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAGTTCAGAGATGCC	1
M00764_CADM1_MIP153	GGCTTTCAGATTCACTGATATATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAACTCACACCTTCA	1
M00764_CADM1_MIP154	CGACTTTTTGACATGTTCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTACCTGTACGGT	1
M00764_CADM1_MIP155	AGTATATGTTGTCCTAGCCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCACCTCATAAATG	1
M00764_CADM1_MIP156	GTATCCCCTACTATGCCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCTCCCCTTCCCAA	1
M00764_CADM1_MIP157	GCTATCTCACAGGGCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGCAGTAGATGTAATGG	1
M00764_CADM1_MIP158	GCTGGGTTACTAAGTGCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGCAATAGGTTCACAC	1
M00764_CADM1_MIP159	GTCATGCTTGTCACATTTAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCCAGATGCCTTCAT	1
M00764_CADM1_MIP16	GATAGGGCCAATCGCTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGCATTTTTAAAAGAGG	1
M00764_CADM1_MIP160	CAGAACAAGCACCAACAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGAATTTTGGTCTCTT	1
M00764_CADM1_MIP162	ATTTTTGAGTGACTGCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTATAAGATGCCAAAATC	1
M00764_CADM1_MIP163	GAATAGAACAGCAAGTAGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTATAGTTCCTTCTGCAGT	1
M00764_CADM1_MIP164	GGAAGCTTCCTGACATGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTAAAAATACTGTGAGT	1
M00764_CADM1_MIP165	CATACCTTTCAATAGAATAACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCGTGGAGCTCT	1
M00764_CADM1_MIP166	CACTGGAGACAACCAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAACAAGATGGTCCTTT	1
M00764_CADM1_MIP167	GGTAGTGTTCAAATACAATTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTCGTAACTCAGTA	1
M00764_CADM1_MIP169	ATCCCAAAAAAATGGTTAGGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCTGAAGACAAGG	1
M00764_CADM1_MIP17	CAAGGACCCACTGGAATAGTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCACCGATGCTGT	1
M00764_CADM1_MIP171	CCTAAAGTTTTCAAAGCACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTGGCTGTCTCCTT	1
M00764_CADM1_MIP172	GAGGGAGAGTTAGTCTCTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATTCAAGAAGATGGC	1
M00764_CADM1_MIP173	GAAGGGTCTTTGGCTGAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTATCACAGTGCTCCAA	1
M00764_CADM1_MIP174	CACCTATTGAGTAAATGAGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTGAGCCATGGG	1
M00764_CADM1_MIP175	GTTGGGAAGATTAAATCAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTTTTGGAGTTGTA	1
M00764_CADM1_MIP176	GTGCAATCTCAGAGACTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGTTATCACACAGTAA	1
M00764_CADM1_MIP177	AAGAATAAAAGGACCAGCTTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCTGGGCCAGGGG	1
M00764_CADM1_MIP178	GAAACCCTCAAAATCCATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGAAGCAAAGTGTTT	1
M00764_CADM1_MIP179	GATGCTGTAGCAGTAAGTCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAGGTGAATGTCTAC	1
M00764_CADM1_MIP18	CCTGACAGGAACTTTAATATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAACATCAAGGTTTG	1
M00764_CADM1_MIP180	ACTTTACTAGAAACTCTTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGATTGTTTTCCAGGG	1
M00764_CADM1_MIP181	GTAAGTGTTTAGCCTGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAACATTTAAACTATAA	1
M00764_CADM1_MIP182	GCCTGATTTAAGTAGATTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATTGGCACATAGATG	1
M00764_CADM1_MIP183	AAAGAGATTTGCTTGAACTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAGTCTAAAGTCGT	1
M00764_CADM1_MIP184	ATATGGAGTGGTTGCAGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGCATTTTAAAAGGA	1
M00764_CADM1_MIP185	ACTGGGATTTGAAACCAATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTCGTTTGCTCTCA	1
M00764_CADM1_MIP186	GTTAATTTCACCAAGTGGTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTACTATTATGAGAT	1
M00764_CADM1_MIP187	GGTGCACACTACCACGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTTTTGACAGGTCTC	1
M00764_CADM1_MIP188	ACTGCTTTAAGACAGAAGAATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAGCACGGGAAGG	1
M00764_CADM1_MIP19	GCAGTAGTCACCCAGCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATTTGTATTCACAGCCA	1
M00764_CADM1_MIP194	CCTTAAGAGGGTCCTCTGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAAGTGTTCTCCCG	1
M00764_CADM1_MIP195	GTCTGATACAGCGATTGCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGTTCCCAAAGATCT	1
M00764_CADM1_MIP196	AACAATCTGGGAGAAGTGCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGCATCTGGCCTAG	1
M00764_CADM1_MIP197	GTCAATCCGGGGACCTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAAATCTCAGAACCCG	1
M00764_CADM1_MIP198	CCTCCCTGGTTTTAATATATAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGATAGTTGGAGAA	1
M00764_CADM1_MIP199	GAGGAGCCTGAGCATACCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCACCTGAAGCCTTGA	1
M00764_CADM1_MIP2	CATCTCCCGGGCTACATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCCTTTGTAACTGAAGC	1
M00764_CADM1_MIP20	AAAGGTGTATTAATCTTGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCTCCTGTACGGGG	1
M00764_CADM1_MIP200	GGTCTGCCGTGTTCCTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGAATATATGTGTGAAA	1
M00764_CADM1_MIP201	CACCACACTCCCTCTCCCCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTCTCCCAGAGACA	1
M00764_CADM1_MIP202	GCTCTCTTGTTTGTCTGCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGACCAACAGGTG	1
M00764_CADM1_MIP21	ATCCCAAATACGCAGCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATTCTGTCATCAAGAAC	1
M00764_CADM1_MIP22	ATTGCACCAATTAACACCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACCTGTAACACAGTGG	1
M00764_CADM1_MIP23	CACTGTCCTCTGTCTACCTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGTACGAGAGTGAA	1
M00764_CADM1_MIP24	AAAAGGCAAATGTACAGCAGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGAAACGAGGGC	1
M00764_CADM1_MIP25	CCACAGGGTATGCAAATGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCTCTCCCTCTTG	1

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ID	MIP	*c*
M00764_CADM1_MIP26	GTTTGCAAGGGCATGATGTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGCCTCATGCTGC	1
M00764_CADM1_MIP27	ACGACTTAGAAGGTTTAATGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCACAGGATAGAGGC	1
M00764_CADM1_MIP28	GCTATGGTGATGTCCACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTATCGTTTTAGTCAC	1
M00764_CADM1_MIP29	CGAAGGTTGTTAGGAAAGATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACACACTAGAGAGAG	1
M00764_CADM1_MIP3	AAATAATAGATTTCCTTGCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTACTTCCCTGC	1
M00764_CADM1_MIP30	GAATGAGTACTCCCTACTGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTGGGCTACTCACC	1
M00764_CADM1_MIP31	GCATCTCTATAAAAAGACCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTCCGTGTGCAGGG	1
M00764_CADM1_MIP32	CCTTCTCCACGAAACCATCCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTGCCCGGACTT	1
M00764_CADM1_MIP33	ATGTGAGTCAAAAGTACAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGCCCAGAGAGTGC	1
M00764_CADM1_MIP34	CCTTATACTTCTCTGCATCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTACCCTTCTCCAGAAA	1
M00764_CADM1_MIP35	CCTGAGCCATGGGTGCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAAAATCAGATATGCA	1
M00764_CADM1_MIP36	GTCTTTCTGGAGCTTACCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATACAGCAGGTGCTCAA	1
M00764_CADM1_MIP37	CCCCTTGAGCCACTTCCATCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGCCCTTTTCCCACC	1
M00764_CADM1_MIP38	CAACAGAGCAAATCCTGCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCACAGCTGAGGGGA	1
M00764_CADM1_MIP39	CATCGTCCTTGCCTTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCCTTTCATAAAAAGA	1
M00764_CADM1_MIP4	ACACTATAGCTGCCCTCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTCAGCAGCAGCAAT	1
M00764_CADM1_MIP40	GAGCAGCCAACACAGGGAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCTTCTGCAGGCAGC	1
M00764_CADM1_MIP41	ACCTGTCTCTTACTTTGGGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTGCAGGTGTGCGA	1
M00764_CADM1_MIP42	GAGAACAAGGACAGGAAGGATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGCGGCCTGTTCC	1
M00764_CADM1_MIP43	CCCACTCTCAGTGGACAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCCTCCTTAGGACCA	1
M00764_CADM1_MIP45	GGACTTCTTATGGACGCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCGCATTTTGTATTGGT	1
M00764_CADM1_MIP46	GTGTGACTAAAGAACAAGCTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATGGTATACATG	1
M00764_CADM1_MIP47	GTCTTATTTTTCCCTTTAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTACAGGTTGATCACT	1
M00764_CADM1_MIP48	CATAATTTCCTGTTTTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAACAAGTTTGTTCTTT	1
M00764_CADM1_MIP49	GTATACAGTGCACTGTTTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTGTTTTCCGTCTC	1
M00764_CADM1_MIP5	GGACAAGGAAGGGAAAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTATCCATCTCTCTCTC	1
M00764_CADM1_MIP50	GGGAGGTCCCAAAAATGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACACTTTGCAATCTACC	1
M00764_CADM1_MIP51	AAGTGTACAGTAGTGCAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAGGTTTTTTTTCAGT	1
M00764_CADM1_MIP54	CCGAGCCCTTAGCACCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTATGTAAAAGAAAATCC	1
M00764_CADM1_MIP55	ATAAAGACAAGAAAAATAAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTCTTGGTTAAGTG	1
M00764_CADM1_MIP56	GCAATATGGGGGCCTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTTTACTATTGTTACA	1
M00764_CADM1_MIP57	CATAGGGACTGTTAGCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATAAGTTTTCCACATA	1
M00764_CADM1_MIP58	ATGGCATCAAAAAAGATAGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAGAAGTGTGGGG	1
M00764_CADM1_MIP59	ACTATGGCTGCCATCATGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTAGACGTTTCAGTGAA	1
M00764_CADM1_MIP6	CAAACAGCTTTTGTGGATTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGAGAGAGGGAGAGAA	1
M00764_CADM1_MIP60	GGGAAAAGGTAGAGGAGTCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGCCTTGGCCTCTT	1
M00764_CADM1_MIP61	CCTATCGAGAACTGAGAGCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGTTCTTAAGGCTGA	1
M00764_CADM1_MIP62	CAGAGCAGAGGTGGAAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATTTCCAACTCGAAT	1
M00764_CADM1_MIP63	ACTCTGTCCCATTCAGTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAATGAAAGTTTCAC	1
M00764_CADM1_MIP64	GTGCTTAGTTAGGAAGGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTTCCAAATGATTCC	1
M00764_CADM1_MIP65	CCTGTCAGGTCTGTTTAGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGATTGGGAAAGGTGGA	1
M00764_CADM1_MIP66	GGACAAATTTTGAGTTGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCTGTATCTGTAGACG	1
M00764_CADM1_MIP68	GCTGTGGAACTACATTACTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTCTTCTCTGTTGTC	1
M00764_CADM1_MIP69	GGAACAGAAAGCAGTTACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCAAAGAGTTTTCAT	1
M00764_CADM1_MIP7	CCAGACACAGCAGACCTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAATATTGAAATGTG	1
M00764_CADM1_MIP70	CATAAAAGGAGAACCAGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTCCAAAATCTCCCA	1
M00764_CADM1_MIP71	ATTTTCTGCAATCTACTGAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCAGGCAAATTC	1
M00764_CADM1_MIP73	AACACACGAATTTCTCGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAACAAACAAACAAACG	1
M00764_CADM1_MIP74	GAGACTGGGAAGGCTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTACTTCATCTAGATCAG	1
M00764_CADM1_MIP75	CATGAGTGAAGTATGTACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACACCTCATTGAAACA	1
M00764_CADM1_MIP76	GCAGACGCAGACACAGCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATGGCCATAAAGCAA	1
M00764_CADM1_MIP77	GAGCAAGCACAGCATGGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATACATCAAATTGCCTA	1
M00764_CADM1_MIP78	GCCTTCTTCACCTGCTCGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCTGAAGCTTTGCT	1
M00764_CADM1_MIP79	GATCATGCCGTGATCGGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTGACCCTCTGACCCT	1
M00764_CADM1_MIP8	CCAGCTCTGGAAGACTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATGAAATACACAACTAC	1
M00764_CADM1_MIP80	GTGCTGAATCGATCTGTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACAAGGCACCAGAAGC	1
M00764_CADM1_MIP81	GGTCAGCCTGTTACCTCAGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCAGGGCCGGATAG	1
M00764_CADM1_MIP82	CAACAGAAGGGTACAGCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGAAGGAAGAAATAG	1
M00764_CADM1_MIP83	GTGTCATTCAGAGCACCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCTTGTTTTATCTCTAG	1
M00764_CADM1_MIP84	GACAGCAAGGAATAATTGTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAAAAGCCACAGTTG	1
M00764_CADM1_MIP85	GGTTTTAAATTGAGGCTTACTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATCCTGAGGGGGT	1
M00764_CADM1_MIP86	GATGCAGAATGGATGTATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTAACACCTTGCAAT	1
M00764_CADM1_MIP89	GTCCTCTCCTGCGTTAATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATAATCCAACATCCTT	1
M00764_CADM1_MIP9	GTTGGAAGAGCCTAATGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCAGCAGGAAGTCCAT	1
M00764_CADM1_MIP90	GTTCAGTGGCTTCAAATAATGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCCTCCCCGGT	1
M00764_CADM1_MIP91	CAGGTTGGACACTGCAGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAACAGGTGAGTGGGT	1
M00764_CADM1_MIP92	GGGTGCTCTATCCACTTCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAAGAAAAACGATTTG	1
M00764_CADM1_MIP93	ATCTCTTGCTATCTATGTTTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCGGAATTGGGC	1
M00764_CADM1_MIP94	ATGTTTTTAAAGAAATTCATCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGGAGACTGAGG	1
M00764_CADM1_MIP95	GCCTGATTGTTAGCTGTCGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTGTTCTTAATAC	1
M00764_CADM1_MIP96	GATTTTCTTTTTGCATGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTATTGGCAGCGGATT	1
M00764_CADM1_MIP97	GCAGGTTATGCCTTCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACATTTTATTTCGCATT	1
M00764_CADM1_MIP98	ATCTGCAGTTAGCAGATGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTCCTGACCTAACTG	1

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ID	MIP	*c*
M00764_CADM1_MIP99	GGTGAAGAGGGAAGTAGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTCAAAGCTGAAAAA	1
M00764_CALML4_MIP1	GTTACCTTCCTTGTGGGTGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTCACAGTCTCCTG	1
M00764_CALML4_MIP10	GCTCCAAAGGGGTGGTGGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGATGCCTGCAGTTG	1
M00764_CALML4_MIP12	GCAGACCCACGGGATAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGCAGAGTACAAGGAAT	1
M00764_CALML4_MIP14	AGGGGAAAAGAGGGAGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGGCATACAATAAAA	1
M00764_CALML4_MIP16	AATACAGGACACCCAGTTAAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTCCTGCTCTCCC	1
M00764_CALML4_MIP17	ATTACTGTGAGAGCCAGAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAACTCCCAGGACAGT	1
M00764_CALML4_MIP18	CCCATTGTCCAGAAAAGTTGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGGGGCAATAGG	1
M00764_CALML4_MIP19	CAGGGTCTGAAGCCCTTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCTGGGGCATTTCTG	1
M00764_CALML4_MIP2	GCCTGGGTCCTGTCTCCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCCAAAGAAAGAAATT	1
M00764_CALML4_MIP20	CCCGAGTCCAAGGACAGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTGTGGGTTTAGGGG	1
M00764_CALML4_MIP22	CCTGAGGTTCACGCCCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATTGCCTAATGAGACCC	1
M00764_CALML4_MIP23	CCAAGTTTCTTTCCCAAGACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCCCACGGGTAGC	1
M00764_CALML4_MIP24	GTAATAAATGCTCGGCTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGACCCTCACACTC	1
M00764_CALML4_MIP25	CCACCCAGCTTGGCAGACTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCCATTTCCTCAAA	1
M00764_CALML4_MIP26	ATGCCAGTGTTTCTTCCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATTCCAGCTTCCTGAG	1
M00764_CALML4_MIP27	GCTTCTGGAGGCAGAGACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGTAAAGTGTCCAAC	1
M00764_CALML4_MIP28	GAGGAAGGGAACCCTTCCAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGACTCCAGGAAG	1
M00764_CALML4_MIP29	AGATGGTGTGTGAGGAGCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACGGGGAGGACTGAATC	1
M00764_CALML4_MIP3	AGCAGAGGGAAAAAGACTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATCAACATGGCTAGAA	1
M00764_CALML4_MIP30	CAGCTGGCAAAATCAAGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCAGGGATACAAGCTT	1
M00764_CALML4_MIP31	CCTGTAATTCAGCTGGTGAGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCTGTGGTGGGGC	1
M00764_CALML4_MIP33	GGCCAGGGTAACCGGCACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATTTCCTCCTATGTGG	1
M00764_CALML4_MIP35	CAGCTGTGGACAAAAGCCTCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGGCACAATGCCC	1
M00764_CALML4_MIP36	GCTTTTCTCCCAAATCACATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGCACTGCCAAT	1
M00764_CALML4_MIP37	CACTTTCCACACAGAGGCGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGCCATGGGGTTTG	1
M00764_CALML4_MIP38	GGCCAACATGCTCCCTCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGTTTGAGGCTCCCC	1
M00764_CALML4_MIP4	GCTGTGTTTGCGGGTTTCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGCATCCTCTTCACT	1
M00764_CALML4_MIP5	AAGCTCAAGAAAGTGGGTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGTGGCAGTGGTC	1
M00764_CALML4_MIP6	GGGGTGATGATAAGCATCGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCTGTCAAAGGTGG	1
M00764_CALML4_MIP7	CCTTCCCCTCACTGCAGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAACTGGAGGGAAACA	1
M00764_CALML4_MIP8	CCATCCTGGTAAGATGTACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTCCTGCAGTTACA	1
M00764_CALML4_MIP9	GATCTCAGGTATCAGACCACTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCTCCTCCACGG	1
M00764_CALML4_PIAS1_MIP1	GTCAAGTTGCCATCATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGTAACTACTAAGTTT	1
M00764_CALML4_PIAS1_MIP10	GCCATTTTACTGGTTTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACATCTAAAGAGCTCT	1
M00764_CALML4_PIAS1_MIP11	GTGCTTCCAAAGCACCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAATGTTACCTGTTTATG	1
M00764_CALML4_PIAS1_MIP12	CACTTGTCTCATAGGGATTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAACAAGAAAGGGAAA	1
M00764_CALML4_PIAS1_MIP13	GGTGCTAGAGAAACCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGTAATGAATATAGCCA	1
M00764_CALML4_PIAS1_MIP14	GTGTTGTTTACAAGAAGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTGGTCCAGAGTCTAA	1
M00764_CALML4_PIAS1_MIP15	GTTTTTGGCAAGTTATATTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCGGGTAGAGGTT	1
M00764_CALML4_PIAS1_MIP16	GGTCATTAGAACCTGGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAGCTTTTCTATGTCT	1
M00764_CALML4_PIAS1_MIP17	GCCATCTAAATCATTGGTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAGGCAAATGAGATT	1
M00764_CALML4_PIAS1_MIP18	CAGGAAGAGCAAGTTCTGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCTCAAAGGTCCTA	1
M00764_CALML4_PIAS1_MIP19	AGTTTAAGCACCAGGACCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTCCATGACTGGAGCT	1
M00764_CALML4_PIAS1_MIP2	GAGAACTGCTATTTGTCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGATGTGTGCATACA	1
M00764_CALML4_PIAS1_MIP20	CATGGTAAATCCACCAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTTTGTGGGGTCTGAG	1
M00764_CALML4_PIAS1_MIP21	CAAAACTCTTTGGCTCCTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCCAAATCTCGTAAA	1
M00764_CALML4_PIAS1_MIP22	GGGGTGAGGGTAAATAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTAGTGCAACTGTCT	1
M00764_CALML4_PIAS1_MIP23	ATTTGGTTTTCTTCTACTTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCACACAGCATCGT	1
M00764_CALML4_PIAS1_MIP24	AAATGGGATGTGTCTTTTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACACAGGTAGGGGT	1
M00764_CALML4_PIAS1_MIP25	CCTGGCACCTTCTAGCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGTACTTGAAGCCCT	1
M00764_CALML4_PIAS1_MIP26	CAGAGGTGCCATACACTTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGCCAGGGTACAAC	1
M00764_CALML4_PIAS1_MIP27	CCTCTCTGCCTGTTAACAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTACTGTTTTCCAGGG	1
M00764_CALML4_PIAS1_MIP28	GGATGGTCTGCTCAAGTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCACACCAAAGGAAAC	1
M00764_CALML4_PIAS1_MIP29	ACTCTACACTCTGTGTTTATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCAAGGCCAGTCA	1
M00764_CALML4_PIAS1_MIP3	GTGTTATTGGATACATCTTAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATATGTTTGTTTCT	1
M00764_CALML4_PIAS1_MIP30	ACACATGCTACAATGAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTATGACAACAATTCTTGC	1
M00764_CALML4_PIAS1_MIP31	AATACAGAATAAGTCTCTTGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGGCCTCTGGCAC	1
M00764_CALML4_PIAS1_MIP32	CATCTTCCATATTTCCAAGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCAAAGCCCCCC	1
M00764_CALML4_PIAS1_MIP33	GCTTGAAAGGGCCGGACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAAGAAGTGGGAATCCA	1
M00764_CALML4_PIAS1_MIP34	GGAGTCTGGCCTGGGTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGCTAACTAGCAACA	1
M00764_CALML4_PIAS1_MIP35	GTTTTCAGGCCCAGGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGGCTGAAATCATCTAT	1
M00764_CALML4_PIAS1_MIP36	AAAGTGTTCTTTTCACTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCCAATGGCAAAGTG	1
M00764_CALML4_PIAS1_MIP37	GTTTTTTGGGGACTGGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGTGGATAAATTCATCA	1
M00764_CALML4_PIAS1_MIP4	AAGCCACTTTAACCCTGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATTGTGATCATGTCTA	1
M00764_CALML4_PIAS1_MIP5	CAAGTGTCTGAAATGGAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTGACTATTTTGAGCA	1
M00764_CALML4_PIAS1_MIP6	GAAAATCTGCCAAAGAATCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTTTAAAAAGTCCTG	1
M00764_CALML4_PIAS1_MIP7	GGAAAATAGCTGGTGGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAAAACTTTCAAGATCT	1
M00764_CALML4_PIAS1_MIP9	ATGTCAGTTTGTATAAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAACAGATAAAGTTACC	1
M00764_CASC16_MIP1	CAGAAAACAGGCAGGACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTATCGTGAAGAGTTCAGTGA	1
M00764_CASC16_MIP10	GGTGTTTAAGCACACAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGAGCATATAGTTAGAA	1
M00764_CASC16_MIP11	GTGCCATAGGAAAAGCATTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGCTGACTGTGCC	1
M00764_CASC16_MIP12	CCTCATGTCTTGTCATGTTTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTTCTAAGCAGCA	1

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ID	**MIP**	***c***
M00764_CASC16_MIP13	GCCTACAGTTGAGACAAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCACACTGAAATGTAAT	1
M00764_CASC16_MIP14	CAACATGGGAAACTGAAATCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCACAGTGGGTGCTC	1
M00764_CASC16_MIP15	CAGAACAGGCTTTGGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAATAGCTCTTTTATGA	1
M00764_CASC16_MIP16	CATAATATAATGAAAACCCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTACCTGGTCTCA	1
M00764_CASC16_MIP17	GATTAAATCACCTGCAAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTATTTTCAGGCTCT	1
M00764_CASC16_MIP18	GCTAACAGTTGTGGCATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTACATGGAACTGTAAG	1
M00764_CASC16_MIP19	ATCCAATGGAGGACTTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGCATATTTTCCAACT	1
M00764_CASC16_MIP2	CATTTTTTTTCCCCAAGGAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAAAACAATTTATT	1
M00764_CASC16_MIP20	ATGAGGGAAATGAGAGAGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGTGGGACAGCAGG	1
M00764_CASC16_MIP21	CATATGGTATTACATTTTGGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGCCAGGCTCTTG	1
M00764_CASC16_MIP22	GCTGATTAAGCTCCAACCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCGTCTCTAGAACCCA	1
M00764_CASC16_MIP23	GCACTTTTTTTTAATGTCACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAACGCTGTGTGGA	1
M00764_CASC16_MIP24	GTGGAGGGAGAGAGTAAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCTTAGATACAACGAA	1
M00764_CASC16_MIP25	CACACTCTGAGAACTGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTATACTAGGGTTCTAAA	1
M00764_CASC16_MIP26	ATTCTCAAACTTCCTCCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTCATGATGATGTCAC	1
M00764_CASC16_MIP27	GGCTGGGAAGTGCTATCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGCATTAATGATCTGC	1
M00764_CASC16_MIP28	CATGCTCATCACAGAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTTCAGGGAAGTTAAAT	1
M00764_CASC16_MIP29	GTTAGGCACTAGAGTCAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTTAAGAGCACTCAAA	1
M00764_CASC16_MIP3	ACTACCCAGTATTTGTTTCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGGGGCCCCTCC	1
M00764_CASC16_MIP30	GTTACTGAGCAGGTGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAAACATGAACAAGT	1
M00764_CASC16_MIP31	GGAATAATTTTCCCCAGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGCAACAAATAAAGTG	1
M00764_CASC16_MIP32	GGTTCAGGGAGAAGAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAACATTCCCCAACTTT	1
M00764_CASC16_MIP33	GAGACCTGCATCTCAGGTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTCTTGACCTCAA	1
M00764_CASC16_MIP34	CCTAGGGTGCCTGGGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTTTTTGTTCCCTGTTC	1
M00764_CASC16_MIP35	CCTGGAACTGAACATCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATTTAGGAGTTAGGAG	1
M00764_CASC16_MIP37	GTTAAACCTCTGATTTTCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGCACTACAAGTT	1
M00764_CASC16_MIP38	ACATGATCAAGATCTCCTAACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGACTGAGGCTGT	1
M00764_CASC16_MIP39	GAGCTGGAGGGGGATACTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATGTTTGTACCACG	1
M00764_CASC16_MIP4	CACAGTTTTATTCTTCGCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGTGAAAATCAGGAA	1
M00764_CASC16_MIP40	CGGCTAAAATATGTCCCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTGAAGCTAAGCAG	1
M00764_CASC16_MIP41	CCTACTCCACCATCACTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAAATAAAGCAACTGT	1
M00764_CASC16_MIP42	GGCAGGCTTTTTTCTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATGAGACATATGATGG	1
M00764_CASC16_MIP43	ACTAGCTTTTTACTGCCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGGGTGGTGTGACA	1
M00764_CASC16_MIP5	GTACTGGGTCTTCAGCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGTATATAGATCTGTC	1
M00764_CASC16_MIP6	CAATCTGCATGCCTTATGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATTTATGGCTGCAGC	1
M00764_CASC16_MIP7	GTCCTGGTTAATGTTTGTGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACCCCTTCTTGGGA	1
M00764_CASC16_MIP8	GTTGTTGTTGTTGCTGTTGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGACTGCAGAAGAAG	1
M00764_CASC16_MIP9	GAGAGCTGTGTTCAGTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCATCTCACCAGTCTAAA	1
M00764_CCDC148_MIP1	CCAAAATTCATTCTAACACCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAATCCAACTAGTGG	1
M00764_CCDC148_MIP11	ACTTTGCCTTTCTTTTGTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGCTCATCCTCAAAT	1
M00764_CCDC148_MIP12	AAGTCCAGCTTCTCGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAATGCTCTTTACATA	1
M00764_CCDC148_MIP14	GATGAAAAAGCCATGATGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGTCAGATACAATGGC	1
M00764_CCDC148_MIP15	AAGCATGGCTACTTGGAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGAAGAGTGGCTTTT	1
M00764_CCDC148_MIP17	CCAAATGGGGATACTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAGGAAACAGGTGTTTTT	1
M00764_CCDC148_MIP18	CCACTTCCTTTTTCTCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATTAAGAGCACTTAGA	1
M00764_CCDC148_MIP19	CCTTCAAGAAGCTCATGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTATGCTGTTTTCTGTAC	1
M00764_CCDC148_MIP2	GGAAATGTCAGGGAGCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTATTTTTTATTTCC	1
M00764_CCDC148_MIP21	GCCATAACCATATCCACTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACGCTGAAGATCTCT	1
M00764_CCDC148_MIP22	CGGTACCATTCTTTCTGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGTTGAATCTCTGAAG	1
M00764_CCDC148_MIP23	ATATGGCTGTGAATCCATCTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCAGGCTTTGGA	1
M00764_CCDC148_MIP24	ATATGGCTGTGAATCCATCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGCAGGCTTTGGA	1
M00764_CCDC148_MIP25	CCTCTTCCTTTTCTCTTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGACCAAAAAGCTCA	1
M00764_CCDC148_MIP26	AAGAGAAACTGTGGAAGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTGTGCATAGTTACT	1
M00764_CCDC148_MIP27	GTTTAAATTCTATGTGCACATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCATTGACGAACCT	1
M00764_CCDC148_MIP28	GTTCTTTATTTTGCAAAGCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAGGCTGCTCTGCC	1
M00764_CCDC148_MIP3	ACCTACCTCCCAGGGGTTGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGACTATTTCTA	1
M00764_CCDC148_MIP30	GTAGGACAGTATTTGCCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAACTTGGCAAATAGTT	1
M00764_CCDC148_MIP31	GCTTTGTAATGAGTGTTGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCTTTCCACTGTTT	1
M00764_CCDC148_MIP32	AACAAGTCTAGGATTATGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGCCTATGGCACAGA	1
M00764_CCDC148_MIP33	GGATACCCAGTTGTCCCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCATGAATCCATTTTCC	1
M00764_CCDC148_MIP34	GGGAGGCCTTAGAATCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAGCCTTTAGAAGATTA	1
M00764_CCDC148_MIP35	CACAGGGCAGAGTGTAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTTTGAGGAGAAATAC	1
M00764_CCDC148_MIP37	GCAAAAAGAGTCATCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTTAAAACTGAATGCCTTT	1
M00764_CCDC148_MIP38	CATTCAAAAAGTCTCTAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAGTCTCTAGGGCAG	1
M00764_CCDC148_MIP39	ATATGAACAATGAGGTCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGACTTTGGAACTGGTA	1
M00764_CCDC148_MIP4	GGAATTTTTGACAGCATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTCAACAACACTAAC	1
M00764_CCDC148_MIP40	ACTGTATTAGTCCATTTTCATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACATTTTCCCGTCT	1
M00764_CCDC148_MIP41	AGTGTATTAGTCCATTTTCATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACATTTTCCCGTCT	1
M00764_CCDC148_MIP42	ATTGGTACCAGTAGAGTGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTTGCCTCCTGACA	1
M00764_CCDC148_MIP43	GTTTGAACTGTATAAAATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAAGATGCTGCACAGG	1
M00764_CCDC148_MIP44	GTCAGCACAGCCTTCTGTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGACAAATACTGAAAC	1
M00764_CCDC148_MIP45	CACTGAGGCTTGTGCAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTATCTTTTCAGGTTG	1
M00764_CCDC148_MIP46	ATGATTTTGAAAAACTGGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGATATTGGTCACAATA	1

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ID	MIP	*c*
M00764_CCDC148_MIP48	CATATTATTGAGCAATCATGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACATGTCCAGATA	1
M00764_CCDC148_MIP49	GTGAAGAAGACCACTGGATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACACAGAAACCTCGTTT	1
M00764_CCDC148_MIP51	GAATAGAGAGGGTTTTATTTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGTCCTGTGTAG	1
M00764_CCDC148_MIP52	ATTGAAGATTTCAAATCAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGTTAGTGTCAAAA	1
M00764_CCDC148_MIP53	CAAGACTTTAATCTGCAGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAAAAGACTAACCC	1
M00764_CCDC148_MIP54	ACACTTACCTTTATACTCCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGGCAGTTCACTA	1
M00764_CCDC148_MIP55	ATGTGGCTAATAATTTATGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTTGTTCCAAATGT	1
M00764_CCDC148_MIP56	GTGGAAGAGAGTTAAAGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCACAAAGTCAACCT	1
M00764_CCDC148_MIP58	CAAAATTGAATTAAAGGAACACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGTGTGAATGCTG	1
M00764_CCDC148_MIP59	AGCTATCAGAACAACAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATATTAACTGCCATTTG	1
M00764_CCDC148_MIP6	GAAAGGTTGAGTCTCCTCTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATATTCCCATGCTTGA	1
M00764_CCDC148_MIP60	GAAGAATGAGAATGGGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAGATGTAAAATGGAAT	1
M00764_CCDC148_MIP61	GGCTTTGTCATCTGCTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATTGAGAAGGGATTT	1
M00764_CCDC148_MIP62	GGCTTTGTCATCTGTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATTGAGAAGGGATTT	1
M00764_CCDC148_MIP63	GACTTCATTCAGCCTCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTCAAATCGTAACTTT	1
M00764_CCDC148_MIP64	GGTAAGAACTGGGGGACATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTCTTTTGTTCCTC	1
M00764_CCDC148_MIP65	GTGCATCTCCTAACACAAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTTCTGATCTAGATT	1
M00764_CCDC148_MIP66	GCATTTCTGTTGTGAAAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCCAACCATTTTTCT	1
M00764_CCDC148_MIP67	CATATAACCCCAGAAAAGTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAGCAGGGAGGAGA	1
M00764_CCDC148_MIP68	GGAAAATAGAATGACTTTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCCAAAAATGTGAA	1
M00764_CCDC148_MIP69	ATGTTTAGATTGGCTTCTATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCTGTCAGGCATAA	1
M00764_CCDC148_MIP7	ATTTAGAAACCAATTTGGTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTACCTGCTAATGT	1
M00764_CCDC148_MIP70	GACCACATCTTTTAACTTCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTGAAGCCAGGCCT	1
M00764_CCDC148_MIP71	GCAGAAGCCAATTTCTTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTTTCTAACAACTAT	1
M00764_CCDC148_MIP73	GGCAACATGTTGACTTCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTCTACTGGTTTGTACT	1
M00764_CCDC148_MIP75	ATTATAATACCAAGCTACAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAGGCCTCTATTT	1
M00764_CCDC148_MIP76	ACCCTTTCAGAAGTAATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGTTGATGTCTATCA	1
M00764_CCDC148_MIP78	GATTTTTCTAAGTTAAAAATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACTAGGACATTGTA	1
M00764_CCDC148_MIP79	GGAAAGCTCACTTTCTGGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGACAATTCAGAGAAA	1
M00764_CCDC148_MIP8	ACTATATGTGCCATAATTAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAACAAGCAGAAATG	1
M00764_CCDC148_MIP80	CTGTGTTACTTGAAGTATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAATACCTGAGCTATC	1
M00764_CCDC148_MIP82	GCACAGCAGTATGACTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTTAGATCTGCAGTAC	1
M00764_CCDC148_MIP83	ACCTTGGAATTGGCAAAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGGAAAAAGTGATTCT	1
M00764_CCDC148_MIP84	GTTCTCCTTTGTTTTCTTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCCCTTAATGGTGTC	1
M00764_CCDC148_MIP85	CAAATTAATGAGAAAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACCATCTATTCATCCAA	1
M00764_CCDC148_MIP86	AATATTTTGAAGAGATATATGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCACTTGGGTATCC	1
M00764_CCDC148_MIP87	GGTAGCTGAAATGAAAAAGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTCAACAGACACTC	1
M00764_CCDC148_MIP88	GGATAAAGTTGAGCGCATTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGTGTGAACGCTC	1
M00764_CCDC148_MIP89	ATAGGTCGAATGCTGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTGAATATAAGCAAATG	1
M00764_CCDC148_MIP91	GGTGATGTATAAGGTGAGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACATGAAGGAACTCTG	1
M00764_CCDC148_PKP4_MIP1	GGAGGAAGCAGCGATGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCTCTTTGAGTCTTTCA	1
M00764_CCDC148_PKP4_MIP2	GACGTCACTGAGCCACCTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTGGGCGTTTCACTT	1
M00764_CCDC148_PKP4_MIP22	GAAGATGCTCCGGTGACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGAAGACCAATGCAG	1
M00764_CCDC148_PKP4_MIP3	ATTGGCAGTAAGGCAAGGAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGGGACTCCCCAAA	1
M00764_CCDC148_PKP4_MIP4	CAACTGTGCCTGGTAGGGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGGTGGGTGTGAGA	1
M00764_CNTN4_MIP100	GTTTTTCTTGCACTGTTCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGTGCAGTTCCCAGA	1
M00764_CNTN4_MIP101	CCCTAATTTTCAGCAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCTAGTTTGATTCAC	1
M00764_CNTN4_MIP102	GTGTCTTCTGGCTTTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATACACTTACCATAGA	1
M00764_CNTN4_MIP103	GATGGTGCAGAATAGGACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAAAAATGTAGCAAGG	1
M00764_CNTN4_MIP104	GAAGGTGACAGACTGCAGTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCTGGCAGAAGGT	1
M00764_CNTN4_MIP106	CATTGTTGGTTAGGACGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTCAAGGCAGGAGG	1
M00764_CNTN4_MIP108	GCTAGAGGTTCTGAAACTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAATAGGATATGCTCA	1
M00764_CNTN4_MIP109	ATCTAGCTCTGTTTTTTACTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAAGCCTCCATCTG	1
M00764_CNTN4_MIP11	GAAGAAAAGCCCCGCCGGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACAGACATCAGCCTC	1
M00764_CNTN4_MIP110	GTCTGGGAACCACATAGTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGAATTCTGGGTCTC	1
M00764_CNTN4_MIP111	AAGCAGCTCCACATCCACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTCTTTTTCCCTTCA	1
M00764_CNTN4_MIP112	GTTACCTCTAGCTGCAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGCTGGTCTTTTCCA	1
M00764_CNTN4_MIP113	AGTTCATGCCAACTGTATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTTTTTTCCTTTCAG	1
M00764_CNTN4_MIP115	GCAAAATTAACTGTCCCTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAATAACAAGACTGG	1
M00764_CNTN4_MIP116	CCTTTCTTTGCTTTTTGGATGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCTCCCTGAATGT	1
M00764_CNTN4_MIP117	CAAAGGGCAAAAGTACACTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATTTTCTTCCATGGC	1
M00764_CNTN4_MIP118	ACTCGGGTAAGCAAGTTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAACCTAATTGGATTCA	1
M00764_CNTN4_MIP119	GTAGGCTTAGGCCTTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAATTCACCATTCTCCC	1
M00764_CNTN4_MIP120	AGACTTTAAGGCAATTTTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCCAAACACTGATA	1
M00764_CNTN4_MIP121	ACTCTTTAGATCACTAAACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATAGTGAACCTCTC	1
M00764_CNTN4_MIP122	CACCTATAACACTAAGCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGTAGCATCTTTGGC	1
M00764_CNTN4_MIP123	CGTCTCCAAAACCTGTTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTCTTGCATAATAAT	1
M00764_CNTN4_MIP124	CACTCAATGACAACTTCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACAGACCAACACATTTT	1
M00764_CNTN4_MIP125	AAGAGCCAAACATGCATGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTATAACAACAAAAG	1
M00764_CNTN4_MIP126	CCAGAGCATCTTGGTCCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGTTGCAGGAACAT	1
M00764_CNTN4_MIP127	CAACTGCTACAGCTTAACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTTCACTCACATTTCA	1
M00764_CNTN4_MIP128	GCAGTCATTAATACTGTTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTAAGTCAAGTGGT	1
M00764_CNTN4_MIP129	CGCTGGGAGTTATACCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAATGACAGAACTAATT	1

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ID	MIP	*c*
M00764_CNTN4_MIP13	CCTGGCCTGTCGCTCGCCGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGGGGCGGTTGTCT	1
M00764_CNTN4_MIP130	GATTTAGTAACGTTGATGATTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACACGAGGACACAT	1
M00764_CNTN4_MIP131	ATCACGGCAAACATGATATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAAGGTAATGGCTAAC	1
M00764_CNTN4_MIP133	ATTAAAAACTCAAGACTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAATTTTGAGAATTATA	1
M00764_CNTN4_MIP135	CATAGCCTGGGTGCTTTATAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCTGTCCCATTTATTC	1
M00764_CNTN4_MIP136	CCTTAAAACTGACAAGGTTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTTCCAGCCCATGC	1
M00764_CNTN4_MIP137	CATATGCTGGTGATAACTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATACAGCCTGGATG	1
M00764_CNTN4_MIP139	ATCTGAGAACAGATACATACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAACCAGGCTAGT	1
M00764_CNTN4_MIP140	CAGGTAACGCATGATCACTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCACACAAGCTCACAG	1
M00764_CNTN4_MIP141	CCAACAGTGACATCCATACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCCTCCAACTCTTTC	1
M00764_CNTN4_MIP143	CCCTACTTTATCAGCAGGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTAACAGGCCATGG	1
M00764_CNTN4_MIP144	AAAGTGGCTGCAATTACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATCAGGTCTGCAGCAG	1
M00764_CNTN4_MIP145	AATTATGGGAAAAAGTCAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTGGACAGGCTATCT	1
M00764_CNTN4_MIP146	AAATCACAGATACCACTGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAATGGGTCAATGCC	1
M00764_CNTN4_MIP147	GGAAAGAGCAAGACCCCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTCCTGGCTTGAATG	1
M00764_CNTN4_MIP148	GTGGCAAGGAACGTCTAAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCATCACCATGTAT	1
M00764_CNTN4_MIP149	ACATTCACAGCGACCGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATACAATAATGATGAGGA	1
M00764_CNTN4_MIP15	GTGGGTGAAAAAGAACAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTATGTCCTTTAGAGA	1
M00764_CNTN4_MIP150	CCCATCAATGAGTTCTGGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTCTTCTGTTCTCC	1
M00764_CNTN4_MIP151	GTTTGAATTCTTGCTGCTCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGCCAACGTGATT	1
M00764_CNTN4_MIP152	GCTGGCAGAACAGATGATCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTCAGCTGGGCTTCT	1
M00764_CNTN4_MIP153	CCTTTCTTCATTGGTTCATTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGATAGAAATCAGG	1
M00764_CNTN4_MIP156	ACAGGATTACCCCATGGTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTGCTGACTGGTCT	1
M00764_CNTN4_MIP157	GTAAAGCAAGAGGCCTACATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAACATCGTGCTCAT	1
M00764_CNTN4_MIP158	GTACGGCTGACCCTGATGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAGTAGGGTCAGAACT	1
M00764_CNTN4_MIP159	GGAAGGTTGCCTGGCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACCTCCCAGGTTATAAC	1
M00764_CNTN4_MIP16	GCTATTAGGCAGACTTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAATAAACTTACGGGT	1
M00764_CNTN4_MIP160	CCTCTGTTTTTAACAGTGAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGAGGCAGCAAAT	1
M00764_CNTN4_MIP161	GGAAACTTCCCAGCTATGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACTGTGATGGATTGAA	1
M00764_CNTN4_MIP162	GCTGCATGGCCAATTGATTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGTTGAGGCAAGTTT	1
M00764_CNTN4_MIP163	ACTAGTTTTCTCTGAAACAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCTCCTAAAAGAGGG	1
M00764_CNTN4_MIP164	GTTCTTCATGTTTTTGAAAGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAATTGGCTTTGC	1
M00764_CNTN4_MIP165	GCTCCCACCTCTTCTCTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTCAGAGGGAAGAG	1
M00764_CNTN4_MIP166	GTTGGAAATGTGGTTTTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCACTCATCCCTCCA	1
M00764_CNTN4_MIP167	GCCAAATAGACAAAAGATCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTCTTTGATGGGGCA	1
M00764_CNTN4_MIP168	ACTGTTAACAAAACGCCAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTTCAGAGCTGGGT	1
M00764_CNTN4_MIP169	ATTTAGGGCTTGCAGTCAGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGGTGGTCTTCAG	1
M00764_CNTN4_MIP17	GATCAAAAACAAGTTTCATGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTGGGTGGCATTCA	1
M00764_CNTN4_MIP170	ATCTGGATGCTGACAGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTGCATTTGAGTGAA	1
M00764_CNTN4_MIP171	ATTTTACCGTAGGGCCGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGGGCCTTCTCCTTT	1
M00764_CNTN4_MIP172	CATTGACTGTTAATATTTCTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGCGTGCACCCCT	1
M00764_CNTN4_MIP173	GAATCGTCCTTAATGATTGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAAGATACTGGCT	1
M00764_CNTN4_MIP174	CATATGTGCCTTGGGTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTACAGAACCCACCAAA	1
M00764_CNTN4_MIP175	GCCTACCTCATAACCTTGTATTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTGGAAGCCAGG	1
M00764_CNTN4_MIP176	CAGGTAATTTTGTACGCAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGATTTCCAACTGT	1
M00764_CNTN4_MIP177	GTGCAACAGTCAATGTGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGAAGAAAATGCTAGA	1
M00764_CNTN4_MIP178	GGGGCCTGTCCCAGCAGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATGCAAATGATCATTGG	1
M00764_CNTN4_MIP179	GAATTCGAGAGTGGAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATAATTTTGGAGTCTGA	1
M00764_CNTN4_MIP180	GCTGTGAGTGGGGGCAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACATCATATGGAATTC	1
M00764_CNTN4_MIP181	GAAATTACCTACTTTGTATCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTTGGAGGCAGCG	1
M00764_CNTN4_MIP182	ATATGGAGCATTCATTTGTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAAGAAAGCTCCAC	1
M00764_CNTN4_MIP183	ATTCCAAAGATATCAAGTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCACATCTGTCAT	1
M00764_CNTN4_MIP184	CGAATTTGTTCACTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCTATTTTAAGTCTGC	1
M00764_CNTN4_MIP185	GCAGAACTGCATGGATTCTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGTACATGCATTCGAA	1
M00764_CNTN4_MIP186	GTTATCTGAAGGACTTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGAATTTGTTCTCTCT	1
M00764_CNTN4_MIP187	ACTGGACCTAGCTGTGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACATTTTTATTCCAGT	1
M00764_CNTN4_MIP188	GTTTCTTTGGAAACTCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAAGACACCCAGTAC	1
M00764_CNTN4_MIP189	AGACAAAGCTAGATTTGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTTTAAAAAATTCTAT	1
M00764_CNTN4_MIP190	GGGCAACACAATCATGCAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGTTACCAAAGCAGTT	1
M00764_CNTN4_MIP191	CATTTTACAGCCGAGGAAAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTCTGCCATGAGA	1
M00764_CNTN4_MIP193	AAGTGCATTAACCACTAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGCTTTTGAGATTGC	1
M00764_CNTN4_MIP194	CATTGTCTTTGTGGTAGCATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGATGGTTTCAGGAA	1
M00764_CNTN4_MIP195	CCTGTACAATGCTAAATTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAGACTTGGTTGACT	1
M00764_CNTN4_MIP196	GTAATTCTCTGTCAATGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATTTGAAGTAACATAT	1
M00764_CNTN4_MIP197	GATAATAAAATGATCTTTTATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAAAGAAGGGCTC	1
M00764_CNTN4_MIP198	ACAATTGTATGGTTTCTTGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTATCTCTGTAATA	1
M00764_CNTN4_MIP199	GAAATAGGAGCAATCTTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCTAGAAGGTAAAGC	1
M00764_CNTN4_MIP200	CCCTACTGGACAGTGACATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGCCTAGTTGCTTTAT	1
M00764_CNTN4_MIP201	GTTTTGTTGATATTGTCATTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTGGCAGCATGTT	1
M00764_CNTN4_MIP202	ATAAAGACATAATCGGGATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTATAAACATTTTCTCA	1
M00764_CNTN4_MIP203	ATAAAGTCATAATCGGGATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTATAAACATTTTCTCA	1
M00764_CNTN4_MIP204	GCAAAAATGACAAACTATAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAACACAGCTTGAAAT	1
M00764_CNTN4_MIP205	AATGACACCCAGGGAGTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAAAAAAATATTGTCAG	1

continued table…

ID	MIP	*c*
M00764_CNTN4_MIP206	GCTGATTTTTTTTTTGCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAATGACAGAATATTT	1
M00764_CNTN4_MIP207	GTGCTAGTTATAATTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACCAGTGATCTAGCATA	1
M00764_CNTN4_MIP21	GTATTTAGCAATTCAGATAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAAACGCACAGTT	1
M00764_CNTN4_MIP22	ATTTTTAATTATCAGTTGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGGCTTTAAATATT	1
M00764_CNTN4_MIP23	GAGCCAGGCCGGGCACGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAATTCTCCAGTATAT	1
M00764_CNTN4_MIP24	GAGCCAGGCCGGGCGCGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAATTCTCCAGTATAT	1
M00764_CNTN4_MIP25	GAAATTATCTGGAAAAATTGGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTGGCAGTGTTT	1
M00764_CNTN4_MIP26	GTGGATTTTATAAGCTCGGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACTTCGCTAACTGA	1
M00764_CNTN4_MIP28	GCCATAAAATATTGCAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACCCTCATTTTATGTA	1
M00764_CNTN4_MIP29	GAGACAATTTCTTAAGAGGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATTCTCCGCCTTG	1
M00764_CNTN4_MIP31	ATTAGGACAAAGTAAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCTATGTCAATGATTCC	1
M00764_CNTN4_MIP32	CCACAAGGGAAGATTTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCCATAAGCCTATCTA	1
M00764_CNTN4_MIP33	GGGAAGCTCTTGAAGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACATCAAAAACAATCTC	1
M00764_CNTN4_MIP34	GCTTTTGCCCAGACATGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAGTCAGGGGTTATAAA	1
M00764_CNTN4_MIP35	GTGTGCCATGCCAAACCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTCCACAGGCTACTG	1
M00764_CNTN4_MIP36	GGGACATCTAGTATTCTAAAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGGGACACTGGC	1
M00764_CNTN4_MIP37	CCCTAACAGACAAACCGAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACACCAGCTTTAGTTC	1
M00764_CNTN4_MIP38	CAGCAGCTCCCAAGAAGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGGAGATTAAGGCTT	1
M00764_CNTN4_MIP39	AGGTTCGATGCGAGGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATTGCCCATTGGGAAA	1
M00764_CNTN4_MIP40	CAAATGTGTTCAACCTTTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTGTTCCCCAAAG	1
M00764_CNTN4_MIP41	GTCCCATTATCTCCCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTGCTAATTATGTCGAT	1
M00764_CNTN4_MIP42	CAGCTGGGACTAGAGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACATGTTACAGCAAATC	1
M00764_CNTN4_MIP43	AGCTGCATTTGATTTTCTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCTGAAATCTCTGTT	1
M00764_CNTN4_MIP44	GCAAAGTCACATTCACATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCTATTTCCTTGTAT	1
M00764_CNTN4_MIP45	GTGCCAGGATGATTAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGCTGTTTCTGTTAAAT	1
M00764_CNTN4_MIP46	AAGATAATGCAACCACACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACTTCTTTTATACAGG	1
M00764_CNTN4_MIP48	GTGTTTCACTTCTAACATGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACAGAACAAGATAG	1
M00764_CNTN4_MIP49	GCCTTCAGGTTGGTTCATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTCCACCAGTGTTAAG	1
M00764_CNTN4_MIP50	GGGGAATGCACTATGCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAAGCTAATAAGACTCC	1
M00764_CNTN4_MIP51	GCAGAGACCACAAGGAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTATTATCTGCAAGAAA	1
M00764_CNTN4_MIP52	GGGAAAGTACCATTGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTTCTTTTAAGTTTTG	1
M00764_CNTN4_MIP53	GCTGGTACTGCAATCATTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATGTCTCTTCTTTCCC	1
M00764_CNTN4_MIP54	CATGGCAACCTCATCTTCAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCCGTCTAAAGTGA	1
M00764_CNTN4_MIP55	AAACCAAGTGGTGATCACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTATAAAGTCAACTCAC	1
M00764_CNTN4_MIP56	CATCTCTCTAGCTTTTGTCATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCTGCCAGCCTT	1
M00764_CNTN4_MIP57	CAGTTTCTCTTATTGAGAGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAATATTTATTGTG	1
M00764_CNTN4_MIP58	ATGCATGAGACTTATTTTGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGTAACGCCCAAA	1
M00764_CNTN4_MIP59	ACCTAGTCCTTCGCTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGTGGACTCAAATCATT	1
M00764_CNTN4_MIP60	AGCCATATATGGTCTACCTTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTATTGCTAATATAC	1
M00764_CNTN4_MIP61	CTTTATGACACTAGACAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTCATTTTGAGGAAG	1
M00764_CNTN4_MIP62	ACATTTTTTTCTGTGCTGTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGACGTCTCCCTTT	1
M00764_CNTN4_MIP63	CACTTCATCATAATCCACAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAAAGGGGTAGGCT	1
M00764_CNTN4_MIP64	AAATATAAGCCCTCTTATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACAACAACATAAGGA	1
M00764_CNTN4_MIP65	CATGGCCCGATTTTTATTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCTTACTATTTTTTGT	1
M00764_CNTN4_MIP66	AAGAATCCCTTCCAAATAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCACAATTGAGCTTC	1
M00764_CNTN4_MIP67	CAAATACTTATACAATGCTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTTGGATTCTGAGG	1
M00764_CNTN4_MIP68	ATAGCATGAAAAATCATTTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGAAATCCATACCAG	1
M00764_CNTN4_MIP69	ACAATTGTTAGCAGAGAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATGGAACAGATGTTGA	1
M00764_CNTN4_MIP70	GAGTTTGTCGCTGTGCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAAAATGAAACTGCTATA	1
M00764_CNTN4_MIP71	CAAAACTGCGTTGGTAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGTGCTTCTTGTTCTT	1
M00764_CNTN4_MIP72	CATGCTTCACTCTCTGTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAACAGATCTTGACA	1
M00764_CNTN4_MIP73	GTACCTCCAGAATGGGGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCTCCACATGGAGGG	1
M00764_CNTN4_MIP75	GTGGGATGAATTTCATAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTGACTGACTAGTTG	1
M00764_CNTN4_MIP76	GAAAAGTATTCAACCTCACAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTCCCTCGTGGA	1
M00764_CNTN4_MIP78	GCTATGCAAGTATGGGGCATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTGACACTCAGGA	1
M00764_CNTN4_MIP79	CCATTAACTGAGAAACGGGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAAGCCACCCTGGA	1
M00764_CNTN4_MIP80	ACACCTGATTAGCAAACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTATTATCTATAAAACAA	1
M00764_CNTN4_MIP81	AAATTACAGACCCAGGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTCCAGAGAAGTAAAA	1
M00764_CNTN4_MIP82	GGAATCTGTATATTGCCAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGTTCCAGTGCCA	1
M00764_CNTN4_MIP83	GTCTCTTGAGAAACAAAGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCACCATCATTTCTCAA	1
M00764_CNTN4_MIP85	GCCTCCTAAATTGCTGGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGTTGCTAGGACTACAG	1
M00764_CNTN4_MIP9	GTCGTCGGGGCCCTGAGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGCTGACTTGAAGGC	1
M00764_CNTN4_MIP90	CAGGCTAGAGTGTGGTGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTACAATTATGCCCAA	1
M00764_CNTN4_MIP91	ATAAGTGTGCCATTGGCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAAAGAAATAACTGA	1
M00764_CNTN4_MIP92	CCACTTTTCCTATATCCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACATCAAATGCCTGTA	1
M00764_CNTN4_MIP94	GTGGCCACAACTTTTACTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAATTAAATTATCTCT	1
M00764_CNTN4_MIP95	ATTTAATCCAGGCAAATGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCTGCAGTATACTTC	1
M00764_CNTN4_MIP97	GCCCCTTTATTTATTCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGCTAGAGATAGGAC	1
M00764_CNTN4_MIP98	GCCCCTTTATTTATTCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGCTGGAGATAGGAC	1
M00764_CNTN4_MIP99	AACTCATTTTTCTGTTAATGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTTTTGCAGTCG	1
M00764_COL20A1_MIP110	CTTCCCTAGGCAGGGTGGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGCAGGGCTTCCCA	1
M00764_COL20A1_MIP111	CAGACTGGAGCATCTGAAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGCCAGGAAAATTCT	1
M00764_COL20A1_MIP112	GCATTCGCTTTATAGATATACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTCCTCTTTTGTA	1

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ID	MIP	*c*
M00764_COL20A1_MIP113	GTCGATTCTACAGTTCACTGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGATGGCTGTGTTT	1
M00764_COL20A1_MIP114	GTCCTCTTTTTTGTTGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGTTGAATCTTCTCATC	1
M00764_COL20A1_MIP115	GATGAAGGAGAACCGAGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGAGAAAGAAAACTGG	1
M00764_COL20A1_MIP116	GTCTTGATCACTCAAATTTCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTGACCGCTGTGT	1
M00764_COL20A1_MIP117	AAGGTGAAGTGTTTATTTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTTCTGTTAGGCCAA	1
M00764_COL20A1_MIP118	AGACAGGTGCATTTTGTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTAATGGTGTTGGTGAA	1
M00764_COL20A1_MIP119	CGCTTCCAGGACAGCACTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGACGCACAGTCATTTC	1
M00764_COL20A1_MIP120	CATGTGCTGCAGAGCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGTGCTGTTATGGACATA	1
M00764_COL20A1_MIP121	ATAACGAGAATTCAGCGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTATCTTTTGAACAAAGC	1
M00764_COL20A1_MIP122	AAAGTTTTCTGTCTCTTCCATACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTTGGAACCTCAG	1
M00764_COL20A1_MIP123	GACTCAGGTTTTATGGGAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAACTCTGGGTTCTA	1
M00764_COL20A1_MIP125	GTGAAGCCAGTTCCAACCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACCGACATGGAGACA	1
M00764_COL20A1_MIP136	ACTTCTGTGTCTATGCAGGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATGGCCTGAAGGAG	1
M00764_COL20A1_MIP138	ACCACCTAGGGACTTCCTGTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGTGGGGCCCACAG	1
M00764_COL20A1_MIP139	AGTAGGAAGTCCCTGAGCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCAACAGGAAGTCCA	1
M00764_COL20A1_MIP140	GACTTTCTGTTGACTGCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTGTTGACCCCCCT	1
M00764_COL20A1_MIP141	GAGTGGTAAACAGGAAGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGTCAATAGGAAGTC	1
M00764_COL20A1_MIP142	GTGTAGCTAAGGGCTGGTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTGTTGGCCACTCAG	1
M00764_COL20A1_MIP147	GGACTTGCCTCTGGCTGTAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGAAAGCCCCATCC	1
M00764_COL20A1_MIP148	CATCTCTGCTGACTTCTTTTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGACCACAGGCTCC	1
M00764_COL20A1_MIP151	GAAGGGAAGGTGGTGCAGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTGTGAGGACAGAC	1
M00764_COL20A1_MIP170	CGGTGTCCAGACAAACCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGAACTTGGAAATGCT	1
M00764_COL20A1_MIP174	CAGAGAAAGGGGCGGGGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGAGTGCTGTTCTGAG	1
M00764_COL20A1_MIP176	GGGACAGAGGGGACGATGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACCCTAAGGACCAGG	1
M00764_COL20A1_MIP177	CCTGGACTTCCTGCCTTATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACTTGGCACCATCAG	1
M00764_COL20A1_MIP178	ATGGTTGGGAGAGACCTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAAGTTCCCACATCAC	1
M00764_COL20A1_MIP180	CCTCTTCATTTCTGGCACCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGGGGTATGCTTTG	1
M00764_COL20A1_MIP181	ACCAAATAGAGAGTCATAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCCACCAAGATCACC	1
M00764_COL20A1_MIP182	AACAGTTGAATCATAGATGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCATTTGGGGCT	1
M00764_COL20A1_MIP183	ATTTTGCACTGAGGGACAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACTGAGGCCAGGAAG	1
M00764_COL20A1_MIP184	GACTTCTTCGACGTCTGATTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTCAACAACTGTGT	1
M00764_COL20A1_MIP185	GCAAAACAGCTTGGTTGCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCAGTGCAGGTATC	1
M00764_COL20A1_MIP186	CTCCCCAACAGAAGCCAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCCTGCTCACTCCA	1
M00764_COL20A1_MIP188	GGAAGGCTCTGGATGCCCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGTGGGGATTAGAGC	1
M00764_COL20A1_MIP190	GAAGACAGCCGGACTCCCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGCTCCACTGCAC	1
M00764_COL20A1_MIP199	ATGTGTAGCAGGAGGCAGGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCCTTCACAGCCC	1
M00764_COL20A1_MIP20	CCCCAGCTGCTCCCCTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTGGTGGTCAGTATCAC	1
M00764_COL20A1_MIP201	CCAGGGCAGTGGGGACGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCTGGCCCAGGCAG	1
M00764_COL20A1_MIP203	ATGGTAAGTACAGAACTCCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGGGCAGATGGTGG	1
M00764_COL20A1_MIP204	AGATCACGATGGGGGGCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGTTCTGAACAGCAGG	1
M00764_COL20A1_MIP205	ACCCATGACTCCACAGTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAACTGGGCCATAAGA	1
M00764_COL20A1_MIP206	GTCTTTTAGCTTCTAGAGGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGGTACCACTGCAG	1
M00764_COL20A1_MIP207	GCTGCAGCACAGAGATTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGCATTGAGCCGAGATC	1
M00764_COL20A1_MIP208	AAAACAAGAAAACAAAACAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTTCCTGCTACTC	1
M00764_COL20A1_MIP209	GGAGCAGGAGGACCACTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATCGTTTGAGCTCAGAAG	1
M00764_COL20A1_MIP21	CGGAGGGAGTTTGTGAGTAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACTCGGAACAGGA	1
M00764_COL20A1_MIP210	AAAATACAAAAAACATTAGCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGGGCCGGTGAGG	1
M00764_COL20A1_MIP211	GGAGGCCAAGGAGGGTGGATCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACTAATGAATGCAC	1
M00764_COL20A1_MIP212	GGAATCTTCCCTAAAAACTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTGATGGCAAAAACT	1
M00764_COL20A1_MIP213	CCCAGCCCTTCATCACAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTGGCTTCCCTAAAT	1
M00764_COL20A1_MIP214	CCCTGCCCTTCATCACAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTGGCTTCCCTAAAT	1
M00764_COL20A1_MIP24	AGCCCAGAACTGCTTCACACATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCACATACACCCC	1
M00764_COL20A1_MIP27	GTTTCCCACATTTCCCACCATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACGGGGAGCCCAGA	1
M00764_COL20A1_MIP76	GGGCAGTGTCACGTGGCTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTCTACCTGGGTCT	1
M00764_COL20A1_MIP8	GTCTAGATAGAGGCCAAGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGAGGACTGGGGTC	1
M00764_COL20A1_MIP85	CCATCCCAGGTCACATCCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATGAGGCCACACTGG	1
M00764_COL20A1_MIP93	GGGAAGGGGTGGAGCAGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCACCAGGACCTTG	1
M00764_COL6A6_MIP1	CCCAGAACTGCATGAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACACGTTTTTTCCTTTTCC	1
M00764_COL6A6_MIP10	CATGCTGAACCACCTAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAAATGTTCATCACCA	1
M00764_COL6A6_MIP100	AATTCAAAGGTGAAAATTCAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGGTTCCCCAGG	1
M00764_COL6A6_MIP101	CAAATGTGCATGCCTTCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCAGGAGAGATGGGA	1
M00764_COL6A6_MIP102	AAAGGAGCCAAAGGCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTACAATTTAATGAGA	1
M00764_COL6A6_MIP103	ACAAACAAAACATTGTTTTAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAACTGCTAGGCCC	1
M00764_COL6A6_MIP104	CCTGCTTAAAATGATCACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGCTCCATTCAATTTAC	1
M00764_COL6A6_MIP105	GCACATACTGAATGAGCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGACATCTCCAATTT	1
M00764_COL6A6_MIP106	CCTGTCTGCTTTTTGTAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGATTAAAGCATGCTGT	1
M00764_COL6A6_MIP107	GCCTCATACTGGTAGCAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGGTGAGTAATCTTTA	1
M00764_COL6A6_MIP108	CTGTAATCCCAGCTGCTTGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGCACTTGGGAGC	1
M00764_COL6A6_MIP109	CTGTAATCCCAGCTACTTGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGCACTTGGGAGC	1
M00764_COL6A6_MIP11	GGCTCCTGCCTTTGAAGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAACTGTTTCTTGTCT	1
M00764_COL6A6_MIP110	AAACCGGAATGCCCAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGTTTTAATACTTAAAT	1
M00764_COL6A6_MIP111	CCTAAAAGACCATATCCCTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGACCTTAATGTCTCT	1
M00764_COL6A6_MIP112	AGTCAACTTCTCAGAGAAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATGGCTTTCCTGGT	1

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ID	**MIP**	***c***
M00764_COL6A6_MIP113	GTGCCTGGCGTGGGAGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAAGACATTCCTGGAAA	1
M00764_COL6A6_MIP114	CACCACGGCTGCCATGGAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCAGGGAGATTGGCA	1
M00764_COL6A6_MIP115	CGGACTGACCGCTGCTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTGAAAGGTTTCATCCT	1
M00764_COL6A6_MIP116	AAATTCTGGATTGGCAGAGTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGCGCGCATTTG	1
M00764_COL6A6_MIP117	CAGCATGTAAGCATGGCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATCTAAAAGAAGCAGA	1
M00764_COL6A6_MIP118	GTAAGACCCACAGAGAGAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAGTTCTTTCTGCTGC	1
M00764_COL6A6_MIP119	CGCTGGAGTCTCTCTAATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCTCCCAAGGCCATA	1
M00764_COL6A6_MIP12	GTGAAAATCATCTCTGTAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGACTTATTTCTCTGC	1
M00764_COL6A6_MIP120	GACATTTGGAAACTGCATAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGACTGCACAGGGG	1
M00764_COL6A6_MIP121	ACTTTGAAATCACCCCAGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGTGACCAAGCCAGA	1
M00764_COL6A6_MIP122	GTGCTCCAAGGAAGGCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAACTCAGCTCTAACT	1
M00764_COL6A6_MIP123	CCTTACAGTGGACTCTGGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCCAACACTCAGAAG	1
M00764_COL6A6_MIP124	GTTGTTTAACTGACTCGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCTAAGTGGCTGGTT	1
M00764_COL6A6_MIP125	GGATGACAAGGAACTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAACAAAGTCATATTTG	1
M00764_COL6A6_MIP126	AATAGGGCCAAGGGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGATTGAGTTTATAAAGG	1
M00764_COL6A6_MIP127	AACCTCTTGTCTGTCTTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGTGAAGTTTGTGAA	1
M00764_COL6A6_MIP128	ACTTTTCTCTTCTAGGTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTTTCATTTCATGTG	1
M00764_COL6A6_MIP129	CATGACTGTTAACATTACTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCGGAATGGTCGTG	1
M00764_COL6A6_MIP13	GCAGGGCCTTTGATGCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTGGGAAAACATGCTG	1
M00764_COL6A6_MIP130	GCTTTTCTTCCTCCTCCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAACAGACTTAACTCT	1
M00764_COL6A6_MIP131	GTTGCAGCCTTCCTCCAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGCTTTAAGTGGTCCA	1
M00764_COL6A6_MIP132	GAAGTGGCAGAGATGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTATCTTCTATGATGT	1
M00764_COL6A6_MIP133	ATTTTGCCTTCTGTAATACATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTTGGGAGCACTT	1
M00764_COL6A6_MIP134	CAGAACTCAAGCAACAGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCATACCTTTAAGAAT	1
M00764_COL6A6_MIP135	GTCCAGAGTCTTACCATGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATTGTCAGGAGTGG	1
M00764_COL6A6_MIP136	GTGTTTTGAAAAGTCTAATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGACCCCCTGCATTC	1
M00764_COL6A6_MIP137	AGTTCTTCGACATATCAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACAGAGATAAAAGAAT	1
M00764_COL6A6_MIP139	GATGAGCATTAGACATTACTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCACAGTGGTGTGT	1
M00764_COL6A6_MIP14	CATCTTTGTAGAAGGTGGGCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAGGCCATGGCCA	1
M00764_COL6A6_MIP140	ATTATTGCTTTTGAGCTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTTCTATTCCACTTA	1
M00764_COL6A6_MIP141	AGTTTTTCAGTGAGTTCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACAGGAAAGACAGACT	1
M00764_COL6A6_MIP142	GTTACTTTTACCCATCAGGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAAGCCCCCATTTT	1
M00764_COL6A6_MIP143	GTTTCTTGACTCTCCTTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCTAAACTCAGTGTG	1
M00764_COL6A6_MIP144	GAGTAAGTTAAAGTAGGAAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACCAAAACAGGATT	1
M00764_COL6A6_MIP145	GATCTCTTTTGCATCTCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACTGAGGTAAGGTCTG	1
M00764_COL6A6_MIP146	CCTGGATGCATGGAGCAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGATATTTTCAACAA	1
M00764_COL6A6_MIP147	GGGCTTCTTTCCATTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAATAGCAGAAGTCGTT	1
M00764_COL6A6_MIP148	GAGCAAGAAGTTCAAGGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCAGATTTTCTTTCCT	1
M00764_COL6A6_MIP149	ACATGAGGTGCTATCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGAAACATTTTTCTGA	1
M00764_COL6A6_MIP150	CACGAACTCCTTTCTTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTTTGCTTCATCTAT	1
M00764_COL6A6_MIP151	AGAGTTAACTAGAAAAATCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAAAATAATCTGTC	1
M00764_COL6A6_MIP152	GTATTTTCCCTGATTTACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATAAAACAAATATTC	1
M00764_COL6A6_MIP153	AAAGGAACTTCTATTTGCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCTGGCTTGTGTGA	1
M00764_COL6A6_MIP154	CATTATCTCTGCACTGAGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTGGAAACAGCAAA	1
M00764_COL6A6_MIP155	AGGCAGTTCCTTTACAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGTTTTAAAAAAAAGTT	1
M00764_COL6A6_MIP156	GTCAGCCCACTCCATTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCATCAGATTGTAATAC	1
M00764_COL6A6_MIP157	CACCCATTCTTCTCTGTCCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTGGACTTCAGCCT	1
M00764_COL6A6_MIP158	GTCTTAGCAGACATTAAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTTATCTATCTAATGG	1
M00764_COL6A6_MIP159	GTCAGATTTAGAGTCTCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATGGACTAACTAGGC	1
M00764_COL6A6_MIP16	GTGAGGAGAACTTTGACTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCTAATGCTCACCA	1
M00764_COL6A6_MIP160	GGGTGTTCCACATCCATGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATCCACTAAGCTATC	1
M00764_COL6A6_MIP161	AGCCAACTGTACTTAGTTTTTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTATTGTTTAGAG	1
M00764_COL6A6_MIP162	AGTATATGAGAAGATGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGAAGGATGGTTGTGTC	1
M00764_COL6A6_MIP163	CATAATACACTGTAAATGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGGACCTCCCAAGG	1
M00764_COL6A6_MIP17	GGGCCTTGGCAAGCTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACCCTCATGCAATTTTC	1
M00764_COL6A6_MIP18	CCTTTCTCCCCGAACTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTATCTGCCCTTGACA	1
M00764_COL6A6_MIP19	GTATATGCTGGAGAACCTCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCAGCACGGCAATC	1
M00764_COL6A6_MIP2	GTGTCCTAACTGTGAACCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACTGTTTCAGTTAGG	1
M00764_COL6A6_MIP20	CGACACCCAGTTGGAAAAGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCAGGGGGTGCCCC	1
M00764_COL6A6_MIP21	GCCCTCTATGCCCAGGGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTTATTTGGTTCCGCA	1
M00764_COL6A6_MIP22	GATTCTTTTTTTCTTCTCTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTGCTCACAACCA	1
M00764_COL6A6_MIP23	AGAAGAAATGAGAGCACATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTTCATGGAAATCTG	1
M00764_COL6A6_MIP24	ACTTGGAATTTGAGATCAATAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCAGGGAGCACC	1
M00764_COL6A6_MIP25	CCAGCTGTCAGCATACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTGCAACAGACTCAGTG	1
M00764_COL6A6_MIP26	CAGACTGAGAGAAGAGCACATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCGCAGCACTGAATT	1
M00764_COL6A6_MIP27	CCAAGATGCTATCCTTGGACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAAAGTCATGCACG	1
M00764_COL6A6_MIP28	CAAATTGCTATCCTGGCAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGGAAAAGAGAGTG	1
M00764_COL6A6_MIP29	GAGTAAACAGGAAAATCCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAAGTTTTCAGGT	1
M00764_COL6A6_MIP3	CCCCAAGACCTATTTCATAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGAAGGAGCCAGAT	1
M00764_COL6A6_MIP30	GGAAGAGTTTCAGCTCAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGTTCTGGAAGTATAG	1
M00764_COL6A6_MIP31	GATGTCGCTGAACTGGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAGTACTGAGACACAA	1
M00764_COL6A6_MIP32	GTGCTTCGGCAAGAAGGTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGGTAGTGCCCTGAG	1
M00764_COL6A6_MIP33	GCTGGTTCCTTTACTATGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCAGAATGTCAAAATT	1

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ID	MIP	*c*
M00764_COL6A6_MIP34	CATACTCACTAGCAGGACTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACCCAGCTTGAGGA	1
M00764_COL6A6_MIP35	CACGGGGGCTGCATATTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGGAGAAACATTTCA	1
M00764_COL6A6_MIP36	GTTGTGTTTGTCATTGATAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCTTGGAGAGAAAA	1
M00764_COL6A6_MIP37	CAATCCGCTTGCATTCTGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACCGGACCTGATTC	1
M00764_COL6A6_MIP38	AGCCATGGGTGGCAGTACTTATACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCTGATGTGGGCA	1
M00764_COL6A6_MIP39	GTCATTCTGGAGCACTGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCCCATCGGTGATCA	1
M00764_COL6A6_MIP4	GTTTTCTCTAAGGCATTTCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAGGAACGCGTAATA	1
M00764_COL6A6_MIP41	CAAGGCCTTTGCCGTGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAATATTCCCTTCAGAC	1
M00764_COL6A6_MIP42	ATGAGAGAGAAAGCAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACTTCTTCGTGGAGAC	1
M00764_COL6A6_MIP43	GGCATCTGTTGTTCAAGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATCTGGGTTTTCTGT	1
M00764_COL6A6_MIP44	GAAGTCATTTGGCTGAATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTATGAAAGTTCCCA	1
M00764_COL6A6_MIP45	CATTACTTCAGGCCAGACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCGATACCTATCACCC	1
M00764_COL6A6_MIP46	GTGTGTTTCCAAAGATCTGCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGCCACCTCGTCT	1
M00764_COL6A6_MIP47	CAGAGAAAAAACTGACAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACAGATGGCCAGTCC	1
M00764_COL6A6_MIP48	GTCCCGGTGATCTGAATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGGGAATCGAATGAAGA	1
M00764_COL6A6_MIP49	ATTTCAAATTGAGCTTTTCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGGGTGAAAGCAGTA	1
M00764_COL6A6_MIP5	GAGTTTTTCTTGTCCCCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATACAAGAGCATACAAAA	1
M00764_COL6A6_MIP52	GTGTTCCAACTTTATAACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAGAACTTCATTATA	1
M00764_COL6A6_MIP53	GAAAGAGGCTAAGAATCAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGAAAAGCATGTCTT	1
M00764_COL6A6_MIP54	AAACCTACCTTCAAGACATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCGTTTGTTGATTTAT	1
M00764_COL6A6_MIP55	AAGCAAAGTCTGCCCTTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGGCATTGGTCACTT	1
M00764_COL6A6_MIP56	ACCTCTTGGATTCTCTATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTCAGTGTGGCTTTT	1
M00764_COL6A6_MIP57	GCATTGAGAAGAGATGGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAAAAAGTAAAATGAA	1
M00764_COL6A6_MIP58	GATGTTGAGAAACTTGAACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGAGGAAAGGTAACA	1
M00764_COL6A6_MIP59	CATCCAATCCATCTGAAAATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAATTTAAGAGCC	1
M00764_COL6A6_MIP6	ATGTTGCTAATTTTGTTCCTCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAATTTATTATATA	1
M00764_COL6A6_MIP60	GCTGATTCAAGTGACTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTTCACTGAGAATAACA	1
M00764_COL6A6_MIP61	GGTCCATCCAGAGCAACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAATAACTTACCAGCTG	1
M00764_COL6A6_MIP62	GGAGTGAAGAAAGGTTTTTATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTGGAAGCCGGCTG	1
M00764_COL6A6_MIP63	CCATTCAAATGACTGTGCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTTCAGCAACATTGA	1
M00764_COL6A6_MIP64	CAGGGAAAAGGGTGATTTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAAGCAATACCACCA	1
M00764_COL6A6_MIP65	CCCATTGTGCCATCTCCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTCTATTTAGAAGT	1
M00764_COL6A6_MIP66	CAGAGACATAGCCCTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAAAATAGACCACACA	1
M00764_COL6A6_MIP67	GTTTAGAAAGAAGCTCTGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAGAAAGAATGGAAA	1
M00764_COL6A6_MIP68	CAGGGCTCTTTTTTACCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTTGGTTTGGTTACC	1
M00764_COL6A6_MIP69	CAGCGATTCCCTCCTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAGATCTGAGATTCTG	1
M00764_COL6A6_MIP7	GACCTGAAAAATCTTCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACTCATGTATTATCTAT	1
M00764_COL6A6_MIP70	GCTTATAAAAACTAAGAGTAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGAGAAAGGGCA	1
M00764_COL6A6_MIP71	GATGCTATGGCACCAAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGTAACAAAAAACTTGT	1
M00764_COL6A6_MIP72	GTACCTTGCTCTCCCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAGTCCTCTGTTTCCCT	1
M00764_COL6A6_MIP74	GAGGCTGGGCCTGGGTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTCCATTTTCCCCAAC	1
M00764_COL6A6_MIP75	GTGTAAAGAAGTCAGATGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATAGCTCAGAAGGGT	1
M00764_COL6A6_MIP76	AAGGAGAAAAGGGAGATGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGGAGAACAGGTAGAG	1
M00764_COL6A6_MIP77	CCAGGAAGACCATTATCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTTTTGTAGCAATAGC	1
M00764_COL6A6_MIP78	CCCTGGTGTGAATAATTAAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGCCCTTTGCTCC	1
M00764_COL6A6_MIP79	ATAGTAACCCTGAGTTTAAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTCCTGGTGACCG	1
M00764_COL6A6_MIP80	GTACCTTGAAATCGAGACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAAAAGACATGTAAGG	1
M00764_COL6A6_MIP81	AGCTCCTGGAGTTGACAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTATTTCTGCTTTCAAAT	1
M00764_COL6A6_MIP83	CACTGTTTTGGTGGCTCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCAATGCTGCATAATT	1
M00764_COL6A6_MIP84	ACATACATAACAATTCCCACATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTGGGCCTGTAT	1
M00764_COL6A6_MIP85	CCTTTTTGATGATATTGGTTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGCTCATGGCAG	1
M00764_COL6A6_MIP86	GGACTTGAAGGCTCCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTGCATTGACATTGTGA	1
M00764_COL6A6_MIP87	GGTCCTGGGATGCCTGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGATTTGAAGGTTTCTA	1
M00764_COL6A6_MIP88	ACTTAGGGCCCAAGAGGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAAAGGCATGATTGG	1
M00764_COL6A6_MIP9	GAACGAACCAAAAACTTTAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGACTGCTGATCAT	1
M00764_COL6A6_MIP90	GTTTTGTTTCAGGGGCCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATACTTTTTCCAGAG	1
M00764_COL6A6_MIP91	AGGGGTTTGCAAATATAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCTCTTGAGCAGAAA	1
M00764_COL6A6_MIP92	CGTGCAAGTGATACAAGAGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGATCTCCAGGTTCT	1
M00764_COL6A6_MIP93	AGTAGACATCTGGTGTGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTTCTGTTTAACAGG	1
M00764_COL6A6_MIP94	CAAGGGAGCAAAGGTAAGTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCAAAAAGCTGGCAA	1
M00764_COL6A6_MIP95	GACACTACCATAACCTGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGTCCAAGATTGCCTT	1
M00764_COL6A6_MIP96	CCTGTCCATTACAGGGACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCACTTCCAGATTTCA	1
M00764_COL6A6_MIP97	GGAAAGATTTATACAGGCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTACTGGCCTAGGATA	1
M00764_COL6A6_MIP98	GAAGGGAGCTAGAGGCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATGTTAGAATCAGTTT	1
M00764_COL6A6_MIP99	GCCCAGTCTCTCCTGGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTGCAAGTCACTGGTA	1
M00764_COLEC11_MIP1	AGCCCTATGCCAAGGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAAAATAATGGATTCT	1
M00764_COLEC11_MIP11	CCAACCCGGGCAGTCAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTCTACAAAAAAGCAGC	1
M00764_COLEC11_MIP13	GCCTGGGCAACATGGCTAAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGTCCAAGAATGGCT	1
M00764_COLEC11_MIP16	GATTTCAAATGACTTCCCTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATCAACCCTTGCCT	1
M00764_COLEC11_MIP17	AATCTGAAAAAAATCGCCTCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCGAGAGCCCACC	1
M00764_COLEC11_MIP18	GCTTTTGTAGCAGGGCTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTGGGAGAACTCCT	1
M00764_COLEC11_MIP19	GGACAACATGGTGAAACCGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTTCATCGTGAAGG	1
M00764_COLEC11_MIP20	ACTTGGAAAACAAGACCAGGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAACCCAGGGGCCT	1

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ID	MIP	*c*
M00764_COLEC11_MIP21	GTAGCCCTCCTGGTGCCTGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGATTCCCCCTCA	1
M00764_COLEC11_MIP22	ATGACGCCTGCTCTGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTTCCTCTGTGTAGGA	1
M00764_COLEC11_MIP23	ATGTCCAGATGGCAGCAGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTGCATGGGAGTCT	1
M00764_COLEC11_MIP24	ACCACTAGACCACCAGGGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTCAGATACCGCAG	1
M00764_COLEC11_MIP25	ATGTGGGCCCCTTGTTCAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGAAAGTCCCTGAG	1
M00764_COLEC11_MIP29	GGAGGGGAGTCACGTGGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCGAGGAGGGGAGGGGA	1
M00764_COLEC11_MIP3	GGTTCAAAGGTGAATATTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAAACAAATGTTAGT	1
M00764_COLEC11_MIP31	CAGTCACCACGAAAGACAAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACCTGAATCCGGT	1
M00764_COLEC11_MIP32	GATCATGGGTTTGAATCTACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCAGAGCTGCACA	1
M00764_COLEC11_MIP34	GGGCTGCAGGACAGTCCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACTTTCACCAAAACTT	1
M00764_COLEC11_MIP35	GGACTTTTGGCTGTGGAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTTGGATGCCTACGG	1
M00764_COLEC11_MIP36	AAGGTTCCACTCACAAACCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTGACCTGGCAGGG	1
M00764_COLEC11_MIP39	AAAAGGTACCTGCAGCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATCACTCTGAGACGCT	1
M00764_COLEC11_MIP4	GTGTGGCCAGGTCTCCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAACATGCAAGATTCG	1
M00764_COLEC11_MIP41	ATAACTTTGCAAAGTCTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTACAAAGGACGAGGTG	1
M00764_COLEC11_MIP42	GGCCACATGGCTTGGACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACATCTCCAAAAGGAA	1
M00764_COLEC11_MIP43	GCGATTCTTGCCTCATTTCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCACCTGTGCATCG	1
M00764_COLEC11_MIP44	CGACCCACACTGCCTTTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGACGAGACAATTCA	1
M00764_COLEC11_MIP45	CCTTGTTTTTTATTTTCAGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGAATGGGGCTC	1
M00764_COLEC11_MIP46	CCAAGTCACCAGGCAGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAAGTGCAATTTTTAAT	1
M00764_COLEC11_MIP47	AGATCAGTGTCACTGACTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGAGGGGCTGGATT	1
M00764_COLEC11_MIP49	GTTAAATGAGGAAAGGAATCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGCCCGGACAAAG	1
M00764_COLEC11_MIP5	AGTCCGGAAACTCACTCTACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATCACCTGGCACCAA	1
M00764_COLEC11_MIP50	GGCCTCCCATGTGAGTGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCGGCCTCAAAGGC	1
M00764_COLEC11_MIP51	CGTTACAAACGCTGGATGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGCCACATACCATT	1
M00764_COLEC11_MIP53	CAGCTGTCCTGCCAGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAAGTTTGTTGCACACA	1
M00764_COLEC11_MIP55	ACAATGCCTACGACGAGGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATACCTGGCGCAAGCC	1
M00764_COLEC11_MIP56	GCCACTTGTTGAAGGTCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACATGTTCTCCTTGTCA	1
M00764_COLEC11_MIP57	GTCCCTCTGTGAAGGGTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTACTTCATGTGTGAG	1
M00764_COLEC11_MIP58	CTCCCTGGCTGGCACCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAATGAAACTCTGCTTCT	1
M00764_COLEC11_MIP59	ATCTTTAAGTAGTGCAGTAGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGGGGTGCTGTCT	1
M00764_COLEC11_MIP6	CCAAAAAAGAAACAAAATTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGTCAGCTGCCCT	1
M00764_COLEC11_MIP60	GGACAAAGGCACAAGCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTAATTTACAGAAGTGT	1
M00764_COLEC11_MIP61	ACCCAGATTTCAGGAAAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTTGAATTACTACCTT	1
M00764_COLEC11_MIP7	CGTTTTTTGAAAAAATAAGCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACGCCTGGAACTC	1
M00764_CORO6_MIP1	GGGAAGGGGGTGGGAGGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCTGAGGTTCAGAAGG	1
M00764_CORO6_MIP18	CAGCGCCTACCATGCATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATAGGTTCACACTTTC	1
M00764_CORO6_MIP19	GGCGGGGGGATAAGACAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGTCAGCAAGTGTGAGAT	1
M00764_CORO6_MIP20	CAGCAGCCTTGGCCCCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTTTGAGATTACCGAC	1
M00764_CORO6_MIP21	CCCTGTTCTCCCTGCCCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAACGTGTTCAGGTAGTG	1
M00764_CORO6_MIP22	GCCCCTGAACCGACTGATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAACGGGGTCCTAT	1
M00764_CORO6_MIP3	GACCTGGCGATGCACTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTCTCAGAAAAACAAG	1
M00764_CORO6_MIP31	GCCTGGAGAGAGCAGGAGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGAGCAACCAGCTT	1
M00764_CORO6_MIP39	GACCTGTGGTTGCAGAGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGAGTTTCCAGCTTCTC	1
M00764_CORO6_MIP4	GTTCTCTCGAGATTTCTTCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAGGAGGCACAGACT	1
M00764_CORO6_MIP41	GTGGTGGCTAGCAGGCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATGGTGGGTACAAGGGT	1
M00764_CORO6_MIP42	GCGCATCATTGACCCCAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCATCTGGAATGTGG	1
M00764_CORO6_MIP43	CATCTATGGGGGACCCCTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTGCATATCATCCA	1
M00764_CORO6_MIP44	GTGGGTGGTGGCAAAGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATTACGGAACCTATCA	1
M00764_CORO6_MIP45	CCTTCCCTACCTTTTTTTTTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCCCTCAAGTGTG	1
M00764_CORO6_MIP46	ACACCAGTCAATATCCAGCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCTTCCCCAGCACA	1
M00764_CORO6_MIP47	CACACAATGACAACGTTATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCCCCAAAAAACACA	1
M00764_CORO6_MIP48	GGGAACTCCTGAGCCTTTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCGTCAACCCCAAATT	1
M00764_CORO6_MIP49	ACTTGCTTTGCCGAACCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCCTCCACAATAATG	1
M00764_CORO6_MIP5	GGCATGAGGAGTTAGGTTCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGAGCCGGACCC	1
M00764_CORO6_MIP50	GGCCTACGAGGACATCCGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACAGGACTAAGGACCA	1
M00764_CORO6_MIP51	AGCAGGGAGCTTTCTTCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCCCAGAAATGCCT	1
M00764_CORO6_MIP52	GGACCAGACACTATATGGATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCTCAGCCTGGGT	1
M00764_CORO6_MIP53	CGCCAGCCTTGATGAGCATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGAATTCTCCACAGA	1
M00764_CORO6_MIP54	CCCAAAAACATTCCAACGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAATGGTCAAGTCTTC	1
M00764_CORO6_MIP55	CCTTTTCCTAAAATTTTGCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCTGTCCAGAAGC	1
M00764_CORO6_MIP56	CATCTGCCTGAACTATTCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACCTCACTCTGTG	1
M00764_CORO6_MIP63	GATTGAGGCTGGAATGCGGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCCCTCTCACTTGC	1
M00764_CORO6_MIP64	GCTGTGTGCTAGGCATTTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCCTAGAGAATGAGG	1
M00764_CORO6_MIP65	GCATTTTAGGTTTCTCAAATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGGGAGGGGAGGG	1
M00764_CORO6_MIP7	CCCCAGTTCTGCAGACACATACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGCCTGAGCTTGAC	1
M00764_CRBN_MIP1	GGGGACCTCTGTAGAACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTCTGAGTTACATAAAG	1
M00764_CRBN_MIP101	ACTGACCACTGCAATTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGATGGTAATGAAATGAA	1
M00764_CRBN_MIP102	AAGCCAAAGCAGGCTGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGAAGTCAGTATGGTGC	1
M00764_CRBN_MIP103	AAGCCAAAGCAGGCTGGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGAAGTCAGTATGGTGC	1
M00764_CRBN_MIP104	CACCTGACAGCTGTCGTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGAACAGCAAAGGTTC	1
M00764_CRBN_MIP105	ATCCTGATTCCCGGACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGATCATGACACTATACC	1
M00764_CRBN_MIP106	GAAATACAGGCCGGGCACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGTCCTGCCATGAAAT	1

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ID	MIP	*c*
M00764_CRBN_MIP107	GTGATTTGCTCTTTAGTCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAGGGTTCCACCATG	1
M00764_CRBN_MIP109	GTATTTTTAGTAGCAACAGGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGTGAGTGCAGTGG	1
M00764_CRBN_MIP111	GCAGACTGGTGTCAAAATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATCCACAATTTCTG	1
M00764_CRBN_MIP113	GTGAAGAGGGAGCCAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCTCTGCTATAAAAGTA	1
M00764_CRBN_MIP114	GTGCTGTAGAGTTTACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCATTCTGTACTATCTTT	1
M00764_CRBN_MIP115	GAAGGAATCAGTCTTGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCAACTGTGAATTTTA	1
M00764_CRBN_MIP116	GTGGCAAATGTACCATACTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGGGGACCTGATA	1
M00764_CRBN_MIP117	GTATCCCTCAACTGGGTTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTTTGCGTTCCAGG	1
M00764_CRBN_MIP118	CGAGGCTCGGAGCCGCTAGCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCCTTTGCGGGTAA	1
M00764_CRBN_MIP12	ACAAAGATGTTATGACTGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTACTGACCTGTATGCA	1
M00764_CRBN_MIP121	ATATTTTGCATATGGAGAAACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTACAGGCCTGCG	1
M00764_CRBN_MIP122	GAACAAAGTGAGGGCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGCTGCATGAACAGGTT	1
M00764_CRBN_MIP123	GAACAAAGCGAGGGCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGCTGCATGAACAGGTT	1
M00764_CRBN_MIP124	GATTTTCTTCAGTAGTTTCAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGAAGGGGGCAGGG	1
M00764_CRBN_MIP125	GCAATAATTCAACCACCCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGCAATCATCATTTC	1
M00764_CRBN_MIP13	CCAACGTCATATAATACATACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGGCTATGATGC	1
M00764_CRBN_MIP14	ATCTGTATTTTGGCAGTACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTGTAAAAACACACA	1
M00764_CRBN_MIP15	GAGTTCAGCCTACAGAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTTTCAGTAGTAGTAT	1
M00764_CRBN_MIP16	CCCTCTGAAAAGTTAAAATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGGTCTGGTTTGT	1
M00764_CRBN_MIP17	ATAAGGCAGGGGCATATCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGCTACTGACAGGAAC	1
M00764_CRBN_MIP18	GGTCTACTTTTACTACTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGCCAAAATACATGCCT	1
M00764_CRBN_MIP2	GGTGTAGTCTCTAAAACCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAACTGTACATTTCAG	1
M00764_CRBN_MIP20	ACATTTGTATGATAACTTTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAAACTAAACATG	1
M00764_CRBN_MIP21	GTTTTGGCATCTTTTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGATATTTTACATTATTT	1
M00764_CRBN_MIP22	ACTTGATACTGTATTATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGCTCAGTATCTGAAC	1
M00764_CRBN_MIP23	ATTTACAAATCAGTATCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGTATAAATGGGCTT	1
M00764_CRBN_MIP24	GAAAATTAGTTAAAATATGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAGCTAGGGTGAC	1
M00764_CRBN_MIP26	GTATCTGTACCAGTGCTCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCATTGATGGGACATG	1
M00764_CRBN_MIP27	CCGTTCATGCTTGTTTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAACACAGGAAATAATCTCAT	1
M00764_CRBN_MIP28	CCTGTGGAATCTGATATGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATTACTTGGAGGGTT	1
M00764_CRBN_MIP29	GAGGCAATAATTTCCAAAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCGTTCATGCTTGTT	1
M00764_CRBN_MIP3	AAAAACTGTTTTTGCATAGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAACTAAACAGAGAT	1
M00764_CRBN_MIP31	GTAAACTTCCATCCAATATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATCTGTTTACAAGCA	1
M00764_CRBN_MIP32	ACATGTCACCTCAAAAATTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGCTTGGAGTACAGA	1
M00764_CRBN_MIP33	ATAGCTAGAAACATCTGTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAACCTGGAAGGCAAG	1
M00764_CRBN_MIP34	CCCTGCCCCCATACCCGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGACAGATTCTCACTC	1
M00764_CRBN_MIP37	GCCTTATACACAGTAAGTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTAGGACTCTGGATT	1
M00764_CRBN_MIP38	GCAACTTGAATCTGATAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTAGACTTCTCGTTTT	1
M00764_CRBN_MIP39	GGGAATTAGCTCACTTTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCAGGTAAGGTCTTTAT	1
M00764_CRBN_MIP40	AAAACTGGCATTCACTTTATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTATATTAAAAACGT	1
M00764_CRBN_MIP41	GTGTACTTCCCTTTGCTGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGGAAGGAAAATGTG	1
M00764_CRBN_MIP42	GTAAAGGAATAGTGATATATAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGCTCTCTCTGA	1
M00764_CRBN_MIP43	AGTTTCAGTGACTTTCGTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATATGAATACATTTATC	1
M00764_CRBN_MIP44	GGACTCTATACAGAGCTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGATATTTCCATGCAGA	1
M00764_CRBN_MIP45	GTAATGTAGTCATGCAATTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGACTTCGCTGTGAATT	1
M00764_CRBN_MIP46	GCAGCTACTCTGTAAGAAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATGGGCATCAAAAA	1
M00764_CRBN_MIP47	CAGCTCCTTAAAATTGGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATATTATCCGATTTGT	1
M00764_CRBN_MIP48	CACTTTTCAGAAGCTCTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAGGAGTCAGATAAGC	1
M00764_CRBN_MIP49	GACAGCTGGTATATTTTTGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTATTTTTCTAGTCTC	1
M00764_CRBN_MIP50	GGGAAAGGAGTCCTTACACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAGAAGTTATTTGCCA	1
M00764_CRBN_MIP51	AAGAAGTGAGTCTAGTTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATATTCTGTGAGCA	1
M00764_CRBN_MIP52	ATGTTTTAATCAGTCTTAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAACTTTTTATGGAA	1
M00764_CRBN_MIP53	AAGCATAATTTCCTTTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATAGGTATGAAAAGTT	1
M00764_CRBN_MIP54	CCTTGTTTAAAATAAAGGTAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAGACATCCCAGG	1
M00764_CRBN_MIP55	ATCAAGAAACAGCTACGTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGACTGAGTGATTAAA	1
M00764_CRBN_MIP56	CCTTCCAGCCTTTTCTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTTTCAACTCTTAAAA	1
M00764_CRBN_MIP57	GGCAAAGGAGCTGGAGCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAATAGAAGGCAGAAGA	1
M00764_CRBN_MIP58	CATACCTTACTTGGCACCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTTGCAGATTGTTC	1
M00764_CRBN_MIP59	GGTGCCATAATCCCTATGGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCTTTTCAGCAAT	1
M00764_CRBN_MIP6	GAATTCAGATAAGAACTGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAAGCATAGCTTGC	1
M00764_CRBN_MIP60	GCAGTGATTCATTAAGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAACATGCAAAAACT	1
M00764_CRBN_MIP61	CAAATCTGGAGTCCTGGGAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGGGCCTGGAGC	1
M00764_CRBN_MIP62	CAGATTCTTTAAACCATTTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTATGCACACCAGGT	1
M00764_CRBN_MIP63	AGATCAGAGACTGACTTCAGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGATCATTAGTCT	1
M00764_CRBN_MIP64	CAACAAAATTTCACATGCTTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCTCCTGGATGCA	1
M00764_CRBN_MIP66	ACTGTACTCCAGCCTGGACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTCTACAAATACAAAA	1
M00764_CRBN_MIP67	CAGGTGTGAGCCACCACTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACATGCCACCAAACC	1
M00764_CRBN_MIP68	CCTTAATTATGACATGGCCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAAGCAATCCCCCT	1
M00764_CRBN_MIP69	CCATGAAGTTAGATTTGCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTAGAAACTGGAA	1
M00764_CRBN_MIP7	GGTCACTATTGAGCCTATTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTGCTGGCATTCAT	1
M00764_CRBN_MIP70	GCTGGAATGAGCAACATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAAGTTACTTACAGCAT	1
M00764_CRBN_MIP71	GTGGGGTTTTTAAGTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTCACACTTCATAGATA	1
M00764_CRBN_MIP72	GACAACTTTGGGAAGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTAGATAATCCCATGAC	1

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ID	**MIP**	***c***
M00764_CRBN_MIP73	CAGCATTGAAATTTTAATGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGTTTGGATTATAT	1
M00764_CRBN_MIP74	GTTCGTTTACTTGAGACTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGTATCTGAAGTGAA	1
M00764_CRBN_MIP75	CACTTCTTAATGTTTGCCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTTTGGATTTCAGTT	1
M00764_CRBN_MIP76	GTATTTGAGGGGGAGAAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAAACCGATTATTT	1
M00764_CRBN_MIP77	GAAATTCTACAATTTCTACAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCCATTCTCACTGG	1
M00764_CRBN_MIP78	ATTTTTGAAAGAGAAGCAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGAGACTCAATAC	1
M00764_CRBN_MIP79	GTTACTTTTGCAGTTATGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTCACTCTATTTTTG	1
M00764_CRBN_MIP8	CAGGCTCTGCATGCATAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATGACACCTAATACACAT	1
M00764_CRBN_MIP80	ACAAAACCTACATACGTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAACAACCTAAACATC	1
M00764_CRBN_MIP81	CCTTCTTCCAAACCAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATGGGAAATGCTTA	1
M00764_CRBN_MIP82	GCTTTTACATAAAGTAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATCTAATTTGATCATA	1
M00764_CRBN_MIP83	GCTTATCAGCTATATTAATCGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACCTTGTATGGCA	1
M00764_CRBN_MIP84	CACCTTCTGGTATTTCTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAATGTAGCTGGAATA	1
M00764_CRBN_MIP85	GCATCTTCAAAAAATGAAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGTCTGCAGTTCAAT	1
M00764_CRBN_MIP86	ACCAAGCATGGTATTCATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGACAGGTTTTGAAG	1
M00764_CRBN_MIP89	GCCTTGTGACATTTAGAAATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGCCTACTGCTCC	1
M00764_CRBN_MIP9	ATGCTTTCATCAGGTAAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTATGTGGTATCTGAC	1
M00764_CRBN_MIP90	CCTATCCTCTTATGCTCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATGGCTTTTATAGCTC	1
M00764_CRBN_MIP91	GACCAGAGGCTTGTGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAAATGATTTTCAGGTG	1
M00764_CRBN_MIP92	ATGCATAGCAAGGTTGGAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGGAGAGACATTAGA	1
M00764_CRBN_MIP93	GAAGCTTGAGTTCCAACCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTGTTCTACTGAGC	1
M00764_CRBN_MIP94	ACTTTGAACCTTTGTCTTCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTTACAAAATATG	1
M00764_CRBN_MIP95	ACACAGTCAGATGGGTAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGAAAGGGAAGCACA	1
M00764_CRBN_MIP96	CAATTTATAGAATCAACCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGCTGTTGTTCCAAA	1
M00764_CRBN_MIP97	GCATATATTTAAAACTCAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTAGTCTGGGCAA	1
M00764_CRBN_MIP98	GCCCCAGCTGCCTGAGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCTAGGATAATTTTAT	1
M00764_CRBN_MIP99	ATAATTTAGAACTTACAGGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATAGGCGTGAGCTA	1
M00764_CREB5_MIP1	GATTGACTGAAGATGGAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAATGCATCCGGCT	1
M00764_CREB5_MIP100	ACTGAGGCTGAATTCCCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAGGGGGAGAAAATG	1
M00764_CREB5_MIP101	GACAGAGACAGCCCATGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTGTTGTCCCTGCTGT	1
M00764_CREB5_MIP102	GAGAGCCTGGGACAGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGACACACAGAAACACTT	1
M00764_CREB5_MIP103	ACTGCTTCTGAATGGAGGGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCCGCCGTCTTGA	1
M00764_CREB5_MIP104	AGGTGGTGGGCCTTCCTGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAGGATAAATAATAT	1
M00764_CREB5_MIP105	CAGCCATACAAATAAGCACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGTTAACCATTTGG	1
M00764_CREB5_MIP106	CCATACAAAAGCTATAGGAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCCAAAGAGAACT	1
M00764_CREB5_MIP107	GCCTTCTCAGGATTTCTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATCTGCCATGACAATG	1
M00764_CREB5_MIP108	GGTTTGGTGTGTGGTAAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCATCTAAGAGAAAGG	1
M00764_CREB5_MIP109	GCATTCAGAAGCCAAAATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGCAGACTTCTAATTC	1
M00764_CREB5_MIP110	GAAGCACAGGGGTTGCTGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACCTAGCTGAACTA	1
M00764_CREB5_MIP111	ATGTAACAAGCACTGGATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACTCTGACTCCAAAAC	1
M00764_CREB5_MIP112	GAGAGGCAGTCTCTGCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTATATCCTACCCCAACTT	1
M00764_CREB5_MIP113	CACTCTTCCTGTCCCCATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGGAGTTTTGGTAGAT	1
M00764_CREB5_MIP114	GAAACTGTAACTACCTTGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTCATCCTTTCAA	1
M00764_CREB5_MIP115	GCAGTAAGGTCAGTCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTTTTCTGTTATATTGT	1
M00764_CREB5_MIP116	ATTTTCACCTGAAATCATGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCAAAGACAGACAC	1
M00764_CREB5_MIP117	GGTATCACATGACTGCAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCAAAACCAATGCAA	1
M00764_CREB5_MIP118	CCTATTTCAAGTAACTCCACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAACTTCTAGCACA	1
M00764_CREB5_MIP119	CCTGTGCAGGGTGGAGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATATTGGATAAGGATAG	1
M00764_CREB5_MIP120	CCTGTGTAGGGTGGAGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATATTGGATAAGGATAG	1
M00764_CREB5_MIP121	ATTGATGGCTAACTTTCAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTCGGGTCAAGAAG	1
M00764_CREB5_MIP122	CAAATGGCACCAGCATTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTTCACGCATTTGACTT	1
M00764_CREB5_MIP123	CACATCACAGGGACTGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGTTGCCAGTTTGAAC	1
M00764_CREB5_MIP124	ATGAACTGTGAAGGTACTTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATACTTGCTGGCAG	1
M00764_CREB5_MIP125	AGGCTCTGGCTGACATTAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTTTGGAAAAGTCC	1
M00764_CREB5_MIP126	AAACACTGCAGACTTATTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGTTTCACTGTTTTCA	1
M00764_CREB5_MIP127	CCCTTGGCAGGCCCATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTAATTTCAGCAACTTT	1
M00764_CREB5_MIP128	AATAAATCACTGGCCTGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGATCAGAGGACTG	1
M00764_CREB5_MIP129	GGTTGAATACAAATAACGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGTGGCTGATTTACA	1
M00764_CREB5_MIP130	CAACCGCTGGGTGCCACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGGCCAATATACAACTG	1
M00764_CREB5_MIP131	GTTTTTATAGTTGTTGTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGACTACTCCTCCC	1
M00764_CREB5_MIP132	CCTCAGTTTAGAATGAATGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGAAAATGGACGCAT	1
M00764_CREB5_MIP133	CATGTGTAGGTGTGTGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGACTCAGAAAATCC	1
M00764_CREB5_MIP134	GATACATGCCAACTCCTGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGAGCTGGATATGGC	1
M00764_CREB5_MIP135	GTTCTGTTTCAGAGGTTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGATAGCTACTGGTA	1
M00764_CREB5_MIP136	AAAGGGAGGAGAGAGAACAACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGTGTGGCGTCTG	1
M00764_CREB5_MIP137	CACCCTCAACCCCATCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGAGATGATGGGCTC	1
M00764_CREB5_MIP139	ATCTTGTTTGACAAGCCCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGACCTCGCCACAT	1
M00764_CREB5_MIP142	CAGCCTAGGTAACATAGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCATGGTAGAGGAAAC	1
M00764_CREB5_MIP143	GGTCAGTGATGCTTTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATAGTTGAAGGAGAAA	1
M00764_CREB5_MIP144	GGCAAGATATAGGAATGACTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAGCACAGAAAGT	1
M00764_CREB5_MIP145	CAACACAACAGATGCAGCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGCTGACTGAAACGAT	1
M00764_CREB5_MIP146	GGAAGGACGTGGTTAGGTAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCGTCTACCACCC	1
M00764_CREB5_MIP147	ATTGGAAAAGAAAGCAGAAGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCACAGGGGGGC	1

continued table…

ID	MIP	*c*
M00764_CREB5_MIP148	ACATCACCCAGACCTTCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAAGTGCCTGTCAGG	1
M00764_CREB5_MIP149	GCGAATAGGCCAGATGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCAGTAGAGGATATGGA	1
M00764_CREB5_MIP15	CATCTCGGGAGTGTACTTGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGTGGTCCCTTCACC	1
M00764_CREB5_MIP150	GCCAAGTCCCAGACCTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGGGCTCTACAATATA	1
M00764_CREB5_MIP151	ACTGCAAATGTAGCTATTAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAAAAGCTGGGGG	1
M00764_CREB5_MIP152	GATAAATCCACAATGCTTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTTGGGATGAAGCA	1
M00764_CREB5_MIP153	GCTTTAGAGGAGCAAACTCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGCTTGCTGAAAGT	1
M00764_CREB5_MIP154	GTTAGCTGTTTAGCGACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTTTTAGGTCTTAATAT	1
M00764_CREB5_MIP155	CAAGGTAATTCAGAGTAAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCACCAGACAATCAA	1
M00764_CREB5_MIP156	AAATCACCATTTTGTATTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGATAGCAAATGTTT	1
M00764_CREB5_MIP157	GTGCATTTCCTACACTAATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACATTTGATTTCTTG	1
M00764_CREB5_MIP159	CATTCCCTTTCTCTTCCAAACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTCCCATTTCTAA	1
M00764_CREB5_MIP16	CCTGCGGCAAGTGCAACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACCCTCCAGAAAAAA	1
M00764_CREB5_MIP160	GGCTGAAAAGCCAAGTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATATGTGGTTGCTTATA	1
M00764_CREB5_MIP161	CACCTAGGAAAGTATGTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGGCATTATACCTCA	1
M00764_CREB5_MIP162	CATTTACGTTCACTTTTATCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGGTGTGCATGCATT	1
M00764_CREB5_MIP163	ATAATATCCTCTCTTTGGTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAACTTGGCACCCA	1
M00764_CREB5_MIP164	GAGTAAATAAGAAGAAAACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAGCTACCATCTATT	1
M00764_CREB5_MIP165	CACAAAGGCATGCTCATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGGTCAATTTTGGTCT	1
M00764_CREB5_MIP166	CACAAAGGCATGCTCATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGGTCAATTTCGGTCT	1
M00764_CREB5_MIP167	CAGCTGACCAACATGTGTACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAGGGGGGAAAGAG	1
M00764_CREB5_MIP168	GGATGATGTCAGCTCAGGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCTCCCCACCATCTC	1
M00764_CREB5_MIP169	AGTCAGCTTATTCTGATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCATGAACAGTAATTG	1
M00764_CREB5_MIP17	ACTGTGGAATTCGGCTGTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTTGGTCCAGTGGGC	1
M00764_CREB5_MIP170	CAGATTTTCCAAAAGAAGTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTTCACAAGCTCAG	1
M00764_CREB5_MIP171	CCTCATAGTAACACAAATAATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGCCTCATATTCA	1
M00764_CREB5_MIP172	GATGGGAAACAGAACAATACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTACTCCACACTGACT	1
M00764_CREB5_MIP173	AAGCCCCTGGGAAATGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAATCTACCTAGGGTCAC	1
M00764_CREB5_MIP174	ACTCAAGAGCTGAACCTTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAACTCTTCCATTA	1
M00764_CREB5_MIP175	GTCTATGTTGAAAAATGAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTCTTAATGTCATTTA	1
M00764_CREB5_MIP176	GAGAAGACCAGAGGATACAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGTGATTCTTTCTGC	1
M00764_CREB5_MIP177	GAAAGAGCAAAAGTAAAGTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACATAAAGACTGCC	1
M00764_CREB5_MIP178	CATGTGAGTATTTTTCCACATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATCTGGAATGCCA	1
M00764_CREB5_MIP179	ATGGGGAAGTTCACATATCCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGGATTCATGGC	1
M00764_CREB5_MIP180	GGTGGGAGAATCTGTGTTGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGCAAAGCCATGCT	1
M00764_CREB5_MIP181	AGAGAAACTGTACTAGATATTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAGCAAGCTGGG	1
M00764_CREB5_MIP182	ACTCACAGAACAGACCTGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGAGAGTAGCCCTCC	1
M00764_CREB5_MIP183	GCTGGCTGAGGGTGGAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCAGGTCTGAGTTAATT	1
M00764_CREB5_MIP184	GAAAAAAGGGAGTTATGCAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCGTCCTTTCTTTT	1
M00764_CREB5_MIP185	AAATGAAAGCCAGTCTTTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTAACTGGTACCAGA	1
M00764_CREB5_MIP186	AGCTTTTAGCTAAAATGAGGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGTGCTTTTCTCCA	1
M00764_CREB5_MIP187	ACAAGATTCAATGTTTCAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATTCTGGTGACACCA	1
M00764_CREB5_MIP188	CATCTCTTCACCTCTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTAACTCATGTTGAGTT	1
M00764_CREB5_MIP189	AAAAAAAAGGTATGGGAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCTAAGAAAAAGTGG	1
M00764_CREB5_MIP190	AAAAAAAAAAAAAAGCAAACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAATGCCCAGTTTTC	1
M00764_CREB5_MIP191	AACAGAAGGAAGTCAAAATGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTCCAGCTGTGGG	1
M00764_CREB5_MIP192	GTTATAAGTGAAGCATGGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTCACTTACACTTC	1
M00764_CREB5_MIP193	ACCACCTTTCATTTGCTGTGATTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCGCAATCCAAGGG	1
M00764_CREB5_MIP194	ATCAGCTGCTAATAGCCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGGGCTATAACATGA	1
M00764_CREB5_MIP195	GTGTAGTGAATAGAGCCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCTCTTTGTTTCTCCA	1
M00764_CREB5_MIP196	GCAGGCTACTTCACTCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGAAAATAGACTAAC	1
M00764_CREB5_MIP197	CCTCATCCATGGGGTTCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGTGGAAGGATAGCTT	1
M00764_CREB5_MIP198	GCCTGGCTAATTTATTTTTACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCACCTATTGCCCA	1
M00764_CREB5_MIP2	GCTTTGTCTTATAGCCTTTCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGCACCGTCAGGA	1
M00764_CREB5_MIP200	ACTTTTGTGAACTTGCCCGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCTTATGTTGCCCA	1
M00764_CREB5_MIP201	CAGAAGAGTGAAGTAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGATGTGATATTAAAAC	1
M00764_CREB5_MIP202	GGGACTATCTGCTTTGTATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGAGATGAAACACCAG	1
M00764_CREB5_MIP203	GTAGCTTTTATAAGAGTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTAGCAATCTAGGC	1
M00764_CREB5_MIP205	GAAACTTATGACTTGGATATATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTCGAAGCATGA	1
M00764_CREB5_MIP206	GAAAGCACTGCATACAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAAAATTATTCCATTTGC	1
M00764_CREB5_MIP207	ACAGCTGAATGGTTTAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAAAAAGAAAAGAGAAA	1
M00764_CREB5_MIP209	GTTTTGCTTTGTTTTAAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAATCAAAAATCATAT	1
M00764_CREB5_MIP211	AAGCCTCGGCAGTTAAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTTAATAAAATGGATTT	1
M00764_CREB5_MIP212	CAGCCTAACAACTAAATATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTGGTTGGTTTT	1
M00764_CREB5_MIP213	GCCTTTAGGTGTGTTCATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGACTGATGTGCATTAT	1
M00764_CREB5_MIP214	GAGTAGAACAAGAAGACAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGATAAGCCAAGTGT	1
M00764_CREB5_MIP215	GCCTGTTTGGGAGAATATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAGATACATTGGTCAA	1
M00764_CREB5_MIP217	AACGTCTATAGTGCCTCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAATCATCACGGCCTG	1
M00764_CREB5_MIP218	CCAGGGAGGCTGGCAGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAGGAGAAACAATTAAG	1
M00764_CREB5_MIP219	ATGTTTTCCCGTTACACTACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAATGGAGGTGTCCAC	1
M00764_CREB5_MIP220	GACTTAACACTTGGCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAATTACTATAATATAT	1
M00764_CREB5_MIP221	GTGAATGTTCTGGTGGTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGACAAGCAGTTTGTG	1
M00764_CREB5_MIP222	CCTTCTATCAGAATACGCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCTTAAAACTCCCCA	1

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ID	MIP	*c*
M00764_CREB5_MIP225	ATTTTTCAGGGTTTCAAATGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAATTTTATAAGA	1
M00764_CREB5_MIP227	ACTGGAACAGCTTTCTTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCTGTGAGTTATTTTT	1
M00764_CREB5_MIP228	GAGTTACTGATTCCCTTTAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCGGGAAGGGACA	1
M00764_CREB5_MIP229	CCTATGCGAACAGTAGCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTCAGCTCCCTTAGTGC	1
M00764_CREB5_MIP230	GCATAATGGAGCTTGAATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTAAAGTGCAATTTTT	1
M00764_CREB5_MIP231	CCCCCACCCCTCCTCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTTTCTGCTTTTAAAA	1
M00764_CREB5_MIP232	GTAAAGGAGAGCAAAGGCAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGCTGATGTGAGAC	1
M00764_CREB5_MIP233	GTTATATTATGCAACAGATGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGCTGAGACCTG	1
M00764_CREB5_MIP234	CATATAGTGTACTGGCTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTCAGGACACTTTGGT	1
M00764_CREB5_MIP235	GCCCTATCGATTTCATTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAATTTTCTCTCACCT	1
M00764_CREB5_MIP236	ACTGTTCTTTCAGTGGCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTAAGTTTATTGCTGC	1
M00764_CREB5_MIP237	CATCATGTTGTGAAAATGAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGACAGCACCTCTA	1
M00764_CREB5_MIP239	ATTAATACTCTTAAGTGGCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGTAGCCAAATTG	1
M00764_CREB5_MIP24	ATGCCAGCAAGAAAGCAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTTCAAGTGATTCTGC	1
M00764_CREB5_MIP240	CCTTACCCCCCACTTCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAGCTAGATATTGTAAG	1
M00764_CREB5_MIP243	CAGCAGCCAGTAGAAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGCACAATAAGCTCAT	1
M00764_CREB5_MIP244	GGGAAGGGTCCTTTCTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCAAGCTTATCTGTT	1
M00764_CREB5_MIP245	GGCCCAGAAAAATAGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCTAAGTTCTGCTAAA	1
M00764_CREB5_MIP246	ATCCCAAACCCTATGTCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGTTAACACTTACTT	1
M00764_CREB5_MIP247	GTAAAGCAACCACCTTCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAGTTTAGCACTGTG	1
M00764_CREB5_MIP248	CAAACAAACACAAATGCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATGTGTTCACGATGC	1
M00764_CREB5_MIP249	GAAGAGACAAGATTTTGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGCATTTAATATGTTT	1
M00764_CREB5_MIP25	ATTTATTTTTAAGGGGCGTCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCGGCAGATTCT	1
M00764_CREB5_MIP250	GAGATGTAAAAATCTGACCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAACCCCAAATTTC	1
M00764_CREB5_MIP251	GTCTTGTCAGAGGCATGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGTGCATTTGTACAAA	1
M00764_CREB5_MIP26	GGGATGCAGCTGCTGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGAGCAAGCATCAAGT	1
M00764_CREB5_MIP27	GTGTCAAGGAATAAAGACTGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCTGGACCGGTGC	1
M00764_CREB5_MIP3	GGCTTTAAAAGGGCCTCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCTTACTGCTTATC	1
M00764_CREB5_MIP32	CGCGCTGATCAGGTACAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGAGGACAGAGTATTATC	1
M00764_CREB5_MIP33	AATAAATACTAAATCCTGCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTATCACACTTTCCAGTGC	1
M00764_CREB5_MIP34	CATCAGAGGATTAACAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGATGCATAGACTTAA	1
M00764_CREB5_MIP35	AGGTAACAGTTTGAATAAAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAGACGGGAATGAT	1
M00764_CREB5_MIP36	GCCATTATAACCTAAATTTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCAGGGACAACTTT	1
M00764_CREB5_MIP38	GAGTATAAACTGAGCATGTAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCAGCTGAACCCT	1
M00764_CREB5_MIP39	GCTACGCAGCAGAGAACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAACTGACATGGAAAAT	1
M00764_CREB5_MIP4	GACCTCTTTAGAGACTTCCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGAAAGGCCACAGA	1
M00764_CREB5_MIP40	ACCTCTGGGTTGCAGAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACAGTTCCACAAATTTT	1
M00764_CREB5_MIP41	CCTAGACTCTGGTACCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAAGATTAGGAAGAAAA	1
M00764_CREB5_MIP42	CGTTGCTGCTTTTATTCTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTATCTTCTGGTCTGA	1
M00764_CREB5_MIP43	GTTGCTTCCTGCAGTCACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCATTTCTGAATTCCAT	1
M00764_CREB5_MIP44	ATACCTTCTGTAATTTACAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCACCTAGGCCACCT	1
M00764_CREB5_MIP45	GTTTATAGATTGGGAAACTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTGCCAAATGACAC	1
M00764_CREB5_MIP46	ATTTTGCATACTGATAAGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGGCTTGTGAAAAT	1
M00764_CREB5_MIP47	GAAAAGGTCAAAATGCACATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCAGCAGAAGCTA	1
M00764_CREB5_MIP48	AAACATTTATTTTCTTTGCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATCAGACGTTTCCAG	1
M00764_CREB5_MIP49	GTTTCTCCTGATGAAGATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATACAACCCCACCAC	1
M00764_CREB5_MIP5	ATCCAAGGAGTGGAGCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTTTATAAAAGTGAGGG	1
M00764_CREB5_MIP50	GCTCACTTGTTCTTCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTCATATTTATTTTCAG	1
M00764_CREB5_MIP51	GCTCCCAGGTGAGTGTGCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGGTAGAAGCAGAAGA	1
M00764_CREB5_MIP52	CCTGGGGCACTGCAGACAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTGGTGGTGTCTTGGT	1
M00764_CREB5_MIP53	GTAGCTGTCCTGTGTGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTAAGCCATATCTAAT	1
M00764_CREB5_MIP54	CAAGACACAGAATTATCCAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCACAGGGGACATT	1
M00764_CREB5_MIP55	GTTGAGAATGACTACCCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTTGTACGACGTTT	1
M00764_CREB5_MIP56	GTGGGCCCACAGGGGACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAATACATAAAATAGTT	1
M00764_CREB5_MIP57	ACTGGTGTCAGGCACCGCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCTTGTCTTTGGGGA	1
M00764_CREB5_MIP58	GAAGAAGGGTTTACAGCAATACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCACCCAGCTGCCA	1
M00764_CREB5_MIP59	GCAAGCATAGAGAACTCTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGGCCTGGGCAGAG	1
M00764_CREB5_MIP6	CCTATAGAATAACAACACAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGAGCATAAATGCT	1
M00764_CREB5_MIP60	CCACCCACTCACTCATTAATCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCGGCTATCCTT	1
M00764_CREB5_MIP61	CCTGGGGAGGAGTGGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAACAGTTTTTTTAAAA	1
M00764_CREB5_MIP63	GTGCTTTCAAAAAAAGTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTACTTCTTCCTGTT	1
M00764_CREB5_MIP65	CATTTGCTTGCATAAAAAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAAAAATTTTCTGCT	1
M00764_CREB5_MIP66	GCTGGGATGTTCCTTTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCATTATTGAGAAAAAG	1
M00764_CREB5_MIP67	CATCTGATGATTCATAGGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTCATGTTTGCAAT	1
M00764_CREB5_MIP68	GGAGGGGAGAAGAGGAGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGCTCCTTACCTGAT	1
M00764_CREB5_MIP69	ACTGGTAAATTGTGCACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGACTTTGAAGTTTCCTT	1
M00764_CREB5_MIP7	CAGACCCTCAGTCATACTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGACAGAAACTGCCTA	1
M00764_CREB5_MIP70	GAACTGCGAGGAGGTGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATTAAGGCAAGGGGAGG	1
M00764_CREB5_MIP71	GGGTCGGAGTTTGATCTGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCCATCCAAGCAAA	1
M00764_CREB5_MIP72	CCATTTGTGAGTATTTGTCTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGAGCAGCAAGCG	1
M00764_CREB5_MIP73	CAATGACTGAAAACCCTAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGTTTGCTTAATCCT	1
M00764_CREB5_MIP75	ATGTGTTTTAGGTCACTAGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTCCTTGCAGGTT	1
M00764_CREB5_MIP76	CCAGTTTATCCACTGGTTTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTGAAGCAGAACCT	1

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ID	**MIP**	***c***
M00764_CREB5_MIP77	AGGGTATCCTGAAAGTAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTATTTACTTCCACAT	1
M00764_CREB5_MIP78	CAGGACTGAGGACACAAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTCACTCTGCATCCTG	1
M00764_CREB5_MIP79	ATATCTCTGATGCAAACCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTGTGCTTGTCAT	1
M00764_CREB5_MIP8	CCTTATGGTGCACACTCTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCTCCTTTTTGCTT	1
M00764_CREB5_MIP81	GTTTTGGCCTTTGAGAGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACATGCTTTACTCTAAG	1
M00764_CREB5_MIP82	CATGTCAACTACATAGAGAGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGGCCCCACCAAC	1
M00764_CREB5_MIP83	CTCTGTCATCACTCAGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATATCTCGATGCATAATG	1
M00764_CREB5_MIP84	GACGGCATGGCTTGCTGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAAACCAGGAGGAAGT	1
M00764_CREB5_MIP85	CCTCCCCACCAGCACAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGTTAATGAGCCTGTG	1
M00764_CREB5_MIP86	AGATTGGGAGGAGGGTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTTGTATGGTAATGATT	1
M00764_CREB5_MIP87	GGGACTGTTGGTTTTGTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATCATTTACTCCTTCA	1
M00764_CREB5_MIP88	GCCTTTATTGGCCTAAGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATGCCAACAATTGCAA	1
M00764_CREB5_MIP89	AAAGAACTCCTCTTGGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTAATTTAACAGGGAGAT	1
M00764_CREB5_MIP9	ACATCCTTCAGCATCCCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTCTGAAAAGCCAGG	1
M00764_CREB5_MIP90	CACGAATGAACACTGATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGTATCTGCAAGGCT	1
M00764_CREB5_MIP91	GTATGTTAAATTACTTTTTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTACAGCTTTAAA	1
M00764_CREB5_MIP92	ACCACCAGCCCTCCGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGTCTGAGTGTGAAAA	1
M00764_CREB5_MIP93	CCTTTCTCCAAACACAGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCCTGTCACCTGGTTC	1
M00764_CREB5_MIP94	ACATCAAGACACGTGTAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAGAGAGCTCCAAGAG	1
M00764_CREB5_MIP95	ACTCAGCCTGGGGCTGTTTTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAACTCCGGGTC	1
M00764_CREB5_MIP96	GGGTAAACAAAGGGGGAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCTCAGTGCTAGTGA	1
M00764_CREB5_MIP97	CAAAAGAAGGGCCAGCACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTTCTGCCAGATTTAA	1
M00764_CREB5_MIP98	GCTGGGCTCTCGCTCACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGTGTGTGTAGAATTTG	1
M00764_CREB5_MIP99	ATGTCCATGAGGTTTGTTTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCTTGGCCTGGAATC	1
M00764_DCLK2_MIP1	CATAGTGGAAATCTTAATGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGTTTCTGTCACTGG	1
M00764_DCLK2_MIP100	CCACTCACCATGATGACGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATGCCAAGCCAATCT	1
M00764_DCLK2_MIP101	GGCGTCAAGGAGCTCCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTTCCGTAGTCCTATTT	1
M00764_DCLK2_MIP102	CCCTCACACCAGGCCTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGCAGGGAGTTAATTC	1
M00764_DCLK2_MIP103	ATAAGAAACAGCCAAAGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGCCTTCTCATCTA	1
M00764_DCLK2_MIP104	CCAAGTCTCAAAGAATAATTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCAACCCTGAAAA	1
M00764_DCLK2_MIP105	GTTTCTTAAGGCAACTCTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTGGGGCTTTTAAAG	1
M00764_DCLK2_MIP106	AGAGTTTCCTTCTTTACCCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGCCTGAGACTTCA	1
M00764_DCLK2_MIP107	AGGTGCCTCTCAAACTGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACTGAGACAAGCATGC	1
M00764_DCLK2_MIP108	ATTTTCTGCAGCAAGCACTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTGAGGCCCGTGC	1
M00764_DCLK2_MIP109	GTGTTCTGAGGAGGAAACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACTGCTTCCCCAGG	1
M00764_DCLK2_MIP113	GATGCCTCCAGGAACCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCATCGAATGCTGGAAT	1
M00764_DCLK2_MIP114	ACTCAGAACACTCCCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCAGTTTGTTGGACAT	1
M00764_DCLK2_MIP115	GGTTCATCCAAAGTGTTTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTCTCACAGGACAC	1
M00764_DCLK2_MIP116	GCTTTGAGAAGCGCTCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGACTTAGAATTGCATTT	1
M00764_DCLK2_MIP117	GCAATCCGTGTCCAATGACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGAAGAAGTGGCTT	1
M00764_DCLK2_MIP118	GCTTTTTAATGAGAGGCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAGACAATGCTCAG	1
M00764_DCLK2_MIP119	CAGAGGGCAAGTTCACGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGATGAAATGCAGATG	1
M00764_DCLK2_MIP120	ATATACTCTGTGAACCTTCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAATGAGCTCTGCT	1
M00764_DCLK2_MIP121	GGGCATGCCTCCTCCTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATACACGGATTATGTAC	1
M00764_DCLK2_MIP122	CAATAAACTTTTCCCTCTTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCACCCTGCTCTTTTT	1
M00764_DCLK2_MIP123	GTTGGGGACACTTGTAAAAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGCACCCGCTGGA	1
M00764_DCLK2_MIP16	GCCTGGTGTTTGCCATCTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCATCCCCAGTCCG	1
M00764_DCLK2_MIP17	CGCCTTCTTGGCCTTCTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCAGGTTCACGTTGT	1
M00764_DCLK2_MIP18	GAGCTGCTGGAAGGTAGGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCTTCCGGTCCTT	1
M00764_DCLK2_MIP2	ACGTACCATATTAGCGAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCCTTTGTTAGGGCAT	1
M00764_DCLK2_MIP20	GCATGATTATCTCTATCATAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGTCCCACCCTT	1
M00764_DCLK2_MIP21	AAGCCTAGAAAAGCCGTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACTGGTCTGTGAACAT	1
M00764_DCLK2_MIP22	CCACTTCGAATCACAGTCACTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCAGAGCCTCTT	1
M00764_DCLK2_MIP23	ATTTAGTAGTGTGCTAGAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAGACTCAGGAGTCG	1
M00764_DCLK2_MIP24	GGAGTGAGACTCCGTCGCAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGGTGGTGGTGATG	1
M00764_DCLK2_MIP25	CCATACGCTGAACAGAACCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTTTGTTCAGCAAA	1
M00764_DCLK2_MIP26	ACTAATTTCTGGGTGTTTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATTTCAACCAAGGAC	1
M00764_DCLK2_MIP27	CCCTCCTGAATCTGGAGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCACTTGCATTTCTCA	1
M00764_DCLK2_MIP28	GTCTTTGTCCCAGGCCTCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGACTAAGGCAGAACA	1
M00764_DCLK2_MIP29	ACCAAGTCCTTCCTCCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACATATTCTACAGTAAGT	1
M00764_DCLK2_MIP3	AGTAACTTTGAATGAATGATGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGCCCAGCATTGA	1
M00764_DCLK2_MIP30	GTATTGAAGTGGAAGAGAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCGTCATCACCAAAAA	1
M00764_DCLK2_MIP31	CATTTTTCCATCTTTGTAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTTACTTGTCTGCA	1
M00764_DCLK2_MIP32	ATCCAGGACAAAGTCATCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGCTATCTTTCCTCA	1
M00764_DCLK2_MIP33	ACTTTTGTTCTTTTCTAGAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGACAATTGCTTTG	1
M00764_DCLK2_MIP34	ATCTGGTTTTAATAACGACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCTGGTGATTTGCT	1
M00764_DCLK2_MIP35	CATTTTCCTTCTGTTTTCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCATCTTATTCTCGAT	1
M00764_DCLK2_MIP36	GCGTTCAAAAGGGTAAAACGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGCTCACCTGGGGA	1
M00764_DCLK2_MIP37	GCTTATTCCAGTGCACATCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCCTATTCTACAGC	1
M00764_DCLK2_MIP38	ACTCCCAGCAGCCAACTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGCTGAAAACGAGTTG	1
M00764_DCLK2_MIP39	ACTGCCCATGAGACAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAATCACACAAATATGCC	1
M00764_DCLK2_MIP4	CCTGCGCGGTTACGTTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGAATGGTGTGCCCC	1
M00764_DCLK2_MIP41	ATCACTTGGGGTCAAGAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGAGAACCTGTGAC	1

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M00764_DCLK2_MIP42	AAGAGTTCAAGACCAGCCTGGCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATGAAGCCTAAAA	1
M00764_DCLK2_MIP43	ACAAAATGCTTACAGAATGTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAAGCTCAGGTCC	1
M00764_DCLK2_MIP44	CACTTGTGCTAAATTACGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGATCTTCTTCCAATG	1
M00764_DCLK2_MIP45	AATATCTGCACACATTTCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCACACCTGCAAAAA	1
M00764_DCLK2_MIP46	AGTGTATAGACAGGTGAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTCTTTAGAATTTGCA	1
M00764_DCLK2_MIP47	GACTACTGCAAAATTGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGCCTTTTTAAAATTA	1
M00764_DCLK2_MIP48	AGATGAGATCTCATTATGTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTAGGGCAAACTCC	1
M00764_DCLK2_MIP49	AGAGGAAGACCATTTAAAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACACCTCACCAAGTT	1
M00764_DCLK2_MIP50	GGGAAAAACAGTTAAGCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGGTATAGTATGCATAA	1
M00764_DCLK2_MIP51	CAAAAGGCTCCATGGTGCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATGCCAAAGAAAGCA	1
M00764_DCLK2_MIP52	AGGAACACCTGATTGAGAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTTGTGCCAAGAGCA	1
M00764_DCLK2_MIP53	ATGAACGGTATAGAGAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTTTGACCAATTCCAT	1
M00764_DCLK2_MIP54	ACTTTCATTATTTATAATCGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAACTGAGCTCTTTC	1
M00764_DCLK2_MIP55	GATTAGGTCCTTCAAGGATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATCAACAGTGCAAT	1
M00764_DCLK2_MIP56	CATGGTGTACAACTTAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATCTTTCTTACCTTC	1
M00764_DCLK2_MIP57	ACTGCCATCTCTCTCAGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGAGGCATTCATTGG	1
M00764_DCLK2_MIP58	CAAGACTTATGTCAATGACCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTATGTCATCCCTGC	1
M00764_DCLK2_MIP59	ATTGGTATAGACTATAAAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAGCAGAGTGAGAAAT	1
M00764_DCLK2_MIP60	GCTTAACAGGAAGGCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATGGAGTTCTTGAATTT	1
M00764_DCLK2_MIP61	GAGGGAAGTGCCACACATTTTTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTTGATTGACTC	1
M00764_DCLK2_MIP62	CCCCCAACATTGGGAATTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGAAAGAGAGCGAG	1
M00764_DCLK2_MIP63	CCCCAACATTGGGAATTACAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAAGAGAGCGAGG	1
M00764_DCLK2_MIP64	AGGCACCTTATGGGAGGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCACCTTTAAGTCAG	1
M00764_DCLK2_MIP65	GACAGGAGTAGAATGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGATACAAGAAAATACAT	1
M00764_DCLK2_MIP66	GAGCCTCTAATTCTGTCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAAAAAAATGGCATC	1
M00764_DCLK2_MIP67	GTCTTTTCAGCTTCCTGTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATGGAAACAGAGAC	1
M00764_DCLK2_MIP68	GCCTCCTTTTTTCTTGTCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGGTGCTTGTGA	1
M00764_DCLK2_MIP69	GAAACTCTGAGTGGAAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCATTACATTACTTAC	1
M00764_DCLK2_MIP70	ATGAGCGTCCACCCCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAATTGGCTAAAATTTA	1
M00764_DCLK2_MIP71	GGACAGGTGAGACTCAATGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAGCCTTTCTACAT	1
M00764_DCLK2_MIP72	GTCAGCAGGTTGGTATTGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAGAGGCGAATATGT	1
M00764_DCLK2_MIP73	GAAACTGCCAAGTGATCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCTGGTGTTTAAAAAC	1
M00764_DCLK2_MIP74	GTATGGGTAGCTGTGTCAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGACTGTCGGCCTC	1
M00764_DCLK2_MIP75	GTATAAGGAGACCCCGTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGATGAATCATGGTGT	1
M00764_DCLK2_MIP76	GATCGTGAGATCTGCCCACCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCCCCACGGAAC	1
M00764_DCLK2_MIP77	AAAATCACAAGGAGAGATTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCTACTTGTTGGG	1
M00764_DCLK2_MIP78	AAGACACGGTCTCGCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCAGCCAACAATCAGAA	1
M00764_DCLK2_MIP79	CAGTCTGTGGCACACCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTGAGGAAAAAAAAAT	1
M00764_DCLK2_MIP80	GTATAAAGGGCCTTCTACCACACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAAGCAGCAATAGCA	1
M00764_DCLK2_MIP82	AAACAGACCTTTCTTACCAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTCTGGCCAGGTAA	1
M00764_DCLK2_MIP83	GATGCCTTTTTCTAAAGTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGATTTTGACCTCAG	1
M00764_DCLK2_MIP84	AAGAGTGGCCTTAGAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAGGAAAAGGATTATTTT	1
M00764_DCLK2_MIP85	GCTATGGCCTGAAGGTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATGTGAAATGAAATGAA	1
M00764_DCLK2_MIP86	GGAAAACAAAGTGGGTGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGGAGAACATTTGCA	1
M00764_DCLK2_MIP87	GCATTCCGTATCTCAATTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTGGAGATTGTTCTC	1
M00764_DCLK2_MIP88	GTTTCTGTGGGTTGTATTACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGTCACTGGCTTAG	1
M00764_DCLK2_MIP89	GGCCTGGAGGGTACCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCATGGGATAAACTTAAA	1
M00764_DCLK2_MIP90	GTCACCCCTGGGTGTCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTATTTATGCTGGAAT	1
M00764_DCLK2_MIP91	CAGGATTTGTCCCGCGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCATGGAGCTTGGATG	1
M00764_DCLK2_MIP92	AGTCACCTGGGCAAGTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCACATGCAAAAGTTAT	1
M00764_DCLK2_MIP93	GGGGCAGGGTCTAAGACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACTCTCAAACCCCAAA	1
M00764_DCLK2_MIP94	GCAAGCAGGGTCCAGAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCAAAGATCATTGTTTT	1
M00764_DCLK2_MIP95	AGACCTGTGCCCTCTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAACTAAATGAATTCTTGA	1
M00764_DCLK2_MIP96	CCGGGACACAAAGCAGGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATTAGGGAAACAATG	1
M00764_DCLK2_MIP97	AAACGGGAGGATGGAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACTGAATAACAATAGTT	1
M00764_DCLK2_MIP99	GCCTTGAAGTTTTTGAATTAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGAGGTGACAGGT	1
M00764_DMPK_MIP102	CTTGGGGGGCTGGCTTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATTCATCACACCTGTGG	1
M00764_DMPK_MIP103	ACTGGGGGCTAGGGGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAAGGTAGAGCACAGAG	1
M00764_DMPK_MIP105	GTGGTGAGGACAGGACCAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGGCAGCTTCTTGG	1
M00764_DMPK_MIP16	GGCCTGAACGGAGGGAGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGCTGGAGAGAGAAGG	1
M00764_DMPK_MIP28	ATTGCAGGAGCTATGGGGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTTGAGCAGCAGAGG	1
M00764_DMPK_MIP32	GACCTCCTGATTTGAGGAAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGGTGTGGGGCCTG	1
M00764_DMPK_MIP33	AATCAGCATTCTGTCTCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGAGGGGCTATTG	1
M00764_DMPK_MIP34	GTTCTAGGGTCAGCTCATCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACAGAGTCCCAGGTA	1
M00764_DMPK_MIP35	CAAGTCCCTGCAGAAGGTTTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCAGAGCCAAGCA	1
M00764_DMPK_MIP36	ATGGCAACTTGAGGTCAGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGACATGTGACCGCT	1
M00764_DMPK_MIP37	CCAGTCTTAGGACCACATCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTGTTCCCACAGGA	1
M00764_DMPK_MIP38	CCCTAGCGGCGCACCTTCCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCCATTGGCTGCCAA	1
M00764_DMPK_MIP39	CACCTGCCTTTTGTGGGCTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTGGGGGGAACATGT	1
M00764_DMPK_MIP40	ATACGGAGTCTCGCTCTGTTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGTCGTCAGGGC	1
M00764_DMPK_MIP41	AAAAAAGAAAAAATGCTGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAGCTACTCAGGAC	1
M00764_DMPK_MIP44	GTCTCCCAGCCTAGAGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTGTTGTAGTCCCAA	1
M00764_DMPK_MIP46	GTAGACACAGGGTTTCACCATGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAACCCCAGCCCA	1

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M00764_DMPK_MIP48	AAAATGTTTTAAAAATTGGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATGGGGCCAGGCA	1
M00764_DMPK_MIP49	ATGAGGGCAGGGACCAGAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAAATTGCTGGGGTTA	1
M00764_DMPK_MIP50	CAGTTGCAGTCTAGAGAATTAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAGGCCGTCTCTC	1
M00764_DMPK_MIP52	GGAGCTATCTGAGCTGAGACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGGGGGAACACAG	1
M00764_DMPK_MIP54	GTGCCCATCTACTACTGAGGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGGTAGGTACCTG	1
M00764_DMPK_MIP56	CACCGGATTTCGAAGGTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTTCATTCAGCGGTTG	1
M00764_DMPK_MIP58	GGTGGACGAAGGGGTCCCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGAGACCTATGGCAA	1
M00764_DMPK_MIP59	GTCCCAGGCCCACCGCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCTTGTAGTGGACGAT	1
M00764_DMPK_MIP62	GCATTTGGGGAGTGGTTGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGATGAGGGATGGAAG	1
M00764_DMPK_MIP66	GAACCCGAGGAAGTGGGGTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCTGGCCGGGTTCT	1
M00764_DMPK_MIP68	GGCTTGGCTACGTGCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACCTGGTCATGGAGTAT	1
M00764_DMPK_MIP70	AGGGGACTACCAACCACCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCAGGTGGTCTCTGATT	1
M00764_DMPK_MIP72	GAACATCTCAGGGGGAGTGAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTGCGGGGGGTCT	1
M00764_DMPK_MIP74	GGATGAGGGGCCTTCCCTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTAGGAAGAGGGACAA	1
M00764_DMPK_MIP84	CCCCCAGAACCTTACACGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTGTCCTTCTGCAG	1
M00764_DMPK_MIP85	GTGACAGTTCAGGTGCAGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGAGGGCTCCAAG	1
M00764_DMPK_MIP87	CACATATCCCAGACTCAAGTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCAGACGTGGGGT	1
M00764_DMPK_MIP88	CCATGCTACCTTTGTCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTAGTCATAGGACCT	1
M00764_DMPK_MIP95	CCAGACATATGAGGGCCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGGAACCAGGCCTGG	1
M00764_EBF3_MIP1	GGCCAAGATAAAAATGTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTATTTCTTGTCTGTGA	1
M00764_EBF3_MIP10	CATCAGAAAAGTTAATGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGTGCTTTTTTGTGT	1
M00764_EBF3_MIP11	AAGTGAACTTCTTTAAAGAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCATTGACTTTGCCA	1
M00764_EBF3_MIP12	ACATGCACAGAATCTACTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTAAACACAGTTCAG	1
M00764_EBF3_MIP13	GAGCGGCCGCGAAGAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTCATTGTTTATTTTTA	1
M00764_EBF3_MIP14	GGTTCAGCTTAACGAAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTTCAGATAACTTAAAA	1
M00764_EBF3_MIP15	GTGTCTTTACATTTCATTTGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCCCACCTTTTCC	1
M00764_EBF3_MIP16	CAAGTGTTCATGGGAAAGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGATCAAAAACCAAT	1
M00764_EBF3_MIP17	GTTGCTAAGGGACTTTATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATACACTTGTCTTGA	1
M00764_EBF3_MIP18	GAAGTCAAAAGGACAATTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAATATTTTAAGTGGA	1
M00764_EBF3_MIP19	ATCCTTCTTCCCTAATGTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTCCTGTTAAGCA	1
M00764_EBF3_MIP20	GTGCTTGTTGAAGGCAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAAGAATGCAATAGTAT	1
M00764_EBF3_MIP21	AAATGCTACTGTCTGTTGGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGAGGGAGGGTTT	1
M00764_EBF3_MIP22	GGCCCTCTTTTTATCACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATAAGTTACAAAGTTTCA	1
M00764_EBF3_MIP23	AGGAGGTATGAGCCATCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTTTGATGATCATGA	1
M00764_EBF3_MIP24	CGCTTTGTTTTCCTTATTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTTTGGAGGCATTTT	1
M00764_EBF3_MIP25	GTTTCCGACTCCGTCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAGAATCAACATGCAAA	1
M00764_EBF3_MIP26	AAGATACTGTTTCCATCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAAAGTTCAGTCAATA	1
M00764_EBF3_MIP27	AAAAAAATCAGCAGCAATTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTCTGGGCTGGTAG	1
M00764_EBF3_MIP29	GTAACTGCTCTGTCCTTCTGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCACGCCCTAACCA	1
M00764_EBF3_MIP3	GTTAAAGACCCTACAATAAGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGCACTGAGAACG	1
M00764_EBF3_MIP31	GAGGGGCAGGACTGGGGGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGGCTTTGCACCTGT	1
M00764_EBF3_MIP32	GCTCCCTATGTGAGAACCAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACTGACCGGTGCAC	1
M00764_EBF3_MIP33	GTCACGGGAGTGACCAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCACCATTACGATACAG	1
M00764_EBF3_MIP34	CCTCGGGACCTTTTTTCTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACCGTGCGGTCATC	1
M00764_EBF3_MIP35	GGTGCCATGACTCACGTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAACACCAGCGGTAAA	1
M00764_EBF3_MIP36	AGCTTCAATTTCTCAGTTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACATGAACTCCTGGT	1
M00764_EBF3_MIP37	GTTTGGAAGCCCTGTGCGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGATCGTTCTCATTAAT	1
M00764_EBF3_MIP38	CAAAGTGAAATATGCCACCGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCACGCAGGCCAG	1
M00764_EBF3_MIP39	GGTTGAATGGGTTCATGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTGAGCATTAGTTCA	1
M00764_EBF3_MIP4	CTAGACCTTGTCAACCATCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGGGGAAGCTGGC	1
M00764_EBF3_MIP41	GAAAATGCCGTGTGTGCTGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCTCACCTTGCAGTC	1
M00764_EBF3_MIP42	CAGTGAAACAGAAGAGCGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACCGTGTTTGCTTT	1
M00764_EBF3_MIP44	CATGGCGCCACTTCCATATCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTCGACTCGGTAGT	1
M00764_EBF3_MIP45	CGCCTGGATTTCTTAATGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACAAGCAGCGTGTCC	1
M00764_EBF3_MIP46	CCCCGAGAATCTATATCATATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGTACTGCTGGG	1
M00764_EBF3_MIP47	CCCGTGTGTGCAGGGTTGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACCAACCCTCGGAGG	1
M00764_EBF3_MIP48	CAGCAGCCAGCTAGCCGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGGAGATCATCTTGA	1
M00764_EBF3_MIP5	CATGGGAAAGCCTGAGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTCTTGACAAAAATCAA	1
M00764_EBF3_MIP50	CCCCGAGAGTGCGGCCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGCCCAGCCAGATATTG	1
M00764_EBF3_MIP51	GCACACTTTCAAAAGCGTCAGTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGATGGGATTTC	1
M00764_EBF3_MIP52	GCACACTTTCAAAAGCATCAGTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGATGGGATTTC	1
M00764_EBF3_MIP55	GCTTCAGTAACACCTCCTAAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACACTGGAGCCACGC	1
M00764_EBF3_MIP57	GCTCTTTTACTAACCTTGGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACACCTGTCGGCC	1
M00764_EBF3_MIP58	GCTGGTTCTGGTTTGGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAACCAACCATAGATTAC	1
M00764_EBF3_MIP59	GTAGTTCTCCTGCTCTGATGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAACCTCTGAAAGC	1
M00764_EBF3_MIP6	GCACTTAGTGCAAAGGAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGAATGAACACTTTGT	1
M00764_EBF3_MIP60	GGATTTGTAGGAGAGGGTCACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCCTCCCGTGCCC	1
M00764_EBF3_MIP61	GCTCCTGGGCGCTTTGTCTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTGTTCACCGTGTG	1
M00764_EBF3_MIP62	CCTAGCTGTCACCCAGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTTATCAGCTACAAAAA	1
M00764_EBF3_MIP64	GGCTGCAAGTTGTATTCGGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCTCTAAGGTCTGC	1
M00764_EBF3_MIP65	ATGCTTCTTTTTCTTTGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACAACATGTTTGTGC	1
M00764_EBF3_MIP66	GAAGTGGATTTGAAAATGGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTGACGGGTCTAG	1
M00764_EBF3_MIP67	GCAGGTTGTTGTATCGACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCGATCAACAGTGTCCA	1

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M00764_EBF3_MIP68	GAGTTCTTTAAGGGCTTGGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGCAGGCAACCCTC	1
M00764_EBF3_MIP69	AAAGACTCAAACTTTTTAAAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGAATCTCCGCAT	1
M00764_EBF3_MIP7	CAGACACGGCACAGCAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTGTCCGTACTTTTA	1
M00764_EBF3_MIP70	GATTCTTTCTAAAGTTTTTCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTAGAGGGAAGTG	1
M00764_EBF3_MIP71	ACCATTTGTTGTCCGCGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATTGACAGGTAAGGATG	1
M00764_EBF3_MIP72	GTAAACAGTGGTTTTAATATGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGCTGCTGCGGTTT	1
M00764_EBF3_MIP73	CCACAGCCGGTGCTGTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTTTAAATTCTCCAAAC	1
M00764_EBF3_MIP77	ATGGAAAACAAATACACGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATATGATTCCAATCACAAG	1
M00764_EBF3_MIP78	CCTTGACATGCTAATGAGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAATGACCAAACAGGT	1
M00764_EBF3_MIP79	ATTCTCATCAGGATTTGAGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAACCCAGGCCCAG	1
M00764_EBF3_MIP8	GAGGTGGGCCCAGGAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATATCTGAAGGAGGTCAT	1
M00764_EBF3_MIP80	GTCTCTGTTTTTTTGCAGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCTTTCTCCCTTTCA	1
M00764_EBF3_MIP82	AAATTAAGCGAGAAGTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAAAAATAAACGACCA	1
M00764_EBF3_MIP83	AGGAAGTAAGTTATGCTCCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGCTGTGTGCGGTGG	1
M00764_EBF3_MIP84	CCTCGAGAGACATTAGAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCAGCAGAACATCA	1
M00764_EBF3_MIP85	GCCATCGACTTATTGATCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCCCATCCTAATAATTA	1
M00764_EBF3_MIP86	ATTAACCGGTGGGGCTTGAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTGCGCTGGTGA	1
M00764_EBF3_MIP87	CCGTTGTTGGTTTTCTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGTCATTTTAATCTCAA	1
M00764_EBF3_MIP9	ATTCACAGAGGTTTCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACTTCATTTGGAGATGT	1
M00764_extra_100_CRBN	CTCCAACTTGCACTATCAAACTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACTAAGATTCCAG	1
M00764_extra_101_CRBN	GACCACTGCAATTACCCATGAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAAATGAACAAAA	1
M00764_extra_102_CRBN	GATAAAAGTTCATAAAAACAAGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGACCAGGATAGT	1
M00764_extra_103_CREB5	TTGTACCTCCCAACTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCCTTTCTCTTCCAAACTTT	1
M00764_extra_104_CREB5	ATATGAGGGTCTCGAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGTGTGTTCATGGGTTTT	1
M00764_extra_105_CREB5	CAAAAGATGGTTTTGAGTGTCCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGAGAAAAAAAGAA	1
M00764_extra_106_CREB5	CATCCAGTTAGGATAGAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTTGTTGCCTGTTAAGT	1
M00764_extra_107_CREB5	GGATCTACTTGTTTTTAAAGTGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGTATACAGTGGA	1
M00764_extra_108_CREB5	GATCCTACAGAATACTGTTCAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATGCACAGAGATC	1
M00764_extra_109_CREB5	GATCCTACAGAATACTGTTCAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATGCACATAGATC	1
M00764_extra_10_ADAM22	GGCTTACATTTCTTTTCTATTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAGTCTGGCATAG	1
M00764_extra_110_CREB5	GTAGCCAAATTGCTTAAAGAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAAACAAACACAAAG	1
M00764_extra_111_CREB5	CCTGGCTTCTAATGAGCTAGATATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTTCCACATTCT	1
M00764_extra_112_CREB5	CCTGGCTTCTAATGAGCTAGATATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTTACACATTCT	1
M00764_extra_113_CREB5	CAGTCCTGAGGCTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATACCTTTCATTATCTCCT	1
M00764_extra_114_DCLK2	GCAGGAGCCGTCAGGCGGGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATGCTGGCTGGGG	1
M00764_extra_115_DMPK	AAATATCCAAACCGCCGAAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTGGGGGTCCTAGG	1
M00764_extra_116_DMPK	GGGGCGCAGGGAAGAGTGCGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCAGGAGGGCGGAT	1
M00764_extra_117_DMPK	GAGCCACAGGCAGCCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTAGGGAAGGGAGGGGGC	1
M00764_extra_118_DMPK	GCCATGAAGATCATGAACAAGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGTGCAGAAGCGG	1
M00764_extra_119_DMPK	GCTGGGGGGGTGGTGGGGGAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGTCAAGTCAGGC	1
M00764_extra_11_ADAM22	TCTCTGAAAGTGCAGAGAATATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGGTAACAGGTAAAG	1
M00764_extra_120_DMPK	GGAGTGCTCCTCCCGGGAGCGCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGACGGGGGAGGG	1
M00764_extra_121_DMPK	GTGGGAGGTTGGGAGAAGGTTTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCGGGCCACAAAA	1
M00764_extra_122_DMPK	GGGCCTGGACAGGGGCTGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGCGGGAGGGGGG	1
M00764_extra_123_DMPK	CTGGACCAAGGGGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGACAGTGTGACAGCTGAG	1
M00764_extra_124_DMPK	GTGGGAGAAAGGGGTTGAGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGAACCTGCCCA	1
M00764_extra_125_EBF3	CTCCAGGGGTGGGGATGGGAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACAGAAGAGCGCC	1
M00764_extra_126_EBF3	GAAGCGGGAGGCAGGCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTTCCACTTCGTGCTGGCG	1
M00764_extra_127_EBF3	GGCGGGGCGGGGGGCTGTAAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGCGGCCAAGGAA	1
M00764_extra_128_FAM171A1	CTCTCGGCGAGCCCGAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGGGGCGCGGGAGGGAG	1
M00764_extra_129_GALNT12	CCTCAGCTGCGGGGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCGTGCCTTTTACTCTCATTAG	1
M00764_extra_12_ARFRP1	CGGCGAGTGTGGCTCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTAAGGCTGGTCCTGGGG	1
M00764_extra_130_GALNT12	GGTCATTGAGATCTTCTAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATATCTGCATGGGTGG	1
M00764_extra_131_GLO1	GAGTGTGTGATTTCGTGTGTCCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTCTTCAAACCA	1
M00764_extra_132_GRIN2B	GAAATAAGTTGATTTCATTCTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGGGGGGAGGGGC	1
M00764_extra_133_GRIN2B	GAGTTCAGGTTTAAAGTGTGGAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAATAGACGTTGG	1
M00764_extra_134_GRIN2B	GGAGGTGGAGCAGATTCTAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCAAGAATTAAGGTAC	1
M00764_extra_135_IQCH	GCAGTGTTTTCCACTAACTTAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTCTTTGGTTCTAC	1
M00764_extra_136_IQCH	GTGCCAGTAACATTTTCTGTACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCAAAAAGCACAG	1
M00764_extra_137_KCNA4	GCACATTAACTGGAAAAGATGTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGTTATACATGGC	1
M00764_extra_138_KCNA4	CATAACTGCACTCTCTATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTATTCCTCCCTCTTCTCC	1
M00764_extra_139_KCNA4	GTTTGGCAGGTGGAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGGCGGGGCGAAAAATAAAAA	1
M00764_extra_13_ARFRP1	GCCGTCTTGATGTCAGGGATTGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGAGGCGGGGGG	1
M00764_extra_140_KRTAP19-5	GCTGTATGTATGTGTGTGCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGACTCAAAATGGC	1
M00764_extra_141_KRTAP19-5	GTGGTTATTTGTAATTATATCCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCTCTGGATGTGT	1
M00764_extra_142_KRTAP19-5	TTATGTCTCTGGATGTGTCTTACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAGAAGATCACCC	1
M00764_extra_143_KRTAP19-5	CAAGCCAAGATCAAGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCATCATGCTATGGAGGA	1
M00764_extra_144_LAMA1	GTTTAATTGTTTTGCCTGTGATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCATTGCCTCATA	1
M00764_extra_145_LAMA1	ATTTAATTGTTTTGCCTGTGATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCATTGCCTCATA	1
M00764_extra_146_LAMA1	GGGTCATGAGATCTGCATTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAAGAAGAAAAATAA	1
M00764_extra_147_LAMA1	CAACTTGGGTGAAAGATCGTCAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACGCGTCTGGTAAC	1
M00764_extra_148_LAMA1	GCCAGGAGCTGGGCGAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGGGCTGAGGGGAGGAG	1
M00764_extra_149_LAMA1	GGGGCGCGTGGGTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAAAGTCGGGAACAAGTTGC	1

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M00764_extra_14_ARFRP1	GCTGTCTTGATGTCAGGGATTGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGAGGCGGGGGG	1
M00764_extra_150_LEO1	GGTGGATCACAAGGTCGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATTTGCTTTTGTGTAATTTT	1
M00764_extra_151_LEO1	GTAAAACCTGGAGATACTAACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGACCTTTTGATCCTC	1
M00764_extra_152_MAP2K5	CCACTAAAATGCTTTATGTGTCGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCATTTTATACACA	1
M00764_extra_153_MAP2K5	CCAGTGTAATATCTAGTAGTATGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAATAAGACAAAA	1
M00764_extra_154_MAP2K5	GTACAGAATTCATGGATGGTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAAGCATGCCTATGG	1
M00764_extra_155_MAP2K5	CAGTGTCTAAGAGAAGTCATGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTTTCCCATATTC	1
M00764_extra_156_MAP2K5	CCAGCACCTGAAGAATTGATGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAACATTCAAATTCC	1
M00764_extra_157_MAP2K5	GGAATTTGAAACAGCCATAGGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTATGCGAAAACAG	1
M00764_extra_158_MDGA1	GTGGGAAATGTCACAGGGGCCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATTGGGGGAAAGA	1
M00764_extra_159_MDGA1	GAAGCTGAAGGGCCACTTAGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGAAGGGAAGGAG	1
M00764_extra_15_ARFRP1	TCCTCACGGCCTTACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCACTGCTGTGGTCTCTGTGG	1
M00764_extra_160_MDGA1	ATTGGCTTGAATTATGCAGTTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACCCATGTTCCAC	1
M00764_extra_161_MDGA1	GCATCCACGTGGCACGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCAATGAGCTCTAGGCTG	1
M00764_extra_162_MDGA1	GCGTTCTTCATGGCTGTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATTCTTGAACCACTG	1
M00764_extra_163_MDGA1	TCGCCGCCTCCGCTCGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCCCCGCGGGAATCTGGAG	1
M00764_extra_164_MDGA1	AGCCGAGCGGCCGCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACGCGAGGAGGAGGGAGG	1
M00764_extra_165_MDGA1	AGCCCAGCGGCCGCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACGCGAGGAGGAGGGAGG	1
M00764_extra_166_MDGA1	GAGAGAGAGGAGAGAGAGAGAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTTGGGGGGGAAT	1
M00764_extra_167_MDGA1	GCGGGGGTCCTAGGGAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTGGCCGAGCCGGGTG	1
M00764_extra_168_MEIS1	CTGGTTCATTGTCCATATTTAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCATTTGGGGTATC	1
M00764_extra_169_MEIS1	GCAAAAACTGTGGGAACACAGTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCACAAGTGCACA	1
M00764_extra_16_ARFRP1	GTGGGGGAGGCTGGGGACTCGGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGTCTGGAGAGG	1
M00764_extra_170_MEIS1	GCATGAGATTCTCTTAAGATCCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCACTTAAGTTAC	1
M00764_extra_171_MEIS1	CTTCAGTCTATGTTTTAGAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCAGTCCTTTTTGC	1
M00764_extra_172_MEIS1	CATGACCGATGCTTTGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATACCAAACTGCTACTTT	1
M00764_extra_173_MEIS2	GCTTCCCTCTCATTTTTGCTATTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGTAGAATTTTT	1
M00764_extra_174_MEIS2	AAAGGCCCTGCCTCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCACGGCTGAGGGCGGGCTGG	1
M00764_extra_175_MEIS2	TGTTTGCCGGGGCAGGCGGCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGAACGCGGTGGGG	1
M00764_extra_176_MEIS2	GTGGGGAGTTACTTCTGTATGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACGACGCCTTGAAG	1
M00764_extra_177_MEIS2	GGGAAAAAGAGCAGGGAGAAGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACATGGAAGCGGGA	1
M00764_extra_178_MICALL2	GGACCTCGTTGCGGGCTGGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGACGCTGAGGATAG	1
M00764_extra_179_MICALL2	GCTGTGTCCTGGTCACGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGGCTGGGCCTGG	1
M00764_extra_17_ARFRP1	GCTGCGGGAGGCAGGGGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGAAGCTGCTGGGGG	1
M00764_extra_180_MICALL2	GCATGTGTGCATGTGTTCATGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTGGGGGCCCCGG	1
M00764_extra_181_MICALL2	GTGTCTGCAAGGGTGGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCTGTCCACGGGCTTCAG	1
M00764_extra_182_MICALL2	GGAGCACCGGGCAGGGAGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTCTGGGTGTGAGG	1
M00764_extra_183_MICALL2	GCAGGACGTGCGGATGGGGTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCGCAAAACACCAC	1
M00764_extra_184_MICALL2	GCAGGTGTCACGGAGGACAGAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCTGGGCTGCAGG	1
M00764_extra_185_MICALL2	GCTTGGCCGCCTGGACTGGAGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGGTGGGGTGGG	1
M00764_extra_186_MICALL2	CCCCCAGTGAGTCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCGCGTGGCCGAGGAGCACTT	1
M00764_extra_187_MICALL2	GGCTGCAGAGTCCCTGGGCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCGCTTTGGTCAGTG	1
M00764_extra_188_MICALL2	GCTCAGCTGCTCAGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGAGGTTAGGGCTCCAATGTG	1
M00764_extra_189_MICALL2	GGTAGCCCTCGCACTGCTGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAACAGCAGAAGAATCA	1
M00764_extra_18_ARFRP1	GGGGAGGGCAGGAGAGGCAGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGGGGAGGCTGGGG	1
M00764_extra_190_MPPED2	GCTGCGAGGCTTAAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAAACATTGTTTTTGGAACC	1
M00764_extra_191_MPPED2	GCTGCGAAGCTTAAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAAACATTGTTTTTGGAACC	1
M00764_extra_192_MPPED2	AGGAACCTGGCAGCGCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCGGGGGGGTGGGACA	1
M00764_extra_193_MYT1	ACAGAATAATTAAACTAACTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCCCTGGTGTGGGGT	1
M00764_extra_194_MYT1	GGTGCCCTGGTGTGGGGTCTAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAATATATAAAAAA	1
M00764_extra_195_NENF	GCGCGCGAAGGGCGGGAGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGTGACATTTTTTGGT	1
M00764_extra_196_NPBWR2	CGGAAGTTGTCATCTAGAAAGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCCTGATGGGGGT	1
M00764_extra_197_NPBWR2	CAGAAGTTGTCATCTAGAAAGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCCTGATGGGGGT	1
M00764_extra_198_NPBWR2	CACGAGTTGGCGTAGCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATGATGATGGGGGGTGA	1
M00764_extra_199_NRG3	GTTAGGAGTTCGAGACCAGCCTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAATATGACATC	1
M00764_extra_19_ARFRP1	GTGCAGGTGCACAGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGGGGGTGGGGGGGCCT	1
M00764_extra_1_AAGAB	GCACATGAGCCGTCTGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGAATAAACTGGAAAGAA	1
M00764_extra_200_NRG3	ATTTTTTCCCCATATCCCTTCTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGAAGAAAAATAA	1
M00764_extra_201_NRG3	GATCCTCTCAAAAGTATTCACATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATGGTAACTGTC	1
M00764_extra_202_NRSN2	GGGTCTTCCACGGGAGGGGTGGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGAGGGCGGGGG	1
M00764_extra_203_NRSN2	TTCAAAAACCCATTCCTACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTGGGAGGTGGGGGTC	1
M00764_extra_204_NRSN2	GGGAGGCGGGAAATGGCCTGATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACACTTCAAAAACCC	1
M00764_extra_205_NRSN2	GGGGGGGATGGGTAGGGGGTGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCCCGAAGATGGA	1
M00764_extra_206_NRSN2	TTGACGCTGCCTCCCGCTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGGAGGTGTGGAGGGG	1
M00764_extra_207_NTNG1	GGTACACGAGGAGTTACTGGAAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAAAGGAAGTGCT	1
M00764_extra_208_NTNG1	GAGGTCGTGGAGCGGCAGCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGAGGGGTGGGATGG	1
M00764_extra_209_NTNG1	GATGCATAGTACTCCAAGGTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTGGCATTTCATTT	1
M00764_extra_20_ASTN2	ATATGCACCCAATATAGGAGCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATAAACTATACAATCA	1
M00764_extra_210_OPRL1	GCTTGGGAAAGAGGAGGCTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGTAGTAGATGGGGG	1
M00764_extra_211_OPRL1	ACGGATGGCAAAGCAGGAACGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGCGAGGGGTGGG	1
M00764_extra_212_OPRL1	GCGGGGCTGGGGAGAACTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGACCGATCGGCGGG	1
M00764_extra_213_OPRL1	GCGGGGCTGGGGAGAACTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGACCGATCGGGGGG	1
M00764_extra_214_OPRL1	GCTAAGGAGGGGCGGGGGCGTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGCTGGGCAACCG	1

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ID	**MIP**	***c***
M00764_extra_215_OPRL1	AGGCGGCCGCAGACGCGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTGGCGGGGGGCAGGGT	1
M00764_extra_216_OPRL1	AAAGGAGGCTCAGACCCACAGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGGGGAGGGGCTA	1
M00764_extra_217_OPRL1	GCAGGCTGGAGGAGGTGGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGCAGAGCAGGGTAG	1
M00764_extra_218_OPRL1	GCAAATGCACTTCCTACAGATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTGGCTGTGAGG	1
M00764_extra_219_OSGIN1	ATTTCCCTGGAACCTCTGTTGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAAAATACAGGCTG	1
M00764_extra_21_ASTN2	CGGGGTGTAGCATGTGGGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGGATTCGTGGGG	1
M00764_extra_220_PCDHB5	TCTATTTACTCTTTTTTGCAGCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGCTAAAATGCAA	1
M00764_extra_221_PDE11A	GCAATGCCACTGTAATGAAGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATACTAGGGAAAG	1
M00764_extra_222_PDE11A	CACGTCTTGGTCCTTTGGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTACATCTACCCCATA	1
M00764_extra_223_PDE11A	CACGTCTTGGTCCTTTGGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTACATCTGCCCCATA	1
M00764_extra_224_PDE11A	ATAGATGGAGATTCTAAGACTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTAGGTTTGTTGCT	1
M00764_extra_225_PDE11A	GTGAGTGGGAAGAAGACAGAAGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATGACCGTATTTG	1
M00764_extra_226_PIAS1	GAGCTGGCCGAGCTAGGATGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTGGGGGTTGGGG	1
M00764_extra_227_PIAS1	GCGAGAGGGATGCTGGCCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTACAGCTGCGAGACAGG	1
M00764_extra_228_PIAS1	GCGGAGACGGCGCCGCTGCTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTAGAGGGGCGGGT	1
M00764_extra_229_PIAS1	GGGGAGAAACCCCCTCGAAGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGATAGGGTGGG	1
M00764_extra_22_ASTN2	TCAGATGGATTCTGTGATGTCACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGATGTGACCGGG	1
M00764_extra_230_PIAS1	GCTTTTATTTCAGATAGAGTCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGGGAAGAGAAACC	1
M00764_extra_231_PIAS1	GCGTAAGGATCAAAATTAAGTAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACATAAAACAAAAGC	1
M00764_extra_232_PIAS1	CTTCGTGTATTCAGATAATTTCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAGCATGTGTCA	1
M00764_extra_233_PIAS1	GGGAAATGGGAAGGGCATCTTGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTCATGAGCTAT	1
M00764_extra_234_PIAS1	CCACCTTCAGTTCATTTTTTTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGAGAACAAAACT	1
M00764_extra_235_PIAS1	GGTGCTTGTTTTTCTTTTTTCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAATTCCTTTTC	1
M00764_extra_236_PIK3R4	GTACATCTTAACCATTTTGGGTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATACAAAATAAACA	1
M00764_extra_237_PIK3R4	CAAGCCAAAAAAAAGAAAGATTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGGCAGCTAATGA	1
M00764_extra_238_PIK3R4	GCTTTTTTTTGCCCTTGAATTCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAGCTTCTTTCTTA	1
M00764_extra_239_PIK3R4	CCTGAAATTGCTCAAGAAAATCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAAGAAGAAAATGG	1
M00764_extra_23_ASTN2	GTCGGGGATTGCGTGGGGGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGCAGCTCCGGGCAG	1
M00764_extra_240_PIK3R4	GTTCTGCTGTCCTGGGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAAACTACTGCTTTGTAC	1
M00764_extra_241_PKP4	GCAACAAGGTCACCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATGAGAAGAATGTTTTACC	1
M00764_extra_242_PKP4	GCAACAAGGTCACCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATGAGAAGAATGTTGTACC	1
M00764_extra_243_PKP4	GCAGAAAAAAATAAATGCAGAGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTTACGCACAATG	1
M00764_extra_244_PKP4	TGTGAAGAATGCTGTTGATGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTACAAAGAGACAAG	1
M00764_extra_245_PKP4	ATTTTAACACTTCGTGTACCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTAACAAAACTGAGAG	1
M00764_extra_246_PKP4	GTTTCACTTTTGCTGTTTCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTTGTTTTTACCACT	1
M00764_extra_247_PLXNA2	GCGGGCAGGGAGAGGGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGACTGAGGGGCGCGCGG	1
M00764_extra_248_PLXNA2	AGCCGGGGCTCTGCTTCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGATCTGGAAAGCCAGGC	1
M00764_extra_249_PTPRD	CTTACTTCGTTACATTGGTGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTTTTGGATGCATAGAC	1
M00764_extra_24_ATP2C1	GCAAGTCTAAAAAAATGTATATACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTGGTTTGAGACC	1
M00764_extra_250_PTPRD	AGTATCTAGAAGGCTACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTCCACATTTTCCCATTG	1
M00764_extra_251_PTPRD	GAGTTCCTTGGGTATTTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATGTTTGGTCTCTTGG	1
M00764_extra_252_PTPRD	GCCATGGATGATGGCATAAGTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACAAATATCATTGG	1
M00764_extra_253_PTPRD	GTAACAGGGGCAAAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGAAAGGTCAGTGCATAT	1
M00764_extra_254_PTPRD	CAGTTTTTCTTTATGTTTTGTTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTTTGTGGGGCCC	1
M00764_extra_255_PTPRD	TGATTCTATGCAGGCATGTATATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACACACTAATACAA	1
M00764_extra_256_PTPRD	GGATACAACCATTGGATCTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGATGTGCCCAGA	1
M00764_extra_257_PTPRD	GTGTTGGCGGCGGCGCGGGAGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACGAGGGCTGGGCGG	1
M00764_extra_258_PTPRD	GCGGCGACCAGGGGGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTAGGGGTGGAGGGAGG	1
M00764_extra_259_PTPRD	GTATTGTGATTTGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCTTAAGAGGTTAGTAATT	1
M00764_extra_25_ATP2C1	GCGTGAGCTGGGGACGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGTCCGGGGCTTTGGGT	1
M00764_extra_260_PTPRD	CTCTGGCAGTTGTATTATGTCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGAGTGAGACTTAC	1
M00764_extra_261_PTPRD	GTTCATGCTGTAGGACACTAATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATACTGCCCAAAGC	1
M00764_extra_262_PTPRD	GGTGTTCGCGTGCTTTCGGTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGATTCCAGGGATCCAG	1
M00764_extra_263_PTPRM	GTTTCCTGTGTCAAATAAAGAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTAAGTTCCAGTT	1
M00764_extra_264_PTPRM	GCATGTATGTATTAGGATCTGATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATATTCTCCTAAT	1
M00764_extra_265_PTPRM	GTTGGTGCTGACAATGGTGACAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCGATATTGCCTC	1
M00764_extra_266_RASGRP4	GCGGGCGTAGTTGTTGTGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTAGGTGCAGGCGG	1
M00764_extra_267_RIMS2	TTGCCTCCCCGCTTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCCCTCCCCCTGCTTTTCT	1
M00764_extra_268_RIMS2	GTGGTTAGAGTCTTTTTTTCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTCAGTAAGAAAAC	1
M00764_extra_269_RIMS2	GTTTAGAGAGGTCGTACAATCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGTAATTGGATTTTG	1
M00764_extra_26_ATP2C1	GGCTTATAGCCACTTATTTGTAGATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATGGAAATCAGT	1
M00764_extra_270_RIMS2	GTTGATGCAAAATGTCAGCACCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAGCTGGTTTGTG	1
M00764_extra_271_RIMS2	GCTCCAGTTTTTAGGTGACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTGCTAAAAATTGGGA	1
M00764_extra_272_SEMA6D	GAGTTGTATATTCTTTTGATGTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAAGATTGAAGG	1
M00764_extra_273_SEMA6D	GGGGCGGGGGGGTAATGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGAATGGCTTTCAT	1
M00764_extra_274_SEMA6D	TTCACGGAACAACTGCGCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGCTTTCTTCCCAGC	1
M00764_extra_275_SKOR1	GAGGTGGTGGAAGCGGCCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCATCCCTGCCATTA	1
M00764_extra_276_SKOR1	GGTGAGCGGAGGTGCGCGGCGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACAACAGCCACAG	1
M00764_extra_277_SKOR1	GCTGTGTGGCCTTGGGCAAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGCAGAGGGGCGG	1
M00764_extra_278_SKOR1	GTTGGCGGCATCGGGCTGCGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGTAGGGAGAAGG	1
M00764_extra_279_SKOR1	CCGGGATCACCGGGTAGCTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGCTCGCCCGCGCCT	1
M00764_extra_27_ATP2C1	GCTTCATTCTGCAAATGTCGTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTTCACATAATTCC	1
M00764_extra_280_SKOR1	GGAAGGGAAGCTGGGGGCGGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGAGAACGGGAA	1

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M00764_extra_281_SKOR1	CAAGGAAGCTAAGCTAGTACTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCGCGGCCGCTGG	1
M00764_extra_282_SKOR1	AAGCCGGGGCCCTGGACAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATACAATGGGAGGGGGCG	1
M00764_extra_283_STEAP4	CCCATCTTGTTTGGTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCCTATCCCCCATTACCTT	1
M00764_extra_284_STEAP4	GTGACAGGAGTAGAAGCACTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGGTACAAAATAAC	1
M00764_extra_285_STEAP4	GGGATGATGGCTTTTATAAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGATCCAAACTAT	1
M00764_extra_286_SUN1	GTCTTGGGGGAGGGGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAAGGGTCTGCATCTTCGG	1
M00764_extra_287_SUN1	GCACATATGAACTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTGATACTAAGTTGATTGTGG	1
M00764_extra_288_SUN1	GCCCGGCAAGGAGCGTGATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCGTCCTGACTGCAG	1
M00764_extra_289_SYT5	GTGTGTCCGCGAGGGTCGGGGGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGGGCTGTGTTG	1
M00764_extra_28_ATP2C1	GAGACTTGTGAAGAAACTGCATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAATTGAAAACTAG	1
M00764_extra_290_SYT5	GGGGGAGCAGCCTCCTAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGAGACGAGAGGGA	1
M00764_extra_291_SYT5	GCGGGAGGAGGTGAGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCTGGTCATGGCGGTGT	1
M00764_extra_292_SYT5	CGAAATGGGGTAAAAGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGGGGCCGAGCAGAG	1
M00764_extra_293_SYT5	GGGGAGAGGGAAGAGGGAACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGGCAGCGTGGAGA	1
M00764_extra_294_SYT5	GAGACAGGGATCTGGGGACGCGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGGAGCTGCTGGG	1
M00764_extra_295_TANC1	GTGTTTGTGGGAAGGGATTGGCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAATTATGACATT	1
M00764_extra_296_TANC1	GAGGAACACAGAACTGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCACGATTTGCTCCCTA	1
M00764_extra_297_TANC1	GCCATGGCTTCAGACAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGTCTGCTGGGTGTTC	1
M00764_extra_298_TANC1	CTCTCCCACGTCTCATGACTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGACTGTATTAAGTA	1
M00764_extra_299_TANC1	TCTTCCTTGCCTTTGCTATATGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCTAGAAATCACC	1
M00764_extra_29_ATP2C1	GATGGAATCATTGAGAAGGTTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCTTTAATGATCC	1
M00764_extra_2_ADAM22	GGGATTCTGACTTCAAAAACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCCCTTGAGTTCCAGG	1
M00764_extra_300_TANC1	TCCTCCTTGCCTTTGCTATATGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCTAGAAATCACC	1
M00764_extra_301_TANC1	GCCTCAAATAGAAAGAAAGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAATAGTGAAAAGCA	1
M00764_extra_302_TANC1	GTCTGTTTTTACTGGCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATAAGGGTGACAGCTGCT	1
M00764_extra_303_TOX3	GTTTTCCTAAATGAGGCTTTAACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAAAAGCAAGAGT	1
M00764_extra_304_TOX3	GGGAGAAGAGGGGCCCCGGAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGAGGAGGGTGGG	1
M00764_extra_305_TOX3	GGAGGGTGGGACACACGGGACGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCGAGGAGAGGGG	1
M00764_extra_306_TOX3	GACGGCTTGGGGATGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCGTCTGGGTTAGGTGTG	1
M00764_extra_307_TREM1	AGCAACCTGACATCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAGAAGTTCTTTGAATCAATG	1
M00764_extra_308_TUBB3	CTGGTGCTGGGGAGCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTGGAGGGTCTGTGTTC	1
M00764_extra_309_TUBB3	TCCGTGGGTCGCCGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTTGCCGGTTTTGGGTGGGGG	1
M00764_extra_30_ATP2C1	GCTTCCATTAAGGAAAAACAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGTCAAGAAATATG	1
M00764_extra_310_TUBB3	GGGGCCATTGTCCTCCCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGATGGTGCGGGTTGG	1
M00764_extra_311_TUBB3	GGGGCCATTGTCCTCCCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCATGGTGCGGGTTGG	1
M00764_extra_312_UNCX	ATTTGCGGAGGGGCGGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCTATTTGCCGCTCAATG	1
M00764_extra_313_UNCX	AACAAGACGGGCTGGGGGCGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGACCAATAAGAA	1
M00764_extra_314_UNCX	ACAATCAGGCGGCGGGCTGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCACGTGGTCGGGTG	1
M00764_extra_315_UNCX	GAAGAAGAAGCGCAAGCACGAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGGAAGAAGGAG	1
M00764_extra_316_UNCX	TACGCGCCTCTCCCGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTTTCGTTTACTCTTAAA	1
M00764_extra_317_VAV3	GCAGTGTATGTGTGGAGGTCACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTCTAAGAGTTGG	1
M00764_extra_318_VAV3	GAAAATGGATGGCACTGGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAATTAGAGTGGTAT	1
M00764_extra_319_VAV3	CAAAATATAAGGATGGGGCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCCATTGCAGCCTTGA	1
M00764_extra_31_ATP2C1	GCATAATCTAGTACATTAGCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTGCCATTCCAAAT	1
M00764_extra_320_VAV3	GATCCTCCAAAGTGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAAAAAGGACAGTAGTAG	1
M00764_extra_321_VAV3	GGACAAATTACCTATAATCCTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAAATGAGGCAGC	1
M00764_extra_322_VAV3	GTGGGGGGGGAGGGGGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGGAGAGGACACATCTAG	1
M00764_extra_323_VAV3	GGATTTAAAGTAGCTAAATATGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGGCTGGTTGGG	1
M00764_extra_324_VAV3	GTGAGATATGGCTTATCAATCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGTACAAGATAGC	1
M00764_extra_325_VAV3	GAGATTGATTGATTGATTTTAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTTGTAGGATTATT	1
M00764_extra_326_VAV3	ACACACAGTCATCTGTGATTCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTGACACATTTC	1
M00764_extra_327_VAV3	GGGAAGCCGCCCCGAGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACTTTTTTCATTGCTCTG	1
M00764_extra_328_ZNF175	GCTCTCTATACCTGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTCTCTATATTTTTCCCTCT	1
M00764_extra_329_ZNF175	GTGATGAGGGGCTTGTTGGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGCGACCATTTAGC	1
M00764_extra_32_ATP2C1	GAGACCAAAGAAACTATCCATTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCGGAAACTACTT	1
M00764_extra_330_ZNF175	GGGGTGGGTGATGGGTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCTGGCTTTGGGGGA	1
M00764_extra_331_ZNF175	GGGGTGGGTGATGGGTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCTGGCTTTGGGTGA	1
M00764_extra_33_ATP2C1	GTTTTTGACTCTATGACTAAGCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGGTATTTGGATT	1
M00764_extra_34_ATP2C1	GTTCATAAACCATTTGTTTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAAGAAGGTACAGAAC	1
M00764_extra_35_ATP2C1	GCCAAGTGTTGACTTTTACAAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCCATTTTGAGC	1
M00764_extra_36_BBS7	GTCCAGAATTTCCAATAGAAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATACACAGTTAACTTC	1
M00764_extra_37_BBS7	GTTCAAAACTTTGGTGGTGAGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTGTATTTCACACA	1
M00764_extra_38_BBS7	GAGAGGGAGTTTTTAAATCTGACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATACAGAAGAAATC	1
M00764_extra_39_BBS7	GCTGTGATTCTGAGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAAAACATAATTTATGAACA	1
M00764_extra_3_ADAM22	GCCGAATTCTACCAGAGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACATACACTCTCCCAAT	1
M00764_extra_40_BBS7	CCCCAGCTGGTTCCTATGCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGATGTCATTGAAATC	1
M00764_extra_41_BTBD9	GAGGCCCTGCAGCCAGGAGCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGGCCTCATGGCCTG	1
M00764_extra_42_C15orf61	CCACTGATATTTATGTTCTTTGACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTCACCTCTTGA	1
M00764_extra_43_C15orf61	CCCTAGAACTAGGTTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTACAGTATCTGCTTCTTT	1
M00764_extra_44_C15orf61	GTAGAGAAAGTGAGTGGAAGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATAATTACAAACA	1
M00764_extra_45_C7orf62	GTGACATGACTAAAGGTTACATAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAACAAATAAAGGG	1
M00764_extra_46_CACNG8	GGAGGGGAGCGGCGGGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGAAGGAGGGGAGAGG	1
M00764_extra_47_CACNG8	GCCCGACTCGTGATATGGGACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCAGTGGTGGGGG	1

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M00764_extra_48_CACNG8	GGCGCAGGCGGCCGCGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACCGAGAAATAGAGAAATT	1
M00764_extra_49_CACNG8	ATTCTGGGCGCAGGGATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCTTTCCTTCCTCCCCCG	1
M00764_extra_4_ADAM22	AGTTTACACATATCTGCTTTAACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTCTTGCCTCCA	1
M00764_extra_50_CACNG8	GAGGGGAGGGAGGGACTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGAGGGAGCGTCGTG	1
M00764_extra_51_CACNG8	TAAAGAGACACAGCGAAGGGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGTGTGCATGGGG	1
M00764_extra_52_CADM1	GCAAGGACTATAGTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTTCAGGTCTCAGTTCAGGG	1
M00764_extra_53_CADM1	ACATTTTGGAGTGGAAGCTAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTATGGCAGTGTAA	1
M00764_extra_54_CADM1	GCCATTAGGATTTCAGCAAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTAATGGAGGTG	1
M00764_extra_55_CADM1	GCGGAGAAGAGCAACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTAGGAAGTGGGGGGA	1
M00764_extra_56_CADM1	GCGGAGAAGAGCAACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTTAGGAAGTGGGGGGA	1
M00764_extra_57_CCDC148	CTTTGCCTTTCTTTTGTGATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTCATCCTCAAATTCT	1
M00764_extra_58_CCDC148_PKP4	CTGATCCCTGGAGCGACGACGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTGGTGGGAGAG	1
M00764_extra_59_CNTN4	GCGGCCAGGGATGCGCCGAGGCGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGAGAGGCGGCAG	1
M00764_extra_5_ADAM22	GTTCAATGTGTCTCTCTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCAAAACTGTACATTAGA	1
M00764_extra_60_CNTN4	GGATCTCTCTGAATGATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTTTTGTGATAAGGATAT	1
M00764_extra_61_CNTN4	GGATCTCTCTGAATGATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTTTTGTGACAAGGATAT	1
M00764_extra_62_CNTN4	ATGGATTGAATACAGCCTGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTAGAAAGATACTA	1
M00764_extra_63_COL20A1	GTGTTGGGCTGGTCCAGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGGGACAGCTGTGAG	1
M00764_extra_64_COL20A1	GTGGGTTGGGTGGTGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCCAGGGCAGGGGCAGGG	1
M00764_extra_65_COL20A1	TAGTGTCCAGCACCCACACGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGTTGGGTGGTGG	1
M00764_extra_66_COL20A1	GGGATTCTGGCTGCCCACTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGAGGCAGGGGCTG	1
M00764_extra_67_COL20A1	GAGATTCTGGCTGCCCACTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGAGGCAGGGGCTG	1
M00764_extra_68_COL20A1	AAACCAGGCCCGGCCCACTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGTCTGGGGGA	1
M00764_extra_69_COL20A1	CGGGGGTGCAGGGTGTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGCTGGACATGTGGAG	1
M00764_extra_6_ADAM22	GTTCAATGTATCTCTCTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCAAAACTGTACATTAGA	1
M00764_extra_70_COL20A1	GGGGGGTGCAGGGTGTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGCTGGACATGTGGAG	1
M00764_extra_71_COL20A1	GGGGCCCACTGCCAGTGTCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTGCCTTTGTTGTGGG	1
M00764_extra_72_COL20A1	GCTCCAAGGGACAGCCGTGAGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGAGAACACCCAG	1
M00764_extra_73_COL20A1	GGGCCCTGTCTGGCAGGCATGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTCTGGGAGGGTG	1
M00764_extra_74_COL20A1	GTGGCGTGGTGTGGGTGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCAGCACTTCCTTGAG	1
M00764_extra_75_COL20A1	CAGCCACGGTGAGCAGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTAGGGGTGTGGCATG	1
M00764_extra_76_COL20A1	GAGATGGCAGGGGAGGGAGGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGAAGGCAGAGGGC	1
M00764_extra_77_COL20A1	GGCTGCTCTGAGGGTCATGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGGGGGCTGGGT	1
M00764_extra_78_COL20A1	GCCTGGCTCACAAGCTGGTAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCCAGGTGTGCTAA	1
M00764_extra_79_COL20A1	GGCCAGTGTGAGGACAGACAGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTGTGGGGAGGAGG	1
M00764_extra_7_ADAM22	CTAAGCTCTCATCTTAGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACAGCTCTGACTTTAGAT	1
M00764_extra_80_COL20A1	GCCTCTGGGGTGCTGGGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGTACTGGGCTCCTGG	1
M00764_extra_81_COL20A1	GCCATGACTGGCTTTGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGGAGGAAGGATGGG	1
M00764_extra_82_COL20A1	GAGGAGCTCCTGAGGGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGCCTGGAGCTGTTGG	1
M00764_extra_83_COL6A6	CACTTTTACAGGTTAGAAAAGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTACTTTAGGGAT	1
M00764_extra_84_COL6A6	CTCTTATGCAATCCTTACCTTAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGTAGGTAAATGG	1
M00764_extra_85_COL6A6	GTCCATTTAGTCCTCTGTTTCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAATAAAAAAGGAAA	1
M00764_extra_86_COL6A6	GGGCTTGTAAAATCGTGATGCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGAAATGTCCAAA	1
M00764_extra_87_COL6A6	GGACTTGTAAAATCGTGATGCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGAAATGTCCAAA	1
M00764_extra_88_COL6A6	CCTGTGGGTCCTTCTATGCTACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTTGATTCCAGTT	1
M00764_extra_89_COL6A6	GCATTGGTTCCAGGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTACTTGCTTAGAAATACTG	1
M00764_extra_8_ADAM22	GCTTGAGGTACTGGAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTTATAAAATTTAAGTTA	1
M00764_extra_90_COLEC11	GAAAACACGAACTACAACATGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTGTAAAAACAC	1
M00764_extra_91_COLEC11	ATTCCACACACATAATAAAATTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGGGATAGCGGA	1
M00764_extra_92_COLEC11	GCCGCTGAGGGGAGTCACGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGCCCGGTGTGAAATG	1
M00764_extra_93_COLEC11	GCTGCTGAGGGGAGTCACGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGCCCGGTGTGAAATG	1
M00764_extra_94_COLEC11	TGCCCCTCCCCCTCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGGGTTTGAATCTACTTTTCT	1
M00764_extra_95_COLEC11	GCTGGGAGGTGGGAGGGAGCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTTGAAAAGTGAG	1
M00764_extra_96_CORO6	GCGTGGAGCAAGCGCGCCGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCGGGGGATGGGG	1
M00764_extra_97_CRBN	GCTGCTATAATTTCAGCTGCTATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTCTTTAAAGTG	1
M00764_extra_98_CRBN	GGGCTTTGTTCCTTTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAACTAATAATTTGATCCTG	1
M00764_extra_99_CRBN	GGGCTTTGTTGCTTTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAACTAATAATTTGATCCTG	1
M00764_extra_9_ADAM22	CGTCTGTGTGTCTTTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTATAAAAGAGTTTATAGAT	1
M00764_EYA2_MIP1	AGACCCCTGAACCGTTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGATGGAGTAAGTGGGG	1
M00764_EYA2_MIP100	ACATGCCTGGTTAATCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCAATGGGCATTTTTGA	1
M00764_EYA2_MIP101	GAACTGGGACTTTTGCATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGGTGGGAATTTGGGG	1
M00764_EYA2_MIP102	CAGCACATACAACTTCTCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCTGTGCATTTCGAG	1
M00764_EYA2_MIP103	GGGAGGGACAGTGTTAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTAGCGGAAGGCCAGCTT	1
M00764_EYA2_MIP104	ATGGATGCTGTCAGTGTCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGTGGACTGGATGAG	1
M00764_EYA2_MIP105	AACAGGAATCTAGCTACTGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAGAGCTTCCAGCT	1
M00764_EYA2_MIP107	GATGAGGTTTAGTGCCTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAAGTGTACAAGTGA	1
M00764_EYA2_MIP108	CAGTTGGCGGGAAATCTGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGGGCAGGAATTAG	1
M00764_EYA2_MIP109	CAACCAAGACAGGTAGGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTCCTTTGTCCTT	1
M00764_EYA2_MIP110	ACTGTAGATGTTCTCAATAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACACTCCATCCAT	1
M00764_EYA2_MIP111	GGATTGCAGCCAATACCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTCCACACCATCAC	1
M00764_EYA2_MIP112	CATGATTTCCTCCACTCCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCTGTCTACGTGGTG	1
M00764_EYA2_MIP113	CCACGCCTGTGGTTAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATACTCCAGCTCCAGGG	1
M00764_EYA2_MIP114	CCACGCCCGTGGTTAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATACTCCAGCTCCAGGG	1

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ID	**MIP**	***c***
M00764_EYA2_MIP115	CACCGAGAACTCCAGAGACCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCGGATATCCTGCCA	1
M00764_EYA2_MIP116	GAGGGGGTCTGAGGGTGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAACCCCCATTTGGA	1
M00764_EYA2_MIP117	CAGAACAAAAGCAAGGAATTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCATCTCAGAAGCCG	1
M00764_EYA2_MIP118	GAGTCTTACAGAAGAGTCTAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGGTACAAGAGCA	1
M00764_EYA2_MIP119	CAAGTTGTGCTTTGTGGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTAGTCTCATTACTCC	1
M00764_EYA2_MIP12	GATCAGGAACACAGCTGACACTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTTAACATGGGGA	1
M00764_EYA2_MIP120	GAGTGCTTACATTAGAACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGTCCACATGACGT	1
M00764_EYA2_MIP121	GCTTTGTGATGGATAAAAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAAGCTGTTGAAAAG	1
M00764_EYA2_MIP122	CCCATTCCTTCCCAGCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACTGATAAAGTCTTTA	1
M00764_EYA2_MIP13	AAGTTGTTGAAGTGACAACAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCCCCACAACTT	1
M00764_EYA2_MIP14	AGCCACAAGGAAGTGATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGTTTTGATACAGGTAT	1
M00764_EYA2_MIP15	GCTTGTGTGCAGCAGGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGCTGATTCCTACTC	1
M00764_EYA2_MIP16	GGAAGATGCCTACCTGGAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATCTCCCATTCCTCG	1
M00764_EYA2_MIP17	CACAAACACCTGTAAAAACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGCCAATCACTGTAG	1
M00764_EYA2_MIP18	GTTATTTAATTTCCCTAGGTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCAGTTCCGGCAG	1
M00764_EYA2_MIP19	GTGTGGAGCGAGAGAAAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGAAATCGCTTACTCA	1
M00764_EYA2_MIP2	CCCTATGTTTCACCCATTTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGGGAGTGGAGGAGA	1
M00764_EYA2_MIP20	CCCTCTTGCCACAGGGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGCTTATAACCTCTGAC	1
M00764_EYA2_MIP21	GAGAACAAACTGGAGGGAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGCCAGATCAAGGC	1
M00764_EYA2_MIP22	GGGGGCAGTTGCTCAAACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCACAGGCTTCTGGACA	1
M00764_EYA2_MIP23	CCCAAACCTGGACGTCTCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGCAGAGGACAGATG	1
M00764_EYA2_MIP24	CACGGGGGTGTGGAAAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTTTGATTTCTCAGCC	1
M00764_EYA2_MIP25	GTACACCAGCTACCTTGGCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTGGGGGAGCCCG	1
M00764_EYA2_MIP27	GGCTTGTGCCATTTGTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTCTTTCTTTGTTGCAT	1
M00764_EYA2_MIP28	CCTTGAAGGCTGTCTGAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATCAGGGTTTTGCAAC	1
M00764_EYA2_MIP29	GCTTCCCTTTCACGAAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTCACATTCTCCCCAC	1
M00764_EYA2_MIP3	CCTCTCCATGTGAATGCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGCTCTAGCTAAAAT	1
M00764_EYA2_MIP31	GATCACCCGGAAACCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGAGTCAGAGAAGGCAC	1
M00764_EYA2_MIP32	AAATGCCGTCTCTACTAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTGACTGTGGTTAAGA	1
M00764_EYA2_MIP33	CCTAGTTTGCTCTGGCTCATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCCGGCCTGTTTT	1
M00764_EYA2_MIP34	GCTGAGAAAGAGACAGACAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGAGAATACACCCAG	1
M00764_EYA2_MIP37	CACTGTAAACAGCGATTGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATATTTATACTCTTAG	1
M00764_EYA2_MIP38	GTTCTACCATTTCCTTGTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGACCCAAACTCACA	1
M00764_EYA2_MIP39	CCCCTGCCATTTAAATGCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGACAGACAAGGTAGG	1
M00764_EYA2_MIP4	AGCAAGACAGTTTCAGAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGAGCATCTACTGTG	1
M00764_EYA2_MIP40	CATCCAGGAGTGGAAATGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGGAGGAACATCAA	1
M00764_EYA2_MIP41	AAAACCGCTCCCTTCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCATCCATTGTACAGATG	1
M00764_EYA2_MIP42	AGTGCACCCAGAAAGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACATTCTTTCTGTCTCT	1
M00764_EYA2_MIP43	GTGCAGTTAAGGAAAAATGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCAGGAGCAGACTT	1
M00764_EYA2_MIP44	ATTTTTCTTTTTCTCCTGCAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCCTCAGATAAGC	1
M00764_EYA2_MIP46	CACCAAATCCCATTTTATTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGTGGAAAGAGGG	1
M00764_EYA2_MIP47	GACGCAGTACAGTGCGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTTGATATCAAGATAAG	1
M00764_EYA2_MIP48	GGCCGTAGGCTGCCATGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGGGGACCTGAGGAGGA	1
M00764_EYA2_MIP49	GAGATAAAGGGAAAAGAGTAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCCTACAGTGAGT	1
M00764_EYA2_MIP5	GCCGTCGTTCCTTTCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAGTCTGTCTTGTTCTA	1
M00764_EYA2_MIP50	GGTGGCTTGTCAGCCAAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAAGGAAGAGGGGGA	1
M00764_EYA2_MIP51	AGCCCATACACCTACCAGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCTTGGTCCTTTTTT	1
M00764_EYA2_MIP52	GGTGCTGAAGCTGGAGCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAAAATCTGCTGAATG	1
M00764_EYA2_MIP53	AAGGAGGAAATGGACTGGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGTCACCCTTGAAGC	1
M00764_EYA2_MIP54	GCCTGTGGGAAGGAGGAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGATGTAAGGGGAATA	1
M00764_EYA2_MIP55	CATGCAGATGCTGGCACCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCAAGGGAGTGGAGG	1
M00764_EYA2_MIP56	CAGGCTGCTCTCCCGCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACAAGTTGATGTATAAA	1
M00764_EYA2_MIP57	GGTGCTTCTGTGGTAGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCATTTTGGTTTCCC	1
M00764_EYA2_MIP58	GTCCTTGGTTTGTTTTTCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGGGGTCTGCTTC	1
M00764_EYA2_MIP59	CACCATTAGAATAAAAGCTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGGGTACTGGCTC	1
M00764_EYA2_MIP60	CAGGAGGCATCTCACAACGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACTATCCTTCCTACCC	1
M00764_EYA2_MIP61	GGACGTAGGGAGGGTTGTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAATGGCCCCACCAG	1
M00764_EYA2_MIP62	CCTGAGAGCTTCTCTGAAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGCTGGTAGGTGCAG	1
M00764_EYA2_MIP63	GGTCGCTTGAGCCCAGGAGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCGCTTGATTGCTTT	1
M00764_EYA2_MIP64	GTGGCACATTTCCCTCCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCATAGAGACAGGGTCT	1
M00764_EYA2_MIP65	GAGAATTAACAAGTCAGGGGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGCACTGCTCCAGG	1
M00764_EYA2_MIP66	ATTTAAGGGACTTCCAAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATGACTGTCTCCTCTC	1
M00764_EYA2_MIP67	GCCCATTGGTGACCTTCATTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTGGGTGTCTCC	1
M00764_EYA2_MIP68	ACACAATGGACCTTCCACACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGCTGCCTTGGAA	1
M00764_EYA2_MIP69	GTTGTATTCACCTGGCGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCTCATTGTCCCCTG	1
M00764_EYA2_MIP70	CAAGTACGAGGCGGAGAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTAAGAGGAGCAGTGA	1
M00764_EYA2_MIP71	AAACAAGGAAGAAAACCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAAATTGGAATTCTGT	1
M00764_EYA2_MIP72	ATACATCCTTAAGTTGCTTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTCCAATGTGGACT	1
M00764_EYA2_MIP73	GAAGGTACATTGTTGCAAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAACCCAGAAATACAA	1
M00764_EYA2_MIP74	AATGTCAAATTCAGCCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCCATCATAATTAAAAT	1
M00764_EYA2_MIP75	GCATCCAGATACGGGAAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACATTAAGTCAGATG	1
M00764_EYA2_MIP76	AATGTCCCCGTGAGTAAGGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTTGGAGAAGCTGC	1
M00764_EYA2_MIP77	GAGCCTGAGGAATCTTAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACCTCCAGGTCATTGA	1

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M00764_EYA2_MIP78	AAGAAGGATGCTGCCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGCCTTATGATGGAAGA	1
M00764_EYA2_MIP79	GCGACAGATTGAAACTCCATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTAGCCAGGTGTGGTG	1
M00764_EYA2_MIP80	GCAACAGATTGAAACTCCATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTAGCCAGGTGTGGTG	1
M00764_EYA2_MIP81	GCAAGAGAAGAAAATGGACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGAGATCAAGCCACTG	1
M00764_EYA2_MIP82	GGACTATTGCAGTAGCCTCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTCCTTGCCACCTC	1
M00764_EYA2_MIP83	CCCCTGTCTGGGGTACGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACTAGATGTGGAGGTTG	1
M00764_EYA2_MIP84	ATCCTCCACTGCATACCAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTATTCCATGCCTG	1
M00764_EYA2_MIP85	CTGATGTCTTCAGAGTCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAGCAGATAGATGAG	1
M00764_EYA2_MIP86	CACAGAAATCCCACAAAATACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAACTGGCTTCCCTA	1
M00764_EYA2_MIP87	AACCACGTTATACGATGATGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTGGAAGGAGGA	1
M00764_EYA2_MIP88	GCTTCTGGCACTGGGACATTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAAGGCTGTGCTT	1
M00764_EYA2_MIP89	CCTCTAAGGGAGTTCCTTCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTCCCTGTCAAAAT	1
M00764_EYA2_MIP90	CCTGTAAGGGAGTTCCTTCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTCCCTGTCAAAAT	1
M00764_EYA2_MIP91	GGTACTACTACAGGCTCGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCCTTGTGGGCACG	1
M00764_EYA2_MIP92	AGAGACCAAGAGAGTCAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGCTGTGGATTCAGCA	1
M00764_EYA2_MIP93	CCATTGTTTATGGTCAGCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGTCAGAGGAGCCT	1
M00764_EYA2_MIP94	CAAAAGCCCTGGTGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGAGGCAGAGGTTGCAGTGC	1
M00764_EYA2_MIP98	ACCAGCAAGACTGAAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGAGCAAAGACCTGAAG	1
M00764_EYA2_MIP99	CAAATTTTCCATAGGATTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATCCAGACTAGAACCC	1
M00764_FAM114A1_MIP10	GAGTGTTGGCTGGACTGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGTGCCTGGAAATA	1
M00764_FAM114A1_MIP100	CAGTTAGTTAAAACACACATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGAAGCAGGTGTA	1
M00764_FAM114A1_MIP101	GAAACCTCTTATTCACATTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCAGCTGCATGTTC	1
M00764_FAM114A1_MIP102	AACTGTGAGCTTCATTTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGACAAATGAAATGCT	1
M00764_FAM114A1_MIP103	GAACACTTTATGTACAATCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCCTTTGTTCCAT	1
M00764_FAM114A1_MIP104	GTTCTCTATTTGGATGTTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACATTTTCATCAG	1
M00764_FAM114A1_MIP11	ATTTCCCATCCTAAACATCTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGCCATCCGGTG	1
M00764_FAM114A1_MIP12	AAAAGTTTGCCCTGGCCGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGAAGCTGTGCTCACT	1
M00764_FAM114A1_MIP13	CAACATGGAAAAACCCCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTACATAGAGTATTGGT	1
M00764_FAM114A1_MIP14	GCCCTGGATAAATAAATCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATCTCAGTAACTTC	1
M00764_FAM114A1_MIP15	GGATGCAGAAGTGCATTGTGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGAAAGCATGAGGTG	1
M00764_FAM114A1_MIP16	AAAATGCAGCTGTGCAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGGAGACAAAGCAGAA	1
M00764_FAM114A1_MIP17	ATGCCCCTCCCCTCTGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATCAATACATTCAGCAA	1
M00764_FAM114A1_MIP18	GTTCTTGCTTATATCTACCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACGTGACTGAGGATACA	1
M00764_FAM114A1_MIP19	CAGTATATCTCTGAATGGAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTACCTACTGTGGCA	1
M00764_FAM114A1_MIP2	CCAAAGCTAATACATCGGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTGGGGGACATTGAG	1
M00764_FAM114A1_MIP20	CCCGTGAGCAAACCATGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCTCTGCTGTCGTCAG	1
M00764_FAM114A1_MIP21	AATCTTACAAAGCTGTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAATTTACACCATGAAT	1
M00764_FAM114A1_MIP22	ACCATGTGCATAATCAGAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGGAGCCACTCTA	1
M00764_FAM114A1_MIP23	GTCCAAGAACACCCAGAGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGCTTTCTGCAG	1
M00764_FAM114A1_MIP24	CCCTGTATTTCCCAGGGCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCAGCCACAGATCAG	1
M00764_FAM114A1_MIP25	ATTCATCGGCAAGAAAACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGAAGATAGTGCCAGT	1
M00764_FAM114A1_MIP26	GACACTTTTACCCTGCAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAACCTGAGACAAGG	1
M00764_FAM114A1_MIP27	ATCAAATGACACCAAAGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCATGGAGAGAACTGT	1
M00764_FAM114A1_MIP28	GGACTTAAAGTTAATCCTGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTACCCTTGCACTCCA	1
M00764_FAM114A1_MIP29	GCAGAAATAAGCTGGCCTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCGGCCAAATTTCTT	1
M00764_FAM114A1_MIP3	GGCAGTCAAATGGGCAAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAACAAACAAACCCC	1
M00764_FAM114A1_MIP30	GCTGAGGGAGGAGGATCACTTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATAAGAGATTCAA	1
M00764_FAM114A1_MIP31	GGGTCTGTAGTCCCAGCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAATCCCAGCATGTTGA	1
M00764_FAM114A1_MIP34	ACGGGTTCAAGCGATTCTCCTGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACATGAGTGATTA	1
M00764_FAM114A1_MIP35	GGAGTCTCACTCTGTTGCTCAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGCCTGGGAATAA	1
M00764_FAM114A1_MIP37	GTGAAAGGCAAAACAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGACTGATTTTGTGT	1
M00764_FAM114A1_MIP39	CCTTAACATCTGCAGAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGGACAGAATTTCCA	1
M00764_FAM114A1_MIP4	GACCTCTTCCCAGTGACACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTGGAAAGTGGGTTT	1
M00764_FAM114A1_MIP40	GCCATTAAAAGATCTCATTTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGTCACACCTGGA	1
M00764_FAM114A1_MIP41	CATGTTTAAGCAACACATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCATAGGACAGAGAAG	1
M00764_FAM114A1_MIP42	AATGACCTAATTTCCATTAAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGGGGACCGCTGT	1
M00764_FAM114A1_MIP43	GAGTTCCAGCTTCTCTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTAAGGATTATGCCAACA	1
M00764_FAM114A1_MIP44	GCATCTGCTCTTGTTACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTAAAGGAAAATAACTT	1
M00764_FAM114A1_MIP45	CATGAGGGAAACAGATCAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTATTTTCTGTTTTAT	1
M00764_FAM114A1_MIP46	AGTATTTTCTTCTTAGAGAGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGCAGATCAACCA	1
M00764_FAM114A1_MIP47	GGCTTATGCCAGTGGGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTAACAGTTCTGAAAG	1
M00764_FAM114A1_MIP48	ATCTCTTTATTGCCCACAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTATTCTCCCCCAA	1
M00764_FAM114A1_MIP50	AGAGTGAGCAGAAGAAATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTATACTGTCTGTTATA	1
M00764_FAM114A1_MIP51	CACATATCATAGGTGCTAAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGATACCTGGCTGGT	1
M00764_FAM114A1_MIP52	GGCACCTGGGTACCATTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGGAAGACAGATCATTA	1
M00764_FAM114A1_MIP53	GTCCACAGAGCCACAGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGAAGGACTGGGATGAA	1
M00764_FAM114A1_MIP54	CCTTTGGGTTGTCCTGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTGTCCCAGGTCTCTTA	1
M00764_FAM114A1_MIP55	GGGACCTCGCTTGTCTTGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCCATTCGTGAGC	1
M00764_FAM114A1_MIP56	CCTGAAGGATGAAAAATAAATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGCCTCACTGCCA	1
M00764_FAM114A1_MIP57	CAGCCTGCAGCTGGGGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCAAAGAGAAGCTCTGT	1
M00764_FAM114A1_MIP58	GAGAGTCTCTGTTGTAAAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGAAGAATTTGCTC	1
M00764_FAM114A1_MIP59	CCAACCCCAAGACTAGAATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACTTTTGCCACATCT	1
M00764_FAM114A1_MIP60	ACTAAGACCATAGAGGTAAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGTGGAAGAGGA	1

continued table…

ID	MIP	*c*
M00764_FAM114A1_MIP61	CCTCCTTTTTGTCTTCTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGGAACAAATGAAAAAG	1
M00764_FAM114A1_MIP62	GTGACATTAGAAGTGATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGAAGCTGCTCAATAC	1
M00764_FAM114A1_MIP63	AGGACCAAGCAAAAGTTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTATTCATTTCAGGAA	1
M00764_FAM114A1_MIP64	AGCTGGTTTTTCCTCTTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAATCTTCTAGTGGCTT	1
M00764_FAM114A1_MIP65	ATTAGGCACACAAAAGTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCACAGCTGAGATTACA	1
M00764_FAM114A1_MIP67	AGGTCAAGTGAGTTGGATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTGAATGCTCATGATT	1
M00764_FAM114A1_MIP68	GCTTGAGCTCCACATGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAATCATCTTCCATGATT	1
M00764_FAM114A1_MIP70	GCTTGAAGATGCTCTACAGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCAGTAGTTAATC	1
M00764_FAM114A1_MIP72	GTCTAATTTCAGGCCTTCAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCTGTCCCCCACA	1
M00764_FAM114A1_MIP73	AAGGTGTTGTTTTACAAAATAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGACCACACGAGGG	1
M00764_FAM114A1_MIP74	CCTAAGGCTCTATTGCACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGACAAAATGCATTTG	1
M00764_FAM114A1_MIP75	ACCGGTGTCACTAAGGCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGATAACCAACTGGGAA	1
M00764_FAM114A1_MIP76	AAGCAGAATGCTTCCTACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTTCTTGTTGCTCTG	1
M00764_FAM114A1_MIP77	GAAAGTGCTTCTGAATCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAGCCTTGTAGTAT	1
M00764_FAM114A1_MIP78	CAGAGGCCACTTACCTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACACAAATTTACTCAAAA	1
M00764_FAM114A1_MIP79	CCAATTGGATAATGTTCCCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAGACCTGCAGAAC	1
M00764_FAM114A1_MIP80	GTACCATTTAAGGGGATGTTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCTTCCAGCTGCT	1
M00764_FAM114A1_MIP81	GATGGAGTCTGGCCAGGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTCTCAATATTGTCT	1
M00764_FAM114A1_MIP82	ACAGCTTATATTGAAAATTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGACACTACAAGCAA	1
M00764_FAM114A1_MIP83	CACATTGAGAGAAATGATAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGCTTAACCAGGAA	1
M00764_FAM114A1_MIP85	GGAACATTTAAAGGTTGAAACATACTTCAGCTTCCCGATATCCGACGGTAGTGTATGACAATATGTTCCT	1
M00764_FAM114A1_MIP86	GAGTGCGTTGGCACAATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTACATAAATGTCGCAGG	1
M00764_FAM114A1_MIP90	CACCCCCAGGCCACAGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATTCATTCTTGCAACAA	1
M00764_FAM114A1_MIP91	GGACCCCTGTTTTAAGCAGTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGCTCTGGGGAGC	1
M00764_FAM114A1_MIP92	CATTAGAGTCTCATGGGAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTAGGAACCAGGCCA	1
M00764_FAM114A1_MIP93	GCTGCTGACCTGATGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGCTATTCAACCTCAGA	1
M00764_FAM114A1_MIP94	GCTGCTGACCTGACGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGCTATTCAACCTCAGA	1
M00764_FAM114A1_MIP95	GGGACCACTGGCTTAAAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATCTAATGCCTCATG	1
M00764_FAM114A1_MIP96	ACCTTTCTGGTACCAGGGACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGTGTAAAGAGTATA	1
M00764_FAM114A1_MIP97	GCACATGGTGGCATAATTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTTAATTTGTTGCATT	1
M00764_FAM114A1_MIP98	CGTGATCGTAAGAAATTAATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGCCACCAGCGA	1
M00764_FAM114A1_MIP99	ACAGAAGACCCTGCGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCAGGACTGCATTTTAA	1
M00764_FAM171A1_MIP1	GTTATTAAGACTTTGTCAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGTGCATTCTTCTT	1
M00764_FAM171A1_MIP10	GGTTTCTTAATGTCCCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTCTCAACGACAGCTT	1
M00764_FAM171A1_MIP101	GTCAAGCAGAGACTCTTTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGATCAGATATCCA	1
M00764_FAM171A1_MIP102	GAACTACAGTCAGGCTCCGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTATGCACTTTTGGA	1
M00764_FAM171A1_MIP11	CACGTGATGTCGCTATGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTAAAGTTATTACTCGG	1
M00764_FAM171A1_MIP12	GTACGCGCTTCCATGAGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCAAAGTCATCCTTTA	1
M00764_FAM171A1_MIP13	GGACGGACGTGGACGTTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGATGGCGTTTAACAT	1
M00764_FAM171A1_MIP14	GTGGGCAGATCTTCTCTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCACAGTCAGGTGGGT	1
M00764_FAM171A1_MIP15	AGGAAGAGGAAGACGATGATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTTGGAGGGGTCG	1
M00764_FAM171A1_MIP16	ACTCTGTTCCACGTCATCCAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTCCGTCTGGTCG	1
M00764_FAM171A1_MIP17	CGAATGTGGGACCACGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGATGCTTTGTCTC	1
M00764_FAM171A1_MIP18	ATTACTTCCGTTCCTTCCAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCGAGGCTCTTTCT	1
M00764_FAM171A1_MIP19	GGACTCTGGCGTAGATATGAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGGAAGCCGCTTC	1
M00764_FAM171A1_MIP2	GACTCCCACATTGGGTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATAACCAAGCAGCTCTT	1
M00764_FAM171A1_MIP20	GGATGGAGAGAGACTCCGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGGAGACGAACCAC	1
M00764_FAM171A1_MIP21	GCTCAGATGAACAGTGAGGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCTGTCTTCCCA	1
M00764_FAM171A1_MIP22	GTAGTCTTTCTATCTCAAGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCACTCCCGGGTG	1
M00764_FAM171A1_MIP23	GGCTGAGCTGTCCAATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCGTTTACAGGAAAGTAC	1
M00764_FAM171A1_MIP24	GTGATCTACTGATCGCGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGTTTCATATAATGAG	1
M00764_FAM171A1_MIP25	GCCAGTTAATCTGCTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTCAGGAACATCTGTAC	1
M00764_FAM171A1_MIP26	GTAACTACCCCTGTAGTCATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGCTGTTCTTTCT	1
M00764_FAM171A1_MIP27	GTGCTCTCACAGCCTTTATTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTGGGACGCTGGG	1
M00764_FAM171A1_MIP28	AGCTTGAGCATGGGGGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACTTATGGTAGTCTTT	1
M00764_FAM171A1_MIP29	CCTCTCTTGCAAGGAAGAGGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACGAAGGAACTGA	1
M00764_FAM171A1_MIP3	GTTTGAGCAAGCGAGCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACGTTAGAGATGCCCTT	1
M00764_FAM171A1_MIP30	GTGGACTGGTCTCTTTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAAATGGACTCCACT	1
M00764_FAM171A1_MIP31	ACACATTAACTTGCTGTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTAATCTTTGGCTTTGG	1
M00764_FAM171A1_MIP32	CAAGTCAGGAGCAGCCAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCAAGCACTTCCTCCT	1
M00764_FAM171A1_MIP34	GGTAAAGTGTTACCATTTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTGACCTTCTAGGT	1
M00764_FAM171A1_MIP35	GAGCAGTGGCCAGAGGAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCCTGTGTTACAACGG	1
M00764_FAM171A1_MIP36	CCGTGTTACCTGGGATGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTCATTTTCAGACTTTT	1
M00764_FAM171A1_MIP37	GCCAACACTTGCGATGATGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAACGTGGCTGAAGA	1
M00764_FAM171A1_MIP38	CCTTTGTAAGGCTTGAGCATATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCAACTGGGGGGC	1
M00764_FAM171A1_MIP39	CAGAGTCTCTTACAAGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAGGTATTAGTTATCAAC	1
M00764_FAM171A1_MIP4	GACCCCAAATGGCACTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACCATAATGGTGCCACA	1
M00764_FAM171A1_MIP40	GTTTTGTACAGTTTTGGCAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGTGTTACACAGC	1
M00764_FAM171A1_MIP41	AAATTACCCATAAGTCTCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTAATCTTCATCCT	1
M00764_FAM171A1_MIP42	ATGAGTTCCCAAGAGAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATGACCTTCTGATGAATA	1
M00764_FAM171A1_MIP43	CCTAATTTACTTGAAAAGAATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTGCTGCTCACAT	1
M00764_FAM171A1_MIP44	ACTCTTGCTTACCCAGCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGAGAAACCACACAAT	1
M00764_FAM171A1_MIP45	CAGATGGCTTCGTTACTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGATGGTCCCATCTAT	1

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M00764_FAM171A1_MIP46	GCATTTTCCATCATTTGCATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGGGGCACAGTGA	1
M00764_FAM171A1_MIP47	CCTTCTAGGAAACAGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTATGTATGTAAAGTGC	1
M00764_FAM171A1_MIP48	CATACACTCAGTATGGGCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAGGGACTGCATGA	1
M00764_FAM171A1_MIP5	GCATCCTCGTTTCAACACAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGTCCCTCGCTTTTT	1
M00764_FAM171A1_MIP50	ACTACCCTGATGGATAATTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGAAGTCTCATTCCG	1
M00764_FAM171A1_MIP51	CACCTCCGAAGGGGAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGCTAAAACTCCCAATCA	1
M00764_FAM171A1_MIP52	AGGATTAGACGGAAATGGAACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGCCTCGCGTTC	1
M00764_FAM171A1_MIP53	GCCTCTCTAAGGTTTCAGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAGGCAACCTCAGAG	1
M00764_FAM171A1_MIP54	AAACAGAAACTGCTCCTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCATAATAGCATGTTGT	1
M00764_FAM171A1_MIP55	CAGTCTTGTCACTGCCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAGGACACAGAGATG	1
M00764_FAM171A1_MIP56	GGAACTTGGAAAAAGCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGAGTATCTCTTACATT	1
M00764_FAM171A1_MIP57	GGCAAGGGAATTAACAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGAAACAAGTAGATGAC	1
M00764_FAM171A1_MIP58	CCTTCAATTTGGTTCATGGCATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAAGCACGCCTCC	1
M00764_FAM171A1_MIP59	GACAGGTTGGGCTGACAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCATCATCCAGTCTATT	1
M00764_FAM171A1_MIP6	GCTTGGATGTTAAGAGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAAGAAAACCAACAACA	1
M00764_FAM171A1_MIP60	CAAAAGTCTCATCCTAAATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGAAAATTTGGAGC	1
M00764_FAM171A1_MIP61	CCTCCCGTTCAAGCGATTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGCAGCTTAACTTT	1
M00764_FAM171A1_MIP62	GCAGGGTTTCACCATGTTGGCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGATCTCAACTCC	1
M00764_FAM171A1_MIP63	GTTCAGGTTTTATGATCAAAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTCTGCCTCAAG	1
M00764_FAM171A1_MIP64	ATATACCATTAGAGTGGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATACAAACATCACATC	1
M00764_FAM171A1_MIP65	AATAGTATCAGGATTCCAAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGCACTTAAATATGA	1
M00764_FAM171A1_MIP67	ATCCGTGGGTAGTGCTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTGAATTCTAAAACAC	1
M00764_FAM171A1_MIP68	GCTGCCTTCACCCACCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGATGTTCCTTTCCCTC	1
M00764_FAM171A1_MIP69	ATAAAAGAAGTTTGCCGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGGAGGTGCTGTTCAT	1
M00764_FAM171A1_MIP7	CCTGGTCCCATTAACTCCAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATCTGTTCCGCTTC	1
M00764_FAM171A1_MIP70	GATCGCATAAGGCCAGGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGTCAGTTGATTGTC	1
M00764_FAM171A1_MIP71	GAGGCTATGGAGGCCTGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTAACCGGATTGGCTT	1
M00764_FAM171A1_MIP72	GATGGCGTCGCCTTTATCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTCTCTACCTCCAGA	1
M00764_FAM171A1_MIP73	GTTGACACTCAAAATATGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCACCTTTAACGTCAC	1
M00764_FAM171A1_MIP74	GATGTCCTTACAGAGCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTAAAGAAGAAAGCA	1
M00764_FAM171A1_MIP75	CATTGGGCAACCAATGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGGTCTACTTTTACTT	1
M00764_FAM171A1_MIP76	AAGAAAGCAGTTTGGGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACAGAGTGAGACTGT	1
M00764_FAM171A1_MIP78	GTTTTGCCATGTTGCAAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGTGCGTGATGATGG	1
M00764_FAM171A1_MIP79	GCTATCTGGGTACTCACTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAGTTTCCATGCAA	1
M00764_FAM171A1_MIP8	ATCTAAGCAAAATCAGACAACGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACGCTGAGATGGA	1
M00764_FAM171A1_MIP80	ACGACCCTTCATAGTATCAGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGCCCGTGGTACC	1
M00764_FAM171A1_MIP81	GAAAAAATGGGCTGCGGTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAAGCTGGTGCTGGA	1
M00764_FAM171A1_MIP82	GGGAGGCTGGGAAAATGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCCTTTGGCCAGAAA	1
M00764_FAM171A1_MIP83	CCCACAAGTTCTGTGTGCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAAGAAGCAGGGCCT	1
M00764_FAM171A1_MIP84	GGAGGAGGCTCACAGCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCCAGCTAGATAGAAT	1
M00764_FAM171A1_MIP85	CCTTCCTTCTCAGTACCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCATTAAACCAGCTA	1
M00764_FAM171A1_MIP86	GCACGGTGGAAGGAGAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTGATGGTGAAATAAA	1
M00764_FAM171A1_MIP87	CGCTCAGGAATTCTTCCCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTCACACCTCTTCTT	1
M00764_FAM171A1_MIP88	CGTTTCTTCCTCCTTGGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACCCACAAAGCAGAT	1
M00764_FAM171A1_MIP9	GGTTAGGTTGCGTTTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCACAATAATCCTACTGT	1
M00764_FAM171A1_MIP97	ACACGTGTGAAAGCACAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGACAGCTTCAGGAG	1
M00764_FAM171A1_MIP98	GGACAGAAAGTTTTAAAGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGAACCCAACCTTTC	1
M00764_FAM171A1_MIP99	GGGGATTCTTGAAAGTCAGACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCTGCAGTCGGGG	1
M00764_FTSJ2_MIP1	AAGTCTGGAAACCCAGGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAAGGTACTTTCATGC	1
M00764_FTSJ2_MIP10	ATCCTCACTGCTTCACAGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAGACTCCCCACT	1
M00764_FTSJ2_MIP11	CCTTTTAAGCTAGAAACGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCATCAAACCTGAAGC	1
M00764_FTSJ2_MIP12	CAGGATGTCTGGGGTCACGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGATGACTCTTTCCTGC	1
M00764_FTSJ2_MIP13	ACCTGGGGGGACATTCCTTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGGCAGGAGAGCAG	1
M00764_FTSJ2_MIP14	ATATGTGAAGAAGATCTACCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATTGGGCGCCATG	1
M00764_FTSJ2_MIP15	CCCCCTGGAAGGAGCAACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTTGTTGCATGTACT	1
M00764_FTSJ2_MIP16	GTTTTCTCACCAATAAATGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGGGATGCAGGTAGA	1
M00764_FTSJ2_MIP17	GGCTCAGGGTTTCATGACTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAAAGCCAGGGTAG	1
M00764_FTSJ2_MIP18	GTTAAAGAACCTACGGTGCAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAAATGCCAGTGCA	1
M00764_FTSJ2_MIP19	CACTGTGGCATCAAGGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATATAAAAAGGTTCTCC	1
M00764_FTSJ2_MIP2	GCTTGCTTTGGCAATTACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTTTAAAAAAAACAA	1
M00764_FTSJ2_MIP20	ATCCATAGCCCTGGCCATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCTTCAGTTGCATGGG	1
M00764_FTSJ2_MIP21	GCTCTGGATGAAGCTGAGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATCTTTCCCCAACA	1
M00764_FTSJ2_MIP22	AGAGTTCGAGATCAGCCTAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACTTGGAAATTTAGC	1
M00764_FTSJ2_MIP23	GCTGGGATTACAGATGTGAGCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCCACCGCACCCA	1
M00764_FTSJ2_MIP25	CCAGATGGAGTCTCACTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTGGAGCTATTTTTGC	1
M00764_FTSJ2_MIP26	CCAGGCTTGTGCATGCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGATGATAAAAATAGG	1
M00764_FTSJ2_MIP27	AGCCTCAGGGGAGCCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTTGAAAATGGCAGCA	1
M00764_FTSJ2_MIP28	GGGCATGGGCAAGCTGCCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCGGGTGTTAGACTG	1
M00764_FTSJ2_MIP29	CACAAATGGGTCCCTGAGATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCAGGCCCCAGGAG	1
M00764_FTSJ2_MIP3	GTGATGTGGTGTGTTTATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCGGAACAATTAGG	1
M00764_FTSJ2_MIP30	GCGAAGGTGGAGAGTTACCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTTGAAGCTGGTGTG	1
M00764_FTSJ2_MIP31	ACTCATTCATTTCTAGAGATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGTGGAACCCTTG	1
M00764_FTSJ2_MIP32	GTCATCCCAGCACTTTGGAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGTCAGCACGCTTT	1

continued table…

ID	**MIP**	***c***
M00764_FTSJ2_MIP33	AAAATGGCACAAGCCGGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTACCACCCTCATGGC	1
M00764_FTSJ2_MIP4	CAGATTTTTCTTTTGGTTTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACTGCCTGGATAAA	1
M00764_FTSJ2_MIP41	ATCAGTGTCGGGACAAAGTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGGAGACGAGGAGA	1
M00764_FTSJ2_MIP42	GCCACGGTTTCCAAAGTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACCTTTCCCATTTCAC	1
M00764_FTSJ2_MIP43	CCTCTAGGGGAACATACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATTTACCCTGTCTGAC	1
M00764_FTSJ2_MIP5	ATTTCCATCTGGGGATTAACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTAGAAGGCTGAG	1
M00764_FTSJ2_MIP6	AGAGCAGGGGTGGAAAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCAAGCAATCCCCCAG	1
M00764_FTSJ2_MIP7	AGATTTCCAGTTCTTAGTGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGAAGGAATCCGC	1
M00764_FTSJ2_MIP8	CATTTTCCATGGCCCCTGAACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACCCATCCCTGC	1
M00764_FTSJ2_MIP9	GTCCGCTATATTGTGATTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAGATTTGAGCTGA	1
M00764_GALNT12_MIP1	CCATCTCTACAGAAAAATTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGAGGCTAGGAGC	1
M00764_GALNT12_MIP14	ACATAGGTCATGGTCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTATGATAACAGATGTC	1
M00764_GALNT12_MIP15	CCTTGAGACATCCCCGGATATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAAGTTCCGCTGTA	1
M00764_GALNT12_MIP16	CACTGTAAACTGTCCGAAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCACCTCCCAGACAC	1
M00764_GALNT12_MIP17	GAGGAGCGCCTCATCCCAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGGCCCTCTCTCTT	1
M00764_GALNT12_MIP18	ACCTTCCTGGACTGTCACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTGAAGGAGCGCTT	1
M00764_GALNT12_MIP19	AGAACATCGCCCCTCGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGAGTCTGTTCCTCATG	1
M00764_GALNT12_MIP2	AAGTCAGTGGGGCAGCGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAACTATCATGTACAGCC	1
M00764_GALNT12_MIP20	CGTTAAATGATTTAGTGCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTACCTGGAGTAGGTA	1
M00764_GALNT12_MIP21	CTGAGCCCAGGCAACCCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAGCAAACAGTGACAC	1
M00764_GALNT12_MIP22	GCACCCTCTGCCTCCCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTGCCAGCTGGAGAAGG	1
M00764_GALNT12_MIP23	ATAATAAAAGCAAACAGTGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTGAGGAGGAGAAT	1
M00764_GALNT12_MIP24	ACTGCTTTGGTCAGGCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGCACCCTCTGCCTCCCG	1
M00764_GALNT12_MIP26	CAAGAACATTTTAAAAAATCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTTTGGTCAGGCT	1
M00764_GALNT12_MIP27	CAATGCCTAGGGCCCATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCGAGGAAGTATCATCAA	1
M00764_GALNT12_MIP28	GTCAGCCCTGCTTGAAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTATTACATACCCATT	1
M00764_GALNT12_MIP29	GGAAGGGTCCCTGAAAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTAAAATCAGAAGGGAA	1
M00764_GALNT12_MIP3	GCCATACTCTTTGGAGTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTTACACAGTCCAAT	1
M00764_GALNT12_MIP30	ACTGGAACACCTTCGAATACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCACCCTTGAATTTCC	1
M00764_GALNT12_MIP31	ACCACTGCCGACTCCTCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCCTCTCCCTCTCAGG	1
M00764_GALNT12_MIP32	ATTGAATCTGGCTGACCTGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCGACTGGAGGCTG	1
M00764_GALNT12_MIP33	ATATTACTCAGCCATCACAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGACTCAAGCAGA	1
M00764_GALNT12_MIP34	CCCTTTGACCTGGGGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTAAATAATGCTGCTAT	1
M00764_GALNT12_MIP35	GATGTTTCCTCAAGAATGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCCAGAATGAGAGC	1
M00764_GALNT12_MIP36	GAGGTCAGGACTTCAGCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGTAGAATGGGCCC	1
M00764_GALNT12_MIP37	GCCCAACTCCCACATCTGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGGTCATCTTAAGGTC	1
M00764_GALNT12_MIP38	GGGTTTGGACTTGACCCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGCAGTTGGGCTTCT	1
M00764_GALNT12_MIP39	CCCATCTCTCCAGCCTTATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTACAACGGTCCCCC	1
M00764_GALNT12_MIP4	GGTTTTACCACCACTATCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAATCCTAGTTGATGG	1
M00764_GALNT12_MIP40	AGAATTGGAAGAAATTGAGTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGTGAGGGCCCT	1
M00764_GALNT12_MIP41	AAGTTTGGGGAGGAGAAAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGTTTTCTGCTGTC	1
M00764_GALNT12_MIP42	CATTCCTGTATCATAAGACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTCCACCAGGCTCT	1
M00764_GALNT12_MIP43	CCTTTCAAACTTTGACAGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTATGGAGAGGAGGAA	1
M00764_GALNT12_MIP44	CGCCTCCTGTGTTGAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTTATTTAGCACAGTG	1
M00764_GALNT12_MIP48	AGTTTGAGATCAGCCTGGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTTGTGAATCTGTC	1
M00764_GALNT12_MIP49	CCGTGAAAACCGTATTGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTAAACTTGTTAGAA	1
M00764_GALNT12_MIP50	AGGCTTGTTACAAAAAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAAGCACCAACATTTA	1
M00764_GALNT12_MIP51	ACTCACGCCCTCTGTAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTACATTTTAAGCATCAAAACT	1
M00764_GALNT12_MIP52	CGGTAGAAGGCCAAATTCTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGACTCAACAGGCGA	1
M00764_GALNT12_MIP53	CCTCTTTTCTTCCTTGCTGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAGATGGGCTCAG	1
M00764_GALNT12_MIP54	AAGGGGGAAAGGAAGAGCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGACTCACAGGAGCAT	1
M00764_GALNT12_MIP55	CACATTCTGTGTCATGAGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTGGGTTGCCAGCG	1
M00764_GALNT12_MIP56	GTGGGAACCAAGACCCCAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACGCAAGGCATGAT	1
M00764_GALNT12_MIP57	GGTGGGGTTCTGGAAACACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCATCTTGGCAGTGTC	1
M00764_GALNT12_MIP58	CACTGCCAGATCTGCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTAAATTCATCCATCCA	1
M00764_GALNT12_MIP60	GACCCCATGGGTCCTAGTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGCACATGCAGTTCT	1
M00764_GALNT12_MIP61	CCTGGGCAAGAAAGGCCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTCTTGGAGACTGTGTA	1
M00764_GALNT12_MIP62	GACACTAACAGATGCCACACAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTACAGAATGACCTGG	1
M00764_GALNT12_MIP63	AGAAAGCTGTGTGTTTTGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGGACTAACAGACT	1
M00764_GALNT12_MIP64	GATTCTGGCCCATCCCATGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTGGCCACCCTAG	1
M00764_GALNT12_MIP66	GTTATGTGTAAAAAATGATGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCACTAGGAATGAT	1
M00764_GALNT12_MIP67	CCTTGGGTCAGACAGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTATTAGATACCCCTTGAG	1
M00764_GALNT12_MIP68	AGTACACGTCCCAGAAAGAAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGACGCAGGTGCA	1
M00764_GALNT12_MIP69	AAAAACTAAAAATGGGGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTTCTGATTCTCTGG	1
M00764_GALNT12_MIP70	GTTCTCTCTGGCATAGTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTATCATGCATCTCTG	1
M00764_GALNT12_MIP71	CCTTGAGGGCTTACAATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATCCAATTCAGTATCC	1
M00764_GALNT12_MIP73	AAAGTATTAAGCGTCCTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGTGGGGACATTTCC	1
M00764_GALNT12_MIP74	CAAGGCTGGAGTGCAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAACAGAAACATATGTGA	1
M00764_GALNT12_MIP78	GTTATTCACTCTGCCTGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTTATGTAGGCCTAA	1
M00764_GALNT12_MIP79	GATGTGCTGTTCACTAAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTCTCTCTCAGGCCT	1
M00764_GALNT12_MIP80	CAAGGCATATAACCCACTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGGAAAAGATAAA	1
M00764_GALNT12_MIP81	GCCAATTCCCAAACCCCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAAACAGAGTGTGGAA	1
M00764_GALNT12_MIP82	GTTCCTGATTTCCCTGAAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGTCTGTGGCTGAG	1

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ID	**MIP**	***c***
M00764_GALNT12_MIP83	ATCCTTTGTTTATCTCTTTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTACAGGCTGCGTC	1
M00764_GALNT12_MIP84	CCCTGATCTCTTTAAAACATGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAGAGGCAAGCG	1
M00764_GALNT12_MIP85	AGAAATATTTATTGAGGGGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGACTGTTCGTG	1
M00764_GALNT12_MIP86	GTTCTTCAAAGAGCGCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTATCTTTTGTAGGATG	1
M00764_GALNT12_MIP87	GAGTTGGTGCAGTCTCGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGTTCTGGTCACTGC	1
M00764_GALNT12_MIP88	GTGTTGGATTTAGTAAAAATGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCATCGAAGGAGAC	1
M00764_GALNT12_MIP89	AATGGCAAAATGATTGCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTAAATACCAAGGGT	1
M00764_GALNT12_MIP90	GGTATTTACAAGAATTCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGTAATCGTAAGATG	1
M00764_GALNT12_MIP92	GTTAACACTCCATAATGTTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCGGGGTTAAAGTTT	1
M00764_GALNT12_MIP93	GTGGTAGCAACACATAACCAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACACTACAGTGCGGCA	1
M00764_GALNT12_MIP94	GGTAGTGTCAGGGAGAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGAACAATTTGCTTTA	1
M00764_GALNT12_MIP95	GTCATAGTGGTAGAACCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAACGCTGATTTAAATT	1
M00764_GALNT12_MIP96	GTCAACCTGATTAAGTCAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAAGTTTGTTCATTA	1
M00764_GALNT12_MIP97	AAATCTCAGGGTTGGTCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTAGGAGTATAGGCGT	1
M00764_GLO1_MIP11	GGGAAAGGGGAGGAGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTTATTTTACAAAAGA	1
M00764_GLO1_MIP12	ATAACTACAACAAAAACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATTTGAATTGCTCTCAA	1
M00764_GLO1_MIP13	GGGGTTTCAATTCCTCAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTAGAACAGTTCCCTT	1
M00764_GLO1_MIP14	GAACAGCTGAAATAGGAAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAAATGCAGCCTCT	1
M00764_GLO1_MIP15	CATGTCCTTGAATATAGTTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCATCTAGGACTGA	1
M00764_GLO1_MIP16	GTTGCCATTTTGTTAGGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAAGAATAATTTGAA	1
M00764_GLO1_MIP17	GTAGTGCTGTGAGAATTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTCTTTTTTAGTCTTT	1
M00764_GLO1_MIP18	CCCAGTTCTTCAAACCTTTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTTGTAGCCAAAAGG	1
M00764_GLO1_MIP19	GTCAAATTTGTGAAGAAACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACTTGGACACCCTGT	1
M00764_GLO1_MIP2	GCTTCTAGCAGTACAAGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGATGGACAAAGGTTT	1
M00764_GLO1_MIP20	GGGAACAGACTTAGGTAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAATTCCAATATGACC	1
M00764_GLO1_MIP21	AGTGCCTTATGTTTTGAAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGATATTGATTAATT	1
M00764_GLO1_MIP22	ACTATAGCAGCCAGCTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTGCCTTGAATTATAAA	1
M00764_GLO1_MIP23	GGTGTCGATTATTCTTAACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCACATACACTTCTG	1
M00764_GLO1_MIP24	ATCATGGTGAGATGGTAAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCATCTTGATTGAGAG	1
M00764_GLO1_MIP25	GTCTCAGAATTAATTTCCAGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGTATGATCAATTT	1
M00764_GLO1_MIP26	CATAAAAACAGGCAAACTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGTGGAAAATAAAA	1
M00764_GLO1_MIP28	CCCCTGCTACAAAAATATTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCCCCAATTGCTA	1
M00764_GLO1_MIP29	CATATAAACGTGGTAAGATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTTGTCCAGTACC	1
M00764_GLO1_MIP30	AGCTCCATGGGCTAGGTGTGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAGTATGATTTTA	1
M00764_GLO1_MIP31	GGGTTTAAATGAAATATAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCCCTTGATTCAAAAT	1
M00764_GLO1_MIP32	CCTACATTTTTAAGTGCTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGTCTCAGACTCAT	1
M00764_GLO1_MIP33	CCTACATTTTTAAGTGCTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGTCACAGACTCAT	1
M00764_GLO1_MIP36	CGGCCGAGGCAGACAGATCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTACCTAAAAATTAG	1
M00764_GLO1_MIP38	GCCCGCCTCGGCCTCCCAGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTTGGACTACACAT	1
M00764_GLO1_MIP39	CAGAGAGCCTGTCTCTAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAGACCTTGCCTCTA	1
M00764_GLO1_MIP4	ATCAAATGTGAATCATGGCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCATGGCCTTTCCA	1
M00764_GLO1_MIP40	GCCTCTAACTTCTAGGTAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCAAACCAGATCTGC	1
M00764_GLO1_MIP41	GTGTCAGCTCAAGTGTAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATTAAAAATGTGAAGT	1
M00764_GLO1_MIP44	GGCCAGGAGTCTGTGATTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAGAGTTCTTGGAATGAC	1
M00764_GLO1_MIP45	CATCTTTCACTTTTACCATTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAATAAGTACTTGA	1
M00764_GLO1_MIP46	GCAGCAGACCATGCTACGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGCAAGTTGTAGGTGG	1
M00764_GLO1_MIP47	ACCTTCAACCAATGGTCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAGATACAAACACAATT	1
M00764_GLO1_MIP48	CCTGCAGTGGAAACTTTCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGTGGGCAACTGA	1
M00764_GLO1_MIP49	CATTCTCTCTAGTCTGCTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAATCCCCAGCAGGA	1
M00764_GLO1_MIP5	GAAAATCTCTAATGGCTCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTTCATGATGCCAGT	1
M00764_GLO1_MIP50	GAGAAGTGGTCACAGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTCTAGAAGGGCATTTA	1
M00764_GLO1_MIP51	GTTGCTAACACCTTTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACTACAATATTTGTTG	1
M00764_GLO1_MIP53	ATACCCCATGTTGTAGATGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGGCTTGACTGAGA	1
M00764_GLO1_MIP54	GAGACCATCCTAACACGGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACTCACTCAGGTGTG	1
M00764_GLO1_MIP55	GTGTTTCGGTTGCCTTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATTCCTTCTCTTACCC	1
M00764_GLO1_MIP56	AGCAAAGGCCAAGCAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCATTACTGTAAAACGAG	1
M00764_GLO1_MIP57	CCCTTCTTGCCTTCCTCATCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCCTCGTTTTTCC	1
M00764_GLO1_MIP58	AAAGCTGACCCTGGGTTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTAAGACTGCAGTCAG	1
M00764_GLO1_MIP59	GAACAGTAGTTTCAGAACTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTGTTGCCTCAGCT	1
M00764_GLO1_MIP6	GACTTCTAGTGTTTACTCCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACATAATTTATCAT	1
M00764_GLO1_MIP63	CGCGGACCCCAGTACCAAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCGTAGTGTGGGTGA	1
M00764_GLO1_MIP64	CGGAGAGCAAGTTGACTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCACAGACGACGGGAC	1
M00764_GLO1_MIP65	GGAAGTCAGCGGTCTCCCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTTTGCCTCCTTTATG	1
M00764_GLO1_MIP66	CATTCATACCTCAGGGCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCAAGGAGCCTTGC	1
M00764_GLO1_MIP67	GTTAAACAAACAAAATTAGCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCGTAAACTGAGA	1
M00764_GLO1_MIP68	CCTCTCTGAGCTTCCTAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTGTAAGGATTCAGAGG	1
M00764_GLO1_MIP69	GTAATTATTGCAAGTTTCTAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCGAGACACTGTTA	1
M00764_GLO1_MIP7	GTACAAAACTGCTCTAGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAAGTTGTAGTACCTC	1
M00764_GLO1_MIP8	ACATGCCTAGCCTGCTTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCAGTGGAGGTATTG	1
M00764_GLO1_MIP9	CAGCTCAACTCAAGATTTCATACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCCAGACACTGGGCT	1
M00764_GRIN2B_MIP1	GATTCTGGATTTTTTTAACCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCGCCAGTCCAAGA	1
M00764_GRIN2B_MIP10	CACAGCTGCACCCCTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTAGCCACAATGACTG	1
M00764_GRIN2B_MIP100	GGCAGCTGATTTAGCCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAACTTGGCTGAACCAAA	1

continued table…

ID	MIP	*c*
M00764_GRIN2B_MIP101	ATCTGTAAAACTGAAAGATGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCGCTGAGCTAGAC	1
M00764_GRIN2B_MIP102	AGAAGTCAAAGCACAAAATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTAGCCTATGGTACAT	1
M00764_GRIN2B_MIP103	AGTGCCTCTTTACATGGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACTACTGTGATTTACT	1
M00764_GRIN2B_MIP104	GCTCCCCTCCTTGGGGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTTTGGTTATTTCTTGG	1
M00764_GRIN2B_MIP105	CAGTAGAATGACTTCTGCTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCTCGTGCCTGTT	1
M00764_GRIN2B_MIP106	CAGACAGTCCTGTTGCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCATTTTCTTTGTGGTA	1
M00764_GRIN2B_MIP107	ACTGTGCTAGACTGATTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTAGCAGGATAACTATGT	1
M00764_GRIN2B_MIP108	AATCCCACTGCATTTTAATGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACTCTGAGCAGCC	1
M00764_GRIN2B_MIP109	GTGCCCTCATTGACTTCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGTTTGTGTTTTGAGG	1
M00764_GRIN2B_MIP11	CCCATCCCTTCTCTGATCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACACACATGTGCACA	1
M00764_GRIN2B_MIP110	CAGCTGTGTTTCCCTTCACTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGGCAGGAAGCAAG	1
M00764_GRIN2B_MIP111	CGTGAAGGCATTTATCCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTTCTCAGTAAGAGT	1
M00764_GRIN2B_MIP112	GTTCTCTCTCTCCCAGGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGAAACATCATGAGC	1
M00764_GRIN2B_MIP113	GTACCAGTCCATCAACAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGACCTCTCCACCTC	1
M00764_GRIN2B_MIP114	GAGGATGGAGAAGCAGAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATATTCAGGCTTCATGT	1
M00764_GRIN2B_MIP115	ACTGGCTGCATAAATTATGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAAAATGGAGACGA	1
M00764_GRIN2B_MIP116	CCCTCAAGGTTTGACAGAAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAATTTCCTATGT	1
M00764_GRIN2B_MIP117	ATTCTGTGTAGTTGTGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCATTCTAAATGAACAC	1
M00764_GRIN2B_MIP118	GATCTCTTTGCCATGAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACCATGACATAAGAAC	1
M00764_GRIN2B_MIP119	GGCTGAAGTTTTAGGCAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTCTGGTTTGCAGAG	1
M00764_GRIN2B_MIP12	CAGTGAGCTCTTGTCCCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGATTTATGGGAGCTTT	1
M00764_GRIN2B_MIP120	ACTGTCATTGTCACATTTTAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTGAGCTGCCTGC	1
M00764_GRIN2B_MIP121	ATGGAGTCACAGCCTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAACAGGTAATATACTT	1
M00764_GRIN2B_MIP122	GTCCCCCTTGCAGTAAGAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCATTCCTGCCCAGGT	1
M00764_GRIN2B_MIP123	GCTTTGGTCCTTGCTCTTTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGATGATCAAGGGC	1
M00764_GRIN2B_MIP124	GAGATGAGTGAGGAACCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGAGCTTCCTTTTGT	1
M00764_GRIN2B_MIP125	AATGCCTAGAATTTTGGTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGGCTTTATTGGTGA	1
M00764_GRIN2B_MIP126	GCCTACAAATACCCATAAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAAACAGCTGGTGGG	1
M00764_GRIN2B_MIP127	AGGCTATCTAGACCCCATAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCTGTCTTCCTACCC	1
M00764_GRIN2B_MIP128	AGCAAAACCCATTTCATTATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGTGACAACTTGGG	1
M00764_GRIN2B_MIP129	CACTGCCTGTAACTTATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATTTTCACTAGGTATC	1
M00764_GRIN2B_MIP13	CCAGTCTGAAGGAGGGGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATAGTCACTGGGTAA	1
M00764_GRIN2B_MIP130	GTCCACTCTTCATTGAGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATGAATTATTCCCCTT	1
M00764_GRIN2B_MIP131	ACGAGCTCCAAGAGTTTCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAGAAGATGCCTCC	1
M00764_GRIN2B_MIP132	GTCCTTTCACTTCAGCTGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCCTGTATTCTTGAA	1
M00764_GRIN2B_MIP133	AAAGGAGTAGTTTAGAGACTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAGAGAGGAGGAG	1
M00764_GRIN2B_MIP134	GGGATTCATTACCTCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATAAGAGTTGAGGTAATT	1
M00764_GRIN2B_MIP135	CCAGCACAGACAGTTCCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATAAGAGGTAAAGTGCT	1
M00764_GRIN2B_MIP136	CCTGAGTTCTTTGGCTTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCACACAGCCTTGTAG	1
M00764_GRIN2B_MIP137	GGTTATTAGAGACTCAATCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACCACCACCTGGGG	1
M00764_GRIN2B_MIP138	ATCCATGCTGGGACTGATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCAAGTAAGTGACAGA	1
M00764_GRIN2B_MIP139	CAAAGCACTTAGAAAAAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAAAAGCTGATACCT	1
M00764_GRIN2B_MIP14	GGGGTAACCTGGGTACGCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATGACCTCTCTTTGC	1
M00764_GRIN2B_MIP140	CCTTTGAAGTTGTTTTGGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATCCCCCCAGTTTCT	1
M00764_GRIN2B_MIP141	GCCTTTCATATACAAGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGTGTGTGCAGATAT	1
M00764_GRIN2B_MIP142	GAGAAGGAGTCACTTTATTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACAGCATAAGCTCC	1
M00764_GRIN2B_MIP143	CAACGAAAGTGTTATGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGGAGATAAAAAGATTT	1
M00764_GRIN2B_MIP144	GCAGCTATCATGGGCCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCTTGAATAATATCCA	1
M00764_GRIN2B_MIP145	GTAGGGAAAGGTGAAACAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGTCTTTGAAGACTT	1
M00764_GRIN2B_MIP146	GCTTGTTTTCCCACTTGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGATCAAGAAACAACCTT	1
M00764_GRIN2B_MIP147	ATAATCCAGACTAGAAGGAAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAGTGAAGCCCAC	1
M00764_GRIN2B_MIP148	CAGCGTCTTTTAGCATTGTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTTTTGCCTCCT	1
M00764_GRIN2B_MIP149	GTGATTATGTTGGTTTGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAATTAGTAGGCTTT	1
M00764_GRIN2B_MIP15	GACTGAGTTGGCTGTGATACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAAAGAGTGGATTCC	1
M00764_GRIN2B_MIP151	AGCTCAGATATACCATGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATGAAGGAAAAGCAAA	1
M00764_GRIN2B_MIP152	CCTTATCTTAATGCTTCTGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTGGGAGGCAATA	1
M00764_GRIN2B_MIP153	CCTGAGAGTAGTTTCAGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCAGAGAACTAAGAT	1
M00764_GRIN2B_MIP154	ACGTTCCAATGAAGTTCTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTATCGCTATCTTTT	1
M00764_GRIN2B_MIP155	GTGGAAGGAATTAAAGATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTTTTGAGAAGTTGG	1
M00764_GRIN2B_MIP156	CAAAAACACCCGTCCTACAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATCCTTTCTCCCA	1
M00764_GRIN2B_MIP157	ATTGCCTGTTGAAAGACAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGAGGAGCACTTGG	1
M00764_GRIN2B_MIP158	CACATATGCTGTCCTCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAATGTTGACTCAGTG	1
M00764_GRIN2B_MIP159	CGTAGGTTTAAGACTTGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAACATGAAAGGAAAAT	1
M00764_GRIN2B_MIP160	AAGAGCACAAATTCAATCAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAATATTCTCACCGG	1
M00764_GRIN2B_MIP161	GGAAGATATAGAAAAGGCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAGAGGAAAAAGGA	1
M00764_GRIN2B_MIP162	CCTTCAAGACCCCTCTGTTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAGAGATTCAGCTT	1
M00764_GRIN2B_MIP163	CCAGAAAATATTAAACTTGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTTTAGCTCTGGGA	1
M00764_GRIN2B_MIP164	CAGGGTAGGAGTCAAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTCAAAATGGAGTATAT	1
M00764_GRIN2B_MIP165	CTTTTATTTTTTTCTCCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATATATTCTACGTGAG	1
M00764_GRIN2B_MIP167	CACTGAGTTCTTTCACCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCCTAAATCACAACAT	1
M00764_GRIN2B_MIP168	GGTACAATTAAAAAGCACAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAAGGGCTCCTGAA	1
M00764_GRIN2B_MIP169	CTCTTGAGAGATGTAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCTCTGAGGAATTCT	1
M00764_GRIN2B_MIP17	CACCCTGTTCAGGGTTCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGCCAAGATGAACATAA	1

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ID	**MIP**	***c***
M00764_GRIN2B_MIP170	AGTGAGTTTCTGGAGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATTTACAATATTGAAGC	1
M00764_GRIN2B_MIP171	GCTTTCAATTTAAGGTTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTACTTATTCCCAGTA	1
M00764_GRIN2B_MIP172	GTGCTGCTACTTTCATGCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCCTCAACTCATTC	1
M00764_GRIN2B_MIP173	ATATTAGACATTCTCAGACTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCACTGTGTGACTG	1
M00764_GRIN2B_MIP174	GGGGGGTGGGGTTGCAGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTGCTACTTAACCTG	1
M00764_GRIN2B_MIP175	GGAAGATTAATTAAACTGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTAGGCCTAAGAAAC	1
M00764_GRIN2B_MIP176	GCTGAGTTGGTCTATATCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGTGATGCTTCTCC	1
M00764_GRIN2B_MIP177	GAAAATAATTCCTAACCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGTAACATGTAATGG	1
M00764_GRIN2B_MIP178	GGGCAGGTTGAGAACTATGATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGCCTCCGCCTG	1
M00764_GRIN2B_MIP18	GAATGAGATCACAACTACTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACACAGAGGATGCA	1
M00764_GRIN2B_MIP180	GAGAGCAATAGAGTAGGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGAAAGGTGACATATT	1
M00764_GRIN2B_MIP181	GTGGTAGTTGCAGTGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTAATGTAAATTAGGTGA	1
M00764_GRIN2B_MIP182	CCCACACAGATTTGTTGCTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAGCAGCTGAAAG	1
M00764_GRIN2B_MIP183	GTAGCAGCCTACTGAGCATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATACATAAGGCCAGACCC	1
M00764_GRIN2B_MIP184	CACTACAGCAGAGCTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGTGCATAAATGATGTC	1
M00764_GRIN2B_MIP185	CCTTTTTAGAGAGATGATGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCACAGTCCCTGG	1
M00764_GRIN2B_MIP186	ATTGCTTGACACCCTGTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGGTTTTTAGTTAGTTAG	1
M00764_GRIN2B_MIP187	CCCTTGGGCAACTCCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATCTGGTTATTCTATCT	1
M00764_GRIN2B_MIP188	GTGCTGGTCACCTGCACATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGTCAGTAGTGCCA	1
M00764_GRIN2B_MIP189	GTTCTGGCTGAGGATACACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATGTCATACATGCGT	1
M00764_GRIN2B_MIP19	CCTTGCCAAACTACTTGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCACAGGAAATAGAA	1
M00764_GRIN2B_MIP190	GCCACAGCCATGTTGTGATTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGAGTCGAGACTTTG	1
M00764_GRIN2B_MIP191	ACTCACCAACCACTTCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCACTGTACATGCATC	1
M00764_GRIN2B_MIP192	CAATGCTTAAATCTCAGCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCTCAGGAGCACCT	1
M00764_GRIN2B_MIP193	CCTCATGCATTTTACTTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGGATTCTGAAGAAC	1
M00764_GRIN2B_MIP194	AGAATTCAGCTATAAGCCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGATATTTGCACTGGG	1
M00764_GRIN2B_MIP195	CTAACAGCTTTTATGATGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGCCCAGCCTTCCTT	1
M00764_GRIN2B_MIP196	ACTTATTTGGCCCCAGTTGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTGTGGAGGTTGG	1
M00764_GRIN2B_MIP197	GATGGCAGTAATGAGGACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAATTTTATCCTGTGA	1
M00764_GRIN2B_MIP198	GTGCTACTGGCCTCGAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTCAGTGGTGAGATGAT	1
M00764_GRIN2B_MIP199	CACATGCTTCAAAAAGTAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAACTTCAGCAATCTT	1
M00764_GRIN2B_MIP2	GGTCTTTGTGCTTTCTTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTAAATAGTCAAAGAT	1
M00764_GRIN2B_MIP20	ACTGTGTAGGCATTTGGAGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGGAGAGGGCTTA	1
M00764_GRIN2B_MIP200	GGTCACAGAGAGGTAGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGTCTTTTCTTCTTT	1
M00764_GRIN2B_MIP201	CCAAGAATGGGAAGTTAATTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGAGTGAGTCAGC	1
M00764_GRIN2B_MIP202	GTGACTGAAAGGTTTCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAGGTTACCACATTC	1
M00764_GRIN2B_MIP203	CAAACCAGTAAGAAGACTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGCCTGTCTTTGTGT	1
M00764_GRIN2B_MIP204	GGCCAGGGTTTTACATAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGTGTCTGGAAAAA	1
M00764_GRIN2B_MIP205	ACCACCCCACTCCCTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCACCATAGTGGCCTC	1
M00764_GRIN2B_MIP206	ATGGGAATGAGAGGGAAAAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCGCTGGCAACAG	1
M00764_GRIN2B_MIP208	CACCCCTTTCAAACAAAAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAGACTGAGAGAGGA	1
M00764_GRIN2B_MIP209	AAGCTTTACAAGGCCTTCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTGCCTCATGCCCT	1
M00764_GRIN2B_MIP210	GTTTTCTTTCTAAAATGAACATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCCCCTGTTTGCCC	1
M00764_GRIN2B_MIP211	GTTTATGTGTCCTGTGTGCAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGCAGTCAAGGGC	1
M00764_GRIN2B_MIP212	GAAAGGTGCTCATCCTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTATTTATTCTATGGGTC	1
M00764_GRIN2B_MIP213	ACCCTCATCCCTGGAGTTTTATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGACAGTGGAAC	1
M00764_GRIN2B_MIP214	GCAGAACTGATGCTCCCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCCCAGAGTGAACAC	1
M00764_GRIN2B_MIP216	GAAAAGAGGGGAAGAGACTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAGCTAGACGAGCAG	1
M00764_GRIN2B_MIP217	GTTCTTCCCCAAACCTTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGTTTTGGGGGGAAGA	1
M00764_GRIN2B_MIP218	AAGCCACCTTTGAAGAAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAGGAAGGCTAAAGG	1
M00764_GRIN2B_MIP219	ACCGCCTTTTTTTGTTTAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAAGAATCATGGCTG	1
M00764_GRIN2B_MIP22	GTGACAGAAACAGTGGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACCTTACTCCTTGTTC	1
M00764_GRIN2B_MIP220	AGGTACATAAACAAGTCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCATGTATTACCTG	1
M00764_GRIN2B_MIP221	ACTACACATGGGTGCAAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGACACAGCCAAAAT	1
M00764_GRIN2B_MIP222	AGGTGCCTCAAGAGAAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGTGGCAGAGTGGATT	1
M00764_GRIN2B_MIP223	CCTCTGCTTGGCACATGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACTTTCCAGTTTGTTCA	1
M00764_GRIN2B_MIP224	AAAAATGCTTGCTTCAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGACCATTTAGCACACT	1
M00764_GRIN2B_MIP225	GTTCTCCCAGCTTCACTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCCAGAGCCTCTTT	1
M00764_GRIN2B_MIP226	AAAAGAGGCTATGTGAGCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATGAGATGATGCCAT	1
M00764_GRIN2B_MIP227	GAAAAGGAGGAGAGATGGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACACCAGGAGGAAGC	1
M00764_GRIN2B_MIP228	CAGTTCTCTCCTTCTTCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGGAGGGTGACGGGGGT	1
M00764_GRIN2B_MIP229	GTTTCTCATAAACATGCCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATGGGAACCAAGTT	1
M00764_GRIN2B_MIP23	CCTGTGAAAATGTGTACTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTCCAATCCTTTTT	1
M00764_GRIN2B_MIP230	GATGTCTGAGTGAGGGAACAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCGTTTCCAGAAGGA	1
M00764_GRIN2B_MIP231	CCCCGCCACCGTGGGCTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACACAGGGGTTGGACT	1
M00764_GRIN2B_MIP232	GGTGGTCTCGGCCCTTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTCATCCCCACTTTTG	1
M00764_GRIN2B_MIP233	AGGACTTGTTGTTGGCAAAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGCACTGGTCGTCC	1
M00764_GRIN2B_MIP234	GTACATGCTCAGCAAGTCGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCCGATTCATGGATG	1
M00764_GRIN2B_MIP235	GTTTGTTCCGGTTCTTCTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAACATGTGGGCGTAG	1
M00764_GRIN2B_MIP236	CGGCAGCACTCCTACGACACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAACTCCCTGCAGGA	1
M00764_GRIN2B_MIP237	GTAGTTGTGCAGCTTGGAGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCCGGCTGGTCCA	1
M00764_GRIN2B_MIP238	CATCCGGTGTGAGGCTTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGGGAGAAGAACCTGA	1
M00764_GRIN2B_MIP239	CGCGCTTAAAGTCATCACTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCCCACTCCACGTTG	1

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ID	MIP	***c***
M00764_GRIN2B_MIP24	GTCCTTTCTAAGGTTCCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTAAAAACCCCACTGC	1
M00764_GRIN2B_MIP240	GGCCCTGTACCAACAGGTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTACGGGACTTCTAC	1
M00764_GRIN2B_MIP242	GGAGTTTGACGAGATCGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCGATGTCTCTGACA	1
M00764_GRIN2B_MIP243	ATTTGCCGTACAGGTCACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGCTGCTTACGCCTC	1
M00764_GRIN2B_MIP244	CCTTCAAGAGCGACCGCTACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGATGGGCTCTACGAC	1
M00764_GRIN2B_MIP246	GGGAACCTGCAGCTGAAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTCATCCGTCTATGA	1
M00764_GRIN2B_MIP247	GACAGGTTAGCCATGTTCTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGGGCGGGTTGTT	1
M00764_GRIN2B_MIP248	GGTGTGAATGGCTCACCGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGCATCCATGGGGT	1
M00764_GRIN2B_MIP249	ATAATTGCTCCAACTGGATAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTACAGACTGGCGC	1
M00764_GRIN2B_MIP25	CATCACCACCTCAATCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATGTTGTGGCCTATC	1
M00764_GRIN2B_MIP250	ACTGCCAATAGAAAAGGTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCTTTGCACAGTGCT	1
M00764_GRIN2B_MIP251	GCTTTATGGGTGTCTGTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGAGGTCATGAGCAGC	1
M00764_GRIN2B_MIP252	GGAGACAGGAAAGGAGCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGTCAATGTCCAGCT	1
M00764_GRIN2B_MIP253	ACCTTTCCTTTTCTTCCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCATCCAAAAAGATT	1
M00764_GRIN2B_MIP254	CATCATAGATGAAGGCATCCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCGCTTCCACCCA	1
M00764_GRIN2B_MIP255	GCAGTGCTGAACTATATGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACATAGTTTTCTGGAA	1
M00764_GRIN2B_MIP256	GCACTAGGTATACCATGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATGGGAAAGTTCAACC	1
M00764_GRIN2B_MIP257	GTCTCTGGAACTGGAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCATCTACACCCCTC	1
M00764_GRIN2B_MIP258	CACCCCCTTTCCGCTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACTAATGCTAACTTAC	1
M00764_GRIN2B_MIP259	GTCTTTCCCTCAATCCTGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCTTTGCTGTCATC	1
M00764_GRIN2B_MIP26	GGGCAGGGACTTGATGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCAAGTGATAAGAGGG	1
M00764_GRIN2B_MIP260	GGAGTTGTTAAACACCAGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACATATTCCTCTTGGA	1
M00764_GRIN2B_MIP261	ACCTGTGCAGAACCCAAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAACAGAACCAGCCAC	1
M00764_GRIN2B_MIP262	CGATGAGCAGCATCACAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTGAAAATAAGGAGAAA	1
M00764_GRIN2B_MIP263	GAGTACTTCAGCCCTGTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTCTTTTGCTCTCTGT	1
M00764_GRIN2B_MIP264	CAGGCTGTTCCAGCTAGAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTCATGGTGTCACGC	1
M00764_GRIN2B_MIP265	CCTCTTCATGACCACCTAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGGTGAGACAGTCC	1
M00764_GRIN2B_MIP266	ACCATCAATGAGGAACGATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAAGAAAACCACTGAT	1
M00764_GRIN2B_MIP267	GCTCACTTTATGCATTTCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGGCAAGCATGGGA	1
M00764_GRIN2B_MIP268	CCCTTGCAGCATTTTTTGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCACCTCTCCAATCAT	1
M00764_GRIN2B_MIP269	GTATTGACATCCTTAAGAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAAGGGTAATAAAT	1
M00764_GRIN2B_MIP27	CCTGCCTAAGAATCAGTGGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGCTTAGGGCAATCA	1
M00764_GRIN2B_MIP270	GATTTCTAGTTGCTTTTGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAACGCATAGTCACT	1
M00764_GRIN2B_MIP271	ATGGTCATCCTCCTGCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGAGAGGATGCCATACT	1
M00764_GRIN2B_MIP272	GAGCATTGTGACCCTGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTGGTTTCTGATTC	1
M00764_GRIN2B_MIP273	GTGCCAACATTGTACATACTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTTTCCACTTCCCC	1
M00764_GRIN2B_MIP274	AATTTTGCAACACAATGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCCTTCAGTGAAGAT	1
M00764_GRIN2B_MIP275	CAGTCAGGTATATAGAGAGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTGCATCTGGTAGC	1
M00764_GRIN2B_MIP276	GAAGCCTGGCCTTGGGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTCCAATATGCTAAATA	1
M00764_GRIN2B_MIP277	ATTATGGCAATTCCATCTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGTTCCACACTCA	1
M00764_GRIN2B_MIP278	CCTGAGCCCAAAAGCAGTTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTCCCCACTGGGCT	1
M00764_GRIN2B_MIP279	ATGTAGGTGGCTTCTTCCTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATATGATACAGAGAT	1
M00764_GRIN2B_MIP28	GGAAATGAGCTGAGATGGGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAGTGATTCAGGG	1
M00764_GRIN2B_MIP280	GAAGTGGCCAACTCAGTAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAGAGGAGGTCCTCCT	1
M00764_GRIN2B_MIP282	ATCCGCAGCACCATTGAGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTTCCAGTTTGGCCC	1
M00764_GRIN2B_MIP283	GGTAATGGAGATTTTGAACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCATGATGTTGAGCA	1
M00764_GRIN2B_MIP284	GTTAATGATGGAAGGTAACCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTGGGCATCCACG	1
M00764_GRIN2B_MIP285	CAGACATGAGATCACAGATGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATCATAGAGGAGCCC	1
M00764_GRIN2B_MIP286	GGGGGTGGTGTTTGCTGATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCCACGAGAAAGATG	1
M00764_GRIN2B_MIP287	GCTCTTCTGAGAACGAGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTCATGGCTACCAGTT	1
M00764_GRIN2B_MIP288	GCTCTTCTGAGAACGAGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTCATGGCTACCAGTT	1
M00764_GRIN2B_MIP289	CATCCTCGTGGGCACTTCCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGACGAGTTGAAGATGA	1
M00764_GRIN2B_MIP29	GCCATTCCAGACCATCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCTTGCTCTTACAGAA	1
M00764_GRIN2B_MIP290	ATTCAAGGACCTTATCTCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTGGGAGAACAGCAC	1
M00764_GRIN2B_MIP291	GACAGATTAAGGGAGTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTTCTTCCAAAAAGAT	1
M00764_GRIN2B_MIP292	GGCTTCTACAAACCAAGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTAAATTGGATTTTAA	1
M00764_GRIN2B_MIP293	CTCACAATGCAGAATCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATAAATGAACGGAAGA	1
M00764_GRIN2B_MIP294	GCTCTCCATACCCTGAATTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAGCCTCCTCCACT	1
M00764_GRIN2B_MIP295	GTCAGGGCTTGATTCGCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATTACGGTTTTTGGTTT	1
M00764_GRIN2B_MIP296	GCCTCTTTTTCCCCCTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCAATTCCTCTCGTGTG	1
M00764_GRIN2B_MIP297	ATGGAAGAGGAGAGAGGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCATTTCCCACAGAGT	1
M00764_GRIN2B_MIP298	CAGGTTGGCTTTCCCACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGTTAAGTGGGAATTGT	1
M00764_GRIN2B_MIP3	CAAACTGGAAATCTATACAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATTAGAAAAGAGAA	1
M00764_GRIN2B_MIP30	ATGAGGGGCAAGAAGGGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGAACATTTCAATCAT	1
M00764_GRIN2B_MIP31	CATATCCTGGCCTCTCAGTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCTGCACCCCTTAC	1
M00764_GRIN2B_MIP32	GATATTGAAGTCAACAAAATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGCTTGCAGTTA	1
M00764_GRIN2B_MIP33	CCTCTGCCTCTAATATGCTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGACCCCAAACCACC	1
M00764_GRIN2B_MIP34	GATCACTCAGTTAGTGAGTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAACTGCAGTGTGTT	1
M00764_GRIN2B_MIP35	CTGAAGGTGACTGAAGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTCCATGACCAAACA	1
M00764_GRIN2B_MIP36	GCTTAAACAGGGTGGCAAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGAGTGAGAACAAA	1
M00764_GRIN2B_MIP37	ACTCTTAACTGATGAACTCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCTAGCATGTCTC	1
M00764_GRIN2B_MIP38	GGGGAAGAGTATTGGAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAATAGCAGGGAGATAG	1
M00764_GRIN2B_MIP39	AAGACATTACTCCAGCAATTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACCAGCCCACTTGC	1

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ID	**MIP**	***c***
M00764_GRIN2B_MIP40	GATGAAGTGAGAGGGCATGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGGGAGGGACTTCTT	1
M00764_GRIN2B_MIP41	CCTCTCCTTCCCCTCTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGCTGTTATTTTTCCCA	1
M00764_GRIN2B_MIP42	GACAACAGGAATAGGCAACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGATAAGACTATCTGG	1
M00764_GRIN2B_MIP43	CCTCAGTCTAGAGAATCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATGACCTCCATGTT	1
M00764_GRIN2B_MIP44	GTTCAAAGCTCCAGGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGTATAGCCTGAAGATA	1
M00764_GRIN2B_MIP45	CCTTCCCAGTCAGCCTCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACGCATACAAATTTTA	1
M00764_GRIN2B_MIP46	GATTAGGCAATTAGATATATGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTGGCCTGAGCTA	1
M00764_GRIN2B_MIP47	CCAACTGCTTCTTATCACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAACTCCAAACTTTCA	1
M00764_GRIN2B_MIP48	GAATCGATATCACACAGTTTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGAAGCGGCTGAA	1
M00764_GRIN2B_MIP49	CCTTCTAGCAACTTCTCATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCAAGAGCTTCCTA	1
M00764_GRIN2B_MIP50	CGGAGCATAGAGTGATATGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGGGAGGAGGAGAG	1
M00764_GRIN2B_MIP51	CAAGTCTCACTCCCTCATTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACCTCACCTCTCA	1
M00764_GRIN2B_MIP52	GGCTTTCTATGCAAAGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGTCATGCAGAAAAA	1
M00764_GRIN2B_MIP53	GTTCGTTCTTATATTCCAGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCCCTTAATCTGCC	1
M00764_GRIN2B_MIP54	ACACAAAGTCCATACCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCTTATTTTGGGGATA	1
M00764_GRIN2B_MIP55	AGTGCAGAGCTCACTTTTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGAAGCCACAGACCA	1
M00764_GRIN2B_MIP56	GTTTTGGGGGAGGAGTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTAACTTTTTCTTACCT	1
M00764_GRIN2B_MIP58	GCTGAAGGGGATTTGGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACTCAGACATGATCTTC	1
M00764_GRIN2B_MIP59	AATGCCTATTTGTAATCGAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTCCTGGTTTGCTT	1
M00764_GRIN2B_MIP60	ATTTAATCCTGAGTCTTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAAAATCTGTTAAA	1
M00764_GRIN2B_MIP61	GTTCTCAGTGCCCCTTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGGAGATGGGAAGATA	1
M00764_GRIN2B_MIP62	GGAATGGAGTTAGCTGAACCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGCCCCTCTCCAA	1
M00764_GRIN2B_MIP63	GTCACCATTTCTGAGCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGGAGAATGGAAATC	1
M00764_GRIN2B_MIP64	GGCTGGCTTTAGAAAGAGACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGTGGTGAAGAGACG	1
M00764_GRIN2B_MIP65	GCTTGTCACTGAATCTATTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGGATGTGGGTGT	1
M00764_GRIN2B_MIP66	GACAAAAAGCTTGGTTCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATAGGAGGCAAGTGTT	1
M00764_GRIN2B_MIP67	GGGCTTGTGCCTTGAAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAATAACATGCAACAAC	1
M00764_GRIN2B_MIP68	GTGATGGAGGATGTCTAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGAATATTAAGCCAC	1
M00764_GRIN2B_MIP69	ATTCTTTCTCCAACTTCCTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGACACATGCTCAG	1
M00764_GRIN2B_MIP7	GGAGGTGGATGGGCTGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAAATAAAAAGACCCA	1
M00764_GRIN2B_MIP70	ACAAGCAGGCAAATGAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTATGAAAATGGGATATA	1
M00764_GRIN2B_MIP71	AGCTTGGAAGGTTGTTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGAATACAGTTTAAGGG	1
M00764_GRIN2B_MIP72	GGAAACCCTTCCTCACCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAACTTCAGTGGTTGG	1
M00764_GRIN2B_MIP73	AAGACCCTTGGGATTAAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTGTCTTTCCTTTTG	1
M00764_GRIN2B_MIP74	CCTCAAAGTTATCTCTTCTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAAATCTACCTGGC	1
M00764_GRIN2B_MIP75	CCTAGGAGAAGCAGCTCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAATGTTTGACTGGCA	1
M00764_GRIN2B_MIP76	CCAAGAACAAAACTCCCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGGAGTATTTTTGAGA	1
M00764_GRIN2B_MIP77	ATTCCTTGCCCATCTTCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAAGTAAAGACACTGT	1
M00764_GRIN2B_MIP78	AATGCAGATGCCCAATAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATACATAACCCTGTTTGG	1
M00764_GRIN2B_MIP79	GTGAGCTGCCAAGGTGCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTGTCAATAGGCCTT	1
M00764_GRIN2B_MIP8	AGTTCTTTTTTTGTTTATTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGTCCTCTCCAGGG	1
M00764_GRIN2B_MIP80	GTGGGAAAGAGTTTAAGTTCATGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGAAAGCTACAGA	1
M00764_GRIN2B_MIP81	AGCTTATCTTCTCTGTCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGAAGTCTAGCTTGG	1
M00764_GRIN2B_MIP82	AGCTTGCTCCGGAACAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGACTGAAGCCACTAAA	1
M00764_GRIN2B_MIP83	GAAAAGCTGAACTTTTCATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCTAAGGGATACTT	1
M00764_GRIN2B_MIP84	GTACCATAGCGGCCAATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGGGAAAATAGCAGGA	1
M00764_GRIN2B_MIP85	GCCCTGTGACCTGTTTTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGCCCTCAGAGTCCC	1
M00764_GRIN2B_MIP86	GCTGATGAGTATTTGGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAGTAAGCTAAGAGAG	1
M00764_GRIN2B_MIP87	GTCTAGTGCCCACCTCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAAATAGCTACTGCCCC	1
M00764_GRIN2B_MIP88	CCTATTACAAATCTCATTTTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCCTGGTTCAGGA	1
M00764_GRIN2B_MIP89	CCTACCTCCTCTCCTATCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTACCTCCTCCATT	1
M00764_GRIN2B_MIP9	ACCCCATAGTGGATGCATATCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCGCAGAGCTGAG	1
M00764_GRIN2B_MIP90	GAGGAGACTTCTATACCATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACAGTGAAAGAGCT	1
M00764_GRIN2B_MIP92	GGGCTGCAGAAGAAATTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATTTATTAAGCACCCG	1
M00764_GRIN2B_MIP93	GGATTTTGGCAGGCAGTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGCAAGATTCTCTGAT	1
M00764_GRIN2B_MIP94	GAAGAAAGGGAAGCATGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCTAGGATTAAGGCATA	1
M00764_GRIN2B_MIP95	GTGGGCTGACCAAAACTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTATATTTTTCTGTTCA	1
M00764_GRIN2B_MIP96	CAGCCTCAAGGGAGAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAAGAATAAACTGGGAC	1
M00764_GRIN2B_MIP97	CATTTTTATTTGACCAAGTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGGAAGAAATCC	1
M00764_GRIN2B_MIP99	AAAACCTACAGTGGGGGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTCTTTTTGACTTGT	1
M00764_IQCH_MIP10	GAGCTTATATACTCCCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGTAAATTAGCTGAGT	1
M00764_IQCH_MIP100	ACATGCTGATAGAGCCCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCAGATGCAGAATCTG	1
M00764_IQCH_MIP101	GACATTGTCTGCAGGTGGGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACTGAGGTCTGAG	1
M00764_IQCH_MIP102	GATAGATCTGGTGACTTTTATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAAGCCCCTTCA	1
M00764_IQCH_MIP103	AAAAGTAACCAACCACATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATATGCCCTGTTGTACT	1
M00764_IQCH_MIP104	CCCTGACTCAACTCACCTTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGTTTGGTCTGGTTA	1
M00764_IQCH_MIP105	GTTGCCCACACCTGATTAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTCCTTTCCTTTGG	1
M00764_IQCH_MIP106	CAACACCCACTGCCACTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGGATTGCAGTTTGAG	1
M00764_IQCH_MIP107	GAGATTAACAGGAAAATTGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCAGTGAGAGATTGCT	1
M00764_IQCH_MIP108	ACATGCCTGTGGGTGATCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCACCCAGCTAAGACA	1
M00764_IQCH_MIP109	GACCCTGGTGTCCATCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAGAAATGAAAAAAGAA	1
M00764_IQCH_MIP11	CATCATTAACAGAAGTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGAAAATGTTGCCTATA	1
M00764_IQCH_MIP110	GAAAAGATGAAAACTCATCTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCAGAGGCCAGT	1

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ID	MIP	*c*
M00764_IQCH_MIP111	GAAATGTTGTATGGTGAAAAGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGGCTGGGCAC	1
M00764_IQCH_MIP112	CCAGCAATTTGGGAGACTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTCTGTCTTTTAC	1
M00764_IQCH_MIP113	CCAGCACTTTGGGAGACTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTCTGTCTTTTAC	1
M00764_IQCH_MIP114	CCACTGTTCTAAGAGTGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAGAATCATCTAGTGT	1
M00764_IQCH_MIP115	CCTTTCCAAATGTGTTCTCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGCTTGCATGATG	1
M00764_IQCH_MIP117	GAAGTGTATCTGTGAGTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGTACTTTGTTTCTG	1
M00764_IQCH_MIP118	AAACAGTTCCTTGCCTTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAATGCATGAGAAGCA	1
M00764_IQCH_MIP119	ATCTCACAAGGTGGCAATCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCGCCGATTGTT	1
M00764_IQCH_MIP12	GGATAGTTCCATGGGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAACGTTAAATATATACA	1
M00764_IQCH_MIP120	GAGACCAATTTTAAGGTGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGGTAAACTCATTTG	1
M00764_IQCH_MIP121	GATGGATGATGAAGAGATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTAGCACTTGTTTACAA	1
M00764_IQCH_MIP122	AGTTCACCATGGTTTAGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATTTTGTTTTCCTTTG	1
M00764_IQCH_MIP123	GTCTGGAATAAAAAGGGCAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTATTCTAAGAGTA	1
M00764_IQCH_MIP124	CATTTCTTGGGTTTAGAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGTTCTGATTCACCT	1
M00764_IQCH_MIP125	GTTGAACAATCCCTTCTTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTGCTTTGTGTGCT	1
M00764_IQCH_MIP126	AACACAAATAAGTTTTGGTTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCTGAGGCCTATG	1
M00764_IQCH_MIP127	ATTGCTATTTGTCAAAACACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCGCATTTACTTCC	1
M00764_IQCH_MIP128	ATGCAGAAGATCGATGGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAACACGATGAATGA	1
M00764_IQCH_MIP129	GATAAGCCAGCATCTAGTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTTTTTCAAAGCTT	1
M00764_IQCH_MIP13	GTTAATCATATAAACTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCACTTAGGGACCATCAT	1
M00764_IQCH_MIP130	GCAGACAATAGTGGCTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTATTCAAGCTACAGAGC	1
M00764_IQCH_MIP131	GTTAAGATTGTAGTAGTGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAGATGGAGTGTAGC	1
M00764_IQCH_MIP132	ACTTGAAAAAATCCTACTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCTTCAGTAAAGCTC	1
M00764_IQCH_MIP133	ATAGGATTTTTACCTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAAAATATTTCCACATC	1
M00764_IQCH_MIP134	CCTTTCCCCAATACACTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAATGTATTTCCAACTA	1
M00764_IQCH_MIP135	ACTTGACAGATAGGAAGTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAGCTTTTGTTTTGC	1
M00764_IQCH_MIP136	GAACAATGGGCCCCTCGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGGTTTCATTTACTCTC	1
M00764_IQCH_MIP137	CCCCTGCTTAACAGTACAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGCACAATCGTGTCC	1
M00764_IQCH_MIP138	GACAGTTTTCTTTTAAAGTCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTTGAGCTTCGGG	1
M00764_IQCH_MIP139	CCTTTGCAGCTATCATTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAAAGTTTTGCATGTGA	1
M00764_IQCH_MIP14	GACAGAATTATTGCACTATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTATTATTTTTGCC	1
M00764_IQCH_MIP16	CAATGCTTCCTAATTAAGCTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTCAGATTCCTGAG	1
M00764_IQCH_MIP17	GTTTAGTGATTGCCAGGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATCATTTATTTTC	1
M00764_IQCH_MIP18	GAAGGAGGCTGCATCTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGCTTCTGTAGAGAAT	1
M00764_IQCH_MIP19	GTCAAAGTACATATTTTGGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGACTGGAAAGGGG	1
M00764_IQCH_MIP20	GAAATAGTTGCCACAGGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAGATGAGCACACT	1
M00764_IQCH_MIP21	ACTCTCTGAGGAGTGCTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAACCACCACAGTGAT	1
M00764_IQCH_MIP22	CAGACCCAATGTAACAAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTATTGATGGTCTGTCTT	1
M00764_IQCH_MIP23	GGGAGCTTAAACTTCTCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAATAAGACAGATCAG	1
M00764_IQCH_MIP24	CACAGCATTCTGTTTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATACCTCCATCTAATCT	1
M00764_IQCH_MIP26	AGATTTACCTGTAAATGTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAATAAGTGGTTCAG	1
M00764_IQCH_MIP27	AGTTTGGGCCTGGTAAATTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATTTCTTTTTAGCTT	1
M00764_IQCH_MIP28	ATGGGATACACGGAGGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAAAATCCTTGACCTG	1
M00764_IQCH_MIP29	AGCCAACCAAGGTGGGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTTTATTTAGGCTGC	1
M00764_IQCH_MIP30	GCATTTTTGTTCATCCAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGAATAAAAGGGACT	1
M00764_IQCH_MIP31	CATTTTATATCCTCAAAGGAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCATTTACAGCAGC	1
M00764_IQCH_MIP33	ATCCCTGGTACTGTTCATGTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAAAACATATTAA	1
M00764_IQCH_MIP34	GAGGACCTACTAGAAAAAATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAATAAATCAAAGTC	1
M00764_IQCH_MIP35	AAATAGCCAAACCAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAACACATTAAGAAATCT	1
M00764_IQCH_MIP36	GTTATGCATTCATAATTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGTATAATTCTACAGC	1
M00764_IQCH_MIP39	AAAAGAAAGAGCATTGAGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATATCCAGCCTCACG	1
M00764_IQCH_MIP4	AAATCAGCTTTGTGTCTCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGTTGCAGTGAGCCT	1
M00764_IQCH_MIP41	CCAAGCAATTCCACAAAGTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAGGAGCTGCTCT	1
M00764_IQCH_MIP42	ATCTAGCCTTCTAGTAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCCACCCATTACACC	1
M00764_IQCH_MIP43	AAAGCCCAAGTCTGACATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCTATAAGCAACAACT	1
M00764_IQCH_MIP44	CAATAGAATAGTCCATATGTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTAGGTGTGTTCT	1
M00764_IQCH_MIP45	GACTGAGGGAAGTGACACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTATAAAATGCTTTGT	1
M00764_IQCH_MIP46	CGGGCTGACTTTGTATTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAATCTGGCTATTTAAA	1
M00764_IQCH_MIP47	ATAAAAAGGCAAATTTTAAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTACCTTTCTTTCTGT	1
M00764_IQCH_MIP48	CCTCTTCTTCTGGAAAAGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTTGAAGTCAGTGAT	1
M00764_IQCH_MIP49	GGGTTTGCACCTTGAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTGGGAAAGAACTTCAC	1
M00764_IQCH_MIP5	AAATCAGCTTTGTGTCTCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGAGGTTGCAGTGAGCCT	1
M00764_IQCH_MIP50	ACTTTCTGTGAGATATTTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCCACTTTCACTA	1
M00764_IQCH_MIP51	GTCTCATTCTTCATTGTAGGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCTCCTGCCTGCG	1
M00764_IQCH_MIP52	CAGTTTAAATCAAAACGACTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCAGCAAAAGGA	1
M00764_IQCH_MIP53	CGTGCTTCCTTTGTAAAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCATGATAGGAAGGTCT	1
M00764_IQCH_MIP54	ACTTTTGTTGCCATCTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTTGGACTGAAGCCTG	1
M00764_IQCH_MIP55	ATAAAATGTGAAAAATAAATGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGACTGAATTACTT	1
M00764_IQCH_MIP56	AGATTGATGTGATTCAGCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGTGTGTGTGCATCC	1
M00764_IQCH_MIP57	AGAACGCTGACATGTTGAAAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCTGTGGCGTAA	1
M00764_IQCH_MIP58	AGATGTATAAGCCCATCTTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGGAGGGTACAGA	1
M00764_IQCH_MIP59	GGTTTAACATAGAAAGTGTAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGAACTCAGGGCC	1
M00764_IQCH_MIP6	CAAACCTTTAAGATAAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCAGTCTGAGCAAGAGT	1

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ID	**MIP**	***c***
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M00764_IQCH_MIP61	ACAGCCCCAGATATGTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTTAGAAATTTACCAA	1
M00764_IQCH_MIP62	GGGAGCATTTGCTTTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTATCACCTTTGTCATT	1
M00764_IQCH_MIP63	GATCTTTTATGAAGTCAGAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAACACGTGTCAAG	1
M00764_IQCH_MIP64	CCACTCATTTAAAGGAGATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCTGGTAATGAGTTT	1
M00764_IQCH_MIP65	CATTTAGCATTCAATGGTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGTGATTTCAGGG	1
M00764_IQCH_MIP66	ACATTTTAGCTTAGCTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTTTTTTTCCACAGG	1
M00764_IQCH_MIP67	CCTTGAATGCTAAGAAGTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAACTCTGGAAGGAGG	1
M00764_IQCH_MIP68	CAAGGGCCAAGATGGAAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGGAATAATTTGGTGG	1
M00764_IQCH_MIP69	GCCCTGGAAGATTTATCAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAATCACACCTGAT	1
M00764_IQCH_MIP7	AGAAATTAACAAAATTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCTACCAATTCAAGTA	1
M00764_IQCH_MIP70	CATTCGAGCCAAGGTGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTTCCTCTTTTATCGCC	1
M00764_IQCH_MIP71	GAAAATTCTCCAGGTGTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAAGGAGAGTAGTTG	1
M00764_IQCH_MIP72	CACTGTACAGTTAAGCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGATAATAGTCCTCCT	1
M00764_IQCH_MIP74	CCTTGAACTCAATCAAGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACATAATGACTTTAT	1
M00764_IQCH_MIP75	CCCGAAATAACAGATAATGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAAACGGCGTTTAA	1
M00764_IQCH_MIP76	CAGATGAAAGCGAATTACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAATATCCTGGCTT	1
M00764_IQCH_MIP77	ATGCTTTATTTGCACCTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGTATGTGTTGTTGCT	1
M00764_IQCH_MIP79	GTTGTCTGAAACACACTGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCTGTGTGAACAAGA	1
M00764_IQCH_MIP8	ACTGATAAAGGTCTTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTATTTTAATATCTAAA	1
M00764_IQCH_MIP80	GCTTTTAAGTTCCCCAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATAAGGAAGCAAACAA	1
M00764_IQCH_MIP81	ACAACCCATTGAATCTCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCAACATGTTTGGGA	1
M00764_IQCH_MIP82	CAGAAACAACCCAATCCCGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATACCCTAAAAGGCA	1
M00764_IQCH_MIP83	GCTGTGTGACATCTTAGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTGCCATTTTGCTAT	1
M00764_IQCH_MIP84	CCCCAGCTGCATGTTCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTGTAGAGGAAAAAAA	1
M00764_IQCH_MIP85	GCTGTATTACAAAAAAATCCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATCGGATGCCAGA	1
M00764_IQCH_MIP86	ACTCGTCATTCATATGATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCACAGGGAAGATGTTT	1
M00764_IQCH_MIP87	GCTCTGGTACACATCAGTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTGCAGGACAGGT	1
M00764_IQCH_MIP88	ACTCACCTGATGTACAGTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGCCTGCTATTAA	1
M00764_IQCH_MIP89	GGCACATATGATGCTTCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTCTAACATATCGGCC	1
M00764_IQCH_MIP9	GTCGTCAGCATTCTTGTTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGGGTTAAGAGTAAG	1
M00764_IQCH_MIP90	CAGTTCCTCCTGGAATATATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCCACAGAGATGAT	1
M00764_IQCH_MIP92	ATGGACTCTGAGTTCCGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTACGATAAAAAGGAA	1
M00764_IQCH_MIP93	CGCTGTATTTGCAGGTGATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTCCAGTCTTCAAG	1
M00764_IQCH_MIP94	AAGTTCAGCTAAGAGATGAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACAAATGGGTGCTA	1
M00764_IQCH_MIP95	CCAGAGTCAGAAAGCCATTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAGCTGGCTCCTGC	1
M00764_IQCH_MIP96	CCTCCAAACATTTCTCAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTGTGGTTCTATTTA	1
M00764_IQCH_MIP97	ATTTCCTCCACGTCGGGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAACACAGGAGATGCAA	1
M00764_IQCH_MIP98	GTAGGCTTTATTATGCCCATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCACAGTGTCTTCA	1
M00764_IQCH_MIP99	GATTGTTGTGCATCTTGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCATTTTGTTTGACTTG	1
M00764_KCNA4_MIP1	ATTTCAAAAGATTCAGTTGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCTTGGCATCTT	1
M00764_KCNA4_MIP11	GCCTTTGCATTAGAACAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACTACTGTATGCATTGG	1
M00764_KCNA4_MIP12	GTGGAGACTGATGTGTGAATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACAAGTCAGAGTA	1
M00764_KCNA4_MIP13	CCTCATTTTCAGTCTCTCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCTTCTTCCATCTCT	1
M00764_KCNA4_MIP14	CAGACACAGCTAACGCAGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCACTGTAGGGGGCAA	1
M00764_KCNA4_MIP15	GCCTCTGCAAAATACACAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGGGACCCGACAAT	1
M00764_KCNA4_MIP16	GATGAACCTACTACCCATTTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACTCCAAAGGCCT	1
M00764_KCNA4_MIP17	CAAAGGACATGGCCTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAAGATCAGAAGGCCC	1
M00764_KCNA4_MIP18	CATCCTCAGAATCATTCGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCTTCAAAAACATCA	1
M00764_KCNA4_MIP19	ATATTGTGTGCCCTGAGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAATGTCAATGATGTTC	1
M00764_KCNA4_MIP2	GGTCTGTTAGAATGATGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTTTTCATTGTGTGA	1
M00764_KCNA4_MIP20	CAATGACCCCTTCTTCATCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCCTGGAAACCTTGC	1
M00764_KCNA4_MIP21	CCAAATCTGCTTTTTAAATTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGTCGTCCCTAA	1
M00764_KCNA4_MIP22	CCTCTTTGAATATCCAGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGAGGAGGTGAAGT	1
M00764_KCNA4_MIP23	GTTCCTGTCAAAAAAATACTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGGGCCTCCTCCC	1
M00764_KCNA4_MIP24	CCCAGCTTTGATGCCATCTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGCCTACGCTTTGA	1
M00764_KCNA4_MIP25	CCTCATCCTGAGGCAGCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTCTCCCAACAAAGTC	1
M00764_KCNA4_MIP26	GGCTACAGTTCAGTCCGCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGAGGAGGAGGAAGA	1
M00764_KCNA4_MIP27	GTAGTGGGCTTTCTTCTTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACCTTCCCTCCTCTT	1
M00764_KCNA4_MIP28	GCTCTGACCTGATGCCCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCACCACCACCAGTCA	1
M00764_KCNA4_MIP3	GTCTCTCTCAATCTCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCCTGTGATGTTATCTG	1
M00764_KCNA4_MIP30	AGAGGCTTGCTCACTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCTACAACTGGAACCAG	1
M00764_KCNA4_MIP31	ATATTTTCAGTCCAACTTTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGGTGGTTTTCGG	1
M00764_KCNA4_MIP32	GTCTTCCAAGCAATCTGCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGAGTGCCAGGCTAT	1
M00764_KCNA4_MIP33	GATGTTGCTGCAAGATTCAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGCTGGTCGAGATA	1
M00764_KCNA4_MIP34	CCAAATTTCAACATCTACCCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGCATTGGCCA	1
M00764_KCNA4_MIP35	CCAGCCATTTCTACTCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTTCTGCCATGGAAA	1
M00764_KCNA4_MIP36	CAAACCACATCTTAACATGGTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGGGTCTTTGCC	1
M00764_KCNA4_MIP37	ATCATGCAGAAGAAGCACTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAAACCACAGATAG	1
M00764_KCNA4_MIP39	GGGGGTTAAGATTTAGCATCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGGGCCAACAGTT	1
M00764_KCNA4_MIP4	CAAACTGTGAATGTTTACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAACAGCAAATGTCTAA	1
M00764_KCNA4_MIP40	CGATATTATTTATCCCTCAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCCCGGGTTTGG	1
M00764_KCNA4_MIP41	GGGCATGAATGGAAGGCGGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGGGAACGGTAAGTAT	1

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M00764_KCNA4_MIP42	ACAGCTGGAGGAGGGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAAGGTAGAGGAAAGAT	1
M00764_KCNA4_MIP44	AGTTCAGCACAGGAGGGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCTCCAAATATCCACG	1
M00764_KCNA4_MIP45	GGAACCAGGAGTCTTGGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGAGAGGGATGGATGT	1
M00764_KCNA4_MIP48	GACGGCAGCGCGGGAGTCCCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCACCCCGGCTGGG	1
M00764_KCNA4_MIP49	GGCCCCAACGGGGACACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATATAGAGAAAGCAAGTT	1
M00764_KCNA4_MIP5	CCTTGCAGCCTTTTTAAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATCCAGTCCTGTTAC	1
M00764_KCNA4_MIP51	GTGGGGAAAAGAAGACGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGTGCAAAGGAGACG	1
M00764_KCNA4_MIP52	GGAATGTTACAGAAATTGGAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGAGCGCCCAGAT	1
M00764_KCNA4_MIP8	AATCTGAGCAGTCATTTATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGGAGAGAGAGAGTG	1
M00764_KCNA4_MIP9	CCTATTCCTCCCTCTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTACTTCACACACACAC	1
M00764_KCNK13_MIP15	ATGGCTGGCAAAGGACCTAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTAAAAGATCAGAAA	1
M00764_KCNK13_MIP16	CATCATGAAGTCGTGCCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTTGGGATGACAACTC	1
M00764_KCNK13_MIP18	CCTCAGCCATGTACACCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGCCCTGCCCCAGGAG	1
M00764_KCNK13_MIP19	GCAGCAAGAGATGAGGATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGCTCTCATAGTGGG	1
M00764_KCNK13_MIP20	ATCAAACAGTCCTTGAACTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGGGACCTGGTCAG	1
M00764_KCNK13_MIP21	GACACCCATGAGGATGAAGACGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGCGTGATCGCA	1
M00764_KCNK13_MIP22	GCGCCGGCTCTCAGGGGAGATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCTGCCCGCAAT	1
M00764_KCNK13_MIP23	GTCCGTGTCACTCTCTGCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGTGCTGGTCTGGT	1
M00764_KCNK13_MIP24	AGACCAGTGGGGACAGGTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCCATCCTGCAGAAG	1
M00764_KCNK13_MIP25	GCCAACCTGTTGTTCATGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGCTCCCAGAAGGAA	1
M00764_KCNK13_MIP26	CCTTCCAGGGATGGGGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAATGGAGGATGATTGCC	1
M00764_KCNK13_MIP27	GGCTGTTGGTTGGAGCCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAGATTAATGAAACAAG	1
M00764_KCNK13_MIP28	CGAAGACTCATCTTTCCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGCAGCATTAGACAT	1
M00764_KCNK13_MIP29	GTTCCCAAATAAGGAACAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTGGCAGGTATGC	1
M00764_KCNK13_MIP30	GTGGCGTCTGTGAGACCTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCAGGCTTCCTTCAA	1
M00764_KCNK13_MIP31	GACAACAAAAAACAGAAACAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCACACCCCTACA	1
M00764_KCNK13_MIP32	CCCAATGCAAAGATGATGACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCAGCAAGATGGTG	1
M00764_KCNK13_MIP33	CCCCAAGCCCTGGTAAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATAAATGCCTGTTTAAT	1
M00764_KCNK13_MIP4	AAAGGAACCAGGACCCAGGACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGGCTCAGCGCGA	1
M00764_KCNK13_MIP8	GATTTGAAACTAGGAGTCAAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAAACTGCGCCCG	1
M00764_KRTAP19-5_MIP10	CGTCTACACTTTATGGTATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTACTTAATGTCTTATT	1
M00764_KRTAP19-5_MIP11	GGCAATTCTGTTGAGCATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAATTGAAAAAACAGC	1
M00764_KRTAP19-5_MIP12	CCTATATGCACAATACAGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCGTCATCTTCCAA	1
M00764_KRTAP19-5_MIP13	ACTTTCTGAAGACCTCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGTTATTGTGAATAA	1
M00764_KRTAP19-5_MIP2	ACTGAAAGCAAATACACGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTAGCATCTAAGAG	1
M00764_KRTAP19-5_MIP4	GGGGACATAAGAAGATCACCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTACGGAGGCTACG	1
M00764_KRTAP19-5_MIP6	GGCTACGGAGGCTTCGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGACCAGGGTATATAAG	1
M00764_KRTAP19-5_MIP7	GTAGGGAGATGCCCTCATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACACCAGCATGTGTAGG	1
M00764_KRTAP19-5_MIP8	GCAAAGGAGGGTATACAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGTTCAATCGTGTCCT	1
M00764_KRTAP19-5_MIP9	CATCTACACTTTATGGTATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTACTTAATGTCTTATT	1
M00764_LAMA1_MIP1	GCTCCAATTTCTACAACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACACATTGAATGTTCTGT	1
M00764_LAMA1_MIP10	GGCAGGATAACAGCTGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCTTTTAAACATAATG	1
M00764_LAMA1_MIP100	AAAAAGAAATCATGCTTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCCTTTAGAACGTC	1
M00764_LAMA1_MIP101	AGGTTGAACCGTGTCCTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACGGTAACAGGATTT	1
M00764_LAMA1_MIP102	GTCTCGCCCTGCTTGGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAATAAAGTTGGAAATC	1
M00764_LAMA1_MIP103	CCGGGAGCATCTTCTGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTGCATTTTACCTTAAC	1
M00764_LAMA1_MIP104	GGAAGCCAGTGTTGTCTTTGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAAGCAAGGTAGGG	1
M00764_LAMA1_MIP105	CCTTCACTCTGCCACGAAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGGTGAGTCCATCT	1
M00764_LAMA1_MIP106	GACTGACCTGGGTTCAGGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTCAGCCATCCCTGA	1
M00764_LAMA1_MIP107	GGCTTTCTAGAACACTACACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTATCCCAGGTTTC	1
M00764_LAMA1_MIP108	CGTGGGCATTTTTGGTTTCGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAACGGGCCCCTTG	1
M00764_LAMA1_MIP109	ATTCAAACAATGTCACGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATCTCCTCGTATCTT	1
M00764_LAMA1_MIP11	GAAACAGCAGATTCAAATTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGCGTCCTCCTGGG	1
M00764_LAMA1_MIP110	CATGTTCTTGTTTGCATCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTAGCCTTCTAGTCT	1
M00764_LAMA1_MIP111	GGAAATTGTTTAGCACACACACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTATTTGAGCTCGAAAT	1
M00764_LAMA1_MIP112	CATTGTAGAACCTTTAGAAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTATGTTTAATGA	1
M00764_LAMA1_MIP114	CGGCACAGTAAGAGTGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCTTCCTTCCATTTTG	1
M00764_LAMA1_MIP115	AACCAAGAACACACTTACTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGGTAGCCGGAAGTG	1
M00764_LAMA1_MIP116	CCTCCTGAGAATGGATTCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCATCTTCACATGGCA	1
M00764_LAMA1_MIP117	GTAGGCAGTATTCATTGTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGATCACTGTAGAGC	1
M00764_LAMA1_MIP118	CCTTATAAAGCAGCTGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGACAGTTATATTAAAG	1
M00764_LAMA1_MIP119	CACTTTGCTGATGAGGTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTTACAGGAGGATAA	1
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M00764_LAMA1_MIP120	ATTATTCTGAAGGCACCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCAGTGATGATTGTTT	1
M00764_LAMA1_MIP121	ACTTGCCTTCCCTTTCAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGATATCACAAACTCTA	1
M00764_LAMA1_MIP122	GTGGGTGCTTCGGAAGGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTTGCTTGTTTGCAT	1
M00764_LAMA1_MIP123	GAGAGAGCCACATTAGAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGCAGGAGATTTCT	1
M00764_LAMA1_MIP124	GATCTGTTAGATTGAAGCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTAGTCACTGAGATG	1
M00764_LAMA1_MIP125	CTGGACCTGAGACCTAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATCCTAGAATGAGTAAC	1
M00764_LAMA1_MIP126	GGGCCCTCACTACCAATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAATCAGTGTTTAGCAAA	1
M00764_LAMA1_MIP127	AAGAAACCCAAACAGCAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAAATATGGTGGGCTT	1
M00764_LAMA1_MIP128	CCAGTGATGAACAGGAAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTTGTTTTGCTTTC	1
M00764_LAMA1_MIP129	CAGAGTTAGGCTGGTTTTGTACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCAACAGGAGCAAA	1

continued table…

ID	MIP	*c*
M00764_LAMA1_MIP13	GTGTGTTACAGTCAAAGAGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGACCTGCTGGTGG	1
M00764_LAMA1_MIP131	CAGAACATTAGCTGTCCCAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCGGCCCATGACTT	1
M00764_LAMA1_MIP132	ACTCAGTGAACCAATGTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTACCTTGATTTGTCCTC	1
M00764_LAMA1_MIP133	CAAAAGTCACCAACAAAAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGGTGTGAAGGAA	1
M00764_LAMA1_MIP134	GAAGGCCACTCTCCCTCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTAAAAAAGAGAGCTGC	1
M00764_LAMA1_MIP135	CGGGTCCACACGCTTGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAAGTGTTGTGGTGGTCA	1
M00764_LAMA1_MIP136	CGAAAAAAAAATAGGCCTTAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACACAGGAACCCG	1
M00764_LAMA1_MIP137	ATCTCTGTCTGCAGACACGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGTCCATAACTTACAG	1
M00764_LAMA1_MIP138	CATCCGGGCCTACCAGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGTGAAAATTCATTAC	1
M00764_LAMA1_MIP139	ATCCCAATAATCTGGGCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAGCTTCTGTGAGT	1
M00764_LAMA1_MIP14	ACACATACCAAGAGCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATCAACTGGAATACTAA	1
M00764_LAMA1_MIP140	ATCAAACAAAAGGTTGGCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGTTACGAAAGCCAC	1
M00764_LAMA1_MIP141	GAAGATGTTAGAGGAGAATCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTTTTCCCTCTCCC	1
M00764_LAMA1_MIP142	CTAGCTAAGCACACAGTGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGCCAGCCTGTCCA	1
M00764_LAMA1_MIP143	CTCTTTGGTTTTGGCTCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGCTGGTGTGTCTCTC	1
M00764_LAMA1_MIP144	GCCACGTCTGCAAGCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATATATTTCTGTGCGAAA	1
M00764_LAMA1_MIP145	CAAAATTTTTACTTGCAAAGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTAAGTGGAAAGG	1
M00764_LAMA1_MIP146	CACTCAGTTCCAATGCAATACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTATTTACAGAAGAA	1
M00764_LAMA1_MIP147	CAAACAGATTTCAAGAGAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTCTGTCGATGGTCA	1
M00764_LAMA1_MIP148	GCATGCAGCAACTTGAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCCAGATTTCTAAAA	1
M00764_LAMA1_MIP149	ACAGAACCACTTAAGCGTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTACACCGTCCGAGC	1
M00764_LAMA1_MIP15	GCAACACTCTCGAAGGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGACGGTTAACAGCAAAC	1
M00764_LAMA1_MIP150	CCAGCTCTCAGAATCCCTTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACCTGGTACCTGGC	1
M00764_LAMA1_MIP151	AGCCACGTCGTTTCCTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGATCATATGATGACA	1
M00764_LAMA1_MIP153	GATAAACTAAATCAAACTTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTTCCTCCGATTC	1
M00764_LAMA1_MIP154	GAAAACATCAGAAATGTGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTTCTAAGGGGAAAG	1
M00764_LAMA1_MIP155	GTGTAAAAATGAGCACTCCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCCAGAGACTAGCA	1
M00764_LAMA1_MIP156	GGCAGACCATAAAAGTAGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTACCTGTACAGAA	1
M00764_LAMA1_MIP157	AAATCAGGCACCACATAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAATCTTCACACATCTT	1
M00764_LAMA1_MIP158	CAATCCTCTTCCTTGGACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAACAGATATGTGTGCA	1
M00764_LAMA1_MIP159	GATGCTGCTGCTGCACAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGTCAGAAGCAGGGTT	1
M00764_LAMA1_MIP16	CAAGAGTAGACAGTGGTGATTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCACTGCGTAGCAC	1
M00764_LAMA1_MIP160	GTTATTTTCATTTTTTGAGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTTTATCCTGCAG	1
M00764_LAMA1_MIP161	CATCTTTGCCTCAGCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTCACTTTTAATTGCTT	1
M00764_LAMA1_MIP162	GGAAAGCAACCACCTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAAATTACCAGAAGC	1
M00764_LAMA1_MIP163	GCTCCTATCTCTGAAATAATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTGCTTCTTTCAA	1
M00764_LAMA1_MIP164	ACAGTAATTAGAAACTTACTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGACCACAGGGCC	1
M00764_LAMA1_MIP165	CAATGCAACCAAGTAGAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAATTCTACTCTTCA	1
M00764_LAMA1_MIP166	AAGTGGCTAGTACCAAGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCATTCTGTTGCATGT	1
M00764_LAMA1_MIP167	CCATAGAAATTATGGAAAAGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGGCCTGACATGG	1
M00764_LAMA1_MIP168	GGAACCAGAGGGGCTGGAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCTGCAGATGAGCAT	1
M00764_LAMA1_MIP169	GTGGAAAAATAAAGTCTCAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCCCACACTACCTG	1
M00764_LAMA1_MIP17	CATTTGGCTTAGATCACCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGGCAATTAAAGTTTT	1
M00764_LAMA1_MIP170	GCTCACTAGGATGTTAGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTACTCTATATTCTGGA	1
M00764_LAMA1_MIP171	CCTGAGCAGTTGCCTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAAATATGCAAAAGGA	1
M00764_LAMA1_MIP172	CACTTGCATTTCTTTTTTGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACACCTTCAAGCTT	1
M00764_LAMA1_MIP173	CAGTACCTACCTGGAGATATTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACCTGCCCGCAGG	1
M00764_LAMA1_MIP174	AAATACAGAGATGAACAGACACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTGAATGACTTGG	1
M00764_LAMA1_MIP175	GTTGCGCAAGTTGTTTTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACGGCATCACCAATCTC	1
M00764_LAMA1_MIP176	CCCAGATGTGCGGTCACAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGAGGAAAAACCATCT	1
M00764_LAMA1_MIP177	CGGTGCGATGAGTGTGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTATTATGGGAACCCTCA	1
M00764_LAMA1_MIP178	CAAATGAAATGCAAAGCACAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCAACTGCCACCTG	1
M00764_LAMA1_MIP179	GGTATTGGGCATATTTACTATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCTTGGAAGGGG	1
M00764_LAMA1_MIP18	ATGCTGCTTACATTTCCAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTGCAAAGTAAACC	1
M00764_LAMA1_MIP180	ATTACTCTTAGGATACACCATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACAGGCGTCACA	1
M00764_LAMA1_MIP181	GCAAAAGGCTAATTTTAAGAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCTCCTGCCAGGT	1
M00764_LAMA1_MIP182	CACAATGGTCACCTGCTGTGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCAGCCCAGCATG	1
M00764_LAMA1_MIP183	GTGTGTACTTCTGGCTACTACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATAAAACGTGGCAGTG	1
M00764_LAMA1_MIP184	CACAAGGAGCAACCAGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCGGAAATCTGACACT	1
M00764_LAMA1_MIP185	CCCTGCAGTTGCAACAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCACTCATTAATCAGA	1
M00764_LAMA1_MIP186	CCTCTTCTTCTGGGTGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGGAGTTGCTGTAAC	1
M00764_LAMA1_MIP187	GTGTCTGTCCTCCTGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTTTTCAAATGTTAGCG	1
M00764_LAMA1_MIP188	CCATGTAGTTCAGTTCCTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTATGGTCAAGGATTA	1
M00764_LAMA1_MIP189	AAAATTCTGTAGAATGAGAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTACCTGCTCTGCT	1
M00764_LAMA1_MIP19	CCATACTGACATTTTACCTTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGAGAGTCTCCCA	1
M00764_LAMA1_MIP190	GGAAATATTTTAACTCTGTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCATGCACAGAACA	1
M00764_LAMA1_MIP191	CCCACCACTTTGAGAAGCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGAGAGGTGATAATGG	1
M00764_LAMA1_MIP192	ACTTGAGGCTCAAAATTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAACTTCTATGAAAAGA	1
M00764_LAMA1_MIP193	ATTTACATGGATGCACCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTGATAGCTCATGGC	1
M00764_LAMA1_MIP194	AATACATCACATGGGTGAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGTTTGCCACCAT	1
M00764_LAMA1_MIP195	CCAGTCGGTGCTTCCTAGGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTACCAGGCCCCCGA	1
M00764_LAMA1_MIP196	GAAAGTGCACTTCAAAATGCGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCATCCAGCAGGAA	1
M00764_LAMA1_MIP197	GAAAGTGCACTTCAAAATGCGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCATCCAGCAGGAA	1

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ID	**MIP**	***c***
M00764_LAMA1_MIP198	CGTGGTTTAGGTAACGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTTAAAGGAAAAGTCTT	1
M00764_LAMA1_MIP199	GGAAACACAGCCAAGTGTTCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGCTTCTGCTCCG	1
M00764_LAMA1_MIP2	GGTATTTGTTGCACATGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCAAAATGAAAAACAT	1
M00764_LAMA1_MIP20	GCAAAGTGAAAACATGCATAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTCCTAGGTAGAAC	1
M00764_LAMA1_MIP200	ATAAAGGACTCGTTTTTGCCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGAGGTGGGACAGC	1
M00764_LAMA1_MIP201	GCTCCCCTGTAGGAAAATGTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCTGGCTAGAGGA	1
M00764_LAMA1_MIP202	GTAAATACCTTGCAAGGGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTCAGATGCGGAAG	1
M00764_LAMA1_MIP203	CCATCCTCCTCTTTCATCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACTTTCCCGACTGTG	1
M00764_LAMA1_MIP204	ACCCCACGAGACTGCAATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCACAGTCACAGGGA	1
M00764_LAMA1_MIP205	GTGCAAGTCAAAATTTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATATGTGTGCATTTGGA	1
M00764_LAMA1_MIP206	CCATCCTCACATTCTTCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATTAAAGTCCAGAAAA	1
M00764_LAMA1_MIP207	GGAGGTGGGGTGCCAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTATTTCAGCCTGTGACT	1
M00764_LAMA1_MIP208	GAGCTGATGCTGTTATTTCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTGAGGGGGGCA	1
M00764_LAMA1_MIP209	GGTTAAGTGCCTTTACTTTTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGCCCATGGCTT	1
M00764_LAMA1_MIP21	GTAGGTCAAGACAGACTATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACCTTCCTTTAGCAT	1
M00764_LAMA1_MIP210	GTGCAGCCATCTGACACGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAAAGTCTCAAACAAGG	1
M00764_LAMA1_MIP211	GATGAAGGCCAGTGTCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTAAAACGTATGTTGGTT	1
M00764_LAMA1_MIP212	GTCACATGCATCTTACCAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTGATAAATTCCCCAG	1
M00764_LAMA1_MIP213	GACACCTTAGCCTTGGTACAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTGAATGCCATGT	1
M00764_LAMA1_MIP214	ACTTTCAATGTTTCAAATCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCAGAATGGGAGC	1
M00764_LAMA1_MIP215	AGTCTTCAACCGTATAGTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGGAACACAGATGG	1
M00764_LAMA1_MIP216	GGCACTGTTGGGTTTCCATAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTTCACAGTGGGC	1
M00764_LAMA1_MIP217	GGCGAATCTTGTGTTCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGATTTATTAGCCATTC	1
M00764_LAMA1_MIP219	ATTTTCCAATGGATGAAGCCGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGATGCAGAGTACC	1
M00764_LAMA1_MIP22	CACTCGGGTTCACTCCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTCATGTTTGACCTT	1
M00764_LAMA1_MIP221	CCAACAAGTAAGCCTCGGACCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAGGCGTGTGCG	1
M00764_LAMA1_MIP222	ATGCTAAAACCAGTCACCAACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGCCGGTGGTGTT	1
M00764_LAMA1_MIP223	GCCGTGAACATTACACTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGGTCTATGAGGCTA	1
M00764_LAMA1_MIP224	GCATTGTGAGTCTCTCACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGACTTTCCCTTCTC	1
M00764_LAMA1_MIP225	GCTACACAATTCACCCATTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGGCACGACTGCA	1
M00764_LAMA1_MIP226	CCACCAGGTCGATGGCATTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCCTTCAGTGCACTG	1
M00764_LAMA1_MIP227	GCTGATGTGGAGCACTGTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCCATCTTCATTGAG	1
M00764_LAMA1_MIP228	CACGATCAATCTGCCTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGGAAGTACCTTCACC	1
M00764_LAMA1_MIP229	CCAGCTGATGACTGTCCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACGGACTCACTTTAA	1
M00764_LAMA1_MIP23	GCTTAGCTCAACCGAGAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTTGTTCTGCCTTTGC	1
M00764_LAMA1_MIP230	GTTTTTCATTCGTGCCTAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGACCCTCAGCCTG	1
M00764_LAMA1_MIP231	GATGACGTCAGCATGCGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACTGAATGGCCACCTG	1
M00764_LAMA1_MIP232	GGTGATTGTTTTTGCTTTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTTCATTCTCGCTT	1
M00764_LAMA1_MIP233	CATGACAGACAAGGAAATTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCAGTCAGCTGAAATG	1
M00764_LAMA1_MIP234	CAGTAGTACTTGGGAGCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTATGAGACTACCTA	1
M00764_LAMA1_MIP235	CGAGGCCTACCTTGGAAATAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCACCGACTTGATCA	1
M00764_LAMA1_MIP236	GTGCAGCAGTAATATTTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTGCTGAGACGGGA	1
M00764_LAMA1_MIP237	GCTAAGGAGTAGGAGGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGTTTCAATTTCTTCTG	1
M00764_LAMA1_MIP238	ATGTGTGTGGGAGTAAGCACATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCCTGAGAGCAGC	1
M00764_LAMA1_MIP239	GAAAAAACAGGATGATGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGAGGATGACTTCCT	1
M00764_LAMA1_MIP24	GATTTACTACATGGCTCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAATTGTTGGGTCCT	1
M00764_LAMA1_MIP240	GAAAAAACAGGATGATGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGAGGATGACTTCCC	1
M00764_LAMA1_MIP241	CAAGAGAGGCTGCTGCAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCGATGAGAGTGGTGT	1
M00764_LAMA1_MIP242	GGCGGGATTTAATGAGCAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGCCAGGATTCTATA	1
M00764_LAMA1_MIP243	GTCTGTCCAGAGAGAATAAAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTCGGAGCAGCC	1
M00764_LAMA1_MIP244	GGCTCATCACTGGCACTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTTACCACTTTGCTCAA	1
M00764_LAMA1_MIP245	CACAGGGCCCTGTGTTTGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTCAGTGCCCATGTA	1
M00764_LAMA1_MIP246	GTTTTCTGTAAAGGGTCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCGATCACATTTTTC	1
M00764_LAMA1_MIP248	GTTTGCCAATTCCTTGTTTAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCAGCTCAGCCAT	1
M00764_LAMA1_MIP25	GCTGGTAAATGGTAGAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGATTTTTACACAGATGC	1
M00764_LAMA1_MIP250	ACATACACCCACAAAAGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCTGGGAATATAAAAT	1
M00764_LAMA1_MIP251	GGGTGTTTACTTAGGAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTATGGACATACCAT	1
M00764_LAMA1_MIP252	CCCACAGGGTCACAATTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTAGTTCCAGTATGTG	1
M00764_LAMA1_MIP253	CCCTCAGTTCTGTCTGTATTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTTATTTATACTA	1
M00764_LAMA1_MIP254	GTGGGGGTTAGGTTTGAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACCTGAAAGGCAGAG	1
M00764_LAMA1_MIP255	CAAAATCATCGTAATAGTCCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGGATAATAGAA	1
M00764_LAMA1_MIP256	ATTAAAGATTGGCTGAACACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACCCTTAGCAAAGTG	1
M00764_LAMA1_MIP257	CCTTGTGGTGTCCTGGTTATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAATCCCTTGACCTT	1
M00764_LAMA1_MIP26	GCTGGTCTGTGAGGAGTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTCCTCATAGGAGAAT	1
M00764_LAMA1_MIP260	GCTAATGGACCCCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAGACTCCGTCTCAAAAAATAA	1
M00764_LAMA1_MIP261	ACTAAAGCAGCTGTCTCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTACTCTATCCTGCTT	1
M00764_LAMA1_MIP262	AAGTCTCTTTTCCACCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGACTGACATCTTATTTTG	1
M00764_LAMA1_MIP263	GGAGACTTTTGTAATATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATCAACTGTGAAACCTG	1
M00764_LAMA1_MIP264	GCTTTGCAACACTTTCATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCTTACTTTGTGTGGT	1
M00764_LAMA1_MIP265	GACAGTTCAGAGGAGGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAGGCATGCTATGTAA	1
M00764_LAMA1_MIP266	ACAGCACCTGTTACAGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGACACCATAAACTTGG	1
M00764_LAMA1_MIP267	GGAACCGTGTCCTCCGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGATACATTTTCTAATT	1
M00764_LAMA1_MIP268	ATTATCATCAAAGCAAACTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGTTTCTACACAAT	1

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ID	**MIP**	***c***
M00764_LAMA1_MIP269	GCAGATACACATGCCTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGTTTGGAATAAAAAAG	1
M00764_LAMA1_MIP27	CAGATGCCGCTGTCACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGCTACCACAGATGAA	1
M00764_LAMA1_MIP270	CCATGCTAGTAGCTGCCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTGTTGGTGTGCCAAC	1
M00764_LAMA1_MIP273	ATTTTTTGAGATGGCGTCTCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGCAGAAGTGAATTCCA	1
M00764_LAMA1_MIP274	GCTCAAGTGGCACCAATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTTAAATAGAGCTAGA	1
M00764_LAMA1_MIP275	GGAGAGGTAGGTATGGTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATGCAGTCAGCGACTC	1
M00764_LAMA1_MIP276	GCAACTTGAAAGACCTGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAACGAGACAAACACTC	1
M00764_LAMA1_MIP277	CCAATGCCCCTCGACCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAGATTCTACCTTTAAGT	1
M00764_LAMA1_MIP278	GATGACCTTTGGGAAAGTCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGCAAAGTCCCAG	1
M00764_LAMA1_MIP279	ACATGAATTCCTCTCGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTAAGTCCAGAGTGAT	1
M00764_LAMA1_MIP28	CATCAGCTGGGGTGGGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCTTTGCTAGGAACA	1
M00764_LAMA1_MIP280	CAACAGAACGCCATCCAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGACTTCTGTTAGGAAG	1
M00764_LAMA1_MIP281	ATCCGGCACTGTGGGTTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTGAACACAATGTTTAT	1
M00764_LAMA1_MIP282	GTGATGGCAACAGCGCAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCTCAATCTTGCCAGC	1
M00764_LAMA1_MIP283	AATCAAAAGGAGATTGAAAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCTGATGTGAGCAT	1
M00764_LAMA1_MIP29	CCTTCATCCGTCCACCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTCTAATATGTTCATGG	1
M00764_LAMA1_MIP291	ACGCAACTTCAACTGCTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGGATTTTTTCTGAAA	1
M00764_LAMA1_MIP3	GAATTCCCTGGCTCTCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAATCTCTTCAGTTCA	1
M00764_LAMA1_MIP30	CCTTGGCCTTGGTCTCCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTCATGGAGAATAAAA	1
M00764_LAMA1_MIP31	GATGGATGTCTCCTTCCTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCAGTGTTACAGGTG	1
M00764_LAMA1_MIP32	GCTAGCGGCTTAGAGGTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGTGGGAGAGAGAAAG	1
M00764_LAMA1_MIP33	GCCCTCCCACCACTATCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATCCCTCTCACAGTCT	1
M00764_LAMA1_MIP34	GAAAGGTCAGGTGTTAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATAGGAGGCTTTTAAAGT	1
M00764_LAMA1_MIP35	GTGCTCAAACTGTGATCTGTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCGTCTTGTTGTC	1
M00764_LAMA1_MIP36	CAAGCTCCAGGCCTTGAGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTATGACAGGGTGG	1
M00764_LAMA1_MIP37	GGCTCCCGGACTCCATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAAACTCTTACACTGTG	1
M00764_LAMA1_MIP38	ACTTAATTTAGATGCCCACACGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGTGGGTGTGGC	1
M00764_LAMA1_MIP39	ACTTAATTTAGATGCCCACACGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGTGGGTGTGGC	1
M00764_LAMA1_MIP4	AGGAAAACTCCGTGCAGTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAGTTGGAAATGAAAT	1
M00764_LAMA1_MIP40	CATTCCACTTTAAGCATTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTCTGTGGTTTCT	1
M00764_LAMA1_MIP41	ATAAAAGCAGGTTCTTTTGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTCCAGAAGGGAAA	1
M00764_LAMA1_MIP42	GATGAAGTGCTTGATTTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTAATCAGTCGGCTGT	1
M00764_LAMA1_MIP43	AGACACACAGGGACACTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGATACCTACTTCTTTCT	1
M00764_LAMA1_MIP44	GGAACAGTGTGTGGTGGATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAGGCACTGGTGGTT	1
M00764_LAMA1_MIP45	CCTGAAGAAAGCACTTAGAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACGCGTGTTCCG	1
M00764_LAMA1_MIP46	GCTGGCGAGTGCATCATTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTTTGCCCCTTAAG	1
M00764_LAMA1_MIP47	AACTGGAGGTGCCCACAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTACAAATTTTCATCAG	1
M00764_LAMA1_MIP48	CATCCTTAGGGCCATTCCCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCTCTTGTCTGCA	1
M00764_LAMA1_MIP49	GTTTTCTGCTTCAGCACAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAACCTAGGTCCACA	1
M00764_LAMA1_MIP5	CATTCCTGTCCTGGGACCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAAGCAAAAATGCCT	1
M00764_LAMA1_MIP50	GCATCTGGGACCCCCATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTAAAGTGTGCACTCTA	1
M00764_LAMA1_MIP51	GCCATTCAAAATATTTGGCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCTCGCCCTGCTC	1
M00764_LAMA1_MIP52	GCTCTGCCAAAAGCATATTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTTCCTAATGAAT	1
M00764_LAMA1_MIP53	GCTCTGCCAAAAGCTTATTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTTCCTAATGAAT	1
M00764_LAMA1_MIP54	ATTTACATTTAGCCAGGAAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGGGTGCCTCAAG	1
M00764_LAMA1_MIP55	CAGCAAGGCCCCATTTTAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCCTACAATCTATGGA	1
M00764_LAMA1_MIP56	GCTAAAAATCAGAGCGGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAGCGGCTTCCTTTA	1
M00764_LAMA1_MIP57	GTCCAGGTCGACTTGCTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTTTGCTGACTGGA	1
M00764_LAMA1_MIP58	CCTGCTGGCTGTCAGAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTACAGTTATCAGATGAC	1
M00764_LAMA1_MIP59	CACTGTGACTCAGAGTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGAGAGTGTTTTCAAAA	1
M00764_LAMA1_MIP6	GCGGGTTTTTTTATTTTTTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAACGAGGTCTGGC	1
M00764_LAMA1_MIP60	AGGATTGGCACTTTGGTTACTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACCTGGGGGGTGC	1
M00764_LAMA1_MIP61	GAAAACTTTGCAAATTCCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGCTGTATCAAAAAC	1
M00764_LAMA1_MIP62	CATTTATCGTCCTGCTTTCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAGAGAGCAGGTAC	1
M00764_LAMA1_MIP63	GGGGGAATTCCAGAGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTTTCATTTATTTTCT	1
M00764_LAMA1_MIP64	CAAGACACTGTCTGTGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAATTCTAAAAGACCAA	1
M00764_LAMA1_MIP65	GATGGAATGCGCTTGTCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGATGACCCCAGTCATC	1
M00764_LAMA1_MIP66	CCTTGGTCAGGAATCGGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTTTTCCGTCATGCTG	1
M00764_LAMA1_MIP67	ATTAACATCAAGTGAGTAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCAATGTTGCCTCC	1
M00764_LAMA1_MIP7	CATAAATGGGATTGTTGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTGTCACCCAAACCA	1
M00764_LAMA1_MIP71	ATTGGAACGTGAGTATCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTTTGCCTGTGATG	1
M00764_LAMA1_MIP72	GTGTATAAACTACCTCTTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTCTTCTCCATTAG	1
M00764_LAMA1_MIP73	AAGACAGGGACTCAAACAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACTTTGATTTGAAG	1
M00764_LAMA1_MIP74	AATCACTGGTTATATGATAATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATGGATGAACTTT	1
M00764_LAMA1_MIP75	ACTTCAAAGACATGCTAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGGCAGAAATGCCC	1
M00764_LAMA1_MIP76	CATCCCCATTGGAGCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTCCCCACTCCTGGCA	1
M00764_LAMA1_MIP77	ATGCACTAAACGCTGCTGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAAAGCAAATTGGTGG	1
M00764_LAMA1_MIP78	CACAATGTTACGAGGCCACCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACAGTGACTACGA	1
M00764_LAMA1_MIP79	GACTGTGACTCATACCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATTTCAGCTCAACTA	1
M00764_LAMA1_MIP8	GTACGGGTACCTGCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGCTAACAAAAGCAAAC	1
M00764_LAMA1_MIP80	ACACAAGTTTGCAGAACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAATTAATCACAACCAT	1
M00764_LAMA1_MIP81	CATTCTGTAAAGTCTCTTCAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATTCCCCTTGCAG	1
M00764_LAMA1_MIP82	GCACACTGTCTTAATCAAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGAAAGGAGAGAAAT	1

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ID	MIP	*c*
M00764_LAMA1_MIP83	CAGCAGTAGACTGAAGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAACATAAATAAGGAAAA	1
M00764_LAMA1_MIP84	GGATTGAAAGGAGCAGCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCATATACGGAGTTTTC	1
M00764_LAMA1_MIP85	ACGTGTGCTTCCTCACGATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAAATGCACATCCATA	1
M00764_LAMA1_MIP86	GGTGACAAAGATTTGGGTGGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCACTGGCCCTACT	1
M00764_LAMA1_MIP87	CACCACGAACAGCAGTGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAACTCACCATGCTGT	1
M00764_LAMA1_MIP88	GTTGATAAATCAATGGACACTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCTGGACACAGAG	1
M00764_LAMA1_MIP89	ACACAACAAACCAGTGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCAGATCAACCTTTGAC	1
M00764_LAMA1_MIP9	GCACCATTGTTGACATGGAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCAACTGCGTTCCC	1
M00764_LAMA1_MIP90	AGAACAATCACAAAATTTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTAAACAGCCTTTTC	1
M00764_LAMA1_MIP91	ATGCCCTTCCCTACAGGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGTAATCCTTCTACCTC	1
M00764_LAMA1_MIP94	GGGGGGAACCCTATACTTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGACTGAGGCAGGAGGAT	1
M00764_LAMA1_MIP95	CATGGAAACAGGTATTCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGCCAAACTCACTAAG	1
M00764_LAMA1_MIP96	CCAGTCTCCATGTAGAGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACTCTCCTTAGGACTA	1
M00764_LAMA1_MIP97	CAATGCACTGTGCACTGTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACGTAAACAACAGCCA	1
M00764_LAMA1_MIP98	CCTCAGTTTTGTAATTTTGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGACCAGCATCAAG	1
M00764_LAMA1_MIP99	CCTTAAAAGAGATCTACTTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCCATTTCATTCCA	1
M00764_LEO1_MIP10	GCGTTATCCTGGGATTCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGAAAGATGACTCTG	1
M00764_LEO1_MIP11	GTTTACCAAATACATTTGTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCATTGGCAAGATT	1
M00764_LEO1_MIP12	GCCACCTGATTGATGTAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGACAAGGTACTGGTC	1
M00764_LEO1_MIP13	GCTGGAAAGAGAAACATTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGAGTTTCGTTTTAA	1
M00764_LEO1_MIP14	ATGAAGTGTTTGATGTGTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATTACACATGTGGG	1
M00764_LEO1_MIP16	CACATAATCACAGAATAAGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATTTCATTTCCTTC	1
M00764_LEO1_MIP17	GAGGAAAAACAAGATGCATAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTTTTCCCTGCTT	1
M00764_LEO1_MIP18	CACTAACCCCGAGATGTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATCACCTAGAGAGGTT	1
M00764_LEO1_MIP19	GAGACGGAGTCTTGCTCTGTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGAGCAGATGGCAG	1
M00764_LEO1_MIP2	AATGAATCGATTTGCTTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAAGCATAAGAAGTA	1
M00764_LEO1_MIP23	GAAAACCCCAGATTTCAATAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTGTATAAAGCAAGT	1
M00764_LEO1_MIP24	GGGAAGTTTATCTCTCTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTAACAGTGGTTTTCA	1
M00764_LEO1_MIP25	CAATGAAGAGTAAAAACAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACACCAGAGTTGG	1
M00764_LEO1_MIP26	GAGGCAGCAGTGATAAACTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGCATGGTCTTGG	1
M00764_LEO1_MIP27	CACTTCACTATATGGCTGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGAAGGTAGAACCA	1
M00764_LEO1_MIP29	CCTTACCTGGGCTCTACACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGACTAATTTTTTCA	1
M00764_LEO1_MIP3	CATTTTTAGGATGGTTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTCATCGCTGATCAC	1
M00764_LEO1_MIP30	ATTTTTTCAGGATGTTGAGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCCAATTCCTGAGA	1
M00764_LEO1_MIP31	GAAATGGCTTCCTTCAACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGTGTTTACTTTGGGT	1
M00764_LEO1_MIP32	GAAAATACCATGAACAGATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTACTCCAGGACAG	1
M00764_LEO1_MIP33	CCAAATAAATCCATGGTTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCTTCACCTTTGAAA	1
M00764_LEO1_MIP34	GGTGCAGATGATATCTCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTGGTCCAGAAACC	1
M00764_LEO1_MIP35	GAGTGTGTTTACCCCAGATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAATGCGATTGCATCT	1
M00764_LEO1_MIP36	CATAATCAGTCGCATTAGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGCACCTCAGTGTC	1
M00764_LEO1_MIP37	GCAGTGATAGTGAAGATGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTATTGCTGAGTAGTAG	1
M00764_LEO1_MIP39	CAGCTGTGGTTGTTCTTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATTCTGGTTCTCATAA	1
M00764_LEO1_MIP4	ACAGATCAGGCAGGCACAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGAAGAAGATAAAGC	1
M00764_LEO1_MIP40	GCAAAATTCTGATGATGAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGACAACAGCTATCTG	1
M00764_LEO1_MIP42	GATCTGATGAAGATAAGCTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATCATTCAGAAGCA	1
M00764_LEO1_MIP43	GTCAGAACGCTCAGAAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTTTTTCAGAACCTT	1
M00764_LEO1_MIP44	GAGGACAATGACCCCTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGACAACCAAGTAATAA	1
M00764_LEO1_MIP45	GGCAGCATTCTCTTGATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATCACTACCACTATGAT	1
M00764_LEO1_MIP46	GTCCATCCCAACATAAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAGGCATTACTGCCA	1
M00764_LEO1_MIP47	TAGAATTAACATTCTAAGGCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCAGATCCAGAATC	1
M00764_LEO1_MIP48	CAAACATAGCGAAACCCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAACTGGCAAAAACT	1
M00764_LEO1_MIP5	GTCTTGCTTTGAGGCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGCTTTGAGTAATCTTT	1
M00764_LEO1_MIP51	GGGCTCAACCAAAGATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGAAGTTGCAGTGAGCG	1
M00764_LEO1_MIP52	GGGCTCAACCAAAGATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGAAGTTGCAGTGAGTG	1
M00764_LEO1_MIP56	GTCTTCGGAGGATGGGTGCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCGTAAAGAGAGGCC	1
M00764_LEO1_MIP57	GACCTAGTTTTCGCTCGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATATCCGCCATTATCGCTC	1
M00764_LEO1_MIP58	GAATCTTTGCGACACTGTCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTAAGAATCCTGGCA	1
M00764_LEO1_MIP6	CAGGTAACTGGCGCTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATCCCGAAATGATGAA	1
M00764_LEO1_MIP7	GTCGTGTATGGAAATTACATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGCACCAGCGGG	1
M00764_LEO1_MIP8	AAAGGAGCTACTTTTGTGCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAACTGGCGCTCAGC	1
M00764_LEO1_MIP9	GGCTTAGCAAACATACCTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGGAAATGAATCCA	1
M00764_MAP2K5_MIP1	GCCTGGGGACAGCTGCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCTTTCTCCCACATTAG	1
M00764_MAP2K5_MIP10	CACCATAGCGTTCGCTCAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGTCCCCTCCAGT	1
M00764_MAP2K5_MIP100	GGAGCCAACTGGGATTGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATACCAAGGTCCCTGCAA	1
M00764_MAP2K5_MIP101	GCTGTTTTTTGTTTTGTTTTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCACCCAACATC	1
M00764_MAP2K5_MIP103	CCCTTTGTGATTTAAAGCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTTGTTAAAGCAGTC	1
M00764_MAP2K5_MIP105	AGTGGTTTAATGCAGAACAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTACTATAATGTTCTC	1
M00764_MAP2K5_MIP106	GTTATCATCGTGCCTTTAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACTAAATAAGTGTCCA	1
M00764_MAP2K5_MIP109	AAGTAAACCAGATTTACAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTGATTTTTGTGGTA	1
M00764_MAP2K5_MIP11	GTGTGGGTATGAGGAGGCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTGTCGGGGGTCT	1
M00764_MAP2K5_MIP110	CACAGTAAAATTCACTCACCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTTTTGGCAGGGA	1
M00764_MAP2K5_MIP112	GTTTTGAGGTTGATTTTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAACTGATCTTTCATA	1
M00764_MAP2K5_MIP113	CAACTTGATTTCTCATTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAAACTGGATTATGGTT	1

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ID	**MIP**	***c***
M00764_MAP2K5_MIP114	CCCAGGGAACCACTGATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTCAGTGATTTTTAGT	1
M00764_MAP2K5_MIP115	CCAAGTTGCAGAAATGACATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAACCTGTCCTCTTGT	1
M00764_MAP2K5_MIP116	GTTTTCTCTGCAACAACCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATGGCCTTTTCTGG	1
M00764_MAP2K5_MIP117	GGAAAAGAGACATACCTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATAACACACTCCCA	1
M00764_MAP2K5_MIP118	CTGGTGAATTCTATAGCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTTGTTCCCTTTTACA	1
M00764_MAP2K5_MIP119	GAGACAAAACAGTCTGTTAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATTATACATTACCA	1
M00764_MAP2K5_MIP120	CAGACCAATCTATCAAAATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGTTGAACAGCAGA	1
M00764_MAP2K5_MIP121	AACAGGAGGGTTTCTTTTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTGAATGAGCTGAG	1
M00764_MAP2K5_MIP122	GGGACTTGGTGAGGATTCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTTGGAGGGAGAGGA	1
M00764_MAP2K5_MIP123	GGAAGTCATTTCACAGATGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGGATGACAAAACAAT	1
M00764_MAP2K5_MIP124	CCACTCACAGGCTCCCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTATGCACAAATACATAT	1
M00764_MAP2K5_MIP125	GCTAAGGTGAGGAGCCACCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAGCTCCAGACATCA	1
M00764_MAP2K5_MIP126	ATCAGGAAAAGTGAAGATTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGCCTGAAAGGATT	1
M00764_MAP2K5_MIP127	CCTACCCAAAATTAGTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGACTCCTTGACTAATA	1
M00764_MAP2K5_MIP128	GCAGTAATCAATAACTGAAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACTGCAACCTCATG	1
M00764_MAP2K5_MIP129	CATCTCCCCTTCATGGCTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTAGCATCAAAAGCCT	1
M00764_MAP2K5_MIP13	AAGAGGGGAGGGGTGATCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTCACATCCTGGG	1
M00764_MAP2K5_MIP130	CCCAGCCACTCCTGGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGAACAATCCTGTGTAA	1
M00764_MAP2K5_MIP131	ATTCTTTTAAGGCCATCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAGATCTGTTAAGGC	1
M00764_MAP2K5_MIP132	AGCCCAAGATGCTCTTTTGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGCTCCTGTTGGA	1
M00764_MAP2K5_MIP133	CAATAGACTAGACCCCAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGATTTGGAGGGCAGTG	1
M00764_MAP2K5_MIP134	GCTCAACTTCACTCACATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACCCCTAATCATGA	1
M00764_MAP2K5_MIP135	GACAAGTACTAAATTTCAGAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTGGCAAACAGC	1
M00764_MAP2K5_MIP136	AAGTGGTATCTTAAAGGGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATATCCTCAGGTAAGA	1
M00764_MAP2K5_MIP137	GTTCCTTCTGCCTGTTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAATTAGAATTTTGGA	1
M00764_MAP2K5_MIP139	ATTGCTAATGTTACGAAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGTACCCTCCAGGTT	1
M00764_MAP2K5_MIP14	GTGCTGGTAATTCGCATCAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTTGTCACCTCTTG	1
M00764_MAP2K5_MIP140	GTGTTAACACATGCCCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTTTTCTCCCTATTCT	1
M00764_MAP2K5_MIP141	CACAAATGTTAATAGCTCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAATATGTAATTAGCA	1
M00764_MAP2K5_MIP142	CCTTTGCATGCTTGAATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAGTCATTTTGATTATG	1
M00764_MAP2K5_MIP143	GAAAAGTGAATTTTTTTCTGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTATTATTTCTAA	1
M00764_MAP2K5_MIP144	CACTCCACTGTAAAGATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTTAACTGCCTGTATTA	1
M00764_MAP2K5_MIP145	GCAAGATTAATCAACAACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCATCAACAATGCAC	1
M00764_MAP2K5_MIP146	CATCCTTGGAGCAAGTTGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTCTCCAGCTTCT	1
M00764_MAP2K5_MIP147	ATTCGCCCGTCCTTCCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATTGGGTGAGGCCTT	1
M00764_MAP2K5_MIP148	GTGATGGAGGAAAAACATGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTGCCGAGTTAATGG	1
M00764_MAP2K5_MIP149	GAGGGACTTCGGGGCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGTACATTTCATCACT	1
M00764_MAP2K5_MIP15	CAGGAAAGGGGCCAAGGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCGGACACTGAGATTA	1
M00764_MAP2K5_MIP150	GTCTCCAAAAGGATGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCAGTTTATTAAATCAG	1
M00764_MAP2K5_MIP151	ACGTACGAAGCTTATTTTTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATACTTCAGAGCCT	1
M00764_MAP2K5_MIP153	AAGGCAACATTATTTACTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGCACCTGAAGA	1
M00764_MAP2K5_MIP156	GGAGCCCCATGTGTGGCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGACCAGTAACCAAGGA	1
M00764_MAP2K5_MIP158	GAGTTGTGTGGTCCAGGGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAATGGAGGCTCCCA	1
M00764_MAP2K5_MIP159	CATCAGTGATGCTGACGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTGTCACACACATC	1
M00764_MAP2K5_MIP16	GGCAGTTTTATTGCTTCAGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTGCTGGTGAGTG	1
M00764_MAP2K5_MIP160	GCAGGAGCAGAGCGCGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGACGAGCTTGGGGAGG	1
M00764_MAP2K5_MIP17	AGTTGTACTACTGGGGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTTCTCTTACTCATTTA	1
M00764_MAP2K5_MIP18	GCAAGTTAAACAACCTGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTACATGTATCAACTC	1
M00764_MAP2K5_MIP19	GTTTCTTGAGCATCTCTAAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTTCTGAGGACTCC	1
M00764_MAP2K5_MIP2	CCCCACGAACATTCAGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAAATGCAAATATGTTT	1
M00764_MAP2K5_MIP20	GAAGACCCAAGTCCAATCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCTGGGCTTACCTAG	1
M00764_MAP2K5_MIP21	CAGATCATGGCAGACTCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGTCTGCACACTTTTG	1
M00764_MAP2K5_MIP22	GCTTGAACATTTGCTAAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCCACGTGACTTTAA	1
M00764_MAP2K5_MIP23	CTAATTTTTGGCAGAACCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGCTTGGAACCTT	1
M00764_MAP2K5_MIP24	GGGTGGCTTTAGCAAGGTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCTATTTGATGCAC	1
M00764_MAP2K5_MIP25	AAGGTAGAGACATTTGGGTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGGCTCCAGTCAC	1
M00764_MAP2K5_MIP26	GAGGGTCAGGTCAGCCTCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCATTCTCTCTCATC	1
M00764_MAP2K5_MIP27	CACTCTTCTGAGTACTTTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCATCCTCCACTGAT	1
M00764_MAP2K5_MIP28	GCACATGGCAAGTGCCATATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTAGCTCTCTGGCA	1
M00764_MAP2K5_MIP29	ACTGGATTGCCTGTGTGCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACAGCTAAGATCTGA	1
M00764_MAP2K5_MIP3	CAAGAAATAGTTCTTTTTTATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGTTTGTCTTTAC	1
M00764_MAP2K5_MIP30	GCCTGAAAACATGAAATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGAGGAAGCATCTATA	1
M00764_MAP2K5_MIP31	ACTGCCTAAGATAGTCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACTATGAGAGTGTAGA	1
M00764_MAP2K5_MIP32	GAGTCTAGTCCTCACAAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCATAATAGTCTTGCC	1
M00764_MAP2K5_MIP33	GCTAAGTGCCCTGCTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGTTTTATATGCACAG	1
M00764_MAP2K5_MIP34	AGTGGCTGCAACTTCCTTCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGGAGCTCTGCCAC	1
M00764_MAP2K5_MIP35	GCTGTCTCAGTATACTAATTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTGGGAGGGACA	1
M00764_MAP2K5_MIP36	GAAACGTTAGCATAAACTATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCAGGCAGAACCT	1
M00764_MAP2K5_MIP37	GCAGTCATTTTTTAAAGGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGATGGCTAATTGTG	1
M00764_MAP2K5_MIP38	CCACAGGAGAACCTAGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATAAAAATGGCTAACAC	1
M00764_MAP2K5_MIP39	GTAGAACAAGACTGGCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTATTGTAGTGTTCAGT	1
M00764_MAP2K5_MIP40	ACAGCACCATACCCCGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCATTCACAACATATCT	1
M00764_MAP2K5_MIP41	CCAAATGGAAAACAAAACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAACCTGTTTTGTCA	1

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ID	**MIP**	***c***
M00764_MAP2K5_MIP42	ATATGATCAGAATCTCAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCATTTGTTTAATGC	1
M00764_MAP2K5_MIP43	CAGTGAGAAGTGATGAGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGGGTTAGAATATCAC	1
M00764_MAP2K5_MIP44	CGATCACCATCTTCATCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTCGTCTTCACTATGC	1
M00764_MAP2K5_MIP45	AAATGTTGGTGGTCCAAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACTTAAATAAAACAGG	1
M00764_MAP2K5_MIP46	ACTACCCCAAGCTAACCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGCATGGCCTGATA	1
M00764_MAP2K5_MIP47	GATTTTTAGGCTGTAGCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTGTTGGCAGAAGGAG	1
M00764_MAP2K5_MIP48	CCTTTATGGTTTTAACCAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCTGTTGCTGAATA	1
M00764_MAP2K5_MIP49	GGAGCCCCAGATGGCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTCTGGGCCCTATTTAT	1
M00764_MAP2K5_MIP5	GAGTCCGCCAAAAGCCAATTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTCGCTCAGGAGA	1
M00764_MAP2K5_MIP50	AAGCTTGTACACATTGTAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCAATAACATGAGCC	1
M00764_MAP2K5_MIP51	ATGAGAAAGAAAATCACAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACCTGGCTTCAGGC	1
M00764_MAP2K5_MIP52	GCATCATAAAGGAAAAGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAGTTATTGAGGAGT	1
M00764_MAP2K5_MIP53	GTTTGATTAACTGGCATGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAACTAGGCTACCTTT	1
M00764_MAP2K5_MIP54	GGAAATCGAAATCACAGAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCAAATTGCCTCTTG	1
M00764_MAP2K5_MIP58	CCATAAGTGTCTGTTCCAGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTAACACACTGGACT	1
M00764_MAP2K5_MIP59	CAGTACTTTTGTAAATTGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTCTATTAACTGT	1
M00764_MAP2K5_MIP60	ACAGTTATGTTTCCAAAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGTATTATTCCACAG	1
M00764_MAP2K5_MIP62	CCTGACACCATCTTGAGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATAAGCAGTCAAAT	1
M00764_MAP2K5_MIP63	CCCTAGCAATCTTTTTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTAAATCTTAGCATATG	1
M00764_MAP2K5_MIP64	CGATGGAACATTCTAGTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCTCATTCTATTACA	1
M00764_MAP2K5_MIP65	GCTCAGTTAACTTGATTTTTATATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCGCTTGCTCACA	1
M00764_MAP2K5_MIP66	AATGATTAGATTCCTTTCATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAATTATGAACCAG	1
M00764_MAP2K5_MIP67	GTAAATGGCCCTGATGTGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCTGCAAGTTAAAAC	1
M00764_MAP2K5_MIP68	GAAATGAGGGTGACACCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAATTCGTACCTTCA	1
M00764_MAP2K5_MIP69	ACTGCACTTTCTCAAGCTCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTCAGCCTGCAAG	1
M00764_MAP2K5_MIP71	GCACCTATTGCTTGGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGAGGTCCTTTCTCTTTG	1
M00764_MAP2K5_MIP72	CACATCCTTCTCCCAATGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGACTTCTTTAAGCT	1
M00764_MAP2K5_MIP73	ACATATTACCGTCCAGTTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTGATGATCTTGCCA	1
M00764_MAP2K5_MIP74	GGGTCATTTCAAGTTCAGCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTGTCCCGATATCG	1
M00764_MAP2K5_MIP75	GTTCTCTGTGGCAAAGATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAGATGAATGAACA	1
M00764_MAP2K5_MIP76	ATCCAAACATTTCTGCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATCCAGTACTTACCTT	1
M00764_MAP2K5_MIP77	GGTTTAGATGGTAGGTAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGTGGGAAAATATTAG	1
M00764_MAP2K5_MIP81	AAAGAAGAAAATGAGTGAGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATCTGTTCCCCACT	1
M00764_MAP2K5_MIP82	CATAATTTGTTGAGTGACTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTATATTGAAAACTCT	1
M00764_MAP2K5_MIP83	GCTTTGTACTATACCCTATATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCTGAACCTGCTTT	1
M00764_MAP2K5_MIP84	GGTTAAGAGTTAGAAGCGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTTTAAAGTAACATC	1
M00764_MAP2K5_MIP85	AAAAAGCTAAGAAATATTCTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTTCACAGCTGAGG	1
M00764_MAP2K5_MIP86	GCATGGAATGATGAGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAGCATGTCACTTGAA	1
M00764_MAP2K5_MIP87	GCGTCAGACCCTGCAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAAACATTTTGAGTAGG	1
M00764_MAP2K5_MIP88	GGCGACATAATTGTCTTTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATCACAAGCTGTCAT	1
M00764_MAP2K5_MIP89	GACTGCTTATATTTAACTTGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACTCCAGCAAAT	1
M00764_MAP2K5_MIP91	CAGCACTCCACACAGGGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCCTCAATATGTACA	1
M00764_MAP2K5_MIP92	GGGTCTAAAAGATAGAACAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTGTTTTTAGGAGA	1
M00764_MAP2K5_MIP93	ACCTCCTTCTTCTTACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGTGTAATATCTAGTA	1
M00764_MAP2K5_MIP97	CATGTTTATCTCTACAGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATTGGACTAAAAAGTT	1
M00764_MAP2K5_MIP98	CAGAACAATGCACTGGGCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAACACTGAAGCCA	1
M00764_MAP2K5_MIP99	CCTTCTTGATTTTCTCCTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGCAGTAGCAGTAAG	1
M00764_MDGA1_MIP1	CACCCTGGCATGACTCAGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAACTGCCACCTGAA	1
M00764_MDGA1_MIP10	ACTGCCTATCCCCATGACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAATCGACCTACCTGA	1
M00764_MDGA1_MIP100	GGACTTCATAAGAAGCTTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGTTTCCACAGCTA	1
M00764_MDGA1_MIP101	AGGAATAATCACCAAGATGATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTGACCCATCACC	1
M00764_MDGA1_MIP104	ACTCAGGCTGGGAGTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGGAAAAAGCAAGTATA	1
M00764_MDGA1_MIP105	CCTCCTTACAGGCACCTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTCTTTCTTTTTTTTT	1
M00764_MDGA1_MIP109	AGGGGATGGAGAAGACAACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGGTGGTGAAGGTTG	1
M00764_MDGA1_MIP11	ATGAGCATTTGCAAAGTGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTTACCCCAGACCTC	1
M00764_MDGA1_MIP110	CACCCACGACCACACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTGAAATGGAGTTTTGCTC	1
M00764_MDGA1_MIP112	ATGCCAGCGCCAAGTTCTACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAGGCCTGGCTGT	1
M00764_MDGA1_MIP116	ATTCCGGGCTTCAAAAGACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGCAGGTGTTGTCTG	1
M00764_MDGA1_MIP117	GCCTTGCTTGGATGCATGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGATTATCCTTAGGC	1
M00764_MDGA1_MIP118	GTTATAAAATCATAAGTAGGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGGCAACTAGTG	1
M00764_MDGA1_MIP12	GTCTGTAGGGCCAGAATAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTCTGAAATTCTAGAA	1
M00764_MDGA1_MIP120	CCATTCATCATTGAAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTGAAATACAAATGGA	1
M00764_MDGA1_MIP121	GTCTCACCTGAAAGGTTCGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTACCCCATGGAAACA	1
M00764_MDGA1_MIP122	GGACACAAAGGCTCTCCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGTATCCTCTGCAG	1
M00764_MDGA1_MIP123	CTTAGGAACCACATGAGGATGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGAGGTGTGGGGC	1
M00764_MDGA1_MIP124	GAGATCGGTCAGGATGTACTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGCCCATCCTTCCT	1
M00764_MDGA1_MIP125	GTGCCCCACAGCTATGAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGACTTCCTAGGCATCT	1
M00764_MDGA1_MIP126	ATAATAAAAATGATGACAGCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCATTGTGCTGGTT	1
M00764_MDGA1_MIP127	AAGACAGCCCTGGGAGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTAATTATGATTTTTGC	1
M00764_MDGA1_MIP128	AGCCACACTCTTACCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAAAATTACAATCCTAT	1
M00764_MDGA1_MIP129	CCAGAACCCAGCTTTGTGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTCCACCATGCAAA	1
M00764_MDGA1_MIP13	CACCCTGCACCCTACTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGGAGGAGGACTAAA	1
M00764_MDGA1_MIP132	ATGCTCATCAAGGCCAGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGTGGACTCAGAGG	1

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M00764_MDGA1_MIP133	GTAGGCTTTGGCTAAGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGTCTGTAGTTGAGCA	1
M00764_MDGA1_MIP135	GAGACAGGGAGATTGGAAATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGATGAGGTGGAAA	1
M00764_MDGA1_MIP137	AGGAGTGGGGAGACAGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAAAGAGAAATTTAGG	1
M00764_MDGA1_MIP139	ACTTAGTCAGTTGGGTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGTGGGAAATGTCA	1
M00764_MDGA1_MIP14	CAACAGGCTAACTCCAATCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCAACCACCATACCA	1
M00764_MDGA1_MIP140	CAATGGGTGGGTCAGAAAGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGCCAGACAGCA	1
M00764_MDGA1_MIP142	CCTGGGCTTGAGGGGCTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAACGTTCCAGAGAAGC	1
M00764_MDGA1_MIP144	CCTAGGCCTGTGGGAAGGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGGAAGCTGGGATTG	1
M00764_MDGA1_MIP15	GAGAGGCTTCTGAGCAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAAGGGAAATTGGTG	1
M00764_MDGA1_MIP153	GAAAATTACCACCATGTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATCTCCCATCTTCATT	1
M00764_MDGA1_MIP154	GTATCAGGAGTAGCTGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCAAAATCAAGTAATTT	1
M00764_MDGA1_MIP156	CATTATAGCGGGCCGTCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGAGGATGAAGAGGG	1
M00764_MDGA1_MIP16	GTGTTTGGTTGGTATTTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCATACCTTCTTTCA	1
M00764_MDGA1_MIP160	ACTAGCTAGATGTGTATTTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGACTCATGGAAGT	1
M00764_MDGA1_MIP161	GTTCTTATTTGTAAATAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACTTAATTCAACCCAA	1
M00764_MDGA1_MIP163	CCTAGACATCAGGCCTATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGATCTTGTTAGTAT	1
M00764_MDGA1_MIP165	CCTTTCCTCCTAAGCTCTATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCGTACAGGCTAAA	1
M00764_MDGA1_MIP166	AACACGTTTCAGATAGTCTCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCACCACTTGTTCA	1
M00764_MDGA1_MIP168	GGAGAGGCCCACAGACAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGACTATGGCACCTACC	1
M00764_MDGA1_MIP169	GTGCCGGCTTGCCATTCTTGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTGGGAAAGAAGCC	1
M00764_MDGA1_MIP17	GCCTTTGTGGAAGCCCCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTTTCTTCTCTTTGGC	1
M00764_MDGA1_MIP171	CAACCCAGACCCAGCTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGGATGTTCTCACTC	1
M00764_MDGA1_MIP172	GGTGGGACATGGACCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTTTTAAAGCACATCT	1
M00764_MDGA1_MIP173	ATTTACTAGTTTAACCCATCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCTGGGAATTGTTT	1
M00764_MDGA1_MIP174	CATGTTAAGTGCTTGGAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAATTCAAGATTGGCT	1
M00764_MDGA1_MIP175	CATTTGGAAGCATGCACTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCTCAGACAGCTTAAG	1
M00764_MDGA1_MIP176	GCATTGTAGGGGTCAAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAAATGTAAGAATTCAA	1
M00764_MDGA1_MIP177	CCTGGTCTTTGGGAGCTACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTCTGGCTACTACAA	1
M00764_MDGA1_MIP178	CATGGGACCACTGCAGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTTCTTGGCAGGGTTG	1
M00764_MDGA1_MIP18	CAACACACACGGCTGACGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCCTCACTGTCCAGG	1
M00764_MDGA1_MIP180	GGGCTAGGAAAACCATAGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCACATTCTCCCCAGG	1
M00764_MDGA1_MIP181	CCTACCTGAGCTAACTCCCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCCAGGACTATGCC	1
M00764_MDGA1_MIP182	CTACACCTGCCAGGTGTCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCTGGGTGAATGAGT	1
M00764_MDGA1_MIP183	GGGTGGATGCTACACTCTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGAGTCTCCAGGGA	1
M00764_MDGA1_MIP184	CCCTGGGGCTAAATGGTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCCAGACTGGAGAAA	1
M00764_MDGA1_MIP185	ATGGCATCACCACCATCTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACTGGCAAGTACCAG	1
M00764_MDGA1_MIP186	GGTGGCTGCAGGCCAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCAGAGTATTGGGAAC	1
M00764_MDGA1_MIP187	CCTGGAGGACATGTTGCCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAGGAGTCATCTCCT	1
M00764_MDGA1_MIP188	GTTAGGAAAAGGCACCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTACTTTGGAAACACACA	1
M00764_MDGA1_MIP189	GCTGCCCATCCTGACCTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGAACTCCAATCAGA	1
M00764_MDGA1_MIP19	CAGAGTGGGCCAGGGTCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTGTTCCCCATTTGC	1
M00764_MDGA1_MIP190	GGGGCTGAGTTTTTGGGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTCCGATACCCTATCC	1
M00764_MDGA1_MIP191	ACATCGCTCACCGTCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGATGTCAACCCCATTGTC	1
M00764_MDGA1_MIP192	GAGGCAACTTCTACCAGGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAAGGGCTGCCAG	1
M00764_MDGA1_MIP194	GTGGACGTGCAGTGTGAGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAAGTTCCAGGAGAC	1
M00764_MDGA1_MIP196	GCCTAGGCTCAGCACTTAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATATCAGCGAGCGTGTCT	1
M00764_MDGA1_MIP197	GTTTAGAGAAGAGGTGCCAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAGGGTGTCCCCCT	1
M00764_MDGA1_MIP198	CCTCCTCCATCCTCTCCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCTTTCCTGGGCTCAG	1
M00764_MDGA1_MIP199	AGTGGGCTGATTGTGTGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTCAGAGGCCTGAC	1
M00764_MDGA1_MIP2	GCTGGGATGGTCAGCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGTCAGGAATTTGGAC	1
M00764_MDGA1_MIP20	GTCTCCTGTTGTGCTTTTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTGGAGGTGAAAGAG	1
M00764_MDGA1_MIP200	AAAAGCACAGCTCTCTTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTCACCTTGGGGAG	1
M00764_MDGA1_MIP201	CAAATGCCTAGATTACCCCCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATCGGTGCCCCT	1
M00764_MDGA1_MIP202	GGCTAAAGGCAATTCCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGGAGTATGACAGTG	1
M00764_MDGA1_MIP203	CATCTTTGCTTGGCTGCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCCCTCTCCCCCACA	1
M00764_MDGA1_MIP204	GCTCAGGAAGCTTAGTCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGGCTCTCTAAAAG	1
M00764_MDGA1_MIP205	GCTCAGGAAGCTTACTCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGGCTCTCTAAAAG	1
M00764_MDGA1_MIP206	AAGGCCTTCATTGTTTTTTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCAACCATCTCAGG	1
M00764_MDGA1_MIP21	GAAATGATTGGGGTTGTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCTGAGACCTCAA	1
M00764_MDGA1_MIP215	CGGCTAACTTCACGGACCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGAATATTTTTCAAAAG	1
M00764_MDGA1_MIP22	CCTAGAGGGCCACCAGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGCTTTTCTCCCAAG	1
M00764_MDGA1_MIP229	CGCTTGTTAGCTGCTGCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTATATGCAGACTAACC	1
M00764_MDGA1_MIP230	ACTCTCCAGGGCTTAAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAACTCAAAGATCTCC	1
M00764_MDGA1_MIP232	CCTCTTCCGTCTTTTCTCTCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTGGTGGCATGGG	1
M00764_MDGA1_MIP233	GAGGCGCAAACGAGTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATCATTCGTGAATTCAC	1
M00764_MDGA1_MIP234	CATCCTTTCACTCCCCAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGGCTGATAGGAAGTC	1
M00764_MDGA1_MIP24	CCTTCTAGTTATAAGGGTCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTATCCTAGGAGGGT	1
M00764_MDGA1_MIP25	GAGCATCTAAGCTGGTGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTGTGTCTGAGAATGT	1
M00764_MDGA1_MIP26	GCTCTGCAGGGACTCTCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACTCCACACATCAC	1
M00764_MDGA1_MIP27	ACTGGCTGAGGTTGGGTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGTTTCCCCAAAGAC	1
M00764_MDGA1_MIP28	AAACAGGGTCTCTTCTGTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAGGATTCTGCACGC	1
M00764_MDGA1_MIP29	GGAGTGAAGGTCAGCATGTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTGCCACACAGAGG	1
M00764_MDGA1_MIP3	CATCTCCACCAAAGCACCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAGGCCTCTTGGAA	1

continued table…

ID	**MIP**	***c***
M00764_MDGA1_MIP30	CCCACCGGCACCCTGGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACTGTGGTGGGAGGGT	1
M00764_MDGA1_MIP31	ATCCTGCCCTCGGCTCCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTACTACAGCCCTGGGG	1
M00764_MDGA1_MIP32	GCTTCAGCTTCTTCATCTGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGCAGGAGACCTCAG	1
M00764_MDGA1_MIP34	GTCTTCAGGCTTCACTCAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCACTCTGACAGCCT	1
M00764_MDGA1_MIP35	CCCCCTCCTCCTGGAATGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCAGGTTGGTGAAAAG	1
M00764_MDGA1_MIP36	GTCACCCTGACCCAGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATAAGCTGCTATACAGC	1
M00764_MDGA1_MIP37	GAGGCATTTTGTGGCCTTAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGCCATGGTGTGTCA	1
M00764_MDGA1_MIP38	ACACTCATTCCTGCTGAGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCAACACACAGACA	1
M00764_MDGA1_MIP39	GTGAGCCAGCATCTCTGTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTATGCCAGTGGGCAC	1
M00764_MDGA1_MIP4	GAGGAAGGGAATTAGACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTAGGTGGCAGTTCAG	1
M00764_MDGA1_MIP40	CCTCAGCATTTCAGCAGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACACACAGAGACCAGC	1
M00764_MDGA1_MIP41	GTGTGAATGGGTGAGGCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGGCACAAGGTGGAG	1
M00764_MDGA1_MIP43	ATCCATAGAGTGGACAGTAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGTGCTCCCTCTTT	1
M00764_MDGA1_MIP44	AACCCAAGGAGCTTTTCAACATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCCTTGGGAACCC	1
M00764_MDGA1_MIP45	CCTGACAGCAGGAACCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTGCAGAATAGAACC	1
M00764_MDGA1_MIP46	ACCAGGCTCACTTGTGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTCAGAACCTCTGAGGT	1
M00764_MDGA1_MIP47	ATTCTGTAATCAGTGGTTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCCCCAACTAGACT	1
M00764_MDGA1_MIP48	ATTTCAGACAGAGGCCTTGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACTTGGAAGGCTCA	1
M00764_MDGA1_MIP49	CCAGGTTCTCAGCATACACTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTGTGTGATCATT	1
M00764_MDGA1_MIP5	GTGCCTTGTTTGTGCAATAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTCTGTATTCTTCTG	1
M00764_MDGA1_MIP50	CCCCACCAAATGCTCCAGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCAGCTGTTGGTGA	1
M00764_MDGA1_MIP51	GAGAAGAGGCCTGGAACTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGCCTGAAATTCCACC	1
M00764_MDGA1_MIP52	GTCTATTCAGCCAGCACCCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTCCTCACCAAAG	1
M00764_MDGA1_MIP53	GTCCAGCCCTGTTCTGTAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCTCACATATCTGCCT	1
M00764_MDGA1_MIP54	ACATACACACATATGCACGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAACGAATGGGTCT	1
M00764_MDGA1_MIP55	GTGTCTAGGTACCACCGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTAGATCTTTCCTCCT	1
M00764_MDGA1_MIP56	CCTCCACCAATCCCAGCTCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGCTCAGGTGATGT	1
M00764_MDGA1_MIP57	ATCCCTGTCCTTGGGTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAAAAAGCACTGTCTAG	1
M00764_MDGA1_MIP58	GTCTGATATGGGGGCACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGAGAAGGGAACTTT	1
M00764_MDGA1_MIP59	GAAGTGGAGAGGGGCCTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGGTCTCAGAGGA	1
M00764_MDGA1_MIP6	GGATTTCTGAGTGCCCATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGAATACAGAAGCA	1
M00764_MDGA1_MIP60	AGTCTTCAGACTGCCCAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCTCACCCCAGAAAAT	1
M00764_MDGA1_MIP61	CCTGAGAACACGGTTCTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTATTTCTGGGACA	1
M00764_MDGA1_MIP62	CGTGGGACAGTCACAGAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGAGGAGGGAAATATG	1
M00764_MDGA1_MIP63	AGGAAGGTAGGGCACCTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGTGGGGCAGACAT	1
M00764_MDGA1_MIP64	CAAGGACAAGGCCTATGTTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAGTCTGACCAAGG	1
M00764_MDGA1_MIP65	AACTCCAGCCTGGTGGCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTACTGCAAAGACAGGG	1
M00764_MDGA1_MIP66	GTCTCCAGGGCCTCAGTGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGCCATTCAGGCAAG	1
M00764_MDGA1_MIP7	GTTTTCCTGAACCAGATGGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGGCTCCCTGAGCA	1
M00764_MDGA1_MIP70	CCTCAGTGCACACAGACAAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGCAACAGGGGAG	1
M00764_MDGA1_MIP72	AGGTAAGTGAAACATGCATATACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGGTTCACATTCAC	1
M00764_MDGA1_MIP73	ACAACAGTTAATCCTCACAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCTCCAGAGGTGAA	1
M00764_MDGA1_MIP74	GCTTCTCATTGTTTACACAAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCCCTGGAAGGC	1
M00764_MDGA1_MIP75	CACCCTCGTGATGAGCATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGTGTTTGGGTCTGAA	1
M00764_MDGA1_MIP77	ATCCCAATAAAGGTGCAAGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTGCTCCTTGCTTT	1
M00764_MDGA1_MIP79	CGTGTCCAGAGCCCCTTTGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAACCACCGAAGCC	1
M00764_MDGA1_MIP8	CAATAAAACTTAGGTGGTAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGAGCGGATTTCTC	1
M00764_MDGA1_MIP80	ACGCCTGGTCTCTCAGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGAGGGCTTGGTAAAT	1
M00764_MDGA1_MIP81	GTGTGGGAAAGAGAAGACTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCCTCACCTTTCCA	1
M00764_MDGA1_MIP82	CAGCTGGGCATGGGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGATTAGCTGATTAGCAG	1
M00764_MDGA1_MIP83	GTGGGACCTCTGTCTGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAGGATGACTTGCAAAT	1
M00764_MDGA1_MIP84	GGGACAGCTCCCTTGCCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTGCCAACTGGGTAT	1
M00764_MDGA1_MIP85	GTCTGTGTGACTGTCCGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGGGCTTTTAAAATG	1
M00764_MDGA1_MIP86	GGCCTTCTGGACCCAACATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATCCGATACATCCAG	1
M00764_MDGA1_MIP87	AGGGGACCCCTGTCTCCAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCAGGAGGCAGATTT	1
M00764_MDGA1_MIP88	CAGCAGCCCTGCTGGATAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAAATGAGATCAGAGA	1
M00764_MDGA1_MIP89	CCTTTGCTTGTGATGTTGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCCTGGCCTTCCAC	1
M00764_MDGA1_MIP9	CATGTTGGGTAACTTCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTACTTGGTTACAATGA	1
M00764_MDGA1_MIP90	GGCAGGAACTGGCCCTCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAAGCCTTATAAAGA	1
M00764_MDGA1_MIP91	GTTCTAGTGTCCTAGAACAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCTCCCTCAAGGAAG	1
M00764_MDGA1_MIP92	AGACAAAGGCCCCTGTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCAGAGTTGGAAGGAC	1
M00764_MDGA1_MIP93	AGGAGTCAAATAGGGAAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCTTCATGAACCCTGA	1
M00764_MDGA1_MIP94	GCAGGAAGGTCTGTGTCAAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAGCCCTCTATCC	1
M00764_MDGA1_MIP95	GGGCATGTTAAGCAGAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGTTAAGGACTCAGAGTTC	1
M00764_MDGA1_MIP96	CACATTCCCCTGGCCAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTCCTCCGTATCTGTC	1
M00764_MDGA1_MIP97	GGCTCAATAATCCTCCCACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCTTTAGATGTGGCA	1
M00764_MDGA1_MIP99	CAGCCACGGGCAAAATGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTAAACCCAAATGAACT	1
M00764_MEIS1_MIP1	CCCTTCCCCGCCCCCAACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTCTCCTTAGGCGACA	1
M00764_MEIS1_MIP10	CCGCGCATAGACTTCATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCAGCTTTATTTTCAG	1
M00764_MEIS1_MIP100	ATTTGGGGGGAGTTCGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACAACTTCACAGATATG	1
M00764_MEIS1_MIP101	GGACAGAGAAGTTCAGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAACAAGAATTATGCTT	1
M00764_MEIS1_MIP102	GAGCACAAAAGTTAGATTTCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTAATGAACTGAAC	1
M00764_MEIS1_MIP103	AACTGAGCATTAGAAGAAATCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCCTTGCTCCTCC	1

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ID	**MIP**	***c***
M00764_MEIS1_MIP104	GTGGAATCCAACATTTCTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTATTCATAGGCCTTC	1
M00764_MEIS1_MIP105	CCAAATTTTGTGCAACCTATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAGGCATTCCGATT	1
M00764_MEIS1_MIP106	CAGATCACAAACACTGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACAATGAAAATGCAAT	1
M00764_MEIS1_MIP107	GCCTACCTTTTTTCATCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAGGATGTAGATTAAT	1
M00764_MEIS1_MIP108	CAAATAAGAGGCATCTGTGAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGTTGTCCCCAC	1
M00764_MEIS1_MIP11	ATTTAATGGAGCGCCTCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTGGGGAGAGAGTC	1
M00764_MEIS1_MIP110	ACCATATTTTGGTATCTAGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGGGAACTTATTG	1
M00764_MEIS1_MIP111	CCAAAGAACTCTTTCTTCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAAACTGGGAAAGG	1
M00764_MEIS1_MIP112	ACTGAGCAGCAAGAGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTCTCATAGACCACCTG	1
M00764_MEIS1_MIP113	GCTCTGTGTTGCTGAGGTTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCTTGAACCACCCA	1
M00764_MEIS1_MIP114	CACAGGCCAATTCAGAAGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATTGGCCGCTGTG	1
M00764_MEIS1_MIP115	CCTAGAATTCCTTCTTGCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCCCTTTCTTTCCC	1
M00764_MEIS1_MIP116	CCTTGGTTTCTGTGACTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGAGCAGTATTCAGT	1
M00764_MEIS1_MIP118	GAGTAGCAAAGTACTGTAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCGTTAGAAACCTGG	1
M00764_MEIS1_MIP119	AAGGATTTAAGATCACTGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCAATCTGCTTTGAT	1
M00764_MEIS1_MIP12	GCACAAACACCACACACCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAACAGGTCGCGTCTT	1
M00764_MEIS1_MIP120	AGTGGCCCGGTCTCATCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCAATTAAGGAGCCAT	1
M00764_MEIS1_MIP121	CAGTCTCTTTTTTCCCCCTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAATGGCCTTTGGC	1
M00764_MEIS1_MIP122	GACATTTTCAGTTTCTGTCACTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTGCGCAGCCC	1
M00764_MEIS1_MIP123	GCCCATGTGTCATGAAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGATGCTATGAGGAAATG	1
M00764_MEIS1_MIP124	CCACCTTTTCAGTTTGCCTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAAAGTCGCCCTATG	1
M00764_MEIS1_MIP125	GATGCTAGTCCATAAACAAGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTACCACACGGCAGCAGG	1
M00764_MEIS1_MIP127	AATGTGGTCTCTCGAGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGTTTAACCTCTTCCA	1
M00764_MEIS1_MIP128	GCTACCTTGACATGCTTTATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGATGCCACGCTT	1
M00764_MEIS1_MIP129	GTAAGTGGATTCTAAATGACATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAGCTTCCCCCAG	1
M00764_MEIS1_MIP13	GTGCAACACACACTTTACACACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCGCGCACCCACC	1
M00764_MEIS1_MIP133	AATTTAAATCATGTTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGCTTTTCTAAGTGTGA	1
M00764_MEIS1_MIP134	ATCCACTAAAGCATCAGAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAGCTCTGACTTA	1
M00764_MEIS1_MIP135	ACTTTTCAAGCAGAGTAACAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGCACTGGCTTCC	1
M00764_MEIS1_MIP136	ACAAGGGACTACACAGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACAAAACAAATCCCC	1
M00764_MEIS1_MIP137	GATACAATGAAGATTTGTGGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCTTTATGCCACT	1
M00764_MEIS1_MIP138	GCACTTACAAAAATATCCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTACAACCTGTCTA	1
M00764_MEIS1_MIP139	GCTTTTCCTAAAGTCAATTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGACAAAGGATGA	1
M00764_MEIS1_MIP14	GAGAGGTGGATTCCGACCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCACTGGAAGGAGAT	1
M00764_MEIS1_MIP140	CCTGATATTAAAAAACAACCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCAGGTATGAAGGT	1
M00764_MEIS1_MIP142	ATAGCCTAAGTGTCTCATGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTCACTTGAAGGATG	1
M00764_MEIS1_MIP143	ACACCCAGTTGCCACTGCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGTTGGCACAAGACA	1
M00764_MEIS1_MIP145	GCTAGCGTTAGGAATATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTAAGAAGCTAATCAA	1
M00764_MEIS1_MIP146	CAGTTCACTTACGCCTAGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAATTAACAAAATCT	1
M00764_MEIS1_MIP147	GACAGAGAAATATCATTTTACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGTTGCCTCCAA	1
M00764_MEIS1_MIP148	ACACTGAGGAATAGAACTAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGAGCCATGTCATT	1
M00764_MEIS1_MIP149	CACTCTACTTACTCCCTGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTATGGCTCTCTGTAA	1
M00764_MEIS1_MIP15	GCTAGGGCTTTGTGCATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTAACCCTCCTTCTCT	1
M00764_MEIS1_MIP150	GGGAAACTACCTTGTGTTTTGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAAGTGAGCAAGT	1
M00764_MEIS1_MIP151	ACTTAGCAATTCAGTTTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGGAAAAGGGCAAA	1
M00764_MEIS1_MIP152	AGGTGAGGAGATCACAGTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCAAGATCTGGCAGA	1
M00764_MEIS1_MIP153	CCAAAGACTGAGAATAAAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAACTAAACTTAGCA	1
M00764_MEIS1_MIP154	GAGCAAGATCTGGCAGAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGTTTTGCTTTGTTC	1
M00764_MEIS1_MIP155	ATCCAGGTCTCAGATTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGGGGACAAAAAAGAA	1
M00764_MEIS1_MIP156	AGGAGAATGGGAAGTGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTTGTTTAAGACTCAA	1
M00764_MEIS1_MIP157	GGCAGCACACCAACATGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATATTTATGTTGGTGC	1
M00764_MEIS1_MIP158	GTTACCTATGTACTTTTGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGACCGCAATTACTTT	1
M00764_MEIS1_MIP159	CCACCTTACTTAAGAGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAATTACACCTCAGG	1
M00764_MEIS1_MIP16	CGCTTCCCTTGAATCAGTCCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTGCCACTCCAGC	1
M00764_MEIS1_MIP160	GGAGACAAGTTTTGGAATACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTACAGCCCTTTTG	1
M00764_MEIS1_MIP161	AACTCAGGTTTGAGTCTATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGCAAAGATAAGGCT	1
M00764_MEIS1_MIP164	CCTAATTTCTCTGAGCCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTATAGTTGCGGTGCTC	1
M00764_MEIS1_MIP165	GAGGTCACATGTTACCAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTCTTTTTCCAGACT	1
M00764_MEIS1_MIP166	CCATTCTCATTATAAGCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCCTGAACTGCTAAT	1
M00764_MEIS1_MIP167	AACACAGGTCTACAACAAATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATTGAAACAAATAA	1
M00764_MEIS1_MIP168	GAAAACCTGTCCCTGTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAAACAGTATACCTTTT	1
M00764_MEIS1_MIP169	AAACAAAAATGCATACTTCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATAAGGCTCTATTAA	1
M00764_MEIS1_MIP17	AGAAGATCTGCTTTTTTTTGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGCCTGTGATTGAC	1
M00764_MEIS1_MIP171	CAACTCAGATCAAATCTGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCAGAGTCATACGC	1
M00764_MEIS1_MIP173	CAATTATTTTTGTAGCCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGCAAGGTCACAGA	1
M00764_MEIS1_MIP174	AGGAATGCATTTCTCTGAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGAAAGCAAAACTA	1
M00764_MEIS1_MIP175	GAGATTTCTTGGGGTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATTCTATTTTAATGCCC	1
M00764_MEIS1_MIP176	GAGGTAACAGATGCCCTTATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATCCCAGTTCATTAT	1
M00764_MEIS1_MIP177	CAATTTTTATCAAAACCACCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTAGCCACCACTCC	1
M00764_MEIS1_MIP178	CCCAAGCCTGTGTACTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCTCTTTGCAAATGAA	1
M00764_MEIS1_MIP179	GTTTGCCTGTTTTACCACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTAGATCTTGGCAAAA	1
M00764_MEIS1_MIP18	CCCCCAAAAATCAGTTTAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCAACGTGAGCTAC	1
M00764_MEIS1_MIP180	GTTTATTAATGCCCGGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGAGAACTGAAGGAGT	1

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ID	**MIP**	***c***
M00764_MEIS1_MIP181	GTTGAGGAAGAGGAAAAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACTATGGGGGACTTG	1
M00764_MEIS1_MIP182	CCTGGCAATTAAAATTAAACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGTCCAACCGAGCA	1
M00764_MEIS1_MIP183	CAGTTTATTTACCAGGTAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTACTTTTCTCTGTTG	1
M00764_MEIS1_MIP184	CCAGCTCTTTCTGCTACTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAAACGTTTGGAGAAG	1
M00764_MEIS1_MIP185	ACAAAGAATATTGTAACTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTTTTGACAGGTAA	1
M00764_MEIS1_MIP186	CTTACTTCTGAAGCAGCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGGAATTGCTGTAA	1
M00764_MEIS1_MIP187	GGGTTATTAAAGCACACAAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTCGAACACCAGAA	1
M00764_MEIS1_MIP188	CTTAAAATGGCGATACTTCTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATTCAGGTAGTGGT	1
M00764_MEIS1_MIP19	GTTTCTTTTCACACTGGCCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCTTTGCTTCAGGT	1
M00764_MEIS1_MIP190	GCATTGAGGCAACACACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTTGTTTTTGCATTATA	1
M00764_MEIS1_MIP191	ACATAGTTTTCCATAGTGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTAGCTCAAAGAGGG	1
M00764_MEIS1_MIP192	GTCTCTTTCTCTGGTATGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCACACCTTAACTG	1
M00764_MEIS1_MIP193	CACCAGGTAAGACTTTGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTCAGAGACTGTTAT	1
M00764_MEIS1_MIP194	CCCATATGTTGCTGACCGTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGCAGCCAGCTTG	1
M00764_MEIS1_MIP195	CCCATATGTTGCTGACCATCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGCAGCCAGCTTG	1
M00764_MEIS1_MIP196	CACTATTTCTCAACCCTCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCATCAACACAGGTA	1
M00764_MEIS1_MIP197	ATCCTGGCTTCCCCTCTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTAGAAGGGAGATAAAA	1
M00764_MEIS1_MIP198	AAGTAAGTACAAATGGGGTCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCTCTTCTTGGA	1
M00764_MEIS1_MIP199	GATGAAGGTTACATGTAGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAACAAGCATGAAGC	1
M00764_MEIS1_MIP2	ACTCTATAGAATCTTCAGTCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGACTCCTGCGAA	1
M00764_MEIS1_MIP20	AATATTCAAACTCCCCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAATTTAATCTCACATT	1
M00764_MEIS1_MIP201	GCTTAAAAGCTTGATCACAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGCAAATCAGTCTGT	1
M00764_MEIS1_MIP202	CATTTCTACACTAACCTGCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGAGTGGGTTGTCA	1
M00764_MEIS1_MIP203	GACAGATTTATGACACTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTCAAAATATGCCTT	1
M00764_MEIS1_MIP204	CAAAATAGAGGTGTGCACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTTACTTAGGGTAAG	1
M00764_MEIS1_MIP205	GCCACACGTAATCCCATTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAATAAGTCAAATCCA	1
M00764_MEIS1_MIP206	CACTCTTGCATTTTCTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTAAGTATGCCATCACT	1
M00764_MEIS1_MIP207	GAATCTGGGACAGTTTTCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAAAGCAAGAACAGT	1
M00764_MEIS1_MIP208	CGTACTGGTCATCTTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAAATTACCCCTAATA	1
M00764_MEIS1_MIP209	CCCTGGCCTCAGCAGTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAACTAAGCTAGAGAATTC	1
M00764_MEIS1_MIP21	ATGCAATACTAATTTCCCCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAACATTCATCTTT	1
M00764_MEIS1_MIP210	CGTGACCAATTAAATTACTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAACATTCCATTGAGC	1
M00764_MEIS1_MIP211	CATCATTTAAATTTAATTGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAAGGAACATTTTTGA	1
M00764_MEIS1_MIP212	CAGTGCACTATTACTTAGAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGCTGTGGGTACA	1
M00764_MEIS1_MIP213	ATACGATGAACACCTTCGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTTGATGGAAACTGAC	1
M00764_MEIS1_MIP214	GGTGGACAGTGTTTTGTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCAGAAACAATACACC	1
M00764_MEIS1_MIP215	GCTTTGAGGGGGCCTCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGTTATCAATGAATTCT	1
M00764_MEIS1_MIP216	GAGATGTTTGGTGACCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTTTTCCCCAGCTCTA	1
M00764_MEIS1_MIP217	CAGGCAGCTGAACTACACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACTGAGGTCTTATTTAT	1
M00764_MEIS1_MIP218	CCAGCATGATGTTTCTCATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAGACAAAAGTGCT	1
M00764_MEIS1_MIP219	AACTCACATTTTGCCACTATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATAGTGTGGTCCTG	1
M00764_MEIS1_MIP22	GTGAGTAACTGTGTGCTTAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGAAGGCTTTTTGTA	1
M00764_MEIS1_MIP220	ATGGGTGTGAGTATGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTTATAGGATTGTCAT	1
M00764_MEIS1_MIP221	GGACCACCCCGGGCTACATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCATCACTGTTGGGTG	1
M00764_MEIS1_MIP222	GGACAAGTCATGGACATTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCATACGTACATTCC	1
M00764_MEIS1_MIP223	CATTGTTGGGTCTCCTGTATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGAGTAGATGCCAA	1
M00764_MEIS1_MIP224	GACATTAAGAGAACAAAGAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGTGGAGTTCCAT	1
M00764_MEIS1_MIP225	GTTATTTAGCATGTCCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGAAACAACACACATAGT	1
M00764_MEIS1_MIP226	GGAAGGTCTGATTTGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGTTGTTTCTTATAGATTT	1
M00764_MEIS1_MIP227	GCTTCTGGAGGAAGTGAAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCATGGCTGAAATCCTA	1
M00764_MEIS1_MIP229	GCAAATTCAAGCCCCAGGCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCAGTCTCCTTAAGA	1
M00764_MEIS1_MIP23	CAGCGTTCTTCCAAACTCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTAAAAGAAAGGGGGT	1
M00764_MEIS1_MIP230	CATCACTTCCTGTTTTAAGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTGTTGCAGGCA	1
M00764_MEIS1_MIP231	GATGCTTGATGTGACAATTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACACACATGACCGAT	1
M00764_MEIS1_MIP233	CATTTTTCCAGTCCTTTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTATCAACAAGCATTT	1
M00764_MEIS1_MIP234	GTATAATAACGCCAAGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTATACTTTTTGTTGTGG	1
M00764_MEIS1_MIP235	ATCCAAACTGTTTCCATCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGGGGGGCAGTAAAC	1
M00764_MEIS1_MIP236	ACCGCAAAGTAAGTTGTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTATTTTTGTCATGCTG	1
M00764_MEIS1_MIP237	GCTTAGGGAGCCAAAATTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTAGAGTTAGTTTAGTG	1
M00764_MEIS1_MIP238	GCACATAAAGGCAAACCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGATTTCTTTAAGCTGA	1
M00764_MEIS1_MIP24	CATTTGCCTGAACCAAAGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCATTCCAGGCAGTTA	1
M00764_MEIS1_MIP240	CAAGATTTCTGCATGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTATATGTTTATTAGGA	1
M00764_MEIS1_MIP241	CAGCTGTTCTGGAAAATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGTATATTTTCCTTAGC	1
M00764_MEIS1_MIP242	GCCTTAAACTCAAGTCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTATAAAAAGTGCTT	1
M00764_MEIS1_MIP243	ACCCATCCTTTGTTTACAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATCACCTAGTAAAGC	1
M00764_MEIS1_MIP244	CAAGGCTCAGCCTACTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAGAGAAACCAGCTGTG	1
M00764_MEIS1_MIP245	GCGCATCCACGTGTTTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATCGACTATTTAGGTAG	1
M00764_MEIS1_MIP246	GTCTATTTGCTCCTCCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACCTAGTGGCAATTC	1
M00764_MEIS1_MIP247	GGTTGTTAACTGCTAGCAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCCACCCATCCTGA	1
M00764_MEIS1_MIP25	AGATGGAAAGTTGTGCATTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAAATCTTGGGAAA	1
M00764_MEIS1_MIP26	GTGTGTGTGAAATTTAGCTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGAAGTCAAGGAGGC	1
M00764_MEIS1_MIP27	CCAATTCTAAATTCAGCTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACCTGGTGAGTAACA	1
M00764_MEIS1_MIP28	CAATTCCCCACCCCCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAGACACTGCATTTCTT	1

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ID	MIP	*c*
M00764_MEIS1_MIP29	CGTAGCTGTTCCCATCGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAGTTAGTTTTGTATAA	1
M00764_MEIS1_MIP3	GAGGAGCAGGAGACACAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCATCCGAAGATTGTTT	1
M00764_MEIS1_MIP30	GCACGTGAATTTAGACAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGAAATTCAAAATCAC	1
M00764_MEIS1_MIP31	CCTGAATTTCTAAACTAGTTGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCTGGCACGTTTT	1
M00764_MEIS1_MIP32	CCTTTGGCAAGAAGGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAGCTGAGTTTTTCTTA	1
M00764_MEIS1_MIP33	CCTTATATAAGCTCGGTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCATCCCAGACGAGTC	1
M00764_MEIS1_MIP34	CAATACAGCTGGGTCCTTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCCTACTCCATCCAT	1
M00764_MEIS1_MIP35	GTACCCGCACACAGCTCATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACGATCTACCCCATTACG	1
M00764_MEIS1_MIP36	GATGCGAGTGCAGAGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTCAACTACTTAACCT	1
M00764_MEIS1_MIP37	GGAGGTACATCTTTGGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACGCTTTAAAGAGAGAT	1
M00764_MEIS1_MIP38	GGACAGTTGCAGGTCAAGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCCTTTGTGTTGTAA	1
M00764_MEIS1_MIP39	AAACTTCTAGATGTTTTAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACTGCACAATAAA	1
M00764_MEIS1_MIP4	GGGTGGGGGCGATGGAGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTTTAGAGCTCCTAACC	1
M00764_MEIS1_MIP40	GTGTAACAATTCAGAGCAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAAGCAGTATAAACC	1
M00764_MEIS1_MIP41	CCTCTTTTTACTTTGCAGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTTCCTCGGAGGTT	1
M00764_MEIS1_MIP42	AAGGATTCTACTAGCCCAGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTCCAGCGAGGG	1
M00764_MEIS1_MIP43	GTTTAGGCTCTGGGACAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCAGGACACACTGACC	1
M00764_MEIS1_MIP44	GTAGTTAACTCTGCGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCTTCTTCTAATGCCC	1
M00764_MEIS1_MIP45	GCTTTGCCACTTCGCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAGACTTGAGATACCT	1
M00764_MEIS1_MIP47	GTGCAGCCCGTTGACAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACTGCAGGAACATTTG	1
M00764_MEIS1_MIP49	GGTGGGAAACTTAATTCAAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGAGCCTGGGCTTC	1
M00764_MEIS1_MIP50	CGTCCCCTCCACTGCACATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGCCATGGACGGTAT	1
M00764_MEIS1_MIP51	ACACAATCGGAGAGGGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGATACGCTAAACCGAT	1
M00764_MEIS1_MIP53	ATTAGCTACTTGTACCCCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAGCTGTTTTTCTT	1
M00764_MEIS1_MIP55	CCACACTTTCAAAAGTAGCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCCGTGTTCGCCAAA	1
M00764_MEIS1_MIP56	GCACACTTTCAAAAGTAGCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCCGTGTTCGCCAAA	1
M00764_MEIS1_MIP57	AAGGGGGGGCTCTCTTTTTGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAATCTGAGGTTG	1
M00764_MEIS1_MIP58	AATAAAATCAAGAACACCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCATGCATGTTACCT	1
M00764_MEIS1_MIP6	CCTCCTGATTGGCCGAGCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGCCACCTTCAGGG	1
M00764_MEIS1_MIP60	ACTAGGAAGGCGACCAGATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAGCTCTGGGCTTG	1
M00764_MEIS1_MIP61	GAGGGACCCGGTGACACCGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAATCTAAATACAAGTGA	1
M00764_MEIS1_MIP64	GCGGGGAAACGCGAGCTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCTGAGATTTCTAGAC	1
M00764_MEIS1_MIP65	GGCCCCTCTCGAGATGAATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAGGAAGTCCGCAAA	1
M00764_MEIS1_MIP66	ATGGGAAAAGCCACAGTTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCATGTGTGCTTAAA	1
M00764_MEIS1_MIP68	ATATAAACCTCTAGATGGTACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCCCTTTTGGGGT	1
M00764_MEIS1_MIP69	AAAAAAAAACTAGCTAAAACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACAGCTCTACCA	1
M00764_MEIS1_MIP70	ATTAGAGAAGGTAATTTCTCTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGTGGGCTGGAG	1
M00764_MEIS1_MIP71	GTATGGCTTGAATCATCTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCAGAAGGCTGAACT	1
M00764_MEIS1_MIP72	CCTAGAGGTCCCAGGCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTACTCCTGATATGG	1
M00764_MEIS1_MIP73	ACTTGGGTTGTCAGGCATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGTGTGGCTGTATGT	1
M00764_MEIS1_MIP74	GTAATGAAGGTTTTTATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAATCCCTTTCTAATGT	1
M00764_MEIS1_MIP75	AGCCCCAGGAGCAGATGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGCATATATACACACG	1
M00764_MEIS1_MIP76	GGTGACCTGCGTAGGTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAATAACTTTCTTTTCT	1
M00764_MEIS1_MIP77	GGATTGCACTTGTCAATGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTTTCTGGGATATCT	1
M00764_MEIS1_MIP78	ATCCAAACTTCCAAATAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTAATATACCGGTGG	1
M00764_MEIS1_MIP79	ATCTAACTGACCAGGTATGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACGAATTATGTGACAAT	1
M00764_MEIS1_MIP8	CGGGCTTTCTGCAGACCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTACTGAATTCTCAGAA	1
M00764_MEIS1_MIP80	ATCCTCCTTCTCTATCGTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGTGGTAGTGACCCA	1
M00764_MEIS1_MIP81	GCTGGCTCTGGGATTCGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTGTATGCATATTGCTT	1
M00764_MEIS1_MIP82	ATGTATCTAAAAGGGACTTAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGACAAGAAACAGG	1
M00764_MEIS1_MIP83	CATTTTTCCCCCTTCTATCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTTGCTAGCAAACT	1
M00764_MEIS1_MIP84	CCGGAACAAAGCCCCTACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCATTTGCTAGATTTC	1
M00764_MEIS1_MIP85	GGTGTTCACTGCAAGCTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAGACAGCGAGAGTT	1
M00764_MEIS1_MIP86	CAATGTTCAGTGAGGTCTAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGAGGATGAGTGG	1
M00764_MEIS1_MIP87	CCTCGCACCGCCTTTGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGACTTTTCTCCTCCTTC	1
M00764_MEIS1_MIP88	CCCCCACACTCCTTACCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACAGCAATTCCAAAT	1
M00764_MEIS1_MIP9	AAATAACTCCCGCTGCTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTTTTCTCCTTGCAGT	1
M00764_MEIS1_MIP90	GGCTGAACCAGACGTGAGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCACTCCGGAGCTTTT	1
M00764_MEIS1_MIP91	ATTTATACCCCATTTTCTCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGCCTAACTGGAAA	1
M00764_MEIS1_MIP92	CATTTTGGAGGCAATTAAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGCTCCATGATATT	1
M00764_MEIS1_MIP93	AACTTCTCATTTTATTGTCTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGAGGGGGGAGAGA	1
M00764_MEIS1_MIP94	CCGATACAATTGCATACCAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCCAGGCGCATAG	1
M00764_MEIS1_MIP95	AGGACAGCAAACCCAAGGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTGACTTCTGGTCCCC	1
M00764_MEIS1_MIP96	CGACCAGCTGAAACTTGGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGTGCTTCATTCGTC	1
M00764_MEIS1_MIP97	GCAGAACAAGGAGCACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATACAATGTTTTCTGCATT	1
M00764_MEIS1_MIP98	CAAACTTTCTAGGCAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTTATAAGACTGTTT	1
M00764_MEIS2_MIP1	AAGGTTTCCCTTTCTTTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTTTGACAACCATATAG	1
M00764_MEIS2_MIP10	ATGGAAGAGCCCCAAATAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAACACAACACTTAAA	1
M00764_MEIS2_MIP100	CAGAAAAAATGGAGCATTCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAATGTAATCCTTT	1
M00764_MEIS2_MIP101	GAGCTGGGTAAACGTCCAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAATGGCATTACAC	1
M00764_MEIS2_MIP102	CAGGCAGTGGATAAACATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTAAGTTACTCGGGG	1
M00764_MEIS2_MIP103	ACAGATAAATCTGTCAGGCTAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATATTGACATGAC	1
M00764_MEIS2_MIP104	GTTTCTACCTCGAGGTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAACAACTGGTGAGTG	1

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ID	**MIP**	***c***
M00764_MEIS2_MIP105	GGAAGGGTACGGATGCTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGAAAACCATTATTTAG	1
M00764_MEIS2_MIP106	AGAGCAGAAGAAACAGTTAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAAATCAAGCCATAG	1
M00764_MEIS2_MIP107	ACAAATTCAGAAGGGTTATAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGTCTCCTCTAGG	1
M00764_MEIS2_MIP108	GTATCCGAAGTTGCTCTCATACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGCAAGGTGCTT	1
M00764_MEIS2_MIP109	CAACAGCAACCAAGGGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGAAAGTAGCAGGTTTT	1
M00764_MEIS2_MIP11	CCATTTCAGACAGCATTTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGAAAGAATAATGTC	1
M00764_MEIS2_MIP110	GCACCTTAGTTTAAAAAAAAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATTCCCAGCTTCT	1
M00764_MEIS2_MIP111	GAAATCTGATGACTAACAGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTTCCAGCATCTCA	1
M00764_MEIS2_MIP112	CAGGTGAAGCTACACTGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCATCTTGACTTACT	1
M00764_MEIS2_MIP113	ATCCGGATAAGGACAAAAAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGCTCATCATTAGC	1
M00764_MEIS2_MIP115	AAAGAGAATATACTCGCTTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGTCAAGTGCACAG	1
M00764_MEIS2_MIP116	CCCAGAGTGAACACATACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTGCCCATATCATTA	1
M00764_MEIS2_MIP117	GGATGCGTTTCCACTGAATAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGGCAGTGCGTTA	1
M00764_MEIS2_MIP118	GCTCTCTGCACCACTGATCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACTGTTCGTTGCAC	1
M00764_MEIS2_MIP119	GTTTTCATGTCATGCAAATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATTAATGCCAGAGA	1
M00764_MEIS2_MIP12	GCAGACATTGTTTGTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATATCTAGCCAAAGTAT	1
M00764_MEIS2_MIP120	GCCTGGAGGGCATCTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAGTTTCTATCAACAT	1
M00764_MEIS2_MIP121	GGCTTTCAAGGCATTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGCTGCTCTTGATTGA	1
M00764_MEIS2_MIP122	ATAAATGAAGAATACGGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCTGTTTTTGGGAA	1
M00764_MEIS2_MIP123	GCATTTGATTATGCCACAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGCAGGGAGCATAA	1
M00764_MEIS2_MIP124	GCCATAAATCCCATGCTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAACAGAGAAGTGGAGA	1
M00764_MEIS2_MIP125	ATTACAAAAACCCCCATCTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAGCTACAGAGCA	1
M00764_MEIS2_MIP126	CCTTCTAACTTCTGGGTCTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGTAGCCTGAGCTG	1
M00764_MEIS2_MIP127	GGATGGCTGTGCTGTAGCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGCTGTGGCTTTTCT	1
M00764_MEIS2_MIP128	GACAGGCCACTTCATTACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTTTGACTAGAGAAG	1
M00764_MEIS2_MIP129	GAGGGTCATCTCTTCCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAACAGAAGGCAAAGAAA	1
M00764_MEIS2_MIP13	CAAAAAGGGTGAGGCATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACTTTTTCTGAAAACA	1
M00764_MEIS2_MIP130	CATTTGACTCTTTCAATACTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATCTGCCCAAACA	1
M00764_MEIS2_MIP131	GTTTCACTGTATACTGATTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTGTGCGTGTATGT	1
M00764_MEIS2_MIP132	CCTTGGCAACCCTAGCATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGACAAGGAGACACA	1
M00764_MEIS2_MIP133	AGAAGCCATTAGTGTGGGTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGCCTGGCTCCTA	1
M00764_MEIS2_MIP134	GTTTGAAGTCAGTCAGTCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATGGAGAGTGGCTA	1
M00764_MEIS2_MIP135	CCGGGTACTGCTTTTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAATGTACATTCAGATA	1
M00764_MEIS2_MIP136	GTAAACAATGCCTGTGTGTATACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTACCATGGATAAAGA	1
M00764_MEIS2_MIP137	GAGTGTGTTTTTATATTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTGCATTCAAAAATCTA	1
M00764_MEIS2_MIP138	GACAGCATTTCCACAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCTCATTTAGCTTTTT	1
M00764_MEIS2_MIP139	CATTTTTAAGGTCATTGATTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCAAAGGATGCTCA	1
M00764_MEIS2_MIP140	GCAACCCGTTGTATATAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGGTAACACCTTCGA	1
M00764_MEIS2_MIP141	GTGATGCTCCTGTCTTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTTTGTGTCTAGTATGT	1
M00764_MEIS2_MIP142	GGACTGTGGACCAAATCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCTAGTTTTGTATTAA	1
M00764_MEIS2_MIP144	AATTTTATTTTAGGTTGCAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAAGGATTGCCA	1
M00764_MEIS2_MIP145	AAGGTATGTATACCAGCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACATGGATATTGGTG	1
M00764_MEIS2_MIP146	ACATGTGCCAAGGATTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAAACAGTTAACTGCCC	1
M00764_MEIS2_MIP147	ATTATGAGAAGATACCTCCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTGAAAAAGGTAT	1
M00764_MEIS2_MIP148	AAAAGATAAGCAAGAAACAGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGGGTTGGCAAAA	1
M00764_MEIS2_MIP15	CCATGTGCAGGGATGCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAATTTACATATGGGTG	1
M00764_MEIS2_MIP150	ACAGTCAAGTAACTGACCCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGACAGTCACTTGCC	1
M00764_MEIS2_MIP152	CCTTTTACCTTGCTCACTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTTAAATAGCAGCTG	1
M00764_MEIS2_MIP153	CAAACATTTTCCTCGTGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAGAACCCTTCTTCT	1
M00764_MEIS2_MIP154	CATATTAGTATTTGTGGCAGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATCGTGGTCTCGC	1
M00764_MEIS2_MIP157	GTGAGTCTGATGCTAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTTTAACACTTTAAC	1
M00764_MEIS2_MIP158	CATTGTTAATAATTGGTTCATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGGCCTGACATAC	1
M00764_MEIS2_MIP159	GGGAATTATGATTGAGTAACCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGCTTTTGCTAT	1
M00764_MEIS2_MIP16	GTAAAATTAACCCTGAAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTTACTTATCTATGA	1
M00764_MEIS2_MIP160	GGAAATCAGCACTCACTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCTATTCTGACAATAA	1
M00764_MEIS2_MIP161	GAGAATTATTGGCAATCTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGTAATCAGTGCAGC	1
M00764_MEIS2_MIP162	CATTAAGAGCACAAATCACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAACTGTCTTGCTTCT	1
M00764_MEIS2_MIP163	GATTTGGTGACTTGGGTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTTCTTGCTTTCTCTG	1
M00764_MEIS2_MIP164	GCCCAGTGGCCTTAAAAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATGAAAATGAAGGGT	1
M00764_MEIS2_MIP165	ACCTTGTTTTAACATCTAGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGAAAGAGACGGCA	1
M00764_MEIS2_MIP166	GTGGAGGGTTTAGCTCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATGATCTGACTTGGAG	1
M00764_MEIS2_MIP168	ACTTCTCTGAGCAACAAGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTTGCAAGGTTACAT	1
M00764_MEIS2_MIP169	GCCTTCAACTATTACACCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCCCTGGACTCCCAC	1
M00764_MEIS2_MIP17	GTCTGTGCTCAAAGGTAATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACATGCTCAACCTCC	1
M00764_MEIS2_MIP170	GTTTCCAGGGGAAAGTAATTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATAACTGGGTTCA	1
M00764_MEIS2_MIP171	CCCCAGCTCCAATGTTGTAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTGCATTAGGTGCA	1
M00764_MEIS2_MIP172	ATAATCCTGAATGCCTGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGACACCCAGCAAGGA	1
M00764_MEIS2_MIP173	CAAACCATTTATGTTACTGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCATCCTTCAACTCG	1
M00764_MEIS2_MIP175	CCCTCTCCTAGTTGAGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGAGCTCTAACTCCAT	1
M00764_MEIS2_MIP176	GTGGCCAGGAAAAACTTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGTATCATCTGAAAG	1
M00764_MEIS2_MIP177	GCCCGTTTCTTCTCCCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGAAAGATATTAATGC	1
M00764_MEIS2_MIP178	CCTCAGGACAACTTTTTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACTCAACCTGAGC	1
M00764_MEIS2_MIP179	GAGGACTAAGAGGAGAAAAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGATTTCGCTGGG	1

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ID	MIP	*c*
M00764_MEIS2_MIP18	GCTGGTGGAACTTATAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAAAAGCTTTATCTGA	1
M00764_MEIS2_MIP180	AAAGAATCGCACCTAAAAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTTAGAACAGCAT	1
M00764_MEIS2_MIP184	AGGGTTCTGTTCTAACTCCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGGTCTCCCGTTTC	1
M00764_MEIS2_MIP185	GGAGCTCTAGGGAGAGAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAATCCAGAGCTGGAC	1
M00764_MEIS2_MIP186	ATGGGTACGGTGGAGGGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAGAGCCTTACCAAAT	1
M00764_MEIS2_MIP187	CACATTTCAGCTTTCTTATTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCCAGGACCAGAA	1
M00764_MEIS2_MIP188	GCAGTCCAAGAGGCTGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTTAAATTAGTGGAGTC	1
M00764_MEIS2_MIP19	GTGTACATGATGAGCCAGGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCCCCCCAGCAGT	1
M00764_MEIS2_MIP190	CCCATATTTATCTCCACTTCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCTCTCCCCAAT	1
M00764_MEIS2_MIP192	CCTCGTTGAAGGAGTCGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACAGATAGGGTGTCCC	1
M00764_MEIS2_MIP193	CCAAGCAGGTCCAGCCTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGTTGTTTCCTCTGTTA	1
M00764_MEIS2_MIP194	GGTGTGGAGTCCTTCTTTAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTTCTCAAAGACCA	1
M00764_MEIS2_MIP195	CCAAACTTGTTGATTACAGTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCTCTGAGCTGCG	1
M00764_MEIS2_MIP196	GACGCTCAGGCAGTCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACAGAAAGGGAAAAGGG	1
M00764_MEIS2_MIP197	CATTACGTTCCAACTGAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTTCACACAGTGTTCC	1
M00764_MEIS2_MIP198	ATGCAAGAGAATGCTCTTTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGACCTCCCAAGAA	1
M00764_MEIS2_MIP199	GAAGTGTCACTCCGGTGTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAAGCTCTCCAGTG	1
M00764_MEIS2_MIP2	AGCAAGTGCCTTCCGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTACAGTATTTCCTTTAAC	1
M00764_MEIS2_MIP20	CCATTAAAAACGCAAAAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGACATTGAAAGGCTA	1
M00764_MEIS2_MIP200	CAAGTGCTCTCAGAATATAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCTTGGGGCTCA	1
M00764_MEIS2_MIP201	GAGCTCTTCCGGCTGAGGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAGGTGGAAGGGACTC	1
M00764_MEIS2_MIP202	GGGAGTAAGGAAGATGGCTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGGGCTGCTTCTG	1
M00764_MEIS2_MIP203	ATCGGCAGGAAACTTTCTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATTAGGACTTCCTGG	1
M00764_MEIS2_MIP204	AGAAGCAACTTTGGGTTTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGAGTCCCCAGAA	1
M00764_MEIS2_MIP205	GCTAGTTCTTCGGGGCTTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAACGAGCAGTCCTG	1
M00764_MEIS2_MIP206	CCCGACCACTCCAGACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTAAGTGGGGAGTTACTT	1
M00764_MEIS2_MIP208	GTGTGTGTTTGTCTCTGTGGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCGCACCCCAATG	1
M00764_MEIS2_MIP21	CAATGCCAACTCTATACAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGTATGAGGACTGTG	1
M00764_MEIS2_MIP214	ACAAGTTGAGCACACAGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAGAGAAGAGAGGAGG	1
M00764_MEIS2_MIP215	ACTTTTCTCCTTTCTGACTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTCTCTAAACGT	1
M00764_MEIS2_MIP218	CGTGAAAGTTACCAGAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGGCGAAATGAAAC	1
M00764_MEIS2_MIP22	AGAAAAGAAGAATTCATGGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCGCTTTTTGTGACT	1
M00764_MEIS2_MIP223	CCGTGCCTCTGCGTGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATCCTCTCCTAAGAGG	1
M00764_MEIS2_MIP224	CAGTCCGGATAAGAAAGTGATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATCGGGACAGGC	1
M00764_MEIS2_MIP225	ATATACGACACATCCAGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTAGACTGGGCTTTTT	1
M00764_MEIS2_MIP226	ATCTTCCTCCTCCTCCTCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTTCTCCCAATTCTC	1
M00764_MEIS2_MIP229	GGGCCGCTCGTAACCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAAGATTCCTCCTCTTC	1
M00764_MEIS2_MIP23	AGCACGTGTTCCTCACTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCGGTCTATTAATTGTT	1
M00764_MEIS2_MIP233	GAGCGAGCGAGAAAGAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGAGGCTCTTCAATA	1
M00764_MEIS2_MIP234	CGTACGGCGGAGACACATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGTGAGTGTCAGTAGGT	1
M00764_MEIS2_MIP238	ACTTACTTCTAGTTCATTTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGAACAGGGAGAG	1
M00764_MEIS2_MIP239	CCTGTGGTTTTCTGCAGTTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGAGCGCCATGCCAA	1
M00764_MEIS2_MIP24	CCCCAAGCTTTGAGTTTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCTGATACTAGCAAAA	1
M00764_MEIS2_MIP240	AGCTCTGCAGACGGTACCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTGGGTCTTGCCGGG	1
M00764_MEIS2_MIP241	GCCCTTGGACGTTAGCAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGTTAAGCTGGTCTCT	1
M00764_MEIS2_MIP242	GTCATCTGGGTCCGATGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATTTTTTTCCAGGACCA	1
M00764_MEIS2_MIP244	CCAGCTTTGTTGTGGTCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGCGCGCGCGACTAGT	1
M00764_MEIS2_MIP246	GTGGAAACTAGTTGTGGCCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAACGCCTGCTAATGG	1
M00764_MEIS2_MIP249	CAGCGCCTGTCCGCCCGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCTCCACTTCTCAGAAT	1
M00764_MEIS2_MIP25	ATAAAAAGGAGCAAGAGAATACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAGTTCTGAGCCT	1
M00764_MEIS2_MIP26	GCTTATGAAGCACGAACTATAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCAACTTAAGATTG	1
M00764_MEIS2_MIP27	GGGGGACTCTTCTTCAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATCACTCGAACTCCAG	1
M00764_MEIS2_MIP28	GGTGAATTCACTGATGAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGAAAACACATTCTTG	1
M00764_MEIS2_MIP29	GTGGTATATATTTTAAACCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGTTATGTTGCCTCA	1
M00764_MEIS2_MIP3	GTGTAAAGAGTTCCGATTTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTACCTTGCTCTCCC	1
M00764_MEIS2_MIP30	CGGAGTCTTTTTCCAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGTGTGGAAAACAAGG	1
M00764_MEIS2_MIP31	GGAACTAAGTTAAACTTGTACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAACAGAGGACC	1
M00764_MEIS2_MIP32	GTCAAAGTTCAGAAAGTCTTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCAGTCAGCCCA	1
M00764_MEIS2_MIP33	GAAATTCCAGACAGCTGTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCAATGTTGGCGGAC	1
M00764_MEIS2_MIP34	GATGGCTTGGCAAATATGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGAATGTCCATAACC	1
M00764_MEIS2_MIP35	CCAGCCATGATGATGCACGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCAGGGTGGTCCTAT	1
M00764_MEIS2_MIP36	CATTTTTATACTTTACCCATCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGAGGAGTGTAAC	1
M00764_MEIS2_MIP37	GCTTTCTTTTTCCCTCTCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTCTGCAAACATTGG	1
M00764_MEIS2_MIP38	GTGGAACTGTTTTTCAAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAATTTAGCTGCAGA	1
M00764_MEIS2_MIP39	GCATTATACTGCTGTGCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAACTGATAAAACTCGAC	1
M00764_MEIS2_MIP4	GACGTGGGTTTGACGAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTGGACAAATCTATCA	1
M00764_MEIS2_MIP41	GTCTACAAATGCAACACAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACACGTAAAAGCTCATT	1
M00764_MEIS2_MIP42	GTCATATGACATGCCCGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGCATATTCATTTTGAA	1
M00764_MEIS2_MIP43	GACCTTTACAATCTCTTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGCATATCTCAATTGA	1
M00764_MEIS2_MIP44	GCCTAGTCTAGATATATGACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTTCAATGAAGCG	1
M00764_MEIS2_MIP45	GGGGCCACAGCAAATAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACTTTTCCTTTTTTTTT	1
M00764_MEIS2_MIP46	GGGGCCACAGTAAATAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACTTTTCCTTTTTTTTT	1
M00764_MEIS2_MIP47	CAAACACAGACATCAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATATATCACCCATCTCTG	1

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ID	MIP	*c*
M00764_MEIS2_MIP48	GTCTCTGAAGTGATAGTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACATCAGTGTCATCTG	1
M00764_MEIS2_MIP49	CCTTGCCCATAACTGCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACATGTAACCTTCATCAT	1
M00764_MEIS2_MIP5	CATGTTAACTTTAACCTTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTTTAGGATGTGTTT	1
M00764_MEIS2_MIP50	AGCAATAATTGATGGTGAAAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTTGCGATTGCT	1
M00764_MEIS2_MIP51	ATTTTCCGGCCTCTTCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAAGATTTTACCACAGT	1
M00764_MEIS2_MIP52	ATAGTAGAGTGGATGGAGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGGCAGAGTATAATG	1
M00764_MEIS2_MIP53	CCACTGTCATGGTGGGTTTAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGCTTTGTGTTGG	1
M00764_MEIS2_MIP54	GTCATTCGAGGACACAGAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACCTACCTGCAGGC	1
M00764_MEIS2_MIP55	ATCCTTCAGTGAGCCAAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTAGAGTGCCAACCACA	1
M00764_MEIS2_MIP56	GTTTCCCAGGGGGTTCGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAAACGTTATAGCAACA	1
M00764_MEIS2_MIP57	GGCCAGTGAAGTCTTTCTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCCCAACCAAATGG	1
M00764_MEIS2_MIP58	CACAAGGTTAAATAGACTCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAGGGGTACCCCATA	1
M00764_MEIS2_MIP59	AATTGTATTCAGGTTTAAAATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATGTTCCCACTATT	1
M00764_MEIS2_MIP6	ACCTGATGTGAGAGTTGATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGCTCTGGTCTCTAA	1
M00764_MEIS2_MIP60	CGTTGTTAGTGGCAGCAGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTTCTCCCTAGCCTC	1
M00764_MEIS2_MIP61	GTACTATTCTTCTTCTGGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGAAGCACTTATTTA	1
M00764_MEIS2_MIP62	GCCCATGATTGACCAGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGATTTGACTGTATTT	1
M00764_MEIS2_MIP63	ACTCCAAAACAACTTGCTAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATGCTGAGGAGCA	1
M00764_MEIS2_MIP64	ACTACGCAGTGACGACGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGCCTGTGAACTTTAA	1
M00764_MEIS2_MIP66	GAGTGCTAGAGCCTGGTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTTAAACTGCAGGAGT	1
M00764_MEIS2_MIP67	CCAACCATAAACCCAGCCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTCTGCTCTTCGGC	1
M00764_MEIS2_MIP68	GTTACCTTATCCTCTGCCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTTTGCATTCCTGC	1
M00764_MEIS2_MIP7	CCACTCAGTAAATTCTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACATGAAGTCTTTTTGT	1
M00764_MEIS2_MIP70	ACATTAAAGTAACATGAAGTAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCACAGGGACAAGG	1
M00764_MEIS2_MIP71	GATTCACTGACCACGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGATGATAAGAAATCTCC	1
M00764_MEIS2_MIP72	GTGCATGAGCTCAAATGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATGAAGTCCCCCTG	1
M00764_MEIS2_MIP74	GAACACAGAGCTGCCAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAAAAGACTCCTTTGGT	1
M00764_MEIS2_MIP75	GTGAAAACAAAAGGAGAGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATAATAGCTGGGAGA	1
M00764_MEIS2_MIP76	GCTGATCACTTTCTTTTTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGGAGGAGGGATG	1
M00764_MEIS2_MIP77	AGCTCACCTTGAAACCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCACAAAGACTTCCAGAA	1
M00764_MEIS2_MIP78	GTGGAAATATCAGGTCAGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACATAAAAGGGGGTAA	1
M00764_MEIS2_MIP79	CCCTTTTTAATTTCACTCTTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACTCGGCAGGGGT	1
M00764_MEIS2_MIP80	AATAAAAATAAAAAACGCAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGAACTGGAGAGA	1
M00764_MEIS2_MIP81	GGGAAGGTTAGAGGTTCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTGTTCCCTTATTTA	1
M00764_MEIS2_MIP82	GTTTGAAGACAGTGTGGAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCATTGTTGTGTGT	1
M00764_MEIS2_MIP83	ACTTGGAAATGCCACTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGATACTAGTCAGAATGTT	1
M00764_MEIS2_MIP84	GACCTGCTAGCTCACAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATATTTGCTTAGGAGAAGT	1
M00764_MEIS2_MIP85	CATTTAGCCTCTCTGGATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGCAGTTATGGCAA	1
M00764_MEIS2_MIP87	AATTAACAATTAATGAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAATCACACAGAATTT	1
M00764_MEIS2_MIP88	GATTCTGCATGGATTGCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACACCTGGTAACCA	1
M00764_MEIS2_MIP89	CAATTCCAGCTATTCTTGATTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGGGCCTTTTCA	1
M00764_MEIS2_MIP9	GAGAAATTCAGTGCCACTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGGAAATACACTTCTA	1
M00764_MEIS2_MIP90	GCAAGTCACTTATCAAATTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGACCTGTTAAAAC	1
M00764_MEIS2_MIP91	CCATTATGTTCCTAGCCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGCACAATCATTTT	1
M00764_MEIS2_MIP92	ACTGGTTGATTTGCAAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATACTTCAATCAAAGGTG	1
M00764_MEIS2_MIP93	GTTTGAAGAGATCAAGGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGCTTTTTAGCTTTCA	1
M00764_MEIS2_MIP94	CATAATTGCTAAACAGCTTGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCCTGCTAGACT	1
M00764_MEIS2_MIP95	GTAGGACTTTGTTCTTCCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGCTGATTCTCCCATA	1
M00764_MEIS2_MIP96	CAGCTGCTCCTTGCCAGATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTTGCAGTTGTCAGAG	1
M00764_MEIS2_MIP97	CCCCCACCATTTTTTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAGAAAAAAAAAGTGCC	1
M00764_MEIS2_MIP99	AGTTTCTATTTTTGGTGCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATAAACACACCTGTA	1
M00764_MICALL2_MIP1	GGGCCATTTCTAGTCTCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATCTTATCACAAATTGA	1
M00764_MICALL2_MIP105	GAGGGGCAGCCTGGTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTAATCTCAGCCAACA	1
M00764_MICALL2_MIP137	GTGCTGAGCAGGGCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCTGGGATTACAGGTGCG	1
M00764_MICALL2_MIP143	AACAAGGGTCTGGGGGTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAGCCTCTTATCTTGG	1
M00764_MICALL2_MIP152	GCTTCACAAATACCAACCTAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGGCCAGCCACG	1
M00764_MICALL2_MIP153	CCAACAACAGAAGCGATGATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGCTGTCTCTGTGA	1
M00764_MICALL2_MIP158	GCCTGGGTAACACACTGAGACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGCTTCTGGGAGGG	1
M00764_MICALL2_MIP16	ACATGATTGAGAAGCTGGGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCAGGGCTGGGGTG	1
M00764_MICALL2_MIP160	CAAGCCGTGTCCTGCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAATATAGTGATCGTG	1
M00764_MICALL2_MIP171	GGGGACATGGCCGCTTTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAGAGCCGCTGCTGGC	1
M00764_MICALL2_MIP175	GGGCAGGATGGGTGGTGGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACAGCAAGGTGCAT	1
M00764_MICALL2_MIP179	GGCAAAATGAATTCTCACCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGCCTTCACATCCT	1
M00764_MICALL2_MIP18	GGAAGAGGGCAGGGACTTGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCCCTCCTGTCCAG	1
M00764_MICALL2_MIP32	CACTGCAACCTGTCCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGCTGACTGGTACAGTA	1
M00764_MICALL2_MIP4	CCTGACACTTTATAAAGCACGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTTGGATTCTGCGC	1
M00764_MICALL2_MIP47	CCTCGAAGGCCAGGACCTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCTCTCCCCAGATG	1
M00764_MICALL2_MIP5	ATGGGGTGTCAGGACCCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTTCCAGCCCACCT	1
M00764_MICALL2_MIP57	CCTTCACGTACACCCCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGTCTCTATTCATGAGG	1
M00764_MICALL2_MIP58	GGAGGATGCATTCACAGGACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTGGAAGGAGGAGG	1
M00764_MICALL2_MIP66	GTGTGCACCCGTGTTCGTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCATGTGCGATGCAT	1
M00764_MICALL2_MIP67	ACATGGACACGCATCACACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGTTGCACACACAT	1
M00764_MICALL2_MIP68	ACATGGACACGCATCACACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACGGTTGCACACACAT	1

continued table…

ID	MIP	*c*
M00764_MICALL2_MIP69	GTGTTCGTGTGTGTGATGCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTGCACGTGATGC	1
M00764_MICALL2_MIP70	GTGTTCGTGTATGTGATGCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTGCACGTGATGC	1
M00764_MICALL2_MIP83	GAGGAAGGAGTGCTGGGAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTAACCTCTCAGCTG	1
M00764_MICALL2_MIP87	CAATGAGAACTCAGCCAAAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAGGGTGAGCCC	1
M00764_MICALL2_MIP88	ATCCTGCAGGACCCAGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGTGTGTAGAAAAAAGC	1
M00764_MICALL2_MIP92	AGCTTTCTTCTAGGCAACTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGTCTGGTGACGAT	1
M00764_MPPED2_MIP1	CGCCTCCAGGGTTCAAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCTCAACCATGTTTAG	1
M00764_MPPED2_MIP10	GCTGGGTCTTTGTAGCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTACTAGTTTAGGTGAAG	1
M00764_MPPED2_MIP100	AATTTCTGCAAAACTCTTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGGGACCCTTGTAA	1
M00764_MPPED2_MIP101	ACTGATAAGGAAGGTAAGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTATCGGTTCCTTCC	1
M00764_MPPED2_MIP102	GTCTTTGATGGAAGTGGAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAATGTCTGGTGCAC	1
M00764_MPPED2_MIP103	CAGCTCCTTTGCTACTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTAGATGGTAAGAAAA	1
M00764_MPPED2_MIP104	ATTAAGCACTTACTAGATGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTATGTGTGTGCATT	1
M00764_MPPED2_MIP106	GAAAGAGCCAAGTTCAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGAAAGTTTACATGTAT	1
M00764_MPPED2_MIP107	GCTATGCTGCTGCTACATCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACCTGCTCCTTGAGT	1
M00764_MPPED2_MIP108	CATCTAAATCTGAGCTGTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATCTTGCCTAAAGGG	1
M00764_MPPED2_MIP109	AATGATTAGGATGAAAGGAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAGGTAACAGTGAAG	1
M00764_MPPED2_MIP11	GCAATATAAACAAGACCAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACAGTGTGCTTGCA	1
M00764_MPPED2_MIP110	CCTGTTTAACAAGGTCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCACCGTATATCCTGAAT	1
M00764_MPPED2_MIP111	CGTTTCCCCTCTGTGTCCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTAATTGGTGCTCTT	1
M00764_MPPED2_MIP112	CATTTCCATGTGAACTGGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGTTTCCTGAAAT	1
M00764_MPPED2_MIP113	GTAGCTGAGTCAAGTGAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCTCCATCAGCAAGT	1
M00764_MPPED2_MIP114	CAATGGGAAACCAGGTCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCATTAATTTTCACA	1
M00764_MPPED2_MIP115	AGCATGGAAGAAACCCTAATGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGCAGTGGACCAC	1
M00764_MPPED2_MIP116	GGAAAGCTTTGAAACCCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCTCGTATGATATGC	1
M00764_MPPED2_MIP117	AACGCAATCATTCCTTACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAATTGGATTAAAGCT	1
M00764_MPPED2_MIP118	GCGGCCCCAATTAACCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGAACAGATGGTATC	1
M00764_MPPED2_MIP119	ACCCTAAAGTAGACATAACAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCGCCTGTGTGGAG	1
M00764_MPPED2_MIP12	ACTGTCTTCTTATTGCAATTATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTCTGCTGCTGTG	1
M00764_MPPED2_MIP120	GACCCCATCCCATATGACACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCTGCCTTTGCGT	1
M00764_MPPED2_MIP121	ACTGGGCAAATTCAAAAGGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTCGCACATACATAT	1
M00764_MPPED2_MIP122	GGGTGATGCTGTCTCTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAAACTTCACCATTAAT	1
M00764_MPPED2_MIP124	ATCAATTGGAGCATGATGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTGCTATCTCTCCAC	1
M00764_MPPED2_MIP125	CCTTATTCCTTTGTTCCCCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCAAAATCCTTGCC	1
M00764_MPPED2_MIP126	ACAGTGGAACAGTTGGTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGGGAAATAGGCCT	1
M00764_MPPED2_MIP127	GCAATACAATGTAAAGCAAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTAGCTGGACAATT	1
M00764_MPPED2_MIP128	CCCACACCTCACCCCACTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGTTAAAGTATTTGCCA	1
M00764_MPPED2_MIP129	GCTCTGAAAATTTGAAATGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAAATTCGCTGT	1
M00764_MPPED2_MIP13	AAGGTTTTTTGGCGGGGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGTATAGCCAGAGAA	1
M00764_MPPED2_MIP130	ATTGAAATTAGATTTTCAGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGCTAGGGAGACT	1
M00764_MPPED2_MIP131	GAGGCTGGAATCTGCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTGTAAATCATTTACC	1
M00764_MPPED2_MIP132	ACATGTACATATGTAAGTATCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGGAGGAAGGATGG	1
M00764_MPPED2_MIP133	ATCTACTCATCAATACCGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAACTTTGCCTTGAG	1
M00764_MPPED2_MIP134	GGATTCAGAGGTTGGCTGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGAACTAGTTTCATG	1
M00764_MPPED2_MIP135	CATATTGCTGGGTGCTAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACATAAATTTAACATC	1
M00764_MPPED2_MIP136	GAGTGTAATATCCACTTTGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGATGCCATGGCAA	1
M00764_MPPED2_MIP137	ATTTGAAAGCTCCATGTTTAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGAAGGGGCATATCC	1
M00764_MPPED2_MIP138	ACATTCCAATTAGCAGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGTTATAGTAATACACA	1
M00764_MPPED2_MIP139	GGCCCAGAACCTTATGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGTTGTGCTTATAACAA	1
M00764_MPPED2_MIP14	CCACATCACTTAGACCTTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTCCTTACCTCCT	1
M00764_MPPED2_MIP140	GCCCACTTCCAGTTACTCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAAGATCTCCAGACC	1
M00764_MPPED2_MIP141	AAGAGTAGGGGCGTGAATTAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGGTGGACAGAAGCA	1
M00764_MPPED2_MIP142	ACTTTTCTCCGGAGCCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGGCTGACATAAAGT	1
M00764_MPPED2_MIP144	CCTTCTAGGCTCACGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGATTGGTTTGTTTGT	1
M00764_MPPED2_MIP145	GTGTGTGTGTGTGTGTAGTTCATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAACGGGGGACTGA	1
M00764_MPPED2_MIP149	CAGGCGTAGAGCAGGGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAACAAAAGTTTAAGTGA	1
M00764_MPPED2_MIP15	GAGGCAGCCACTTGAAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAAAATAAGAAATGGGA	1
M00764_MPPED2_MIP151	GAGATGCTGCAAACAAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCGTCAGCAAGAAAATAA	1
M00764_MPPED2_MIP152	CCTTGTTATACGTAAATAGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCACTGGGGCATCC	1
M00764_MPPED2_MIP153	GGAGGTGAAGGGGGCATTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGAGTACCGAGGAA	1
M00764_MPPED2_MIP16	GCCAGGACCCCTTCTTATTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTGCCATGCCAGCT	1
M00764_MPPED2_MIP162	CCACCGACCTGCCAGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATCATCATGAGTGCGAT	1
M00764_MPPED2_MIP164	ACGCTCACTCACTCACTCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTCGCTCAGACCTA	1
M00764_MPPED2_MIP165	GCGCTCACTCACTCACTCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTCGCTCAGACCTA	1
M00764_MPPED2_MIP166	GTGTGTGTGTGTGTGTCTGTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTTCCTGTCCTGA	1
M00764_MPPED2_MIP167	GTGTGTGTGTGTCTGTCTGTCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTTCCTGTCCTGA	1
M00764_MPPED2_MIP168	ACTTAGTCCAGTTTTGTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCCATGAATTAAGGCA	1
M00764_MPPED2_MIP169	GATTTTTAAAATGCTTTTGACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCTCTCCCTTGT	1
M00764_MPPED2_MIP170	CAACCAGATCTAATTCCTTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAATGCTGGAAGA	1
M00764_MPPED2_MIP171	ACAATGGCATAACATCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATACTTAGCACACTTCT	1
M00764_MPPED2_MIP172	GCCTCTGTGCTGAGACTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAAATCCAATGTATATA	1
M00764_MPPED2_MIP18	GCATGGCTAAAGGGGAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAATTAAAAGGGAAGCA	1
M00764_MPPED2_MIP19	ACAGCCTGCTCATATTTCACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGCCTGTGATGGGG	1

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ID	MIP	*c*
M00764_MPPED2_MIP2	GCTGGGACTACCACGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTTTTTTTTTTTTTTTTAG	1
M00764_MPPED2_MIP20	CAATTCCAGTCTTGGCTCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTTTCAAGGCCACC	1
M00764_MPPED2_MIP21	GGATGTGCAGAGCAGTGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTGCAAGCCTAACACC	1
M00764_MPPED2_MIP22	GACTGTTTTCCCAGCACCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGCTGTAAGCCTTGGC	1
M00764_MPPED2_MIP24	GGGTGCATAGTCCATGATTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGTTCAGAATTTGGA	1
M00764_MPPED2_MIP25	GCATAATCAGGAGGGTTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTTAATAAGTGTTGG	1
M00764_MPPED2_MIP26	GGCTTGCAGATCAGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAATAGTAGTAGTAGTA	1
M00764_MPPED2_MIP27	GGGACTGTGGTAAACGTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCAGCTGTGCTTATAT	1
M00764_MPPED2_MIP28	AACAAACGTCTACAGGGACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGCACAGCGTGCAC	1
M00764_MPPED2_MIP29	GTGTCTATGTGTGATTCACTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACAGCATCTGCT	1
M00764_MPPED2_MIP30	GCATATTCCCAGTCCCCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTGAACTCTGAATAATT	1
M00764_MPPED2_MIP31	GAATGTTTCAAAGAAATGAAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCCTGACAGTCTC	1
M00764_MPPED2_MIP32	CAGAAAAGGAACGGAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTCTGAACAGATAGTCT	1
M00764_MPPED2_MIP33	GAGCAGAGCATGGGATGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAAAGAAGCTGGCAT	1
M00764_MPPED2_MIP34	CCCCCCTCTCTCCAGGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAATATGTGGGAGCTT	1
M00764_MPPED2_MIP35	GCTGGGACTGTTCACTATAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTAAAAGGGCCAGG	1
M00764_MPPED2_MIP36	GATGATGCTGGCTTTGTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGCATTCCACACTGTG	1
M00764_MPPED2_MIP37	CATCTGCCAAGGACACGATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGGTAGACAGCTGG	1
M00764_MPPED2_MIP38	CTGGTCTATTAGAAGATAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGACTGAGGGTGAT	1
M00764_MPPED2_MIP39	GCTTTATTAGGCCGCCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAGACAATTCCATATTT	1
M00764_MPPED2_MIP41	ACTGTGCACCTGCCCCTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCCAAACCACAAAGAG	1
M00764_MPPED2_MIP42	AGGAATCAGCTCTGTCTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGTGCTGGGAAGGC	1
M00764_MPPED2_MIP43	CAACAGTCCCTCCTGCTCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCATAAAGGGCCAC	1
M00764_MPPED2_MIP44	CCTCATGCCTTCTTTGTCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACAACCCCTTCCTG	1
M00764_MPPED2_MIP45	AGGCGACAGGGAAGCTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAATTAATTGATGATCTG	1
M00764_MPPED2_MIP46	GTTTACTAAAGGGGAGAGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTAGCTCACACAATGC	1
M00764_MPPED2_MIP47	GTGAGCATCTCCAAGGCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGGGGTTGTTTATGA	1
M00764_MPPED2_MIP48	GTCATCTGTCTTGCCTTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGCCTTTCAGAAGAAT	1
M00764_MPPED2_MIP49	CAACCCTCTAAACAGCACGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGGTAATAAAAATTTA	1
M00764_MPPED2_MIP5	GCTCATGCCTCCCAGCACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCTTCTAACTAGCAA	1
M00764_MPPED2_MIP51	GACAATATTTTGTGCTAGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGCTAGATATAGAATA	1
M00764_MPPED2_MIP52	GTTTTCCCATTGTAAATGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGGCTTAGTTGTCCTT	1
M00764_MPPED2_MIP54	ATCTAGGTACAGTTACAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTACGTTAGGAGTTTA	1
M00764_MPPED2_MIP55	GCTCTTGACAGATTCCATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCAGTTGTACTGTCC	1
M00764_MPPED2_MIP56	AAAAATGAACATGCAGACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGTTTAACTAGTGAG	1
M00764_MPPED2_MIP57	GCCTACTTCTGTTGAGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAACAAACAATGAGACC	1
M00764_MPPED2_MIP58	GCTGCATTGAGAAGAAAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAATGTTTTGTTGTTG	1
M00764_MPPED2_MIP59	CACTGCCTGTTTCTTATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATAAATTGGGACCAC	1
M00764_MPPED2_MIP6	CCATACCAGTGTGCCCTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCTCTTGTCCAAGATT	1
M00764_MPPED2_MIP60	AAACCAACACAGATTTGCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCATGCCATTGTAAAT	1
M00764_MPPED2_MIP61	CCTCTAGCATCATTTGTGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTGGCGAACACTAAC	1
M00764_MPPED2_MIP62	ATGGGGCATCCATTTGAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAACTGCCATTTTTCT	1
M00764_MPPED2_MIP63	CAAATATAATTGGAGGGTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAACTCACAGGGTTTG	1
M00764_MPPED2_MIP64	CAAACCCACAGGGTTCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACAGTAAATGTGACAC	1
M00764_MPPED2_MIP65	CCTCCTCAGATATAATGACTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAACCTGTGGGGAGA	1
M00764_MPPED2_MIP66	GATTCCACCAAACACATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCTTATAAAAGGGTCC	1
M00764_MPPED2_MIP67	GAAGGTAAGAACAGCGGAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGCATTTTGCCCTT	1
M00764_MPPED2_MIP68	GCCTCTCCATTAAAGCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCCAGTCTCGAAAACC	1
M00764_MPPED2_MIP69	GACCTCTGGGTAGGTTAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTATGCCTGGAAAAAA	1
M00764_MPPED2_MIP7	GTCAGTTTGTGGTCTGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACATTGGGTACTTGCTTAG	1
M00764_MPPED2_MIP70	GCTGGACAAGTGGAACCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATGTGCGAGAGAGAAA	1
M00764_MPPED2_MIP72	GCTCTGACACAGGCACTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCTAAGAAATTCTGC	1
M00764_MPPED2_MIP73	CATCCTTTTCTCCAAGGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAGTTCTGTGTTTAC	1
M00764_MPPED2_MIP74	ACTTCTGCTCCAAGAATGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAACACAGTAAACAGA	1
M00764_MPPED2_MIP75	CCTGGGATGGAAAAAGGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCATTACTTGTATCTT	1
M00764_MPPED2_MIP76	CCAAACATCTAGATCTTATCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGATCGGTGCTGA	1
M00764_MPPED2_MIP77	ATAACACTGGGAACTACTTAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGCTTGGCCAGAA	1
M00764_MPPED2_MIP78	CAGCTAATCAAATGGAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATACATGTAACAGACAA	1
M00764_MPPED2_MIP79	GATTGACAAGGTTAGGGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTGACTATACATGTCC	1
M00764_MPPED2_MIP8	ACAGACATGGAAGCCAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCATTATTTCCTTTCCT	1
M00764_MPPED2_MIP80	GAGAGAAGAGACTGTGTAGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTTTCATTTGGTGG	1
M00764_MPPED2_MIP81	CATATCAGCGTGAACTGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTATAAGCAAGCACCC	1
M00764_MPPED2_MIP82	GCTTTTTCTGTGTCAAGGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAGGAGAAACTAGGA	1
M00764_MPPED2_MIP84	CCACCATATAATTCCTCTTCTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCATGAGGTGGGCA	1
M00764_MPPED2_MIP85	AAGGGCATTTCCTTGGTTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGTCTGGGAAGATTA	1
M00764_MPPED2_MIP88	GTGGTTTAGGCTCATATTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAATCACTTAGAAACA	1
M00764_MPPED2_MIP89	CAGATCTTTTGCCAGGCTCCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAGAATGAAGGCT	1
M00764_MPPED2_MIP9	CCTAAGTTCCTGTCCCTTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCTGCTTAGGGGTTT	1
M00764_MPPED2_MIP90	CACAGCCCATTCCCCAGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAACATTTCTAAAGCTTCGG	1
M00764_MPPED2_MIP91	AATCAGGAATGGGGAAACCTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGCAGTTTCATGG	1
M00764_MPPED2_MIP92	GCCTGGCATGCAGAAGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTTATTCCTGATTTAT	1
M00764_MPPED2_MIP93	ATAAGAGGACACTGGGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAACGTCTCCCATGGAG	1
M00764_MPPED2_MIP94	ATACAACTGTTTTCTGCTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTACCACCCTCACTCTC	1

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ID	**MIP**	***c***
M00764_MPPED2_MIP95	GTTAAGTGAACATTTGAAATACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCAGACACCTGAAA	1
M00764_MPPED2_MIP96	CTCAATGCAATTGTGGGCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTTGAGGGGTGGGAG	1
M00764_MPPED2_MIP97	CCAGATCTCCAGCTGACTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTCCTACTTCCCACAT	1
M00764_MPPED2_MIP98	CACTGTGGAAAGAAAGCAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATTCGGCCTCAAAGA	1
M00764_MPPED2_MIP99	ACAAAAAGGGCAAAATGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGTTTAGTCTTAGGC	1
M00764_MYT1_MIP1	GTTCTCAGTGGTGGCATCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGGACTTGGAGGAGG	1
M00764_MYT1_MIP100	GGAAGCAGAGGCCACATATCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATGAGCAGGGAAAT	1
M00764_MYT1_MIP101	GAATGAGTCACGGCAGAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTCAAGACTAGCGAC	1
M00764_MYT1_MIP102	AGACCTGAACGAGTCCAACTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGAAAGCAGGCTTCC	1
M00764_MYT1_MIP103	GATCTCCTGGTTCAGCTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGTCCCCAAGACGAA	1
M00764_MYT1_MIP107	CCTCTGTGCCATGCTTTCTAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGACCCTGCCTTCC	1
M00764_MYT1_MIP109	GCCTCTCACAACCCTCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTCAATGAGCTTGTT	1
M00764_MYT1_MIP11	GAGCAGGACACAGGACTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGAATGTGGTGGTTGT	1
M00764_MYT1_MIP110	CATGGTAGGCAGCACGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGAGAAGAACCTGAAGA	1
M00764_MYT1_MIP111	CTCCAGAAACAGGGCTTCATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTCCTGCTTTCC	1
M00764_MYT1_MIP112	GAGACAAGCCCACACCAACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATCGAAATTCTGTT	1
M00764_MYT1_MIP113	GTCTAGGCCGTGTGGTACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCTAGGAGCCAATATG	1
M00764_MYT1_MIP114	GATGCTCTCCAGGAGGTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACGGGAAGTCACTGTG	1
M00764_MYT1_MIP115	GTGGTGGCCCTATCTGTGTGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCACCGTGGGGATG	1
M00764_MYT1_MIP116	GGCCGATTTCCAGCCATCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGACTTTGAGCTGCT	1
M00764_MYT1_MIP117	GGCCAATTTCCAGCCATCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGACTTTGAGCTGCT	1
M00764_MYT1_MIP118	GTGGTGGGTGGGTGGTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTGAAAGAAATCTGAA	1
M00764_MYT1_MIP119	ACAAAGGAATACTGTGGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGAAAACGCACTTTCT	1
M00764_MYT1_MIP12	GCCTATGTTTGTCCACACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTACTCTCTGAGGTG	1
M00764_MYT1_MIP120	ACAAAGGAATACTGTGGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGAAAACACACTTTCT	1
M00764_MYT1_MIP121	ATACTCCAGACAGTTGACAAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGTGTCTGTGCTCA	1
M00764_MYT1_MIP122	GAACAGAGCTTTGTTCCACCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCCCAGACATTA	1
M00764_MYT1_MIP123	GGACCACTCTGGCTTCTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACTCCTGAAAATCAGC	1
M00764_MYT1_MIP124	GCTGTGACCCAAGGCCATACACATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTCGGCCATGACC	1
M00764_MYT1_MIP125	CCACAAAGGTTTCACTTCTTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACCCAGGCCCCC	1
M00764_MYT1_MIP126	ATTTACCCTCTGACCTTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAATTGACTTGGATTC	1
M00764_MYT1_MIP127	GCACTTCCTGGAAAAAATTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCCAATATGCGAAA	1
M00764_MYT1_MIP129	ACTATAATATAGGCCACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTCTTATGTTAACGTT	1
M00764_MYT1_MIP13	CCCGTGCCACCGCTGCTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCCAATTCAGCAGAT	1
M00764_MYT1_MIP131	GGAGAGAAAGACATTTTGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGATGCAACCAAGT	1
M00764_MYT1_MIP132	GACCAAGGGAAAACAAAATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAAGCACACACATC	1
M00764_MYT1_MIP133	GAGTCCTGTTGCTGTGAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTTCCTTTTGTTTCA	1
M00764_MYT1_MIP134	ACCGCAAGAGCCGACACGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAACGCGCTTCCTGAG	1
M00764_MYT1_MIP135	GTCTCCATTCTTGGTGAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATACTGTGACCCTCCTT	1
M00764_MYT1_MIP14	CCTTTGTAAATACGCTACCCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTGCGGGTTTCAAT	1
M00764_MYT1_MIP15	CCCCCATGTAAATTTCATGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGCTTAGGAGTTC	1
M00764_MYT1_MIP16	AAGGCAGCTGCCTCCCGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTCAGAAAGAACGTAA	1
M00764_MYT1_MIP17	CAGGAAAAGCAGGTCTGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGAAAGGTAAGTCAAC	1
M00764_MYT1_MIP18	CATATATTCAATGCCTATTTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCACCTCGGAAC	1
M00764_MYT1_MIP19	GAGGGCAGCCCCTGTCGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAACCTTTTTAAACCCT	1
M00764_MYT1_MIP20	CACGTCTCACCTTGCAGTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCTTCACCTAACCCG	1
M00764_MYT1_MIP21	AAGGGCTTCAGCCTAAGCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGCCCTCCTTGCCTA	1
M00764_MYT1_MIP22	CATTTTAATGGGTCTGTTATAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACAGTGATGGCGT	1
M00764_MYT1_MIP23	CGCCACCAGATTCAAAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTACTGACTCTTCCTTGT	1
M00764_MYT1_MIP24	GCATCATGTTGATGTTTCTAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGGCTCCCGCAG	1
M00764_MYT1_MIP25	CCCTAATAAACAAGATACCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTACAGCGCTAT	1
M00764_MYT1_MIP26	AGCTTTGACAGCAAAGGTGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGAGCTCGCTTGT	1
M00764_MYT1_MIP27	CCCTAACCACACATGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGATGAGCTTAGAAAATG	1
M00764_MYT1_MIP28	ATTGCCCTAACAGCATAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACATAGACGATGCT	1
M00764_MYT1_MIP29	CCGAAGGTAAGAGGACCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGGTCTGCGACAGG	1
M00764_MYT1_MIP3	CCTTTGTCCACAGGATGCTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGGTTCAGAAGAG	1
M00764_MYT1_MIP30	GTGCATCCTGGGGTGGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGATGGAAAGTTCTCC	1
M00764_MYT1_MIP32	GTGAGGACACTGAGGTGAAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGAGCTGCCCCCTG	1
M00764_MYT1_MIP33	CCAGCTTCAGGGGGTGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTCGTCCTGTCCTGAC	1
M00764_MYT1_MIP34	GAGAATTGCAGCCTGTGAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATCGGAAGGAACTCTG	1
M00764_MYT1_MIP37	CTGCCTCCTAAAATATATTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTTAAGCTCCATTGT	1
M00764_MYT1_MIP38	GGCAGGTCATGGGCCACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGACCTACCACTCACTC	1
M00764_MYT1_MIP39	GTCTTCCCACGTGCTCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGTTGACAGAAAGGTC	1
M00764_MYT1_MIP4	GACAGGGGAACGCAGGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTGTCTGTAATTTGTGC	1
M00764_MYT1_MIP40	CCAGGTCTCCAGTCCCCAACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGTATCTGCCCTT	1
M00764_MYT1_MIP41	CCAGGTCTCCAGTCCCCAACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGTAGCTGCCCTT	1
M00764_MYT1_MIP42	AATTGCTGAAGAGACCCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTGCAGGAAGGAGCC	1
M00764_MYT1_MIP43	GACCCAAGTTCAGGAGAGAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGAGGCCCTTTTCA	1
M00764_MYT1_MIP44	GAGTCCAGCAAGCAGAAAGGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTGCCAGCGAGGA	1
M00764_MYT1_MIP46	GGAAGAGGAAGAGGAGGAGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACGAAGAGGAGGA	1
M00764_MYT1_MIP47	GAATCACCCAGTCCCAAGCCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGAAGAGGAAGAGG	1
M00764_MYT1_MIP48	GGAGATGCAGGACATGATGACCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCTGAGCTCCGGG	1
M00764_MYT1_MIP5	CATTTGCACAAAGGGAGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAGGTGGCAATTCCAA	1

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ID	MIP	*c*
M00764_MYT1_MIP51	AGACTGCCCATGAGCTTGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCAGCTCTTGAAGGA	1
M00764_MYT1_MIP52	GCTGTCCCCACAAGGATAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTAACTGATGTGACTTG	1
M00764_MYT1_MIP53	GGTGAGGGTACAACCCGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCCCCATAGACACCA	1
M00764_MYT1_MIP54	CCAAAGGCTGCTGCTTGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCAGCACGTTCTCATG	1
M00764_MYT1_MIP55	CCAGGGTGGGGGCCGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTACAGTCTTAGCCAT	1
M00764_MYT1_MIP57	CCTCTAGTTTGTCTGGGTGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGGCTTCTCTGGAG	1
M00764_MYT1_MIP58	GTCCTGGGTGTCTGTGTGTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCCTGTCTGCGGC	1
M00764_MYT1_MIP59	GGGCTTCTCAGTCTCCCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCCAAATCCCATGAGAAG	1
M00764_MYT1_MIP6	CATGCTTGCAAAAAGCTGATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACATTCTGCCACCG	1
M00764_MYT1_MIP60	GGCCAAGGAGCTGGAGAAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCCCATCTCACTGGC	1
M00764_MYT1_MIP61	GTTGGGCCGGTAGCTCCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCTGAATCTTTGGGG	1
M00764_MYT1_MIP62	ATTCAAGGGGCAGTGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCAGGTTTTTGGCAAA	1
M00764_MYT1_MIP63	CAATGCAGACAAGTCAGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAAGAGGATGAAGT	1
M00764_MYT1_MIP64	CCATCCTGAACCTCTCCACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAACCTTTCCCAAAG	1
M00764_MYT1_MIP65	GTGGCAGCCATGTGTGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTCCACCAACTCACCTC	1
M00764_MYT1_MIP66	ACTTTTTCTCCCTCCTGGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGTACATCTGCCAC	1
M00764_MYT1_MIP67	GAATGAGAATTGCCAGCTAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCTAACACGTGGGA	1
M00764_MYT1_MIP68	GTGTTTCCTTCTGACTCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAACCTGGTGTGCTGA	1
M00764_MYT1_MIP69	GTGTGTGCACCACCCTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATGTCATAAACACGGGT	1
M00764_MYT1_MIP7	ATGGGTACACATCTCGGTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGGAATGTCTGGGA	1
M00764_MYT1_MIP70	GGAAATGGCAGCTGGATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTTGCTGACACACT	1
M00764_MYT1_MIP71	CATGAAGGGGGCCCTACAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGCCTTCTGGTCCA	1
M00764_MYT1_MIP72	GCACAAACACCGCAAACGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGTACGTTTGATTCAA	1
M00764_MYT1_MIP73	CAAGTCCAGGGTTCCATTTTCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGAGCTGCTGGGGG	1
M00764_MYT1_MIP75	GCTAGGCTTGGTGTAGTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTGAGGAGAAGCTT	1
M00764_MYT1_MIP76	GTATGTTATTACCCTCGTTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCTCTGAGCCTCC	1
M00764_MYT1_MIP77	AATTACAACAATCGCAGTAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAGCATAAACATCA	1
M00764_MYT1_MIP78	AATTACAACAATCGCAGTAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAGCGTAAACATCA	1
M00764_MYT1_MIP79	ATTTCTAGGGCAACGCAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTGTCTATTGAGTGCC	1
M00764_MYT1_MIP8	CAGACCAAAAAATAGAGTCATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCGGGCTGCAGAA	1
M00764_MYT1_MIP80	GACACCCTCCCTGGCCTCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTTAACTCCCCCCAG	1
M00764_MYT1_MIP81	CCAGGCCTCCCCGCCAGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTGTCTTCTGTGTTTT	1
M00764_MYT1_MIP83	GTTTGGCTGGCACAGCTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGATGACCAGGAAGT	1
M00764_MYT1_MIP84	GTGAGCAGCTCCTTCTTTATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGAGGTGGTCAGGAC	1
M00764_MYT1_MIP86	GTGGGTCTTCCTCCTCTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACACTCTTTTTCCTT	1
M00764_MYT1_MIP87	GGAGGCGTAGTTCCCGGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGCTGAAAGAGAAGA	1
M00764_MYT1_MIP88	GTCTCTTGGGCGGCACCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGCTTACCCCAATATC	1
M00764_MYT1_MIP89	GCAAACATACTTGAGGTCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGCCCATCTCAGG	1
M00764_MYT1_MIP9	GGGGCATCTGTCATTCCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGAGCCGATATGTAATA	1
M00764_MYT1_MIP90	GTTCTGCTTCCCTCTGCAGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGGCGATGCTCCTCT	1
M00764_MYT1_MIP92	GTTGCTGACAGCTAGAGTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGACGGCTCTGGCCAC	1
M00764_MYT1_MIP93	GTCAAGGTGGCACCCACCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTCACAGAGCTTGAG	1
M00764_MYT1_MIP94	CCACTTTTCTTTGCACGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGAGTTTTTTTACATTA	1
M00764_MYT1_MIP95	CACGTTGATACCTGTGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGATTTTCGTGTGTTT	1
M00764_MYT1_MIP96	GGAAATACGCCTCTCACAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCCCTTGTGTCTGG	1
M00764_MYT1_MIP97	ACACAGCCTGGAACTGGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATTCTTCAGGGACTT	1
M00764_MYT1_MIP99	GTTTGTCAGGCTGTCCCAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGGTCGTGGTGGG	1
M00764_NECAP1_MIP1	GATTGCTGGGAAATGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCACAGTTGGATTTTAAT	1
M00764_NECAP1_MIP11	GATTTAGTGCCTTACACTCTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAGAAAAGAGGCA	1
M00764_NECAP1_MIP12	CCTAGAGTAAGATGGCGCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTCTGGGACTACCGG	1
M00764_NECAP1_MIP13	AGGACGAGGACCATATTGAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCACCGTCTTGGATA	1
M00764_NECAP1_MIP14	ACTTGAACTCGCGCGGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCCATAACGAGAGTCAC	1
M00764_NECAP1_MIP15	GTTTCTGAGATTAACCTTTTCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTCGCCATCTTGGG	1
M00764_NECAP1_MIP17	CGGAATCCGGTAGACGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACAATACAGAGGTAGTAGT	1
M00764_NECAP1_MIP18	GTCATCACCATATTTCTGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGACAGCTTCCTTCT	1
M00764_NECAP1_MIP19	GTCCAGAGTGGAGATGGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAAGTGCATGATGGG	1
M00764_NECAP1_MIP2	AAACTCCCAGGTTACAGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGCTCTATCAATTTGT	1
M00764_NECAP1_MIP20	CAGCTTATCATCCTCATCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCACTCTGCGTTATTC	1
M00764_NECAP1_MIP21	GCAGGGAAGAGCGAATGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAACACGATTACCCA	1
M00764_NECAP1_MIP22	GTTTTACCAGTGAGCAAAGGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTCCCCATGCAC	1
M00764_NECAP1_MIP23	GCTGAAGGAAAAACCGAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTAAGAAGGGAGGTA	1
M00764_NECAP1_MIP24	GGGAAGACTGCCTATATCAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGATTGTGGGTGGG	1
M00764_NECAP1_MIP25	AAGTGATTCGGAGGCGACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATTCCAGTCCCCAAAT	1
M00764_NECAP1_MIP26	GGCACCAGTAGAACAATATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGCTTTTATAAGTAC	1
M00764_NECAP1_MIP27	GAGCAAAGAGCTCCCCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCTAACTTCGTTCCA	1
M00764_NECAP1_MIP28	CCTTTCTCTAAAGTTGCTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAGGATGGTACTGGT	1
M00764_NECAP1_MIP29	GCAATCGGAAACACTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACATATGAATTACCACAT	1
M00764_NECAP1_MIP3	AGACCAGCGTGGGCAGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTATGGAGGCAGAAAT	1
M00764_NECAP1_MIP30	CACATTTGGCACTTTAGGAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTGCTCTAGTTGC	1
M00764_NECAP1_MIP32	CTGGCCTCAAACTCCTGACCTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTCCCCAATTCAA	1
M00764_NECAP1_MIP33	CACCCGAGTAGCCGGGATTACCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGGCAAAAAGTGTTCAT	1
M00764_NECAP1_MIP34	CAACCTCCACTTCCCCAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATTCAAGATAGTCCCA	1
M00764_NECAP1_MIP36	GTCTGTTTGCCAACCTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGTTTCATGGAACATA	1

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ID	**MIP**	***c***
M00764_NECAP1_MIP37	GGATGATTCAAGTGCATCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTAGGGTGACTGTTAT	1
M00764_NECAP1_MIP38	GAAACCATCCCCTAATGCCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAAACAAGCCCAAG	1
M00764_NECAP1_MIP4	CCAGATTTAACATATTTTGATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCCAGCTGGTGTG	1
M00764_NECAP1_MIP40	GGAAAACAAGCCCAAGGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTAGATTCTCAGAGGG	1
M00764_NECAP1_MIP41	GGCTGTAAATACAATGAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGGAGCTCATAACCT	1
M00764_NECAP1_MIP42	GTCACTTGCATGACCACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGTATCCTCTATGGCA	1
M00764_NECAP1_MIP43	ATCGGGGAGATGCCTTCGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCTGGTTTCTAACAG	1
M00764_NECAP1_MIP44	GTGAAGCCAATGCCAATGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGATACTGCCCATTC	1
M00764_NECAP1_MIP45	CCCATTCACTTTTGTTTCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGAAGCTTGTCCTT	1
M00764_NECAP1_MIP46	GAAACAAAGAAACCAGGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAACTACTGCACAA	1
M00764_NECAP1_MIP49	GCTTTAACTTGGAAAGACTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCACTTGATTTTGG	1
M00764_NECAP1_MIP5	GAGGCAGAAATGGTGCAAGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGCCGCTGTCTAT	1
M00764_NECAP1_MIP50	ACTTCAGAGAGTCCTAAGGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAATTGCCCCTTCC	1
M00764_NECAP1_MIP51	CCTTCTGTTTCTCACTCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGGAATGGGAATTGG	1
M00764_NECAP1_MIP52	GGGGTTCAATTCCACTGGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTGAAAGCAGAGTCT	1
M00764_NECAP1_MIP53	GATGCTCGTCCTAAGTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAAAGTAAATACACCC	1
M00764_NECAP1_MIP54	CCTTGGAAATCTCAGATTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATAGGCTTATGGAAG	1
M00764_NECAP1_MIP55	GAGCTTACTCCCACCCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAATTTTGTTTTCCTGT	1
M00764_NECAP1_MIP56	GCAGTCCTGGGCTTAGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCTCCATGGTTAGATTT	1
M00764_NECAP1_MIP57	GGAGAGTTAATGTTTTTGCTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCAATCATGTCACC	1
M00764_NECAP1_MIP58	GACAAACAGGTGTTGCTTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCCAAAGAACCTATG	1
M00764_NECAP1_MIP59	ATTTTGGTCATGGCTCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTAGTGAACTAAGAG	1
M00764_NECAP1_MIP60	GACCATTATGAATAAAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGAGATTCATTCAAGT	1
M00764_NECAP1_MIP61	CAGCAATAAAAAGAAACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGCACAAAAATCTGTAT	1
M00764_NECAP1_MIP62	CAGCAATAAAAAGAAACAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCACAAAAATCTGTAT	1
M00764_NECAP1_MIP63	AGACTTCAGCACTGCCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGATTTTGATTATGTTT	1
M00764_NECAP1_MIP64	GGAGATATGTACAGTCAATTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCTCCTGCTCCTGT	1
M00764_NECAP1_MIP65	GGTTTTGGAAATTCTAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGAGTCTTTTGGAAG	1
M00764_NECAP1_MIP66	CACTTCATGGCAATTCTACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTGCCTGGTTTGGAA	1
M00764_NECAP1_MIP67	AGGGAAGTTAGGAACCCATTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCTTGCAGCTCT	1
M00764_NECAP1_MIP68	ACAGATTGGTGCCCTCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTTTCTTGGCTGTACA	1
M00764_NECAP1_MIP69	GTCTGTTTGAGGGGGAATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGTCACTCCCCTGTGT	1
M00764_NECAP1_MIP70	GGCCTTTTAAGCCCTGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAATTGCTAAATAGGGC	1
M00764_NECAP1_MIP72	GAATTTGTAAACACTGAGGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACACAAGAGGGTGA	1
M00764_NECAP1_MIP73	CAGTGGGTGTATCTGTAATGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGGTGCAGCTCC	1
M00764_NECAP1_MIP74	CACAATTCAAACTCAACAAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATGCTTCAAATGC	1
M00764_NECAP1_MIP75	GCAGAGAGGTTGAAAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTCTATAGGAGTGTTTA	1
M00764_NECAP1_MIP76	ACCCTTCAACTTTAGGTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTACATGAACTGAAAA	1
M00764_NECAP1_MIP77	ATACCTGTCACCCAGGGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTTTCCATAAACATTT	1
M00764_NECAP1_MIP78	AAAGCCTTGGGCAAAACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATAGAAAGTACCCATTC	1
M00764_NECAP1_MIP79	GAAGGGAGTCCTTATGTTTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAAAAAAGTTCTGCT	1
M00764_NECAP1_MIP80	GTACATACCCAATAGGTGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAATAGAGCTGCCTG	1
M00764_NECAP1_MIP81	AAGTCTGTGGAATCACTAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGATTCTCTTCTTCAC	1
M00764_NECAP1_MIP82	CCTTTTAGTGTTTTCTATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATTTTCCATTTTTCA	1
M00764_NECAP1_MIP84	AATTAAAAGATAAAAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGAACACAGAGGTCTAGT	1
M00764_NECAP1_MIP9	ATACAAAGAATTAGCTAGGCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGGCCGGGCGAAG	1
M00764_NENF_MIP1	CAGGTGCATAAATGCGGAGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGTTATGGGGATGGT	1
M00764_NENF_MIP10	CGCTTTTATTTTTGGCTGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACTACAGACTGGAA	1
M00764_NENF_MIP16	ATCTAAGGAAAGAGAGAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCCCCTAGATTCTCC	1
M00764_NENF_MIP17	GTCAGTTGGAGAGTCCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACATCAACATCAAAAAAC	1
M00764_NENF_MIP19	CAGGCTCCACTCCCAAAACAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATAGACCAGAACA	1
M00764_NENF_MIP2	CAGCATATAGTGAAACCTCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTAACCTGCCTATT	1
M00764_NENF_MIP20	CCTGTTCTGCTGTGTGATTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCGCTGTTGTTTGA	1
M00764_NENF_MIP21	CATCTACTTGGCAGTGAAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTGGGACTTGACCC	1
M00764_NENF_MIP22	GCTGATCTTCCTAGAAAGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCACACCTCCAAGT	1
M00764_NENF_MIP23	GACTCCACGCTCACGGAGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGGGCTCCTCGTCCA	1
M00764_NENF_MIP24	AGCCAGATTATAAGCCTTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCCTTCCTTCCCAC	1
M00764_NENF_MIP25	CCCCGTCAAGGCATTGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGAAAAAGAGAAAAAGG	1
M00764_NENF_MIP26	CCGGAGAATTCTCAATGAGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCCCATCTCCTGTC	1
M00764_NENF_MIP27	GACGATGGGGTATTTGGCTTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGAACCTGCTCC	1
M00764_NENF_MIP28	GAGGCCCTGAGCCACCCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAAGCCTGAAGACCAGC	1
M00764_NENF_MIP29	CAGTTTTGCAGGAGATTCAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCTGGTGTGCAGAC	1
M00764_NENF_MIP30	GCGACCTTTACTTTATACTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTGTTGTCCTTGG	1
M00764_NENF_MIP31	GCCCAGCCAGCTGATACTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGGGAAGAATTCTCCT	1
M00764_NENF_MIP32	CAGGAAAAGAGAGTGGTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGGTCCCATTTTTACA	1
M00764_NENF_MIP6	AGCACTGGGATGGACATTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCACTGAACAAGACAG	1
M00764_NENF_MIP7	GGGAGAAAAAGTAGGGCAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTCCATGTACCAGGT	1
M00764_NENF_MIP8	CACTGGGGACTCACCACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGGAGATTTTTGCAAA	1
M00764_NENF_MIP9	ATATACCTTTCTAGGTTCTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTATCGGTAACAGCAC	1
M00764_NRG3_MIP100	GGACATGGCTCTTCACCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGCAAAACCCTATAAAG	1
M00764_NRG3_MIP101	GTTCCTGCCTTTTCTGATGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAAGAAAGAAGTAAA	1
M00764_NRG3_MIP102	GGATGTGCACGTGCAGGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCAGTTAAGGCAAGGA	1
M00764_NRG3_MIP103	GTAATGTCACCAGTTAAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTTGGGTAGGTAAAG	1

continued table…

ID	**MIP**	***c***
M00764_NRG3_MIP105	CAAGTGAAAGAAAATCCCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATAAAACGGCCCCAC	1
M00764_NRG3_MIP106	AGTATTCAAAGGTGGAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCTCCTGCTCCTCTAG	1
M00764_NRG3_MIP107	GGGAAATCACACGTACAGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGTTTGACAGACTG	1
M00764_NRG3_MIP108	GAGACAACTGTTCTTGCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCCTGACAGAGGAAG	1
M00764_NRG3_MIP109	CCTAAGTCATGCTGCCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTTCTATCAGGTTTCTT	1
M00764_NRG3_MIP110	GCCTTTTCTAGATTACACAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGCAGACAGCATT	1
M00764_NRG3_MIP111	CCTTTATTATTTGAGCACTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGAGAGACTGGTTT	1
M00764_NRG3_MIP113	GTTAAGGCCTGTGGTATAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACAGTAGGGTCAATTC	1
M00764_NRG3_MIP114	ACTGAGAATTCCTACATAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTTTTAATAAACAT	1
M00764_NRG3_MIP116	ACCTCAGATTTTAATCAATCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTGACAAAAACTGA	1
M00764_NRG3_MIP117	GAGGAGCTTGAGAATTCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAATTTTTTCCCCATA	1
M00764_NRG3_MIP118	CCCATCCATCCTGATTATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAGACACTGAGAAAA	1
M00764_NRG3_MIP119	CAGATTCAGTGTTTGCAAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATCCAGGAACTTCCC	1
M00764_NRG3_MIP120	CCCAAATTCTCAAAGTTCTAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGCTGCAGCAAG	1
M00764_NRG3_MIP121	GACCAGCATATCAGCAACTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTTCATTCCACCCC	1
M00764_NRG3_MIP122	CAATTCCACCTAGCCTACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAACTTAAAGCTATGGC	1
M00764_NRG3_MIP123	ACTTAAAGTAAGAAGATCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGTTTGTCACAATG	1
M00764_NRG3_MIP124	CAACACACCACGGCTGTATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTCCCAGTTAAACAGA	1
M00764_NRG3_MIP125	CAACACACCACAGCTGTATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTCCCAGTTAAACAGA	1
M00764_NRG3_MIP126	CAATCCACAAAGCACTTTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTCTTGAAGGCAGT	1
M00764_NRG3_MIP127	CATCATCCCTTCAGTGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGGTTTAAAAACCCAAC	1
M00764_NRG3_MIP128	GCACAGAACTGGCCCTTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGCTGACTGGAATACTC	1
M00764_NRG3_MIP129	AGAAGACTACGAACTGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTATTCAGCTGACGTTG	1
M00764_NRG3_MIP130	GCTCCTGGACAGTTTCTAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTCGTTCTGATTTG	1
M00764_NRG3_MIP131	ATGTAGGAATCTGTGCATTCTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGGACAGTGCAAG	1
M00764_NRG3_MIP132	CAAGTCACTTGGTCAATGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATATGAGGGCGATAGAC	1
M00764_NRG3_MIP133	ATGTTTCAGGAGGGATAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGAGAGGAAATCAAA	1
M00764_NRG3_MIP135	GGTGGCTCTTGCCATTTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCTTAGAAGATGTGG	1
M00764_NRG3_MIP136	GCTCACTGGTGCATCCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTTGTGGCATTCTCCAA	1
M00764_NRG3_MIP137	AGATTTGAATGCACAGATCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGACACATGTAGTGTTTT	1
M00764_NRG3_MIP138	CCTTCTATCTCCTGTCCTCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTGACACGATATAAG	1
M00764_NRG3_MIP139	GCGAGCGTGTGTGTGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAAGAGACAAAAAAAT	1
M00764_NRG3_MIP140	CACACATGTGCACACAGGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGATGTTTCAGAAC	1
M00764_NRG3_MIP141	CACTTGCATGGTGGGGTCGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACGCTTGCTAAAATT	1
M00764_NRG3_MIP142	CCTTGATTTAAGAACTAACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTGATGAACTCACC	1
M00764_NRG3_MIP144	ATGATGAGAAAGCAAATGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGCTTCTTGTGAAC	1
M00764_NRG3_MIP146	GTGGTAAAAATATTGCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTACATAACAACTCAACACCAC	1
M00764_NRG3_MIP147	GCAGTTTTGGAAAACCTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGACATATGAGGAAATT	1
M00764_NRG3_MIP148	GCTTTCAAATACGGTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTGAAATAAGAATTGTA	1
M00764_NRG3_MIP149	GTCATCCAGAAAAAAGAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGAAGGAATGTAACT	1
M00764_NRG3_MIP150	ACTCATGTTCCCAAGGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTTTTGTTAAATGTAAA	1
M00764_NRG3_MIP152	GAAATTCTACCAATATTACCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAACTTGTCGGGT	1
M00764_NRG3_MIP153	ACTTTGTTGAAGTCAACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTGTGGGAACATTTTA	1
M00764_NRG3_MIP17	CAGGAGGGAGTAGAATCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAATCATAGTTGAGACA	1
M00764_NRG3_MIP19	GTCTTTTAAGCTGATCTGATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATGATAGCTTTCTGT	1
M00764_NRG3_MIP20	GAATAAGAACAAGGTGGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTGCAAAATAGCCTTG	1
M00764_NRG3_MIP21	ATGATGGGAATACTGGGTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTAGTTCAAGTTCTGT	1
M00764_NRG3_MIP22	CAGATGCTATGGCTCAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCAAGGGTTAAGTAAC	1
M00764_NRG3_MIP23	GGAAAAAAACCGTCTAGAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCCCTATGATCTTAC	1
M00764_NRG3_MIP24	GCAAAGTAGGTTTGCTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGACTGCTTCAGCCA	1
M00764_NRG3_MIP25	GAGTGTATGTGTGAACATATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTAACTTGCTGCTT	1
M00764_NRG3_MIP26	CCTTCTACAAAACACAAGCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGAGGTATACCACACT	1
M00764_NRG3_MIP27	AGGTCTTTAAAGAAAAGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGCAGTTGATAGAATA	1
M00764_NRG3_MIP28	GGAAATCAATTGAGAAAGAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCTGTCAATAATCA	1
M00764_NRG3_MIP29	GGGTTAAATCTAGGGCTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGCCTCTGAAAAACC	1
M00764_NRG3_MIP30	GACATCGCATCAGATTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAACCTCTTACTGTCTTT	1
M00764_NRG3_MIP31	GCATTCAATTCCAAAAGGTGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGGCACTCTCTG	1
M00764_NRG3_MIP32	ATAAGAATCCAGTTCATCACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGGCTCTTGCACGG	1
M00764_NRG3_MIP33	ACTAATTTTAGCTGCCGATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTACACAGCGCTAT	1
M00764_NRG3_MIP34	AGCTGACATATACAAGTGTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCAGACAGAGGGGC	1
M00764_NRG3_MIP36	ATGTGTAATGATCAACTCAGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGTAGGCCTCCC	1
M00764_NRG3_MIP37	CATGTAACAAAATATGACATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAACAATATATTGTAC	1
M00764_NRG3_MIP38	CACTCGAACCACTGCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCTTGCTATTTACAAA	1
M00764_NRG3_MIP39	GAGTGATAAAGAGGGGTTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCACTCTTGCTCTCT	1
M00764_NRG3_MIP40	GCTGAAGGTTGGTAGTGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTCTGGTATGTATCAT	1
M00764_NRG3_MIP41	ACTGCCCTCTCTTGACTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAACTCTTATTTGCT	1
M00764_NRG3_MIP42	ACTGCCATCTCTTGACTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAACTCTTATTTGCT	1
M00764_NRG3_MIP44	AAGAGCACCAGAAATGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTTTCAGACTTACAAA	1
M00764_NRG3_MIP45	GTCTTCTTGCTCGCATTATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGCTGACGAATTCAT	1
M00764_NRG3_MIP46	AGGAGCAAGGTAAGTTGTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGGCTACAAGAGGAG	1
M00764_NRG3_MIP47	GCCTCCTGACCACTCTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACTCCTGTTTCCCAAAT	1
M00764_NRG3_MIP48	GGATTCCACAGAACAGTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAATCTGTTTCAGAATT	1
M00764_NRG3_MIP49	CAGTTACAGCTATAATTGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATGTTGTATGAAGG	1

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M00764_NRG3_MIP50	CCAGAGTGACTCCAATAGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGGAATGTTGTTTC	1
M00764_NRG3_MIP51	GAAGCCCCATTTGTGGACAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACCTCTGGGACTC	1
M00764_NRG3_MIP52	CCCTGACAGATACGACGACATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGGAGCTGTCTGTCT	1
M00764_NRG3_MIP53	GGAAACGCTGTCAGCAGTACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGGTTTCGATCAC	1
M00764_NRG3_MIP54	CATCTGGTATGTGTCATATCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAATGATGGCGAGTG	1
M00764_NRG3_MIP55	CCAGCACCCTCCACCCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTTTCCATTTTGTCTT	1
M00764_NRG3_MIP56	AAGCGTCTGTTTATGATGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTCTTTAACAGTGGAA	1
M00764_NRG3_MIP57	GCAGATCTAAAAGTAAATCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTCTCCTGCCAC	1
M00764_NRG3_MIP58	GTTTCTGCCTTCCTTTATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGTTCTTGAGAACCTA	1
M00764_NRG3_MIP59	GTTCTCTCTGGACACAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGTTCTCTACCTAGAC	1
M00764_NRG3_MIP61	GTGAGCCACCACACCTGGCCCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACCTGGCTGATTT	1
M00764_NRG3_MIP62	ATGAGCCACCACACCTGGCCCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACCTGGCTGATTT	1
M00764_NRG3_MIP63	CCACACCTGGCCCATAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGGCTGATTTTTTGTAG	1
M00764_NRG3_MIP64	ATTTATCCCCTTTTCTCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAGGTCAGAAACAGA	1
M00764_NRG3_MIP65	AACATACGCATGTGGTTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCATTAGAGAGAAGAA	1
M00764_NRG3_MIP66	CTGATGGCAGATGTTGATGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGTAGGTCAAGCATT	1
M00764_NRG3_MIP67	CATTTTCTAGACACCGGAGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACCGCATTGGCCAG	1
M00764_NRG3_MIP68	GAACTCCTGACTTCGGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCCCGGTTCAAGTGACT	1
M00764_NRG3_MIP69	GCATTGGCCAGGCTGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTCACTGCAACCTCTGA	1
M00764_NRG3_MIP70	CCCCGGTTCAAGTGACTCTCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTAGAGAGATTT	1
M00764_NRG3_MIP71	CCCAATGGTGAACTCTAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTTCAGTCTAACGTAA	1
M00764_NRG3_MIP72	CATCAGTGTTGTCAACAAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTTGCTCAGTACC	1
M00764_NRG3_MIP73	AGTTCAACTGGAAGAGTGGTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGTCTCCAGGCA	1
M00764_NRG3_MIP74	ATAGCCCATATGTGAGACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCATAGATATGCCTGA	1
M00764_NRG3_MIP76	GAGGAATTATGTCATGAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGACTACTGTATTAG	1
M00764_NRG3_MIP77	ATGTCCCACTTCGTAATACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATCAGTCCATGATGG	1
M00764_NRG3_MIP78	GAGTGACAGATTTCAGTTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGTGGAAGACTCAA	1
M00764_NRG3_MIP79	CACTGGTGACACTCCAGGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGGAATGTGGAGCAA	1
M00764_NRG3_MIP80	ACTGAATTACTGCCCATGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTAATTGAGTGGGTGG	1
M00764_NRG3_MIP81	ACTTCAAGGCAGTAGTCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACTGGGGGCTCCATGA	1
M00764_NRG3_MIP82	ACTTCAAGGCAGTAGTCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACTGGGGGCTCCATGC	1
M00764_NRG3_MIP85	ACCCCGTCTCTACCAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTGTGTTTTAAAAAGTT	1
M00764_NRG3_MIP86	ATTGAATTCATGGGTAAGACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGCCTTGCCTTGG	1
M00764_NRG3_MIP87	CCCAAGTGGTCTGCTACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATAGCATCTGATAATGA	1
M00764_NRG3_MIP88	CCTATTGATTTTTTCTTCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTTTTGAATTATTGT	1
M00764_NRG3_MIP89	GTATTTTATTCACCCAGTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCTTCTGTGGTGCT	1
M00764_NRG3_MIP91	GTGAAATTGTGGTAAGGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACAGGATAACTGGTTG	1
M00764_NRG3_MIP92	GGCTTTGAAAGACTCCTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTATGAGTTCTGATGT	1
M00764_NRG3_MIP94	CATTCTACTTCAAAAGCAAGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCGCTAGCATCC	1
M00764_NRG3_MIP96	ATGATCAAGAGAGCTTTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCTTTCCTCAGACACA	1
M00764_NRG3_MIP97	CCCATAGCAACTCTAAAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGACTTCATCAGAA	1
M00764_NRG3_MIP98	GCTAAAGTTAAATAAACTCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTGCTCTTGGATT	1
M00764_NRG3_MIP99	AATGTAAGTGACATGTCTACACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGGAAACAAGCTAA	1
M00764_NRSN2_MIP1	GTTTAAGCGTTTTGTATGTTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTCTTGTTCGTGT	1
M00764_NRSN2_MIP10	ACTGAGTGAGATGTGAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGTGGAGGTCACTTCT	1
M00764_NRSN2_MIP12	ACCTGGAAAAGGGACTGACGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCAAGGCAAGTGGGA	1
M00764_NRSN2_MIP19	GAAGCCTCTACCCAGCCTATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCTTCCTGACAGG	1
M00764_NRSN2_MIP2	CAGCCTGGGCATCATGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGGAGGCTCACAGATA	1
M00764_NRSN2_MIP25	CGCTGCCTCCCGCTCGGCCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTGTGGAGGGGGC	1
M00764_NRSN2_MIP29	GCAGAGACTGAAAGCGAAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTCAAGAAAGCCTGT	1
M00764_NRSN2_MIP30	ACCGTGTGTGTGTGTGTGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCTCCTTTCCTTCC	1
M00764_NRSN2_MIP31	GGAGGTTCTGCTTGGAGTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGAGAAACTCACCGA	1
M00764_NRSN2_MIP32	CAGGAGGCTGCTAATTAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTTTCTCTGTGCTG	1
M00764_NRSN2_MIP33	AATGAAACAATGTGCTTGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATGGAAGGTACTTGT	1
M00764_NRSN2_MIP34	GTCTTTAATCCTGAGGGACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGGGCCAAACCTGTAT	1
M00764_NRSN2_MIP35	GTTAGATTTCCAGAGAAACCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCAAGGCTATAAA	1
M00764_NRSN2_MIP36	GCTCTCTCATTCCAGATATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCTGGAGGCTTTCAG	1
M00764_NRSN2_MIP37	GGGGTAATTGTCATGGCTGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAGAAATGGTAGC	1
M00764_NRSN2_MIP38	ACTTGTCTAAGGTCACGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCAAAAAAATTACAGTAC	1
M00764_NRSN2_MIP39	CCACCTTTCTGGGTCTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGTCAATAAATGTGCAT	1
M00764_NRSN2_MIP40	ACTGTGCTATGCGTGTAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCCTCCAGAGTAAA	1
M00764_NRSN2_MIP41	CCTGTCCTTCCCAAAGCACACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGAGGGATTAGTGGG	1
M00764_NRSN2_MIP42	ATGGCAAGTGGTATGGGGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGAAGGTCACCATGAG	1
M00764_NRSN2_MIP43	GAACGATTGCAGCTCGGCATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACCGGAGGTCCCTC	1
M00764_NRSN2_MIP44	GAGGAAATGAGTCTGAATTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTGCAAGCACTGCT	1
M00764_NRSN2_MIP45	GAGGAAATGAGTCTGAATTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTGCAGGCACTGCT	1
M00764_NRSN2_MIP46	ATCCTCACCAGACTTAAGGGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGTCAGAGCCGCC	1
M00764_NRSN2_MIP48	CAGGAACTCACCCTCACCGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCCAGCCTATCATGG	1
M00764_NRSN2_MIP49	GCAGCAGTTGTCACCCATTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGCTGGAGTTCTGC	1
M00764_NRSN2_MIP5	GATCTCCCAAGGCTCAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGATAGGGCCACATCTT	1
M00764_NRSN2_MIP50	CAAGGGCTCTGCCTTGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAAGATTGCCCAAAGG	1
M00764_NRSN2_MIP52	CACATCTTAGGCCATGTGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGAGCACTGGGATT	1
M00764_NRSN2_MIP53	CCTACCCACACCCTCTTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTTAGCAGGGTCCCT	1

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M00764_NRSN2_MIP56	GGCAGTGCGTGTCCTCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCAAAATGCAGGTAGAA	1
M00764_NRSN2_MIP57	GTCACACAACAAAGCAGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGCCTCTCACAGTGTG	1
M00764_NRSN2_MIP58	GACATGTCACCTCCAGCCTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAGGACCCTCAGGG	1
M00764_NRSN2_MIP59	GGATATGGATTTAAATGGTCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACAGGTGGGGCGG	1
M00764_NRSN2_MIP6	GAATAGATGCTCAAGACACAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGACGCTGTCTCAA	1
M00764_NRSN2_MIP60	CCAGAGCCACCTGGGACCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGTCACGGCCAAG	1
M00764_NRSN2_MIP62	AGGGAGGGGCTGGCGCCTCTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCAGGCTGGTGGA	1
M00764_NRSN2_MIP64	GGATGGAAGGGGTGCAGGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAATGGGTCGTGCCCAG	1
M00764_NRSN2_MIP67	GGTATGTGCCTGTAGTAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCATTTCCTAGATGGC	1
M00764_NRSN2_MIP68	AAAAATCTGGCAGACACCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATGTTCTTTGATGCTC	1
M00764_NRSN2_MIP69	CACTGTGAAGTCACTGTTTTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGAAGAATGCCAC	1
M00764_NRSN2_MIP7	GTTTCTCCTTGTGCTAGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCATGAGCTGTCAG	1
M00764_NRSN2_MIP70	CGAAAGACAAGGAAAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAATGATGTGGTGAGAA	1
M00764_NRSN2_MIP71	CATGATTAGGCTGACGTTACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGTATCCTTCAGCC	1
M00764_NRSN2_MIP9	GCCCACTGCCCATCTCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACCTTGAGAAGGGAGTT	1
M00764_NTNG1_MIP1	GTTTGTTGAGTTGGGCCTATAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAAGAAATGGGCAA	1
M00764_NTNG1_MIP100	GGAATTTCTAGTACTCTCACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTACACCTGGTTCTC	1
M00764_NTNG1_MIP101	AAATGCCCAGTAACTTTACAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAGAACACTTCCCC	1
M00764_NTNG1_MIP102	GTGAATTTCAGGCTTGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCGGTAATTTATTTGT	1
M00764_NTNG1_MIP103	CAGGGTGATCGCAGTGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTTGAACAACTACTAAG	1
M00764_NTNG1_MIP104	ACAAGCCTGTGAGGGGATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTATAAGAAGCAGGA	1
M00764_NTNG1_MIP105	ATGTGGTAAATGCCATGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATACTCTGATAATTTGGA	1
M00764_NTNG1_MIP106	CACAAGCTCAAGTAAACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAAGAGGATGCTGTAG	1
M00764_NTNG1_MIP107	CCCCTTGGCATTTGCCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACATCCATTTAGAGATAC	1
M00764_NTNG1_MIP108	AATTAGACTATTAGAGCTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGCTTCTACTTGCT	1
M00764_NTNG1_MIP109	GTCTTTCTGTTTGGAGTGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCATTTTAGTGCAACA	1
M00764_NTNG1_MIP11	GTGCTGCTCCGGCTGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGTTTCACTTAAAAAGCA	1
M00764_NTNG1_MIP110	CCCCAACGCCAAAGAACTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAAAAGGTCAACATCT	1
M00764_NTNG1_MIP111	CGTTGTGCCTTTGAAAAAAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCTCCACCACATT	1
M00764_NTNG1_MIP112	GCATCCTTTCAGGTCACCACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGCCAGAGGCATA	1
M00764_NTNG1_MIP113	CTTACCTGTTTCCTGGCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGATATTTTGGACTCTC	1
M00764_NTNG1_MIP114	GTCATGTGTGATGTTGGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGCAAAAAGCAACTTATA	1
M00764_NTNG1_MIP115	GTTTTCAAGGTGCAAGCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATTCGAAAGTTCCTTC	1
M00764_NTNG1_MIP116	GGCAGTGTCGTCTACGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTCATTGATTCCTTCTT	1
M00764_NTNG1_MIP117	CAGCATAGCTCAAGGAAAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAAGTTATGGGTGTT	1
M00764_NTNG1_MIP118	GATAATCGGGGTCTCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTGAAATTTATTAGGGC	1
M00764_NTNG1_MIP12	CACTCTTTAATTGGCACTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATCCTTCCACTTGCTG	1
M00764_NTNG1_MIP120	GAACCTTAATACAGGCGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAGGATTATGGGAGAC	1
M00764_NTNG1_MIP121	GAACCTTAATACAGGCGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAGGATTATGGGAAAC	1
M00764_NTNG1_MIP122	CAGCAATTAATGAATCCCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCATTCGTACCTGC	1
M00764_NTNG1_MIP123	GGCCAAAGCAGATCAGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAAATGCAATCTGAAGG	1
M00764_NTNG1_MIP124	GCTCTTTAACTTGGCTGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCGGCCATATCCTATTA	1
M00764_NTNG1_MIP125	CATGTTTGGGGGAAAATCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCTGATTTTTCCTGAT	1
M00764_NTNG1_MIP126	GTTGTTTCTAGGAGTTTGTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGAGCAACTGGATA	1
M00764_NTNG1_MIP127	GTTATGTGTTGTGAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAATTTACTGTTCATTC	1
M00764_NTNG1_MIP128	CAAGAATTCCTACCTCTCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCGATGCATTGATTGA	1
M00764_NTNG1_MIP129	GGCAACAGGTGGTTGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAACAGAAATGTATAC	1
M00764_NTNG1_MIP130	ACTAGAGGGCAGCACTGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCTACTGTATACACT	1
M00764_NTNG1_MIP131	GTGTTTACAGCTCACGCAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGGCACAGAAGAAT	1
M00764_NTNG1_MIP132	CAGAATGAACTTTCTCAATGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACAACTGGACGATG	1
M00764_NTNG1_MIP133	GATCGTTGTAATGGCTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAGTAAGTGATGCATTT	1
M00764_NTNG1_MIP134	GGATTGAGCCCAAAGGGTTACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGCTCCCAGAGT	1
M00764_NTNG1_MIP135	GTTTTAAAAGCTACTTAATGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTACGGCTGTCAA	1
M00764_NTNG1_MIP136	ACTGCAGCCATTTCTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTTAGTGTGCGTAAAAA	1
M00764_NTNG1_MIP137	GACCTGGGAGTGCGCTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGTAAAATCTGTCCTGC	1
M00764_NTNG1_MIP138	CCCATGGTTTAATATTGACTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGCCCTCACAGAT	1
M00764_NTNG1_MIP142	CGGTTCCCAGCAGCGTGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGAGTGGGGGTGTCT	1
M00764_NTNG1_MIP143	AGGAGTTGGCAGCTGTTGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGGAAACACACACATA	1
M00764_NTNG1_MIP144	GGAGTCAGAAATTAACAGTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCGGTTGATTTGTT	1
M00764_NTNG1_MIP145	GTGGGCATAAGGAAATCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGGAAAGACAAAAAA	1
M00764_NTNG1_MIP146	ATGCACCTGACAGCAAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACATCAGACAAAGAAATC	1
M00764_NTNG1_MIP147	CCCACTATACAAGAGTGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACCCTTGTTGGTTGAA	1
M00764_NTNG1_MIP148	GTGTGCTCGCACTGGACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGGTAACACAAATTGG	1
M00764_NTNG1_MIP149	ATTTCTCTGTAAGGGCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATATGTAGATTTTTTGT	1
M00764_NTNG1_MIP15	CGCACCCAAAGTCCGTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAATCAGGACAATTAGC	1
M00764_NTNG1_MIP150	GTGAAACAAAACAGAACGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGTGTTAAAGCAACA	1
M00764_NTNG1_MIP151	CAGTTTCACACTCACTTTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCAAAGGACATTCTA	1
M00764_NTNG1_MIP152	GAAATTGCAATACAAATTCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGTCCAAGCTAGTG	1
M00764_NTNG1_MIP153	ATTATGCCAAAGCCTGTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCAGGAAGATGGATTG	1
M00764_NTNG1_MIP154	GTAATTTTTCCCAAGTGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATCACCATCAATCTGT	1
M00764_NTNG1_MIP155	GTAATTTTTCCCAAGGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATCACCATCAATCTGT	1
M00764_NTNG1_MIP156	GGAGCAGGGAAATTGAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATTTTTAAGTCATGCT	1

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M00764_NTNG1_MIP159	AGAATTTATTACACCTTGGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGACAACAGTGTGC	1
M00764_NTNG1_MIP16	CGGGAACCAGAAAATCGTCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTCTTGGCGCCAA	1
M00764_NTNG1_MIP160	ATTCTACATGACTTGGTAGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTAAGACAGTGT	1
M00764_NTNG1_MIP161	CATTGTCCTTAAGACTCTGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAGACATTCCTCC	1
M00764_NTNG1_MIP162	GTAAACAGGTAATGCCTGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTGCTGAAACAGGG	1
M00764_NTNG1_MIP163	ACATGCTGTTCCTTCATCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGACTGTTGGTTTG	1
M00764_NTNG1_MIP165	GTTGGCCACTCTGGCACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATATCAGAAATCCACC	1
M00764_NTNG1_MIP166	ACTTTATCGTTATCTGCTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGATAACATAGGGAGT	1
M00764_NTNG1_MIP167	GCCAGAAATAACATGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATCAGTTTAAATCAGGC	1
M00764_NTNG1_MIP168	GGAATATCTTTCATTCCGTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAATCAGACACTGCA	1
M00764_NTNG1_MIP169	CATCAATTTAGATTCTTATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGATTTAAAAAGAACA	1
M00764_NTNG1_MIP17	CGCTTGGCACCGCTTTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTTACTGAGGGATATTT	1
M00764_NTNG1_MIP170	CAAAGCTGGTTTCATCTACAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGTACAACAAATGGA	1
M00764_NTNG1_MIP19	GAGGTCGTGCCAGCCCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAAAGATCAGTGACTTT	1
M00764_NTNG1_MIP25	GCGGGGCCCCTGTCAGTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGGGCAAGTGTTTTTTT	1
M00764_NTNG1_MIP26	CCCATGTTGTGCAGCTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAGCAAACAAAAAAAA	1
M00764_NTNG1_MIP27	GTTTTAATCTAGCACCAATAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAATCCATCAACCGA	1
M00764_NTNG1_MIP28	ATTAAGTGATTCATACAAGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTACTGGCATCATA	1
M00764_NTNG1_MIP29	GGTTATTTTAGGCCCAATAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGCCTACTCTTAAGT	1
M00764_NTNG1_MIP3	CCAGGGACCTGCTGGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTCACTTCAAGACCCT	1
M00764_NTNG1_MIP30	ACTTTACTTGGAAAAGTCGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTCTGCTGTTAATT	1
M00764_NTNG1_MIP31	GCTTTAAAATCCCCGCTAGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGGAGTGGCTCCAT	1
M00764_NTNG1_MIP32	GCTCTAGAAATAAGGCCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCCATTCTTCTCTTTA	1
M00764_NTNG1_MIP33	ATTCTACTGCCAGATTCACCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTACTAAGCATATCT	1
M00764_NTNG1_MIP34	GGGAGGCTTTTCTGTTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGTTTTATCTTACAGAA	1
M00764_NTNG1_MIP35	GGAAAACTTTCCAACAAGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATTCAAAGTGACAC	1
M00764_NTNG1_MIP36	ACTGTCCAAGATTCTTTTTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCCTTGAGGAGGA	1
M00764_NTNG1_MIP37	GAGCTGCTTTTCCTTTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACAACATTACATGTGAA	1
M00764_NTNG1_MIP38	CACTACTAATTTGGTGGTATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGTGCATCAAGTA	1
M00764_NTNG1_MIP39	GCCTTCATGGTGGTCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATATTAACAGGAAACCA	1
M00764_NTNG1_MIP4	CAGATTTCTGAGATCAGAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTTCTTGTTCAACCAA	1
M00764_NTNG1_MIP40	CCTTTTTAGGAGGAGGCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATTTAAGACGGATAA	1
M00764_NTNG1_MIP41	ACCTGAATCATTTTAACACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTAACTTTTTAAACAA	1
M00764_NTNG1_MIP42	GTTTTAGTTACAAAGGCATCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAGTGGTGCAAATA	1
M00764_NTNG1_MIP43	CAGATACTGATATCTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATTTCGTAATATATTGA	1
M00764_NTNG1_MIP44	GCCCGGTGTCTGTTTCCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTAGCAAAGCGATGGC	1
M00764_NTNG1_MIP45	CAAGTTGTTAACGCCTAACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGTTATCGGATGT	1
M00764_NTNG1_MIP46	GCTTTTTCTTTGTCTTAGAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGATGGGACCTCA	1
M00764_NTNG1_MIP47	GTAAACTAGACAAAGATCGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGAATACGCACAATA	1
M00764_NTNG1_MIP48	CACATATGTATGTATGCGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCGTAACCCAAAGGGCAT	1
M00764_NTNG1_MIP49	GTTTGGGATTACATGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATGTATTTGTCAAGATT	1
M00764_NTNG1_MIP5	GGGGGAGCAAGCAATAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAATTTAGATAAGATAGGG	1
M00764_NTNG1_MIP50	GTGTAAATCTGAGTCTTACACAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCACAGAACGTCTC	1
M00764_NTNG1_MIP51	ATAAGTTGAATCTGCAGGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTGTGGAGACCCTC	1
M00764_NTNG1_MIP52	ACTTCTTTTCACACTCACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTCCAGATATCCTACT	1
M00764_NTNG1_MIP53	CCAAAGCAGCCCCAGAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGCTGTTGTGATGACT	1
M00764_NTNG1_MIP54	GTAGAAGCACCTGTCTCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTCTACAGCAGGCAGA	1
M00764_NTNG1_MIP55	GGCACGTGACTCCAGGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATGTCAAACAGGAGTAA	1
M00764_NTNG1_MIP56	CAAGAAATCAGTCAGGTGAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAATGCCAGGGCTGA	1
M00764_NTNG1_MIP57	GGTAATAATGGTGGGGATGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACAGAAGCAGCAGA	1
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M00764_NTNG1_MIP59	GGTGAGTAGTCCCAGCTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTTCTCTGGGCTCTGA	1
M00764_NTNG1_MIP6	GAGCATCGGAGCATTTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATAGTCTTTCTTTCTAA	1
M00764_NTNG1_MIP60	CATTTTTATTTGCCCTAACTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGGATTGCCCTATG	1
M00764_NTNG1_MIP61	GGCAGTCTGCCACTTGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTCTTTTGTTCTTCTT	1
M00764_NTNG1_MIP62	AAATGTGGAGGGATGTCTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGGTCTGGACGCC	1
M00764_NTNG1_MIP63	CAGACTGCTTAGATGCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTGGAGCAAAACCATT	1
M00764_NTNG1_MIP64	ATAGGGCTGCCATGTTCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTATTTGTTGTATACC	1
M00764_NTNG1_MIP65	CCAAGAAACTCAGAGATTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAAGAGTACTCAACA	1
M00764_NTNG1_MIP66	GTATCCAGCTGTCCGTAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTATGTCTGAGATCGC	1
M00764_NTNG1_MIP67	CAGAGTGTCTCACAGCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGGGGAAATATTTGTAG	1
M00764_NTNG1_MIP68	GACACACCCGTTCCCATTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCTGAGGATGAGGGA	1
M00764_NTNG1_MIP69	GAGGTCCTTTAGGTCTTTAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAAGGCATTCTGAG	1
M00764_NTNG1_MIP7	GGCTTCATTCCCCACCAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAGCCCTAGACTGGAA	1
M00764_NTNG1_MIP70	CGACTCAGGGAGTTACTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACCATGTTGAATCCC	1
M00764_NTNG1_MIP72	CAGTACCTTGATATATGGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCGATAATTACCTTC	1
M00764_NTNG1_MIP73	GTTGACTGCCATAATAGTGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCATCAACATCTTCA	1
M00764_NTNG1_MIP74	GTTCATAGGTATAAATGACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGTTAGGGATTTGAAA	1
M00764_NTNG1_MIP75	AAAAAATCCTCAATGTCATCGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTCATTCCCTTCT	1
M00764_NTNG1_MIP76	AAAAAAAAAAAAAAGAGATACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATTTCACTAGCCTA	1
M00764_NTNG1_MIP79	CAGACATCCCACTCACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTTAGAAACCCAAGAAA	1

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M00764_NTNG1_MIP80	CATTGTTCTTTAAACCCAAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAATGAGAACACTTG	1
M00764_NTNG1_MIP82	ACTGACTTGACTGCTATTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCAGATGAAATTGTC	1
M00764_NTNG1_MIP83	GCCTGAAGCTCCCGCAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATAGATTTGCAGGCCC	1
M00764_NTNG1_MIP84	ACAATGAACTCTTTGTCTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGATTCTGAGGGC	1
M00764_NTNG1_MIP85	AGATAAGTTGGTCTTGGTGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCCCACAGTCTGGAC	1
M00764_NTNG1_MIP87	AAGTTACTCACAGGTATTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGACTGAAACTTTCG	1
M00764_NTNG1_MIP88	ATGATACTTGACATCACAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTGTCTCATTCTTCT	1
M00764_NTNG1_MIP93	ACTCCATGAACATGGCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTCCTCAGATCTATTT	1
M00764_NTNG1_MIP94	GAAAACCAACACAAAAATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAAGGAATTGCACCTG	1
M00764_NTNG1_MIP95	GGATTTGGATGTCTGACATAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTAACCAGTGAGGG	1
M00764_NTNG1_MIP96	AATTTGTTTGTTGGTTGCTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCCCTTCCCTTGGT	1
M00764_NTNG1_MIP97	GTCTCTCTGGAGAGATAAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAATGCCTTGGGT	1
M00764_NTNG1_MIP98	CAGGCCTTCACAAAACATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTATATCAAACTCAAAGCT	1
M00764_NTNG1_MIP99	GTTAGTATGAATCCAAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCTCCTTCCTAAAAT	1
M00764_OLFML2B_MIP1	ACAAAAGTGCACTGGGGGATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGAGGAGCTCCTAG	1
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M00764_OLFML2B_MIP11	GTGAAGGCGCGATTGTAGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCACAGCAAAGTCCAC	1
M00764_OLFML2B_MIP12	CGCAACATCATCAAGTACGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGAAGCCTCCTGT	1
M00764_OLFML2B_MIP13	ACTTTCTAGCATCCTGTAGCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACCTGCAGGTGGG	1
M00764_OLFML2B_MIP14	GCAGAGCCAAGACACAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACCACATTCATGTATAT	1
M00764_OLFML2B_MIP15	CCTCTGTTTTTATCACAGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGATGAGCGGATTTA	1
M00764_OLFML2B_MIP16	CCTGGTGGAGAAGAGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTAGTAATAGTTGGTTAC	1
M00764_OLFML2B_MIP17	AGGTGCAAGGACACTCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAGGTTATACAGGGC	1
M00764_OLFML2B_MIP18	CCATCTTTGGCAACTTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGAGTCTGGACTCCTC	1
M00764_OLFML2B_MIP19	GGTGGAGGCTCAAGTGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATAGAATAGTTCTCCAGA	1
M00764_OLFML2B_MIP2	CAGCACCGATATGTCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAAGAAAGAAGTGCTAT	1
M00764_OLFML2B_MIP20	CATCTCCACAATGTTTGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTTCAAAGACCTAAG	1
M00764_OLFML2B_MIP21	GGATGACATGCTCTGTAAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACACCGTGTTCTGAG	1
M00764_OLFML2B_MIP22	GTGTAACCAGGAACTCGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTGGCTTTTCCTCATT	1
M00764_OLFML2B_MIP23	GGCCACACTTCTCATGCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGGACAGCAGGTGGG	1
M00764_OLFML2B_MIP24	AATAAGGAGCTGACTCTGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATTCATGTCCCTGAG	1
M00764_OLFML2B_MIP25	GTACAATGAACTTACCTATGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGGTCAAAGGCTT	1
M00764_OLFML2B_MIP26	GGCCTTGGTCTCCTGATCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCACAGTCAGAACAGA	1
M00764_OLFML2B_MIP27	GTGGGCCACAGTGGTGGCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCATCTTTCCCCAGCG	1
M00764_OLFML2B_MIP28	CAGTGTCTCCCAGGGAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAACACTCCAAACAACC	1
M00764_OLFML2B_MIP29	CATTCAGGTCGCTTGTCACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACTCCCTTGTGGGA	1
M00764_OLFML2B_MIP3	GGGGCTGAAGGCTTGAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTTTTTTCTCGCCA	1
M00764_OLFML2B_MIP30	CGTTCAGGTCGCTTGTCACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACTCCCTTGTGGGA	1
M00764_OLFML2B_MIP31	CCACAGCCCTCGACCTCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATCAGCTCCTGAGACA	1
M00764_OLFML2B_MIP32	ACCTACAGATGACAAGAGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACTGGTCATCAGGCC	1
M00764_OLFML2B_MIP33	GGGAGCCATACACCCCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTACTATAAAGCCAAGGT	1
M00764_OLFML2B_MIP34	GCTGTGACTTCACCACCTCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACTCACGCTGCTCT	1
M00764_OLFML2B_MIP35	GGCCTCCCAGCCCACTGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGCAGGAAGAAACCG	1
M00764_OLFML2B_MIP36	CAAGGCTGTGCTAATAACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTGATCTGCTGGGA	1
M00764_OLFML2B_MIP37	GCTATACCTCTGGGTGGGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGAACAATTGTATGG	1
M00764_OLFML2B_MIP38	CAGCCTCCAAGGGCCTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATTCGAACCGAGATGAA	1
M00764_OLFML2B_MIP39	GTTTTTAGACACTTCCTGAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGGGCTGAGCGGA	1
M00764_OLFML2B_MIP4	AAGGTTTCTTCATCTGGGTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTATGTGCTGGTCTC	1
M00764_OLFML2B_MIP40	GAACAAATCAAAGAGGACATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGTTGTGTCTGTGTG	1
M00764_OLFML2B_MIP41	CAGGTCTCCTGGCAGTATTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACAAGCAGGAGGCA	1
M00764_OLFML2B_MIP42	GCTGGGCACACTCTCTAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAGACTTGTCAATGTT	1
M00764_OLFML2B_MIP43	GCATCCCATACATCTGAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTACCATAGCTTTTCTAT	1
M00764_OLFML2B_MIP44	CAAAGGACAGAAAAAGAACCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCACCTCTTCCAAA	1
M00764_OLFML2B_MIP47	GTAAATTTTCAGCTAGCACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTCCTGAAGCTACAT	1
M00764_OLFML2B_MIP48	AGGGCAGAGTTTCCTTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGTTTGGTGGTGACTG	1
M00764_OLFML2B_MIP49	GATCAAGGTTGATGTCCTAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACCTGGTATGGGGC	1
M00764_OLFML2B_MIP5	CACATACCCACCTACACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATATAAACTGGGGAGGA	1
M00764_OLFML2B_MIP50	ACAGGCACACTTGCACGACGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGTGCCCTCTCGTC	1
M00764_OLFML2B_MIP51	GCACCCCCATCGGCCCTCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAGTGTGTGGTGAG	1
M00764_OLFML2B_MIP52	GACACACAGAAAACGGGTTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTCCTGGAGGCCC	1
M00764_OLFML2B_MIP53	GTTGCTGGGGGACTATGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGTGGTTCAGAGTTT	1
M00764_OLFML2B_MIP55	CCTCAGCCCCTTCAGAGAATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCTGCGCATCTGGG	1
M00764_OLFML2B_MIP6	GCAAATGTAAAATGACAATTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACACCCTTGTCCC	1
M00764_OLFML2B_MIP63	GCTCCAAGGCTGAGCTAGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTTTACTTTCTTCTC	1
M00764_OLFML2B_MIP64	CCAAGAATGGTCGAACCCCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAACGCCTGGGAACA	1
M00764_OLFML2B_MIP65	GCTTTAGAACCTAGTAATACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTAGCACACCTGGG	1
M00764_OLFML2B_MIP66	CGCTAAGTTCAAAGCTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACAGTCATTCCCCTAAC	1
M00764_OLFML2B_MIP67	GGACAAATCTCCGGGTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTGTGTAAACGTTGAA	1
M00764_OLFML2B_MIP68	AACCAGGAAGACAGGAAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATCTTCACTGTAGGTT	1
M00764_OLFML2B_MIP69	GCACCCTTGGGAAATTCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGGACAACCTTTTAT	1
M00764_OLFML2B_MIP7	ATACTCATTCTCGAACAGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGCTTCTGCTTGT	1
M00764_OLFML2B_MIP70	CGAGTGACAGTTGTCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACTATTACTTATATGCG	1

continued table…

ID	**MIP**	***c***
M00764_OLFML2B_MIP71	GGTTTGTGGGGACATCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGTAATAAACTAAGGAA	1
M00764_OLFML2B_MIP72	CATTGAATTTTTGTCCATAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCAAACAAACAATC	1
M00764_OLFML2B_MIP8	CCTATACGACCCAGATAGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTCGTCATCTGTGGG	1
M00764_OLFML2B_MIP9	ATGACCTCCTGGCTGAAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGCTATCCACGGCATA	1
M00764_OSBP_MIP1	AAGGAGAACTGGTCCAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTCAGTTTTTTTGCCT	1
M00764_OSBP_MIP10	CAAAGTCCCTGTTTAGTAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCCACACTCTTCCTG	1
M00764_OSBP_MIP11	CCATGGTTTGTATCATGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTCCCTGAGACTCTT	1
M00764_OSBP_MIP12	CATTATTCCAGAGGTGGCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAACACGTGTCCAAG	1
M00764_OSBP_MIP14	GAAAGACAATGAAGGATGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGAAAACTTTTGTTCC	1
M00764_OSBP_MIP15	GGCTTCTCTTCTTCTGGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCTCACAAAGGGGTT	1
M00764_OSBP_MIP16	AACTTCCAAGAATGTAACTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGAGGAAGTCCATA	1
M00764_OSBP_MIP17	ACACCCCTCTGTTGTTCTCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTCGGTTTAATGGA	1
M00764_OSBP_MIP18	AACTTCTAAATTCGGCTCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCTCCGCGTGGACA	1
M00764_OSBP_MIP19	CATAAGACTTACCAATGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACAATGTCACTCACC	1
M00764_OSBP_MIP20	ACCTCTCCCTTACAGACATAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTGGCTGAGCAGGA	1
M00764_OSBP_MIP21	GTGGCCGAAGGTTAGTGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTGACCAATCATTTT	1
M00764_OSBP_MIP22	CCTCTTTTTTGTTACTGCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCCTTCTGGTGATTG	1
M00764_OSBP_MIP23	GCATATAATGGAGAAGAGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGAAGAAGGACCCTG	1
M00764_OSBP_MIP25	GATGCATGGAGAATGCCAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGATGAAGCAAATG	1
M00764_OSBP_MIP26	AGAAGTAGTACATGTTTTCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCGCTGCTTCTCC	1
M00764_OSBP_MIP27	GACTCTCAATGCTTGGGAAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTTGGCAGTGTACT	1
M00764_OSBP_MIP28	CCCAATGACTGGCTGTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGTCAAGGTCAAAGT	1
M00764_OSBP_MIP29	AAATGGGGGTGATGCTCGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGCCCTGTTCTCCAC	1
M00764_OSBP_MIP3	GAATCTTTCAGGTGGAATAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTTTGGATAGAGTG	1
M00764_OSBP_MIP30	AGTCCTAGGATAAATAATGGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTCCCCAGAAGAGC	1
M00764_OSBP_MIP31	AAGCATACTCCTTTAGGACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGAATCACAAGACAG	1
M00764_OSBP_MIP32	GCCAAACCCATGGTTCATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGAGAAGTAGCTATAAG	1
M00764_OSBP_MIP33	ATTTTTTCATTTTACAGTCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCATTCCCAAGGCTA	1
M00764_OSBP_MIP34	ATTCATCAGTTTCTCCTAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCAAGTTGTGGATA	1
M00764_OSBP_MIP35	GAGGTATCCAAATTAAGCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTTTCCTCACCTGAT	1
M00764_OSBP_MIP36	GCTTCCAGGTACCATTCATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCTTTTTGATTTATT	1
M00764_OSBP_MIP37	ATAGTGCAATCTCAGCTCACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCCATTCCCAGGAC	1
M00764_OSBP_MIP38	ATAGTGCAATCTCAGCTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATTCCATTCCCAGGAC	1
M00764_OSBP_MIP40	CATAAATGATACCTAACCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGAGCTCAGACAAT	1
M00764_OSBP_MIP41	AAAGATCTTACTTGGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATTGCAAGGTTAGGTT	1
M00764_OSBP_MIP42	CCTGACTGCCAAAGTAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAATTCAGCCATTACAT	1
M00764_OSBP_MIP43	GTTTCTTAGCTAATCCTTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTATTTAGAACACAA	1
M00764_OSBP_MIP44	GCCTCCACACTCATTTGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTAAGAGACAGAATT	1
M00764_OSBP_MIP45	GAAACTCTTTAAGGACCCATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCACGATGGAGGA	1
M00764_OSBP_MIP46	GATTTTGATTTCCTGACGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACTCTTTAGCCAGTG	1
M00764_OSBP_MIP47	CCAGCAAGTTTCGAGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCTTTTTCTTCTCCTTT	1
M00764_OSBP_MIP48	GTCTCCAACGCTGACGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATCAGGTTCAAATTAA	1
M00764_OSBP_MIP49	GGAGGTTCTGGGATTCACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACGCATTTCCTTTCTGA	1
M00764_OSBP_MIP5	AATTTCCTCCTAAGAACCTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCAAAGGAAGCCA	1
M00764_OSBP_MIP50	GAATGGCTTACTGGTGCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAAAAATCATCTCTTTC	1
M00764_OSBP_MIP51	ACCCACTGCTTGGGGAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATCTGGAATACCATGAG	1
M00764_OSBP_MIP52	GTTTACCTGTAAGGAGAAGAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACGGTGAAAGCTG	1
M00764_OSBP_MIP53	GAGCCCTTGTCCATGCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGCTCTACTGAGCAAAGC	1
M00764_OSBP_MIP54	GGGAAGAGTGCTGATATGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAACTATAGCCTCA	1
M00764_OSBP_MIP55	CAAAGAACAGAAAACCTGGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTCTTCATGATGCTC	1
M00764_OSBP_MIP56	GGGTGGTTGAATGGCTTTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACGTGGGTTGTGAT	1
M00764_OSBP_MIP57	ACTGATATTGCTGCCAGTACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCAGTTTCTCTTAGCA	1
M00764_OSBP_MIP58	CATCAGCCTTGATGAACAGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACTTGGCATTCTGC	1
M00764_OSBP_MIP59	GTTTACGTAAAAAAGCTGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAACTAGAGTGTGGTC	1
M00764_OSBP_MIP6	GAAGGCACCTCAATTTGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTACCCAGTAAAACCAA	1
M00764_OSBP_MIP62	ATACCACCATATTGATGGTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACAAAGAGATCTT	1
M00764_OSBP_MIP63	GGTTAAAAACATTTCAGTGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACCTGAGATCATCA	1
M00764_OSBP_MIP64	GTTGACTTTGGTTATCTTTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTGTGGCCCAAATT	1
M00764_OSBP_MIP65	AATGGGGCTTTTCTTCTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGGAATTGGAACCCA	1
M00764_OSBP_MIP66	AGAGCTAAGTGTCTTACCTTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGGAAAATCCAGA	1
M00764_OSBP_MIP67	AGGTAGCCTGGTCTAAGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAAGAAACCCTCGAG	1
M00764_OSBP_MIP68	GCAGGCCTGTATGGAGAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCAGGTGATTATGCT	1
M00764_OSBP_MIP69	CCTCATGTTAGCCCAGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCATTGTAATTTGCCAGT	1
M00764_OSBP_MIP7	GTTTTTGTTCCTTAACTGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTCCTTCTCTGTTTG	1
M00764_OSBP_MIP70	CCAGAAAAAAAGTAAATATGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTTCTGCAAGCCC	1
M00764_OSBP_MIP71	ATTTCAGCGTGGAGCTAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTTTTGATGTTGTCAC	1
M00764_OSBP_MIP72	CAACAAATTCTTGACTAAACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAAGTGAGCAGTAAA	1
M00764_OSBP_MIP73	AAGCAGTTATCCTGTGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCTTAGTGACCAAAA	1
M00764_OSBP_MIP74	AGGTTTAGAGAAAAAACCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAACTCATTTGGTTT	1
M00764_OSBP_MIP75	GATTTTTCAAGTAGGCTTCTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCGTATTATGAAGG	1
M00764_OSBP_MIP76	GATTTCTGGCACAGTCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTTATGAACATAAAGAG	1
M00764_OSBP_MIP77	GTGAGCAGTTCAGTGTGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAACTGTAGTCCCAACTG	1
M00764_OSBP_MIP78	GTTGATCATGGCATTGGATGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTTGACCAGTGAA	1

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ID	MIP	*c*
M00764_OSBP_MIP79	GCAGATGGTGTCTGTGTTGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGCAGCGTTCTCT	1
M00764_OSBP_MIP8	ATTCAGCCTATGCGCCGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAACAAGACAACAAAAA	1
M00764_OSBP_MIP80	GTTTGTGAGACAGACTCTTCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACTCCAGCTCACT	1
M00764_OSBP_MIP81	GACAAGACTGAGCTGCAGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGAATGTTGGTTTGT	1
M00764_OSBP_MIP82	GTGTTCTTTGTTCCTGACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGAAATACTGCATG	1
M00764_OSBP_MIP83	GCCTGGGGAACTTTCTTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGCTCAGACCTACCA	1
M00764_OSBP_MIP84	ATTTCTGCCTTTGATCTGTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTCAACTTCTGAACT	1
M00764_OSBP_MIP85	AGACATACCTGCCGTGGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTCCTAAGACTGTCAT	1
M00764_OSBP_MIP86	CCAGCTCCGGCATTACCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGGACCAATTATATCA	1
M00764_OSBP_MIP9	GATGTGGGGCTTAAAGCACCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCTCTTTCCTGCCTC	1
M00764_OSBP_MIP92	GCCCGAGAGAAATGCCAATATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGGAAACTTCAGGAA	1
M00764_OSBP_MIP93	CGCCATTCATTTCAGTTTATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTTCAGATAAAGGCC	1
M00764_OSBP_MIP94	CAGCCAATCGGCGATCAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTAGAAAAGGTGGAGC	1
M00764_OSBP_MIP95	GTGGAGAGGCGGGGCAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTGGTGGTTGGTATCAG	1
M00764_OSBP_MIP96	AAGAAAATAAGGATGTAAAGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTCCTCATTAGGTC	1
M00764_OSBP_MIP97	GCCTCTTAAAAGCGTTTTTTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGACCAGTGAGAG	1
M00764_OSBP_MIP98	CACCTCCCACCAACTTGCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACTGCCGAGAGTTA	1
M00764_OSGIN1_MIP12	ATCCTCCAAATTCAGGCGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGGTCTTTGCAGGCT	1
M00764_OSGIN1_MIP13	GAGCAACTCAGCAATTCTGTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGCCAGCCCCCTC	1
M00764_OSGIN1_MIP14	GAAAGCTTGACTAAGACAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGACCTTGTTCTAGAA	1
M00764_OSGIN1_MIP18	GTGGTTTTGAATGTGTAAACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAACATGAGGGCAG	1
M00764_OSGIN1_MIP23	GGAAGCCACAGCCCAGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGTATGTATTCTGGTG	1
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M00764_OSGIN1_MIP25	ACTGGACGGGGTTTCGCCACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCTAAGGCAGCTTG	1
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M00764_OSGIN1_MIP30	CACGGGGAGGGAGGAGGCGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCGGCCAAGTTGTGC	1
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M00764_OSGIN1_MIP33	CCAAGACCACGGCCATGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTAGTGGCCATTTAC	1
M00764_OSGIN1_MIP34	AATGCCGCACACTTGAAAGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCCACCTCCTGGGG	1
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M00764_OSGIN1_MIP36	ACTAAAAAGCACAAAAGGAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGTTTGCCTTTGTG	1
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M00764_OSGIN1_MIP38	CGGAGTTGGAAGATTCAATTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACAGGACGCCCCA	1
M00764_OSGIN1_MIP4	CCTCGGTTTCCCCATCTGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTCACTGAAAGCCT	1
M00764_OSGIN1_MIP40	AAGTGGGCGGGCACAGGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAACTTCTCAGTGTCA	1
M00764_OSGIN1_MIP41	AAGCATGTCAAATACCCGGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTTCAAAGCCAGCTG	1
M00764_OSGIN1_MIP42	GCAGCCCTGGCCATATTAATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACATGCTGCCATCCT	1
M00764_OSGIN1_MIP43	CAGCTCTAGGACCAGCACTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCTGTGCCCACAAG	1
M00764_OSGIN1_MIP44	CATCAGACCTACCTTCTTCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCCAGGTTTGGGGA	1
M00764_OSGIN1_MIP46	GGAGCTGGGATGGACTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCTGTAAAATGGAAGCA	1
M00764_OSGIN1_MIP47	CACCAGGCCACACTGGGACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTACTGTGTCCCTCAA	1
M00764_OSGIN1_MIP5	CAATGTCCCAGTAGCAAAGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTCCTGGGACAGAG	1
M00764_OSGIN1_MIP50	GGGACACTACTGTGGAGGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGGGTGGATGGCAT	1
M00764_OSGIN1_MIP52	GACCCACCTGGTCCAGGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTTTGTGGACTCTCGA	1
M00764_OSGIN1_MIP53	GAGCCTGAGGCTGGGCAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAAGGGCATCAAAGAGC	1
M00764_OSGIN1_MIP56	GGGCTGGGTAGAGGGAGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCATCCACTGGCCTTG	1
M00764_OSGIN1_MIP57	CCTGTGAACCCAGAAAATCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGGCTCCATGGTGAT	1
M00764_OSGIN1_MIP58	GTTCCGGGGCGGCCTCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGTCATTAGGACTTCCT	1
M00764_OSGIN1_MIP6	GACACACACGTGGCTCTCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACTGAGTCACTGCACT	1
M00764_OSGIN1_MIP66	GGCGACAGGATGGACTGCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGACCAGCACCAGGGA	1
M00764_OSGIN1_MIP72	GTTACCACCTCAGACACTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGCTTTATTTGGGAC	1
M00764_OSGIN1_MIP73	GATTGTGGGAGGAGTCCTGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGCCTTCCAGAAGCA	1
M00764_PCDHB5_MIP1	GCTTCTTCTCCTCAATATTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTGGTTACCACCC	1
M00764_PCDHB5_MIP10	CATTACAAAGGAAACAAAGAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGCTGGCTCTGA	1
M00764_PCDHB5_MIP11	CGAGTGGCCAGTTCCCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGCAATATACAGGGTTC	1
M00764_PCDHB5_MIP12	GAAATGCTCCTAAAAATCCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGTGCGGGGCGAC	1
M00764_PCDHB5_MIP13	CATTTATATCTGTGAGCTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAGTTCTGAACAGTG	1
M00764_PCDHB5_MIP14	CAGAGCTGGTGCTGGACAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGACTGTGTTTCCCTTA	1
M00764_PCDHB5_MIP15	GTATTTTCTGCCATCTCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCCAAGACGACAATGC	1
M00764_PCDHB5_MIP16	CCCCTTAACTCCTTAGTTGTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCACTGGACGGTGG	1
M00764_PCDHB5_MIP17	GTTCTCGGGCACCTGTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGTTTTCTCGTCTATTA	1
M00764_PCDHB5_MIP18	AATGCACTGTGGCTATAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGTTACTCAACCATTT	1
M00764_PCDHB5_MIP19	CCTGAAAGGCCCCCACCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGAAACACTGAAAAC	1
M00764_PCDHB5_MIP2	CCTATGATTTGTGCCATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTTATCTTTTGGGGA	1
M00764_PCDHB5_MIP20	GTGACACAGAGAACACTGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGAAACTGTAGTTGC	1
M00764_PCDHB5_MIP21	AAAAGAAAGGGGAGATCATTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTCGGTTTTCAG	1
M00764_PCDHB5_MIP22	CCCTGCACATCGGCAGTGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGACATGGGGACACCC	1
M00764_PCDHB5_MIP23	AGGGTGTAGGAGGTTTGGGTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGCGCAGGTGTGG	1
M00764_PCDHB5_MIP3	GCAAAGTGAACACACTCCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATATTAAATAAGTGATCA	1
M00764_PCDHB5_MIP37	GCTGGTGAAGAAATAGGGAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGACGTGAGCGG	1
M00764_PCDHB5_MIP38	GGAATAATCGGCTTCAGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCTGAAAAAGTTTGGG	1
M00764_PCDHB5_MIP39	GTCTGTTGAACTTCATGCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGATCTCGTGATGA	1

continued table…

ID	MIP	*c*
M00764_PCDHB5_MIP4	GTTTTTTTCTCAAAAGTATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTTCTTAAACTTTA	1
M00764_PCDHB5_MIP40	AAGCTCAATCTCAAGGTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAGGAAAATCAACAGC	1
M00764_PCDHB5_MIP41	CATTCTATTTCATCACACTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTGTCATTCCAAA	1
M00764_PCDHB5_MIP5	AAGTACCCTTGAGTACACAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATAAGCTCTCCCGA	1
M00764_PCDHB5_MIP6	GCTAAGAGTGTGGATAGTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAAGAGCTGGAGATAC	1
M00764_PCDHB5_MIP7	GCCACCAGGCGTCCTAATTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCCCACCCTGAAGAT	1
M00764_PCDHB5_MIP8	GGACCGGGTCTGAACAATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAAGATCTAGTGGCTA	1
M00764_PCDHB5_MIP9	GAAGGCGCAGTTTAACTCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCTGGTATGGAATAC	1
M00764_PDE11A_MIP1	AGCATCCAAATACCTACAGTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAAGCCTGCTTT	1
M00764_PDE11A_MIP10	GTCTTCAGCTAGTAATTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAGTGAAGAATAATAG	1
M00764_PDE11A_MIP100	GCTTGCCTAATCTTTTCTGGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGTGTGGGAACC	1
M00764_PDE11A_MIP101	GACACTTTGAAGGGTGAGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTGGGTCCAAACCT	1
M00764_PDE11A_MIP102	AAATTGAGATAAGGTGCACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGTGGAAAGAGCC	1
M00764_PDE11A_MIP103	CACTACAAAGCTGGAAACTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTCCAGTTAGTCCAA	1
M00764_PDE11A_MIP104	GGAATGCAATGGTGCGATCTTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTATTTGGTCACAT	1
M00764_PDE11A_MIP105	GAATGAAACTCCATCTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATGGTGGCAGGCACCTGTA	1
M00764_PDE11A_MIP106	CCCAATTACTCAGGAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTCTGGGAGGCCGAGGTGA	1
M00764_PDE11A_MIP107	CTGAGGTCAGGAGTTCAAGATCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCTATCTCCTGAG	1
M00764_PDE11A_MIP108	CAAGAAGGATTTTTTTCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGTAATTTTTATACCT	1
M00764_PDE11A_MIP109	CCCTGTGCACCTCCCAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAGATCATGTAATAAAT	1
M00764_PDE11A_MIP11	GCAGAATAACAATTTCAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTCTATATGTTTT	1
M00764_PDE11A_MIP110	ACAGGACTGGCAGAGACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTATACAAAATTTGCCTAG	1
M00764_PDE11A_MIP112	GGAAAAAGCAAGTTGCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATTTTCATCTTCCAGG	1
M00764_PDE11A_MIP113	CCTTGTACATGTTTCCTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCTTCATACTGATGT	1
M00764_PDE11A_MIP114	GGTTCATAGCTGCATTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTATAACTATAATGAAAATTCA	1
M00764_PDE11A_MIP115	AGTGACTTGTTCAAGGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGACTTCTTTTCTATGT	1
M00764_PDE11A_MIP116	CACCTTCCTTCACCTTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGATTTCAATTAACACA	1
M00764_PDE11A_MIP117	CATAAACCTTTGGGCCAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCATTTCCACCTTTCC	1
M00764_PDE11A_MIP118	CAGAGGGCAGAACCGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTTGGTACAGCAGCCT	1
M00764_PDE11A_MIP119	GTGCCAGGTTGGTGGTTCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCTCATGCTATGTA	1
M00764_PDE11A_MIP12	GGTTAAGTCTGACTACAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAAAAACTCTGGCAA	1
M00764_PDE11A_MIP120	GATGATGGAAAGAACCCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGAATTTCACATTGT	1
M00764_PDE11A_MIP121	AATGCCAATACCTACTCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGAGAAACAACAACA	1
M00764_PDE11A_MIP122	CCATCCTGTAACTAATCTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGCTAACCTGTCCT	1
M00764_PDE11A_MIP123	ATCTGTGGTTGTTGATTACATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGTGAGGTCTGTTGC	1
M00764_PDE11A_MIP124	GGCCTGTACCTCACTTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTAAGGCCCATTAAGTTG	1
M00764_PDE11A_MIP125	GATGTTCTGCTTCTCCCCTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCACTCACCCTCTG	1
M00764_PDE11A_MIP126	ACTGCTTTTGTAGTCCATTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCACTCCTGAAAGAG	1
M00764_PDE11A_MIP127	GTTTAGAACACTTACTTAGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCCCCATGACATGC	1
M00764_PDE11A_MIP128	ACGAATGCTAAAGAGTAAAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTGATTGTGGGATG	1
M00764_PDE11A_MIP129	ATAAGGTTAGGTGCTGAGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCGAGGTCATGACACA	1
M00764_PDE11A_MIP130	ATTTCTCATTCGTAGGAACTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGTGGCTTTTGACAG	1
M00764_PDE11A_MIP131	GCAGTTGTAAGTGATTCTAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCGCGAACATCAGCTG	1
M00764_PDE11A_MIP132	GCAGTTGTAAGTGATTCTAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGCGAACATCAGCTG	1
M00764_PDE11A_MIP133	GGTGCCTTATATCTGAGTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGTTGTGGTATAGA	1
M00764_PDE11A_MIP134	CCAAGCAGTTCACCTGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATTCATTTCGATGACT	1
M00764_PDE11A_MIP135	CCAAGCAGTTCACCTGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATTCATTTTGATGACT	1
M00764_PDE11A_MIP136	CAAGTTCACCAGCTTTCCCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCGGAGAGCAGCTGT	1
M00764_PDE11A_MIP137	GCTCTGTCACATGCCTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTTTCTTCTGAATCA	1
M00764_PDE11A_MIP138	GCTCCGTCACATGCCTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTTTCTTCTGAATCA	1
M00764_PDE11A_MIP139	GGACTTTAATGTATGACAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATGGTATGATAGCAC	1
M00764_PDE11A_MIP14	CAAAAAGGATTCATTAAAGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGTTTCATCTCCAG	1
M00764_PDE11A_MIP140	GCTTTTGGTTTTACAGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTGCCCATTGATTTAA	1
M00764_PDE11A_MIP141	CCTTTACCTTGGCTCTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATACATTTCCAAGGGTG	1
M00764_PDE11A_MIP142	CCTGTTTTCTACACCGGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGGGCCATGTTGTACA	1
M00764_PDE11A_MIP143	GTTTGTATGCTGTCAGTTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTCTTTCCTAGGCT	1
M00764_PDE11A_MIP144	GTTTGTATGCTGTCAGCTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTCTTTCCTAGGCT	1
M00764_PDE11A_MIP145	ACACAGAGGTAGGCCTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCACAAAAGATGACAA	1
M00764_PDE11A_MIP146	GTTTAACACTTGAGCCACTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTTGTCTTTCAAAT	1
M00764_PDE11A_MIP147	GACTTGATGGGAAACCTTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGTGCAGTTCCTTA	1
M00764_PDE11A_MIP148	CAGATCTTATGTGAAAACCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACACATAAAAAAGA	1
M00764_PDE11A_MIP149	GTGTCCCTATTTGGAATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGAATATCTGTTATGAA	1
M00764_PDE11A_MIP15	GCAGATTCTGTTTAATTACCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTCCCACTGGAAG	1
M00764_PDE11A_MIP150	AGGGGCTCCTCTTACCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGTCAACAGTAGGCAAT	1
M00764_PDE11A_MIP151	GTTTCAGTTGTCGCACTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACTGGCTAATAAATAAC	1
M00764_PDE11A_MIP152	AGAAAAGAGAGAAACGTAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCACTGATGTTCACTG	1
M00764_PDE11A_MIP153	GGTGCTCTGATAGTTTCAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTATTGTTCTGTGA	1
M00764_PDE11A_MIP154	CCTACCTGTTCTCAGCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATACAGAAGAGTCACG	1
M00764_PDE11A_MIP156	CAAGCCATGCATGTCAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAAAGGTAGATAAAGAT	1
M00764_PDE11A_MIP157	GTGGATTGCCTCTCTCAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAGTGGTATCAAGCC	1
M00764_PDE11A_MIP158	ACCTGTGGAACTTGGAGAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCACAGACAAACATC	1
M00764_PDE11A_MIP159	GGGCATGCACATGCACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATATCGAAGTAAGGCTAA	1
M00764_PDE11A_MIP16	GACTCTTAGAAATTGCAGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAATCCAGTTGCTT	1

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ID	**MIP**	***c***
M00764_PDE11A_MIP160	CAAACTCTCATACTTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTTACATTTGTATCTAC	1
M00764_PDE11A_MIP161	GCCAAGCAGGTGATGAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAAATTTAAAGCCAAA	1
M00764_PDE11A_MIP162	ACTAGGTAGTCTAACATCAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTGCAACTTGTGT	1
M00764_PDE11A_MIP163	GCAGTCTCCTGTGCTGGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTAGCACTGAAACACA	1
M00764_PDE11A_MIP164	GTTGAAGACTGTGTGAATGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGACTGACCTGGAGAA	1
M00764_PDE11A_MIP166	AGGTGGTTAATGACCTCTTTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAGCTACACAAAAA	1
M00764_PDE11A_MIP167	CACTCTGTTGTCCAGACTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTGAGGAAAAGCTGCT	1
M00764_PDE11A_MIP168	GAGAGGTGAATGCTAATTAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAAAGCACATGGA	1
M00764_PDE11A_MIP169	ACCAAGAACCTGTTTCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAGACTAAATGTAAA	1
M00764_PDE11A_MIP17	AATGCATAGACATCTCAGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTGATACACAGAA	1
M00764_PDE11A_MIP170	GGTTTCTGTAAGTCATTATGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGTATCTTCCATTT	1
M00764_PDE11A_MIP171	CCTGATTGTAATACTTTATTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATATGGCGATTCCA	1
M00764_PDE11A_MIP172	GGGATGTATCAATGTTCTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAACTTTGAAAAATAT	1
M00764_PDE11A_MIP173	CAACAGATTATGAGGGCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATTGAATACAGAGAGT	1
M00764_PDE11A_MIP174	ACTTTATGTCTTCATAGATGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCACATGCCTTAA	1
M00764_PDE11A_MIP175	CAGGGATTTCAGCTTGATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTGTGATATACCTGGA	1
M00764_PDE11A_MIP176	CCATATACATATGGTATATGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCAGAAGGCTGCCA	1
M00764_PDE11A_MIP177	AATGTACGAAGTCAGAAACTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCATCCCAGTTCA	1
M00764_PDE11A_MIP178	ACTCAAAAGTATCTACAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGCATCAAGATGTTG	1
M00764_PDE11A_MIP179	GTTCCCAATCCCTTTTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTCTTTTTCCCTTCCA	1
M00764_PDE11A_MIP180	CCATCTGACTTACTTTTTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATCTGACAGACAGGA	1
M00764_PDE11A_MIP181	CCTACACTCAAAGCCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGCTAATTTTACCTGTTA	1
M00764_PDE11A_MIP182	CCTGTAAGCAATAGGAAGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACATGGGCATGGATA	1
M00764_PDE11A_MIP183	GCATCTGTCAGACTCTACTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTTCTCCCTCTACAT	1
M00764_PDE11A_MIP184	CAAAGTAGGCAAGAAGGTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGCCATTTCTTTGGT	1
M00764_PDE11A_MIP186	GCTCTGCTGCCAAGGCTGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTTATAGCTCTAATGC	1
M00764_PDE11A_MIP188	ACCTGAAACTCCTAGGCTCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCTAGCCCTACCCC	1
M00764_PDE11A_MIP189	GGCCTTCGGGTCCTCAGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAAGAGGAGATCTC	1
M00764_PDE11A_MIP19	GGTGGTTCATATCTCTAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCAATTTTAACTTCTC	1
M00764_PDE11A_MIP190	GGCCTTCAGGTCCTCAGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAAGAGGAGATCTC	1
M00764_PDE11A_MIP191	GGTCAGGGCATTCCTGGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCTTCACTGGTCTTTCT	1
M00764_PDE11A_MIP192	GAAGGCAGTAGGGAGTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGCTATTGTTTGGTTT	1
M00764_PDE11A_MIP193	GCATTTGAAATATATTCTCTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGACCCTGACCCA	1
M00764_PDE11A_MIP194	GTTTGACTAGCTGTCATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAGGAAGTATTTGCTAA	1
M00764_PDE11A_MIP195	AGATTATAAGAGAACAAAACTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACTTGTCGTACT	1
M00764_PDE11A_MIP196	ACAAAATCGGTGCTGGATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAATGGAAGAGTTTCAC	1
M00764_PDE11A_MIP197	ACCTTTGCTGACAATATATCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACACTCCAGGATACCAG	1
M00764_PDE11A_MIP198	ATTGATTGCTATTCTCCTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGTGATGGTGAGA	1
M00764_PDE11A_MIP199	GCATTAACTGCATGTGCATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGGGCCACACCAATA	1
M00764_PDE11A_MIP2	AGCATCCAAATACCTACAGTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAAGCCCGCTTT	1
M00764_PDE11A_MIP20	CACCCACCTTATATGTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCTAAATTTTGTATTGT	1
M00764_PDE11A_MIP200	CAATGATGAAATCGACAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAAATTCATGGGGCT	1
M00764_PDE11A_MIP201	GGCTTGGGAGATAAGCCTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAAATGAGGTGCAGGT	1
M00764_PDE11A_MIP202	CACCAGGAAAAGAGAGCAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATACCTTTGCCCCAGG	1
M00764_PDE11A_MIP203	CAGCTGCTGGCAAGAAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGTTCTTTCTGGAATTG	1
M00764_PDE11A_MIP204	AATATGGGCTGTGGTGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATTGGAGATATCTTTGA	1
M00764_PDE11A_MIP205	GCTGCTGGAATCGAGAGTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACGTGAACAGGACCT	1
M00764_PDE11A_MIP206	GACTCAAGGGAACCCCACCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTCACCTGTTCATCG	1
M00764_PDE11A_MIP207	GAGAGCTTCTCAGAAAGAGCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTGGTGGTGGCACTG	1
M00764_PDE11A_MIP208	GCAGCCACTTTTCAACCATCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGAGCCATTTGGT	1
M00764_PDE11A_MIP209	CCCTCTTTGGCTGGTACCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGTGGAAACTTTCCT	1
M00764_PDE11A_MIP21	GTCAAGGCTGCAGTGGCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCAGTGTGGTCAGCATA	1
M00764_PDE11A_MIP210	CTGTTCCTGCACATGTTCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTCTGGGTGCCTGTC	1
M00764_PDE11A_MIP211	GGGGCAGGAAAACATTTGGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCACTCTGAGCCAGA	1
M00764_PDE11A_MIP213	CAGCTCAGTGCTGGGCACCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGCCCTACCTCCCTG	1
M00764_PDE11A_MIP214	CAGGCGGTTCCTGGAAGAGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGTGGACCGCTGTG	1
M00764_PDE11A_MIP215	GGCTCCCTCCTCTTCTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGTTTCCCTCTTCTAA	1
M00764_PDE11A_MIP216	GGGAGCCCAGTGGGAGTCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCCTGATTGGAACACG	1
M00764_PDE11A_MIP217	GGTGAGTAGGGAGGGTTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAACGACACTCTCGATT	1
M00764_PDE11A_MIP218	GCCTTGTGGGTGCTCAGTAAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGCGGACTCCGAG	1
M00764_PDE11A_MIP219	CCCAGAGATTTGGACCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAATCATATGCTTTATTC	1
M00764_PDE11A_MIP22	GTGATCTTTCCTGCCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAGATGTAGTCATCAAT	1
M00764_PDE11A_MIP220	AAAACAGGAAAAGCACCAGGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAGCAACATGGG	1
M00764_PDE11A_MIP221	AAAAAGAATTCCATCATTTTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCACTGAGCACATT	1
M00764_PDE11A_MIP222	AAAGAGCACCTCACGCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAATGAAACACTTTTTAA	1
M00764_PDE11A_MIP224	CAGTAGCTGTGGATAGCTCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCCAATGGCAAGCC	1
M00764_PDE11A_MIP225	CGCAGAGCCAAGCACTGCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAATTACTTAAAAT	1
M00764_PDE11A_MIP227	GTAGATCACAGGACAAAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAATGGTAGTCTCCT	1
M00764_PDE11A_MIP228	CATATACAACAATCTGAAAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATGCAAACTCAAG	1
M00764_PDE11A_MIP23	AAGATGACTGCTTTAGGTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTTTTTTTAAATTG	1
M00764_PDE11A_MIP25	GTCTGCTATGCACTGAATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACGTCTTGGTCCTTTG	1
M00764_PDE11A_MIP26	GGCCACCAGCTGAACCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTACTAGTCACTATGTAG	1
M00764_PDE11A_MIP27	AACAATTAATGCCAAGAGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGTCCCTACCCACC	1

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ID	**MIP**	***c***
M00764_PDE11A_MIP28	AAATAACTTCATCCTACTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTCCCAGTCCTTATT	1
M00764_PDE11A_MIP29	CATATGCCTCACATTCTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCAGTTTGAGTTTTT	1
M00764_PDE11A_MIP3	CAATGAAACATCAGTCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGAGCTTTAGTTAAA	1
M00764_PDE11A_MIP30	GTTATCCATATAATCTGCTTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGAAGGTAGCAGC	1
M00764_PDE11A_MIP31	AAATAGATGGAGGCAATTACAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTGGCACCAGGA	1
M00764_PDE11A_MIP32	CAAGATTTAGAAACTGCTGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGTTCAACACCA	1
M00764_PDE11A_MIP33	GCTTGTAGGGTTTATGCTATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCACTGTATGGCAG	1
M00764_PDE11A_MIP34	GTTGAGTTTTCCTCTCATTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTGGACCCAGGG	1
M00764_PDE11A_MIP35	GTGGGCTCATCTCTGCCTCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCAGTCTCTGTCAG	1
M00764_PDE11A_MIP36	GATGCCAGTCCATCTACAGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGGGTAATGTGCC	1
M00764_PDE11A_MIP37	GGAGAGACAGCCCTGCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTGATATAAACATGATG	1
M00764_PDE11A_MIP38	GGGTGGAGTCAGGGACAGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAGCAGGTAAGAGG	1
M00764_PDE11A_MIP39	GTAAAGGGTAGCTAGGAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATACAGAAAACTGGC	1
M00764_PDE11A_MIP4	AGGTTGGCCATTTCACAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTCCTTCCTAATTATTA	1
M00764_PDE11A_MIP40	GCTGTCTCTGCAGGGAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAATGAAGGTGTAGAAC	1
M00764_PDE11A_MIP41	CGGTCCCTGTCTTTCCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTCTTTTCTGAGCAAT	1
M00764_PDE11A_MIP42	AACAAAGAAAAATGGCACTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCAGACTAAGAGGGG	1
M00764_PDE11A_MIP48	GTCTACTGTGTGCCAGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGTCTATACATTTCTTT	1
M00764_PDE11A_MIP49	GAAGAAGGAATGGGTAAAATTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCGGCCCTTGTTA	1
M00764_PDE11A_MIP5	AACTTAGCCTCCTATTTCCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTATTTCCTTTCTTTCG	1
M00764_PDE11A_MIP51	ACCTCCTGAGAAGCTGGGATTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGTTTCTTTGTTTGTT	1
M00764_PDE11A_MIP52	GCTAGAATGGCTCTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAGCCGAGATCACGCCAT	1
M00764_PDE11A_MIP53	GCTCTGGATGTCCAAACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTTGTAAATTTCAGATT	1
M00764_PDE11A_MIP54	CCTACAAACCTTCATCTCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATTCTCGAACATGTTT	1
M00764_PDE11A_MIP55	CTAAGGATAGAAATCTATCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAAAGAGTTGTAAGG	1
M00764_PDE11A_MIP56	ACTTCTACAAGCTTGTTTCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTTTGCTCCCTAT	1
M00764_PDE11A_MIP57	GTTATTTCTTAACATTTGAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATACCATGTCCACAATT	1
M00764_PDE11A_MIP58	GAAGCCAGGTTTACAATAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATTACTACCAGTAACC	1
M00764_PDE11A_MIP59	GTTTCTAGATGTCACTTGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCCCTATAGTTTGCT	1
M00764_PDE11A_MIP6	AGTCTCATTCCCTTGGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGTTCATTTTCTGTGT	1
M00764_PDE11A_MIP60	GTTCACAGGACAGAGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTTTAAAATTCAACCTT	1
M00764_PDE11A_MIP61	GAGAACTGGGATTGATCAGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGGGAGAAAACTTTG	1
M00764_PDE11A_MIP62	GATGGGTAATTCTAGACTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTCTTATTGATGGA	1
M00764_PDE11A_MIP63	AGGCAGTGTTTGGCTTGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGGCAATTCTAAAGG	1
M00764_PDE11A_MIP64	AGGCAATGTTTGGCTTGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGGCAATTCTAAAGG	1
M00764_PDE11A_MIP65	GTGCCAGACTGTCCCAAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTACTCTGAGCTGAGGG	1
M00764_PDE11A_MIP66	ATTTCAGCCCATGCGTGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAAGCCCTATACAAA	1
M00764_PDE11A_MIP67	GGCTCTGGGTAGGGGACTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGCTTTCATCTTGA	1
M00764_PDE11A_MIP68	GGCTCTGGGTAGGGGACTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGCTTTCACCTTGA	1
M00764_PDE11A_MIP69	GACTGAAAATGGCCCTTCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTGTCCTTCCCGTT	1
M00764_PDE11A_MIP70	CAATGTCATCCTTTTGTTCTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCTGGCCTCAGC	1
M00764_PDE11A_MIP71	CAATGTCATCCTTTTGTTCTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCTGGCCTCAAC	1
M00764_PDE11A_MIP72	GTTTCATGTTGACCTTCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTCCTGTCTTCCTTG	1
M00764_PDE11A_MIP73	GTTTCACGTTGACCTTCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTCCTGTCTTCCTTG	1
M00764_PDE11A_MIP74	ATGCTAGATTCAGTAGCTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTTCCATTCTCCTC	1
M00764_PDE11A_MIP75	GCAGTTCATCCTTCCGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAATGAGTGCTTTTGAG	1
M00764_PDE11A_MIP76	GGAGTGGATTGATAGCATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATTCTAGCAAAGTGTT	1
M00764_PDE11A_MIP77	CACATACTTTCTTTTCCTTTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGGGGGCAGGAAG	1
M00764_PDE11A_MIP78	GAAGGAGTGAGTTTGAGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTAAACTTTCAGGAGT	1
M00764_PDE11A_MIP79	GTGAGTTCATCCTTTAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGTCTCGTGATAAACT	1
M00764_PDE11A_MIP8	GAAGTATTTGCTGTGAAAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGTTCTTGCATGT	1
M00764_PDE11A_MIP80	GCTCAGCAGAGGAGGGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACAAAAGATTATTCAGG	1
M00764_PDE11A_MIP81	GCACTGTTTATAGTCCCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAACCAAACAAAACA	1
M00764_PDE11A_MIP82	GGAAAGGAAGATGTGAGCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTGATTTGCTGCAGA	1
M00764_PDE11A_MIP83	ACTATAAGCAAGAGAATCAGTATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGGTGGCCCTTT	1
M00764_PDE11A_MIP84	AAAAACCCAACAACATTGTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGCATGTGCCTT	1
M00764_PDE11A_MIP85	GGTTTATAAGCATTATGAAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCACACCAAAGAGG	1
M00764_PDE11A_MIP86	GTTGGAGCCAGGTAGTAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGTATGAATTATGGTT	1
M00764_PDE11A_MIP87	ACTCTGTCCCAAATCTGCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGTTTTGAGGGGCAG	1
M00764_PDE11A_MIP89	GCTTAGATGGCAGGGGGGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAACTGCTTTTGGAAGA	1
M00764_PDE11A_MIP9	GTCATGACAAACAGTGTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATTGGTGTAGTTATGT	1
M00764_PDE11A_MIP90	CATCTGGGCAGCAGACATGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAGAGGGCTGCTGAT	1
M00764_PDE11A_MIP91	CATTATCTTCTTGATTTGTTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAGGGAGAGAGT	1
M00764_PDE11A_MIP93	GTAACAAATCTTAGCTTACATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACATCAAAAACCAT	1
M00764_PDE11A_MIP94	GAGATTTCCCAGTCTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTACCGAAATATATCA	1
M00764_PDE11A_MIP95	CATTTGATTTTCCTGCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGCTTTAGCCTCATGAT	1
M00764_PDE11A_MIP96	CAACTGGCGAGATGGCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAGACAAATGTATAGT	1
M00764_PDE11A_MIP97	GTAAGGTTGTCTTGGAGATTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAATGGGTCAAGTGA	1
M00764_PDE11A_MIP98	GAGAATCTCCAACCCGCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCAGGTGTATACAGTT	1
M00764_PDE11A_MIP99	GGGGAGCTCGTTTTACTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCTCACAGACTGAATC	1
M00764_PIAS1_MIP1	GTGCTAACGGCTAAATATACATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTCAGAGAGGAAAA	1
M00764_PIAS1_MIP14	GTCTTTGGAAGCAGTGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGAAGCTCTGGTAAA	1
M00764_PIAS1_MIP16	CATCTTGCTGGCCATGTTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTTAGCTGGTGTGG	1

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ID	MIP	*c*
M00764_PIAS1_MIP17	GGGTCGAGACATAACCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAGAAGTTGTCGTTTCA	1
M00764_PIAS1_MIP18	CGAAAGAGCTTTTCTCCTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGAGTCTTCTTTTT	1
M00764_PIAS1_MIP19	GAGGATATTCCACAGGAAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTCTCCCTTCAGTA	1
M00764_PIAS1_MIP2	ATTAAGGGCCCCTTAAATGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGTTTGTGCAAGTCA	1
M00764_PIAS1_MIP20	AGATCATCTGGCCATCACACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCACTCTTCTTCCTG	1
M00764_PIAS1_MIP21	AATTCTATTGTTATTTTCTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTGCCATTTTAATTT	1
M00764_PIAS1_MIP23	ACATGGAAGGGGAAATATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCATAGCTAAGAATGA	1
M00764_PIAS1_MIP24	ACATGGAAGGGGAAATACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCATAGCTAAGAATGA	1
M00764_PIAS1_MIP25	ATATTAACTAATGATGGAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGAGTTTTCTGGTA	1
M00764_PIAS1_MIP26	CAAGTACTGTTGGGCTACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTAAACCATAAGAAGGG	1
M00764_PIAS1_MIP27	AGTTCAGAAACTCTAAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTATAGAGTTCCTTAAT	1
M00764_PIAS1_MIP28	CAACTTTGTCTCCATCTACCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTAAAGGCTGGCTGT	1
M00764_PIAS1_MIP29	GGGGATGGACAAGTCTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTCCAGTTCATGTTTAG	1
M00764_PIAS1_MIP3	AAGCATTTCTATCATTATTGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTACGGTCACAGA	1
M00764_PIAS1_MIP30	CCCACCAGTCTAGGTAAGATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGTTTCTCTTCTGGG	1
M00764_PIAS1_MIP31	GAAGTTTTATATCCGGATGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGTCAAAGTAAAAG	1
M00764_PIAS1_MIP33	AATTGCCAAAGTTCCTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGTCATTTTCAAACAA	1
M00764_PIAS1_MIP34	GCATTTGCCTTGACACCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTAATTAAAGACATGTG	1
M00764_PIAS1_MIP35	ATCAGTAGTTCCATGTAAGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGTCTTTACTGGCG	1
M00764_PIAS1_MIP36	AAACAGGTTTCTCGAAAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAATCACTGTTTTTTAAA	1
M00764_PIAS1_MIP38	AAGACCTTGTTACTCCAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTATAGTCAGCACTG	1
M00764_PIAS1_MIP39	CAGTGCTGACTGTAGGATATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGGGATATTTCTGGG	1
M00764_PIAS1_MIP4	GCTAGGATGGGGGGCAGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGGGGACAGCATTGT	1
M00764_PIAS1_MIP40	GGATGATTTCATTAGTATTATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGCTGCAAGGTT	1
M00764_PIAS1_MIP41	GGATGACTTCATTAGTATTATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGCTGCAAGGTT	1
M00764_PIAS1_MIP43	AGTCTATAAGCCTATGGTAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGTACAGTTAGCAG	1
M00764_PIAS1_MIP44	GTTGAAAAAACTTCGCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACATGAGTAGTAGTATT	1
M00764_PIAS1_MIP45	ACCAAAAACAGTCCTCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTTATACTCTCCTTATA	1
M00764_PIAS1_MIP46	GGGGGTTTTTCTTAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATAGTTTTCTCAGGTTTA	1
M00764_PIAS1_MIP47	CAAACTGCATACTAGAAAATATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGTCGCTTTGGT	1
M00764_PIAS1_MIP48	ATTGGAAGAGTAAGTAAATTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTTACCTTCCACC	1
M00764_PIAS1_MIP49	CCAAGAAACAACAATCGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAAATCCTTTTGCAGC	1
M00764_PIAS1_MIP50	GAACTATTCCATGGCAGTATATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAGACTGCTTGACA	1
M00764_PIAS1_MIP51	GTAGAAAACAAACAACATATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACGTACTTAAAGCTCT	1
M00764_PIAS1_MIP54	GGAAGGGCATCTTGGCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCATGAGCTATATTTA	1
M00764_PIAS1_MIP55	CCCAGAATTCCTTAAACATTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACTGGCTCTCTTCA	1
M00764_PIAS1_MIP56	AAGATAAAAACAACCATATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGATATTCATTGAAGA	1
M00764_PIAS1_MIP57	GGGTTTCTCTACTATGTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTATAGTAATGCTCCAG	1
M00764_PIAS1_MIP59	CAGTGTTGACTTTTCATCAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCAGCCGCATTTTA	1
M00764_PIAS1_MIP60	CCTGTCTGTGATAAGAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCCCTTTTTAAAGCT	1
M00764_PIAS1_MIP61	CAAACCCAGGTTGGTTTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCATCCCAAATCTGA	1
M00764_PIAS1_MIP62	GCACTTGGGCACCGATGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAACTTAAGTTGTTCAA	1
M00764_PIAS1_MIP63	GTATTTCATCACAGTCTGTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGCAGTAGGGAGAC	1
M00764_PIAS1_MIP64	GCTTTTAGTATGTTTTTGCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCAAAGTAATGTAA	1
M00764_PIAS1_MIP65	GTCTGCTCTCAAATTACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTTTTTTCATTTATT	1
M00764_PIAS1_MIP67	GATGTCATAGCTCTTCCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTACTATTATTAAATAA	1
M00764_PIAS1_MIP68	CAGTTACAGTTTAGATTCACAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACTGGTGGTGAGA	1
M00764_PIAS1_MIP69	CCTTCCCTATCTCCCACATCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTGGAGCATCAGGT	1
M00764_PIAS1_MIP70	GGTCCTCTTGGCAGATGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGAATCATTTTATTTGG	1
M00764_PIAS1_MIP71	GCTTCATTCCCTCTGTCTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGCTTTTATGCAAA	1
M00764_PIAS1_MIP72	ATCTGAGTGGTTCGGAGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGAAAGATACCTACA	1
M00764_PIAS1_MIP73	GTGAGGTTTGTGAATGTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGTTGTTTTAAAAGGG	1
M00764_PIAS1_MIP74	GGAATATCATCACCTATGCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTATAATTTAGATT	1
M00764_PIAS1_MIP75	GTTCATTGTGAGATACAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCACTTCTTCCTGT	1
M00764_PIAS1_MIP76	CGGTTTAGTGCTGGAAATAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGATACTGGAGATGC	1
M00764_PIAS1_MIP77	CGGTTTAGTGCTGGAAGTAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGATACTGGAGATGC	1
M00764_PIAS1_MIP78	GACTTACAAGGTGAGTCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAAGTCTTCCACATCA	1
M00764_PIAS1_MIP79	GCATGGGTGTCATGTGGAAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCCCTGTTGGCTCA	1
M00764_PIAS1_MIP80	CCAGTGGTAAAACTAGTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAAGGAAGAACTGGAAG	1
M00764_PIAS1_MIP81	GTACAATCAACGAACTGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACCAAAATTCAAACCC	1
M00764_PIAS1_MIP82	GCCTGGGCTGGAGTGCGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTTAGTTTTTGTGAGC	1
M00764_PIAS1_MIP83	CAGAGCAAGACTCCGTTCCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGTGGTAGTGGGC	1
M00764_PIAS1_MIP84	GGTCCTGACCTCGTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTCCCAGGTTCAAACAATTCT	1
M00764_PIAS1_MIP85	CAGGAGACAATCAGGTATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGACATAGCATATAA	1
M00764_PIAS1_MIP86	GAAATCTAATCCTGTGGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATGCATATATGGCC	1
M00764_PIAS1_MIP87	CACTCGTCTCGGTTTTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGGAGAAAATATATTA	1
M00764_PIAS1_MIP88	GGAGGTCTTGATCATCTGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAACCAGGCTGCTG	1
M00764_PIAS1_MIP89	ATTGGACTGATTCCCAGGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCAGTAGTGGCAGTA	1
M00764_PIAS1_MIP90	GTCTGGTATGATGCCAAAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCTTGTATACTTTTC	1
M00764_PIAS1_MIP91	ACTGCCTGTGTGATAAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTTTACCTTACTCTG	1
M00764_PIAS1_MIP94	CGATTGAAAACTTCATACATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACAGATGAGCTTTAT	1
M00764_PIAS1_MIP95	GTATGATGTTCTCAGGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGTCTGATCTACTCT	1
M00764_PIAS1_MIP96	GTAGAACCACTTTTCCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAGTCTGGAAAACCAG	1

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ID	**MIP**	***c***
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M00764_PIK3R4_MIP10	CCAAAACCTAGGAAAGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGAAAGGAATGAAAAG	1
M00764_PIK3R4_MIP100	GTTATGGTTCAGAACCTTATTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCTGAGGAAAGCA	1
M00764_PIK3R4_MIP101	AACACCATAGACTAATATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGATCACAGTATCAGA	1
M00764_PIK3R4_MIP102	CTCAGCTATCACACAACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGCATAGTTACCAATT	1
M00764_PIK3R4_MIP104	GTCTACAAGCGGAGTTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCACATTTCTGTTTAAC	1
M00764_PIK3R4_MIP105	GCAATCAGAGAACAAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTATTTCTTTGACACA	1
M00764_PIK3R4_MIP106	CATTCTCAGTCTTGATGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATATAGCAAGTTCTCCTC	1
M00764_PIK3R4_MIP107	ACCAGTTGGAATTGGGTTCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGTACCCGTCCATT	1
M00764_PIK3R4_MIP108	ATTCTGTGCAGAATTAAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGCTTCTCAATGTTAT	1
M00764_PIK3R4_MIP109	GTCTACCTTTCCAGAAAGCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGCCAAGCACCGA	1
M00764_PIK3R4_MIP11	AGGACAATGGGAGGAACTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCTTCAATTATTTTCC	1
M00764_PIK3R4_MIP110	GAATATCTGAAAAATAACTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTGGTTAAAGGCAAT	1
M00764_PIK3R4_MIP112	CAAAAAGACAGATGCAGCATACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAGCACCTCTGT	1
M00764_PIK3R4_MIP113	ACGAGGTCATAGTAGACTACTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCAGGGTTCTGCT	1
M00764_PIK3R4_MIP114	ACGATTTTGACACTTTCCCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCACCAACAGCC	1
M00764_PIK3R4_MIP115	CGCTAAAGAGTCTCCACAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTTTCTTCATAGACAG	1
M00764_PIK3R4_MIP116	GGCTTCTTCTCTCTGCTGAGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGGCTCGGACGG	1
M00764_PIK3R4_MIP117	CAGACCGCCAGTCCCAAGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACCTGCCCTGGGG	1
M00764_PIK3R4_MIP118	GGGTTCCATCTCCCCCCGCCCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCACTTCCGCTCGG	1
M00764_PIK3R4_MIP119	GAAAATGATGCTCTGACAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACCTCACTTCCTGT	1
M00764_PIK3R4_MIP12	GCTGTTATTATAGATACTGATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTCATAGCGTCC	1
M00764_PIK3R4_MIP120	CCCTGTAGACTCGCCCAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTCTGCTGTCCTGG	1
M00764_PIK3R4_MIP121	GAGTGAAGGCGTGTCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTACATTTTAAGCAGGT	1
M00764_PIK3R4_MIP124	CAGTGGAGCGATCTCGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATACATCTATCGAGTT	1
M00764_PIK3R4_MIP125	GCACAAAAAAGAAAAATGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAACACAAAGCAGACTT	1
M00764_PIK3R4_MIP126	ATAAAGAGGCATCTCTGAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGCCCCAGAAAAAG	1
M00764_PIK3R4_MIP127	GCTAAACAACCACAGCATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTGGGGGCAGGGAAA	1
M00764_PIK3R4_MIP128	GCTAAACACCCACAGCATGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTGGGGGCAGGGAAA	1
M00764_PIK3R4_MIP129	GCTTTTCTGGGTCATGAACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAAGGGCAGTTAGTG	1
M00764_PIK3R4_MIP13	GATAGTGCTATTTCTAGAGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCCAGCTGTTAGTA	1
M00764_PIK3R4_MIP130	GTTTTTCTGGGTCATGAACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAAGGGCAGTTAGTG	1
M00764_PIK3R4_MIP131	AAGTATAGAAAGCCAGATACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTCTGTATGCTGG	1
M00764_PIK3R4_MIP132	GCAATATGTAAATGACTTCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTCATTAGAGTCA	1
M00764_PIK3R4_MIP133	CCCTTCTGTCACCTCTCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCCATCTGTCAGGTT	1
M00764_PIK3R4_MIP134	CCAGGGGGACAACTAAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCACCTTGCTAGTGGG	1
M00764_PIK3R4_MIP135	CAGCCTCCCTGACACTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGAGTTTTCTTTAAGG	1
M00764_PIK3R4_MIP136	CAGCTACTGTAAAGTTTAAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGAAAAACCAGGGC	1
M00764_PIK3R4_MIP137	GAAAACAGACTGGACATCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGATCACAGGGTTTT	1
M00764_PIK3R4_MIP14	CACGGATGTCTTTTATTTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGGAAAAGGCCAGATT	1
M00764_PIK3R4_MIP15	GCAGAACACTAGCAAGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAAATGAGAGACCAGTT	1
M00764_PIK3R4_MIP16	GGGTAAATAAGTTGCTAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCAGGCATTTAATCAA	1
M00764_PIK3R4_MIP17	GAGTAAATCTTCTGTCACCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCAACAGATACTAGG	1
M00764_PIK3R4_MIP19	CATCTTACCTGCAATCACCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACCTCCATAATCAGA	1
M00764_PIK3R4_MIP2	CATTGTTGGCTGGCTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCAAAAATGTGTTTATAC	1
M00764_PIK3R4_MIP20	GGCTGGCTTTCATGTGTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCATGGCTTGTTGGGA	1
M00764_PIK3R4_MIP21	AGCTGCATTTATACAAATGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGAAGGATGACAG	1
M00764_PIK3R4_MIP22	GTGAAATCAGTTTTTTCCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTAAAGTCGGGCC	1
M00764_PIK3R4_MIP23	AGTTGAAGTGATGCATATCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCAAAGGAAGTGATG	1
M00764_PIK3R4_MIP24	GGAGCACAGTCTGTTCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAAGTCATCTTAAAGGG	1
M00764_PIK3R4_MIP25	GATGTAGAGAAGAATTGCAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTTCCAGTCACTGAA	1
M00764_PIK3R4_MIP26	GTGTCGGCTTTCGTTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTAATTTCTTAGTTTTG	1
M00764_PIK3R4_MIP27	GTGTCCTTTTACTATTCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAAGCTTCCCCTTAG	1
M00764_PIK3R4_MIP28	CAGAACACGTTCTGTACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTCAAAAATATCAAGGT	1
M00764_PIK3R4_MIP29	CACAGAAGTGATGTGCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTTCCTCAGTCTTTCAT	1
M00764_PIK3R4_MIP30	GATCAACTAAGGGCCTCTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAAGCTGCCCAAGTC	1
M00764_PIK3R4_MIP31	CCAATTCGGCTGTATGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGGATGGATTTTAGG	1
M00764_PIK3R4_MIP32	ACGAGTCAAGACGCTCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGACCCCAAAGTAATAAT	1
M00764_PIK3R4_MIP33	CATCTGCACACACTTCTCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCCATTAGCAAGCAA	1
M00764_PIK3R4_MIP34	CCAGTGGTGCGATCACAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCCGATATTTTCAAAT	1
M00764_PIK3R4_MIP35	GCGTGCATCACCATGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGACAGGGTCTCACTCTGTT	1
M00764_PIK3R4_MIP36	GTAGTCACAGCTGCCAGGGTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAAGAAGATAGGA	1
M00764_PIK3R4_MIP37	GCTTTGGAATCACGGACTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTAATGAGAACTCC	1
M00764_PIK3R4_MIP38	ACAAAAATCCTTCTTCTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCACCACTACCAGGTAC	1
M00764_PIK3R4_MIP39	CGATTCACAGCAGATTTATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATTCATTCCTGAGCAT	1
M00764_PIK3R4_MIP40	AGTCTCTGATGAACACTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATGATGGGGACATTGT	1
M00764_PIK3R4_MIP42	GTTGTAGTCTAGTCTAGGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAACTTCAGCAACTCA	1
M00764_PIK3R4_MIP43	ACTTCTGGAACCTACAAAACAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCGCTTTTGCTG	1
M00764_PIK3R4_MIP44	CAATCTTACCATCCACCTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCATACACTTCTGTC	1
M00764_PIK3R4_MIP45	GAGGAGGTTTCCCAGTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTACACAGCCTTTAAACA	1
M00764_PIK3R4_MIP46	CCGAGTCCTCTGCTGGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTAAAACAAGACTCAAAT	1
M00764_PIK3R4_MIP47	GTAGAGGAGGCAGGGATAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTTCCATTCTTCATTT	1
M00764_PIK3R4_MIP48	GTCCCCTCCAAAGGCAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCACATATGTTCCATC	1

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ID	MIP	*c*
M00764_PIK3R4_MIP49	CCAAAGCCAGCTCAATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTTCCTTAAGATTTCTA	1
M00764_PIK3R4_MIP5	ACTCGAGAAAAGGCATTTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGATGTCGCCACATT	1
M00764_PIK3R4_MIP50	AAACTAGGAAGTAATTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACAGACAACTGATAGAA	1
M00764_PIK3R4_MIP52	CAAATACAGTGACTCCATTACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGACAAACGGGGT	1
M00764_PIK3R4_MIP53	GCTCTGGTCCACTATATTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACAAACAAGCATACT	1
M00764_PIK3R4_MIP54	GGTGTAATTGACTTGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATTTGGTTTTAGGGAAT	1
M00764_PIK3R4_MIP55	AAAAGAGACAGAAGGGTGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCCTCTTCCTCTG	1
M00764_PIK3R4_MIP56	GGAAGAGAACCATTTCGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAAATGGACACTTCAAT	1
M00764_PIK3R4_MIP57	ATCCTGCCATAGCACAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGGAACCAGTAAGTCGT	1
M00764_PIK3R4_MIP59	AAAAAATGTTTAGAGAGTCCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATAAGTACAGCTG	1
M00764_PIK3R4_MIP6	GTTTGGTGATTAAAAGGGAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCCCTGTGTGGTC	1
M00764_PIK3R4_MIP60	GGGGCTAAAGAGGAAAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGGTAATATATGGGTC	1
M00764_PIK3R4_MIP61	CCTGTGTCATCCCAATTTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCTCCTGATAGTAAC	1
M00764_PIK3R4_MIP62	GTTCCTACTATTGATTGTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGAATTTGCCAGTGA	1
M00764_PIK3R4_MIP63	GTTCCTACTATTGATTATGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGAATTTGCCAGTGA	1
M00764_PIK3R4_MIP64	CCTTGTTGCAGCAGAGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGAAACAGAAACTTACC	1
M00764_PIK3R4_MIP65	GTATGTGCCAGTTAGGACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTTTCATTTCCAGGT	1
M00764_PIK3R4_MIP66	ATTACCTAGGAAAGAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTTGCCAGCCAACATA	1
M00764_PIK3R4_MIP67	GATTAATATGTTTGGCTTTTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGTAAGTTCTTA	1
M00764_PIK3R4_MIP68	AGCAAGGCATTAAAAGTTATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCACAGAAAAGCTAAG	1
M00764_PIK3R4_MIP69	GCCTATGTCTTGTCTTCTAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAGAAAGGGTTGC	1
M00764_PIK3R4_MIP7	CAGAATAAGCAGAAAGTAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGACTACAAAAGGTGT	1
M00764_PIK3R4_MIP70	AATGTCATCAAGAAGAAAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGTTTGCCTCCCA	1
M00764_PIK3R4_MIP72	ATCCACTGGCCTTGCTATAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACTTTTCTTTCTA	1
M00764_PIK3R4_MIP73	CCTCTTCTAGTTACTAAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATTTTATTGACTGTGG	1
M00764_PIK3R4_MIP75	ATAAATTCACATTCTTTAACACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCAACAGGCAAGG	1
M00764_PIK3R4_MIP76	GATGATATCATTTTGCATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACGTATGTATGTAAG	1
M00764_PIK3R4_MIP8	ATTCAAAGTACTCCTCGCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACGATGTTATAAAGTA	1
M00764_PIK3R4_MIP80	CAACCAGTAAGACAGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGATATGAGAAAATGCTTA	1
M00764_PIK3R4_MIP81	GGGGGATAGAATGAATTAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTATACTGTTGGGTTCAG	1
M00764_PIK3R4_MIP82	CATCCTCTCAAATACTTCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAACGATGTTTTGTTG	1
M00764_PIK3R4_MIP83	CAACTTTCTGCTGGACCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAAAGTAATCATGTGG	1
M00764_PIK3R4_MIP84	GCTAAGTGACCCTGAAAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACTATCTGTATGGGG	1
M00764_PIK3R4_MIP85	ATTATTGGGGTCATTTTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAAACTACAAATGATAG	1
M00764_PIK3R4_MIP86	ACAGGTTGTATAATTTTCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGCTCTGCTGGC	1
M00764_PIK3R4_MIP87	CCTCCCTGTCTTTATACATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTTTTTAACTGTACTA	1
M00764_PIK3R4_MIP9	GGAAATTTATTTTTTCTTGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACTGAAGTTGTCC	1
M00764_PIK3R4_MIP90	GGCTAAGTGGGCTATGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAATTCTCAAACAAATC	1
M00764_PIK3R4_MIP91	AGATGATGCTACTATCGTTAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCCTAGGGTGAGGG	1
M00764_PIK3R4_MIP92	AATGAAGAATCAGTTCCAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGAGCAAGAACTTTG	1
M00764_PIK3R4_MIP93	GGCTCCAAGATTAAGTGTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAGAAAAAGCCGAAG	1
M00764_PIK3R4_MIP94	ACTGGGCCATGTAGGGCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATTTTCCTTAGGCTCT	1
M00764_PIK3R4_MIP95	CAAGGAAACGTTTCTTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGTAACTCAGATGATTC	1
M00764_PIK3R4_MIP96	ATCTTTCAGAACCTGACTGCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTATCTGGCTCACGG	1
M00764_PIK3R4_MIP97	CTTTCATCTGGTTTACTTTTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCAGGGCCATCT	1
M00764_PIK3R4_MIP98	GCTGTCCACAACTCAAAGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGACTCCATCATCCTA	1
M00764_PIK3R4_MIP99	GGGGAATACTGAGCCATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGTATACATTTTTCTC	1
M00764_PKP4_MIP1	GTCACCCCAGCTGGAATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGAAATAACCATCAAGA	1
M00764_PKP4_MIP10	CATATTACTTTGAAAACAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACTTTTATTTTTAA	1
M00764_PKP4_MIP100	GTTGACCACTATGATTGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAGGAAACGTCTA	1
M00764_PKP4_MIP101	GCCATTTAAAATATTCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAAGTGTTTGGCAAATC	1
M00764_PKP4_MIP102	GGACAAGGTCAGTTTTTCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTGCATACATGCC	1
M00764_PKP4_MIP103	GGACAAGGTCAGTTTTTCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTGCATACACGCC	1
M00764_PKP4_MIP104	GCAGCCTACCAACTTGTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGTGAAATTGTTGCTA	1
M00764_PKP4_MIP105	ACAATTTTCCAGTGAAGCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGATTTCCCACTCAA	1
M00764_PKP4_MIP106	GCTACTCCTGGTTTGCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGTCATTAAAACAAAA	1
M00764_PKP4_MIP107	GAAGTGAATAAGTGAAGCGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATCTCTGACAAGCTG	1
M00764_PKP4_MIP108	GTAATTTAGACCATCCCTTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTCTAATAACACCT	1
M00764_PKP4_MIP109	AAACTCTTTTGGGAATTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCAAAACTGAAGTCT	1
M00764_PKP4_MIP11	ACACAAAAAGACATCTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGATCAAAAACTTGTGAA	1
M00764_PKP4_MIP110	CATAAAACTGATGGCTGTCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTTTAATATGTGTC	1
M00764_PKP4_MIP111	CACACTATGAATAGCTGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTCCAGTTTTAGCTAG	1
M00764_PKP4_MIP112	GCAAATGCAGCGGCCTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAGTGTATTTTTACAAC	1
M00764_PKP4_MIP113	AAGCATGTGAATGACCTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGGCATTATTTTCCC	1
M00764_PKP4_MIP114	ACATGGTGGTGCATGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGGCTCATGCCTATAATCT	1
M00764_PKP4_MIP116	ATGTGTTTTATGGGATTCTAGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGAAGGAGGTTG	1
M00764_PKP4_MIP117	GACAGAGTCTCGCTCCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTGATGGTTATAATCCT	1
M00764_PKP4_MIP118	CATTGGCTCACTAGTTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTATGTTTCTATAAAT	1
M00764_PKP4_MIP119	GAAGTGTTTTTCATCATTTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAGGGTTTTTTTGG	1
M00764_PKP4_MIP12	GCCTGCTTGATTGCAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTAGAAAATTTAGCAA	1
M00764_PKP4_MIP120	ACACAGTGGGTCAGAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCATTTGTCAATTCAT	1
M00764_PKP4_MIP121	CCTGCAGATAGCTTTGCTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCAGAAATACTCAAAT	1
M00764_PKP4_MIP122	GTTTCTAGAATGAGTTCTCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCTCAGAACACACA	1

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ID	**MIP**	***c***
M00764_PKP4_MIP123	ACCACTTAAATCTCCTATCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAGCCCTGCAGAT	1
M00764_PKP4_MIP124	AGCCTCAGAACACACATCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCACCAAAAAAACAG	1
M00764_PKP4_MIP125	GGACACTCTTGTAGATGATACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACAAGAATCGCTGG	1
M00764_PKP4_MIP126	CAACAGAGTGAGACTCTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTAGCTGGGTGTTGA	1
M00764_PKP4_MIP129	CATTCTAAGGAGAGGCCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCAGGCCTAAGTAAC	1
M00764_PKP4_MIP13	AAGGGTTAACACTTTCTTCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTGGCTGTGGTCTC	1
M00764_PKP4_MIP130	GTTTTGGAAGTTCAGAAGAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCATAACGGACTTC	1
M00764_PKP4_MIP131	GTGGTCCAGAAGGTCAACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCAACAGTCGCAACA	1
M00764_PKP4_MIP132	GTGCCCTTGTATAGTGGCACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTTGGTGGGATACCT	1
M00764_PKP4_MIP133	CAGAAAATTAAACAACCTGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGAGCTGCATTTT	1
M00764_PKP4_MIP134	GGGAGTCACCCTTTTCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGTTGAAAATATCCTA	1
M00764_PKP4_MIP135	GTGATTCCTAATGCCATTGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTCACGCTGGGCC	1
M00764_PKP4_MIP136	GTCTTCTGTTTTCACTCCCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTATGCTCCTGGA	1
M00764_PKP4_MIP137	GGGTCAAGGCATAGCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATCTAAAAGACATTTGA	1
M00764_PKP4_MIP138	GAAGCTGCTCTGAGTCAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAGACTGCCAAAAAAA	1
M00764_PKP4_MIP139	GAGCACAGTTTAAAACCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTGAGCATAGATAATAT	1
M00764_PKP4_MIP140	ATCCTGGGGGTTTTGCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCATTATGGGTGCTTAT	1
M00764_PKP4_MIP141	CAGAGCAAGCTTTTGGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAACTGTAGAATTTAAGT	1
M00764_PKP4_MIP142	GTTCATGATAGACCTTTGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACTCCTATTCCACCA	1
M00764_PKP4_MIP143	GGTGCAGAGCAGAACACAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCCTGAAGGCTGTA	1
M00764_PKP4_MIP144	CCTCTTTCACTTGGCTTTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAAACTGCGTGAGGAC	1
M00764_PKP4_MIP145	ATCCTGTGGCTTTAGAAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAACAATCACAGTG	1
M00764_PKP4_MIP146	GGTTGCCTAAGGTAAATTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATTCGAGATGCTCT	1
M00764_PKP4_MIP147	CGCAGAACTAGTGAAGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTGGAAACTTAGATAG	1
M00764_PKP4_MIP148	GTAGACTCACTGTTGTATGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGGTTAAGTCCACGT	1
M00764_PKP4_MIP149	GCATTTGCTTCCGAGCTTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATCATGGTCACCTG	1
M00764_PKP4_MIP15	CACTGCAACTTTCAATACGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCCAGTCATCCCAATG	1
M00764_PKP4_MIP150	AAGGGCAAGTCTCCAAAGTTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCCGGCCTGGTT	1
M00764_PKP4_MIP151	GGAGAGTGGCCTCCTGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATGAGCCTAGGGGAAC	1
M00764_PKP4_MIP152	CCTGGTTGAGGCACTGTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTAAAGGCTTTCTCTC	1
M00764_PKP4_MIP153	CAGTAGATACTCAAATACTGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCAGGAGGGGGT	1
M00764_PKP4_MIP155	CATGCTGGGGACAGACCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTCAGTCCCTCTTTCC	1
M00764_PKP4_MIP156	CCTGAGACAAAAAAGGATGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGAAAGTGGAAAGA	1
M00764_PKP4_MIP157	CCTGAGAGAAAAAAGGATGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGAAAGTGGAAAGA	1
M00764_PKP4_MIP158	CACCCTTACAATCCAACACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCCAACTTGCTTACT	1
M00764_PKP4_MIP159	CAGTCTTTTAGGGAACAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGATGAAATTGAGAG	1
M00764_PKP4_MIP160	ACACCTCTGATTGGGAGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGTCCCATGTCTGC	1
M00764_PKP4_MIP161	AGCATCATGGGTGCAGTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGGAGGGTGGAGTTG	1
M00764_PKP4_MIP162	GAGCCTCACTTCTCACTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGACAGGATGCAGA	1
M00764_PKP4_MIP163	CATTTATTTCCTGTCTGTAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCAGCAGGACTGA	1
M00764_PKP4_MIP164	GAGAACTTGAAACAATCTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCACCGTCTGAAACC	1
M00764_PKP4_MIP165	GGCCCGGTTACTGGGACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTACAGAAGTGTTTTGC	1
M00764_PKP4_MIP166	AGGTTCCTCAGGGTGCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTTTCTTCTTCTTCCC	1
M00764_PKP4_MIP167	GGCAAGAAAATAAATTTTCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGCCAAGTTGCTG	1
M00764_PKP4_MIP168	ACTCCCAGAAAAATTAAACTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACAAACAGCACACG	1
M00764_PKP4_MIP169	ACTCTTCTAGCAGAAAGTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTCTGCCTCCATTTA	1
M00764_PKP4_MIP17	GTCCTTACTTGCAGACGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACAGGCCTCAGGTTG	1
M00764_PKP4_MIP170	AGATATGGTTTTACCACCGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCAAAGATGGAAAGA	1
M00764_PKP4_MIP171	GTCACCTAAAAAAGATGTTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAGAAGCTCCACAA	1
M00764_PKP4_MIP172	GACAAGATGAGCTGTAAATGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGGGCTCCCCATC	1
M00764_PKP4_MIP173	CCAGAACATACCTATGAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCAAATATGCCAAGAA	1
M00764_PKP4_MIP174	AGACGGGAATAGGGAAACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTAGTGCTGATGAT	1
M00764_PKP4_MIP175	GCTGTCTGGAGCTGCAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCCTCTTTTTTCACAT	1
M00764_PKP4_MIP176	GGGTGGGTCCCACTCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATGTAATTTGTCATTT	1
M00764_PKP4_MIP177	GTCAGCACTGTTTTTCCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAGTTATGCCTTAGC	1
M00764_PKP4_MIP179	ATTTCTTTTGTTTGTAGTGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTAGCTGAGACCTGT	1
M00764_PKP4_MIP18	GAAGTGAAAAAGACTAAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTAAGAAAAAAAATGA	1
M00764_PKP4_MIP180	GAGTGGATGTGCAATCGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAAAAGAGATTACCTC	1
M00764_PKP4_MIP181	GCATTATTCCTGGGAGATAACACTTCAGCTTCCCGATATCCGACGGTAGTGTATCGAAGTTGAAAAAGCT	1
M00764_PKP4_MIP182	GAAATTCTTGCTAAGACAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTGAGGTGTACAGCA	1
M00764_PKP4_MIP183	CCAGATTCAAAGGTAAGTTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACCGTTGTCAGA	1
M00764_PKP4_MIP184	GTCAGGCTGCCAAACAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATTTTCAGTAACATTGA	1
M00764_PKP4_MIP185	GCTTTCAGCAATTGACAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGATGCATAGGAATTC	1
M00764_PKP4_MIP186	AATGTAAATCAATGCGTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAAAAATCAAAACCCA	1
M00764_PKP4_MIP187	GTAGAATTTACTCTTTTGCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCTTTTCTTCTTTGC	1
M00764_PKP4_MIP188	GTTATTGTTGTTCAGATTCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATGGTCTCATCAGA	1
M00764_PKP4_MIP189	CCGACTCAGGAGGCATAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCGAGACCTGGTCAAC	1
M00764_PKP4_MIP19	ACTAGCCATTGTTTGCTGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTCTGTGGCATTGG	1
M00764_PKP4_MIP190	CAGGGCTTTTGCGTTCTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCAACAAAGGCCTCAT	1
M00764_PKP4_MIP191	CAGCCCCACTCAGAGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTTTTATAAATGCTCCG	1
M00764_PKP4_MIP192	GAGGTTTCTTTTTCTCTTAACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAATATCGGGACCT	1
M00764_PKP4_MIP193	ATGATTATGAGTGTGTGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGTGATTTGAATCGGT	1
M00764_PKP4_MIP194	ATGCCACTCCTTGGCGAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGGTGGAATCAGAAC	1

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M00764_PKP4_MIP195	CCACTGACCTGACTGAATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTACAGAAGGTTCTCT	1
M00764_PKP4_MIP196	ATGTCCCCACTTGAACTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCATTTGGACTTTTAA	1
M00764_PKP4_MIP197	GGCCATGTATATTCGTCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTAGGTTTCTTTCAA	1
M00764_PKP4_MIP198	GAATAGAGGTGCCAGGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTTAAATTATGGGTTG	1
M00764_PKP4_MIP199	CAAGACCCTAAAAGGTTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCTGGGACGCATAAAA	1
M00764_PKP4_MIP2	GTCTGGCCTAGGCTCAGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTATCCCCGTCATCT	1
M00764_PKP4_MIP20	AATATAAATCCCCGTGATCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCTGCTACAGTGCC	1
M00764_PKP4_MIP200	CCTCAGTTATTGTTAATGTTAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACGAGCTTGTCCA	1
M00764_PKP4_MIP202	GTTGGCTAGCCCCATTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCAAGATAATTATTACT	1
M00764_PKP4_MIP204	CCTACTACTTTCTGGAAAGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCACTTCTGCTTCT	1
M00764_PKP4_MIP205	CAGAAAGCATACCCGCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTGACAATGAAATACTT	1
M00764_PKP4_MIP206	GGCCACTCTTATTTGAAATTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAGTGAGGTGACTT	1
M00764_PKP4_MIP208	AGTATCTGTGGAAAATCCTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTGGGTCCTATCGT	1
M00764_PKP4_MIP209	GTCTCTTGAAAAGCCGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTAGGAATCAGAGACC	1
M00764_PKP4_MIP21	CCTTTAGATTTGAAAAAGCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGAAGCCTTAACT	1
M00764_PKP4_MIP210	GTATCACACACCCAACTGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACAATCCCCAAAGTAG	1
M00764_PKP4_MIP211	AGGGCTGTATCCAAATAAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCATGTTCCAGTCATT	1
M00764_PKP4_MIP212	GTGCCCACCGTACAACTACATACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGGGCTGACGGTTC	1
M00764_PKP4_MIP213	CATTTTCATGGAGAAGAGTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGAGCAGTCTCTGT	1
M00764_PKP4_MIP214	AAGATGTGGCCCCTGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTAAAAAATAATCACGT	1
M00764_PKP4_MIP215	GCCCAAAGGGTTACTAAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCAAAAGGTATAATGTG	1
M00764_PKP4_MIP216	ATTGTATGCACAGCTTTCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTACTTTTTGTGGGG	1
M00764_PKP4_MIP217	GCAGTCTCCATTGTACTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCGATTATAACTACT	1
M00764_PKP4_MIP218	CAGCAGGAGTAAAGCTGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCTTGGTGTTGAAATG	1
M00764_PKP4_MIP219	CATGCCCTTCTGTATCTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAAATTGCAGATGCT	1
M00764_PKP4_MIP22	GCCTTTATTTGGCATAAAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACAGGAAACATAGG	1
M00764_PKP4_MIP220	GATAAAGCAGGCTGCTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTATTATTAAGGCTAGCA	1
M00764_PKP4_MIP221	ACATACTTAAATATGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTTTCCTCATTAAAAA	1
M00764_PKP4_MIP222	GAGATAATTGTCTTCAAAAGTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCATGCCTTCCAA	1
M00764_PKP4_MIP223	GAACAAAATAGACGGCTACAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGGAGACCACCC	1
M00764_PKP4_MIP224	GCTGGTGAGGAATAGGAACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACCCTGCCATGTTG	1
M00764_PKP4_MIP225	GCAGTTTAAGGTTAAAAGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATACAGCTGTTGATGC	1
M00764_PKP4_MIP226	AGTTCACTTTCCAGCTTCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTTTCATTTTGTCAAC	1
M00764_PKP4_MIP227	GATCTTCATAGCTATGAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTACTGTTCTGCTCTA	1
M00764_PKP4_MIP228	CATCTTGCTGATTTGATGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTCCACTAAACGACC	1
M00764_PKP4_MIP229	ACTTTTCACCTCAATCTGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTTAGAAAGTCCTCT	1
M00764_PKP4_MIP23	CACCCGAGAACTGGAAGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTATGTTATGGGTACGT	1
M00764_PKP4_MIP230	ATGGGGGATATGTAGGTCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGAGGAAATGTTTGG	1
M00764_PKP4_MIP231	CGTCACCCACACCTTCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCATCCATTTTATTTTT	1
M00764_PKP4_MIP232	ATGCCACATTGGTTAAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATAAAGTTATGTTCTGA	1
M00764_PKP4_MIP233	AAGAAATTTACAAGACATAATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGTTCCTTGGGC	1
M00764_PKP4_MIP234	CCATGCCCATTCCTCGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACTGACAACTTCAAAAA	1
M00764_PKP4_MIP235	GACGTTGTGCTTCCAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAAGAATAGAGAACACA	1
M00764_PKP4_MIP236	GCATGTTGGAAACAGCTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGCCATTTTCTATTC	1
M00764_PKP4_MIP237	GTTAGATTTGTGTTTATTAAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACCTAGATTGTCA	1
M00764_PKP4_MIP239	ACATGATAAAACTGTGAAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGGTGCCAACCAAAT	1
M00764_PKP4_MIP24	GTCGCTGAAACTGAAGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAGTGTGCATAAAGATG	1
M00764_PKP4_MIP241	GGGGCTTCTTTCCCCTACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGTGGAAACTGCAAGA	1
M00764_PKP4_MIP242	GTAGCTGTACTAGGAAAACTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCTGAGGCCTTCTC	1
M00764_PKP4_MIP243	ACCAATGTGGCATTTCCATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATTACACTTGCAGGG	1
M00764_PKP4_MIP244	CAAGATGAGCATCCAAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGTCTTAGCTCAATAT	1
M00764_PKP4_MIP245	GGGTGTCTTTCCATATACTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCACCCCAGAAGGG	1
M00764_PKP4_MIP246	CCTTGTTAGATGGCAGAGGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTAAGATCTGCAAG	1
M00764_PKP4_MIP247	GCTGAGCTCCGCCAGGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAACCCAGATCTGAAGAT	1
M00764_PKP4_MIP248	GTTTGGGGTAATGCTGTAACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTTCCCTGAACCTG	1
M00764_PKP4_MIP249	GCAGTCACTAAAAGAAAGTTATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTCCCCGTGTACA	1
M00764_PKP4_MIP25	ACCAAAAATGTCCATTTATTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCAGGTACAGGGC	1
M00764_PKP4_MIP250	ATTGATGAAAAAACAAAGCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTAACAGAGCCAGA	1
M00764_PKP4_MIP251	ATGCACTTTTGTATCATTCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAGTGGGCTGAATT	1
M00764_PKP4_MIP26	GATTGTTGGTATGAACATTAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGACATGCCTGCA	1
M00764_PKP4_MIP28	GTGAACCAGGATATATGTTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGCAACTGTTGAG	1
M00764_PKP4_MIP29	GCTCTTTAATTTTTGCCAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCAGCTTTCTGAAGT	1
M00764_PKP4_MIP3	GAAGAACCTCCTTGCCAACTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACACACAGCCCAGCA	1
M00764_PKP4_MIP30	ACAAGCTTAGAAATTTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTCAGTTTCTATTTCC	1
M00764_PKP4_MIP32	ACTGAGAAGTCATTTCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAAGGTTTTTGTGCTC	1
M00764_PKP4_MIP33	AAAAAGAAAGAAAAAAATGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTATTTCACCAAGAGA	1
M00764_PKP4_MIP34	GTTCAGATGTTTGTCAACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGATAGTTGTTGGGC	1
M00764_PKP4_MIP35	GGTCTGTTGTGTTATCTTTTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAAATACTGGTGT	1
M00764_PKP4_MIP36	GTCTGTTCTGGTGAATAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGTAAGAATGAAACCA	1
M00764_PKP4_MIP37	CAGTGGATACCAGGAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTTGCTTTTAAGATTTT	1
M00764_PKP4_MIP38	CGGAATAAGAATTCATTTGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTTCAGCTCTTGAA	1
M00764_PKP4_MIP39	ATACCTTCCGGCCGGGCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCAAGGCAGACAACAG	1
M00764_PKP4_MIP4	GCACAAGATCACATCTGCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCGAATGGCTGTGA	1

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M00764_PKP4_MIP40	GATCTTGATGCGTTTGGCTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTTCGCCATGTTAGG	1
M00764_PKP4_MIP43	GACTCTTCTCCTCATGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATGCAGGTGTGGGTAT	1
M00764_PKP4_MIP44	GCACCCTGCCCTCTAGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTAAGCAGGAATAGCTG	1
M00764_PKP4_MIP45	GGGTTCTCTAACTTGATAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAAGGTTATTACCATC	1
M00764_PKP4_MIP46	ACTTAACAGAATGGATATGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCCTCTCTGAATCC	1
M00764_PKP4_MIP47	GATAATCAAATAAGTTAGGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCCACCAGCATGT	1
M00764_PKP4_MIP48	GCTACTTTTCAGCTCTAAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGTGCCAAAGTTGT	1
M00764_PKP4_MIP49	ATCTTGTGCATGTGGCAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCACAGAGAAACATA	1
M00764_PKP4_MIP5	GAAGCTAAATCTTAAGAGGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCAATTTTGCTGCT	1
M00764_PKP4_MIP50	CAAACATGTTTTAAATGACTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCCCAACAGCAA	1
M00764_PKP4_MIP51	AAATCACACTTTTCAACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGTCCTCAGATTAT	1
M00764_PKP4_MIP52	AGACCTGCTGACACAGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAAACAATTCTTTAGC	1
M00764_PKP4_MIP53	GCAAGTCATGTGGGATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAAGTTGATTTTCTC	1
M00764_PKP4_MIP54	ACTACCAAAATGAAGTGATAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATATTGTACTCCAGC	1
M00764_PKP4_MIP55	ACTCAGCCTCCTGGAGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATGCTTTTTTTGTTGT	1
M00764_PKP4_MIP56	AGACTATAGTGAGCTATGATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTGAGGCCCAGC	1
M00764_PKP4_MIP57	GTCTCCCAATGTGTAGGGATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGACTGCAGGCACAT	1
M00764_PKP4_MIP58	GAGGCCAGGAGCTTGACACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAGGCAAAAAAGATGG	1
M00764_PKP4_MIP59	CAAGTGTTTCAGCCAGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGTCTACTAATTTTTA	1
M00764_PKP4_MIP6	GTTGAGACTACACAGAAGGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTCCTGCAATTTT	1
M00764_PKP4_MIP60	GGGAAGGCAATAGCAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGATGAGGGCTTTGTAT	1
M00764_PKP4_MIP61	CCTGGTCCTAGTCTTCTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATATGACCCCTAAGG	1
M00764_PKP4_MIP62	GCTCTGTTACCTCCTTAGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTGTGCAACAATAAA	1
M00764_PKP4_MIP64	GAATCTGTTGATTCCTGCAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAAAGGCACCCCC	1
M00764_PKP4_MIP65	GGAATCAACAAATTTGCCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGCTGGAATAGATT	1
M00764_PKP4_MIP66	AGCATAGCTTCTCACTTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTTTCATTGTGGAAT	1
M00764_PKP4_MIP67	CCACTAGCTACATTTAGACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGAAGTAAATTCACA	1
M00764_PKP4_MIP68	GGTCCCATTAACAAAAGGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATTCCCTATGAAGC	1
M00764_PKP4_MIP7	GAGAGGAGTGAGGAGCTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATAAAAGGAAATTCTGCA	1
M00764_PKP4_MIP70	GCCTATGCATTTTTCACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACGGTGCTTTAGTTGT	1
M00764_PKP4_MIP71	CATTCTGTAGTGAGCTATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCATTTGGTTTAAACC	1
M00764_PKP4_MIP72	ACTATTTTAGGCATCTAAGATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATGGCCCGATTG	1
M00764_PKP4_MIP73	GGGTAGTGGATTTGGCTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTTCATCAGCCATCAG	1
M00764_PKP4_MIP74	AAGGAGACTGTGCTCTAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATGTGGTGGAGGAATAT	1
M00764_PKP4_MIP75	CAATCCCAACGGACCAACCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTGAACCCCAGTG	1
M00764_PKP4_MIP76	CCGGGAGGTGACTGACCCAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGACGACCCCACCT	1
M00764_PKP4_MIP77	GTATGACATTTATGAGAGGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTCCCCATCCCAAG	1
M00764_PKP4_MIP78	GCTGCTGTCCGAATTGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCATTCTTTGTTTCAA	1
M00764_PKP4_MIP8	GAAACCAAGCTAGCTATAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTAGGAAAGGCATTCC	1
M00764_PKP4_MIP80	GTAATGTGCAAGTCGGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTAAACAGAGTTGATG	1
M00764_PKP4_MIP81	ATAAGCAGCTGTGACAGCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGCACAGGTTCAGGTG	1
M00764_PKP4_MIP82	GACAACCAAATGGGCAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTGAATTAACAGTATA	1
M00764_PKP4_MIP84	GAATATGCATCTAACCCGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATACACTTGGGCTTC	1
M00764_PKP4_MIP85	ACTCAAACTGGTACAGGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGTTACTTGGCCATC	1
M00764_PKP4_MIP86	ACTATTCAGAGAACATCCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCATAAACATGAGGAC	1
M00764_PKP4_MIP87	GTCTCAAGACTACTTTTTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGAGCATCACAC	1
M00764_PKP4_MIP88	GCAGCACAACCTGGCAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGGTGTTCTAGAGTTG	1
M00764_PKP4_MIP90	GGTTCAGTAACAAAACTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTAAAATTCTACCTTAT	1
M00764_PKP4_MIP92	GGACTATATTTTTTGGCAATTATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTTCGTTGGCTG	1
M00764_PKP4_MIP93	CGAGTGCAAGAGTGCAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGACTTTCTAGTAGGTAT	1
M00764_PKP4_MIP94	GTATAGGCCTGTAGGGCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGAGACTCCTAACTGGT	1
M00764_PKP4_MIP95	ACTTTTTTAAGTTGCTAAGTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCGGCTGATGATGG	1
M00764_PKP4_MIP96	AAAATGGAGGAACTGGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAATCTATCTTTAAAA	1
M00764_PKP4_MIP97	CCTGGAATAGCCTCTTGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCATTGAGGTTAATTT	1
M00764_PKP4_MIP98	ATGAATGCTGCAGATATTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATCCATTTTTTGAAGC	1
M00764_PKP4_MIP99	ACAATTTGTGACATTTAGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGACTTCTTCGATAAC	1
M00764_PLXNA2_MIP1	CCTCAGCTTGCAAAATAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCATTCTTAAATATGCC	1
M00764_PLXNA2_MIP10	GGGAACTTGGGAGATGAACTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCTGTGTCTTGCAT	1
M00764_PLXNA2_MIP100	CAGTGGACATGGACTTGGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAACCCTGACAACGAG	1
M00764_PLXNA2_MIP101	CCTCAGAATCTTCTTTTTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAACACCTTCACTGGG	1
M00764_PLXNA2_MIP102	GGTCTGGGGTGAGCCCAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCGAGTACAAGACCCT	1
M00764_PLXNA2_MIP103	CAGTATAGCATGAAGAGTGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCCGGCTTCCTCAC	1
M00764_PLXNA2_MIP104	GAAGGGCCCCATTGATGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGAGAGGAAAGGGAA	1
M00764_PLXNA2_MIP105	AACCTGGACTGGCTGTGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCTCCTGCACAAGT	1
M00764_PLXNA2_MIP106	GTGGGGCCTGGGCTTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTTTCTCACCTTTAGG	1
M00764_PLXNA2_MIP107	GGAGACCCCTCTGTGAAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCCCCAGGTCACAGT	1
M00764_PLXNA2_MIP108	GAGGTTGGCCTTTTCAGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGAGCATGGGAGAAC	1
M00764_PLXNA2_MIP109	AGGCCCAGAAAGAAGCCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTTTATAGCCCTGTG	1
M00764_PLXNA2_MIP11	CACCTGGAGATTTATCAGCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGGCCCCAGGAGT	1
M00764_PLXNA2_MIP110	GCATGTGTGAGTACCCTGTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTGAGACAGGGTCT	1
M00764_PLXNA2_MIP111	CCCAGAGGGACTGGGAAACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCACACAGCCAACGTA	1
M00764_PLXNA2_MIP112	GTTGTCAGGGTTGAATGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTGGGTTCAAATCCT	1
M00764_PLXNA2_MIP113	ACCACTGGGGTTGGATGTTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACCTGAGGGCTGG	1

continued table…

ID	MIP	*c*
M00764_PLXNA2_MIP114	ATTTGGGAAGGAACAAAGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTCATGTGGGGTCTT	1
M00764_PLXNA2_MIP115	GAACCTGGACAGAGCACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATATGCCACTGATGTCCTC	1
M00764_PLXNA2_MIP116	GAAGGTCAGCAGGAACACCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGAGAGCAGCTGCT	1
M00764_PLXNA2_MIP118	ACTAGCTGTAGGACCCTATGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCTTCTCCACGTG	1
M00764_PLXNA2_MIP119	AGGACTCGCATAGCGTAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTACTGCTGAGTCTCA	1
M00764_PLXNA2_MIP12	CATTAACCTGCTCCTGGTAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAGCGTGAAACAG	1
M00764_PLXNA2_MIP120	GAGGTAATGCCTGCCTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCCAGACGGATATCAA	1
M00764_PLXNA2_MIP121	GAGGGGAGGACCTTTTGTAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCACTGGTCAACTC	1
M00764_PLXNA2_MIP123	GCTGCAAATGCAGATGGACAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAGCTTGCTGACCC	1
M00764_PLXNA2_MIP125	CCTGGCTCGGTGAGTGTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTGGTCTGTCATGTCC	1
M00764_PLXNA2_MIP126	GACTCACCCCCTCCATATCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCTCCCAACCTCAC	1
M00764_PLXNA2_MIP127	AGGGGTCTCTCCGATGAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATCACACATGCACCAC	1
M00764_PLXNA2_MIP128	GTGCTGTCACCGTATCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATTAACTTGTGCGTGCA	1
M00764_PLXNA2_MIP129	AGTTTTTGTGGAGGGGACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTGTAGAGAATAGCAG	1
M00764_PLXNA2_MIP13	AGAGATGGTGGCAGTAGAAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCACTCATCCATT	1
M00764_PLXNA2_MIP130	ACTTGCAAAGCTGTCTCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCGCCCATCATTCTGA	1
M00764_PLXNA2_MIP131	ATTGGACATTGTTAAAGACAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGCACTCCTACC	1
M00764_PLXNA2_MIP132	CAACCCGACCTTTGAACTGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACCCTCTCTGACCA	1
M00764_PLXNA2_MIP133	GGCACAGAGCCCAGGGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGTTCCACAGTGTCCAG	1
M00764_PLXNA2_MIP134	CATTGACAGATTCTTTGCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAGTCTTAAGCCAGT	1
M00764_PLXNA2_MIP135	GAGTAACTGTTGGTCTGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTTTACCTAACCGAGC	1
M00764_PLXNA2_MIP136	AGCCAGACTTGGGCTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGACATCCAGGTTGAA	1
M00764_PLXNA2_MIP137	ATCCCTAAGGTGGAGGTTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGATGACCCTCGGGT	1
M00764_PLXNA2_MIP138	ACACACACGATCTCACTCATTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGGCTCGATGCG	1
M00764_PLXNA2_MIP139	CACCCCCATCATCCAATGGCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTTACCCGCAGAC	1
M00764_PLXNA2_MIP14	GGCTGCACTTCACCTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTACCAGTTTTGTAGGA	1
M00764_PLXNA2_MIP140	GTGCATGTTCATTCATAGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTACCTTGGGGCTGGGA	1
M00764_PLXNA2_MIP141	ATGACTACAGCTTAGGTTTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGACTGCCACGCTG	1
M00764_PLXNA2_MIP142	CCAAAGAACCCTTCTGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTAGGATTGAAAAGGA	1
M00764_PLXNA2_MIP143	GTACTCACCACGAAGGTGTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGGAGGGTCCTTTT	1
M00764_PLXNA2_MIP144	GGGTCCAGGGCCAGGTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGATTGTCTGTGAGAT	1
M00764_PLXNA2_MIP145	GTCTTGCAATAATGCCAGACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCCACGAGGGCATG	1
M00764_PLXNA2_MIP146	CAGCCACCTGCACATGGTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGCCCAGGAAGGGAG	1
M00764_PLXNA2_MIP147	ACGCCCCTCCCAGGGGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCCCTCCTGCAGATTTT	1
M00764_PLXNA2_MIP148	ACCTCCATAGGTTCTTAAATTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCGTCCCTCCTTCC	1
M00764_PLXNA2_MIP149	GACAGTGGGAGAGGAGTGCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTACCAGCCCTTCCA	1
M00764_PLXNA2_MIP15	AGAAAGACCTTGGTTTTGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTGCTTTCTTCCTTT	1
M00764_PLXNA2_MIP150	CCACACTCAAACTTCCGGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTGCAGGACTTACCTC	1
M00764_PLXNA2_MIP151	GCAGGTGCACCCTCCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTGGTTTCATCTGTGA	1
M00764_PLXNA2_MIP152	ATTGCAAGAATGACTGAGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAAAGAGAGCAGGTG	1
M00764_PLXNA2_MIP153	CAGATTGCTGATGTCCATGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTAGCCCCAGTCTTT	1
M00764_PLXNA2_MIP154	CCGTGGATTTCGCTGTGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAATAATCTGAGCAGC	1
M00764_PLXNA2_MIP155	GTTGAGGACACACTCATAGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACGAGTGTGAGAGG	1
M00764_PLXNA2_MIP156	GCTCTGCGCTTCAACAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGATCTTGATTCCAGT	1
M00764_PLXNA2_MIP157	CAGGCCCCTCTTGTATCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGGCTTTACCTCCC	1
M00764_PLXNA2_MIP159	CAATATTTCAGAGGTAAGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTCTCACCATCTCT	1
M00764_PLXNA2_MIP16	GCTGGTTCCTGCCACCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTCCTGCATTCATTCA	1
M00764_PLXNA2_MIP160	GTTTAAATCCTAGTCTCATTCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAATGGCAGCGGA	1
M00764_PLXNA2_MIP161	GCTCTGGGTCTGGATGTGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCAGACTGGTTTGG	1
M00764_PLXNA2_MIP162	GCTCTCTTAGGATGTAGATACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTCAGCTGTAGCTC	1
M00764_PLXNA2_MIP163	GGATGACAGGGACATCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTAAGCCAATATTAGT	1
M00764_PLXNA2_MIP164	CAAGGTAAGAAATATCTGCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTGATCTATCTGC	1
M00764_PLXNA2_MIP165	GACCCACTTTGCTCACTGATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCACAGGCGATACC	1
M00764_PLXNA2_MIP166	GATACTGAGATGCTGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTGGATTTAAAGTCTGAT	1
M00764_PLXNA2_MIP167	GAGCACAGCCGGTTGGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGAATCTGTGTTTATGG	1
M00764_PLXNA2_MIP168	GTCTTCTCAAGAAGACTTTTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGTCCCTGCGGG	1
M00764_PLXNA2_MIP169	GTATACTGCTCACATGACTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCATTCCCGGAAAG	1
M00764_PLXNA2_MIP17	ATGGTTTTGAGAGCCCTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTCAAGAAGGTTCCCA	1
M00764_PLXNA2_MIP170	ACTTGTGGGGAGTGCCTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAGTGTGAGTACACA	1
M00764_PLXNA2_MIP171	ACTTACCTGTCTCTCAGACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGCCTCTCTCAAGA	1
M00764_PLXNA2_MIP172	ACATCCATCTCTGCTTTCCAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCATGGTGGGGTC	1
M00764_PLXNA2_MIP173	CAGGTAGCTTACAGAAGACCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGAGACCATCTCG	1
M00764_PLXNA2_MIP174	GTTTACCCCAGGTCTTAGAATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCACCTGGCAGCT	1
M00764_PLXNA2_MIP175	GCTGCTCTCTGATGGTATATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATCTCCAAAATCGCA	1
M00764_PLXNA2_MIP178	ATTCCCAAATCAAGCAAAACTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAGCCATCAGTCA	1
M00764_PLXNA2_MIP179	ATCTCCACCAATAGCTACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGCATTCCTTACATAC	1
M00764_PLXNA2_MIP18	GGCAGAGGGTTCCCCTCTTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGAGAGCACTCCCTC	1
M00764_PLXNA2_MIP180	ACTATAGGCAACTTTATTTTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGTTTTTGTGGGG	1
M00764_PLXNA2_MIP181	GGGCTGGTTGATGTCCAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGCTTGCCACTCTTAG	1
M00764_PLXNA2_MIP182	GGGAGGCTCAACTCCAGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGTTGTGGATATGGGT	1
M00764_PLXNA2_MIP183	CCTGCTCCATGACACAGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCAACTTGCAGATCAA	1
M00764_PLXNA2_MIP184	ACATCGTCCTGGCTGGTGATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGTAGCAGGACTG	1
M00764_PLXNA2_MIP186	GTGAGGTGTAGAAGAGGTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGTCCCCAGGCTTG	1

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M00764_PLXNA2_MIP187	GTGCGGCTCTGCAAGGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCACTTTGACATCTTCTA	1
M00764_PLXNA2_MIP188	CATGGCTGAGGACTCAGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAGTAGACAAAGCCCC	1
M00764_PLXNA2_MIP189	GACTATGAGCTACACAGCGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATTGTGCGCTCTGA	1
M00764_PLXNA2_MIP19	CAGATCAATGAAACGAAGCGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAGAGGACGGGAG	1
M00764_PLXNA2_MIP190	CCTTCTTGTGGGATGGCTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGGGTCGGGAAGTAA	1
M00764_PLXNA2_MIP191	GCACTACCTGTCCAGTGTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACAAGCTGCTCATCA	1
M00764_PLXNA2_MIP192	GTCCTCTTCTGGCCCTGTCTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGGCTCCCACAGG	1
M00764_PLXNA2_MIP193	GTTACCCGCCCCTCATCGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCACTTGACCGTCCAC	1
M00764_PLXNA2_MIP194	GCCAGCAGCACCCAGACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTATAGACCCGGTTGAT	1
M00764_PLXNA2_MIP196	AAACACAAGGCAGAGTGGTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCACCTCCAGGGC	1
M00764_PLXNA2_MIP197	GAATCATGTGAGGGCCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAGAAAAACCAAAATGC	1
M00764_PLXNA2_MIP198	CCTTTATGCTATAAAATACTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGGGTCCCCATC	1
M00764_PLXNA2_MIP199	ACCAAAATAGATAACAGGATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTGAACTTCAACAG	1
M00764_PLXNA2_MIP2	CACAATTTGTACTGTTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTGTGGAATAAAAACTG	1
M00764_PLXNA2_MIP20	CAAGAGACAATGCTCTGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACCTTGGGTAAGGATG	1
M00764_PLXNA2_MIP200	AAGCTTGTTAGGCAGGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCCCAGAGAGGTTAAAA	1
M00764_PLXNA2_MIP201	GGATAGGGAAGACTGGGTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGGAATTTTGTGTG	1
M00764_PLXNA2_MIP202	CTGGTCACCCTGAGTGAGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCAGGTCAACTGCT	1
M00764_PLXNA2_MIP203	CCTTGCCTCTCTGTGGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGCTACAACATTTTTCCC	1
M00764_PLXNA2_MIP204	CCTTCTCAAGGTGGACGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAGAACAGCTGTTAGAAC	1
M00764_PLXNA2_MIP205	GGGGGAATCTCAAGAGATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGCAAGGAGACTGGTT	1
M00764_PLXNA2_MIP206	GTGAGATTCAGTCTCATTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGAAGCCAGGACACA	1
M00764_PLXNA2_MIP207	GCTCCCCACATTCTCCCAAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGCTAGAGACTGG	1
M00764_PLXNA2_MIP208	GCTTATTCTTCCCTGTTCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCATGAAATCACCAG	1
M00764_PLXNA2_MIP209	GTCAGGAGGCAGGGGGAAGAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCCAGACTGCCC	1
M00764_PLXNA2_MIP21	ATTGGTTCTTGGTGGCCCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTGTGGAGAGGAGCT	1
M00764_PLXNA2_MIP210	GACTTATGGAGAGGGACAGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACAGCCTGTAGCCA	1
M00764_PLXNA2_MIP211	GTATGATGGTGACAAACTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTGAGAATCAATGAGA	1
M00764_PLXNA2_MIP212	AGGCAGCCAAGGAGATGATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCCTGTTTGTTTCTT	1
M00764_PLXNA2_MIP213	CATTTCTATCAGTGGTCCCATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGCAGCAGAACCTG	1
M00764_PLXNA2_MIP214	GGGAATGACAACTCAAGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCCACACCCTTCTGT	1
M00764_PLXNA2_MIP215	CATTCTCTGGGCCCTTCCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGTTGCTCTTGCTGG	1
M00764_PLXNA2_MIP218	GCGGGCAGGGAGAGGGGCCTCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGAGGGGCGCGCGG	1
M00764_PLXNA2_MIP22	AAGTCCACACCCTTTGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTAAGAAAAGGGAAAAAG	1
M00764_PLXNA2_MIP221	ATCTATTTCGAGGTTTGCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGCTGTCTTCAGATTT	1
M00764_PLXNA2_MIP222	CAGGCTCCCGGAGGAAATGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCAGTTGCTGGGAA	1
M00764_PLXNA2_MIP227	AAGGTCTAGCGTTGGGGTTAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCGCCCAGCTCAGC	1
M00764_PLXNA2_MIP228	GCAAGGCCCGACTCGAATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGACAGGTGATGCGAAT	1
M00764_PLXNA2_MIP229	ACTAGAGTCTTGGAATTTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTAGGGACAGGGAAT	1
M00764_PLXNA2_MIP23	CCTGAGAAATGTGGCCAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGCCTTATAACCTTTC	1
M00764_PLXNA2_MIP230	CCCCACTCACCCCTCACTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAACAACAACTTCAAGC	1
M00764_PLXNA2_MIP24	GGGGAACTTGGGCTGACAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTTTCCTTGAAGGTTT	1
M00764_PLXNA2_MIP25	CCGACTGCCTTTAACTTCTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTCCACGCTCTCCA	1
M00764_PLXNA2_MIP26	CATCTCAGTAGCATCTCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTACCTGTAAAAAAGTT	1
M00764_PLXNA2_MIP27	GCTATGAAGAGCAAACACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGTTAGATGGGGTG	1
M00764_PLXNA2_MIP28	CTTATCAGCGCAGAGCCCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAAGGCCACTTTCTT	1
M00764_PLXNA2_MIP29	AAACTAGAGCTGGGGAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAGAAGTGGATTTTCA	1
M00764_PLXNA2_MIP3	CAAGAGGAGTGGGTTTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTTATTGGAACATTTT	1
M00764_PLXNA2_MIP30	GCCTGAATGCGGCTGACAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATGTGATTCCCAGGAG	1
M00764_PLXNA2_MIP31	GTTAATAACAGAGAAAATGACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGAAGCCAGACC	1
M00764_PLXNA2_MIP32	GCCCTGCTTTACCTCCAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCTTCCTCACTTTTC	1
M00764_PLXNA2_MIP33	CCTCCTACCCCCTGACTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGTCTCTCTTGGAGGAG	1
M00764_PLXNA2_MIP34	CAAGTGGAAGCAAAGGTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGTGAGTGTCAGGA	1
M00764_PLXNA2_MIP35	GAATTGGTTATCCATAGTTTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTGGCCACCAAG	1
M00764_PLXNA2_MIP36	CCAAACAAAGAGACCAAAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTCTTTCTGCCTCTC	1
M00764_PLXNA2_MIP37	GGTGGTCTCCCCTCTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTTCACACTCACAAGTC	1
M00764_PLXNA2_MIP38	ATATACGGAAGCTCCTGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACAAAAATCAAACACTG	1
M00764_PLXNA2_MIP39	GAACCTCGTGGAGGCCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATGCTCTTCAAGTATTGC	1
M00764_PLXNA2_MIP4	GAAAATACAATGATGGTTGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCAGAAGGGACAAG	1
M00764_PLXNA2_MIP40	GATTTGGAGACATAGGTGTTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCCTCTCCCAGA	1
M00764_PLXNA2_MIP41	AAACAAAAAACAGTAGCAAAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGCCAGGTGTCTG	1
M00764_PLXNA2_MIP42	CCTAAACCTCAACAAATGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCCTGGCTGACTGG	1
M00764_PLXNA2_MIP44	AAAACAGAGGCCAGTAAAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGCAGAGATGCTGAG	1
M00764_PLXNA2_MIP45	GGATTAACAGGGCGGCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTTCTCTCCAATGTC	1
M00764_PLXNA2_MIP46	GTCCAACTTTTGTTTAATTCTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGACTGCTGCTT	1
M00764_PLXNA2_MIP47	ATGGACGACGCCCACTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCCAATATACATCAAAT	1
M00764_PLXNA2_MIP48	CAGTGAGAACACCAGAGAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGGCCCCAGAGCTT	1
M00764_PLXNA2_MIP49	ATGGACATGGCATTAATGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTCTCAGGGGACAG	1
M00764_PLXNA2_MIP5	AGGACTTTGAAATGCAGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTCATGGGATAGAGA	1
M00764_PLXNA2_MIP50	GAGAGCTGAGAGGAGGAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGAGTCCTGAAGTCT	1
M00764_PLXNA2_MIP51	AGCTCGAAAATTATCATTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTATAGTGAGGAGGT	1
M00764_PLXNA2_MIP52	CATTCATGTCCTGGTCACTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTTCTGTCCCTGCTG	1
M00764_PLXNA2_MIP53	GCACGCCGTGGAGTTCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGTAAATGTTTGCTGAG	1

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ID	**MIP**	***c***
M00764_PLXNA2_MIP54	GCTCTGACGTTGAACAAGAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGGGCAGGGAGACA	1
M00764_PLXNA2_MIP55	GCAAGGACTCCCCCTCCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGGGTGAACGTGATT	1
M00764_PLXNA2_MIP56	AAGGTCAAATTGTCCACCTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGAACTGGGGGTTCT	1
M00764_PLXNA2_MIP57	GATGGGGAAGAATATCAGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTAGGGTACAAAGTGC	1
M00764_PLXNA2_MIP58	CCCTAGGCAAGCCCAAGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTGGGAGAAATGGAAG	1
M00764_PLXNA2_MIP59	CCTTTAGAAAAGTCTCCCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGGCTGCCTTCTTC	1
M00764_PLXNA2_MIP6	ACTTTGACTTATTTGGCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATTCTTCTCACAGCA	1
M00764_PLXNA2_MIP62	CCCAAGAGGAACCGATCAGTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCCTGGGGGAAGTT	1
M00764_PLXNA2_MIP63	AAAATCTCTGAGCTACAGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGGAGAGTAAATGGG	1
M00764_PLXNA2_MIP64	CCTCTGTGGAACCGGTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCTCCTTAGACCATAA	1
M00764_PLXNA2_MIP65	GTCAAAAGAGTTAAAGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGGGAAAGTTTGGGG	1
M00764_PLXNA2_MIP66	ATTTCTGCCTATCTTCCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCTTCTTCTTCTCTC	1
M00764_PLXNA2_MIP67	GAGGCTGGGTAAAGCAGATCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCAGAAGAAGGGGA	1
M00764_PLXNA2_MIP68	GGTAGTCCATTTCTATTACTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGAGCTGACTCAT	1
M00764_PLXNA2_MIP69	GTTTCCTTAACCAGACCTCAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGGGAGAGGGCAC	1
M00764_PLXNA2_MIP7	ACTTTCCCTAGCACTAGTTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAGGGAGAGCTTC	1
M00764_PLXNA2_MIP70	GCTCTTAACCCCAGGGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTTTCTCTTGATTTCCC	1
M00764_PLXNA2_MIP71	GGACAGGCCTTCCATCTGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTCTTCCTTCCTCCT	1
M00764_PLXNA2_MIP72	CATCTGTGTCGGCTCTGTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACTGAGGAAGGCT	1
M00764_PLXNA2_MIP73	GCCCAGGCTGTTATTTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAAAGGCTTCCTTTGG	1
M00764_PLXNA2_MIP74	GGATAAAGTCTCATACCAGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCTCCCCTCTCCCC	1
M00764_PLXNA2_MIP75	CATGGGTTTTGAACCTGGACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCGCCATAGCTTTCA	1
M00764_PLXNA2_MIP76	CAGTGGGCTCAAGTCTATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTGCAGAGATGACTTT	1
M00764_PLXNA2_MIP77	AACTTGATCTCTTAAGGCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAAGGCACTTCCTGA	1
M00764_PLXNA2_MIP78	CCTTCTCCTGAGAACCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTTAATTCAGGGATTCC	1
M00764_PLXNA2_MIP8	CAGCCACTGCTTGGCATACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTCTTCCCTAGTTTCC	1
M00764_PLXNA2_MIP80	AACATGTACTTGATGGCCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCTCCAGGCCTCTC	1
M00764_PLXNA2_MIP81	ACACAGATGTGCGGCACACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCAGAAGTTTGTGGAC	1
M00764_PLXNA2_MIP82	GCCTTGGAAATTTGTCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAAGGTCTCAAACAAGT	1
M00764_PLXNA2_MIP84	GGCTTCCCATGGGTGAATGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGAGAAACTGGGTGG	1
M00764_PLXNA2_MIP85	CCCGGGGCACTTCCTGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTAACAGACTCTCCTG	1
M00764_PLXNA2_MIP86	GTCTAGACTCAAGAACCACCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGGACTGGGTGCC	1
M00764_PLXNA2_MIP87	CAGGTACAGCCAGACCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTGGCCACCAAGGTAA	1
M00764_PLXNA2_MIP88	GATGCCACACCTTGACCCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCACTCCCTGGTCTG	1
M00764_PLXNA2_MIP89	GTGAAGAACCATGACCACGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGCCCTCCACCAA	1
M00764_PLXNA2_MIP9	GTCGATCTGCTCCCACAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTAAAACGTCACACTTCA	1
M00764_PLXNA2_MIP90	CCGTTGGGACCTCATATATGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTGAGGAGAAGGG	1
M00764_PLXNA2_MIP91	GCTGGCAGAGGCAGGGATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGCAAGGGCTGCCTG	1
M00764_PLXNA2_MIP92	CCCGGACGTCCATCAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCCCAAGACACCTACAT	1
M00764_PLXNA2_MIP93	ATACCAGAAACAACCATTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGACACCTGAGAAGG	1
M00764_PLXNA2_MIP94	AGCATAGAACAGGGATTCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCAGGTGAGAGGGGG	1
M00764_PLXNA2_MIP95	GATGTCCTCATCTTGCAGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGCCTTAGAGCAAGG	1
M00764_PLXNA2_MIP97	GCTAGAGACATCTAGGGCTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTGGGTGGAGGGGG	1
M00764_PLXNA2_MIP98	AATCTTCTCCTTGACCTGTGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCAGCTCCCCTTC	1
M00764_PLXNA2_MIP99	AATCTTCTCCTTGACCTGTGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCAGCTTCCCTTC	1
M00764_PTPRD_MIP1	AAGGCCAGGGCTGCATAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGATATTTGTAAACAGT	1
M00764_PTPRD_MIP10	AAAGTGATTTGTACAGAACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCACAAGCTTTCAAGTT	1
M00764_PTPRD_MIP100	CGTTATTTAATCTGCTGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAGAGGTTACTACAT	1
M00764_PTPRD_MIP101	ATTATGGATATGGGGTGACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCAAAGGCACAATT	1
M00764_PTPRD_MIP102	ACTTACTTTATATTCTCATTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGAGTCTGAGCA	1
M00764_PTPRD_MIP103	ATTGAAGGCTTAGGGCTGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCACGGCAAAGACT	1
M00764_PTPRD_MIP105	AATCATATTCATTTGTGCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTCTGATAACCAG	1
M00764_PTPRD_MIP106	ACAGCAAGCAGACCACTTTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTTGCTGTCTTGGG	1
M00764_PTPRD_MIP107	CCTGTCCTTTCCACCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTATAATTCTCTGGAAT	1
M00764_PTPRD_MIP108	GTTTTTCCTTTTCCAGCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAATGCTCTAAACAGG	1
M00764_PTPRD_MIP109	AGCCAGACTTGCTTGACATTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGTATGATTTTCCT	1
M00764_PTPRD_MIP11	ATGACAGTAAGGGAGTTAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTACTGGTTATGATGA	1
M00764_PTPRD_MIP110	CAATAGAGTTGGCTGAATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATAGGTTCAGCAAAAAC	1
M00764_PTPRD_MIP111	CCGTAAGCAGACAAATCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGACGTAGTAAGTTTTA	1
M00764_PTPRD_MIP112	CCTCCTTTAAAGGATTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAAAACCAGATACCACAT	1
M00764_PTPRD_MIP113	CCTATAAAGAAGGGTATACTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCCTTTGCTCGTAT	1
M00764_PTPRD_MIP114	CCCCTTCTCCCGATGGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTCCCTCAAAACCTTCA	1
M00764_PTPRD_MIP115	ACGTATGATGCTCCCTTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACGGAGGTTGAAGTGGT	1
M00764_PTPRD_MIP116	CAGGCTCTCAGCCAGAAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGACCTCTTCAGGGCT	1
M00764_PTPRD_MIP117	GGATGGAGTGGTAAGACCAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAAATTTTAGACGG	1
M00764_PTPRD_MIP119	AGAAATTATCATTGAAACAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTCTTACTTACCA	1
M00764_PTPRD_MIP12	ACCATTCAAGTTTTAATTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGGGATGCATACC	1
M00764_PTPRD_MIP121	GTATGTGCCTTGAACAGTAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTCTGGGCTCCAG	1
M00764_PTPRD_MIP122	AATGCTCGCACATCCCTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGTAGGAAGTTTCAG	1
M00764_PTPRD_MIP124	GCTCTTATTTTAGTTTTTCGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAATGGTGAGCCCA	1
M00764_PTPRD_MIP125	GTTGACAGCCTCTACCTCGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTTCAGCATGGGCT	1
M00764_PTPRD_MIP126	ACAGCATGGCCAGATAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAAGTGCCTATAATTTC	1
M00764_PTPRD_MIP127	GCTACAGCCTGGCCTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGTTTGCACCCTTCTG	1

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ID	**MIP**	***c***
M00764_PTPRD_MIP129	ACTGTGACAGCCCATACAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGAATACTCCATCAA	1
M00764_PTPRD_MIP13	CAATCATTCTGGTGTGCAGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCGCAATAGTCTCC	1
M00764_PTPRD_MIP130	GCTGACGGCTCTTATTTTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCCACTGCAGTGTA	1
M00764_PTPRD_MIP131	CCTCAAGACATTAGTTGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGTCCTTATTGTTCG	1
M00764_PTPRD_MIP132	ACCTTGGCTTAGTAATATGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGAAAGGACAGGAG	1
M00764_PTPRD_MIP134	GCTAGTATTTACTTGAGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGACCTCGAGATAAT	1
M00764_PTPRD_MIP135	AGTATAGTGGGGGTGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGAGTACTGTATGTAA	1
M00764_PTPRD_MIP136	ATAAACAACAAACATAAGAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGCTTTCACTTCT	1
M00764_PTPRD_MIP137	GGAACTGGTAGAAGGGCATTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGCATGCTCACTGTA	1
M00764_PTPRD_MIP138	GGAACTGGTAGAAGGGCATTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGCATGCTCACTATA	1
M00764_PTPRD_MIP14	CCAATGAGCAGCTTCTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGCCAGATTACTCAGT	1
M00764_PTPRD_MIP140	GAATTGAAGAGTTTTGTTGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGATTGTTTTGCAT	1
M00764_PTPRD_MIP141	CCCCAGGAAACAAAATACAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAACTTTCCACCAAA	1
M00764_PTPRD_MIP142	ATTTCTTTTTGGAGCTGTTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCTGTGTGTAGTACC	1
M00764_PTPRD_MIP143	GCTAAAGCCTGTGTGCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATACAGATTTTCTGTCAAT	1
M00764_PTPRD_MIP144	GCAATCAAACAAGTCCTTATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACAAGTCTTTAAAGC	1
M00764_PTPRD_MIP145	GTAGGAAGTGGGAAGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTATTTTACAGGGTTCTC	1
M00764_PTPRD_MIP146	AAGGTAGTAGACGTCCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTTAGTCTCTAGGTTAG	1
M00764_PTPRD_MIP147	ACACCTACTTGACTGCATGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAAGTGTGATGCAT	1
M00764_PTPRD_MIP148	GCTTACTTTCTGCCTTTTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGCTGCAAGGACTGA	1
M00764_PTPRD_MIP149	ATTAAGGTTCATGCAAATACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGAGGGGAGCGTGC	1
M00764_PTPRD_MIP150	GATGACCACATTCTCTTATTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTAGTATAGCCCTGG	1
M00764_PTPRD_MIP151	CAGTCAGCCAAATACATCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAAAAGAGTCAATAGTG	1
M00764_PTPRD_MIP152	CCCTTATTCCAGTTACCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTGATCTGTGTCACA	1
M00764_PTPRD_MIP153	CCTTCTGAAATCTCAATTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTGCCGTTAAATGT	1
M00764_PTPRD_MIP154	GTAGACCAGTTCATAGTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTCCTCAATAGCTCTC	1
M00764_PTPRD_MIP155	AAGATGGGGAGCATGGAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCCTCCCTGTTTTTA	1
M00764_PTPRD_MIP156	CTTAGTGGAAAACAAGCTCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGTGGCTGCCCTGG	1
M00764_PTPRD_MIP157	ATGTTCTATCTGAGATCTCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGACTCAAAGACCAA	1
M00764_PTPRD_MIP158	GCCTGATTGATTAACTTTGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTATATTTGCCAGA	1
M00764_PTPRD_MIP159	GTCTTGAACCATCCAATCTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGCCATACAGAGA	1
M00764_PTPRD_MIP16	AGAAGAATGTGCACTATGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGCATTGTATTTGAG	1
M00764_PTPRD_MIP160	AAAATAAAACTGTTACAGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAATGTCTCCCCCAT	1
M00764_PTPRD_MIP163	GTCTGAGTGATGACTTGTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAAGCCCTAAATCTC	1
M00764_PTPRD_MIP164	GAGGAGGGAAATAGGGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCACTACTATTGGCAAC	1
M00764_PTPRD_MIP166	ACTCAACATGTCAACAACTGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCAGTGCCCCGAG	1
M00764_PTPRD_MIP167	GGACTTAGTCCAGCGACACTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCGTGCCTGGACATC	1
M00764_PTPRD_MIP168	CGGATTATGAATTCAGGGTTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGGAACCCTGAG	1
M00764_PTPRD_MIP169	GCTTGGATGGGGGAAGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCAGAGTTTTTAGGTTT	1
M00764_PTPRD_MIP170	AGAGCACAGCTACAAGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATAATCCTGTCATTTTC	1
M00764_PTPRD_MIP171	AGGTGTAATTTGCTGACTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCTTTCTAGAGGCAT	1
M00764_PTPRD_MIP172	GTTGCTATGTCAACACTGGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGTCACCAATGCC	1
M00764_PTPRD_MIP173	GAACAAAACACAAGGGAAATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCAACATCCACTTT	1
M00764_PTPRD_MIP174	GTTCGCCGTGTCCCACCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATGTTTTGTTTTTGGAC	1
M00764_PTPRD_MIP175	GTCATTGATATCTTAGACACACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGTACAGACACGATT	1
M00764_PTPRD_MIP178	GTATTGATTGAACTGTGCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATAGAAAAGTTAAA	1
M00764_PTPRD_MIP179	CCCCTGAGCCTGAATGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGAGTTAAACAACACA	1
M00764_PTPRD_MIP180	GTTAACAAGCTGGTTTGGTAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCACTCGCTATTCC	1
M00764_PTPRD_MIP181	GCCAAAGAGATGATCAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACATATAAATTGGCAG	1
M00764_PTPRD_MIP182	CCATACAGGAGCCCTTCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTTAGCAAGAGATTGA	1
M00764_PTPRD_MIP183	AATATCTCTTTTCCCAAGCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGCGAAGGTCCAC	1
M00764_PTPRD_MIP184	GTCCTGTTTTCAGCGTCATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCTTTCTAATCTTATT	1
M00764_PTPRD_MIP186	GAGATTTAAATACGGAGAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGTCTACACTGACA	1
M00764_PTPRD_MIP187	GTGCTTAGTTCTGAAGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACATGTAACATAGATGATTT	1
M00764_PTPRD_MIP189	CATAAACTTGGGATGGGAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCAATATTACTACCA	1
M00764_PTPRD_MIP190	GGGTTCAAAAACCTTGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAATCTAAGAGAGCAAA	1
M00764_PTPRD_MIP191	GAAGTCTGCTTTTGGTGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATACCAGTAAAAGGAGG	1
M00764_PTPRD_MIP192	AAAGCAGATGTGCCCAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCACAATGTTATTATCA	1
M00764_PTPRD_MIP194	AAGAAAGAGGAGAAAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGAAACATTTTAGGGTT	1
M00764_PTPRD_MIP195	CATTGGACTTCATTCAGAACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCTCACTGCTGTGA	1
M00764_PTPRD_MIP196	AACATGGACCACCCATTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAAAAAGCAGTAAATTA	1
M00764_PTPRD_MIP197	GAGTCTGTCTTTCTCCTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAATTTTTCTCTCTC	1
M00764_PTPRD_MIP198	CGACCATTGTTGTTGCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAATCAGTACCTAGAA	1
M00764_PTPRD_MIP2	CCATGCAAACACTTTGGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTACTTCGTTACATTGG	1
M00764_PTPRD_MIP20	GTATCTTACCCCCAATTCTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCGCTCTGGAACAT	1
M00764_PTPRD_MIP200	CCAAATTCAAGAGATTCCCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCCGTGCGAGTA	1
M00764_PTPRD_MIP201	CCCTCGGAGTCCGTAAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATACAGAATTGTAACAA	1
M00764_PTPRD_MIP202	GAGGCCATTTATGAATGTGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTAGCTGAGAGGT	1
M00764_PTPRD_MIP203	GTGACAGCTATTGTTTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAAATATTTTTTCACC	1
M00764_PTPRD_MIP204	CCTACTAAAAACTACCAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAGGCATCATTCTGA	1
M00764_PTPRD_MIP205	GCAAGAGGCTTGCAGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAACAAGGAGAAAGATATG	1
M00764_PTPRD_MIP206	GTAGGGACTAGAAATCTCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGAGAGAAAGAATA	1
M00764_PTPRD_MIP207	GCTAGTTTAAACTGTCTCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTTGCAGCTATAA	1

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ID	MIP	*c*
M00764_PTPRD_MIP208	CACCTTACAGTCCCATTATTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGTCTCGTTGGC	1
M00764_PTPRD_MIP209	CATTTTCTGCATTTTTAGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAACCACGAAAAGA	1
M00764_PTPRD_MIP21	GCTGGTACAATCACTAACATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTTTGGTGCAGTTAC	1
M00764_PTPRD_MIP210	CATTTTTTGCATTTTTAGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAACCACGAAAAGA	1
M00764_PTPRD_MIP211	ACAATTTTAGGTCTTGGGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAGTAAAGCAAGCAA	1
M00764_PTPRD_MIP212	AAGAAAGTCAGCAATCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTATTTCAGCACCTCC	1
M00764_PTPRD_MIP213	AAGACATACATTTTTACAATGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTGTTCGTGTAAA	1
M00764_PTPRD_MIP214	GTGAGGAGCAGCAGCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACTTCCAAAGGAAATGT	1
M00764_PTPRD_MIP216	ATTTCTTACTCTTTCCCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCTTGGAATCACTG	1
M00764_PTPRD_MIP217	CCTTTTCTTTTCTCTTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTCCTAATACAAACAA	1
M00764_PTPRD_MIP218	GCATTCCCAATTTTAGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACACAATCCATTGTAA	1
M00764_PTPRD_MIP219	AACCCGGATAGTCTAAGACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTCATAAGAAGTGACA	1
M00764_PTPRD_MIP22	GGATAATCAGGGCCCTTCTTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTATCTGTTACTT	1
M00764_PTPRD_MIP221	GACTTTTATCCTGCATGGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGGGAAGAAGCCA	1
M00764_PTPRD_MIP229	GTAGCTTAAAATTGTTAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGACGTCTGGTGAA	1
M00764_PTPRD_MIP23	CAAAACGAAACAAAGTACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAAACAGATAATGCTT	1
M00764_PTPRD_MIP230	GCTCATTTAGGTGATGCATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACACAACCCAGTAT	1
M00764_PTPRD_MIP231	CAGTCCCTGGCCTCAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTAACCAATATTCGTTG	1
M00764_PTPRD_MIP232	GAAAACACCGACGGTGGCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCACTAAAAAATGGG	1
M00764_PTPRD_MIP233	ATCATAAAAACTACCAAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCTTTAGAATATCAAA	1
M00764_PTPRD_MIP234	ATGGTTCTAATCTTGCAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTGGGAGATGATAGC	1
M00764_PTPRD_MIP236	AATTCAAATAAGTCATTTGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTGGTGAACTTTTT	1
M00764_PTPRD_MIP238	CAGATTTTTGAAGTTACCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAATGAGGGGAGAT	1
M00764_PTPRD_MIP239	GAGATATTTTTTTCTTTGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATATTGTAGAATTATAGC	1
M00764_PTPRD_MIP24	GATGCCTATTTTAATAGCATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGGCAAAGCCAA	1
M00764_PTPRD_MIP240	GTCTGGTAATATGTAATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGGACAAAGGTGAGTAT	1
M00764_PTPRD_MIP242	GTCCTGAGACCACAGCAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATACACAATATGAGCAA	1
M00764_PTPRD_MIP243	CAAAATACGAAAACACTGCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGCTTCGGCTCC	1
M00764_PTPRD_MIP244	AACTGCTTGCCTTTTATTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACATCTTGTGTCATGG	1
M00764_PTPRD_MIP246	GCTGGAGGATGAAAAGTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTACATCTTTTGAATCATGCT	1
M00764_PTPRD_MIP248	CAAATTAGGGCTAAGAAATGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGAAAGGAAAAGTG	1
M00764_PTPRD_MIP249	CAAGGCAGTTTTTCCTGTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTCTTCTAAAAGATT	1
M00764_PTPRD_MIP25	ACTTTTTTTAAACAACTCGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGGAATGCTGTAT	1
M00764_PTPRD_MIP251	GTGAAATAGGAATAGCATTTAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGTGGGTTTGTG	1
M00764_PTPRD_MIP252	ACCTCTATTCCTTCTGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACACTAATTTGTTGAT	1
M00764_PTPRD_MIP253	ATATTACTTACTAGTTGTGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACCATATGTGATT	1
M00764_PTPRD_MIP255	AGGAGAAAATCTAGGACCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGACATTGGGCTAGAT	1
M00764_PTPRD_MIP256	CCCTGAGGAGTCTTCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAATGAATAAACTGTCCA	1
M00764_PTPRD_MIP257	CCAAGGAGGACTGGAGCGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCCAAACCCTGACGG	1
M00764_PTPRD_MIP258	AAGAAAGCGCGCTCGGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATAAACTGCAAAAAGG	1
M00764_PTPRD_MIP27	ATTAGGTAGGAAATCAGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACCTCTTAGCTATTTA	1
M00764_PTPRD_MIP28	CCCCACCTAACCAATCAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTATTGTAAACATCTCT	1
M00764_PTPRD_MIP30	CAGTCAGTTCTTCCATGATTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATCAACAGGGAGG	1
M00764_PTPRD_MIP31	CGAGACTGATACTGTAGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAACTTTATACTTTGC	1
M00764_PTPRD_MIP32	GATTGGTGAGAAAGTACCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGTAGAACTGTTATCT	1
M00764_PTPRD_MIP34	GAATTTTAAAAAAGTTACATAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGGAGGGAATGTT	1
M00764_PTPRD_MIP35	GTGCTGAACTGCAGCATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCAAGGACTTTCTTTTT	1
M00764_PTPRD_MIP36	GTGCTGGTGTGGCTTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTACAGATACCTCAAG	1
M00764_PTPRD_MIP37	ATTCTTGGTCCACCTGGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGTTCTTTGCTGTGAT	1
M00764_PTPRD_MIP38	AATAATGAAGAGAATCCTGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCACTTGAGAAGTCC	1
M00764_PTPRD_MIP39	CTGCCCAGGTACTCTAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTAGCTAGAAGTTAAG	1
M00764_PTPRD_MIP4	CAATTACCTCTAATTAGTAGTACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCTTTGCCATCCC	1
M00764_PTPRD_MIP40	CCCATTCTGGATTTTTACTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGCTCATGGTCCCTT	1
M00764_PTPRD_MIP41	GGAAGATATCTACAACTCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGTATGGAGTCCG	1
M00764_PTPRD_MIP42	GACTGTCAAAATGTTAAGAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACATCTCACCCAGT	1
M00764_PTPRD_MIP43	CATGGTATCACATTCATCAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGCCACAATAACAA	1
M00764_PTPRD_MIP44	GGTGGTGTTTCTTCATTGTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGTCCGGAGAAGGA	1
M00764_PTPRD_MIP45	GGAAGACGCCAGGAGGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCGATGAAGTCAATAA	1
M00764_PTPRD_MIP46	CAGTCCCGAACAGTAAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTAACTTTTTCTACC	1
M00764_PTPRD_MIP47	ATCCTAAATTTATTTACTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTCCCGAAAACAAAA	1
M00764_PTPRD_MIP48	GGTATGTGAGTGTGGACAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTCTCAGAAACATT	1
M00764_PTPRD_MIP49	CCATTTCAAAAATTTCAGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGTTAGTAGCCATCC	1
M00764_PTPRD_MIP5	CAAAAGGAACCAAAACCCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAGAACACAACTGT	1
M00764_PTPRD_MIP50	GGAAGGAATGCAGACATGATGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACAACTGCAAAAG	1
M00764_PTPRD_MIP52	CACCATTTGTCATTTGACAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTAACAGCACAGT	1
M00764_PTPRD_MIP53	GAGAAGCACTTGCCACTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTACAACATGCCACAG	1
M00764_PTPRD_MIP54	CCTAAAAGGAGAGAAGATTAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCCTGGCATCTGTG	1
M00764_PTPRD_MIP55	GAAATGTCACCAATACTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTGCCTTGAATTTTGA	1
M00764_PTPRD_MIP56	CATTTTTTTTGAAATGCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATAGTTGTGATGCTC	1
M00764_PTPRD_MIP57	GCTTTCTGTTGTCTGAATTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCACACACTTACTCT	1
M00764_PTPRD_MIP58	GGCCCTTGGCAGAGACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTCGTTTTTTATTAGC	1
M00764_PTPRD_MIP59	GGTCATCATTTAGTCCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTTTATTGATGGATAC	1
M00764_PTPRD_MIP6	GTTTATGGGTGCCCTGATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGGAAGGGAAAAAAGT	1

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ID	**MIP**	***c***
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M00764_PTPRD_MIP61	GCCATATGAATCCACAAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGTTGGGTTTTTCCT	1
M00764_PTPRD_MIP62	GTTTCTAGCTGGCACTTCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACAAACCCAGAATGAC	1
M00764_PTPRD_MIP63	GTATGCCTACATTCAGAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGCCATGTAACTTTAA	1
M00764_PTPRD_MIP64	AATAGAGAAGAAAAGCCCAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCCTCTGGGCTCTC	1
M00764_PTPRD_MIP65	CCTCATAGTGCGGGAGTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACAAAGTCATCCCAATA	1
M00764_PTPRD_MIP66	CATTGGATGTTTCTGCAACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCTTTTCTAGCTTTC	1
M00764_PTPRD_MIP67	GTGAAATAGGAATATCAGCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGGGTTACAGGTT	1
M00764_PTPRD_MIP68	GAATGGTTCAAGTGAGAAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCCAAAGGCTACAG	1
M00764_PTPRD_MIP69	TCTCTATTGTTTAAAGAAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGCACAGAAACC	1
M00764_PTPRD_MIP7	GGTGTAGAATCAATAGGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGAAAAAAAATACGT	1
M00764_PTPRD_MIP70	CCTCTATTGTTTAAAGAAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGCACAGAAACC	1
M00764_PTPRD_MIP72	GTTCAGAATCTAACCTTTCCCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAACAACGGAGTGC	1
M00764_PTPRD_MIP73	GGCATTCACATAGTCACTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTGTCATCATGACAA	1
M00764_PTPRD_MIP74	CCCCGAAACATTTGGGGACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGATGTGCTCACCT	1
M00764_PTPRD_MIP75	ATAGGAGAACCCGGGAATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCACAGCCATCTTAAT	1
M00764_PTPRD_MIP76	GGTAAGGAAATGCAGACATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAAAGTCAATTGACCC	1
M00764_PTPRD_MIP77	ATTCTGAAGCCATACTTCATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAAGTGAACTGCTG	1
M00764_PTPRD_MIP78	GAAAATTAACTTCATCAGTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACCACATTGAAAG	1
M00764_PTPRD_MIP79	ATGAAAATGATGCTAACTATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGAAAACTTCAAG	1
M00764_PTPRD_MIP8	AACCCATCTGTAAGAAACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGATTTGCATGGTTAGA	1
M00764_PTPRD_MIP80	CAATAGGTATGGCTAGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTCCTCACCTAAAACA	1
M00764_PTPRD_MIP82	GCAAGTTTTTACAGAATTCACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTAACCGGAATCAT	1
M00764_PTPRD_MIP83	GTCTGTTGGGTGGTGTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAATAAAGTGATACCTT	1
M00764_PTPRD_MIP84	GTAGAACTGAGGCGCCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTTCAATTGATTTTTC	1
M00764_PTPRD_MIP86	GCTAAATGTTAGTTGGCCAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTTCAACAACTCTG	1
M00764_PTPRD_MIP87	GATAAGCACTTTTCATAACAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTACATTACAGTA	1
M00764_PTPRD_MIP88	GGCAGCCTCCAAAATTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGTCTTTACATTTTGA	1
M00764_PTPRD_MIP89	GAAGACTTGATCATTGTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTGATCTGGGTTGTA	1
M00764_PTPRD_MIP9	CATAACTACACGTACATAGGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCTGTCCTCGCC	1
M00764_PTPRD_MIP90	CATCTTCTGAGGAAAAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAATGCAGATGATAAAGA	1
M00764_PTPRD_MIP92	ATGTGGTTATTTGGGGATTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAACAAGCAACTCCA	1
M00764_PTPRD_MIP93	CCATAACGGATGCTTCTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACATATTCTTGACCACT	1
M00764_PTPRD_MIP94	ACTGAGTTCACCCTGGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTTCTTTTTCTGTTTCC	1
M00764_PTPRD_MIP95	GCACATCAGCATCACTAAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCTTAAGGAAAAAAG	1
M00764_PTPRD_MIP96	GAACAAATTGCATTTGGGTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTGTGTTTATAGC	1
M00764_PTPRD_MIP97	AGCTTGATTCATAAAAGCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTGGACTGCTCTGACA	1
M00764_PTPRD_MIP98	GACAAGTTATGATGCACTTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGCACTAACCTCTT	1
M00764_PTPRD_MIP99	ATCTAATTCCATTTCATCTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAACCAGCTAGGTAT	1
M00764_PTPRM_MIP1	ATGATTCTGGCTAGAAGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAATAAGCACATTGAG	1
M00764_PTPRM_MIP100	CCACTGTATAGAAACAATTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCCTCCTCCTGTTT	1
M00764_PTPRM_MIP101	ACAAACAGGCTGCAATTCATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCACTGGAACTGTTCG	1
M00764_PTPRM_MIP102	GCTTTTCACAGAAAATAGGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGGAGCTCAAGCAA	1
M00764_PTPRM_MIP103	CCAAGTTTCTGTGTTGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAAAGGATACTAGCAC	1
M00764_PTPRM_MIP104	GTAACTCGTTGCCACAGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTTCTCTCTCATGT	1
M00764_PTPRM_MIP106	AAGCCAAGAACTCATAGTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACAAGTGCGAGAAG	1
M00764_PTPRM_MIP107	CAGTTTCACACTGACATTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCGAAACAAAAGTTGTT	1
M00764_PTPRM_MIP108	CAGTGGAGAGAACCAACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGTCTAGAAAAATCTAC	1
M00764_PTPRM_MIP110	AAAGCATGTTGGATGAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGAAATGTGGTTAGTG	1
M00764_PTPRM_MIP111	ACCCATAATGATCACTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTTTCAGTTCCTCAGTC	1
M00764_PTPRM_MIP112	ATAGAACTTTCTGAAATGATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAATGTGGGTGAGGA	1
M00764_PTPRM_MIP113	GGCCTTATCCTTGTCAGTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGAATCTGTCTAGGA	1
M00764_PTPRM_MIP114	GTGGCCATAATTTGACTTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGTTGTTTGCTTTCA	1
M00764_PTPRM_MIP115	GCGGAGTTCCTTCATCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGTTTTACAAAATGACA	1
M00764_PTPRM_MIP116	GCCAGTAGATTAGAATATACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTATGCACTGTCAG	1
M00764_PTPRM_MIP117	CAGTTCCTTTGACCCAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCTTATCATAAAGTG	1
M00764_PTPRM_MIP118	GCTTTGTAGGTGATCTGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTCGGATGGTAAAGGA	1
M00764_PTPRM_MIP119	AGTAACATTTTTGTCCGTTTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCGGGGACCACATA	1
M00764_PTPRM_MIP120	GTTTCCACTTTCTTTTACAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCATGACTGTCACGG	1
M00764_PTPRM_MIP121	CCTCCAATGTGTTTTCTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGAATCAAACTGACAA	1
M00764_PTPRM_MIP122	ACAAAACACAATGTGTAGTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATTTTACAGATA	1
M00764_PTPRM_MIP123	CACTAAATAGTGTTGTTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTAAACTGAGTTAA	1
M00764_PTPRM_MIP124	GAGAAACAAAATTCACCATCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACGCAGTCCATAC	1
M00764_PTPRM_MIP125	ATTGATGGTACTCTTGTTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCATGAGAGTCTGT	1
M00764_PTPRM_MIP126	CCACTCTGCCTTCAACTGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTGGGTAGCACTTTA	1
M00764_PTPRM_MIP127	GCAGCCTTTTACAATTGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGAAGAACTAAAAAGA	1
M00764_PTPRM_MIP128	CAGCTTGGAGGCTGTCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTATCTGTACAACTTACC	1
M00764_PTPRM_MIP129	GGAAGTCATGCTTTTCTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTATAAAAGCTACAGAAT	1
M00764_PTPRM_MIP132	AGTAAGGAAAATAGATCATCTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACATCAGTTCTAACA	1
M00764_PTPRM_MIP133	GGTCTGCTTCAAGACTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCATTTTCCAGCTGTATC	1
M00764_PTPRM_MIP134	GTTTGCCTGCACAGCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAAATGCATCTCCAAG	1
M00764_PTPRM_MIP136	CATGCAGCTTTCCATTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTTTTCAACATTCTATT	1
M00764_PTPRM_MIP137	CACTGCTCAGTCTTCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTAAGAAGAGAAAACATT	1

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M00764_PTPRM_MIP138	ATTGAGTGTGGTGCTGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAACTATGACACAGTTG	1
M00764_PTPRM_MIP139	CAGCACCTTGCTATGTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTTTGTTTTCCTTTTT	1
M00764_PTPRM_MIP140	GAATTCTTTTCCCTTAAACAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGACTGAAGCTAGG	1
M00764_PTPRM_MIP141	ACCTTACATTCGCATCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACAATTTGATATACTGA	1
M00764_PTPRM_MIP142	CGATTATCGCAGCTAAGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAACAGAGCTGAGAAA	1
M00764_PTPRM_MIP144	GAAAGGAAATGAAAAAGGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAACACAACTCCAAG	1
M00764_PTPRM_MIP145	AGTTACTGAACTGGCTTTGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGCTGTTCGTGATT	1
M00764_PTPRM_MIP146	CATCTGTTATTTCATTTTTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGAGCTCTCTGAG	1
M00764_PTPRM_MIP147	GGTGAGGAGTCAAGAACGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACGAAATTATTGTCAACA	1
M00764_PTPRM_MIP148	ACAGTGTTTTAGGCTGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGACACTGTATATGGTG	1
M00764_PTPRM_MIP149	ACAGTGTTTTAGGCTGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGACAGTGTATATGGTG	1
M00764_PTPRM_MIP150	CCAATGATTCTAGTACAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGAGATGAAAAACAG	1
M00764_PTPRM_MIP151	GAATAGGATTAATTCAGTAGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGTTGTTTGGGGT	1
M00764_PTPRM_MIP152	GTGCCTTATTTGTGGCAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTAGGATAAAGAATTC	1
M00764_PTPRM_MIP153	GGGCACAAACTGCGACGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAATGCATGCCTACATAA	1
M00764_PTPRM_MIP154	CCATTGAGTTCACCATCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTGCAAAACCAAGGA	1
M00764_PTPRM_MIP155	GCAAGGAGAGGATTTAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGTTTCAGAGGAATA	1
M00764_PTPRM_MIP156	AAAACAAAGGTGGTGCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAAAAGTAGAAGAAGGT	1
M00764_PTPRM_MIP157	GAATTTCTCTATCCAAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACATTGACATTGGGAATC	1
M00764_PTPRM_MIP158	CAGACTTCTATTTTGACTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTGTTTCTGAGTAC	1
M00764_PTPRM_MIP159	GTGTGTTCAGAGTGTATTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGTCTTCTAAAGGA	1
M00764_PTPRM_MIP160	ATGCTCTGAGACCACCCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATAGGAATTAGGCACC	1
M00764_PTPRM_MIP161	GGGCTTACTGTGTTTGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAATACACTGAGCACAT	1
M00764_PTPRM_MIP162	AGTGACCACTCTGTAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTTTCTCTTTTTACTT	1
M00764_PTPRM_MIP163	ATCTCAGCCCCAATATTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGTGGGAGGTGGGTG	1
M00764_PTPRM_MIP164	CTACACACTTGTGTACCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTAAATTTCAAAGCAA	1
M00764_PTPRM_MIP165	GTTGCTGTTGCTGAAATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGCTCTGAAGAAAATTT	1
M00764_PTPRM_MIP166	ATTCCCTATTGATATACAATCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTGCGATGCAGAT	1
M00764_PTPRM_MIP169	CAAAGCCAGCTGGTGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTTTTCTCCTCCTTTT	1
M00764_PTPRM_MIP17	GACACCTTTGAGATTTCAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAATCTGGGGGGATGA	1
M00764_PTPRM_MIP170	CCTGGTGCAGTCCCATACTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGATGCCAGGAGC	1
M00764_PTPRM_MIP171	GCTGGCCATTGTGTGGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTCATCTGTGTGATGT	1
M00764_PTPRM_MIP172	ACTGTGCTCCCAACTCAATCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAGACCTCCTTCA	1
M00764_PTPRM_MIP173	GGTTTTCTTCTAAGAGTTTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGTTTTGTTGCTTA	1
M00764_PTPRM_MIP174	CAACCTACAGAATGAGAGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAAGCAGTCAATGAC	1
M00764_PTPRM_MIP175	GCTGTACAGAAGTTTTGTACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTGCTATTGAGTTG	1
M00764_PTPRM_MIP177	GGTTATTTGCTCATTCTTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATTCTGAAAGGTGTG	1
M00764_PTPRM_MIP178	GAGGTGATATCTCATTGTGGTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAATCTCCACAC	1
M00764_PTPRM_MIP179	GCTTCTTTGAAGGGCAGTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTCATTTCTGTCGG	1
M00764_PTPRM_MIP18	CCTCCACAGAGATAATCCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTCCTTGTGGTGGGG	1
M00764_PTPRM_MIP180	GAAGGAAAGTGAGACTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGTTCTACAACAGCAC	1
M00764_PTPRM_MIP181	ATCCTTCTAGAACAGCTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATACGGGAATATCATT	1
M00764_PTPRM_MIP182	GCCCACCTGAATTTAATGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTTTTTCTGACTGACT	1
M00764_PTPRM_MIP183	AGAACCTGCATGGCAGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGAGAGCTCTGACACA	1
M00764_PTPRM_MIP186	GGTGGCTCTGAGCCCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATACATCGATATAATTGCC	1
M00764_PTPRM_MIP188	CACCTGAAAGTTAAATGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGGGTCGATGATAAC	1
M00764_PTPRM_MIP19	GTACAGTAGCCACTAGTCATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATTTGGGTACGTGG	1
M00764_PTPRM_MIP190	GTAGAAATAAACTTACCTTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGGGAAGGCAAGAG	1
M00764_PTPRM_MIP191	AACCGATTGCTAATTGGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAGTCAGCTTTTATGG	1
M00764_PTPRM_MIP192	GTTTCTTCTCCTTCCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTTAACGATGTTTATT	1
M00764_PTPRM_MIP193	GGTGTTACTGTGATCAGTATATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTGCTGCAAAAGG	1
M00764_PTPRM_MIP194	GGAATTAATGTATACTCAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTTGCTTCTGCCTT	1
M00764_PTPRM_MIP195	GATGTGCCTGAACATTTTTATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAAGTAACTTGCCCC	1
M00764_PTPRM_MIP196	GAGCTGGAGCTCAAATATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGAAATGAGAGAAATG	1
M00764_PTPRM_MIP197	ATCTGGATTAAAAGAAATTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCAAGCCTTTGAA	1
M00764_PTPRM_MIP198	ACAGATGGACACAGGTCTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTTTCCTGCATTGGC	1
M00764_PTPRM_MIP199	GGTGACCAATCTTGTGGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAATTTTCCAGTTGAAA	1
M00764_PTPRM_MIP2	AGACCCAAAATCGTAAAACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCTGGTTGGTGCTG	1
M00764_PTPRM_MIP20	AAGTTCTCCTGGACAGTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTAAACTCAAAGTGACT	1
M00764_PTPRM_MIP200	GCAGTGTTTTCGTGCCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAATAGTTCAAAAGCTTG	1
M00764_PTPRM_MIP202	GAAAATCAGATTGAACACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGCATCTCTACTCA	1
M00764_PTPRM_MIP203	AAATATTGTTTTCTTCTGAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGCAGGCCGTTCT	1
M00764_PTPRM_MIP204	GTAAAACCTGGAAAAAATGGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTATGATTTATAGGA	1
M00764_PTPRM_MIP205	ATGCTGCAAATACTGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTGAGTATACAATTA	1
M00764_PTPRM_MIP206	GGTTTTTTTGGAGTTCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATATTCTGCCAGTAGT	1
M00764_PTPRM_MIP207	ACTTACCTAGGATACTTTACACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTACCCTAATAGAAA	1
M00764_PTPRM_MIP208	CCATGCACATGGGATGAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCTGTGACACTTCTCT	1
M00764_PTPRM_MIP209	ACTTTTCTATCCAGAGTTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCTGACATAGGGA	1
M00764_PTPRM_MIP21	CAGCACCTGCCAAGCTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTTTAAGGAAAGAATG	1
M00764_PTPRM_MIP210	GATTCGTGCGGCAAGTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTGTTCTCTTCCTTGTT	1
M00764_PTPRM_MIP211	GGCCAGCCAGTGAAGTGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAAGAGGCTCTGGAG	1
M00764_PTPRM_MIP212	GTGATGATTGCACAACATTTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGCAGGCCCACT	1
M00764_PTPRM_MIP213	AGGGGTCGTAGACATCTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAAAAGCAGCAGCAGC	1

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ID	MIP	*c*
M00764_PTPRM_MIP214	CCCTGCACCAGCACTGAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTACCTCTGTTTGCA	1
M00764_PTPRM_MIP215	ATCCAGGCAATTATCTGTTCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGAGCTGCGGTCA	1
M00764_PTPRM_MIP216	CCTTGTGCCCTTGGTCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTACCTGGAAAACTCC	1
M00764_PTPRM_MIP217	CCTTGTGCCCTTGGCCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTACCTGGAAAACTCC	1
M00764_PTPRM_MIP219	AATGGTATTGAAAGTCTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGAGGCTTCTGTTC	1
M00764_PTPRM_MIP22	GCAAGCACTTCCACATTTACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTACAGTCCTCATCG	1
M00764_PTPRM_MIP220	ATTCAAGGTATATCGGGAATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCTCCCAGGGTCC	1
M00764_PTPRM_MIP221	CAGAGTTACTAGTTAGTATACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGTGGTCGGTGTG	1
M00764_PTPRM_MIP222	AAAGCCTCTGGGAAACCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACATTCGTATTTTTACTCA	1
M00764_PTPRM_MIP223	CACTTCACTTCATGAATCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCCATGAAAGCAGC	1
M00764_PTPRM_MIP224	CAATCAAATGTTGCCACTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTTTTTTAGCTAACATA	1
M00764_PTPRM_MIP225	CAAACACAGTATCCCCTTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCCCAAAAACAGCAC	1
M00764_PTPRM_MIP226	GAGGCTTTTTAAACTTCCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATTTTCAGGTGTTG	1
M00764_PTPRM_MIP227	CAGTTAATTCGGTTTTTTCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCACAGTGTAAATAT	1
M00764_PTPRM_MIP228	GAAATAAGAACTTCTAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTAAGAAAAGTCAGTGC	1
M00764_PTPRM_MIP229	ACCTCTTAGAAGTACAGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGTGCAAAGAAGGTC	1
M00764_PTPRM_MIP23	CACATGAAATATATTTTGGTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGCCCCCTCCTGA	1
M00764_PTPRM_MIP230	GTCTTCAGCCACAGTTTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTAATGCCAAGTTTTTC	1
M00764_PTPRM_MIP231	GAGGAATGAGCAGAATTTTGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTACACAGATTGATT	1
M00764_PTPRM_MIP232	GCTAAAATTGATACCGTCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATTGGGTCCGATTG	1
M00764_PTPRM_MIP233	CACATCATCAAGAGAGTGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCCACAAAGACAGG	1
M00764_PTPRM_MIP234	GAATTCCGGGTAAGTGATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTATCCACGATGCGAT	1
M00764_PTPRM_MIP235	ATGTCATAATACAGAGACCTAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCAGGTGCTGACC	1
M00764_PTPRM_MIP236	GACTGCAAGACGGTCCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTACTCGCAGCGTTGG	1
M00764_PTPRM_MIP237	CCTGCCCTTCCTCATCACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTTTCTTTTCTCACGC	1
M00764_PTPRM_MIP238	CAGGATGTCCATGCACCGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTCCCCAAACACCCC	1
M00764_PTPRM_MIP241	AGCTTTTATAGTCACCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAAACATGTTCAGTGT	1
M00764_PTPRM_MIP242	AAGGCTGTTTATAGCTCTGCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCGGGTCTCACCTGG	1
M00764_PTPRM_MIP243	ATCTCAAGTGCCAGTTGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTATGCTAAATGATGTGG	1
M00764_PTPRM_MIP244	GGCACTAGGGCCTGCACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACCTCAACCATCTATGA	1
M00764_PTPRM_MIP245	CAGGAACCTGAACATCGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAAATACAGGCTGAA	1
M00764_PTPRM_MIP246	CGACCTTGTCAACCTCCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACAGTCACTCCAGGAA	1
M00764_PTPRM_MIP247	GGTAGAGATTGTCATGCAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAACCAGAGGACAG	1
M00764_PTPRM_MIP248	GTATTGACACTCAGTAATCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGGATGGGGCCGT	1
M00764_PTPRM_MIP249	GCCTGTGATTATGGTTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGAAAACGGAGTAC	1
M00764_PTPRM_MIP25	GGGAGCTAGAAGGCTGGCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAATCAAAGGACTTGT	1
M00764_PTPRM_MIP250	CGTCTCTTACTCTGGCGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAATCTATGTTTTTTT	1
M00764_PTPRM_MIP251	GAGTCCTGCCTACAAATTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCATCCGATATCCAT	1
M00764_PTPRM_MIP252	ATTCGCCAGGTGGACAAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCACTCCCCGATTGTT	1
M00764_PTPRM_MIP253	GCTTCAAGAAGGAGCGCTTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGAGAGTGAGTGTGG	1
M00764_PTPRM_MIP254	ATCTTTTTCACGACAGGAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCTGCCCAGGTAAGA	1
M00764_PTPRM_MIP255	AGATGACTGCACTCGGTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTGTTCCTCAGTGTCT	1
M00764_PTPRM_MIP256	ATTTGCAGGGAAACTGATGCGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTCTTTCACGCTG	1
M00764_PTPRM_MIP257	AAGGGACTTCTTTATCATGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGAGTGCTCCAAGGA	1
M00764_PTPRM_MIP259	AGGCCAATTTTATGGTATGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAGTTCAGTTGGATG	1
M00764_PTPRM_MIP26	GACAGTGATGTTTGGGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCCACTTGAAAATGAGG	1
M00764_PTPRM_MIP260	CATGAGAGGCCACTGTTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCCTTCTATGAACAGTA	1
M00764_PTPRM_MIP261	GCACCCCCTTTACAGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACATCAAAAACAACAAAA	1
M00764_PTPRM_MIP262	AGATAACTCTTGGGACATGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGAGCTGGGAGGAG	1
M00764_PTPRM_MIP263	ATGATGTGTGGAAAAGGTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAGCCAAATCCAGA	1
M00764_PTPRM_MIP264	AAAGCTTGGGGGGCTCCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCTTATCCGGCTACAT	1
M00764_PTPRM_MIP265	GTGTAAACAGCTCTGCAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTATGGTAATTGCTTT	1
M00764_PTPRM_MIP266	GAATTCAAGTATTCCAGGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGCCAATTATGCAA	1
M00764_PTPRM_MIP267	CCAAATCCCGTACTCCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAATATGCTTATTTTGC	1
M00764_PTPRM_MIP268	CAGCAGCATTACTGGGATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGGTACAAATTCCTTC	1
M00764_PTPRM_MIP269	GCTATCTGGCATTATGGTAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAGCTGGTAAACTG	1
M00764_PTPRM_MIP27	GAGAGAACAGACCATGAAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTACCAGGGAGCAG	1
M00764_PTPRM_MIP270	CTGTAACAATAACGAGGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTATCTGTTAGTCCTGG	1
M00764_PTPRM_MIP271	GGGAGGACTCAGTTCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTAACATGTTGCATAAT	1
M00764_PTPRM_MIP273	CGATTTTCTGTATGATGTTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACGGACCCAGAGCT	1
M00764_PTPRM_MIP274	CCAGGCCTTAAGAAAAATGATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCGTGTCGGGTG	1
M00764_PTPRM_MIP28	GTGAACTTTGAACTAGTTAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGAGGCAGATCTTA	1
M00764_PTPRM_MIP29	CCCTGCATTAAGCTTCCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACACGCACAGGATTG	1
M00764_PTPRM_MIP3	AAAAACCTTACAATGCTTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGACATAACCCGTGGT	1
M00764_PTPRM_MIP30	ACACTTTGTAATACTTGGGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACTGTGCTGTGGC	1
M00764_PTPRM_MIP31	GAAGAGAGTTTCACCGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATGATAATTCTACCCCT	1
M00764_PTPRM_MIP32	CAAGCTTAGCTTTTTATTTTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTAGCCCTACAGG	1
M00764_PTPRM_MIP33	AGCCTACTTTGAATCTTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCTTCTCATTTCTGG	1
M00764_PTPRM_MIP34	AGCAACTGAGTTGGTGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATATAGTGAGGAGGAAG	1
M00764_PTPRM_MIP35	ACACATGCCCCTCTCCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTAGACAGTTTAAAAGC	1
M00764_PTPRM_MIP36	CCAAAGCATAGCCAAGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATATGAGGATAGGTATAA	1
M00764_PTPRM_MIP37	CCAATGATATTTAAGAAAAGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCGAGCAGCAGGT	1
M00764_PTPRM_MIP38	CACAAAACTTGTTCTCCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTGTTCTACAGATTT	1

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ID	**MIP**	***c***
M00764_PTPRM_MIP4	GAGGACGCAGAACAGCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTCTCAGCACTTTGC	1
M00764_PTPRM_MIP40	GATGATTGCAGGAAGCCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATTGAAGTCATCACCT	1
M00764_PTPRM_MIP41	GTTTTAAAGAGGAACACAAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCGTATAGCACATG	1
M00764_PTPRM_MIP42	ACTTAAAACTAAAAGCAAACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCACCACTCTCACT	1
M00764_PTPRM_MIP43	ACATGGGGACAGAGGGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGTAAATGATTTCAGA	1
M00764_PTPRM_MIP44	GTGGTAATCCTCCATGAACAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTGGGCTGTCAT	1
M00764_PTPRM_MIP45	CCTAGATAAATCTGAACAAGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTTGGCATCAGCATT	1
M00764_PTPRM_MIP46	GTCTTTCCAAATTGCAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCAATAAAAAGATGTC	1
M00764_PTPRM_MIP47	GCACTCTGCTGTGTAGAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTGCAATAAGAAAGCT	1
M00764_PTPRM_MIP49	CAGAAAGGGGGTAGTATCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGGATATAGACAAAT	1
M00764_PTPRM_MIP50	AGCATTGTATGACCACCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGGTAACTTGTTACA	1
M00764_PTPRM_MIP51	AGCATTGTATGACCACCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGGTAACTTGTAACA	1
M00764_PTPRM_MIP52	CAGAGAGCCCACCTGCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAACCCATGTAAATG	1
M00764_PTPRM_MIP53	CAGGTCTCCCAGAGGCATTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACCTTCACGTAGACA	1
M00764_PTPRM_MIP54	CCTAACTTTTATCAGGTATGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCCGGGGTTACT	1
M00764_PTPRM_MIP55	CAGAAAGTACTAATGGCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCTTGCCAACAAAAAT	1
M00764_PTPRM_MIP56	GTACGTAACATCTGCTAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTTCAAAAATCACCTG	1
M00764_PTPRM_MIP57	GTACATCATTGGGGGCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAATCTTTCTTAATTTT	1
M00764_PTPRM_MIP58	AATAAAGACAACTTACTACATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGGCAAACCAACA	1
M00764_PTPRM_MIP60	CAGGAGACAGGCTCTGGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCACTTTTAATATCTTTC	1
M00764_PTPRM_MIP61	CACTGGAAGGTAGCAAACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTGTTTCTCTGGGTTC	1
M00764_PTPRM_MIP62	CCTTTATGGCTTAATTTCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAGATTATTACAAAA	1
M00764_PTPRM_MIP63	CCAAAGAGGCCTTAGGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTTAGACATACTACTCC	1
M00764_PTPRM_MIP64	AGGAACCTTTCTCCTGTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGTGGTTCTTTTTCAG	1
M00764_PTPRM_MIP65	GATTCTCACCCCACCCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACTAAATGCCCTAAAT	1
M00764_PTPRM_MIP66	ATAATGTTGATGGAACTGTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTGTCTATGAGAA	1
M00764_PTPRM_MIP67	GTAAAACAGTCTTGTTTATACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAGCTTCAGCTT	1
M00764_PTPRM_MIP68	CACTGAACATATGGGAGGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCTTTCTCACTGCC	1
M00764_PTPRM_MIP69	GCTGTAAAACTCACAGGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTGAGGAATATGACTT	1
M00764_PTPRM_MIP70	CCTGGATATACAAAACCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACTGACCTCATTTTA	1
M00764_PTPRM_MIP72	CCACATTTGGTCTTATAGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTAAAGACTGAGCGAT	1
M00764_PTPRM_MIP73	GGTACAACTGCCCATGGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTTGCACTAATTAACAT	1
M00764_PTPRM_MIP74	GGAGAATAGCTGAGCAGGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGGGAGGACAAAAAG	1
M00764_PTPRM_MIP75	ACCAGCTCCCGACGCTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATGGATAATATACCATT	1
M00764_PTPRM_MIP76	GGAGCATCTCGCACATCAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTGATATTCCAACACC	1
M00764_PTPRM_MIP77	CCTTTAAAGCTCAAACTTACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGATTCGCACTGAAG	1
M00764_PTPRM_MIP78	GATGAGAAAAATTTTGTTTGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGAACGGGTGGTTC	1
M00764_PTPRM_MIP79	GAGGTGGAGTACTGCACGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTCTGGTTTGTCTTTC	1
M00764_PTPRM_MIP80	CCATCCCCATTGATGGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCACACTAATCTCATA	1
M00764_PTPRM_MIP81	CCTGCAATTAATTGTCATTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGACACCTTGACCCA	1
M00764_PTPRM_MIP82	CCTTATACTCACCAGCACACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGGCTAAGGGCATT	1
M00764_PTPRM_MIP83	CCCCCACCCTTTTTCCTATTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCACGCTTCCCCTA	1
M00764_PTPRM_MIP84	GGCTGAGAAATACCAAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGAGTCTGACCTATTA	1
M00764_PTPRM_MIP85	AGGGGCTCTGGAATAACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTGTTCATATAGGAAT	1
M00764_PTPRM_MIP86	ACTATGAACATAAAACAAAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACAAACAGGCCCAAG	1
M00764_PTPRM_MIP87	AAGTAGGGTTAATGGAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTGCTGGCGAATG	1
M00764_PTPRM_MIP88	ACCACGCCTGGCCTAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTGCATGTTTTTTGTA	1
M00764_PTPRM_MIP89	ATGCACCTGTAATCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAGGTCAGGAGTTTGGACCA	1
M00764_PTPRM_MIP90	GTCACCGCACCCAACTAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGGAGTCTTACTCTG	1
M00764_PTPRM_MIP91	GAGTGCAGTTGCACGATCTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAACTGGAAATATGC	1
M00764_PTPRM_MIP92	GCACTGAGGACGCTCTAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACCTCAGCTATTTCA	1
M00764_PTPRM_MIP93	CCTGGGACGTAAATAGGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGAGTCCACTTTACAA	1
M00764_PTPRM_MIP94	CCATGAATGCTTGGTGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTTTCCATTTGTACCTA	1
M00764_PTPRM_MIP95	GTGAGGAAGTGGTCTTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTAAAAAGAATGATCA	1
M00764_PTPRM_MIP96	CTGACATGGGCTTCAGCATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCCTGAGTCTCCATA	1
M00764_PTPRM_MIP98	CCCATTCCAAACCAATTTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAGAGTGAATGGTT	1
M00764_PTPRM_MIP99	CATAAAGCTATGATATCCACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGTGAAAGACTTC	1
M00764_RASGRP4_MIP10	GGCTGTGTGTTGGATACATTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCGCCTTCCCATC	1
M00764_RASGRP4_MIP11	GATGTCTAGGAATCCAGCTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCACTAAAGGCAGTGT	1
M00764_RASGRP4_MIP12	GGTCTCCTCTCTTCCTCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCTAGACATCATATG	1
M00764_RASGRP4_MIP13	GGGGTAGGAGGGTATGGATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATACGGTGAGGAGA	1
M00764_RASGRP4_MIP14	GCGTGTAGGAGTGATTTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCCCCTGTATCCACT	1
M00764_RASGRP4_MIP15	CCATGCCTGGACCCAGACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTGAGTCCAAGGTCAA	1
M00764_RASGRP4_MIP16	GCTGGTGTGGATGGGACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGTGGGTGGATGGAAG	1
M00764_RASGRP4_MIP17	CCCCATGCCAGCTGTGGTAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCCCCAGAGTGCGG	1
M00764_RASGRP4_MIP18	GGTAGCCTTGCTTGGTGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTTGTGGCAACACAG	1
M00764_RASGRP4_MIP19	GGTGAGTGGGGTGTCAGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTAGCTTCCACACTTC	1
M00764_RASGRP4_MIP2	CATGGGTAAGGAGACATTCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCAAGTCAGGGGTG	1
M00764_RASGRP4_MIP21	GTTAAATCTCTAGCCTTGAGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAGCCTCCAATCC	1
M00764_RASGRP4_MIP23	CCAGGCTGGAGTGCCGTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCATAGAATTTGCATTT	1
M00764_RASGRP4_MIP24	CCAGGCTGGAGTGCCATGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCATAGAATTTGCATTT	1
M00764_RASGRP4_MIP25	ATGAATGTGGGAAGTAATCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAATTTAGAGTTACT	1
M00764_RASGRP4_MIP26	GTAATCCTAGGCCCTGGGGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCAAACTCTGGCT	1

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M00764_RASGRP4_MIP27	AAGACCAGCCTAGGGAACATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGACAATCGCTGA	1
M00764_RASGRP4_MIP28	AAGACCAGCCTAGGGAACATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGACAATTGCTGA	1
M00764_RASGRP4_MIP29	GGGTTTATATGAAACAGGATGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCTCCTATCTAGA	1
M00764_RASGRP4_MIP3	CAGGATAGATGTGCTATAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAACAGGGATTTCTA	1
M00764_RASGRP4_MIP31	ATGGAAGGTGTGCAGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTTGGGGGTTATCTGGG	1
M00764_RASGRP4_MIP32	GTCACCTTCCGAAAGCCTACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATGCTGAGGCTCAGT	1
M00764_RASGRP4_MIP33	GAGTCACAACCACTTACCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCAGCTCCTCTCTG	1
M00764_RASGRP4_MIP34	ATCCTCCGAAGATGAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAATTATGACCCTGAAG	1
M00764_RASGRP4_MIP35	GGGTTCTACAGATGTCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGAGATTGTTCCTCGG	1
M00764_RASGRP4_MIP36	GATCATATTTCGACAACTGGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACACTGGGTCGGC	1
M00764_RASGRP4_MIP37	GTTAGTCACTGCATAGGCTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCACCAGCTGCTCCA	1
M00764_RASGRP4_MIP39	CAGGCTCTTCCCAAAGCCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCCGGGCATAAGAA	1
M00764_RASGRP4_MIP4	GAAAAAGTATAGGCTGTCAGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTACCACCTGCCAG	1
M00764_RASGRP4_MIP41	ACACCAGGTCCTTGAGGTGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGGCGCTGCAGGGT	1
M00764_RASGRP4_MIP43	ACCCAGTGGCATTGTGGAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGTTGTGGGAGGCAA	1
M00764_RASGRP4_MIP44	GGCATGGGAGTCCTTGAGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTACCAGGACCCCTG	1
M00764_RASGRP4_MIP46	CATGTGTGGACCAATGTGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCAGCGTGTTGAAAT	1
M00764_RASGRP4_MIP48	GACAGGTGTGTGTCAGGTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTGTGGGCCTCACAG	1
M00764_RASGRP4_MIP50	AGACAGATGCTAGACAGGTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCAGCCATCTGGGG	1
M00764_RASGRP4_MIP51	ACTCCTCCATATCTCTCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTCTGAGCATTTTCCAT	1
M00764_RASGRP4_MIP53	AGCCCTGCAAAACGTAGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAATGAACTTGTCCAGC	1
M00764_RASGRP4_MIP56	GTGGCTCACAGTTGAGGGCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGTCTCCAAGTGGT	1
M00764_RASGRP4_MIP58	GTACCTGAGAGTGGTTTGGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTCAGAAGAGTCTC	1
M00764_RASGRP4_MIP60	CCCCACAGGCCAAAATCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATCTGTCACCTGGTCA	1
M00764_RASGRP4_MIP61	ATCCATGACCTGCCTGCTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTCCTGAGAGTGGGG	1
M00764_RASGRP4_MIP62	ATCCATGACCTTCCTGCTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTCCTGAGAGTGGGG	1
M00764_RASGRP4_MIP63	ACCAGAACTCAAATACCAGAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCCTGCTGACCTC	1
M00764_RASGRP4_MIP65	CACGAGGACCACATGCTCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACCGTTAGAGCTGG	1
M00764_RASGRP4_MIP66	GTCTTGCTGAAGATTGAAATAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGGACCACCTGGTT	1
M00764_RASGRP4_MIP67	CAGGGGTGATGCTGCCCCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGACTTGTCCCGAA	1
M00764_RASGRP4_MIP69	GAGTGAGGGCGGCTGCAGCGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCCACCAGGAAT	1
M00764_RASGRP4_MIP70	CCTAGAATTCCTTTTGACTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCATGTCTTGTGGCG	1
M00764_RASGRP4_MIP74	GGGGAGCTTGAGGGTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTTTTGAGTGAGTGTGT	1
M00764_RASGRP4_MIP75	ATGGAAACTCACAAGACATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATAAAAGAAGGGGCT	1
M00764_RASGRP4_MIP76	GTCCTTCTAGACAGACAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAAAATGTTTTCCAGG	1
M00764_RASGRP4_MIP77	ACTCATTTAATCCTCACACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTATTCCTAGTTTAAG	1
M00764_RASGRP4_MIP78	GTGCTATGTGGAGGTTTGTTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTGAGCCCCTGTGA	1
M00764_RASGRP4_MIP79	CAAAAAATGTAAAACGTTAGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCAGGCACGGGGG	1
M00764_RASGRP4_MIP9	CAAAAGAGGAAAGTCACTTCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAAAAAAAAGAAAT	1
M00764_RIMS2_MIP10	AAGAGATTTCTATTTACAAATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGCAAAAGTACA	1
M00764_RIMS2_MIP100	CGTTAGTAGGAAAACTTTTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTTACCAGAGCCA	1
M00764_RIMS2_MIP102	GAAAAGCAAAAATATTCATTTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGGAAGAAAGTAA	1
M00764_RIMS2_MIP103	GGGTATTTCAATTCTGTATCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTTCCAGGGAAG	1
M00764_RIMS2_MIP104	GAACCCAAATGGAACCAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTCCTGAGAAATTTT	1
M00764_RIMS2_MIP105	GTTCTTCTCTTGTTTTTATCACTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTCGAACACGAGC	1
M00764_RIMS2_MIP107	GAAATTATGTTAAATGGTCCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAAGAGACATCA	1
M00764_RIMS2_MIP108	ACGGAGGTTGCAAAGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTAGAAACAGCATTAT	1
M00764_RIMS2_MIP109	CGTGGCATATATGGAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAAAGATATCTTCAAGT	1
M00764_RIMS2_MIP11	ATCACTGAACTGGTAAATAACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTGGCTGTAGCTTT	1
M00764_RIMS2_MIP110	ACAAACGAAAATATTCTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTCCATCATCACAGT	1
M00764_RIMS2_MIP111	GAGAAAGATATAACTCGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTGAAGTCTCTGACTAT	1
M00764_RIMS2_MIP112	GTATGTACAAAGTCCTTTGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGACCCTGATGGTG	1
M00764_RIMS2_MIP114	GTGGAGGAGGGACACTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCATATGAGCCAATTCT	1
M00764_RIMS2_MIP115	GTGGAGGAGGGACACTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCATATGAGCCAATTCT	1
M00764_RIMS2_MIP116	CCAGTAGTGGCTTAGTCCAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTCCAGAGGGACAA	1
M00764_RIMS2_MIP117	CCTTCCCCAGCTTGCAGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTGCACCAGTGGCTT	1
M00764_RIMS2_MIP118	AAAACTTAGCAAGCAAGGTTATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGAGAGCCACCAG	1
M00764_RIMS2_MIP119	CCTTTCACTCTTCCTGCCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGAAGACTCACCCA	1
M00764_RIMS2_MIP12	GGGAAACCACCTGTTTAAATAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTATACTATCAGA	1
M00764_RIMS2_MIP120	CATTCAAGTTGACACGTAATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGACTGGATGGTGG	1
M00764_RIMS2_MIP121	AATGAAGGAAGCCTAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAACCATCTTGCTTTC	1
M00764_RIMS2_MIP122	ACTTGTTTTGTAATTTTAGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTCTTGTGGAAAAA	1
M00764_RIMS2_MIP123	GTTTTAATTAATTGCATCTCTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTCCGACTAAAA	1
M00764_RIMS2_MIP124	ACATCGTGTCATGGATGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTTCTTAGTGTTTCAAAT	1
M00764_RIMS2_MIP125	GTATTATAATGTCCGGTCATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTAACCCCTTCCTG	1
M00764_RIMS2_MIP126	ATACAGTCAGACCATTGACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCTGCCTATCTTTTAA	1
M00764_RIMS2_MIP127	CAAGCATGGCAGAAACAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATCATATCAATACACAGGC	1
M00764_RIMS2_MIP128	GAAATATAGAAATATCACCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGGGATGGCAGG	1
M00764_RIMS2_MIP129	ATAGACAGCCATATCACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTACATACTCCATAATTTTAA	1
M00764_RIMS2_MIP13	GTGATGCGCCAACCTGTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGATCATCAGGAAACCA	1
M00764_RIMS2_MIP130	GCTGCTTCACAATCCCTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCATTAATGAAGGCAT	1
M00764_RIMS2_MIP131	ACCATTTTATTTTCCCAACAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTCCTGATACAAACC	1
M00764_RIMS2_MIP132	CATTTGGTTCATATGATAGCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCCTTCGTCCTGC	1

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M00764_RIMS2_MIP133	GCTAAGGTGAATCAAGATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAAGCCCATCAAGT	1
M00764_RIMS2_MIP134	CCAACGTTCCCTTTGGTGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATACAGACAAGGCAT	1
M00764_RIMS2_MIP135	AACAAAAAGGGAACCAAAGCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCCAAAAAGGCTG	1
M00764_RIMS2_MIP136	CGTTGTGTAGACTTAAATACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAGACAATGGAGTCA	1
M00764_RIMS2_MIP137	GTCTGTCTCTTCTGCTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCCTTTCCATCAGTG	1
M00764_RIMS2_MIP139	AATACAAACAGGTAGCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTTCTTCGTTTATAC	1
M00764_RIMS2_MIP14	GTTCTTGCTGTTGCTGTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAGCGTAATGACACT	1
M00764_RIMS2_MIP140	ATTTGGCGATTTCTCTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGAATCTAACTGTTTC	1
M00764_RIMS2_MIP141	CCATGGCCCCATGATATTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGAACAAGATTACCA	1
M00764_RIMS2_MIP142	ATCCTCATAGAGGGGCAGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTTTGCAGTTTCCTC	1
M00764_RIMS2_MIP143	CCATCCTGATCGATACTGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATTGGACAGACATGT	1
M00764_RIMS2_MIP144	CCCGGATGAACATAAAATTATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTCGTTTCAGCA	1
M00764_RIMS2_MIP146	AACAGAGAATCAGGAGACGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAGAAGAGGGAGGGAA	1
M00764_RIMS2_MIP147	CACGTTTTGGCAATCTCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACCTGGTATCATCTTG	1
M00764_RIMS2_MIP148	CCTAAAAATTATTTTGCCATTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGCAAGGGAAAGAA	1
M00764_RIMS2_MIP149	GTTCTGTTCAAAGCAAGTATCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCCCAAGGCAGCA	1
M00764_RIMS2_MIP15	GTGTTTATCTATTCACGTTAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATGGATGTGGCCAT	1
M00764_RIMS2_MIP150	GAGTACAGAAATGTTTGAACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGCAGGTACCAT	1
M00764_RIMS2_MIP152	CCTTGGTGCCAAAATGGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATATCAGGGAAGAACATGA	1
M00764_RIMS2_MIP153	CAAGGTGCCCACTGCAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTTAAAAGTAACATTGA	1
M00764_RIMS2_MIP154	GGGCATTTTAAACTAGTTAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAACGGGTAGGAA	1
M00764_RIMS2_MIP155	GGTTCTTGGTTTCTTTAGTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTACAATGTTGTCA	1
M00764_RIMS2_MIP156	ACACCAGCACTGAAAAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTCAAGTCATGACACA	1
M00764_RIMS2_MIP157	AATTTACCGGTTTACTTATCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGTGGAACTTGGTAAA	1
M00764_RIMS2_MIP158	ACTTTCCCTTTCCTCAGGTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGCTGCTCCGAGT	1
M00764_RIMS2_MIP162	GGGGTCCAGAGGAGGAGATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCGGGACCAGTGGG	1
M00764_RIMS2_MIP165	GTCTCTATCTGTTTAGAAAGTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATGCAGCGCTCCC	1
M00764_RIMS2_MIP166	GAAATATCAGCGAAGGCTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGTTCCTCATTTCCA	1
M00764_RIMS2_MIP167	GTCTCCTCCGTGCCTCACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTACAGAAACAGGCCT	1
M00764_RIMS2_MIP168	CAAGACTAGTCCTATTATTTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCTATCAGAGGCC	1
M00764_RIMS2_MIP169	ACTCTGGCAACACCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGTTGGGGATTTAATCT	1
M00764_RIMS2_MIP17	ATGCATGGTAATTGCTAAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAGGACAAAGTGGT	1
M00764_RIMS2_MIP170	GGCCATCCAGGAAATCACTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATTCTATGAAATTTA	1
M00764_RIMS2_MIP172	CCAAGACACTGCCAGGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTGTATATTAAAGCAC	1
M00764_RIMS2_MIP173	CCTGGTTTTACAACAAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATCCATTAGTAATCTTG	1
M00764_RIMS2_MIP174	GTGTATCTATTAGATAACGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGATTGCTAGCTCT	1
M00764_RIMS2_MIP175	GAGCAATAAACTATGGACATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCTGCTGGTAAAGG	1
M00764_RIMS2_MIP176	CATTATACCCCAAATCTTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAAAAACGCTGGAA	1
M00764_RIMS2_MIP177	GGAGATTATGGCCGCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTTGATCTTTGATGTCA	1
M00764_RIMS2_MIP178	GACGATGATCTGTTGGCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTACTAGGGAGGAAG	1
M00764_RIMS2_MIP179	ATTGTTGTCACAGCAACCAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTCAAACTTTTCCCA	1
M00764_RIMS2_MIP180	CAGCTGCTATGAACGAGAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTGCTTTGTATCCCT	1
M00764_RIMS2_MIP181	GTGAAGAACTATCAGATTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAACACTGCATGCT	1
M00764_RIMS2_MIP182	GCTCTGCTCTTTCACCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAATATAAAGGTGCCAT	1
M00764_RIMS2_MIP183	AGTGTAATCCTAGGAAGCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACAGAAGCCCTTTTC	1
M00764_RIMS2_MIP184	CACCTGTAACACCGCTTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAAAGTCTGCCACTC	1
M00764_RIMS2_MIP185	ACTTTTTTTGCATGGACACAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCAGTCCAGCAGG	1
M00764_RIMS2_MIP186	GCCACAGAATTTTGTTTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGAAAATGGCTGATT	1
M00764_RIMS2_MIP187	GTGATACAAAGATACACCATGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTGGGGCTGCAA	1
M00764_RIMS2_MIP188	CCTTTTTAAAACCATGCACTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGTCACATAAAGAG	1
M00764_RIMS2_MIP189	ATATGTGCAAATTTTTCACATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGTTTTGGCAGAC	1
M00764_RIMS2_MIP191	CTTTCTTTATTTCAAGCATGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAGAGTGAACCTTA	1
M00764_RIMS2_MIP192	CCCTTGAGAAATTCGCAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATAAACTGCAAAAGTT	1
M00764_RIMS2_MIP193	ATTTGTTTTTAGCACCAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATGTATTTGACGAAG	1
M00764_RIMS2_MIP194	CACAATGGCAACATGATTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAATGGAAACTGGCT	1
M00764_RIMS2_MIP196	ACAGCCCTGTGTTTCAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATAATGACTTTCTTTG	1
M00764_RIMS2_MIP197	CATTGGGTGGAGCTGCAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCAGTTTTTAGGTGAC	1
M00764_RIMS2_MIP198	ACCAAAGGCAGGGGTTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGTTATCAAAATGTACA	1
M00764_RIMS2_MIP199	ATTAAGGCCATGCACAAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAAAGTCACTGGTTA	1
M00764_RIMS2_MIP20	CAGCAATTTAGGACTCTAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGTTGCAAAGTTTCT	1
M00764_RIMS2_MIP200	ACAAATGAGATGTATGTGGATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGCACCACATAAA	1
M00764_RIMS2_MIP201	CCTGTGTACCAGCAACAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATCACTAAAAATGCCT	1
M00764_RIMS2_MIP202	GGGTCCATCAGAATGTCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAAATCATAAACCTT	1
M00764_RIMS2_MIP203	ACATACTTGTCATTATGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATACTATCCCTTAGAAT	1
M00764_RIMS2_MIP204	CAAATATTCCGTAGTCACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTATGTACAGGGCAACAAC	1
M00764_RIMS2_MIP205	GGTGATGGTATTTAACACTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTATGCCAGTGA	1
M00764_RIMS2_MIP206	CATTAGTTGGTGTTCATTACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGGAATGAGCTGC	1
M00764_RIMS2_MIP207	GCATTTCTTTAAAACGCCAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACACAGCCCTGAG	1
M00764_RIMS2_MIP208	CCGCTGCTAAGACCAGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCTGTGAGTTGCTGAG	1
M00764_RIMS2_MIP209	ATGGCGAAGGCATAACTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTTTCTTTCTGATTAAA	1
M00764_RIMS2_MIP210	GCAGAGCCTGTGCCTGAGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGTTACCACGTCTC	1
M00764_RIMS2_MIP211	CCTCAACTGGGAGAAGGAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTGGAGGGTGTGTT	1
M00764_RIMS2_MIP212	ATCGCCCCAGAAGGATATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAATAGAGAGACAGCTA	1

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M00764_RIMS2_MIP213	GTCCAATTCCCCCTATCTGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCTTCAGGTTTGA	1
M00764_RIMS2_MIP214	GGAAATGGAGGAAATGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAATGTATATGAACAAC	1
M00764_RIMS2_MIP215	GTTGTTCATTCCTGTTTCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCCTACTCTAGTGA	1
M00764_RIMS2_MIP216	AAGAAACAATTCACTAGAGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGGGACTCGCATGG	1
M00764_RIMS2_MIP217	CCAGGGACCCCAGATGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTACTTTTCTCAATAA	1
M00764_RIMS2_MIP218	GGCAGCCATGTTGTTAGGGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGACAGCTTTGGT	1
M00764_RIMS2_MIP219	GGTTCTGTGGGCATTTATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATGATAGAATTAGGCAAG	1
M00764_RIMS2_MIP22	ACTAATTTTTTCCCCCTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAGTATATATTATTTA	1
M00764_RIMS2_MIP220	AGCTGAGGGAGTTGAGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGTTTGTTCACTTAAAA	1
M00764_RIMS2_MIP221	CCTCACCTGGAAAATATGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACTGTGAAATGTGTAT	1
M00764_RIMS2_MIP222	GTGACCTGAGTCAGGGCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGATACTGAAGATACGG	1
M00764_RIMS2_MIP223	CATAGTAGTGAACAAAACAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAAGCTCCTTCAGGG	1
M00764_RIMS2_MIP23	AAAATTACGTGGTTATCCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGATTTCTTGTTGTT	1
M00764_RIMS2_MIP24	CCTCAGGAGAAGAAACCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTATGTAATTTGTGCCG	1
M00764_RIMS2_MIP25	GCCTCCTCATTTCTTAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCATTTTTAATAGAATG	1
M00764_RIMS2_MIP26	GTCTTCATTCCAAACAGAGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGATCTCATGGGCTCA	1
M00764_RIMS2_MIP27	AAATTCTATCTCCACTGGTTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTGGCAGCCAGT	1
M00764_RIMS2_MIP28	ATGGAAGGGTTATGTGGTCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCTGGACATCTCTT	1
M00764_RIMS2_MIP29	CAACCAGAGCATCAGCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTCTGTAACAGGAATGC	1
M00764_RIMS2_MIP30	AAAGGAGATAAAAATATTCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCGCCTGCTAATGA	1
M00764_RIMS2_MIP31	AACTTCCCTCCAAATCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGGATAATGTTGAATC	1
M00764_RIMS2_MIP32	GCATTTTAAATGCAGATGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTTTAGAAAGGACC	1
M00764_RIMS2_MIP33	GAGAAGTACATTTGGAAAACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGATGCTGCAAAGGA	1
M00764_RIMS2_MIP34	CCAGTAGTAGCATTGAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCACTTATTTTTAGAGTG	1
M00764_RIMS2_MIP35	CCCCAACCCTTTTCTCTTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATAGATGCTGTCGTCA	1
M00764_RIMS2_MIP36	CTTACTGCTGTTTAGAATTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCAGATGTGCTAAA	1
M00764_RIMS2_MIP37	GGGCATTCCCAGCTGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATGAACAGAGGTTGATA	1
M00764_RIMS2_MIP38	GATGGTGTCAGCAAATAGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACTGAATCTTCTACG	1
M00764_RIMS2_MIP39	AACACGCCAATCAAGTTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGATAAAACAGAATTGC	1
M00764_RIMS2_MIP40	GAGCTTTTTGGACAAACACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGGAAAAATAAGAGA	1
M00764_RIMS2_MIP41	GTAAGATATTTGGTGGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGCACTTCAATACAA	1
M00764_RIMS2_MIP44	GGTTCAAGAAGCAGCAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAATTGTGCTGCTTAAG	1
M00764_RIMS2_MIP45	CAGTTTTAAGCGTAGTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTTAAACTATTACTAT	1
M00764_RIMS2_MIP46	CACCTTCTCCTATATGAATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCCTGTAAGGAGGA	1
M00764_RIMS2_MIP47	GGATTCTATGACTCCATCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGGCACTAATCAGCT	1
M00764_RIMS2_MIP48	GTGATGGGCCTGTTAAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGGAGCCATCCTTAATC	1
M00764_RIMS2_MIP49	CAGATGTGCATTGGTTGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGTAGAGACTTTCAAA	1
M00764_RIMS2_MIP50	CGAGCATGAAGCATCATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCTACAAAAAGCTTTGA	1
M00764_RIMS2_MIP52	GGTAGTGGAAGTGTACGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAAGTATTCAACTCT	1
M00764_RIMS2_MIP55	ACAATGGTTTTAGTAGTATTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAGGAAAAGAACAA	1
M00764_RIMS2_MIP56	GAAAGAGAGGAATATTCACAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCAGCAAATCAATGA	1
M00764_RIMS2_MIP57	GATCTCTGGACACAGATGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATAAAACTGAGGTTCA	1
M00764_RIMS2_MIP58	AAGCAGAGATGAATACGAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTATGCTGATAGGCGAT	1
M00764_RIMS2_MIP59	GCCTATGACTTCTCCTGTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTACTGGATAACGG	1
M00764_RIMS2_MIP60	CAAATGCTGATCTGGAAGATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCTACCGAAGTGAT	1
M00764_RIMS2_MIP61	AAGAAACATCACTATGCCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGTTCTTTCCATTGAA	1
M00764_RIMS2_MIP62	ACTTGAGGCGTACTGACTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGAAAATCAGCGATCT	1
M00764_RIMS2_MIP63	GGGTAGTGGACTCCTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGAACTGAGAGAATCAT	1
M00764_RIMS2_MIP64	AGGAATTGGCTTCCACGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGGAAACAATGTTAAGG	1
M00764_RIMS2_MIP65	GCTCAACGAAATCTGGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTTATCTAATCAATTAC	1
M00764_RIMS2_MIP67	CCTTTTTTATTTACACCTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCTCACAGGAGACA	1
M00764_RIMS2_MIP68	ACGAAAATTAAATAGTAAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGCCTGCTCACTA	1
M00764_RIMS2_MIP69	GATTAAGGACTCTGGGGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGGGAAAAAGAAAAA	1
M00764_RIMS2_MIP70	GAGGTTCAGACCATTCCAAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGCAAACGAAGAC	1
M00764_RIMS2_MIP71	GCCCCAATAAATTCCCAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGAAGATTTTGAAAGC	1
M00764_RIMS2_MIP72	GCATCTTTTCTTCCCGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCAAATGTAATGTTTTA	1
M00764_RIMS2_MIP73	AATTCTACGCAAGTGAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTACAGTTCTCTAACA	1
M00764_RIMS2_MIP74	AGTGCTTTGAAATGAAAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGATTTTGTAGAGCTAT	1
M00764_RIMS2_MIP76	ATCGTTTAATTGGTCGCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCGTACAATCAGAGAT	1
M00764_RIMS2_MIP77	CCATCTTTAGATGGTTGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAGAGTATAGAGCCAA	1
M00764_RIMS2_MIP81	CCTGATTCAGGAATTCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTATTAGGTTAGCAC	1
M00764_RIMS2_MIP82	CCATGCTCATTTTAACAATATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGCTCTTAGGGCA	1
M00764_RIMS2_MIP83	CAATTTGCAACACCTAAAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATAAATGCACAAAGCCG	1
M00764_RIMS2_MIP85	GAGAACAACAGTTCCAGTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTATAGTGGGTGTCA	1
M00764_RIMS2_MIP86	AACCTGAACCACAAGTAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGATCAAATTTTCTGT	1
M00764_RIMS2_MIP87	GGCTCCTTGCAGTAGTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTAACACTATTCAACTT	1
M00764_RIMS2_MIP88	ACTTTTTCTCTTTCCTTAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCCTATTGGGTAAG	1
M00764_RIMS2_MIP89	AAGACAGAAACTGTTTCAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATCTCTGATGAATGC	1
M00764_RIMS2_MIP9	CCGTGAGGTGGCTGAGGTCAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGGGGCGGAGGGC	1
M00764_RIMS2_MIP90	GTATTATTTCATGTCACTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGAAGAAAACGTT	1
M00764_RIMS2_MIP91	GCTTACAGACTTGATAACAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTAGTATACCTTAAT	1
M00764_RIMS2_MIP92	CCTGCCACCACGTCCGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGAGACAGAATCTCATT	1
M00764_RIMS2_MIP93	GCTGGAGTGCGGTGGCGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACAGAACATTGCTGATA	1

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ID	MIP	*c*
M00764_RIMS2_MIP94	GCTGGAGTGTGGTGGCGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACAGAACATTGCTGATA	1
M00764_RIMS2_MIP95	CAATGGCTCTTCACAAGTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAACTGTGGGACATC	1
M00764_RIMS2_MIP96	GATGCTTGTTTTTTACAAACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGTTACCTCTCCCA	1
M00764_RIMS2_MIP98	ATTCAAGTTCATAATTTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTTTTGAAATCCAATT	1
M00764_RIMS2_MIP99	GGAACTAAAAGACCAAAAGTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGGCAGACAAGGC	1
M00764_SEMA6D_MIP1	AAAGGGCACGTGTGGCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCATGAAACTAAGAACA	1
M00764_SEMA6D_MIP10	GCACCGCGGGCCCAGGCGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTCAGCAGCTCCTCG	1
M00764_SEMA6D_MIP100	CACCTGATTCTCACCATCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCTGAAACCAAAGGT	1
M00764_SEMA6D_MIP101	ACCATAATTATCCTGCAGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATTGTGCGAAGGG	1
M00764_SEMA6D_MIP102	ACGGCCATCAAGAGGTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATCGAAGCATGGGTGAT	1
M00764_SEMA6D_MIP103	CCAATCTGCCAATGACTTTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGTGTGGCTCTGAA	1
M00764_SEMA6D_MIP104	CATTTGGCTTGAATTGTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACCAGTTTGTTTTTAA	1
M00764_SEMA6D_MIP105	GCCTTGCCTAAATTATTATGTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGTTGGCCCTAT	1
M00764_SEMA6D_MIP106	AATCTAGCAGTCTTCTCTCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAATACACAGCCTG	1
M00764_SEMA6D_MIP107	GTCCCTGGAGATTCGTTTTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTTCTATCCGTTGG	1
M00764_SEMA6D_MIP108	AGTTCAGCCGAGCCTTTAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTGCTCTCACCTA	1
M00764_SEMA6D_MIP109	CCTTTTCAGCATCCCTGGTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTCGGGGTGTTTAC	1
M00764_SEMA6D_MIP11	GCCAGACAAGGGACCCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGGGCAAGCCTTTTCC	1
M00764_SEMA6D_MIP110	AGAAAATCATCAGGAAGAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTGTCTTCGGGAACT	1
M00764_SEMA6D_MIP111	GGCCAACCTCCCACACCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGATTCTGTTTGGACAG	1
M00764_SEMA6D_MIP112	GTTGTGCAAAACACGGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTTCACTCACTCTCCTT	1
M00764_SEMA6D_MIP113	GGAAAACAGCGTTATTTTATGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGGTGGAACGGC	1
M00764_SEMA6D_MIP114	CCCTTCTGATCTGTGCCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCTCATCCCCTGATGGA	1
M00764_SEMA6D_MIP115	AGGCCAACGGGCAGAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTAAGTACCATGCCAG	1
M00764_SEMA6D_MIP116	GAACGCCCTTCAGCACTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCTTTGTTGGCTCTGAA	1
M00764_SEMA6D_MIP117	GTAGGCTTCAATCTCTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAACACTATTATGCCA	1
M00764_SEMA6D_MIP118	ATAATGCAGCCCTTGTTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCTCTAAATTAGCAG	1
M00764_SEMA6D_MIP119	ACTCATCAACCATTCACCCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGTGTATGCAAGCT	1
M00764_SEMA6D_MIP12	GACAGCCTAGTAAATTAAACCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAGGCTGCCGGGA	1
M00764_SEMA6D_MIP121	CATTCTGTGTATGTATGTGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTCTGGTTCTCTCC	1
M00764_SEMA6D_MIP122	CATCATAACAGGAAAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAAATGGAGCCAAGGGG	1
M00764_SEMA6D_MIP123	GATCGTGCTTTAATGCATATAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCTACTTCTCTGCA	1
M00764_SEMA6D_MIP124	GCTAAAGCAAACCACACTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCCTGAAATTTAAC	1
M00764_SEMA6D_MIP125	ATTACTGAGACCTGGGAAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGTGGTGATCTTTATC	1
M00764_SEMA6D_MIP126	GTTTCTTTACTTACCCTGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAAAAAGGTCATCTC	1
M00764_SEMA6D_MIP127	CACAGCGACTGAGGGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCAATACAAGACCTGTG	1
M00764_SEMA6D_MIP128	GATGAACTATCCTCTCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTACATTCTGTTTGGTTT	1
M00764_SEMA6D_MIP129	GCTCATGTGACAAAGTATACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTGTCACGTCTCCT	1
M00764_SEMA6D_MIP13	ATTAGAGTCAGATCTAAGTTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCAAGAGAAAGCGG	1
M00764_SEMA6D_MIP130	GCATTCTAGTTCACCAGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACAGGAAAACGAAAA	1
M00764_SEMA6D_MIP131	GAGAACAGAAGAGAATTGGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAGCAGAACCAAGA	1
M00764_SEMA6D_MIP132	GCAACACAGCTCATCTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTACTAATCAGTCTGTG	1
M00764_SEMA6D_MIP133	GCAAAGAAGTCTTCGGTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAATGTGGTCAAAAA	1
M00764_SEMA6D_MIP134	CAACCTTTTCTTTCCTTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGTTACTTTTCACTG	1
M00764_SEMA6D_MIP135	CAAACTTTTCTTTCCTTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGTTACTTTTCACTG	1
M00764_SEMA6D_MIP136	AAAAAACTAACCAGATGTTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACCATCAGTGGGAA	1
M00764_SEMA6D_MIP137	GCTAACATAGACTGCATTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCGCTTTGACTCAT	1
M00764_SEMA6D_MIP138	GTCAATGATGAAGTGTTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAATACAGATGACCAGAA	1
M00764_SEMA6D_MIP139	CAAATACACATTTCCCATAAATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCCAAGCTTTCT	1
M00764_SEMA6D_MIP14	GCTAGTCGAGTTGCATGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTGTTATTGACAGCTG	1
M00764_SEMA6D_MIP140	GAGGAGAGATGGGGAAAATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCACACCACTGAGA	1
M00764_SEMA6D_MIP141	GTAAAAACACGCCTGAGGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTCCATGTCTGTGGT	1
M00764_SEMA6D_MIP142	ACTGACAAGCTCTCGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCTTGACACTATCCATA	1
M00764_SEMA6D_MIP143	GGTCTCCAGGTATCAATCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTTCCACGCAGTTAG	1
M00764_SEMA6D_MIP144	CCTCACAGGAGCTTCTGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACACTTCTGATTTTACTG	1
M00764_SEMA6D_MIP146	ATTGGAAACCTGATACCATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAATGGTGTTACTA	1
M00764_SEMA6D_MIP147	GCCTTAGTACTAACTTAAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTCTTCTTTCTGCTT	1
M00764_SEMA6D_MIP148	GGAATTCAGTGGCACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTACATGCTATAAACAC	1
M00764_SEMA6D_MIP149	ACTAATTTGCTCTTCTTTTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTACTCTGGGATAGC	1
M00764_SEMA6D_MIP15	GAAGGCACAAATGGAATAAATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAGCATGCGGCCA	1
M00764_SEMA6D_MIP150	ACTTAACCTTTTAATGCAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGACAGTCTAAGGA	1
M00764_SEMA6D_MIP152	GCTATAAATAGAGACTTTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGATATAGGAAAATG	1
M00764_SEMA6D_MIP154	ATAGCTAACTTTAAACTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGATAACTCTAATCTCC	1
M00764_SEMA6D_MIP155	CGAGCTAAGCATATGAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAACAGAAGAATACAGAT	1
M00764_SEMA6D_MIP156	AGGGTCAAGTAGACTCCAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCCATCGTACACCTG	1
M00764_SEMA6D_MIP157	GTGGCAGTATACTGCTATCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGTCCCATGTGTCTAT	1
M00764_SEMA6D_MIP158	CAATGAATGCCCCCAAAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAGAGACCATTCAGT	1
M00764_SEMA6D_MIP159	ATGGAGATACTAAATCCATGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACTCCAGTGGAAGT	1
M00764_SEMA6D_MIP16	GTTCCTTTCGTTGGATGGTAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGTAGACGTCCA	1
M00764_SEMA6D_MIP160	GGTTAGCAGGTTACTATACAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGGGTCTTCTGGT	1
M00764_SEMA6D_MIP161	GTTTTTTCCGTCTAGTCCGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTCCAGAGTTGGCTG	1
M00764_SEMA6D_MIP162	AGGGGTTTCTTTCCTTGAAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTTGTGAGCATTGG	1
M00764_SEMA6D_MIP163	ATCTCCTGAAGCATCTGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACACGTCTTTCTCAAAC	1

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ID	MIP	*c*
M00764_SEMA6D_MIP164	ATTGAGGGTATTTCTGGAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGACTTTAGGTGGGA	1
M00764_SEMA6D_MIP165	CCCACCACTCCTGGAGTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGAACTTAATGCTGGA	1
M00764_SEMA6D_MIP166	ACATCCACTCGCTTGGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGATAACAAAACACCATT	1
M00764_SEMA6D_MIP167	CAGCCTTCCCTCTCCAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAAAAACTTAAACTCACC	1
M00764_SEMA6D_MIP168	GTTCCCTGAATATAGTCCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAGGCTTTGGTGG	1
M00764_SEMA6D_MIP169	GTTGAGAGGATGATGTTGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCCTTAAAACCTGACG	1
M00764_SEMA6D_MIP17	GTATGCAGAAGTCTTTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTCCCAGCAAAATGC	1
M00764_SEMA6D_MIP170	GCCACATGGGAATAGCACACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAAGTTCTGATGTTG	1
M00764_SEMA6D_MIP171	GTGTAGCTCACAGGGGCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAACTCTTTCTAACTTTG	1
M00764_SEMA6D_MIP172	GCTTCAAACAAAAGAAATGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAAGACCACACATA	1
M00764_SEMA6D_MIP173	GATTACCAAGCAGTTTGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAATGTAGACTGCCA	1
M00764_SEMA6D_MIP174	GCAAGGTGAATGCATACATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGATGCCACACATGAA	1
M00764_SEMA6D_MIP175	GGATTTGTTTAGGTGCCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAATCTTTGACCCAAGC	1
M00764_SEMA6D_MIP176	ACACACGCACACACACAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGGAAATAGTATTGTC	1
M00764_SEMA6D_MIP177	CAGAATGTAAGAGTTGCAAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCATGACCGAACGAG	1
M00764_SEMA6D_MIP178	AGCCTCGATTCTATTCCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGATCTCCTTAAGCT	1
M00764_SEMA6D_MIP179	CCTGAGTCACTCTATTTAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTGCTGCTATTCATT	1
M00764_SEMA6D_MIP18	CGCATTTAACTCTAGGAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCAAATGGCACTATTA	1
M00764_SEMA6D_MIP180	GATTCACAGTGGACAGGAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTCTTACCTTGGGG	1
M00764_SEMA6D_MIP181	CAGTGGTGCAATCATGTTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTTTAACTCCTCCTA	1
M00764_SEMA6D_MIP182	CAGACTGTTTCTGTTAAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAAATGCACAGATTCA	1
M00764_SEMA6D_MIP183	AACCAGCACCTAAAAAGACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCACATGTGAGTTTAC	1
M00764_SEMA6D_MIP184	AAACACTTGACAGATTTTAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATGAGGTCGGATTA	1
M00764_SEMA6D_MIP185	GGTAATGTGACACCTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAACCTAGGACAATTATTT	1
M00764_SEMA6D_MIP186	CACTGTTTCATCCTTAGGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTGAAACAGTCAGCA	1
M00764_SEMA6D_MIP187	ACTGGATTTCTTTTGACAATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGATGATGCGCAACC	1
M00764_SEMA6D_MIP188	AGCATACCTCTGCCTTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTGTATCAGTATTTCAC	1
M00764_SEMA6D_MIP189	GCTAAAGCTAAAATTTCTGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGGGGGAGGACATG	1
M00764_SEMA6D_MIP19	ATAGTAAGTGGGAAAATACACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCCTTCTTTTGATT	1
M00764_SEMA6D_MIP190	CCAGAGATCACTGGAAATCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCAAACACGTTTGTTG	1
M00764_SEMA6D_MIP191	GTTTGTAATGTGAGTTCAATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTACTCAGTCCACCA	1
M00764_SEMA6D_MIP192	CAAGGAAGCACAATGTTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGATACAATCTGCGT	1
M00764_SEMA6D_MIP193	GTATTGTGGATGTGTAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCCATTTGTGCAAAGGT	1
M00764_SEMA6D_MIP195	GCTCTCCAGTCATGATTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATTATATCCTGCCTC	1
M00764_SEMA6D_MIP2	GAGCCCGCTTCCTCGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATCTAACCGCTGTTCAT	1
M00764_SEMA6D_MIP20	GTACAGAATGCGACATGTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAAACTTGGGGCTTG	1
M00764_SEMA6D_MIP22	CCAGGGTGAGGCTACTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCCCTTGGTTTTTGAA	1
M00764_SEMA6D_MIP23	AATAGAATCTCTCTCTGTGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCATCTTTTGAGTTGT	1
M00764_SEMA6D_MIP24	GGCCTAAAGTGCCCCAGAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTCTATGGTATGGT	1
M00764_SEMA6D_MIP25	CATGGTTTTCAATCATGCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTATCTCAGAGACAT	1
M00764_SEMA6D_MIP26	CAATGTGATTGGACAAAAAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCTCTCTCTGGGTG	1
M00764_SEMA6D_MIP28	CAGATGAAGAGATGTGTAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACAAGTCTGGGCCC	1
M00764_SEMA6D_MIP29	GAAACTTCTCTTGAGTAAGAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGCATTTCTTCTGTG	1
M00764_SEMA6D_MIP3	GCTCATTTAAAGAAATACATCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACTTTGTGGGCCT	1
M00764_SEMA6D_MIP30	AATTCCCTCTATTGACCTTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGACTTTGGCTGT	1
M00764_SEMA6D_MIP31	CATGTCCTGATTGCAGTTTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTCAACTACCCAA	1
M00764_SEMA6D_MIP32	CATGTCCTGATTGCAGTTTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTCAGCTACCCAA	1
M00764_SEMA6D_MIP33	ACCAACCCAATTTTAATGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATCTCTACCTGGATGT	1
M00764_SEMA6D_MIP34	CAGCTGTGTTTAAGAGGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTATTTGTCCTGCTTG	1
M00764_SEMA6D_MIP35	ATGCAGCGCACCAGTGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAGGAAAACATTCATGA	1
M00764_SEMA6D_MIP36	CACATTTGCTTGCAGTGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGACAGGATTAGAATAA	1
M00764_SEMA6D_MIP37	AGTGTTCCCATGTCAACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATACCTAAACAACTTCAG	1
M00764_SEMA6D_MIP38	GTAAGGCATGAACTTTTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCATTTGTAGCTAT	1
M00764_SEMA6D_MIP39	CCAGCAGTCTTGGGCTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAGGCAAAAATCAAGAT	1
M00764_SEMA6D_MIP4	GTAGAAATGTATTCCCAGGTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACATCTCCCCAGGCC	1
M00764_SEMA6D_MIP40	ACATAGTTGTGGTGTGCTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGAACAGTATGTTGT	1
M00764_SEMA6D_MIP41	AGAATTAGAGTTTACTGGTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAAGCCAACCTTTT	1
M00764_SEMA6D_MIP42	CAGCAAAAACTTATCTAAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTCTCTCTCTCTA	1
M00764_SEMA6D_MIP43	ACTCTTTGTCTCTGATGTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTGACTAAGTACTGG	1
M00764_SEMA6D_MIP44	GGGCAAGAAAAAGATACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCTTTCTAATTCTTCC	1
M00764_SEMA6D_MIP45	ACTTTCCAGGAGTATCTGTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCACCTCTCCAAAG	1
M00764_SEMA6D_MIP46	CCTGCTAGAGTTGGACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAAATGCATTCTGATTT	1
M00764_SEMA6D_MIP47	ACATTTCCAAGTTCTATGTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAATTGAGGATGTGT	1
M00764_SEMA6D_MIP48	CCTGTATTCACAAACCAGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTAGAAATCCACCCC	1
M00764_SEMA6D_MIP49	GCTGGGCTTCCAATTGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTAAGCAGCTCTATTT	1
M00764_SEMA6D_MIP5	AGGGAGCGGCAGGAGCACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAAGCAAGGTCCTTTGC	1
M00764_SEMA6D_MIP50	GGACATTTCTGCCAAACGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGAGTAGATGGACCC	1
M00764_SEMA6D_MIP51	ACTTCATTATGTATTGTATGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCTTTCTAGGTAT	1
M00764_SEMA6D_MIP52	GACTTTTTCTATGATCTGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATATGGGGGTAGCA	1
M00764_SEMA6D_MIP53	GTCATCTTACTCTATGAAACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTCGCTGTTTGTAC	1
M00764_SEMA6D_MIP54	GGAGCAGAGAAAAGACTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTGTTTTTCATCCCTT	1
M00764_SEMA6D_MIP55	ACACTTCAGTGAGAGTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTTACAGATGAGGAAC	1
M00764_SEMA6D_MIP56	CAGAAAGGACTTCCTTTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGAGGGCTCTAAATGG	1

continued table…

ID	MIP	*c*
M00764_SEMA6D_MIP57	GGAATATGTGACTTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCTTTAAACAGGGGCA	1
M00764_SEMA6D_MIP58	CAAACTTCATTTCCAAGAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAAGTGTTTCATGT	1
M00764_SEMA6D_MIP61	GCAGTGATTTGTCCTCTGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGAGAAATGGGGGGC	1
M00764_SEMA6D_MIP62	GAAGTTCTGCCTTAGTTTTCCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTGCGAAGCAAC	1
M00764_SEMA6D_MIP63	GGTGGGGAGAGGGAGGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGCTCTGAAAGAAGTG	1
M00764_SEMA6D_MIP66	GGCTCCCTCCACGCACTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAACTCGCCACCACCCC	1
M00764_SEMA6D_MIP67	ATATTTTTCTTTATTTTCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATCGGTTTGTTTT	1
M00764_SEMA6D_MIP68	GTAAAAATAGATATCCCTCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCACAAGAGCATTA	1
M00764_SEMA6D_MIP69	ATCGCTGTGTGTGTGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCGTTTTCAACAATTTG	1
M00764_SEMA6D_MIP7	GACCCACCAGGACTAGGAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGGGGTGGGAGGAC	1
M00764_SEMA6D_MIP70	GATCTCAGGTTCCGACCCCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCCCTTTGCGCGTC	1
M00764_SEMA6D_MIP71	ACTGTGCACCCCCTTGGAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAAGCTGCTCTCTC	1
M00764_SEMA6D_MIP78	AAGCACGGAAAGTTGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTTCCTTATTTGTTTCC	1
M00764_SEMA6D_MIP81	CCTCTGGCTATTTTTGAGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACGTTGGTCGTAGTA	1
M00764_SEMA6D_MIP82	ATCCTGTCATAATCTCTCCTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGATAAGAATTTTA	1
M00764_SEMA6D_MIP83	ATTCTCGTGAATTTGCTGAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAAGAGGATTGGAA	1
M00764_SEMA6D_MIP84	GGAGGTAATTGTATGTCATCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGGAATGCTGGCA	1
M00764_SEMA6D_MIP85	GCTTCTGTTTTCCAGGTAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGATACCTGATCTAC	1
M00764_SEMA6D_MIP86	CAATGAAGCGGTTTTCTTGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCAGTATGTAGGCA	1
M00764_SEMA6D_MIP87	GTCTTCTATTCTGAGAAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGAGGGTCTTCCTGC	1
M00764_SEMA6D_MIP88	ATAGTCGACAGTATTAAGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGATGCAAATTCAAGG	1
M00764_SEMA6D_MIP89	CATTCAGGATTATGGAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATATAAAGGGTGTCTCG	1
M00764_SEMA6D_MIP90	CATTCAGGATTATGGAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATATAAAGTGTGTCTCG	1
M00764_SEMA6D_MIP91	GTGTGTCTAGTTCATGAAAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCGCAGCACAGGCT	1
M00764_SEMA6D_MIP92	ACAAAGTCAACAAAGAGTACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCTGTTGGAAATAAG	1
M00764_SEMA6D_MIP93	CAACTGTAGTTGGCAAATTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAGCAGCTTAACA	1
M00764_SEMA6D_MIP94	GGTATTACTTCTGTTTTGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTCTGTATTAATCAAG	1
M00764_SEMA6D_MIP95	GATTTAGTCTTTCTGTGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCAGTTAAAAACTGCTT	1
M00764_SEMA6D_MIP96	GCAGACATTTTTCTGTTTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCGTTTCTTGGAACAA	1
M00764_SEMA6D_MIP97	CAACTTTTCTCCCTTCACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCACAACTTTATCAAA	1
M00764_SEMA6D_MIP98	AGAAATTAGTGGCCTGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGACAGAATTCTTCAAAT	1
M00764_SEMA6D_MIP99	CCCCATCATATTCTAAGGTACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATTCCTTTTTCACC	1
M00764_SETBP1_MIP102	GCTCACTGCGCTTCCCACGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCTCCCTGCTTTGCTT	1
M00764_SETBP1_MIP104	ATCCAGCCGTACTGAAGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGTGTTTCCCTTTCGA	1
M00764_SETBP1_MIP105	ATTTTCAAGCTCTGCTAAGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGCTGGCCAGGAAA	1
M00764_SETBP1_MIP106	AAACCAATTAAATGGAACGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTAGAATTCCACCTT	1
M00764_SETBP1_MIP107	CCTTTGCCCATTGTACTTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCTCGATGGAATTGT	1
M00764_SETBP1_MIP108	AAAATAGGAATAGACAATGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGCATGCCAAGG	1
M00764_SETBP1_MIP109	ACCCAGATGTCAACCAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTGTGCTGTAAAGTTCA	1
M00764_SETBP1_MIP110	AACATATCCTTGGCTGCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTGGGGTTTCAGTTT	1
M00764_SETBP1_MIP111	AAACAAAAACACAATAGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAACTGACAAACCACCA	1
M00764_SETBP1_MIP114	GGCAACCACAATTTGGATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTACAACTTGGATGAGAA	1
M00764_SETBP1_MIP115	CCACAGCCCAAATAAAATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCATGGATGCAAACTG	1
M00764_SETBP1_MIP116	CCACGCTAAACCAATGGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTATTTGAAATTTCCACA	1
M00764_SETBP1_MIP117	AGACACTGAGAGAGAGAATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCATTTCCGTAGATG	1
M00764_SETBP1_MIP118	CATGCCAGGTGTTTGATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCGAAATGATAATACAATT	1
M00764_SETBP1_MIP119	GTGATGGGGTATCTATGTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGGTTTACCTCCAAA	1
M00764_SETBP1_MIP120	ATCCATCTCTCTCTAAGGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACGTGGGTAATTTCAAC	1
M00764_SETBP1_MIP121	GACTGCATTCCCCTCTACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTATGGCACCAAGAGTT	1
M00764_SETBP1_MIP122	CATATTGCTAGGATTAAATGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGAATTAAAAATGGCTG	1
M00764_SETBP1_MIP123	GCTATAAAACAGCAACGTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCATTTCACGCAAGTT	1
M00764_SETBP1_MIP124	ATGGTGGGGTGAGAGGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGGAGAGATAGTACAAC	1
M00764_SETBP1_MIP125	CATTAACCTCTAGTAGGTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGCCCTTCTTCCTTC	1
M00764_SETBP1_MIP126	GGTCCTTATTAAAGAAGTTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACGTGTAAGTTGCA	1
M00764_SETBP1_MIP127	GCATGCTAAACAGCTGCTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGATTTAACAGCAGAG	1
M00764_SETBP1_MIP128	CAGCTTTGGTCCTCTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGAGTTAGGTTAATGAA	1
M00764_SETBP1_MIP129	CGTGGGCCAATGCAGCTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGTATCACATTATTTT	1
M00764_SETBP1_MIP130	GAGAGGCTAAAGGAATTGGGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAAGGCAGTGTTG	1
M00764_SETBP1_MIP131	CCCTTGATTTTTATTTCTTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGGTCTCTGGCCC	1
M00764_SETBP1_MIP132	GTGAAGCTGTATGTGGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCATCCTTTTCTCATCAC	1
M00764_SETBP1_MIP133	ATCTCAAATGAGAGGAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTGTAAGGAGTCTGGT	1
M00764_SETBP1_MIP134	GGTGGAAGAGCAAGTAGCTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCCTGCCAAGTCA	1
M00764_SETBP1_MIP135	GTTCAATGGCAGTCAGAATTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTCAGGGGCTGGTT	1
M00764_SETBP1_MIP136	GGCCTCCTAGTCCGGACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCTTAAAACCAAAGCCT	1
M00764_SETBP1_MIP137	AAGATTTACCTGGGAACTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGATGTACTACATGCA	1
M00764_SETBP1_MIP138	AAAGATATTCTCCAAAAGCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGGCTTTTGAGGCA	1
M00764_SETBP1_MIP140	GGGTAGTGTTGAGAATAACGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCTTGTATTGTGGAA	1
M00764_SETBP1_MIP141	GAAGCACATATCAACCAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTCTTGGTGTTTCTT	1
M00764_SETBP1_MIP142	GACTGTTCCCCAAATGACTGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACCGCCCTTCCAC	1
M00764_SETBP1_MIP143	ATGCACATGATGTGTTAAATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACACTAAAGGGGGG	1
M00764_SETBP1_MIP144	AGAAAAAGAAAGACACCAATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTAGCCAGCACGA	1
M00764_SETBP1_MIP146	GTTCTAAAATATGTTTACATACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGCAAGTCCATGTT	1
M00764_SETBP1_MIP147	AAAGCTCAGTCTTTTCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAAGCATTTTTGTACAT	1

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M00764_SETBP1_MIP148	GAAAAAAATGTTTAAAACCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAATTGAATGTCTTTA	1
M00764_SETBP1_MIP149	ACTGGATACAGAATCATTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTCATTGTGTGAAA	1
M00764_SETBP1_MIP15	GTCTCTTTCTTGTGCTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGAATCTAACGTGTCG	1
M00764_SETBP1_MIP16	CATCCTCCCTCCCCTCCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCAGAGCCATAGAC	1
M00764_SETBP1_MIP17	GGTAAAAGACTCATAGTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGAGTGTACCCATA	1
M00764_SETBP1_MIP18	GGGTTGGGACGAAAGTCTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTCCAAAACTTTGTC	1
M00764_SETBP1_MIP19	ATTTTATCTTTCCAATCCTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAACAGCAGAGCTAG	1
M00764_SETBP1_MIP20	GCTTAGGAGATAACAGCCTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATGGACACTCTGTAC	1
M00764_SETBP1_MIP21	CATTTTTACCTTGCCTTGGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCTGCAGGCAGTC	1
M00764_SETBP1_MIP22	GCCTTGTCACATTCCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTTTTTGGTGAGTCTGG	1
M00764_SETBP1_MIP23	CAGACAGGTTAGGTTTCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAATCACAAGAGGACT	1
M00764_SETBP1_MIP24	CATCAGCACACAAAGCTGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATTTGCTGCCTATCC	1
M00764_SETBP1_MIP25	CAGTTGCAGATCTGATCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTAGCTGTTTTTCCATC	1
M00764_SETBP1_MIP26	GAAGCAAAGAGACAGTTAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAAAAGGGAAAGGT	1
M00764_SETBP1_MIP27	GTCAGACTTCCTGCCGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGGTGTCCTCTTTTCT	1
M00764_SETBP1_MIP28	CCCTGGACTCCATGACAATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCTTCCCAGGTCCT	1
M00764_SETBP1_MIP29	ATGGGTGGCAGGAGATGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCTTTGCTCTCCACTC	1
M00764_SETBP1_MIP30	GCGTTGGAGTTGGAATCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGGGGTTTCTTAGC	1
M00764_SETBP1_MIP31	AAGCCACGAAGGAGGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGATTCAGACCACAAAG	1
M00764_SETBP1_MIP32	CCAGCACGGGACACCTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAGACCCTAAGAAGTTG	1
M00764_SETBP1_MIP33	CAGAAGGCAAATGTGAGATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAGGAGCTGCAAAA	1
M00764_SETBP1_MIP34	GTAAGTTCCACTGATGCTTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTCAGTTGTCGTG	1
M00764_SETBP1_MIP35	GTGGCTGAAATCCTTTGAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGCTAGGGAAAGAAGC	1
M00764_SETBP1_MIP36	AGCCTCCTCATTTTCTAGATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGACAGGAATTATC	1
M00764_SETBP1_MIP37	ACTTAGATTTTGGAGAGCTTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGCATGAGAAGCA	1
M00764_SETBP1_MIP38	GCATGGATTCTGCAAAGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCAATTCCTGTCCCAG	1
M00764_SETBP1_MIP39	AAGTTATACTTCTTGTGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTAGCAGGCAGAGAAG	1
M00764_SETBP1_MIP40	CAGCATTCACTGTCTTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGACAGCATTTGGGCTTA	1
M00764_SETBP1_MIP41	GATCTTTTTGGATTATCTTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCATGTGTTTCCTA	1
M00764_SETBP1_MIP42	CCACAGCTGGCCTGTCAAGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTCAGACGATCAC	1
M00764_SETBP1_MIP43	GGAGCCCATACTCTGTATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTATAAGACAAATCCGT	1
M00764_SETBP1_MIP44	GTTAACCAACACTGAGCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAAGCATGTGATTGT	1
M00764_SETBP1_MIP45	AACAGAGCTTATCAAACGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTGGAGGGTGAAC	1
M00764_SETBP1_MIP46	GACACGGGCCTCCCACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTTTTGATGTCAAATAT	1
M00764_SETBP1_MIP47	GTGGAGTGGAGAGGGAGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTGGTTCTGGCTGCT	1
M00764_SETBP1_MIP48	AACTGCAAGCACCAGCAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACCGGTGACACCTTAA	1
M00764_SETBP1_MIP49	GCCAGACTCTGGACTGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAGCAGATCTTTGTTAT	1
M00764_SETBP1_MIP50	AAGATGGAGGAGGTACAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGTCAGTTGTCTAAC	1
M00764_SETBP1_MIP51	GGGTGGGGCTGGTGAGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTGACTTATCACATCTT	1
M00764_SETBP1_MIP52	CCCAAGAGGCATCACCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGAAAAAGTCCAGTAAA	1
M00764_SETBP1_MIP53	ACTATCTGCGGAATAACCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCTCTTATGGTTGG	1
M00764_SETBP1_MIP54	AGGATACTTTCCAACTCTGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCACCCTCTCTGGA	1
M00764_SETBP1_MIP55	ACTACTTCACTGCTCATGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATAACTTTCTCAGC	1
M00764_SETBP1_MIP56	CATCCAAAATTTGCTGCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGAAACTGGTGGAAA	1
M00764_SETBP1_MIP57	GGATTTCTGGCAGCTTTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGATGGGATATGCAGAC	1
M00764_SETBP1_MIP58	ACGACCAAAGAAGCAGCCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGTTATGGCCACCT	1
M00764_SETBP1_MIP59	CCCGCTTCTTTTTGACTGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGCTAAATTGCGTCGT	1
M00764_SETBP1_MIP60	GGATAAGAAGACCATCAAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTTTCCTGGCACTA	1
M00764_SETBP1_MIP61	CCGAGCTTTCCAACTTTCTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCTCTGGGGGAGC	1
M00764_SETBP1_MIP62	CATTGGCAAGAAGCGGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCAGATCTTGTCCTGTT	1
M00764_SETBP1_MIP63	GCTTGCCCAGTTTGCTTTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTAGAAACAGGCCTG	1
M00764_SETBP1_MIP64	CCAATGGCAACCTGAGCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAACAGCCATCAAGCAC	1
M00764_SETBP1_MIP65	CCCACCTAACTGTGTTGAAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCAGGTTCCACTGT	1
M00764_SETBP1_MIP66	GTCCCACAGTGAGGAGACGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACCAAAACCCAAAAGG	1
M00764_SETBP1_MIP67	CACAGGGGACAGCGTGATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGGGAGCAGAAATCAA	1
M00764_SETBP1_MIP68	AAAGCCTCAAGAAGCCAAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCGAAGGAGGTACTCT	1
M00764_SETBP1_MIP69	GTGGGCCAGAAAGTTGTCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCCGGTGGGAGATTC	1
M00764_SETBP1_MIP70	GCTCTATCTTCGTAGGACTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAAGTTCCAAGTGT	1
M00764_SETBP1_MIP71	CGGGTCATACTGGATATATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTTCCACTGGGAATAG	1
M00764_SETBP1_MIP72	ACACGCTTGGAGCAGCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTTACAAGGGTTCAGC	1
M00764_SETBP1_MIP73	CGATAGGTACAAAGGAGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCTGCAGGTGTACTC	1
M00764_SETBP1_MIP74	AACACAAACACAAGCATAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCATAAAGCCAAGCAT	1
M00764_SETBP1_MIP75	CGACCACTGGACAGACTGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTCGCTCAGGATGTG	1
M00764_SETBP1_MIP76	ACAAAGCTTCTAAGAACAACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGCCACAGGCTTC	1
M00764_SETBP1_MIP77	GCTGTGCTGGTGCTTCTGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGTCCACAGGCTCAC	1
M00764_SETBP1_MIP78	AGTGGGACAGTGACGTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAAGGAGACTTGAGC	1
M00764_SETBP1_MIP79	GTCATTCGAAGGGTTCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACATGGAGGAGTCAT	1
M00764_SETBP1_MIP80	ACTAGTTTGCAAAGAGGTGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAAGGAGAGAAGTT	1
M00764_SETBP1_MIP81	GTGCCACAGATGTGTCTGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGCTCCAGGAGAGAA	1
M00764_SETBP1_MIP82	GCCCACTATGGTTATGCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCACATTTGAGTTTGC	1
M00764_SETBP1_MIP83	GGTTATGGCTTCACAGTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTAATGAGTTTTAGAG	1
M00764_SETBP1_MIP84	CTCCACAAGTCACACATCTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCTCATCTGATCTAA	1
M00764_SETBP1_MIP85	ATTAGCTAGTCATTTCCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACAATATGGCCCAAGGCT	1

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M00764_SETBP1_MIP86	CACTAAGTGGAAGGAGGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACTCATCAGGTAGCCA	1
M00764_SETBP1_MIP87	AGTTTTCATTTTAGGGACCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCCCTTTCTAGTGGG	1
M00764_SETBP1_MIP88	CCAACCTCCCCAACCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAGCAGACCTTATAACT	1
M00764_SETBP1_MIP89	GCCAGCAACTGACAAGGAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGGTCTTTATAGGGG	1
M00764_SETBP1_MIP90	GTTCCCCCTGTTCCCAAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTTACATCATATATGA	1
M00764_SETBP1_MIP91	GATGCCAAGTCCCCACTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTCTTGTTGTACCAGA	1
M00764_SETBP1_MIP92	AAAATAACAACCCCAAAGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGGTGGAATTGTAA	1
M00764_SETBP1_MIP93	CAAGATGAATGTGGAGAAAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGAAGAAGCCAGCC	1
M00764_SETBP1_MIP94	CCTCTTCACTGACAGCTAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTCCGCACTTCGC	1
M00764_SETBP1_MIP95	GCAACAACTTCGTGAAGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATCGAAGCCATCCAG	1
M00764_SETBP1_MIP96	GTTTTTGATTGTCTCTGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGGCCTCTTTTGCT	1
M00764_SETBP1_MIP97	CAAGACACCATCATGGCCACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCAGCCCACCCAGTT	1
M00764_SGCZ_MIP1	GAAGGAAAACTCAGGGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGACATTATAATGGC	1
M00764_SGCZ_MIP10	GGAGTTGTAACTTAGGAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTACAGAAGGGGAGGTG	1
M00764_SGCZ_MIP11	GGGAGCTTCCATGATCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAAAGTGGGCAGTATAG	1
M00764_SGCZ_MIP12	GTGGGGTCCAGGTGAGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCTAGTTTATCAAAA	1
M00764_SGCZ_MIP13	GGCATAAAATCCATCATTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATACTGACTGCTATAT	1
M00764_SGCZ_MIP14	CATATGATGTATTAGTCCGTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCTCCTTCAGTGC	1
M00764_SGCZ_MIP15	ACCTGTAACTTTCAGCTTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACAAACGTTGTGAT	1
M00764_SGCZ_MIP16	GTAGATGGAGGTCTTGAAAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCTGATGCTGTGGA	1
M00764_SGCZ_MIP17	ACATGTATTTTTTGGAAATAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAAAACAGCACCC	1
M00764_SGCZ_MIP18	GGTTTTTGGTTCTTGTTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTGACAGGAATGTC	1
M00764_SGCZ_MIP19	GGTTTTTGGTTCTTGTTGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTGACAGGAATGTC	1
M00764_SGCZ_MIP2	GTTTCTTTAATTTCAATGTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCGACTTTTAAAA	1
M00764_SGCZ_MIP20	GTTTGGATATTCTGAAAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTCTTGCATTCACT	1
M00764_SGCZ_MIP21	ATATACCTTCAAGTCGGATTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGATTCTACCCTGC	1
M00764_SGCZ_MIP22	GAGTTTCTACTTCCATTGTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAAGAAAATTATGG	1
M00764_SGCZ_MIP23	CAGCAGAAGGACAAAGAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAACAGAGCTAGATTG	1
M00764_SGCZ_MIP24	ACTTAGCCATGACAATATGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTAGCAACCCAACAG	1
M00764_SGCZ_MIP25	CCCATGATTTTTTTGAAACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGCATTCTCAGTCC	1
M00764_SGCZ_MIP26	GCTTCTTTTTTTTTCCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACAAAATGATTCGAAGT	1
M00764_SGCZ_MIP27	GTCAGATTTGTCCCATTTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGAGCATTCAAATA	1
M00764_SGCZ_MIP29	GGTGATGAGATCATGGCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTCTACCTCCAGTTAC	1
M00764_SGCZ_MIP3	ATCTTGCCATTGGATACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTAAAGCAAGCATTAC	1
M00764_SGCZ_MIP30	CCAGGAGCCATCTCCAACATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTATATGGCAGGAGCA	1
M00764_SGCZ_MIP31	GAGTGGCACCCAAAAACAATCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGCAGGGAGCGCC	1
M00764_SGCZ_MIP32	CGGTTCCTCTCCACTTCGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTAACCCGGTGGAGG	1
M00764_SGCZ_MIP33	GTGCAACACAGCTGAGTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCTCAGTCTCATTCTC	1
M00764_SGCZ_MIP34	AGATCACCTGTCACTAAATCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCAGCAATTCGCT	1
M00764_SGCZ_MIP35	CCTCCGTCAGGCTTACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCAATAAGCTTAGAAC	1
M00764_SGCZ_MIP36	CAGTTTGAACACATTTGCTTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAGGACTTCGGGG	1
M00764_SGCZ_MIP37	AAGGGAACGTTCTCCTTTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCAGGCATTAGCAAT	1
M00764_SGCZ_MIP38	GACTTGATTATCTTCTTTTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACAGCGAAGCAGGA	1
M00764_SGCZ_MIP39	GGATTTCTCTCATCTGTCAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAACGGAGAGAAAAAG	1
M00764_SGCZ_MIP4	ACCCTGTAAGAAAACTTATTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGGTGCCTTTGCT	1
M00764_SGCZ_MIP40	AGAGAGAAGCGAAGTCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTAAAATGATTGTCACC	1
M00764_SGCZ_MIP41	ACTTCAGATCTCTGCTGCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCTGCCCTGTGTCC	1
M00764_SGCZ_MIP42	CATGTGGGTGATACACACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCATAAGAAGCATCGT	1
M00764_SGCZ_MIP44	ATGCACTGACCTGTCAGAATCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCTCAATAGTTTA	1
M00764_SGCZ_MIP5	ACAGTAAATCACAAGAGAAGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCTTCACTTCGCG	1
M00764_SGCZ_MIP6	GCTCAACACAGAGGGTGTGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCGTCTGCTTCACA	1
M00764_SGCZ_MIP7	CCTGCTGGAGAAAGGTAAAGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGGGAAACCGAGC	1
M00764_SGCZ_MIP8	CCAGTAGCAACATCTGCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTACCAACTGGCTCCTTC	1
M00764_SGCZ_MIP9	GTAATCTACATCCCTCCTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGAGCTGGGTGAAGA	1
M00764_SKOR1_MIP1	CCTGGGAGGCTTCTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCTCTCTCTCTCTCTCTA	1
M00764_SKOR1_MIP19	CAGCCAGAGCAGCTTGAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCCTGAGTGAGAGG	1
M00764_SKOR1_MIP2	GAGCCTCAGGAGGGCAGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGCTCTTCTTTTCCT	1
M00764_SKOR1_MIP21	GGGGACTGATGTTTGGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAATCTCAGCCATCTT	1
M00764_SKOR1_MIP23	GCCTCGCTGTCCCGGCTCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTAGCTTCCAGTCGCC	1
M00764_SKOR1_MIP24	CAGAAAATGTGGTTAGAACTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAAAGCTCAAGGAG	1
M00764_SKOR1_MIP25	GCTGTATTCCAGACCAAAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCTCTCACGGCTG	1
M00764_SKOR1_MIP3	GCACCTGGGGATGCAAGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGATGGGTAGAGCTTG	1
M00764_SKOR1_MIP31	GCCAAATCCTGGCTTTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGAGAAGGGGTAAAGG	1
M00764_SKOR1_MIP35	GTACAGCTGGAGATTCTGCGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCATCGACGGCCA	1
M00764_SKOR1_MIP39	GACGTCAAGGCCATGTTTAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCCACTCGCACCG	1
M00764_SKOR1_MIP4	CATCCTACAGATGCAGATATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTAACCTAAGTAGGGC	1
M00764_SKOR1_MIP5	ACATGGACCCCCACTTTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTCTCGGGAACATCAA	1
M00764_SKOR1_MIP58	CCTCTGGTTCCCGGCTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGTCTTCCTTATCTGG	1
M00764_SKOR1_MIP59	GCAAATACAGACAGAGGTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGCCTCTCTTGAAA	1
M00764_SKOR1_MIP6	CAAATCCGGACCCTCTCCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCAATTGTTCTCCCTCC	1
M00764_SKOR1_MIP60	GACTTGGCTGGGAGATACTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGCTTACACTTGAT	1
M00764_SKOR1_MIP61	GTGAGCTTCCCAGGAACCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCAGGTTCTCGATA	1
M00764_SKOR1_MIP62	GTGGAAAAGACACTCACCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCATTTGGTGGAGAAA	1

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ID	**MIP**	***c***
M00764_SKOR1_MIP63	AATTTCAGAGTCTCAAAGGTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCAGAACCTGAGC	1
M00764_SKOR1_MIP64	CCTCATCACCGAGCCTTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCTCCCACTTTTCCC	1
M00764_SKOR1_MIP65	CTTCTTGCGGAGCTCCATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTAGTACCAGTTGCCT	1
M00764_SKOR1_MIP68	GCTCAGTCATTTGGATTTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGAGGGAATTGGC	1
M00764_SKOR1_MIP69	CCATCCAGCAGAAATTGAAAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGAGGAAGCCCG	1
M00764_SKOR1_MIP7	CCTCTGGGTTTCCGCTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAAAAGTGAGGAGAAG	1
M00764_SKOR1_MIP70	CCTGGTCGAGTTCGTTACACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCTCACTAGTCCCA	1
M00764_SKOR1_MIP71	GGGTCAGGGAATCTCAACCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGGAGAAATGGTGCA	1
M00764_SKOR1_MIP73	CGGTGGCTTGAAGGAGCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCTGTATTTACATCGGT	1
M00764_SKOR1_MIP77	GTATTCACAATCGGGTTCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATACTGAACCGAGAGA	1
M00764_SKOR1_MIP78	CATTCCCCTTTGGATTTTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGGCTATGTGCAAT	1
M00764_SKOR1_MIP79	GGGTCCAGGAGAAGGAAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGGCTCCAGGTGGT	1
M00764_SKOR1_MIP80	ACTTCTGGGGCTACGGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGTAACAGCACTTTAAA	1
M00764_SKOR1_MIP9	GCGCTGCTACCCGCGGAAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGGAAGAGAGGGGAG	1
M00764_SLC14A2_MIP1	GTCAGTTCTGTTGCACATGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGCAGGGATTACAGA	1
M00764_SLC14A2_MIP10	GAAGTCTGAAAGCAAGACGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTCTGCCACCCTGA	1
M00764_SLC14A2_MIP100	GTTCTACGTCATCACCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAAGACCCTAGACCCAAC	1
M00764_SLC14A2_MIP101	GCCGAAGTAGATGGAGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATAAAGGAAACAAATCC	1
M00764_SLC14A2_MIP102	ACTATTTTCACTGAATACTCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCACCTCCTCGCCAT	1
M00764_SLC14A2_MIP104	CAACATCCTTCCTGGTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTATTAAATAGTTACTGG	1
M00764_SLC14A2_MIP105	CATTGATACTTCATTGATGACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGCGGCAATCCA	1
M00764_SLC14A2_MIP106	CACCTACCCAGAGGCCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCTTATCTGTGTTCTTT	1
M00764_SLC14A2_MIP107	GGGGTTATTGGTCGTCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACTTAGGAGACATCGT	1
M00764_SLC14A2_MIP108	CCTTTGGTCTGTTCTGTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGGCATCAATCATAAC	1
M00764_SLC14A2_MIP109	GCGTGCTGAAGCCTGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGTTGTGCATCTTAGAA	1
M00764_SLC14A2_MIP11	GCATGTATGTACTAGGTCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGAAGTTCAAAGAGG	1
M00764_SLC14A2_MIP110	CCTCATCCTTAAAGAGAAGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTCCAGAACCTCTC	1
M00764_SLC14A2_MIP111	GCAGAAGAGGGCAAGTTCCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCGCCAGGATGGTCT	1
M00764_SLC14A2_MIP112	CCAAGAACTGTGCATTAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCCAGCCTGGGCAACGGA	1
M00764_SLC14A2_MIP12	ATTGAATGAGAGAGAAAGAGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTGGCCACTTCAG	1
M00764_SLC14A2_MIP13	AGGTGATATTGAGGAATATTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACTTTCCCTCTGC	1
M00764_SLC14A2_MIP14	ACATGAAAAGGTCTGGCATACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTAATTCCTTAGCTAT	1
M00764_SLC14A2_MIP15	CACAACAGCTGCAAGAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAATATAGGTGTAGCTA	1
M00764_SLC14A2_MIP16	ATACATGAGATACACTCACAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCTCCAACGTGAT	1
M00764_SLC14A2_MIP17	ACATGTGCACACACATACAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAGTGTATGTGGGTG	1
M00764_SLC14A2_MIP18	ACGTATGCCATAGATGTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAACTTAAAGACGTAT	1
M00764_SLC14A2_MIP19	GGTACTGTTAACCATGGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGGATGATGGAGGCAG	1
M00764_SLC14A2_MIP2	GCCTCTGAGTCTCACCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGGTGAGACATATTTAT	1
M00764_SLC14A2_MIP20	CATTGAAGTATTTGCACCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCAACTCACCATTTT	1
M00764_SLC14A2_MIP21	GTTCCTGTTCAGAAACACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAAGACATGGACTTAT	1
M00764_SLC14A2_MIP23	AACCACTGACAACACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATATTATTACCTTTTCAAG	1
M00764_SLC14A2_MIP24	AGTAGTAAGCAAGAAACAATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTGATAGCAGCTGT	1
M00764_SLC14A2_MIP25	AGAGTCCCCACTGGAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTTAGATTTCAGAGGA	1
M00764_SLC14A2_MIP26	GCAGAGGTTCTCTATGAGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACAGTGGATTTACC	1
M00764_SLC14A2_MIP27	GAGCTGCCTGAGTCTGTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTACTCCAGACCCCAGA	1
M00764_SLC14A2_MIP28	GCTCTCCTCCTGCTGCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAGTCATTAAATCTTAA	1
M00764_SLC14A2_MIP29	CACCCCCACTGTATCTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGAGATTATTTTGAGA	1
M00764_SLC14A2_MIP3	CCCAAGTTTCAATGGGGAGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCAACAACTGAGA	1
M00764_SLC14A2_MIP31	CAGAGCAAACTGTGTCTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTAGCAGGGTGTGGTGGC	1
M00764_SLC14A2_MIP33	GATGAAACTTTGGACTTTGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCTGACGTCAAGTGA	1
M00764_SLC14A2_MIP34	ATCAAAAGCAAATGGCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTTCAAAACAAAATTGT	1
M00764_SLC14A2_MIP35	CAGTAATCCCCATATGTTGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACTGTTGCTAAGG	1
M00764_SLC14A2_MIP37	GTCCAAGTTTGCTTCCCCTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATGGGAGCGGTTTCC	1
M00764_SLC14A2_MIP38	CCTTCTCAAATGGCGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTACCTGAGAGTGGGTGA	1
M00764_SLC14A2_MIP39	GATCTACAGCTTGTGCTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCTATCGATGGACTA	1
M00764_SLC14A2_MIP40	CGAGGCAGAGTTTACCAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTCACTAGCTCTTTCC	1
M00764_SLC14A2_MIP41	GAGTTTGTATCTGCTGGAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCTCCCAGGAAACA	1
M00764_SLC14A2_MIP42	GGGGATAGAGGAGGGTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCCTTTTACTCCTTTCA	1
M00764_SLC14A2_MIP43	CGACATGAAGGAGTACAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGACAGTCACATTGTGA	1
M00764_SLC14A2_MIP44	CGTGAGGTAGCCCACTGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATGAGTGAGGGAGAAG	1
M00764_SLC14A2_MIP45	GACAAGCACCTTGCCCTCCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGCCTGGCTGAAT	1
M00764_SLC14A2_MIP46	GAAAGAGACAGAGAGCGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCCACCAGGGATTCTG	1
M00764_SLC14A2_MIP47	ATGTGTGGAACAGAAAGTAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATAGGGCTGCTGAT	1
M00764_SLC14A2_MIP48	AAAAAGTCAGTTCGCTCAATGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGCAGACCTGGC	1
M00764_SLC14A2_MIP49	ACTACTACTGGTGGCTTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGTAACACCACCAACT	1
M00764_SLC14A2_MIP5	CAATGCTTATGTGTCCAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCTCTACCAAGCTCA	1
M00764_SLC14A2_MIP50	CCATCAGCAGTCCCACCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGACACAAGTGTCTTGG	1
M00764_SLC14A2_MIP51	GGATGCTGGAAGCATCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGATTTCTATATCAGCT	1
M00764_SLC14A2_MIP52	CCAGTTAAAATCCGTCTCCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGACCCACTCACT	1
M00764_SLC14A2_MIP53	AGGAGAGGAAAAAAAAAAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCCCACAGAGATGA	1
M00764_SLC14A2_MIP54	GGCCCCCTTGAGACTCCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGAAAGAACTGGGCT	1
M00764_SLC14A2_MIP55	ACTACAACCTCTTCTTCCCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGTCTCTTGCATC	1
M00764_SLC14A2_MIP56	GCCTGTGGCTGCAAGGTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGAATATGGGGGTCTC	1

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ID	**MIP**	***c***
M00764_SLC14A2_MIP57	GTACCCTCCAGCATGTGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTGTAACAGCTGCA	1
M00764_SLC14A2_MIP58	GCTTGCATGCAGCCATTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCTGTATTCTGTTAACT	1
M00764_SLC14A2_MIP59	GATGAGTGGCGAGGAGATGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTCTGGAAGATTTGC	1
M00764_SLC14A2_MIP6	GTTGCCCTGAATCTACAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTTCACCATTTGTATA	1
M00764_SLC14A2_MIP60	ACACCTTGTCCCATAGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTTGTAGAGGCTCTTTT	1
M00764_SLC14A2_MIP61	GTATTTCTGTCTGATTCTGGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCCAGGTGAGGGC	1
M00764_SLC14A2_MIP62	CATGGGGACCACTAATCAATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCGGAGGCATGTTC	1
M00764_SLC14A2_MIP64	CACTGACATGATGTTGGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAGATGTCGTGTGAG	1
M00764_SLC14A2_MIP65	CCTAGTTTCCTGTGTTGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGGGAGTCTGAAGAT	1
M00764_SLC14A2_MIP66	ATAGCCATGTTCGGGGAAGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCTCCTGACGACAA	1
M00764_SLC14A2_MIP67	GCTGGGGGCCTTCTCTTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTTCTACACAGGTGCA	1
M00764_SLC14A2_MIP68	GTATTACAGTAAAATTTCCGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTTCTTTGCCTCT	1
M00764_SLC14A2_MIP69	GTCGCACAATAGATAGTTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCCAAGAAGATCACC	1
M00764_SLC14A2_MIP70	GGGAAAAATCACACAGATGCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCGAGCCCTCCTC	1
M00764_SLC14A2_MIP71	ATCCCTGCCTTCCTAGTCTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCAGGCCCAAAGG	1
M00764_SLC14A2_MIP72	GAGGACATGCACACCTTTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGTCAGACGTCAGGT	1
M00764_SLC14A2_MIP73	GCTCAGGCAGCTTAATACTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACCCCACCAGCCAT	1
M00764_SLC14A2_MIP74	GCTCAGGCAGCTTAATACTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATCCCACCAGCCAT	1
M00764_SLC14A2_MIP75	GAGCCATGCATAATCTGTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTCCTGTTCCGCA	1
M00764_SLC14A2_MIP76	GAGCCATGCATAATCTGTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTCCTGTTCCACA	1
M00764_SLC14A2_MIP77	GCTGCTGTTTCCTCATCTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCAAAAACAACCAAG	1
M00764_SLC14A2_MIP78	GCTGCTGTTTCCTCATCTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCAACAACAACCAAG	1
M00764_SLC14A2_MIP79	GAGACAGTGACTTGTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACATCTTCGTATAAACA	1
M00764_SLC14A2_MIP8	GCTCCTGAGGGAAAGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAGTGTCATCCTCATC	1
M00764_SLC14A2_MIP80	GAGACAGTGACTTGTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTACATCTTCATATAAACA	1
M00764_SLC14A2_MIP81	CATGATTCTGTGCTTCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCTGAGCTCCCTAAAT	1
M00764_SLC14A2_MIP82	GCAGCTCGAAGGCTCTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGAGCACCATCAGTTA	1
M00764_SLC14A2_MIP83	GCTTGTGAGTACTGAGTGTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGAGTAGAGGTGTC	1
M00764_SLC14A2_MIP85	GAATTCATGTTTGTGGTCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCGAATCCAGGATGT	1
M00764_SLC14A2_MIP86	GGAGAGGGACTTAAAGGTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGAGAGCTCTGAGAT	1
M00764_SLC14A2_MIP87	CACTCCTTCATCTCTCCTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTCTAGTCTAAGTCT	1
M00764_SLC14A2_MIP88	ATGTTTGTGAACAACCCCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCCTCCATCTGCCC	1
M00764_SLC14A2_MIP89	CGGAGGACCCAGTCAAAGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTCAAGGTGGACAT	1
M00764_SLC14A2_MIP9	GTGAGGGAATAATTGAGTTGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCAACCGATTGCT	1
M00764_SLC14A2_MIP90	CCAGCTGAGAAATCCTCAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGCCTGGGTACCAT	1
M00764_SLC14A2_MIP91	CCTTCAAATAGACCACCCTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGAAATCCTGCAGC	1
M00764_SLC14A2_MIP92	CGACCTGGCAGGAGAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTACCAAGACATGGACA	1
M00764_SLC14A2_MIP93	CATGTATTTAGCTTGCACATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTACCCGTCATCATC	1
M00764_SLC14A2_MIP94	AGTGGGACCTCCCAGTCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGAAGGCACAGGGAG	1
M00764_SLC14A2_MIP95	GCTGATGGCAGAAGCATGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGGGGAAGAAAAGGT	1
M00764_SLC14A2_MIP96	AAGGAGGAAGGGCAGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGTGACTTTGTACCTG	1
M00764_SLC14A2_MIP97	ACCAAGGGCACTTGGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATATATGTAGAATGCTTGGT	1
M00764_SLC14A2_MIP98	AAAGAGACAACTTGACCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATATGAACAGAGCTATGA	1
M00764_SLC14A2_MIP99	GTGAGGGGGTTAGAGCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGATAACCCCTGGACTG	1
M00764_SLC39A11_MIP1	AAGAGCTAACTAAAGTTGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAAATTGTGCTTTCT	1
M00764_SLC39A11_MIP10	GTCTGTCTCTTCTTTCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGTCTCTTAGAAACA	1
M00764_SLC39A11_MIP100	GCACTGTCCTATCCCTCCGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGAACTTTCCATCCG	1
M00764_SLC39A11_MIP101	CAACGTAGAGCCGAAGTTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTGACTCAGCTCAG	1
M00764_SLC39A11_MIP102	ATCCTGAGGGTCCCGCGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCATCTGGGGAATTAAC	1
M00764_SLC39A11_MIP103	ACAGGGAAACTCCCCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGAGACTGGGTAATTTATAAA	1
M00764_SLC39A11_MIP107	AAAACAGATGCCTGGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTAGGAAAAAATCTTAAA	1
M00764_SLC39A11_MIP108	CCCATTTTAACTTTCTAGTTTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACTTAAAACAAAT	1
M00764_SLC39A11_MIP109	ACTTCGCCTGGGAGCATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTACAATTTTAGTTAGA	1
M00764_SLC39A11_MIP11	GAGTGTGGGTTTGTTCGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGGAAGGAAATTGGCTA	1
M00764_SLC39A11_MIP110	GATCAAACCTGACATACCTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGGCTTCACCCTTG	1
M00764_SLC39A11_MIP111	AGCTGCCAACATGACCTACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTCAGCCAAGTAGA	1
M00764_SLC39A11_MIP112	GGTCTCTTCTGGCCCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATGTGAAATTGTAGGGG	1
M00764_SLC39A11_MIP113	GCCCCCAAACAAAGAGGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGTCACTGCAACTTC	1
M00764_SLC39A11_MIP114	CCTTCCCTGTTCCTATGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCGTGAGTGAGTATCT	1
M00764_SLC39A11_MIP115	CACACCACCCCAGATGCTCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGGTAGGAGGGGAGG	1
M00764_SLC39A11_MIP116	CCCAGAGCCCTGCAAACAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGAGGAAGTGATACA	1
M00764_SLC39A11_MIP117	CGTCTCCTTCCTGAGTGTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTTACTTCCCATCA	1
M00764_SLC39A11_MIP118	GCCTCCAAGGTTCTATTCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCGTCCCCAGCATCA	1
M00764_SLC39A11_MIP119	CCCAGCCTCCTAAAGAGAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCCTAGGAAGTCAGG	1
M00764_SLC39A11_MIP12	CATGCTCCTCTCTGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCTTTCCTTCAATAATG	1
M00764_SLC39A11_MIP120	GAAATGAAAGACCCTGAGATGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCTGGGCCACAAC	1
M00764_SLC39A11_MIP121	ATGCATCTCTGTGTTCCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTAGATGGAAGTCTT	1
M00764_SLC39A11_MIP122	CATAAGGCCCAAAAGAGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTACTACATGCTACTT	1
M00764_SLC39A11_MIP123	GTCCCACTCCATGGAGCAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGACCTTCTTCACCT	1
M00764_SLC39A11_MIP124	AGGGTCAGCCACCGGTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTAGAGAATACGAACACG	1
M00764_SLC39A11_MIP125	GCTGTATCCAGCATGCTCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTGGAAGGGTGCATA	1
M00764_SLC39A11_MIP126	AAGGGCCAGCTTACCTGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTCAGTGTGGCTTTG	1
M00764_SLC39A11_MIP127	CCATCCAGCACATATTTTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCTTGGTGGGCGGT	1

continued table…

ID	**MIP**	***c***
M00764_SLC39A11_MIP128	ATCTCTCCCTGTGGAAAGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGAAGCTGAAGTTAC	1
M00764_SLC39A11_MIP129	GCATGTTAAAGTCTGGAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTGATATGAGGCCC	1
M00764_SLC39A11_MIP13	GAAGGAAATTGGCTAGTCTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGTTGGAACTGGAGC	1
M00764_SLC39A11_MIP130	GCTCTGTGAGGAGCCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGTTCTGGTACACAAAC	1
M00764_SLC39A11_MIP131	GTGCTGGCAGACCATCAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCTTCCAGGGTCAATC	1
M00764_SLC39A11_MIP132	GCCCAGGTGAGCCCTGGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAGAGCTGAAGACGCT	1
M00764_SLC39A11_MIP133	CCTTCCTAGGTTTGAGCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTTTCACAGTTGGTG	1
M00764_SLC39A11_MIP134	GGCATGTTAAAAGTTGGAACGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACTCTTGGAAGCG	1
M00764_SLC39A11_MIP135	AATCCAGCAGAAGGATTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTTTAAACCTGTTGTT	1
M00764_SLC39A11_MIP136	CGTGGAGTTAGGGCATGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGTGTGCATTTCTA	1
M00764_SLC39A11_MIP137	GGAGCAGCTGGATTTGTAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCACCCAACCTGGGAA	1
M00764_SLC39A11_MIP138	CCACTTGCTCTGGCTGTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGACATGCCTTCCTTT	1
M00764_SLC39A11_MIP14	GCTTAGGAGACGTCTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGCTTGCTATCTTTAT	1
M00764_SLC39A11_MIP141	CCTTCGGTGCCTTTGGTTGGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCCACGTGTGCGG	1
M00764_SLC39A11_MIP143	GGCGGGAGTTGCCAGTTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTTTGTAGCTTCCCTTA	1
M00764_SLC39A11_MIP144	CAGGATGTGCTGTGTGTGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCGAGTGACTGCAGC	1
M00764_SLC39A11_MIP145	GCACCCAGTGGCATGGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCATTTTGTGTTTGACC	1
M00764_SLC39A11_MIP146	GGCTGACATTTTGGGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCTGGGGGCGGGTAAT	1
M00764_SLC39A11_MIP149	CCCTGCCCCCCTACCATTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGCCTACTCTGGATT	1
M00764_SLC39A11_MIP15	GGTGGCCTAGTGACTCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTCTTCAGTGGGATTA	1
M00764_SLC39A11_MIP150	ATAGGAATGGAAAGGACAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAGCACCTAAAGAAAT	1
M00764_SLC39A11_MIP151	GTACCTGTAGTCCAGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTAATCCCAATATTTTG	1
M00764_SLC39A11_MIP152	GCCTGGGGAAAATCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAATACAAAAACTAGCCAGG	1
M00764_SLC39A11_MIP153	CTTTTTTCTCCCAAGTGTCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGTTGAGGCTTGAG	1
M00764_SLC39A11_MIP154	GTGAAAACAGACTAATACACTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACGTAAGACGTGCC	1
M00764_SLC39A11_MIP155	GTATGGGGAAAACCTCCCCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCACGGCCGAAGGT	1
M00764_SLC39A11_MIP157	GCTCATTCCTGTGGTTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTACGGGAGCTACAATT	1
M00764_SLC39A11_MIP158	GAGGTGGATTCTTCAGCCTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCTCTCACCTCCC	1
M00764_SLC39A11_MIP159	AAGTGACATACCATCATCCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTACGGGGGAAGAGAGGAG	1
M00764_SLC39A11_MIP16	CCCCATTAAATCAAAAATCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGAGGCAGATAGAA	1
M00764_SLC39A11_MIP160	GATTAGGATATGGAAAGCATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTCCAAGATGAGC	1
M00764_SLC39A11_MIP17	GATTCTTTGTTTTGGCCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTTTTTCCTTCCTC	1
M00764_SLC39A11_MIP18	CCTAGCCCAGGCCAACGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCAGGATAATGAGATGAA	1
M00764_SLC39A11_MIP19	GGACCCCGGGAAAGGCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTAAGGTCTTACTTTTCT	1
M00764_SLC39A11_MIP2	GTCTTCAATTTTGATCATCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGAGGTCTTGTCC	1
M00764_SLC39A11_MIP20	GGGGCTTACTATGTGCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGAAGAGAAGGACAGG	1
M00764_SLC39A11_MIP21	ACCATGGCACCGGCAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGGCAAATGAAGAAAG	1
M00764_SLC39A11_MIP22	CGTGGTCATGGACGACATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCCTTAGGTATGGGC	1
M00764_SLC39A11_MIP23	CCATTCTACGTCATATCTGAGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTCCACCATGCCG	1
M00764_SLC39A11_MIP24	GCATCCATGTGCTAGGGTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGAGAGCTTTCTGGT	1
M00764_SLC39A11_MIP25	AAAACCAAGAAAGCACATGAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTTGCCCTTGGGC	1
M00764_SLC39A11_MIP26	CAGGAATTTGGCCATTGGAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTACTGCAGGTCA	1
M00764_SLC39A11_MIP27	CCTGGGCAGGCTCTGTCCTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCCAGGAGGAGACC	1
M00764_SLC39A11_MIP28	CCCCTGCTCTTTACCTAGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAACTCAGGGCACC	1
M00764_SLC39A11_MIP29	GATGGAGTCTCGCTCTGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAACACACTGGCTGG	1
M00764_SLC39A11_MIP3	GATTAACTGGTGTGGTGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGGGTGAATCTCCTG	1
M00764_SLC39A11_MIP30	CGGGTTCAAGTGATTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTTCTACGCCTCTGTTT	1
M00764_SLC39A11_MIP31	CGGGTTCAAGTGATTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTTCTATGCCTCTGTTT	1
M00764_SLC39A11_MIP33	CCTCATGTCGCCTGGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGTTTCACTCTGTTGT	1
M00764_SLC39A11_MIP35	CCTGCTGCTGATCATATCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTTGGTTTCCTGCC	1
M00764_SLC39A11_MIP36	CAGTCCTAAGAGTCCAGGTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTCAGGAAGGCAGG	1
M00764_SLC39A11_MIP37	CCTTCTGTACAAGCCGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGAAAAATCAGGGTAT	1
M00764_SLC39A11_MIP38	GAAGGCTAAGGACCATATATGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCACGCGGTAGCT	1
M00764_SLC39A11_MIP39	AAAACTGAAGAGAAGGAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCTAGCAACCTATG	1
M00764_SLC39A11_MIP4	ACTGAAAGTCTCACGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCTGATAGCATTCACAGA	1
M00764_SLC39A11_MIP40	CCACACTACACAGCCTCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCACATTGTGCTCTCA	1
M00764_SLC39A11_MIP41	GTGAAAGGGTGGGGACAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTGTGATAGGTTCAAGA	1
M00764_SLC39A11_MIP42	GAAAAATGCCCCTCCCACCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCCCAGCCTGGTCTCC	1
M00764_SLC39A11_MIP43	GTCTGGGAGACTGAGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAATTCTCAGGCTAAAAG	1
M00764_SLC39A11_MIP44	CCCATTTTGATGATCTTTTAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGAGCCACTGCACT	1
M00764_SLC39A11_MIP45	GACAGTCAGGTGAAGACAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGGTTTCCATGGTC	1
M00764_SLC39A11_MIP46	ATTTACAAGGCCCAGTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTATGGCTTTATGGGCC	1
M00764_SLC39A11_MIP47	GCCTGGAAATAAACAGGGCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAGGGTTCCCTGT	1
M00764_SLC39A11_MIP48	ACACATGGAAAATAAAGTCACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGGGTACAGCGGT	1
M00764_SLC39A11_MIP49	GATGATACCCAAGTCAAGCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTATGGCCTGTTCTT	1
M00764_SLC39A11_MIP5	AAGGCAGCCCAGGAGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTACTCCTTCTTACAT	1
M00764_SLC39A11_MIP50	GCTTCAAAAAGGAAAGGCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTGGGAACATCACCT	1
M00764_SLC39A11_MIP51	CCCTCTCTCTTTCCACCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTGTACTCTAAGCACT	1
M00764_SLC39A11_MIP52	GATGGCCTTCACCGGACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTAGTCTTCACACCTTTG	1
M00764_SLC39A11_MIP53	GAGGAGTCTCCTAAGAGAGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCAGGGGTGCTCTG	1
M00764_SLC39A11_MIP54	ACAGCGAGACCCTCTGAAATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGTGACACGCACAC	1
M00764_SLC39A11_MIP55	GGAGTTGGATTTGGGGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGATTTTCTTTGACTGGC	1
M00764_SLC39A11_MIP56	GCAACCTAGGAATGATTTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCACTGTCACTGCATT	1

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ID	**MIP**	***c***
M00764_SLC39A11_MIP57	CCCTGGGTTTAAGCTGCTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTACATAATTTTCATG	1
M00764_SLC39A11_MIP58	GAGGCCAAGACAGGCAGATCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCAACCTAGGAATGA	1
M00764_SLC39A11_MIP6	ATTACCTCTTCTTTTCCTATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTACCCCTGTTGGA	1
M00764_SLC39A11_MIP62	AGACAGAGTCTCACTTTGTCACCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTACTATGAAACCC	1
M00764_SLC39A11_MIP63	ATATTTACTTTCTGGAACTTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGTAAATGAAGT	1
M00764_SLC39A11_MIP64	CATACAGTTTCTGTCCCAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCAGTGACATCTTTG	1
M00764_SLC39A11_MIP65	GTTTATCCTATGTTTACTCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCCAGCTGTGTGA	1
M00764_SLC39A11_MIP66	AGACATGCCAAGCAAAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTGGCTAATTTATTTAA	1
M00764_SLC39A11_MIP67	CCTGTCACCATATGAAGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGTGGGAGACAATTG	1
M00764_SLC39A11_MIP68	AAAGACAGTCCTGGTGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAAAAAATCTGAAAAGA	1
M00764_SLC39A11_MIP69	ATTCATTCCTTTGAGTTGTACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAGAAGGGGCCCGT	1
M00764_SLC39A11_MIP7	CCCCTTTAAAGTAAATTTTAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTTCCCTGTTGACC	1
M00764_SLC39A11_MIP70	AATCCCCACTCCACTGACAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGCAAAAGGGACTCC	1
M00764_SLC39A11_MIP71	CACTACTTTGGATGGAGAATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAGACCTGCTTG	1
M00764_SLC39A11_MIP72	AAATTTGAACCTGGTTTCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGGTCCACCTTCTG	1
M00764_SLC39A11_MIP73	GATCACCAACACCTGATATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACAAATTCACAGACT	1
M00764_SLC39A11_MIP74	CAGAACTGAAATGGAGCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTCACCTCTAAGCTT	1
M00764_SLC39A11_MIP76	AAACATAGCACCAGTGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCCCATCTATTCATTAC	1
M00764_SLC39A11_MIP77	GTAGATTAGTGCAGGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACATGCTACAACATCAA	1
M00764_SLC39A11_MIP78	CCCTAACCGGGACTGACTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAAAGAAACCCCACA	1
M00764_SLC39A11_MIP8	GTAATTGAAGAGTTTGAGTTCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGCCTGTTGCAGC	1
M00764_SLC39A11_MIP80	CCTGCTTCAGCCTCCCATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATCTGAAAGGTTGTGCA	1
M00764_SLC39A11_MIP81	CATTGTCCAGGTGGGCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGGTTTTGCCATGTTG	1
M00764_SLC39A11_MIP82	CATTGTCCAGGTGGGCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGGTTTTGCCATGTTG	1
M00764_SLC39A11_MIP83	CGAGGGTCAAGTCTATTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATTGACTATGTTATTGG	1
M00764_SLC39A11_MIP84	GAATTCCTTAATAACATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTGCCCCCTGAGAG	1
M00764_SLC39A11_MIP85	GCATTAAGCAGAACCAGAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTCAGCTGAGGAAGA	1
M00764_SLC39A11_MIP86	ACAGATCTGAACTACGTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTACCAAGTTATTTGG	1
M00764_SLC39A11_MIP87	GACGATCAAAAAATAAAGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCAATCATGTAACA	1
M00764_SLC39A11_MIP88	CATATGTGAAAACTTCCCATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCAGCACAGTTGTC	1
M00764_SLC39A11_MIP89	GGCCAAGATGAGCAGTGCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGACCCACGTCACAAT	1
M00764_SLC39A11_MIP9	AAAGAAGGAGCCATTTCAGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCAAGGCCATTTG	1
M00764_SLC39A11_MIP90	CACTATACACAACGTTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATATCAGAGAAAGAAGG	1
M00764_SLC39A11_MIP91	GTTAACTCTCCAGCAAGCTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGACCCTCTGGAA	1
M00764_SLC39A11_MIP95	AAATCCCAACACTTCGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTCACAATTGCCCAT	1
M00764_SLC39A11_MIP96	GTTCGCTGAATGAATGGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGATGGGATTGTGCCA	1
M00764_SLC39A11_MIP98	CCTCAGTGTCCCCCTCTCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAACCACATGCTTAGT	1
M00764_SLC39A11_MIP99	GCATTTCTCTCACTATTCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTACCGTTACCTTCTGT	1
M00764_STEAP4_MIP10	CAATGTATGTGAACCTACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGCATATCTATAGCATA	1
M00764_STEAP4_MIP100	CATGAAATCTGTCAGTTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTAAAAGATGGTTGGTT	1
M00764_STEAP4_MIP101	GTTAACTAGTGTGTTTTCAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTTCCAGGTTCGCT	1
M00764_STEAP4_MIP104	GGCGGGTACCTCTAATCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACTCCCATAATCCCAG	1
M00764_STEAP4_MIP105	CACTTTGGGATTCCGAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCTTCTTTTTAAAGTA	1
M00764_STEAP4_MIP106	AAGAGATTTACCTGGGTAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACATGACATTTCTAA	1
M00764_STEAP4_MIP107	GCTCCTGAAATCAGAGACTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTAGCTCTGGGATTT	1
M00764_STEAP4_MIP108	ATAACACCAGGGAGGTAAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGGACATGAAGGAA	1
M00764_STEAP4_MIP109	GCTGCCATTCTACAACTGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACGTAATCTACCCTTA	1
M00764_STEAP4_MIP11	GTGGAGAGCAGTTAGGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTATCAATACCATTTCTC	1
M00764_STEAP4_MIP110	CTGCAGGGGGTACTTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATACGAAATGTATTAT	1
M00764_STEAP4_MIP111	CCAATGTGGAGGTTCCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTGTGTGGAAATGACAG	1
M00764_STEAP4_MIP112	AGCACCATGCCAAATGATGACTTCAGCTTCCCGATATCCGACGGTAGTGTACGAACAATATCCATCACTC	1
M00764_STEAP4_MIP113	AAATGCCCACTAAATATTACATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTCCAGTCAGGA	1
M00764_STEAP4_MIP114	GAGGTTGTTGCTGATGTCTACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGACTTGCATCCAGTG	1
M00764_STEAP4_MIP115	CAATCAATATCCAGAATCTAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAGCAGCCAAGA	1
M00764_STEAP4_MIP116	CCACACTGGAGCATTTTCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCTCTCTGTGGATTGC	1
M00764_STEAP4_MIP117	GGAAGTCGAAACCCCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGTATAGATGCACTTCC	1
M00764_STEAP4_MIP118	GCTCTGTGCCTGGAAAATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCACCAGTTCCAAAA	1
M00764_STEAP4_MIP119	GGTGGATTCTCCTTGGGAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCGAGTTGGTAAGA	1
M00764_STEAP4_MIP12	CCTGTGAACTTTGTTCATACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTGCTCAAACATTTG	1
M00764_STEAP4_MIP120	ATTAGATGAATTCCTGCATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGTTCTTTCTTTCT	1
M00764_STEAP4_MIP121	GCCGGGCGAGGTGTGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGCTACATTAATTAGAT	1
M00764_STEAP4_MIP124	CCCGCCCTTCTCTGGCTTCTTATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAGCGGCACCATC	1
M00764_STEAP4_MIP125	CCCCTTTCCTAAAGGAGCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACTTCTATACTGCGG	1
M00764_STEAP4_MIP126	ATTCCTAGACCTCTCCAAACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAGGGGAAAGATACC	1
M00764_STEAP4_MIP127	GTTTTCAGGTCTTAATTTAGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCACCTGGACTAGG	1
M00764_STEAP4_MIP128	CAAGATCTTCCAAGTTATGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACAACCAGGGCTGTG	1
M00764_STEAP4_MIP13	GAAACAAGGCTCTGCAACATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTCATACCACCAGCT	1
M00764_STEAP4_MIP15	ACTTTGTGGCACTTCTGGCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGGAAAGTCTGGA	1
M00764_STEAP4_MIP16	ATACTTTATTCCTTCCCTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGATGAAAAGCACAG	1
M00764_STEAP4_MIP17	GGGCAACTGGAGCTCAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGGCTTCTTGTAAAAGA	1
M00764_STEAP4_MIP18	AAGTGTGGTCTGCCCGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGTATCTAATAATTTG	1
M00764_STEAP4_MIP19	GCACAGTGCTCAAACGTAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACACCCTTAAATGTGAT	1
M00764_STEAP4_MIP2	ATATACAGTGATCAGATTAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCAGGGATATGCA	1

continued table…

ID	MIP	*c*
M00764_STEAP4_MIP20	CCCCATCTCTGATAGTTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGAAAAGTTTAGAAA	1
M00764_STEAP4_MIP21	CCAGTTCATTACAAATCAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTTCTCTCTGTAGAT	1
M00764_STEAP4_MIP22	GAGTTAAGCCTGTAGAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAAGAAAAATGGGTAGA	1
M00764_STEAP4_MIP23	GATGGAGTATTGACCATCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATGGATATGTACAAC	1
M00764_STEAP4_MIP24	GTTGGGAACAGTCAATGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTAAAACTGACAAATAA	1
M00764_STEAP4_MIP25	AAGAAATGATAAATGTTTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCCTGTTCTCATTT	1
M00764_STEAP4_MIP26	GGCTCCTTCAAAATCTGTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCTATGGAACACTAA	1
M00764_STEAP4_MIP27	ACCCAGTGTATTCATTTCATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAAGGCTGCTGGA	1
M00764_STEAP4_MIP28	ACTAAGCCTGGTGTGTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAATTCTGGGTTTCTATT	1
M00764_STEAP4_MIP30	CCCTTCGAGTCCTCAGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGCATGGGTTACTGGA	1
M00764_STEAP4_MIP31	GGATAGCTCTTCTCCAGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCAATTGCCATTTTAA	1
M00764_STEAP4_MIP32	GGACTGGGCAATCAGGAATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGACTAGAGTGGGAAG	1
M00764_STEAP4_MIP33	GCTGATTTCAATTCGTCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATCCACAAAATAGACT	1
M00764_STEAP4_MIP34	CTCTGCCTCTCATTAGTTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGGTTTCGTTCAC	1
M00764_STEAP4_MIP35	CCATCTCCTTTTAACACAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCTCTAAGGTTCTCTT	1
M00764_STEAP4_MIP36	AAGCCTTCCAAAATTCCCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTTCCTCTTCTGATAA	1
M00764_STEAP4_MIP37	GATACTTACAGCAGAGTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCAAAGGGACTGAG	1
M00764_STEAP4_MIP38	GAAAGGGGGTCCAATACAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCACACTCCCCTTT	1
M00764_STEAP4_MIP39	CTCGAGGCAAAGTCCTAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGTCTTAATAAACTTGC	1
M00764_STEAP4_MIP4	CAAATTTCTTCCTATCCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTGAGAACATTCAATA	1
M00764_STEAP4_MIP40	CAAGGGATGGATTATTCATGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAATCCATAAAATGA	1
M00764_STEAP4_MIP41	AATAACTATAACTATACTCAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATGGCCACATCCAG	1
M00764_STEAP4_MIP42	ACAGCCAAAGATCACTTTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCCTGCTTTTAGAAC	1
M00764_STEAP4_MIP43	GCTAATTATAATATATTAGCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCACAAGGTACAG	1
M00764_STEAP4_MIP44	ATGGCGCGATCTTGGCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACTCCTATCTCATCCTG	1
M00764_STEAP4_MIP45	GGGCTGCATTCCCAGGACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGTGCTTGGACCCA	1
M00764_STEAP4_MIP48	CAATGTATCAGAAGCATTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCACAGATAGCCTTA	1
M00764_STEAP4_MIP49	ATTGCAACTACTGTGTGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAATTGAAGTAGGACC	1
M00764_STEAP4_MIP5	AGCTAGATAGGAAGATTAAGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTGTAGACCTTTT	1
M00764_STEAP4_MIP50	CATTCTCCATCATCACAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAGAGCCATGATAAT	1
M00764_STEAP4_MIP52	AAGCAAATGGAAAGCCCCTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCGTGACTGGGCAT	1
M00764_STEAP4_MIP53	ACAAAAATCCAGCGTGGGATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTGTGCAAGGCATTT	1
M00764_STEAP4_MIP54	AGAATTTGGAGGTAAAAAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAGCTTGAGCTCAG	1
M00764_STEAP4_MIP55	ATGCTGGAACTACTGTGATTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGACTGTGCCACCC	1
M00764_STEAP4_MIP58	ACATTATTTTTGTACACTTTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGTGCTTTGGGCG	1
M00764_STEAP4_MIP59	GGGAGGTTGTGGGAAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTAAAAGGAATACAGT	1
M00764_STEAP4_MIP60	ACACAGCTGACTCCTCCAGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGACCTTTGGCCCC	1
M00764_STEAP4_MIP61	AGCATTTTTACTAGGCTATAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTGGGGCTTGGA	1
M00764_STEAP4_MIP62	AAGCAATTCATGAAGCCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTGTTTATCCTGGCTC	1
M00764_STEAP4_MIP63	AGTAAAAGAGCAGTATCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTCGGTGACGGACTA	1
M00764_STEAP4_MIP64	GATTAAAGTTTAGGTACCATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGGTATACGGTGCT	1
M00764_STEAP4_MIP65	GTGTTCTGTGTACCTTTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTAGTGACATTTTCCT	1
M00764_STEAP4_MIP66	ACCCAAGCAAGGATACAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTACCATTGGATGAGGG	1
M00764_STEAP4_MIP68	GCCAGATTCATGCCTGTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATATTATCTGAAATGTT	1
M00764_STEAP4_MIP69	ATCACTTGACGCCAGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATGTTTAATAAGGAAAGA	1
M00764_STEAP4_MIP7	CCTAAAGAAACTCTCAGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACAAACCAAGACACC	1
M00764_STEAP4_MIP72	CAAGTGATTCTTGTTCATCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTAAAGGCTTTGTTT	1
M00764_STEAP4_MIP73	GAGACAGTCTTGCTCTGTCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATATTTTTCTATAAAA	1
M00764_STEAP4_MIP74	GTCTTAGCAGAGCAGGCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGATACAATTATTTTTA	1
M00764_STEAP4_MIP76	ACAGTGAGAACCATCCTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGTGCCTTTTAGTT	1
M00764_STEAP4_MIP77	GTGCTGATAGTACCCTTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACAATGCATAGATGAT	1
M00764_STEAP4_MIP81	CAATAAGCAAAGAAGGGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGTATCCATGTCTTG	1
M00764_STEAP4_MIP82	GGGGTCATTTCACTAGAATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTACATGCCAGCTCT	1
M00764_STEAP4_MIP83	CAGATATTTACTGAGAGGAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAAGTGGGTCACAT	1
M00764_STEAP4_MIP84	AAGCTGCAATACTTCTATTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAACCTCATTCCCT	1
M00764_STEAP4_MIP85	GCTCAAGGGCTGAGTTAAGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAGGCCATGGAGCT	1
M00764_STEAP4_MIP86	CAATGTTTCCCTCAGTCACGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGCTAGTCTCAATCT	1
M00764_STEAP4_MIP87	ACATACTGGAAGAGAACACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTTCAATTTAGCTGGA	1
M00764_STEAP4_MIP88	AGTTCCTTTCCCAGCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGAAAAAAACTTTCCTA	1
M00764_STEAP4_MIP89	AAAACACTAGAAAAAGCATTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCTTCCTGCAGCCT	1
M00764_STEAP4_MIP9	GATTCAAGCATTCATCTTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGGAGTCTCACTCC	1
M00764_STEAP4_MIP90	CCCAGTTTGGACTATAAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTGCAAGGAATGAT	1
M00764_STEAP4_MIP91	ACCCTGATCTTGTGTACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTATAGGTCTCAAATGTT	1
M00764_STEAP4_MIP92	ACTTTTCATTTTGCTCCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGCTTTGGGAATACT	1
M00764_STEAP4_MIP93	ATTCTCCTTCTTGAGTATTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCTCCAGTTGACTG	1
M00764_STEAP4_MIP94	CATTTAGCACCTCCTCAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACAATTTGCTTTGAGCA	1
M00764_STEAP4_MIP95	GAAAAACAGAATTCTGATGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTACAAGTGTCTGATTC	1
M00764_STEAP4_MIP97	GATGCTTCTATGGGTTTCTCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTGAGAATCAGCTG	1
M00764_STEAP4_MIP98	CCCCAAGTCAAACATTAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATAGCACTTCCTCTGAG	1
M00764_STEAP4_MIP99	GACCTCAATAACTAGAAAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTCCTTTTGGAAGTC	1
M00764_SUN1_MIP102	AGGTCAGGAGTTGGAGACCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTCTGGCTGAATCG	1
M00764_SUN1_MIP103	GTGGCTAGCCTTGCACATCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTTGGGCCACACA	1
M00764_SUN1_MIP104	GGCTCCTACCACACAGGTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAACACACGCAAAAGA	1

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M00764_SUN1_MIP105	GTAAGTATGGCTTCGTTTTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGCGTCGGTGAGTT	1
M00764_SUN1_MIP106	CATTTACACTGAGGTGGCCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGTGAGGACCACCAT	1
M00764_SUN1_MIP107	GTGTAATTGAGTTTCCCAGTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAACGGCCCGTGT	1
M00764_SUN1_MIP108	CGAGACAGTCAACAATCAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTTACAGTCGTCG	1
M00764_SUN1_MIP110	CCAGAGGGTCCCTGCCCGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGTTTTTACAGCAAGA	1
M00764_SUN1_MIP111	GCTCCCTTGTAAATATTTTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGTCACCATGCTAT	1
M00764_SUN1_MIP112	GAGAGATTCACCCTGTTTTAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAGGAGAATTGCTT	1
M00764_SUN1_MIP113	GAGAGATTCACCCCGTTTTAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCAGGAGAATTGCTT	1
M00764_SUN1_MIP115	CGAGGCAGGCAGATCACTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCAAAGAAATATGGC	1
M00764_SUN1_MIP116	GGCTTTATGTTTATTCATTAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCACTGTGGGTGGC	1
M00764_SUN1_MIP117	GTAGCAAAACCCTGTCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCACAAGCAGGTGTTA	1
M00764_SUN1_MIP120	AATGGTAACACAGCACTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATACCATATTTTAAAGCA	1
M00764_SUN1_MIP121	ATATCTGCATTTTACACCTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGGTGTCTATGGAA	1
M00764_SUN1_MIP122	CCTAAAAACCCCAGGGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCCAAATAACTCTTGT	1
M00764_SUN1_MIP123	GCTGTCACTGCAGAGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAAATGGTCATGTCAGT	1
M00764_SUN1_MIP124	GTGGGTCAAGAGTCTCCTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCTGCAGCAAGAAG	1
M00764_SUN1_MIP125	GTTTCTGTGTTGCGTTCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACGTCTTCCCTGCACAG	1
M00764_SUN1_MIP126	CAAAATAGCCACCTGGAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAAGAACGAGACACG	1
M00764_SUN1_MIP127	CCTGAATGCCCGGTGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAGGCTCTCATGCTTTG	1
M00764_SUN1_MIP128	GGACTTCCCCCAGACCCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTCGGTGATGCTAGTC	1
M00764_SUN1_MIP129	CATTTCCTTAGAATGTTTGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTTACTGCCTTGCTTC	1
M00764_SUN1_MIP130	GAAAACCAAGCTCCTAAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGAAACACATTCAGC	1
M00764_SUN1_MIP131	ATTTTGTGCCAATTGCAGGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTGGAGTGTTCTGG	1
M00764_SUN1_MIP132	GGTTCCTTAAAGCACCACGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCTCACAGGTTGGTTT	1
M00764_SUN1_MIP133	GCTTCTGCCCTGCTGCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGTGCTTTTATATTCT	1
M00764_SUN1_MIP134	GGACCTGGGTCCCCCATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTTGAGACCTACGTTAC	1
M00764_SUN1_MIP135	ACAAAATTATCTAGAGGGGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGCACCAGAGAGTT	1
M00764_SUN1_MIP136	CAAAATCCACCCCCCCAGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGATGAGCAAGACTA	1
M00764_SUN1_MIP137	CGTGTAAGTCCATGTTTTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAAACATCTGCAAGTT	1
M00764_SUN1_MIP138	CATTTTTTTCCACTAAGTTACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGTTCAACACGG	1
M00764_SUN1_MIP139	AAGGCCTCTCAGCTGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATTTCTTTTCGTTCTTG	1
M00764_SUN1_MIP140	CCTCTTACCTGCAGAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAGACTTGCTTATCTGAC	1
M00764_SUN1_MIP143	ATGCTTGTTTGACTACCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTCAGCCATGTAAGG	1
M00764_SUN1_MIP144	ACAGAGTCAGTTAAACCTCCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCACTGTCCAGA	1
M00764_SUN1_MIP145	GTGGACCAGATGGAAGGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTGAGGCTTTTCCGTG	1
M00764_SUN1_MIP147	GTTCTTAGTTGTTGAGAGCAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGTGGGTGCTGCC	1
M00764_SUN1_MIP148	ACTGAGAGAAAAATCTGAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGCCAGGTTTTTGTT	1
M00764_SUN1_MIP149	CAAGTGTGACATACGCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGAGGAACATTAAATG	1
M00764_SUN1_MIP150	GCCTGTGGGTGGCAGGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGATGGCCTAAAAAGTAT	1
M00764_SUN1_MIP151	GGAGCGGCAGCAGAGTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTCAGTAGACTATTTCT	1
M00764_SUN1_MIP152	GCTTCCCACACTACACACAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGACAGCTCTGACT	1
M00764_SUN1_MIP153	CTTTCTGCATGTTTACTTTTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGCAGCTCCTGC	1
M00764_SUN1_MIP154	CACTCTTTCTTGTACGGCATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACAGCAAGACTCGG	1
M00764_SUN1_MIP155	GTTTTACTAGGTGGACGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAGGAAAACACTGTCA	1
M00764_SUN1_MIP156	GCAGACGGACACAAATGTCCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGTCGCCTTTGCTC	1
M00764_SUN1_MIP157	GTGTCTGCTGTGAGCGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGGTTCTCATCACAGTT	1
M00764_SUN1_MIP158	AGGTTGGGAGCTGCTTGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTCACAGCTAGGTCTT	1
M00764_SUN1_MIP159	AAACTATGTAGGGTTCCTAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGATGGCACGTGCTTG	1
M00764_SUN1_MIP160	GTGAGTAAATAGACGTTCTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGTTCTGGTGTTT	1
M00764_SUN1_MIP161	ACCAGATTCCAGAGCAAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTTTCTCAGATGTTTA	1
M00764_SUN1_MIP162	AATGTTTCCAAGAAAAGTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTTTCGTAAGTTTCA	1
M00764_SUN1_MIP163	GCTGCTCCTCTTCAGCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTGAGTACTCGCTGTT	1
M00764_SUN1_MIP164	GGGGACTGCGAGAAGTACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCACAGACGTGTTCAT	1
M00764_SUN1_MIP166	CACGAATGAAATGCGTGTGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTCAAGGCTCAGCTC	1
M00764_SUN1_MIP167	AAGAGATGGTGAACGATGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGACTGACTGACAAGT	1
M00764_SUN1_MIP178	GAGGGCCACTATCTCCAACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTACCCACTTAGCAGC	1
M00764_SUN1_MIP179	CAGGGGTACCTGGTGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCAGTATAATCAGTCTT	1
M00764_SUN1_MIP180	GAGCCTTTAAATGCCCAGCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGACGGCGAAGTC	1
M00764_SUN1_MIP181	GATGAAAGCAAGTGACGTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCTGGAGCACATCCC	1
M00764_SUN1_MIP182	GAAGGTCATTCCTCCATGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTAATCCCTGAAAAC	1
M00764_SUN1_MIP183	GTAAGAACTGGGACTGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCATTCGTTCATAATTG	1
M00764_SUN1_MIP184	GCCTGGAACATCTGGAGCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGTTAACATTTTTCAA	1
M00764_SUN1_MIP185	CCCCAAATATGACGTCTGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGCCCCAGTTAGAA	1
M00764_SUN1_MIP186	GACAGCGTGAAACACTGGAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGGAACTTCGGATTT	1
M00764_SUN1_MIP187	ACAAAAATAATGAGTAGTGTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACGCTCACGTCCT	1
M00764_SUN1_MIP188	GCTCTCAGACACTCCTTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTCAATAAACGTGGCT	1
M00764_SUN1_MIP189	GTGTTCAACACGCTTCTCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTGCAAGGCTGAAGA	1
M00764_SUN1_MIP190	ATTTTCAGAGTTCTAAACTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCTGGCGTGTTCTTG	1
M00764_SUN1_MIP191	GGTGACATTGTTTTTCCCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGTAAGAGCGAACA	1
M00764_SUN1_MIP192	GAAGTCAGTCTGACTTGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATGGGGAAATAACTAA	1
M00764_SUN1_MIP193	GCGAAACGCTCCCATATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTTTGGGTTTCTGTTTA	1
M00764_SUN1_MIP194	GAGGAGCCGTCTGGTGTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCCTGTTGGGAGTCA	1
M00764_SUN1_MIP195	CACCACCAGTGAGAGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGAATGGTGACAGCTG	1

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ID	**MIP**	***c***
M00764_SUN1_MIP196	GGCACTTAAAGTGTTACAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGAATCTGCCTTTTA	1
M00764_SUN1_MIP197	GATATCTCATTTATAAAGTCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCAGCACCATCGT	1
M00764_SUN1_MIP198	GAACTATGCAGTTAAGGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTTTTCAGAAAAAGAC	1
M00764_SUN1_MIP199	GTGAAAAAAATGCTGCTTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAATATTTCCACCCCA	1
M00764_SUN1_MIP200	GCTTCTGCTGCTGCCACCAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTATATAAAACTGATT	1
M00764_SUN1_MIP201	CAAAGACAGATATTTTGAAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGAAACAGACAAA	1
M00764_SUN1_MIP202	CCTCAAGTGTGCCAGGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGTCTATTTCTTTTCTC	1
M00764_SUN1_MIP205	CCCTGACCTGTTCAGGACAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTCACCCAGCAGC	1
M00764_SUN1_MIP209	CCCCAGGCCTACCTTTCCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCATGGACCGGCC	1
M00764_SUN1_MIP210	GAGGGCTGTGCCAACATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACATGGAGTGTCTTTCCC	1
M00764_SUN1_MIP211	AAAATGATACCTCGACTCACAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGAGCCACAGACA	1
M00764_SUN1_MIP212	CAGGATAAACTGAGTTCACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGACATGTTCGTGG	1
M00764_SUN1_MIP214	GAAACCTGGAAATGAGAACATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAGCAGCAGGAAC	1
M00764_SUN1_MIP215	GCAAGTGTAGCCATGGTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGCTTAACTTCATCT	1
M00764_SUN1_MIP216	AGAGCTTGGGGCTGGGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTGGTCCTGTTCTGCT	1
M00764_SUN1_MIP22	GAGGTCTCTGCTCTCGCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAAAGTGCCCAGAATG	1
M00764_SUN1_MIP23	CCTGGGGAGCCGGGAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTATGACTGAAGCTTAGA	1
M00764_SUN1_MIP231	ATAACCGGTCCAGGAGTGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTGTGCTGGAAATG	1
M00764_SUN1_MIP232	GGTTAAAACCCAAAATGTTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCGTATCAATCTAC	1
M00764_SUN1_MIP233	GGTTAAAACCCAAAATGTTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCGTATCAATCCAC	1
M00764_SUN1_MIP234	AATTTCAGGAAGGCTTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCAAATGTTACCAGAA	1
M00764_SUN1_MIP24	GAGAAAATGATAGATTCCGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTTATTTTCTAGGCT	1
M00764_SUN1_MIP25	GTTCCTTACCCACCCTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCATTCTGATTTCACTTT	1
M00764_SUN1_MIP26	CCCCATCTTCCTTGCTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAAAATTCACGTGATTAT	1
M00764_SUN1_MIP27	GGAAAAGAGGTCACACTCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACACTGGGCTAAC	1
M00764_SUN1_MIP28	GGTTGTTGCTCGGCAGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTCCATAGAACTACTG	1
M00764_SUN1_MIP29	ACACTGGGCTAACTCAGTGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCTCTGGCAGCTTC	1
M00764_SUN1_MIP30	CGTGTGGGTTGAATCTAGATTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGCTGGGTTCTGC	1
M00764_SUN1_MIP31	GGCACAGGACAGGGCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGCAAATAAAACTAACTG	1
M00764_SUN1_MIP32	GCTTGGTTTATGGAGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTAAAATGCAGGAGTTT	1
M00764_SUN1_MIP33	ACAGAAATAAAGACCATTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAATATCTGAGGGAG	1
M00764_SUN1_MIP34	GGAAAGTATGAGTCATTCCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTTTGTCCAGGAGG	1
M00764_SUN1_MIP36	CTTCAGCCATCTAGGAACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAATATACTCAACACTTTC	1
M00764_SUN1_MIP37	CACAAGCATCTCAGAATCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAAATCCTCACTGTGT	1
M00764_SUN1_MIP38	CCCTGGTTTCACGAGTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGTAGTTCTATTTTAGT	1
M00764_SUN1_MIP39	CACCTTCCAAGAAACACGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAAACAGACGAGACAA	1
M00764_SUN1_MIP40	ACAGGAATGCGCTCGATTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTCCTGGGCTTGTAAC	1
M00764_SUN1_MIP41	CAGTCAACCTGAGCTGCCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCACACACTGGGGAGGACT	1
M00764_SUN1_MIP42	GTGGACCTTAACAGGAACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCGGCTTCACATGTA	1
M00764_SUN1_MIP43	GCAGGTGCACACTCACCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATAAGATACAGTTTAT	1
M00764_SUN1_MIP44	GCTTCGACCCCACCCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTTGAAGGTGAAAAAAA	1
M00764_SUN1_MIP45	GCAAGCCATGTGCGATGACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAAATAATTTTCCAGG	1
M00764_SUN1_MIP46	CGGAGTTTTCTGCTTTTATTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACGTATCAGTGGCT	1
M00764_SUN1_MIP47	ACCCTGAGCTTCAACGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCTACTTGGAAAACTG	1
M00764_SUN1_MIP48	CGGATTTGATCAGCAGGTTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTGAAGAGGCGCT	1
M00764_SUN1_MIP49	CCTTCCCTTGCTGCTGACCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACGAAAAAAAAAAAAAG	1
M00764_SUN1_MIP5	GCAAAAAAGGTGAACATGATTGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGTCTGAGGTGG	1
M00764_SUN1_MIP50	GGGAGCATTGACGGCCCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCATCTTTTTATTTAAT	1
M00764_SUN1_MIP51	GAATTTATCTAAAGGCTTCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTGTGTTTCCTCGT	1
M00764_SUN1_MIP52	CATCTGGGAATGTGCTGTCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTCCGCGTAGTGTT	1
M00764_SUN1_MIP53	GGGGCCCAGCGTCTACAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTACTGGGTGACAACCT	1
M00764_SUN1_MIP54	ATGGGGGCTATAAGCACTGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATGCTGGCTGACCT	1
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M00764_SUN1_MIP56	CCTGAAGAACCGAGCGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCACAAATTGGACCCTG	1
M00764_SUN1_MIP57	CATCCCCCAGGGTGCATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTATGGAAGCTTGGTT	1
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M00764_SUN1_MIP59	GTCTGTACACGCACATACACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGCACCAGCGAAGA	1
M00764_SUN1_MIP6	AGACAAGGTCTCCCTCCCGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTTCTCTTCTCCGTG	1
M00764_SUN1_MIP62	GGGAGGCCGAAATGGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATAAATTTAATCCTCCCC	1
M00764_SUN1_MIP63	GCCCAAAATAACCTGGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTTTACCAGCAACTTA	1
M00764_SUN1_MIP64	CCATGACCCCAAGTGGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAACCATTTTCCTATGCC	1
M00764_SUN1_MIP66	CAAAATGATTACATTTGACCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCAGAGGACGTGAC	1
M00764_SUN1_MIP67	ACCACTTCTGGGGTGAGTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAACCACGTGTCAAGG	1
M00764_SUN1_MIP68	GGAGGCGGTGGCCAGGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCCTCCTGTATTGGACG	1
M00764_SUN1_MIP69	CAAAAACTTCAGTGTGTTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTGGTCATTGGGTTA	1
M00764_SUN1_MIP7	CATTCCCCAGAAGGGCGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACAAATCAGTATTTGCA	1
M00764_SUN1_MIP70	CATGGAGTCTGGGCAGTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTTTGAACAAAGACA	1
M00764_SUN1_MIP71	CGTGGAGTCTGGGCAGTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGTTTGAACAAAGACA	1
M00764_SUN1_MIP72	GAACTCTCTAACCCTGGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCATGCTTCCCTCTCC	1
M00764_SUN1_MIP73	CATGTGCTAATTTTGGGAAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGTCCCAAGGCTGT	1
M00764_SUN1_MIP74	GTCTCAAAAGGGCCAACCAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGCAGATGCCTCT	1
M00764_SUN1_MIP75	CCAGGTGCTGTGTGTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTAGTGAGAGTGGTTAC	1
M00764_SUN1_MIP76	GGAGGAAAGCAGAACATGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGCACTGGTCACAGTT	1

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M00764_SUN1_MIP79	GCTGCCATTCAGGGAAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGATCTTAAAGGTAATTA	1
M00764_SUN1_MIP80	CAAACAGTAGATGGAACCTGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGCATGTCCTTGC	1
M00764_SUN1_MIP81	CAAACAGTAGATGGAACCTGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGCACGTCCTTGC	1
M00764_SUN1_MIP82	AAGGTGTGTTTTCCAAATTTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCAGCATGCTGTC	1
M00764_SUN1_MIP83	GAGTTTTAAAGGACTGAGACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGACAAAGCTGGTTT	1
M00764_SUN1_MIP84	AAAATTTCTACGTAAGCGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATAAGAAGTACACCC	1
M00764_SUN1_MIP86	ATGGAGGGGCCTTCAGAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACAGATGTTCACACAT	1
M00764_SUN1_MIP88	CCCTGAGGGTTACTCTGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAGCGCCGTCTCCGG	1
M00764_SUN1_MIP89	CCCTGGGGGTTACTCTGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAGCGCCGTCTCCGG	1
M00764_SUN1_MIP92	GTACCCTGGGGGTTGCTCCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCGCAGTACCCTCTC	1
M00764_SUN1_MIP93	CGAAGACTGGACTGCAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGTAGCCAAATTATTC	1
M00764_SUN1_MIP94	ATTTTGTGGCTGGCCAGATACACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCTAAAAGTGCCTGA	1
M00764_SUN1_MIP95	GAACATGCGTTATTTCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATAACTGAGCTTCATT	1
M00764_SUN1_MIP96	ATATTTTTTCCCTCCTTTTTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTTTCAAGTGGT	1
M00764_SUN1_MIP97	GATTCATGGCTTTTTGACTTATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCCAGCACCAAGA	1
M00764_SYT5_MIP1	CATAAAGACATGCTCTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCAGCCCCAAATTTTCT	1
M00764_SYT5_MIP17	GAAGTCTCACTTTGTCGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTTCACCTCTTTCTTT	1
M00764_SYT5_MIP18	ATGGCAGTAAGTCGCTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAAAAGGAAAAAAGAAA	1
M00764_SYT5_MIP19	AAAACAAAGGAGAGGCGCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTGCATCCCTCCCTC	1
M00764_SYT5_MIP2	GCCAATAATAATCCTCACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCCAAAGGAATTCA	1
M00764_SYT5_MIP20	GTTCTCGCGGACTCCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGACCTCAGGGAATATGG	1
M00764_SYT5_MIP21	ATTCTCGCGGACTCCTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGACCTCAGGGAATATGG	1
M00764_SYT5_MIP22	GCTCACCCATGACTCACATCGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACTCACCACTCTGAG	1
M00764_SYT5_MIP23	GCCCATTCCTGGAAACGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAGGAGGAAACCCAG	1
M00764_SYT5_MIP24	GCTGTTCGTCCTGAAAGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGGGGCCAAATAAAT	1
M00764_SYT5_MIP25	AGGATGGCTGATTGTCAAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGGTCCCAGCCCTT	1
M00764_SYT5_MIP3	GTTTGCTGCCTCCTTTTTAGGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACATGAAAAGTT	1
M00764_SYT5_MIP33	CTGCAGAACTTTAACAGGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGAGGAGGCTCTGG	1
M00764_SYT5_MIP35	GGCGGGGCATCCTGGTCCTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTAAAGAAGTGAGGG	1
M00764_SYT5_MIP36	GCATCTCCCTAGAAACCAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCCTATTACAACGAA	1
M00764_SYT5_MIP37	GGAGGAGTCTTATAGCTCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCTCGAAGCTGAAAG	1
M00764_SYT5_MIP38	GGCAAAAAGGTGCGGAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGAGCTAGGGAGACCC	1
M00764_SYT5_MIP39	AACTGTCAGAACGAGAACCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGGTTGTTGGACC	1
M00764_SYT5_MIP4	GTTTGCTGCCTCCTTTTTTGGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACATGAAAAGTT	1
M00764_SYT5_MIP41	AAAGGAGAGAGGCCCATCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACACACCTGACAGTC	1
M00764_SYT5_MIP42	AAAGGAGAGGGGCCCATCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACACACCTGACAGTC	1
M00764_SYT5_MIP46	GATAGGGTGAGGCACAGCACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCGATGGCGTCATT	1
M00764_SYT5_MIP47	GACTTCCTGCTCTCTACTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGACCCGTGATTTTTT	1
M00764_SYT5_MIP48	GCTGGTAGCTGCCACCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAAATGGGAAAGTCCAG	1
M00764_SYT5_MIP49	GGGCACTACTGACTCCTGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGGCCCCGTGTTCC	1
M00764_SYT5_MIP5	GCTCCTAAGCTTCCTGGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAATTTTGGGTGGTGA	1
M00764_SYT5_MIP50	GTCTCGTACCGCCTCCGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGGGTCGGTCCCTA	1
M00764_SYT5_MIP51	GAACCCTCACTTTGGGGAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGGCATTCTGCAAG	1
M00764_SYT5_MIP52	GGCTCCTTTCAGAAGGGGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGGGGTCCGAGGAG	1
M00764_SYT5_MIP53	CCCCACCTCCCCCACTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTACTCCCTGGATTATG	1
M00764_SYT5_MIP54	GCCAGGGGTAAGGGTGGGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGGCCACTCTGGAAG	1
M00764_SYT5_MIP55	GAGCTGGAGCCAGCACCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAGAGCTCAGGTATAG	1
M00764_SYT5_MIP56	ATTAGTGGTGTCTGCTATGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCACAGGTCCCTTG	1
M00764_SYT5_MIP57	CCTTCACAAACATACTGCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATCCATTAGCATGTGA	1
M00764_SYT5_MIP58	ACTTGCCATTCTAAAGTTGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCACAGGAATAATGC	1
M00764_SYT5_MIP59	ACATGGCAGTTTGGACTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGAATTTTAAGAATTGC	1
M00764_SYT5_MIP6	GAACAATGAGGTCAGATGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGTTCTCTGGCCAAA	1
M00764_SYT5_MIP60	ATTTGCATTTCAACAAGTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCCTTAACCTAGGC	1
M00764_SYT5_MIP61	CAGACATTTTGCCACAGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCCCTGTCCCTTAAA	1
M00764_SYT5_MIP62	ACCACAGACTTGAGGCTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTCTTTGAACATCACTG	1
M00764_SYT5_MIP7	GCTGCCTCCTACTCTGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTTTTTTAGAGATGG	1
M00764_SYT5_MIP71	GGAATGGGGGACTAGGGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGGCTGATACTACAA	1
M00764_SYT5_MIP8	TCCCAGCTACTCAGGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCCCAGCTACTCACACAGGA	1
M00764_SYT5_MIP86	GACCAGAAGGCAGAAAATGCTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGGGGTCTGGGGT	1
M00764_SYT5_MIP88	GATGCTGAACCCTGCAGAGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTCCTCCTGCTTCG	1
M00764_SYT5_MIP9	CCACAGGCACATGCAACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTTCTTTTTTTGACA	1
M00764_SYT5_MIP90	GCTCATTTTTGTAGAGACGGGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCTTGCTCTGTTG	1
M00764_SYT5_MIP91	AGTAAAAGAAAAGCTCAGAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCACCTGGGCCCAG	1
M00764_TANC1_MIP1	CGTTCTGGGGCCGGTGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTCTGCCTCACTTAAC	1
M00764_TANC1_MIP100	GCCCATTCGCTGGTAACAAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAAGTGTACGTGT	1
M00764_TANC1_MIP101	ACCTTCTGATAAAGGAGCCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTTCCCCCTAGGTG	1
M00764_TANC1_MIP102	CAGCTGATGGGACCGGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTTCTCAGGTTTGTGA	1
M00764_TANC1_MIP103	GTAGAAGTGAGGTGGAGCATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGAGTGCTGGAGC	1
M00764_TANC1_MIP104	GATTATGGAGATACGCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGCTGTCTTAGAGAAA	1
M00764_TANC1_MIP105	CAGCTTCATTTAAGCCATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTGAGAATTCTTTGTT	1
M00764_TANC1_MIP106	CTGCTTGAATTGGAAACTATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGAAGTTGATTGTGA	1

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M00764_TANC1_MIP108	GGGGGAGAAAACAAAAACCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTGAGGATGTCCTGG	1
M00764_TANC1_MIP109	GCTCACCCTGGACCTTTTCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGGGTGCACAGCA	1
M00764_TANC1_MIP11	CCTTTAACCATGTAGCTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGATCAGGGTTAAA	1
M00764_TANC1_MIP110	CACCAGGTGGCTGCTCACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGAAGCAAATAGAGCT	1
M00764_TANC1_MIP111	CAGATCTTTCAGGCTATTAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCCGTGTCTCTCTC	1
M00764_TANC1_MIP112	GGGCCACGTTGAGAATCGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTAATGAGGAAGCAG	1
M00764_TANC1_MIP113	AAAACACGGCCTTCCTGTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGGGATGGGAAGAC	1
M00764_TANC1_MIP114	GTCTGCTCTCCATACAAGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCCCTTCCATTGAGA	1
M00764_TANC1_MIP115	GCCTTAGTCACTGATTTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTGCCCTCCTGACGCGA	1
M00764_TANC1_MIP116	AGGTGAGATGCACACCAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCTTTGTATTCCTTCC	1
M00764_TANC1_MIP117	GAAAATGTGCGCCTTCAGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTGCATTTGGGCTG	1
M00764_TANC1_MIP118	GTTTCCAGGGCCTCAGTAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGACCCCGTGCCTT	1
M00764_TANC1_MIP119	ATCGAGACAGATCTTGGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACGTTGGGAGTATAGA	1
M00764_TANC1_MIP120	CAACAGCCCTGTTTCCCTCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAGCACCGAGGGGC	1
M00764_TANC1_MIP121	GTGCACCAGTATCACCTGGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACGGCTCACCTGTTG	1
M00764_TANC1_MIP122	GTTGTCACTCTGCTCCTGGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGGGGGGCCTTGT	1
M00764_TANC1_MIP123	GACGCACAGGATTGGGGCATTACTTCAGCTTCCCGATATCCGACGGTAGTGTACACCAGCTTCATGTGGC	1
M00764_TANC1_MIP124	CAGGGAAATGGCTTCATCTCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGGAACGTCAGAGA	1
M00764_TANC1_MIP125	GTTACAGCTGAGCATTACTTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCGGCGACCACTC	1
M00764_TANC1_MIP127	CCCACTCACCGAGCTGTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAGACCTTCTACTGC	1
M00764_TANC1_MIP128	CCAGTCTCCTAGCCCACACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCAAGTCACAGGTATG	1
M00764_TANC1_MIP129	AACGTATATCGCTTTGTTTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCCAGGCTTCCTGC	1
M00764_TANC1_MIP130	AAATACATTTTCTGCTGGTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACAAAGGACATGGC	1
M00764_TANC1_MIP131	ATTTTTTTTTAATTCTTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGAAACTGCACTTTG	1
M00764_TANC1_MIP132	CAGTGAATTTCAGCAATATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACAGTGTGTTGTTTT	1
M00764_TANC1_MIP133	GGATGGAGAAGGAACATGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGTGTGAGATAATGGT	1
M00764_TANC1_MIP134	GACCACCTGTCAGAAGTGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGCTAAAACATCAAG	1
M00764_TANC1_MIP135	GCTCACATGGCTTTAGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAATAATACCAACCTG	1
M00764_TANC1_MIP136	GAGGTGAGCCATCCCCACCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGGCTGCCAGTTCC	1
M00764_TANC1_MIP137	AAAGAGTGTTCAAGGAAGTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTGCTGGCTGTCT	1
M00764_TANC1_MIP138	AGGAAGCCCAAGCAGTCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGTGACAGCTTTGACC	1
M00764_TANC1_MIP139	ACATGCTAACAGATTCCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTGCTGTGTTCTGT	1
M00764_TANC1_MIP14	ATAGTGCATTCTCAGCATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACATTAATTTTCTTTG	1
M00764_TANC1_MIP140	GTGGAGCACAGATAGCCAGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGTTTGTCCGCG	1
M00764_TANC1_MIP142	GCACAAAACAAAGGTGGAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGACAGGCTCAGG	1
M00764_TANC1_MIP143	GGTAATTCCAAATGTCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAAGATTTTCCAGGC	1
M00764_TANC1_MIP144	CAGGTTTCTCAACCTTTAAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCCGGCCTTGCTTG	1
M00764_TANC1_MIP145	ACGGACACAGAGAGAACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGATGTGAACCTAAGTG	1
M00764_TANC1_MIP146	GGGCATCACGCTGCTACCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTGTGTTGCCTATTCT	1
M00764_TANC1_MIP147	GCTTGACTGACACTTGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTTTTCTGTTAATGGAA	1
M00764_TANC1_MIP148	GGCAGAATGGTCATCGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCATTCACAGAACATG	1
M00764_TANC1_MIP149	CCAGTATCTGGTTGAAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTGTCATCTCATAA	1
M00764_TANC1_MIP15	GTTTAATTCCTCTTCTCTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTTCCCACCATAGTT	1
M00764_TANC1_MIP150	GTGACCTTTCAGACAAGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAACACCTGCTGGTAC	1
M00764_TANC1_MIP151	GGTTGTGTCTCAGTGTCATCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACACCCTTGGACCTG	1
M00764_TANC1_MIP152	CATCTCTTTGAAGTGGATTATACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTAGTGGCCACAGT	1
M00764_TANC1_MIP153	GGAGAGTAAAGATGGCAAGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACAGCAGTGGTGAC	1
M00764_TANC1_MIP154	CCTGGGAAGTGGTGTGAGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGTTGTGTGGGTCTG	1
M00764_TANC1_MIP155	CACAGAGACGGGACATAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCCACAGCTAAAACCTT	1
M00764_TANC1_MIP156	GCCCACCCCTAAATCCGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAATCTCTTCAGCAGT	1
M00764_TANC1_MIP157	GTCTTAGCTTCACTCTGATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCTGTGGTCCACAT	1
M00764_TANC1_MIP158	AGTGAGCACTGCCTCCATTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTGGTGGAGAAGGGA	1
M00764_TANC1_MIP159	ACCTAACTTGGCTCCCTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGACAGAGATCTGCA	1
M00764_TANC1_MIP16	ACTTGTGTCTTGACAAAAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCCTTCTTGCCTCC	1
M00764_TANC1_MIP160	GTCTGGAGTGGTATCAGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGTAAGATGTCAGATG	1
M00764_TANC1_MIP161	CGTGAGCTACTTACACATTGTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTACCCGGCCCCAC	1
M00764_TANC1_MIP162	GGAAAATGGCCACCACAGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCCAGAGAGGAACCA	1
M00764_TANC1_MIP163	GGGAAATGGCCACCACAGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCCAGAGAGGAACCA	1
M00764_TANC1_MIP164	CTGACTGGTGGCTCTAGAACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTGGAAAGGGCTTT	1
M00764_TANC1_MIP165	GGGCACTGTGATGAAAATGCTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACCCTGAGTAGG	1
M00764_TANC1_MIP166	CCAGAGCTGCTCCTGACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGGATTGTCACTGAGAC	1
M00764_TANC1_MIP167	CCCCAGGACTGCCTTGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATAGTGCCAGGAACTAT	1
M00764_TANC1_MIP168	GCTCGGTGCCTTGGTTTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAACCTCTCTAACCCCTG	1
M00764_TANC1_MIP17	GGTCAGAGAGGGTTACCTGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGAGAGGGAGGAAA	1
M00764_TANC1_MIP170	ATCTGCTGTACTCCGAGATGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTCATTCCTCCCTTCC	1
M00764_TANC1_MIP171	GGGAAAGGATTAGCAACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTCATTTAATTAATTT	1
M00764_TANC1_MIP172	GGGCACTCAAATCTGTCCTTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCAATTCCTCCGTG	1
M00764_TANC1_MIP173	CCAAACCTGATATCTTGATTATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCTGCTGGTGCT	1
M00764_TANC1_MIP174	CCATCGCCCAAGCAGCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATTAAGAGGGTGCTCC	1
M00764_TANC1_MIP175	ACTCCAGCACTTTTGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTTTGCCATTGAAAC	1
M00764_TANC1_MIP176	CCAGGTGCCTGTAATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTGGGGTGGCTCACGCCTGTA	1
M00764_TANC1_MIP178	GCCCGTTGTTGGCTTAATATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCAATCTGGGAGGCAGAG	1

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ID	**MIP**	***c***
M00764_TANC1_MIP179	GCCCGTTGTTGGCTTAATATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGAATCTGGGAGGCAGAG	1
M00764_TANC1_MIP18	CCTATAGGGTGAGCTTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATGGATGGTTTAACCT	1
M00764_TANC1_MIP180	CAGGTCAGCACCTCTTGGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGACAGGAAGTCACC	1
M00764_TANC1_MIP181	ACTACAACCTCAAGGATTAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCATGACTGTGCCT	1
M00764_TANC1_MIP183	GGCTTAGGAGACAGAATAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAAGGGAAAATGGA	1
M00764_TANC1_MIP184	GTAAAGGGCCAGACAGTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCAGAAGACTGAATTAA	1
M00764_TANC1_MIP185	GTTTGCTGACCTCTGACCTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGGGACACAGCTGT	1
M00764_TANC1_MIP186	CATAGGTCACTATTCTTTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGCACAGAGTGAATGA	1
M00764_TANC1_MIP187	ACCAGGGGTTGGCAAACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTATACAGCTGCCTAACAGTAA	1
M00764_TANC1_MIP188	GGCTTGGAATCAGCTTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTAGATTATGACCATGTTA	1
M00764_TANC1_MIP189	GGAACCCTGCTGGGTCATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCACAGCAGGTATGAA	1
M00764_TANC1_MIP19	GTGGGAAGACTGCTCACAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTGTTTACCTGGGGA	1
M00764_TANC1_MIP190	GCCCATGTTTTAATTCCTCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGCAATTATGTCAG	1
M00764_TANC1_MIP191	CAGAACAGCACCACACATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTAATAGAAATCAGATG	1
M00764_TANC1_MIP192	GTTTGGTAATTATCAATCTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTACTTGTCCTAGGA	1
M00764_TANC1_MIP193	GAATCAGATTACCTTCTGGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGCTGGCACATGA	1
M00764_TANC1_MIP194	GGTGTGGGAGTTATTCATTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGAGGACAGTGAAGC	1
M00764_TANC1_MIP195	ACACCGTGGGGAGTTTACTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGGAAACTTTCTTAA	1
M00764_TANC1_MIP196	CTGTGCCCCTTTATTCCAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGAGGTACCAGTATG	1
M00764_TANC1_MIP197	AACCCTTAATTCATTGAAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTGGTCTGGAGAAGG	1
M00764_TANC1_MIP198	GACTATCGTTTGGTCACGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTCCAGCAACAGAGC	1
M00764_TANC1_MIP2	AAAGCAGCGAGGAGGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTGTTTGTGTTTGTGTG	1
M00764_TANC1_MIP20	GTTTTTTCTTTGTCGCAGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTGCAATCAAGAGTG	1
M00764_TANC1_MIP200	GCCAGTAACTAATTTGTAACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCAGTCTGCTCCTCT	1
M00764_TANC1_MIP201	GACCCTCTGAGCAAACCTAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCAGCTCAACAGAC	1
M00764_TANC1_MIP202	GCTGTGAGGTTCCACCATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGTAGTACTTCCTACC	1
M00764_TANC1_MIP203	GTGGAGGGGCAGCCTCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCGTTTTCTATCTTGTTTT	1
M00764_TANC1_MIP204	CCAGGCTGCTTCTGACTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAACCATCATTATCTCCT	1
M00764_TANC1_MIP205	GTTTTGTTCTAAAGGGTAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATAGGACTTGGGCT	1
M00764_TANC1_MIP206	GCCTGTTGAATTTGGGGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAGGCTCTCGAATTG	1
M00764_TANC1_MIP207	ACACGAACATGCTCAGAGTGTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTACGCGGGCCAG	1
M00764_TANC1_MIP208	ACCCCTGGCTTAAGTGACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAAGTCAAGAGGCT	1
M00764_TANC1_MIP209	GGGGTGTCCTCTTCGTTCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGGATGTATGAGGAAGG	1
M00764_TANC1_MIP21	CGGCTGTTTGTAATCCTTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTTGGTCTCTCCTA	1
M00764_TANC1_MIP210	CACAGAGCAGGGCAGGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGGAAGAAACTTCTCCC	1
M00764_TANC1_MIP211	GGCCTTCCTTTGGACTGTAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCAGAGCCCAGGTG	1
M00764_TANC1_MIP212	GGGAGCAGAACCCAGCATTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCGTGAAAACCAGCCA	1
M00764_TANC1_MIP213	GACTTGGAGGAGGGTTCTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACATTCTGGCTGGGG	1
M00764_TANC1_MIP214	CATTCCTCCGTGGCTGTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAAGAGCTGGTTGTGG	1
M00764_TANC1_MIP215	GACAGAAGCCTCTCTGTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATCTTTATGCTGCTGGA	1
M00764_TANC1_MIP216	CAAGGTTGTAACCCACGTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGCTCAGGCTCTT	1
M00764_TANC1_MIP217	GTATCTGGTCCTTGGACCTTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTGGAGGATTGCT	1
M00764_TANC1_MIP218	CAAGTGGGAGGATATAATAACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGTTCCAACAGCA	1
M00764_TANC1_MIP219	GAGAGAGGGCTTCTCAGTGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGAGTGGACTGGAA	1
M00764_TANC1_MIP22	CCTGTAACAGCAACACAGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACATGTTCAAACCTGGA	1
M00764_TANC1_MIP220	CCTCACTGCAGCCAAACCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAAGAAAGCAAGTGCC	1
M00764_TANC1_MIP221	GAGGCTGCTGTTTGGAGATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGGAGTCAACACAC	1
M00764_TANC1_MIP222	GGGATAAAACTTCTTTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTTGTGGAATTTGGAAA	1
M00764_TANC1_MIP225	GGCAAAAGCCAAACAATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAGAATACATCACTT	1
M00764_TANC1_MIP226	ATATAAGTGCGACTGTAAACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATGACCAAGTGATGT	1
M00764_TANC1_MIP227	AATGGGATTTGACTCAATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTATAGGAACTGCTAT	1
M00764_TANC1_MIP228	ATATTTGGAAACAGTATAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACACCTAAGTATTCT	1
M00764_TANC1_MIP229	AAAAACACCTTCAAGCACAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCAGTTTGGAAACC	1
M00764_TANC1_MIP23	CAGCTTTTGTTTTTGTTAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTGTCCCATCCTTG	1
M00764_TANC1_MIP230	ACTGGTTGTTACTTTTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATTCTTAGTGGCGCTT	1
M00764_TANC1_MIP231	GGAAGGATTGTTCCAGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTCTGAATAAAACTGGG	1
M00764_TANC1_MIP232	CATCCATGCTGGTTATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATAGTCACATGTTGTAT	1
M00764_TANC1_MIP233	AGCTTACAGAGAACATGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAATACATCAGAGCTTGG	1
M00764_TANC1_MIP234	GCTAATTTGAGAGAAGTAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCTTTGAGGTGCTAC	1
M00764_TANC1_MIP235	ACCAAGGTTCATTCCTGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTTCTCCTCAATTTT	1
M00764_TANC1_MIP236	ACCTCTGATGTCATTCTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATATGTTGGGATGTGA	1
M00764_TANC1_MIP237	CACAGGAACTTCATTACAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACAGCAAAACTCATGG	1
M00764_TANC1_MIP238	GTTTTGTTTCTGCACAACTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGTGTGTACAATT	1
M00764_TANC1_MIP239	ACAAAGGAGTAAGACTTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCAACAGAGATAGC	1
M00764_TANC1_MIP24	ACATGTTCAAACCTGGACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCAGTCTGGCCTGCCAAAG	1
M00764_TANC1_MIP240	GGGTGACAGCTGCTAGAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGAACAGCCTGATGAC	1
M00764_TANC1_MIP25	GAGGGGAAGGCACTGGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAGCTTACTCTTTTCTT	1
M00764_TANC1_MIP26	CCTGGTAAGGACACACACTGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTCGTCTGTACTGA	1
M00764_TANC1_MIP27	GGTAAGGACACACACTGTACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGTCTGTACTGAAAT	1
M00764_TANC1_MIP28	CCTGGAGATGCAGTTATAATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCCTGGTAAGGACA	1
M00764_TANC1_MIP29	ACTCTGGGGCTTTCCACATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGAAATGAAGTGTCATT	1
M00764_TANC1_MIP3	GGACGCTTTGGGGTGGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAGATGGGCCATAGTCT	1
M00764_TANC1_MIP30	CAAGACACCTGCAATAGCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACACCACAGTGGAAT	1

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ID	**MIP**	***c***
M00764_TANC1_MIP31	AAGGAAAGTAAAATCTCTCTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTGGTGAAGGTGG	1
M00764_TANC1_MIP32	AGGACACCGAGGAGAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTACAAAGGCTTTGGT	1
M00764_TANC1_MIP33	ACAGGGATTGGGACCTCCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTTCCCTTCTTCCCC	1
M00764_TANC1_MIP34	CAGAACCTTAACGATACTCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAATTCTGCTTTGAG	1
M00764_TANC1_MIP35	GTTTGCATGTGTGCTCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTGTTAACTTTTCTCCCT	1
M00764_TANC1_MIP36	GGCCACTCCAGCAAGACCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGGCGAAACCGAAAT	1
M00764_TANC1_MIP37	CATGATGTTGGTGGATGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACAAATACAGGACCAGA	1
M00764_TANC1_MIP38	GTGTCTGCAAACAGATACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCTCCACAACAAACAG	1
M00764_TANC1_MIP39	CAGATTGAACCAGAAGCTAGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCACAGGCATGGC	1
M00764_TANC1_MIP4	AGGCGGGACAAGGGGACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATTTTGAAGAGGCTGTA	1
M00764_TANC1_MIP40	CAGGTTGAACCAGAAGCTAGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCACAGGCATGGC	1
M00764_TANC1_MIP41	AACACTCTGTGTAGAGAGCCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGTGGGTGAGGGG	1
M00764_TANC1_MIP42	ATAAAGTAGCTGCCCTGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGTGGAGATTGTTTC	1
M00764_TANC1_MIP43	GCTGGAGGGAGGGAACAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACCAAACCAGATCAGC	1
M00764_TANC1_MIP44	GTAGAGCGGCTTTGGCATGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTTCTGAGGGCCTC	1
M00764_TANC1_MIP45	GGAGGTCCCTTCCTACCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGGGTTAAAAGAGCC	1
M00764_TANC1_MIP46	GAGCTTTTACCAGTAAGCAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTCCAGAAGCATCA	1
M00764_TANC1_MIP47	GGAGTAGGAAGAATGGTTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCACTCACATATCAGT	1
M00764_TANC1_MIP48	GTTGTAGCTCAACGGCAACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTGCATGACTTGCA	1
M00764_TANC1_MIP49	GCACCAACAAAGATCAATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTGTCTAGGTAACTGG	1
M00764_TANC1_MIP50	CCCCTGATGGATGCTGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAATAGGTTCATATGAG	1
M00764_TANC1_MIP51	AAATTTACAAAGCAAGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGAGCTGTAGTTTAAC	1
M00764_TANC1_MIP52	AAGGTGGGCTTTCCCAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATAATTAAGTGCCTTTG	1
M00764_TANC1_MIP53	GGTTCTCCCTGAGGTTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAATCACAGTGAAACT	1
M00764_TANC1_MIP54	GTGCACAGGAAGTTTTCCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACAGTGGTACTGGGT	1
M00764_TANC1_MIP55	AAGTCAAAACCAGGATTTCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGCTGGTAGAGACCC	1
M00764_TANC1_MIP56	AGCTGATGTCTGAAGTACCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAACACCTAAATAGCC	1
M00764_TANC1_MIP57	GGGTAAGAAAAGGGCCTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTGACAGGTTAAGGAA	1
M00764_TANC1_MIP58	CTGTAGTGTGAACTCATCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGTTTTTGTTTTACTG	1
M00764_TANC1_MIP59	GCTTTGTCTGGTGATTTTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCTTGAGCTGCCGG	1
M00764_TANC1_MIP60	GTAATGCCCGAGGAAGACACTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAGGCCGATAATGA	1
M00764_TANC1_MIP61	GGTTTCATTTTTGTCTTCAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACACAACAGCCCAGAA	1
M00764_TANC1_MIP62	AAATGTCCACATTAACCTTCTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGGGAAGCCATT	1
M00764_TANC1_MIP63	CGTTCTGCTTCTTTCTGCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGAGAAGAACGGTGC	1
M00764_TANC1_MIP64	CAGTGGGGTGAGGAAAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTAAAGAGGCTAAAAG	1
M00764_TANC1_MIP65	GCACAGGAAAGCGTATACCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCTTGGAGGGGAA	1
M00764_TANC1_MIP66	CAAGGGAGGGTGTCATGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCATCTATCAGGAAAGCA	1
M00764_TANC1_MIP67	GTGCAGAGACCTTCACCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCTGTTTTTGTGATGT	1
M00764_TANC1_MIP68	CAAATGTGCATCCTCACTAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTGCAGTGTTCGTG	1
M00764_TANC1_MIP69	AATGGCAAACAGGCAGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGTATATGTGGTCTTCC	1
M00764_TANC1_MIP70	GTTTTCCTGTTCTTAGTTTTATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGAACCGAACAA	1
M00764_TANC1_MIP71	GATATGGATTCATGGAGCTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGAGGAGTTAGCAC	1
M00764_TANC1_MIP72	CCTAGCACCGATAGCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAAAACAAAAGCATGTG	1
M00764_TANC1_MIP73	GATGCGGTGCTGCTTGTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCTATAATTCCACTGTC	1
M00764_TANC1_MIP74	CATGGTCTGTGAAGGTCAGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCCCTAGTTCCACC	1
M00764_TANC1_MIP75	AACCCTCTGAGGAAGTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACTGTTATAAAGTAAA	1
M00764_TANC1_MIP76	GTTGGGCATCAGGTCCCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTTACATTCCTTGA	1
M00764_TANC1_MIP77	CCTCCTTGTCTGAGAAAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGATTTTCAAATTTGCA	1
M00764_TANC1_MIP78	CACAGTAAGTAACTGAAAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATACAGCTTACAGTTTCC	1
M00764_TANC1_MIP79	CAAAGCATCACTGAAAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATTCCTTTGAATATG	1
M00764_TANC1_MIP80	AAATCAGATTGGTTTTCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGCAGAAATAGCCTA	1
M00764_TANC1_MIP81	GATAGATGTGCAGAGGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTATATTAGTTTCAAGA	1
M00764_TANC1_MIP82	GGAAAGCTGGGTTTTCTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAAGGCAGATTAAAA	1
M00764_TANC1_MIP83	GGTGCTAGGACAGTTCCATGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGGAGGGGCCGTT	1
M00764_TANC1_MIP84	AGGCCGATTCAGGACACTACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGAGCTGGGCAGGT	1
M00764_TANC1_MIP85	CCTTTCCTTTGCTTTCCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGAGCAGGTATGTAA	1
M00764_TANC1_MIP86	CCTAAGATTAGGGGTTCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATTCTTCAGCCCCAGC	1
M00764_TANC1_MIP87	CGGTCATCATTTTCGGATGAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGACCCGGTGGT	1
M00764_TANC1_MIP88	GCCCAACTCAGTTGCAGGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAACTGCTCCCCAGTGG	1
M00764_TANC1_MIP89	GTGAGCTGGAGCCCTGAGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGCTTGTATCTGGA	1
M00764_TANC1_MIP9	CCCCTGCCCCCTTTTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGTTAATAAATGGTGGA	1
M00764_TANC1_MIP90	CATTTTGATATTGTTTGCCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTGCTGTAATATTA	1
M00764_TANC1_MIP91	AGGTAGGGCACAGGAAGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGATACTAAACTTCAGT	1
M00764_TANC1_MIP92	CGGCCGTATTGTGCCATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCATGTTATAAACACAG	1
M00764_TANC1_MIP93	GAAGCACGATTTGCTCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGGAAATGCTTACAGAC	1
M00764_TANC1_MIP95	CAAGTTGGTGGCCCTGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCTGTGTTTGTGGGAA	1
M00764_TANC1_MIP96	AAATGATTGCCGTCTTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCATCTATCTTATGTT	1
M00764_TANC1_MIP97	GATTTGTGCCAGGGCATATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAAGAACTCGGTG	1
M00764_TANC1_MIP98	GTGAAATATCTTGCTTCTAAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACCCCACTCAGGA	1
M00764_TANC1_MIP99	GCATCCTCTCTTGGTCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCATTAAGCAGTTGTCTCT	1
M00764t_LRRN1_MIP14	GAGGAAAGAAAAAGGGTGTCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGAGGAGGGCTGC	1
M00764t_LRRN1_MIP20	CAAACGTCCTGAGGCTGCCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCACGCAGCACAA	1
M00764t_LRRN1_MIP24	GGCCAGTCGTTCACTCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCACCCAATTAGAATTC	1

continued table…

ID	**MIP**	***c***
M00764t_LRRN1_MIP25	CTCTAGGCAAATGTCGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCTGTAGAACTGTTAAG	1
M00764t_LRRN1_MIP27	ACTGCCATAATCAGTGAGATTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGTTGGTTAGCAAGC	1
M00764t_LRRN1_MIP30	AAGGCATAGTCACTCGCAAATCTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGTCCGTGGCATG	1
M00764t_LRRN1_MIP31	ATTCTACACAGCTCAACCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAATTTGGCTGAAATA	1
M00764t_LRRN1_MIP32	GGGATGGTTTTCAGGAGTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAACTCCTGACACCC	1
M00764t_LRRN1_MIP33	CGAGTCTTCCATACAGAATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTGTTCACGTTTTGTT	1
M00764t_LRRN1_MIP34	GAAGTCATTAGTAGGCCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAAGCGGAGGTCATT	1
M00764t_LRRN1_MIP35	CTGCAGCAGCTTTTCAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCAACTTACAGAGAAGC	1
M00764t_LRRN1_MIP36	GCGATGTTATTGCTCTGTAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCCAAATGCAGCGT	1
M00764t_LRRN1_MIP37	GCTCATGCTTTTGCAGGCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCTAACCCAGCTCAC	1
M00764t_LRRN1_MIP38	GTGGTTGATGTAGAGTTCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATTTCCAGGTTGGGTG	1
M00764t_LRRN1_MIP39	GTATCTCACTGATATTCCTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATAGTCGCTGGTTTG	1
M00764t_LRRN1_MIP40	CCTGCCAAAACTAAGCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAATTTCAAATTTGGAAC	1
M00764t_LRRN1_MIP41	GCTTCGGTTAAAAGAACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTGTCTTTTTATGATA	1
M00764t_LRRN1_MIP42	CCCCTTCTTGGATTTTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTTAGGGTTATTGGTG	1
M00764t_LRRN1_MIP43	AGTCGAATCCCTCCCCAATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTCACAAAGCTGGAAG	1
M00764t_LRRN1_MIP44	CATTCAAGGCATTGTTGTTCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCATGAAGCGGATG	1
M00764t_LRRN1_MIP45	GATATCTCACGACAGCTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAACTCCAACAAAACCA	1
M00764t_LRRN1_MIP46	CCTGGATTAAAACTTCCTTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGTAAATTTCAGGT	1
M00764t_LRRN1_MIP47	ACCTTGGAAATATCTAACATACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACGACGGTTTTCCT	1
M00764t_LRRN1_MIP48	CGCTACTTAGCTTGTATTTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCATCCAGAAGGGTC	1
M00764t_LRRN1_MIP49	AACTTAAAATGGTCGTCTGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTGGCAACAATTAA	1
M00764t_LRRN1_MIP50	ACATTGGAATTAACTTTCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCTGTGGAAGGCTG	1
M00764t_LRRN1_MIP51	CATCTCTGATCAAGAAACCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATACAACCTAACGC	1
M00764t_LRRN1_MIP53	GACAAAGATGGTTCTGCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTGCCAAAAGATTTAA	1
M00764t_LRRN1_MIP54	CGCTGTCACCTTCCCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATAAAGCAAAAACGTCT	1
M00764t_LRRN1_MIP55	GACGGGTGGATATTTCAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTAACTCAGAGGATA	1
M00764t_LRRN1_MIP56	GCCACAAACTAGCAAAGTCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATCATAATAATGATA	1
M00764t_LRRN1_MIP57	GTTCCCCTGTGCTTTTACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGTTTGGTTTTTATTC	1
M00764t_LRRN1_MIP58	GAGCACTGTAGTTAGAACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCAATGCTGCTTCAAA	1
M00764t_LRRN1_MIP59	GTTGAATGATGTTAGTTGACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATCCGTAGAAAGT	1
M00764t_LRRN1_MIP60	GGTAACAAGTCTAGCCTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTAAGCCTCTTTAACTA	1
M00764t_LRRN1_MIP62	CATATTTCTATTGCCTGTTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTATACACCACGTG	1
M00764t_LRRN1_MIP63	GTTCTTGCTAGTTGCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACACTTTTAAAAGAAAAG	1
M00764t_LRRN1_MIP65	AGGGTGGTTCATATGAAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAGCTAGGCCCTAA	1
M00764t_LRRN1_MIP66	GCCCATTAGGTGCTAGTCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGTGTGTGACAGGTT	1
M00764t_LRRN1_MIP68	ACAAAACTCTTACAGAAATGACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTAACACGGGTCTAAG	1
M00764t_LRRN1_MIP69	ACAAAACAACTTCCGTACAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTCTGTGGAGTGTCAC	1
M00764t_LRRN1_MIP70	GTCTCAGCAGATATTGCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCATCTGCTCTAAATG	1
M00764t_NPBWR2_MIP10	GTAGCTGGGACCGTTGACGATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCAGTGGCTCGGA	1
M00764t_NPBWR2_MIP12	CAGGTCAAGGACATGGGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGGTATCTGGTTGGGG	1
M00764t_NPBWR2_MIP14	ACCTCCCAAGCTCATCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATCAGTTCCCTCCTCC	1
M00764t_NPBWR2_MIP15	GTTTCCAAAGGGACCGCTTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAAGAGTAGCTGGAC	1
M00764t_NPBWR2_MIP16	GTTTTGGCCAGTACAGGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGAGTCTGCACCCT	1
M00764t_NPBWR2_MIP17	GAAGCACTGGACAGGTCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGTCTTGAAACTCC	1
M00764t_NPBWR2_MIP2	GACAGAGGCCAGGTGGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGGAAGTTGTCATCTA	1
M00764t_NPBWR2_MIP5	GGTCCTGGGCTTCGTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCACGGTCCTGGTTCTGC	1
M00764t_NPBWR2_MIP8	CCCTTAGGATTACAAGGATGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTCCCCGAAGGGC	1
M00764t_NPBWR2_MIP9	CCAAGATGAAGACGGTGACCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCACAATGCCACC	1
M00764t_OPRL1_MIP10	GGGAGAGGGAGAGCGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCAATTCAAACAGAAC	1
M00764t_OPRL1_MIP12	CGTCACCTAGAGCTCTCCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTCACCTGCCCTCTA	1
M00764t_OPRL1_MIP17	GTTCCTGGCTTGAGGGGTCTTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGGGCGTGGACGC	1
M00764t_OPRL1_MIP18	GATGAAACTTCAAGTCAAATTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAACTGTGAGGGA	1
M00764t_OPRL1_MIP19	CAGGCCTTGGCAGCAATAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCCTTGTGATTTTAAC	1
M00764t_OPRL1_MIP21	AGGTTGCAGAAGTAAGGGCCTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCACTCGGCTGCT	1
M00764t_OPRL1_MIP25	GTCCCTGCATGTGCATGTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTAGCTGCCTCCAGG	1
M00764t_OPRL1_MIP28	ACCTGGGACAGAGCGCAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGCAGACTGTGGTT	1
M00764t_OPRL1_MIP33	ATATTTACATCTTTAACCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCACTGTAGCTTGT	1
M00764t_OPRL1_MIP34	GAAGAAAGGCTTCACTTGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGCCCAGGAGGATG	1
M00764t_OPRL1_MIP35	CCCTAACTGCCATGAGTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACTCTGGTCCTGCTG	1
M00764t_OPRL1_MIP36	GAAGGTGCTGGTGAACATGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGACAACAGAGGCCA	1
M00764t_OPRL1_MIP39	CATCTGCATCTTCCTCTTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCTCCTCTGGGCC	1
M00764t_OPRL1_MIP40	CAAACACCGGGCCCCAGTAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGTTCCGGTCCTTC	1
M00764t_OPRL1_MIP45	GATGGGCTTTTCCCTGTGGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGACTAGGCGTGGAC	1
M00764t_OPRL1_MIP46	ACCTGTGTGAGCTCTGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATGCTTTGACCTGTCC	1
M00764t_OPRL1_MIP47	GGTGGACGGCCGTGACTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGACCTAGTGACATCAT	1
M00764t_OPRL1_MIP53	GTGGGGCAGGTGTCTCAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTGCAGCTTGACTCTG	1
M00764t_OPRL1_MIP54	GGGTTGACGGTCCACAGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCTTCTCCCACCCAAA	1
M00764t_OPRL1_MIP57	GCTGTGGTGGCTGTGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTTCATTTACAAGCCTC	1
M00764t_OPRL1_MIP59	AAAAACTCATTTTTTCCACCAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGGGGATGCCCC	1
M00764t_OPRL1_MIP60	CAATGTTGCAGGTCTTTTAATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTAGACTCCCCAG	1
M00764t_OPRL1_MIP61	GTGGCAGGAGTCCCTGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTTAGGCACCTGCAAA	1
M00764t_OPRL1_MIP62	GACGTCATGGAGACAGCATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAGTAACGCTTGCCA	1

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M00764t_OPRL1_MIP63	GCTCACTGGCTGGGTATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTGTGAATCTGTGCTG	1
M00764t_OPRL1_MIP64	TCTTTTTCATTACCCCAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCATAGCCTCCTCCC	1
M00764t_OPRL1_MIP65	CCTTTTTCATTACCCCAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCATAGCCTCCTCCC	1
M00764_TOX3_MIP1	GCCCAAACATCATCTTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGACTGTATTTTGATGC	1
M00764_TOX3_MIP10	GTCCCAGGATTCATTAAACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTACAACTGTGCTTTT	1
M00764_TOX3_MIP11	GAAAAATGGCCTTATTTCTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAAGCTGTGCTCT	1
M00764_TOX3_MIP12	AGAGGACCGTTTGATCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAATAAATAAAAAAGGC	1
M00764_TOX3_MIP13	AAGTGTCTATTAGATAGGCAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACGCATATGGCAGA	1
M00764_TOX3_MIP14	GCAGGGATGGGGGATGTTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTGGTATACGCAAATC	1
M00764_TOX3_MIP15	CAAATACAGTCTCAGACACAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCTGCAACACAT	1
M00764_TOX3_MIP16	CATGTGGTGCTGGAAATGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGGCTGAGACTGGT	1
M00764_TOX3_MIP17	CCAGCAGCAAATTAATCAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGATGCAACAGATGC	1
M00764_TOX3_MIP18	GAGGGTGCTGAGCCAACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGCTGATGCATTTGGTG	1
M00764_TOX3_MIP19	ACCCAAGTGAGTCCTTCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACCCTTAACCATGAGACT	1
M00764_TOX3_MIP20	GAGGATGTTAGATTGGTCGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAATCTGGTTCATGGG	1
M00764_TOX3_MIP21	CACTCCACTGTCTCAACATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTGTTGTAACAGTCTG	1
M00764_TOX3_MIP22	ACTCTTTGTCTTGTGACTTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCATTTTGGGGGA	1
M00764_TOX3_MIP23	CAGGAGGGCATGAATAATGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGTATCACTGTCATC	1
M00764_TOX3_MIP24	CAGCCAGCCAACTGTGATCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTGGCTAACAGAATG	1
M00764_TOX3_MIP25	GCAGCTTCTGTTTTCCTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTATGTTTTCAATGCTTGA	1
M00764_TOX3_MIP26	AAAAAGAATACCTGAAGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTATGTGAGTTGTGT	1
M00764_TOX3_MIP27	AGAACCCTGCCACCCTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCACAAATTAGGTCACATA	1
M00764_TOX3_MIP28	GTTTTAATATCCGTGTGTGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGTTTTCAGCTGTT	1
M00764_TOX3_MIP29	AAAATAATGAGTTTCTCCATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATTTCTGGATGCAA	1
M00764_TOX3_MIP3	ACAAAAAATGCTTTTATCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTTAACGTAAACACT	1
M00764_TOX3_MIP30	GTAAGCCATTTGCAGCAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGCTTTGCTCTTTTC	1
M00764_TOX3_MIP31	CATCCAAGCTAGGAGATTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGATACCTTTCTAAA	1
M00764_TOX3_MIP32	GACTTTTAATTTTGCTCCAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACTGAACACCCAGC	1
M00764_TOX3_MIP33	GAAAATCAGTCTGCTATCTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTGGGCTTCTCCT	1
M00764_TOX3_MIP34	GAGGGACTGGAAAAGTGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTATTTCAGGAACTCATT	1
M00764_TOX3_MIP35	GTTGATCTATTCTTCTGTGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCACCTTCCCAACAA	1
M00764_TOX3_MIP36	GTTTTCAAGAATGAAGAGTGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGTTCCTTGGGGGT	1
M00764_TOX3_MIP37	AATACCTCTCATACTGCCTTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAGTAAGGGGGGGA	1
M00764_TOX3_MIP38	AGAAATTAGCCATGCTTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGAACCCTTGTGCTGT	1
M00764_TOX3_MIP39	CAAAGGGGAAAAAATTCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAATAATGAGACACGC	1
M00764_TOX3_MIP4	ATTATTCAGATGTGGTGTGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAACACAATAAGCA	1
M00764_TOX3_MIP40	CAAAAAGGGCACTACAAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTTATGGGTGCATGT	1
M00764_TOX3_MIP41	CATATTAAGTGAACACATGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGAATGGGTTCTG	1
M00764_TOX3_MIP42	AACCCAGACATATAAATCTAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCATCAAGGCTCC	1
M00764_TOX3_MIP43	ACCTTTAATTGCAGCCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAATGATCATGAGGTTTA	1
M00764_TOX3_MIP44	AAAACCCCAATGCAACCTTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTCCAGACTCTGGC	1
M00764_TOX3_MIP45	CCATAATTGTTCTTTGAAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTGGAGTCTTGGG	1
M00764_TOX3_MIP46	GTGGCTGATTTGCTTGCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCATGAATGAAATTCAA	1
M00764_TOX3_MIP47	GTAAGTTAGAACTGCCTTAGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGTTGGGGTTGAA	1
M00764_TOX3_MIP48	GACCGCATGATCAGGGAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATGTGTGAGGCATACT	1
M00764_TOX3_MIP49	GACTGCATGATCAGGGAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATGTGTGAGGCATACT	1
M00764_TOX3_MIP50	GTCCACATGACCGATGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAACCTGATAAGTTCACTG	1
M00764_TOX3_MIP51	GGGGGAAACTGGGGTGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGCAAATGATAAAAAAT	1
M00764_TOX3_MIP52	CCCTTCCATTACAATCTCAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTCCAGAGTCAG	1
M00764_TOX3_MIP53	GTTCCTATATCTTATTCCTCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGCCTAGGGCAG	1
M00764_TOX3_MIP54	GTGGCACAAGGTAACTACTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATGCGTTCTTCGCT	1
M00764_TOX3_MIP55	GCTGTGATTTGGAAAGAATGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCACCTACCTCACTG	1
M00764_TOX3_MIP56	GGTAGATAGTTCTGGGGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTAGAATCTGTGTTGTT	1
M00764_TOX3_MIP57	ATTTGACAGCTAATTTTTTTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATAGGTGCCTTCCG	1
M00764_TOX3_MIP58	GATCTGGACAGGCTAACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCATAGAAGATGTAGTG	1
M00764_TOX3_MIP59	AAAAACAACATGGTTGGGCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGGCACTTCATCCT	1
M00764_TOX3_MIP6	AGTGGTCATAGATATTGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAACTGTTTTCATTTA	1
M00764_TOX3_MIP60	CATCCAGCAGAGGACAGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCCCATTCTACTAC	1
M00764_TOX3_MIP7	GTTTTGAGTGACAAGTTTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGACTAATTTCCACTTTT	1
M00764_TOX3_MIP72	GTCGGTTCTCTTCGTATTCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCACGAGTGTCTCC	1
M00764_TOX3_MIP74	CCCAGAGCAGTGAATGATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCCGATGAGAAAAAAAAT	1
M00764_TOX3_MIP75	ATAAAGAGGGGTGGGTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTTCCCATTTAGTATAA	1
M00764_TOX3_MIP76	CCTATGACACTCGCTAACAGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTTGGCGAAGGGA	1
M00764_TOX3_MIP77	AATATTTCAGAATGTCGCCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCCCGATCTACTCT	1
M00764_TOX3_MIP78	GCTCTTCTCTTAGCAAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTTCATTTCTTCTGTT	1
M00764_TOX3_MIP9	ATCACAGACTTTTGCCAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTCCTGAAGCCCTAA	1
M00764_TREM1_MIP1	GACCTTGCCATCTTTCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGTGGGCCATGAAATAA	1
M00764_TREM1_MIP10	ACCATACAATTTTGGCCTGACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCACCAGCCACT	1
M00764_TREM1_MIP11	CCAAGATTATTAGAGGAACGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCCACAAGAGAATTA	1
M00764_TREM1_MIP12	GTGCCTCAGAAAAGAAGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGAGGAGGTAAAAG	1
M00764_TREM1_MIP13	AGCAAACAGGACAGAGAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGTTATTAACTCCCTG	1
M00764_TREM1_MIP14	CACGCTGAGGTCATTTGTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGAGAGACTTTGCCA	1
M00764_TREM1_MIP15	CATAATGGGGAAAAAGGCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAAGATTATGTTCTCT	1

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M00764_TREM1_MIP16	GTTTGGGGAACAAAGTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATTAAATAGTGTGAGT	1
M00764_TREM1_MIP17	GGAAGACCATTGGTAGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTAGCAGGAATGTGAT	1
M00764_TREM1_MIP18	AAAGATTGGAAACAATTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATAACTCTGAGATAAACAT	1
M00764_TREM1_MIP2	ACTGTAAGCAAACAAAAATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAATCCCATCCTCTCCC	1
M00764_TREM1_MIP20	ACTTACATAACCATTGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGCAGTAAGTCTAATT	1
M00764_TREM1_MIP22	CACCACTAGTCTAACATGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTAGGCAAACTTAAG	1
M00764_TREM1_MIP24	GAGGTCCCTCTCAGTATTTTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTAATAACTCTCAG	1
M00764_TREM1_MIP25	ACATTCAGTTAGTCAGGCCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCCCCAGCTCCAGC	1
M00764_TREM1_MIP26	ACTTTGGGTGAGTCAGGAACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGAGGGAAATGGCA	1
M00764_TREM1_MIP27	CCTTCTTCCCCTGGACATTTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCCACTGGAACTTG	1
M00764_TREM1_MIP28	GAGAATAGGGGAGGCTCTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCCTTTGTTTCCCAG	1
M00764_TREM1_MIP29	GATTTCAGAGTCAGGAGTGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTCCCCTTTCCCTC	1
M00764_TREM1_MIP3	AGGGAGCCCATACAGGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAGAACTGACTTATCC	1
M00764_TREM1_MIP30	CATCAGGTATAGTTTCCAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTACCACCACTAAGG	1
M00764_TREM1_MIP31	CATTGGATGGATGGATGGACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTCACAGTTCTGG	1
M00764_TREM1_MIP32	GTCTTCTTGCAGGTTTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCAGCTTCATTTACCG	1
M00764_TREM1_MIP33	AAGAAGAAAAAAAGGGCAGGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACGGGTAGGTGGT	1
M00764_TREM1_MIP34	CAGGTTGACTCCACAGTATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGAAGAACAGAAGG	1
M00764_TREM1_MIP35	CCTGGCTTATGGCATATTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAAGAAAGGAATTTTTT	1
M00764_TREM1_MIP36	GAACGAAAGGCAGAGTGAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGACAGAGGAAAGGG	1
M00764_TREM1_MIP37	GGGGTGCAGAGCCCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCAGGCTTAGAATTCC	1
M00764_TREM1_MIP38	GTAGTTTCTGACACAAAGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCCCCTTGTACACAA	1
M00764_TREM1_MIP39	GTACCCATTCAGTTGGAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTATCCAGTGAGTAGA	1
M00764_TREM1_MIP4	GCTCCTGGAACACCTGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCCTCTTTTCCTGTATCA	1
M00764_TREM1_MIP40	GGGTCTGCATCTCTATTGATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCCTCCCAAGGATG	1
M00764_TREM1_MIP41	CACCCAAAATTAGGCTGTGCTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATGCCACCAAAC	1
M00764_TREM1_MIP42	AATTGGGGTACAATTAAGGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTCCCAGCAGTCTG	1
M00764_TREM1_MIP43	GGTCACCACCAAGCGGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGATAAAGAGGTCCTGG	1
M00764_TREM1_MIP45	CCAGGGTCTTGGGCATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATACAGTCCAGAATCTTCC	1
M00764_TREM1_MIP46	CCTTCAAAGAATTCCCATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAACTGAAAGAGGGGCA	1
M00764_TREM1_MIP47	GGGGAAAAAGGAGAGGAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATTTCACATCCAGGGT	1
M00764_TREM1_MIP48	CTTCAGAGCACAGGGCCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGGAAGGATGAGGAAG	1
M00764_TREM1_MIP49	CAACAGGATATGAGGCCATTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCATCCACAGCAGC	1
M00764_TREM1_MIP5	GGCAGTGGCTTATTCATGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATCCCTGACCCTTGT	1
M00764_TREM1_MIP50	GCAACTTTCCGAAGCCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCAAAGAAACTTAACTGA	1
M00764_TREM1_MIP51	GGGAGAATGATACTTGAATGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCTGACTCCTGACA	1
M00764_TREM1_MIP52	GTAAGGTTGAAAGGTAATTGTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCACTACACTAAA	1
M00764_TREM1_MIP53	GTGGGTTCTCTTGGCTTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTCCATTCACATCCA	1
M00764_TREM1_MIP54	CAGGATGAAGCAACATGTTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGAGCTCCCAGGC	1
M00764_TREM1_MIP55	GTTCAAGACGCTGAAGCAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCATTTGTCCTTCAGCA	1
M00764_TREM1_MIP56	CCAAAAGTTATCTGGGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGTGTTTAGTACTATT	1
M00764_TREM1_MIP58	ATCCAGAAGTTGGTTATTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACATCACACTTAGAGGAA	1
M00764_TREM1_MIP6	GGCAGGAGTGAAAACTGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATAGGAGAGCAACAAC	1
M00764_TREM1_MIP60	GACATTACCAGCAACCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTATTTGAAAGAATAAA	1
M00764_TREM1_MIP62	GCTTGTGTGCATAGAGGTGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGTAGGCCTTTTGCT	1
M00764_TREM1_MIP7	GTCTTATTTCTCCAGGTTCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTACACAGGATGTCTGACA	1
M00764_TREM1_MIP8	GTGAGAAAGTGCATCCTTCTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCCCCATGCTGGGA	1
M00764_TREM1_MIP9	CAGGGCAAAACTGAGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTGGAAAGAACCACAC	1
M00764_TUBB3_MIP101	AGACCTACTGCATCGACAACGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGTGAGGAGTATCCC	1
M00764_TUBB3_MIP102	ATCCGTGTTCTCCACCAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGGAGGTGGTGACTC	1
M00764_TUBB3_MIP107	CCTTCCTGCACTGGTACACGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTGGCCGTGTGTGAC	1
M00764_TUBB3_MIP108	GCTGTTCCCGATGAAGGTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGCTCTCGGCCTCGGTG	1
M00764_TUBB3_MIP109	GAGGCCCAGGGCCCCAAGTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCATGGACGAGATGGA	1
M00764_TUBB3_MIP11	GGTGCCTGGAGGTGTCCATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACTCCTTCCTGCTTC	1
M00764_TUBB3_MIP112	CATAAATACTGCAGGAGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTATTAAGTATCCCCG	1
M00764_TUBB3_MIP113	GGAAAGTTGTGTCCAGTAGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAGCTCCAGGCCT	1
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M00764_TUBB3_MIP115	GTCTCCTCACTGGGCTCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTTCCCCTCAGGTCC	1
M00764_TUBB3_MIP116	CGAGGCAGCAGCAGACATGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCATATATAACAAGAGG	1
M00764_TUBB3_MIP117	CCTGCAGATATCCGACGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAATTTGGCATCTGCT	1
M00764_TUBB3_MIP12	GGCTCCTGTCTGGTTGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGAAGCAGTACATGGGTG	1
M00764_TUBB3_MIP13	AGACGGCCGTCATCCTCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGCTTGGTGGAGAAC	1
M00764_TUBB3_MIP14	AGATGGCCGTCATCCTCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGCTTGGTGGAGAAC	1
M00764_TUBB3_MIP2	GTAGAGCCTGAGGCCACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTCTGGAAACTGAGTGA	1
M00764_TUBB3_MIP22	CGGGGCAGAGGACGATGAGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCCTTGAGCGTCCTG	1
M00764_TUBB3_MIP23	GGGCAGAGGGAGGTGGTGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTCATCATCTGCAAT	1
M00764_TUBB3_MIP24	GTCTCTGGGTGGAAGTGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTCCTAAAGAGACAT	1
M00764_TUBB3_MIP3	GCAGAGGGGACCCCTGTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAAACTCCTGCAGGG	1
M00764_TUBB3_MIP30	GGGACTCCTTTCTTCCCTCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTGTCAGCACGGAGA	1
M00764_TUBB3_MIP31	CCTTCCCTGTGACCACATGTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCTGCTTCTCGGTT	1
M00764_TUBB3_MIP35	GCTGGGGAGCAGTGGCGCCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTGTGTTCAGCC	1
M00764_TUBB3_MIP36	CCAGGCAGCATAGTTCATCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTGAGCCTGTCCCAGG	1
M00764_TUBB3_MIP40	GGAGTCCGGGGTGAGTGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCTCCAGTTTGGAAAG	1

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M00764_TUBB3_MIP51	GGAGAAAACTGCTTGTGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATAGTGCGAGACTGTC	1
M00764_TUBB3_MIP54	TCACCCCCATAATCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGGAGACGGAGGTTGCAGTA	1
M00764_TUBB3_MIP56	CAGGGGTGGTGGCTCACACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAAATAAATAGAGGCCAG	1
M00764_TUBB3_MIP57	CAGCAGTTTCCACTAAAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTGGTATTACAGGCG	1
M00764_TUBB3_MIP61	GCGCATCTTTGTCTACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGGTCTCGATCTCCTGACTT	1
M00764_TUBB3_MIP62	GCATCTTTGTCTACACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGTCTCGATCTCCTGACTTCG	1
M00764_TUBB3_MIP63	GCTTTGGAATGGAGACACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAAGATTCCTCAAGAA	1
M00764_TUBB3_MIP64	GGGCAAGGGGCATTGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCAAATTGTTTTCTAA	1
M00764_TUBB3_MIP66	ATAGTTCTACGTTTGCCATATACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCCTGCAGACACTG	1
M00764_TUBB3_MIP67	CCTTCAGGGAAGTTGCCACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGATGACAGGAGGTCT	1
M00764_TUBB3_MIP68	GTCTGTGAACCCAGCAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACACAGATTAACCCACT	1
M00764_TUBB3_MIP7	CCTGGGGACCTGAGCAGCAGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGGGCTCTGAG	1
M00764_TUBB3_MIP70	CATTTGGGACCCCAAGGACCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTGCAGGCACCT	1
M00764_TUBB3_MIP71	GAAGCGACTTGCCTGAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAACCATGTCCAGTGAT	1
M00764_TUBB3_MIP72	GTCTCTACCCGCTCTGTGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGAGGCCAGTAATGT	1
M00764_TUBB3_MIP73	AGTAGCTGGCAGAGCAGGGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCAAGGGCCTGGAG	1
M00764_TUBB3_MIP74	CCCACCCTGGGGCTGTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGATAGTAAAAACTAACC	1
M00764_TUBB3_MIP75	ACCCACACCCAGGTCCCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCACGAGCCCCATTCA	1
M00764_TUBB3_MIP76	GGGCTATGGGCCGGTGCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTATGGCAATTTTCTGAC	1
M00764_TUBB3_MIP77	CCCTTTCCCTTGTGAAGCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGCAAGTCCGAGT	1
M00764_TUBB3_MIP78	GACTGACCAGGTCTCAGCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGATGAGCATGGCATC	1
M00764_TUBB3_MIP80	ACATATTAGTGCCATGAGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCAGCTCTCAGCAT	1
M00764_TUBB3_MIP81	GGCTCTCACTTTTGTGACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCCCCTGACTAAGC	1
M00764_TUBB3_MIP82	GAGACAGTCTCGATATGTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGGGGTCACCTGGAG	1
M00764_TUBB3_MIP83	AATTTTAAATCACATGTCCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGATGCAGGGGCT	1
M00764_TUBB3_MIP84	CTTGCCTTTGGTCCAGGACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTTGGGAGTGCAGAC	1
M00764_TUBB3_MIP85	CACCCTTAAGCCTCACTGTGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCCAGAGCCTCT	1
M00764_TUBB3_MIP86	GTGTCCGCTCAGGGGCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAATTCAGAAAGAATGA	1
M00764_TUBB3_MIP87	GTACTTGTGAGCTGAGGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCAGAGCTTGGAGCA	1
M00764_TUBB3_MIP88	GGTGGGAACTCATCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTACAATTTCATCTTTGGTAAG	1
M00764_TUBB3_MIP89	GATCATGTGAGGAGCTGACCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCTTCTGTCTGCTTT	1
M00764_TUBB3_MIP90	AGGACGTTCCCATGCCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTTCAAGTGGAATGAA	1
M00764_TUBB3_MIP95	GCTGTGACCCCAAGTTCTCAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGCTGCCAGGGA	1
M00764t_ZNF804B_MIP1	GCGAGGCACATATTTTTGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGGACGAGGAAAGTTT	1
M00764t_ZNF804B_MIP10	CGCCGCCGCCTCTGTCAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGATTCCCTGGTGGAC	1
M00764t_ZNF804B_MIP12	CACATGGCTTGTTACCTGGTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCCCTGCGTCCTG	1
M00764t_ZNF804B_MIP13	CGCAGAGTCTCAACTCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTACCGGAGAGGGAGAT	1
M00764t_ZNF804B_MIP14	GTGGACATCTAAAACGTATACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCTGTGCAAGAAC	1
M00764t_ZNF804B_MIP15	GATCTCGTATTAATCAAGGTGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACATAATTCACAGT	1
M00764t_ZNF804B_MIP16	AAAAGTCCTTCATATTCCTGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCCTGGAAGATGT	1
M00764t_ZNF804B_MIP19	CATTTCGAGCAAATTCCCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGAGAGTTTTGAAGCATC	1
M00764t_ZNF804B_MIP2	CTGTTGCTTCTGCCAACGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTCGTTTCTATACCTTA	1
M00764t_ZNF804B_MIP20	ACTAATAGATATGTCTGAAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCTGAGTTAAGGCA	1
M00764t_ZNF804B_MIP21	GCCATAGAAAAGCAACTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCATCTTAGAAACACT	1
M00764t_ZNF804B_MIP23	CAAATCACAGAACAGGAGTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAAATCTCCCCAGA	1
M00764t_ZNF804B_MIP24	ACCTGATTTCCAAACAAACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGGTTTCTTCTGTGTT	1
M00764t_ZNF804B_MIP25	CCTTACCAAGGAAAAAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAATCTTCAGCATCAG	1
M00764t_ZNF804B_MIP26	GCAAACCTGCAGCACTTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCATCAATAGAGTCGTG	1
M00764t_ZNF804B_MIP27	ATCTAACATTCATCTTTCAGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCAAGCCATCTGG	1
M00764t_ZNF804B_MIP28	GAGAATGAAGCATGAATGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAAGGAAGCATTTGC	1
M00764t_ZNF804B_MIP29	CATCTGAATCCAAATTCCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTAATCACCCATGCCA	1
M00764t_ZNF804B_MIP3	AATGAGCTGTGCAGCCACAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGAGGAGATGGGCA	1
M00764t_ZNF804B_MIP30	GTACTCTTTTGTTCACTTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTGGTTTAGATGCCAC	1
M00764t_ZNF804B_MIP31	GTATCTCTTATGGCTGCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTGTAAAAGAAGCATGT	1
M00764t_ZNF804B_MIP32	GTAAAGAGCAGAAGTTCCGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTCCAAGGGCTTCTT	1
M00764t_ZNF804B_MIP33	AAACCAAAGACGATGATAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCACAATCTAGAGGACTT	1
M00764t_ZNF804B_MIP34	CAGTTAAACCTGAGACTTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCTTATTTGGCTCAGAA	1
M00764t_ZNF804B_MIP35	ATAATAGTAGTGAGAACAAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATTTGGACTACAGT	1
M00764t_ZNF804B_MIP36	GATGTGTTGAGGTAAAGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAGGAAGGAAAAGATAG	1
M00764t_ZNF804B_MIP37	CCTTGTACAGTAGGGGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTCTAAATGATATAGA	1
M00764t_ZNF804B_MIP38	GGACTTGCAGTTGAATTGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGAGTATCTCTTGT	1
M00764t_ZNF804B_MIP39	ATTCAATGGTAATAGCAGAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTTCCGGATGTGGAA	1
M00764t_ZNF804B_MIP4	AGAGATAGGGCAGAAGAACCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCGCTGAAGAAAAGCT	1
M00764t_ZNF804B_MIP40	ACTTCTCAAGCTAGACATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCAGACAAGTAGAAGC	1
M00764t_ZNF804B_MIP41	CGTAGATATTGTCACTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAATGTCTAAAGCACAA	1
M00764t_ZNF804B_MIP42	ATTCCCACAATTTGCAGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAGTTAGAATCACAA	1
M00764t_ZNF804B_MIP43	GACAGATTGGACTCTTACTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACTGGGCAAAAATCA	1
M00764t_ZNF804B_MIP44	GCTGAGTTCCCTGGCAATTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGAGTTACACTTCATG	1
M00764t_ZNF804B_MIP45	CCCTCTAACAGCAAAAATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCACATTTGTGATCTGG	1
M00764t_ZNF804B_MIP46	CAGTTCTTTAGAAGGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGATCTCAACATTACTTGA	1
M00764t_ZNF804B_MIP47	GCCTTTGTCTGAAAAAATACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGAAATGTCAAGAAC	1
M00764t_ZNF804B_MIP48	ATGCTTGTCTGTTACAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTCTGCTAAAATTGTA	1

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M00764t_ZNF804B_MIP50	GTTTAGTGACTGAGACTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACACCAGTATATTTATTAG	1
M00764t_ZNF804B_MIP51	ACTCTTACTATGACAGAACTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCCCTGGTGCTTTT	1
M00764t_ZNF804B_MIP52	GATTTATTTGGTCTTCTTGGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGATAGATTTATGA	1
M00764t_ZNF804B_MIP53	ACTCCTATCAAAGCATCTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGACGGATTAGAAATGT	1
M00764t_ZNF804B_MIP54	GCATATGCTGCTGGGCTTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGTGTGGTGGATGGTG	1
M00764t_ZNF804B_MIP55	GTCCTATTTCATTTTCGACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGCACACTTCTATC	1
M00764t_ZNF804B_MIP56	GAAATGTGCCTGTGAAAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGGCTGAAGTGTTA	1
M00764t_ZNF804B_MIP57	GTATTCCAAGGTCAAGATTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCCTTCCACCCATC	1
M00764t_ZNF804B_MIP58	GGTTGGATTAAAGGATTCAAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACAGGAGGGGCTT	1
M00764t_ZNF804B_MIP59	GATTTAAAATATTGCTGCCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGTGAAAGAGGCCT	1
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M00764_UBL4B_MIP10	ACTTTGAACCACAGGATGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTACTGCATTGGGCCC	1
M00764_UBL4B_MIP11	GCGGCTGGTGGGCCTCCTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTCCAGGCTTATCTTC	1
M00764_UBL4B_MIP13	CGCCTCAAGCTCCCTCTCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACCAGGGAACACGTA	1
M00764_UBL4B_MIP14	CCTGTCCCCTCTTGGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGCATGCTAAAATTCT	1
M00764_UBL4B_MIP15	CAAAAAGGGGTGTGGACGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCGGTGATCAGAAC	1
M00764_UBL4B_MIP16	GTCTCCATGGTTCTAGGCAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATGCTTCCCCTAGA	1
M00764_UBL4B_MIP17	CTGCTGGGTATGTGTGGGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAGGGGAGATGTCAC	1
M00764_UBL4B_MIP18	CTTAAGGGACAGGCACAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTTCCTCCATCCTCAGA	1
M00764_UBL4B_MIP19	GGAAGCACAAGCAGGAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTTTTTTCTGCCTGAGG	1
M00764_UBL4B_MIP2	GCTTGATAAATGCTAGCCAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTCCCCTCCTGGTG	1
M00764_UBL4B_MIP20	ACATTACCTGCCCAGCGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAAGAATAGCAGGAAA	1
M00764_UBL4B_MIP21	AGCTGTGATACCTACTGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCACTTTACTTTTCACAT	1
M00764_UBL4B_MIP22	CATAGAGGGGCCAGTCCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCCCTCACAGAGCAC	1
M00764_UBL4B_MIP23	CCCGTGCATTCAGTCACACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGTGTGGGGACTCCT	1
M00764_UBL4B_MIP24	AGTCCTGAGTGATGGGGATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGTGAGAGAGTGGCC	1
M00764_UBL4B_MIP25	AAACTTTTGCAATAACAGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTCGGACTGGAAGA	1
M00764_UBL4B_MIP26	CATCTACTTACCCCATGAGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCTTGGCCTGCA	1
M00764_UBL4B_MIP27	GTTATAAGGATGCCCATGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCACAAACAGAATGCT	1
M00764_UBL4B_MIP3	GTCAAGCACTTTACACGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGTATTAGGTGCCACCT	1
M00764_UBL4B_MIP5	GACTGGGGGAAATGAGAGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTGATGTCACAATGCT	1
M00764_UBL4B_MIP6	GGAGAAGCCAACATCTCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTGTCCCAAAAGTTCC	1
M00764_UBL4B_MIP7	CAACAAAGGGCTAGTAGTCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCATCTCTGGCCCAG	1
M00764_UBL4B_MIP8	CCGTGGCCAGCTCCTGGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCACAGTCAAGCTGC	1
M00764_UBL4B_MIP9	GCCTGGACACCAGTCTCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCAAGGGCTGCATG	1
M00764_UNCX_MIP1	CCGAAACTGTCACATTGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTTGTGGGGATTTTT	1
M00764_UNCX_MIP28	GACATTTTTGCATTTTACAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGAGGCGTGGAA	1
M00764_VAV3_MIP10	GCTTCTTTTTTTTCCCAACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGTCCACTGAACCTT	1
M00764_VAV3_MIP100	GATTCTTAAAACGAGGCATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGCCAAAATTAAAAA	1
M00764_VAV3_MIP102	GGAGGTAAACTAAATATGAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCTTATCCCCAGA	1
M00764_VAV3_MIP103	CCATCCAACTCCCTCTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGGAAATTTAAGAACT	1
M00764_VAV3_MIP106	GTAACATATCTGCTTTTGAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAGACAATTGTGGC	1
M00764_VAV3_MIP107	CCCCTGAAAGGTGAAATAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACAGAATTGCAACAA	1
M00764_VAV3_MIP108	GTTTTAAGTGTGGAGCGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGAAGAGCACTGTTG	1
M00764_VAV3_MIP109	ATTGGAGTCTGCATAGTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGAAACACTTAGCAATT	1
M00764_VAV3_MIP11	ACTTAGTAGAACTGAACCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCCATTCAAGGCAGT	1
M00764_VAV3_MIP110	CTGCAATTTAGTCATCTAAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAGGATGTGACTCG	1
M00764_VAV3_MIP111	GCTGTGAGCAGGAGTGCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGTGAGTATTTCTATTT	1
M00764_VAV3_MIP113	CCAAGGACAAAATGGGTTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATAATATTGTGAGGAGTT	1
M00764_VAV3_MIP115	GTATAAAGCAACCAAATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTTCATAGTTATCACC	1
M00764_VAV3_MIP116	CAAAAAAATTAATAACCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGCCATTTACAAGGTA	1
M00764_VAV3_MIP117	GCCAAGTGAGATAAGCCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTATAAGAACTGTGTG	1
M00764_VAV3_MIP118	CAACAACTCTGCAGTGTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGATTCCTAGTAACTTC	1
M00764_VAV3_MIP119	ACCACATGCTGGGAAGGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGCTAAAAACCTATAGA	1
M00764_VAV3_MIP12	CCAGTTAATACACTCCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCAAGTTAGTGTCTTA	1
M00764_VAV3_MIP120	GAGGTCGTCCAAAAAGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAATTGTCTTTAAGGTT	1
M00764_VAV3_MIP121	ATGGTGAAATTCGAATAACCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGTAGTTGTCTTGAGT	1
M00764_VAV3_MIP122	GTAATCCCAGGGGGTATGTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAATATTAGTAGAGA	1
M00764_VAV3_MIP123	ATGTAGACCTGAGCTTTTTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAATTTGGACCCTTCC	1
M00764_VAV3_MIP124	GCCCTCATGAAGCACACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATTAGCTATGAAAAGAA	1
M00764_VAV3_MIP125	GTATCATTTTGCCGTACACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGACCAAATTAGCGCG	1
M00764_VAV3_MIP126	CTATTTTCCCAGAGGCTGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTGCCATGAAGGAGTA	1
M00764_VAV3_MIP127	ATAGCTGAAACTGTTTAATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAACCTCCAACAGT	1
M00764_VAV3_MIP128	CCATCCAGCTTCCCCTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTTCTACCCTTTTCTTT	1
M00764_VAV3_MIP129	AAGACAGTAAAATGAATGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCAAGTCCTAGACAA	1
M00764_VAV3_MIP13	GGGAAGATGGGTCTTGCAGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAGGAAAGCACAACT	1
M00764_VAV3_MIP130	CCTATTTGGAAGATATGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATTCCATTGTCTTTAGG	1
M00764_VAV3_MIP131	AAGGTAGGGCAGATTCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTCTTTAGTATGTCTT	1
M00764_VAV3_MIP132	ACCACAAGCAAGTCTCGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACATGGAATATCTGCAAT	1
M00764_VAV3_MIP133	CCTATGCAACGTGTTTTAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGCCTAGGGCCTTT	1
M00764_VAV3_MIP135	ACTGCCCGTAAATAACCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTTTTAGGTTTATTTTG	1
M00764_VAV3_MIP136	GAGTCAGCCATCTCTAGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAATGGTTTTAAAGAGA	1

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ID	**MIP**	***c***
M00764_VAV3_MIP137	AACGTGGGACAATTACTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGAAAGGTAACTTTTG	1
M00764_VAV3_MIP138	GGTTCCGATGAAGTTTTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCACTATAATTACAAGC	1
M00764_VAV3_MIP139	GCAAGAGATTCATGATTCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTGAGTGGCAAGTC	1
M00764_VAV3_MIP14	ATGGGAGGAAAAGGCATGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAAATGAATAAAGGAC	1
M00764_VAV3_MIP140	ATCCCTATTTTAATACTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACCACTAAAAAGATTTC	1
M00764_VAV3_MIP141	ATACGTTTTGAAAGTCAATTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAATTCTGCTGCTG	1
M00764_VAV3_MIP142	GCTTAATTTCTGCTAGACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTACACACCTTCAGAAGAAA	1
M00764_VAV3_MIP143	AATATACAGAAACTTTGGAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTACTTCCCGATAG	1
M00764_VAV3_MIP144	GCTTGCTTATAACTATATAATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCAGAGGAAGCAC	1
M00764_VAV3_MIP145	GGATATCATATAAGGTCATTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCTACGGGCTGA	1
M00764_VAV3_MIP147	ACTGTGGATGTTAAAGTAAGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTTCCCAACAGAAG	1
M00764_VAV3_MIP148	CGCACTTAACCCTCACTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTAAATCAGGAAGGCCT	1
M00764_VAV3_MIP149	GACTGTGGTGACCAGCTGTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAGGCAAGGGTACA	1
M00764_VAV3_MIP15	ACACACAAAGATGACCTGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTAGTTGCCAATAACC	1
M00764_VAV3_MIP150	GTTGTCTGACTTGGGGTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTTCTACTAGTTTTCAT	1
M00764_VAV3_MIP151	GTTTATTAGACAAATGAGTCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCCGTTCACTAG	1
M00764_VAV3_MIP152	CCAATGCTATAGGTGTTCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCATGAATGAGACAT	1
M00764_VAV3_MIP153	AGGTAAGCTCTGTTTTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAAAAATTTTGGAAAAA	1
M00764_VAV3_MIP154	CAGAATGAGAAGGGCTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCTGAGAAAAGAGGAAA	1
M00764_VAV3_MIP155	CAAGAAGGGGTCCACGGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGTTCAGTAACAACAAC	1
M00764_VAV3_MIP156	CATGCAGCTGCCTGATTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTTCAGAAACCAGGATG	1
M00764_VAV3_MIP157	CAGACAGAAGCATAGTCTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAAGGCACAGATGTT	1
M00764_VAV3_MIP158	ATTTCTCCACCCAGCACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACCATCTGGTCTGGTTTAGA	1
M00764_VAV3_MIP159	CGAAACTCTAATTTCACACAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGACACCAGGTTAT	1
M00764_VAV3_MIP16	AGGTTGTGAAGGTTTAATATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTTGATCTGTTTCT	1
M00764_VAV3_MIP160	GAGTTCTGTTGATTTCCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAAGCAACAAGCAGG	1
M00764_VAV3_MIP162	GATCTTATCTGGCTGTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGATTGTTACCAAGGAC	1
M00764_VAV3_MIP163	GTATAATAAGGGGCAAGTTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTATGTACTCATA	1
M00764_VAV3_MIP164	AAAAGTGGTAAGCTCCTATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGACAGTGGATTT	1
M00764_VAV3_MIP165	GCAAGCTCCTCACTTTAGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTAATGACCTAGATGAC	1
M00764_VAV3_MIP166	CCAGAGACAGCTTCATGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTTCTAAGGATATGAT	1
M00764_VAV3_MIP167	GCAAATAAGTGTTGATTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTGTTATTCAAGTTTCT	1
M00764_VAV3_MIP169	ACTCAGATAGAAGAAGCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTAAGAATGTCCTTCC	1
M00764_VAV3_MIP171	GTCACATTGGCTTAAGGGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCTAGGAATATTTGTC	1
M00764_VAV3_MIP172	GTATAATTACCTTTCCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAGCCATCTACATGTGA	1
M00764_VAV3_MIP173	ACTGGAAAGCATTTAAGCAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACATTTCTCACGGC	1
M00764_VAV3_MIP174	ACTGCTCTAAAAATGACAAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACGTCTCACAACA	1
M00764_VAV3_MIP175	CACTTCCATGCCTGTTCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAAACCCCTCAAAGG	1
M00764_VAV3_MIP176	GGAGAGCCATACGTATTTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTCATCTGTGATTC	1
M00764_VAV3_MIP177	GCGTCATAGAGGATTAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATGAAACACTGACACCA	1
M00764_VAV3_MIP179	ACTACTCTTCCACTGAACTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGTCCTCTCCCTTT	1
M00764_VAV3_MIP18	ACAATTTAAGACAAGTAAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGTAATTAAAACCCT	1
M00764_VAV3_MIP180	ACTCGGTTCAGAGCCTCTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTTTGAGGGTTAAG	1
M00764_VAV3_MIP181	ATTTCCTGTCGCTGCTGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCCAACCTTCCAGAG	1
M00764_VAV3_MIP182	AGAAGTTTCACTAGAGATTCCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGAACCCGGAGG	1
M00764_VAV3_MIP183	AAAGAAATAAGTTGTCTTAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCACTTCGGCACC	1
M00764_VAV3_MIP184	ATTAATGGGAGCTGCCGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAAACCATTTCAAGCCA	1
M00764_VAV3_MIP19	GGCAAACACTTTTACCCTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGAAGCAGAAGTGT	1
M00764_VAV3_MIP195	GCGACGATCTCTAAAACTTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCGTCTCCACACAC	1
M00764_VAV3_MIP196	CCGTTGCTGTTCTGGCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAAGTGAGTGAGAGTG	1
M00764_VAV3_MIP20	AAGTAAAGGGAAGCACGAACCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGGAAAAGGAAAAT	1
M00764_VAV3_MIP21	GCCAGTCATCAGTAAATCTTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAACAGCCTGCCA	1
M00764_VAV3_MIP22	GGGCTAAGGAGGGAGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAACAGCTCTTGGTTTTG	1
M00764_VAV3_MIP23	CCTAAGTCTTAATGCTGAGATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGTTGCACCCTGC	1
M00764_VAV3_MIP24	CAGCAACATGACTTTGTATCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCAGGCTTCTATTTA	1
M00764_VAV3_MIP25	GGTTGCTTTTCTTTTTTAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCAGTTAAACCAATC	1
M00764_VAV3_MIP26	GTATAATACAGGGGGGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATGTCCATTGTAGGT	1
M00764_VAV3_MIP27	GCTAGTGGATTAGAACACTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCTGATGTAAATTGG	1
M00764_VAV3_MIP28	GCAGCAAGCTGTCCCACTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGAGGTACTATGTCCCA	1
M00764_VAV3_MIP29	AAGAGTCGAGGAGCATTTCAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTGCCCTCTGGAA	1
M00764_VAV3_MIP3	ACTAAATTGATTTCTAAGAGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAGACAGAAGTAA	1
M00764_VAV3_MIP30	CCCTTCTTTCACATGCACCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCGAGTCCCTGGTAT	1
M00764_VAV3_MIP31	ACTGAGCAGTTGTTTGCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTTGTCCTTGTTGAAAG	1
M00764_VAV3_MIP32	ACTGTCAAGAAATGACAAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCAGCCATTTGCACT	1
M00764_VAV3_MIP34	GCTTGCAAATAAAATATTTGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCCTCTTTGTTC	1
M00764_VAV3_MIP35	CACTTCTTTCCTATCACCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAGTCTGGAGGAGT	1
M00764_VAV3_MIP36	GTTGCCTGCTCTATTACCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTCCTTGCTCATGCAT	1
M00764_VAV3_MIP37	GCTGTCACTTAAAAATTAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCAAGGAAGGGTTCA	1
M00764_VAV3_MIP38	AACTCCTGAGCACATAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGCAGAGTTGTATCT	1
M00764_VAV3_MIP4	GGCTCCAATATCCTCTGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACAAAGTATATGGAAAA	1
M00764_VAV3_MIP41	ATTGCCCACAGGTACAATAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCAGTGTATTGGCA	1
M00764_VAV3_MIP42	ACTTGTCCTACTTACTTAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATTAATGAACTGTCT	1
M00764_VAV3_MIP43	GATTTCCTGTTTTCATAATTGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATTGCAAGCAGAGA	1

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ID	**MIP**	***c***
M00764_VAV3_MIP44	AGAGGCTAAAAGTAAGTATCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTCACAAGGTAAGT	1
M00764_VAV3_MIP45	CAACATATGAGAGCAACAAAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCGATGCCATCAT	1
M00764_VAV3_MIP48	GGATGGAGTGCAGCGATGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATTTAATAAAGCAGAG	1
M00764_VAV3_MIP49	GGTATGGTATTTCAACCTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATATGGAAAGGTCAGC	1
M00764_VAV3_MIP5	GTGACATTACCAATTACATCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATGGTATTGTAGCA	1
M00764_VAV3_MIP50	GGTTTGGGCACCTAGGATATACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGACAAATGGAAATGGA	1
M00764_VAV3_MIP51	GTAGATTATTCTTGCCAACCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGACTGTGCCACTT	1
M00764_VAV3_MIP52	ATCTACAAAGGGTACTGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATTTAGCATCTGGAG	1
M00764_VAV3_MIP53	ATCTACAAAGGATACTGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATTTAGCATCTGGAG	1
M00764_VAV3_MIP54	CATACATAGCACTGTTACTTAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAGGCTTGACTGC	1
M00764_VAV3_MIP55	GTAAAGAGGGTCCTTCATGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGGCAAGATTTAAG	1
M00764_VAV3_MIP56	GTAAAGGGGGTCCTTCATGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGGCAAGATTTAAG	1
M00764_VAV3_MIP57	CAGGCCGGGGATACCGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATGCATCATTGTTTTC	1
M00764_VAV3_MIP58	GAAATTCATACTGAAACACCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGCATGCCTCTGTA	1
M00764_VAV3_MIP59	AGTCAGCGCTGACTATACAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCTGGCAGTATCTTA	1
M00764_VAV3_MIP6	AACATTCCCGAGACAGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACACCATTTATAAGGAGA	1
M00764_VAV3_MIP60	GAAATCCTGAACCCCACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTCAATTTTAAAGAACA	1
M00764_VAV3_MIP61	GCTCAAAGTCTTCTTTCCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAAAAAGAACACAGGG	1
M00764_VAV3_MIP62	GAGTGGAATAGCAGGAGGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAACAATACTGGGTAG	1
M00764_VAV3_MIP64	GCAGCCTTGAGGTTTCTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTATTTCTTTCTTGTCT	1
M00764_VAV3_MIP65	CCTCCTTTTCTTGCACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACAGGGCACATCTAATA	1
M00764_VAV3_MIP66	GGCAGTGTTTCACCATGTTGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAGATCTTGGCTCC	1
M00764_VAV3_MIP68	AGGGAGATACAGAGGGTATACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTTGTTCTTTCAACT	1
M00764_VAV3_MIP69	ATACCAAACTGGAAACATAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAGGGAAAACACAT	1
M00764_VAV3_MIP7	GTTGCCGTCAGCCGAACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTAAATGATCACAAAAA	1
M00764_VAV3_MIP70	ACTTAATTTTGTTTCATTGAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCCTCTCACTCAGCT	1
M00764_VAV3_MIP71	GAAGCTCAAGTGTCATTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGTATACAGGGTGA	1
M00764_VAV3_MIP73	CTTTTAAAAAAATTCAACTGCATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTATTTCTGTCAC	1
M00764_VAV3_MIP74	GGAGTTAACTATTTGAATCAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACACGCCATGTGT	1
M00764_VAV3_MIP75	CATCAGTAATATGACTACTGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCTGGCAGGTCTGT	1
M00764_VAV3_MIP76	GGAGAAATAAATCCTCCTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCACCTCACCTTTGTT	1
M00764_VAV3_MIP77	CAAGGCTCATTCCGAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGATCTTCTTGTAGTCAT	1
M00764_VAV3_MIP78	CATTTGTTCACAGCTTGGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAGGTAGTCCTGAA	1
M00764_VAV3_MIP79	GAGGAGCATGCTCTGGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGCATAATTGTAAATGT	1
M00764_VAV3_MIP8	ATCTATCCTAGATGAAAAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGAACATTTTATAA	1
M00764_VAV3_MIP80	GAAGCAGGTTTGACTGATTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCAGTTTTTTCAAGT	1
M00764_VAV3_MIP81	CCTCTAAAGCTAATTTCTCATCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGGGAGACAAATGCA	1
M00764_VAV3_MIP84	GGATATGGGAATTGCTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTGCTTTGTTTTACT	1
M00764_VAV3_MIP85	CAAGTCAAAGTATGACTAAATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTCCATTGGTCCG	1
M00764_VAV3_MIP86	CCAGTTCATAGTTTATTCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAACATCTCCAGGTTT	1
M00764_VAV3_MIP87	AAGTCTAGGACGGAGCTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGTATTTTATATTGA	1
M00764_VAV3_MIP88	GGGGAGGGGAGTATACGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTGGTGTGAAGCTGTA	1
M00764_VAV3_MIP9	CAGAATTATGTAAACTGTGATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTGTAGCCTGCCC	1
M00764_VAV3_MIP91	ATGGGATGTGAGATGTACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTGCCTCATTACCATT	1
M00764_VAV3_MIP92	GGAGTGGACCTTCGGAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAATAGTTATGATTGTG	1
M00764_VAV3_MIP93	CAGAGCTTACAAATTACAAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGCAAATAAAGTGCA	1
M00764_VAV3_MIP94	CCTCTCTTGAAGACCTTCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCTCTCACCCTATAC	1
M00764_VAV3_MIP95	CAGTGTAAAGTTATTTTGTTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAAGCCTGGTTAA	1
M00764_VAV3_MIP96	CAATGCCAATTTTTACATTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTAGCCCAGCCTG	1
M00764_VAV3_MIP97	CACAGTTTTAAATGACTTCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTAAAACACCACTGC	1
M00764_VAV3_MIP98	AGCCAATAGGGTAAGAGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTATAAATTTAGTGTA	1
M00764_VAV3_MIP99	ACTGCATTGACGATTTGTAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCTACCACATAAAGC	1
M00764_ZNF175_MIP1	GTGGTCGCTTGGTAGGTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTCTGCCCAGTTGGG	1
M00764_ZNF175_MIP10	GTCAGCTAAATATCATGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCAAAATGAAAATGCAG	1
M00764_ZNF175_MIP11	CATTTAGTCCAGACTCAGTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGCTTCATCTTGGTT	1
M00764_ZNF175_MIP12	ATTGCAGCTTTGCCACATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATATTTCCTGAGGGCAC	1
M00764_ZNF175_MIP13	ACATCATTGAGGCTGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTCTACTCCAATGTCTGA	1
M00764_ZNF175_MIP14	GACCTGGGGGTTCTGCAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTTGCTGACAACTCCA	1
M00764_ZNF175_MIP15	GTCCAGAGAAGCAGGATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAATCCAAACACCTATC	1
M00764_ZNF175_MIP16	GGACCTGAGGCTTCTGGGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCAAGACTGACTCAG	1
M00764_ZNF175_MIP17	ATAAAAGAGGATAGTAGAGGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGCAGCAGGTCTG	1
M00764_ZNF175_MIP18	GAACACAGATAGCCTATGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAAAGAGTCAGCTTTT	1
M00764_ZNF175_MIP19	CAAATTCCTTGCTTGGTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGTAGTCCCTGGTCT	1
M00764_ZNF175_MIP2	AGAGAGAATTTAGGGCTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCACTGTCTTTAATAGC	1
M00764_ZNF175_MIP21	ATAGTCAGGATTTGGTAACAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGGGAGGTAGAGT	1
M00764_ZNF175_MIP22	AAACACTGTTTTCCAGCATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGACTTGTAAATA	1
M00764_ZNF175_MIP24	ACCCATCACAGAACAATGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGCAGGTTGAGATGATT	1
M00764_ZNF175_MIP26	GGAGTAGAAGGTAATGCTACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACTCAGAGACTTGGA	1
M00764_ZNF175_MIP27	CACATGTAGTTGCTTCGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCATGTTCCCTTTTTAA	1
M00764_ZNF175_MIP28	GGCTGTAGTTGAGCTGGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCACTGTACACCTACA	1
M00764_ZNF175_MIP29	GTGGGAAGCCTCTGTGATGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTAGAGGGAACCCATTT	1
M00764_ZNF175_MIP30	ACACCTATTTCACATTTTTAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGCCTGTAACAGTG	1
M00764_ZNF175_MIP31	AGCTCTATAGCCATCTCTTCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACAGTGAGCTGGGGT	1

continued table…

ID	**MIP**	***c***
M00764_ZNF175_MIP32	CAGCATCACATCCCGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGTCATGACATACTTT	1
M00764_ZNF175_MIP33	CAGAGGTGTCAAGGTGAGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGAAGAAGCTACAC	1
M00764_ZNF175_MIP34	GTGAGACTTCAGCCTCCTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGAGGCAATCTACGG	1
M00764_ZNF175_MIP35	ACAAGAGATGGTTCATGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCTTTCTTGTTCATT	1
M00764_ZNF175_MIP36	CCTTTTGAAATGAAGCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAGAAAGCACTGTGA	1
M00764_ZNF175_MIP37	ACAACCTCAGAAATGTTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAATCAAATTCAACCCA	1
M00764_ZNF175_MIP38	GTGAAGAAGCAAGGTGGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGCTGAATAGCTGACCA	1
M00764_ZNF175_MIP39	ACTCAAGCAACATCAAATTCATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGATGACGTTGTTGGGT	1
M00764_ZNF175_MIP4	GACATGTATTCTGAAAAATACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCATCGTCAAAGGGC	1
M00764_ZNF175_MIP40	ACTGTTTATGGCCACAGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTCATGGAGGTTTCCT	1
M00764_ZNF175_MIP41	AATGTGGGAAGGTCTTTATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAACAGAGAATTCAT	1
M00764_ZNF175_MIP42	CACCTGTATGATCTGTCAGATACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGGAAAAAGGCTTTT	1
M00764_ZNF175_MIP43	GCTTCTCCCAAAACTCAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACACACTAGAAAGAAG	1
M00764_ZNF175_MIP44	GCCACATTCACTGCATTCATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTCTCTGGTGCAAGC	1
M00764_ZNF175_MIP45	AAAAACCTTATCAGTGCCACAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAGAAGTCAACACTC	1
M00764_ZNF175_MIP46	CCTGTGTGGCTTCTTTGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGGTGAAGGTTTTTCC	1
M00764_ZNF175_MIP47	CAGAAGTCAATACTCAGCATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGAGAAACCTTATGA	1
M00764_ZNF175_MIP48	GCTTTCCCGCATTCACTGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTGAATTCGCTGATG	1
M00764_ZNF175_MIP49	GAGGCCTTTTGTCTGTTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTCTAAGTCTCAATTCA	1
M00764_ZNF175_MIP5	ATAAAGGTACGCCGTTATACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACATTCCATTTGTCCTT	1
M00764_ZNF175_MIP50	GGAAATTTGACCTGCCGTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCATTCATAGGGTTTC	1
M00764_ZNF175_MIP51	AAAGGCCTTCAACAACAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAAGAACTCACATGGGAG	1
M00764_ZNF175_MIP52	CCCGTGTGAATTCGCTGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTGGTAAAGCCTTTCAC	1
M00764_ZNF175_MIP54	CAAGAAACTCGGAGTATATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCTCACTAAAATAAA	1
M00764_ZNF175_MIP55	CGCATTGAGAAAAGCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACATGATAAAAAAGTCAT	1
M00764_ZNF175_MIP56	CCGGGGAGAAAATTTATAATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCACAATAAACAGGG	1
M00764_ZNF175_MIP57	GTGCGCCTTATGTATATAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTTGTTACTCGATTAT	1
M00764_ZNF175_MIP58	CATGACTGTGTTGGCACTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCCAAAATGCTTCTGA	1
M00764_ZNF175_MIP6	CCGCGGTTCATTCAACTTCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTCCGGTTTGGGTTA	1
M00764_ZNF175_MIP61	CCCTCAGTGCAGTGGGGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATTAGGAATACCCAACC	1
M00764_ZNF175_MIP62	GCATACATACACATATGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATAATTTTTATAAAAA	1
M00764_ZNF175_MIP63	CACATGAATGTGCATTTTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGAGATGTAAGCAGA	1
M00764_ZNF175_MIP65	CATTGGCCAAATATGGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCTTCTTTTAGGATTA	1
M00764_ZNF175_MIP66	CACAGTTTGTTGACTCCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAAAACTACTCAATTCT	1
M00764_ZNF175_MIP7	ATATTAGCAGTGGGGGTTCTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAGCGCCTACGGA	1
M00764_ZNF175_MIP9	GGTAAGTGGCGTTTGCTAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGCTTGTTGGGGGT	1
M00764_SUN1_MIP60	ACAGAGCCAGACTCCGGCTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCCGGGCGTGTTGGCG	3
M00764_TUBB3_MIP55	CCACTGTACTCCAGCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAGCCTGTCTCTACTAAAAA	3
M00764_TUBB3_MIP58	ATGGCATGATCTCAGCTCACTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGCTTGCTACCAC	3
M00764_TUBB3_MIP59	ATGGCATGATCTCACCTCACTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATGCTTGCTACCAC	3
M00764_MDGA1_MIP223	GAGAGAGAGAGAGAGAGAGAGAAAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAAGGGAAAGAG	7.69
M00764_MICALL2_MIP27	GTTCAAGACCAGCCTAGCCAACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAAATACAAACAAC	7.69
M00764_MICALL2_MIP30	GCCTGGGCAACAGGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCTACCAAAAATACAAAAAAT	7.69
M00764_PDE11A_MIP47	TCGAGACCGTCCTGGCTAACACGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGAGAAAAAGACTC	7.69
M00764_RASGRP4_MIP5	TGAGGTCAGGAGTTTGAGACCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACGAGATAAAGAGGG	7.69
M00764_STEAP4_MIP102	CCCAGGAGGCTGAGGCAGGAGAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGAGGCAGGTGAA	7.69
M00764_SUN1_MIP20	GAGGTCGAGACCAGCCTGGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCCGACCTGGGCAG	7.69
M00764_AAGAB_IQCH_MIP5	CCAACGTGAGTAGATAGGCGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTGGTGCAGCCCA	10
M00764_AAGAB_IQCH_MIP7	ACGCTGGGAGCGGAAGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTCAGTGTTCTGTGCCA	10
M00764_AAGAB_IQCH_MIP8	CACTTCCGAGCGAGGTCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCGCCTCCGCGGAGGTAG	10
M00764_AAGAB_IQCH_MIP9	CGCGGCTGGGCAGGGCAGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGGGCCGTGGGGGAA	10
M00764_AAGAB_MIP106	ATATTTCATATGAATGAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCATCACCATTTAATTC	10
M00764_AAGAB_MIP107	TTATTTCATATGAATGAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCATCACCATTTAATTC	10
M00764_AAGAB_MIP14	CATCTCAAGCAGCAGGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTCATCGCCTAACATTTC	10
M00764_AAGAB_MIP41	AGTTCATTTTTAGATACAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAAAATTCTGATTAA	10
M00764_AAGAB_MIP72	CAGTATATGTGTGGTGTATAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGATACATTAGATTCCA	10
M00764_ADAM22_MIP169	GTATCTATATGTATACTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTTGAGGTATACAGT	10
M00764_ADAM22_MIP181	ATTTATTCATTTTATCCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCTCTTGTGGCTACTTT	10
M00764_ADAM22_MIP21	ATTAGTCTTTCTTATGATTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAGCACGACATCGAG	10
M00764_ADAM22_MIP210	GAAAGTCACTTTACTAATGTTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTCTGGGACACCA	10
M00764_ADAM22_MIP52	AATCAAATAGTTTATGAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTTTCAGATATGGCAAAC	10
M00764_ADAM22_MIP6	GGGCGAGTGCACCGGGCGCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGGATATAGAGGACC	10
M00764_ADAM22_MIP83	AAAACCACAGTTACTGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAAAATGAACAAAAATC	10
M00764_ALLC_MIP23	CCTGCTTTTCTGGGTTGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGTAGAGCCATAAAC	10
M00764_ARFRP1_MIP10	ACTGAGGAAGAACACAGCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCACCGTGTCCAACA	10
M00764_ARFRP1_MIP12	CTTTTTGCATCAGTCAGCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGCCCCACAGAGA	10
M00764_ARFRP1_MIP24	CATGGCTGGTAGTGCCTGAGACAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCCCGGGACTCT	10
M00764_ARFRP1_MIP25	GGGCTGAGCACAGGGTCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGCCTCAGTCCTCA	10
M00764_ARFRP1_MIP27	CCATCACTGATGCAGGGCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCCGACAAGAGGGA	10
M00764_ARFRP1_MIP29	GTAAGGCTGGCCTCCCCTACAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACTGGCCACGCTG	10
M00764_ARFRP1_MIP3	AGGGTCTGTCTGAGGTAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGCCCCATCCTGTTC	10
M00764_ARFRP1_MIP32	GAGGTGGGAGAACCTCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATCACTTCTTTGAGCT	10
M00764_ARFRP1_MIP39	CAAGACCCTTCTGGGATGCATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATACTGGGAGGAAGCAC	10

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M00764_ARFRP1_MIP40	GCCCTCTTGCCCCTTCCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTTCACCTTTGGCCAC	10
M00764_ARFRP1_MIP43	GTCTCAAAAAAAAGATAGGGTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGCGCCTGCAGTC	10
M00764_ARFRP1_MIP44	GGTCTCTCATTCTCACCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCCGCATGGCCACAC	10
M00764_ARFRP1_MIP52	GGGGGCCTCGCTACCTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTCTCCACCTTAGGGTC	10
M00764_ARFRP1_MIP54	GGAGCCACGTGGAGATTCTCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTGCGGCCCTGC	10
M00764_ARFRP1_MIP62	GTGGGGCCAGTGGCTCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGTAGCCCATCCTTG	10
M00764_ARFRP1_MIP66	GGGTCCCCAGTGTGGGCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGGAGAGGTCGACTCA	10
M00764_ARFRP1_MIP76	AAACCCTGGCTTGGGTTTGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTGTTCACTGGTCATG	10
M00764_ARFRP1_MIP77	GGCATTTAGTGATTCTTTCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCCTGAACCCAGAT	10
M00764_ARFRP1_MIP82	AGGTCATGAGCCTTGCCTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTGATATTCACAGTCC	10
M00764_ARFRP1_MIP86	AATTTCACCTGAGACGGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTGGGCCTGGACAAT	10
M00764_ARFRP1_MIP89	CCTCTCCGCATACACATCGGTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCAGCCGACCGCTC	10
M00764_ASTN2_MIP102	CCCCCATCTCCTGCATTCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATATGCCCCAAATCCC	10
M00764_ASTN2_MIP171	ATAACTTCCTGTAGCCTCAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTTGCTCAAGGCC	10
M00764_ASTN2_MIP172	CAGAGACTAGAAAAGGGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATTAGCAATTAGTGCTA	10
M00764_ASTN2_MIP37	GCCTCCAGTTGACTTTTCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCTGTTCCGAGTCCAG	10
M00764_ASTN2_MIP41	GTCAATAACATATTCAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAATTATGAGCACTAACTT	10
M00764_ASTN2_MIP64	AGAAAATTCAACATCTGTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAACAACCTACACATT	10
M00764_ASTN2_MIP75	GCCAATATTTTATTGAAGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTTTGTTTCAGTTTA	10
M00764_ATP2C1_MIP174	ATTTTACAAATGACATTATACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTCATTTTCTGTCTCT	10
M00764_ATP2C1_MIP187	GTATCTTGTATTTTAACAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACATATGTCATATTGCT	10
M00764_ATP2C1_MIP188	AAATCTTCAATATTAAGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGTAGCAGCATTTTGT	10
M00764_ATP2C1_MIP201	AAGGATTTTCAAGATGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAATCTGTTGATTCTATGATA	10
M00764_ATP2C1_MIP243	ACAACCATCTCCAAAGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTTGCCCCTAGAGTATT	10
M00764_ATP2C1_MIP249	GAATGGAAAATATCAGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGAAAATATCAAGAGAT	10
M00764_ATP2C1_MIP269	CAGTGCCTTCAATACTTTGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATCCAGGAGGTACT	10
M00764_ATP2C1_MIP34	CCCCACGGGAATGCGTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAACGTTGCCTGCTGAG	10
M00764_ATP2C1_MIP45	GCTCCCACCACCCCTAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGATGGCTACAAAGTCTT	10
M00764_BBS7_MIP106	CCCTTTCCCGAAGCACCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCTCAAAAGCCAGCCC	10
M00764_BBS7_MIP15	AACACAAGTAGAATGATTTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTACTTTAATTTCAA	10
M00764_BBS7_MIP31	CAACATATCATACGGTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCTATTCTTTTAAAAAA	10
M00764_BBS7_MIP36	ATTCTGTTGCCAGGCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTAAAAGAAATCTGATA	10
M00764_BBS7_MIP37	GAAAACATTAGCTGGGTGTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTGTAATCTCAGTAG	10
M00764_BBS7_MIP86	CCTATTAAGATATGATACTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAAAAATGATTGTATA	10
M00764_BTBD9_MIP109	AGATAAACACTAATATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAGATATGTGACAGATAT	10
M00764_BTBD9_MIP14	GCCCTGGCCCTGGCGCAGAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCCCCACTAGTG	10
M00764_BTBD9_MIP18	ACCCAGCGAGCTTCCAGTCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTGGCTGCTTCCGA	10
M00764_BTBD9_MIP20	GTTCTCTTTACTCACTTAAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGCACAGTGCTGG	10
M00764_BTBD9_MIP43	GCCAGCCCATCCCATCATCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGAGCTTATCTCCC	10
M00764_BTBD9_MIP48	CACGGGTTCACCTCCTTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACGATGGGGTGGCACTA	10
M00764_BTBD9_MIP51	CAGCACCCCCACCAGCCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCGTATTCCTTTTCAG	10
M00764_BTBD9_MIP55	ATCAGAGCTGAGGGGATAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACCATGCTGGAGGG	10
M00764_BTBD9_MIP6	GCGAAGCCTGTCTTGAATCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTCCTTATGTCCCTGA	10
M00764_BTBD9_MIP7	ACCAAGGCCTGGAGAGCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCCAGGCACTGGGG	10
M00764_BTBD9_MIP72	GGCCTGGTGTGACTTGGTGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACACCAGCCTGGCCG	10
M00764_BTBD9_MIP94	ACTAATTACATTTTCTACATAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTCAATGAAGTA	10
M00764_C15orf61_MIP10	GCTGCTTCCCCTTCATCAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGCAGCGGCGCCTG	10
M00764_C15orf61_MIP11	CCCTGCACCGGCCAGTTGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCGAGGTTGACGAC	10
M00764_C15orf61_MIP38	GCAACTCTACTGAAAAGCTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTCTCCAAGGACACT	10
M00764_C15orf61_MIP44	GTAATTATTAAAACCGTGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGTACAGACGGTTTC	10
M00764_C7orf62_MIP14	GTAAACTTTTAAAAAAGTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAAAAGAAACTGGAAGA	10
M00764_C7orf62_MIP17	ACTTACCATTTTTCTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGAAATGATTCATTTCTC	10
M00764_CACNG8_MIP101	CCTCCCTGAGGCCCAGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACTCGATGAAGAGGAGT	10
M00764_CACNG8_MIP12	GTTAGCCTCCCAGCCAATCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTATCTACTCCGTACG	10
M00764_CACNG8_MIP33	ACTGGGTTAGGCTCCCCTGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGCTGCAAGCTCCT	10
M00764_CACNG8_MIP39	ACAATAAACTGCTTGAGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTCCAGGAAGCCTACC	10
M00764_CACNG8_MIP41	AGTTGTTCTTTGGCCCCACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTACACTCTAGCTTG	10
M00764_CACNG8_MIP42	GCTGGAGTATCACTTGAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGATGCTGATGTACAAG	10
M00764_CACNG8_MIP56	GAGCGCAGTGGTGCCATCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTTTGGCCTTCAGACT	10
M00764_CACNG8_MIP58	CCCCTCCCTCCCCATCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATCTCTGGGACTTCTCTG	10
M00764_CACNG8_MIP62	TGGTGGATCACTTGAGGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAAACACACTGGAGAGA	10
M00764_CACNG8_MIP63	TGGTGGATCACTTGAGGTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAAACTCACTGGAGAGA	10
M00764_CACNG8_MIP70	GAATAAAATTCAGATTTCTTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCCCACTGGACTC	10
M00764_CACNG8_MIP81	CACCACTGCACTGAACTGACATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTGGCCTTTGTGTC	10
M00764_CACNG8_MIP84	ACCCAGGCTAGAGTGCAGTGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGCTAATTGCAGG	10
M00764_CACNG8_MIP89	GTGGCGTGGTGGCTCACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTTGGGGGCTCATGCCTG	10
M00764_CACNG8_MIP90	CTCATTTTTCATTTTTGTAGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCCCAGCCTGAAG	10
M00764_CACNG8_MIP94	GCCTGAGATTGCAGGGCCTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCTAGGGGAGGGGC	10
M00764_CACNG8_MIP96	GAGATGATGGCACACAGACATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAATTCACCTTGGC	10
M00764_CACNG8_MIP98	CCCCGCAGTGTGATTGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACCAACTCCTTCTTCTC	10
M00764_CACNG8_MIP99	GTCCTCTGTCCCTGCTCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGAGCAGCCAACTGT	10
M00764_CADM1_MIP109	AGGATTGGAGGAAGGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGACTACATTTCTCTTTTT	10
M00764_CADM1_MIP120	CAGCGGTATGTACCATTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTTGAGAGTAAATCACA	10

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M00764_CALML4_MIP15	GCTCCCCTTCCCTTTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAATTCAGATAAACACTGA	10
M00764_CALML4_MIP21	ACTGAGCATCTGATTTAGGGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGCCGGAGCTAG	10
M00764_CALML4_MIP34	GTCTATGAGGCTCTACAAGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAGGAGTTCGTGCTG	10
M00764_CCDC148_MIP29	GTATACATTTTCACTTACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTGCATTACATTTTGG	10
M00764_CCDC148_MIP47	GTTTTAGTAGTCAATAATTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGTACCCTGGAGA	10
M00764_CCDC148_MIP50	GTCAGTCTAAACATTTATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTTCTTACCTGTGTAGT	10
M00764_CCDC148_MIP77	ATAATTTTAACTAATTTGAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCCATTCTTTTTA	10
M00764_CCDC148_MIP81	CAGTCTTTAATAAATGGTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTATTGGAGCAAGGA	10
M00764_CCDC148_PKP4_MIP21	CCCATAGCTTCCCTCCATGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCACCAGGGGCAGAGT	10
M00764_CCDC148_PKP4_MIP5	CCATTGGCCTGTTCAATATGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCCTGTCCTCTCCG	10
M00764_CNTN4_MIP1	GCCAGAGGTTTGGGTACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTGGCCTAAGTTCAATG	10
M00764_CNTN4_MIP10	ACAGCCCAGTCACAGCCCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAAGGAACCGAGAGCC	10
M00764_CNTN4_MIP114	GACTACAATATGAACCACAAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGGTGATGGGAAG	10
M00764_CNTN4_MIP134	AATAGTGTTCCTAGACATGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATTAGTATAATAAGC	10
M00764_CNTN4_MIP142	ATTTTGTTCAAGTAATCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTACACCTGATAGACTTTGACA	10
M00764_CNTN4_MIP155	ATAATTTCTTCAGAAATGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAATTTCAAAAAAAAAT	10
M00764_CNTN4_MIP18	GGTTAATTTTAACATCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATAACAGTTTTGATTAC	10
M00764_CNTN4_MIP20	CTATTTATTTGGCTTTAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAATTTCATTTGCTGA	10
M00764_CNTN4_MIP3	CCTTTACTAATTTCGCGCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGATACTCGGGTTGTAAA	10
M00764_CNTN4_MIP30	ATTTAATTTTAGACCGGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCAAAAGTCACTCAG	10
M00764_CNTN4_MIP77	CATTTTAGTAAGAGAGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAACTTATTCAAATTCTTA	10
M00764_CNTN4_MIP86	GCGAGACTTCGTCTCGAAAAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGGTGGTGCACAAC	10
M00764_CNTN4_MIP87	GCGAGACTTCGTCTCGAAAAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGTGGTGCACAAC	10
M00764_CNTN4_MIP88	GCGAGACTTCGTCTCGAAAAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGTGGTGCACAAC	10
M00764_CNTN4_MIP89	GCGAGACTTCGTCTCGAAAAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGTGGTGCACAAC	10
M00764_COL20A1_MIP101	GCATCTGGAGCTGAAACTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGTGACCCTCAGTGG	10
M00764_COL20A1_MIP102	GAGATCAGGGAAGGCTTTCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGAGCTCCCTGCCT	10
M00764_COL20A1_MIP108	GAGCTCAGAGAGAGTGTGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCACTGCTGTCAAGG	10
M00764_COL20A1_MIP12	GCTGGGAGGTATCCCCTAGACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGGGACAACTGGG	10
M00764_COL20A1_MIP124	GGGTTCTCCCAGACCCTCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCTGCAGCGCCCCC	10
M00764_COL20A1_MIP13	GCCTAAAACTCAAGGACCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGACCACAACGCCAGA	10
M00764_COL20A1_MIP135	ACTTCTGCTGGAACTTTCTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAGGCACCGACCTC	10
M00764_COL20A1_MIP14	CACCTCGGCCTCTGCCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCCTGGCCCTCGAGGA	10
M00764_COL20A1_MIP146	GTTCCAGCCCCACTCAGGACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGTGCCAGCACAG	10
M00764_COL20A1_MIP149	GAGACCACACGTGACAAGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCCTTCCCAGGAGAT	10
M00764_COL20A1_MIP15	CCTTCAGCCGTCCCCCCGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCCAGTGTCCTTACCTT	10
M00764_COL20A1_MIP150	GTGAGTCTGCCATTCAGAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGATCTTTGGCTCAC	10
M00764_COL20A1_MIP156	GAGGCTGGACAGTGGCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCATGTTTCCTGAAGACT	10
M00764_COL20A1_MIP164	GGGGGGGCATGGCCAGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTGTCAGGGCCCCTCC	10
M00764_COL20A1_MIP165	CCTCGCAGGGGAGCCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGATCTCAGACTCCCAT	10
M00764_COL20A1_MIP168	GTCCAGCAGGGCCGTGAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAATGTCCTGGCAGG	10
M00764_COL20A1_MIP17	GGGGGACCCCGAAGAGACAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGAGACCGCTTGCT	10
M00764_COL20A1_MIP171	GCTCTGTGCACCCCACCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGCGGCCTCGGCCAAG	10
M00764_COL20A1_MIP172	GGGGACACTCTCCCAGGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAGCTACTGAGACGGC	10
M00764_COL20A1_MIP173	CAGGCAACAGATGGTTCCACTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGCAGTGCCCTG	10
M00764_COL20A1_MIP175	CCTGTGTGTGAATGGCCACCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGCACGATGGCTCC	10
M00764_COL20A1_MIP187	AAGGAGCCCCTCTCCTGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCGGGGAATTACATGT	10
M00764_COL20A1_MIP191	GTTTGCAGGAAGGCAGCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCTTAGGGACTGGTC	10
M00764_COL20A1_MIP192	CAGCTCCCTTGCCATCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTAAAAGGACCCAGAG	10
M00764_COL20A1_MIP194	GCCAGAAACCCAGCGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCCCGGAGCCCCCACAC	10
M00764_COL20A1_MIP195	CAGCCGGGGATGTTCAGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACCCCCAGAGGCAGCAC	10
M00764_COL20A1_MIP197	GACCTGCCCTCCCTAGGTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGACGCTCAGCTCAG	10
M00764_COL20A1_MIP198	GCACGCCCCTTACAGTCCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCTTGCAGGTGGC	10
M00764_COL20A1_MIP202	CCCCCAGGTGCAGATGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGAAATGCACTGAATCTA	10
M00764_COL20A1_MIP22	CCAGAGCCAGTGAGCTCGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAACGCAGCCTGGA	10
M00764_COL20A1_MIP26	CAGGGAGACACAAAGAGCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACTTGGGGCTCAGAA	10
M00764_COL20A1_MIP30	GTGGGGTCACCTGGCCACAGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCTGAGCATCCCCG	10
M00764_COL20A1_MIP31	GAACAGGTGCTGGCAGCTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTGCCAAGCTCCCTG	10
M00764_COL20A1_MIP32	GTGCTGAGGGAGTTCAGGTCCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTGGGAGGGCGGC	10
M00764_COL20A1_MIP33	CCTTTATAGAGGGCAGAGTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGGTACGGCCCAG	10
M00764_COL20A1_MIP35	GTGAACGTCTTCGCTGTGGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTGGGGCAGAACCT	10
M00764_COL20A1_MIP42	AGGCTCGCCAAACGATCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGACCCAGTTATTTGT	10
M00764_COL20A1_MIP56	ACACATTCAAAACCACAGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTCACCTATGTGTCCA	10
M00764_COL20A1_MIP59	CATCAAGTGTTTTGGGAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCACCTGCCTCTACCC	10
M00764_COL20A1_MIP63	AGCCCTAGACTTTGGCTTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTCCCTGGGACAGA	10
M00764_COL20A1_MIP68	GGCCCAGTGATCAGGGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCATACCCCCAACCA	10
M00764_COL20A1_MIP7	CCTCCACAGAAGTCACTGCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCAGGACCACAGGG	10
M00764_COL20A1_MIP75	AGGGTCCTGGTCTCAGCTATCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGCCGCGTGGAC	10
M00764_COL20A1_MIP81	GGGGAAGATGGTGGGGGAAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGCTGGGCGTCCTT	10
M00764_COL20A1_MIP86	CTGGGAAGGGTGTGCGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATGTACCCCATGTTACT	10
M00764_COL20A1_MIP87	GTAGACTGAGCGTGGAGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATGAGCAGACCCAAGG	10

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M00764_COLEC11_MIP48	ACTCAGCCAAGTCACACCGGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACCTGCCTCCAGGT	10
M00764_COLEC11_MIP62	GAAGCAAAGCAAAATTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTACAAAAGTTAATTAA	10
M00764_COLEC11_MIP8	GATTTGCTGGGCTGTCTGATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGGTCCTGCCCCC	10
M00764_CORO6_MIP12	GGGCGGTTGGGGGAGATGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTTCTCCAGAGCCGT	10
M00764_CORO6_MIP16	CCTTCTCCCGGCCCCTCACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGCCTGGCGTATCCG	10
M00764_CORO6_MIP17	GCAAGTCCTCCTGTCCACCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTACAAGCTACACGAA	10
M00764_CORO6_MIP2	CCCAGGAGCCTGGGGGTAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTACCTAACTTTACTTG	10
M00764_CORO6_MIP29	GACAGGGAGGGACATCACCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACAGGCCCAGCTCTC	10
M00764_CORO6_MIP32	CGGATGCTCTCCAGGTCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATTCGGGAAAAGCCT	10
M00764_CORO6_MIP37	GAGGGGTCCAGGAGCTCAGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGATAAGCAACGCG	10
M00764_CORO6_MIP38	CCAGACGCATCTTCCAGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCATCTCAGAAGCTCA	10
M00764_CORO6_MIP62	GCTCCCAATTTAGCTGTCCCGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGAGGCTCGGGTT	10
M00764_CORO6_MIP8	GAGCCCCCCAGGTTACCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAATCGCCACCCGTTT	10
M00764_CORO6_MIP9	GAGGTGGTGTCCCCCTTTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGGAGCTTAGGGGAG	10
M00764_CRBN_MIP110	CGTGGTATATAAGCATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAACCTGGAAGGTGGAGGC	10
M00764_CRBN_MIP120	CCCCTGGGGCCGCCAGGGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGTACGCCGGGCACTC	10
M00764_CRBN_MIP35	GTACTCCCAGCTGCTCGGGAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTACCTTAATTG	10
M00764_CRBN_MIP36	GTACTCCCAGCTGCTCGGGATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTACCTTAATTG	10
M00764_CRBN_MIP4	GAACAGGTTAAGATAGATAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGTCATTGTTAAGGT	10
M00764_CREB5_MIP14	ATTGCGGTCCGCTGGGGAGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAAGGCAAGAGCGGA	10
M00764_CREB5_MIP199	GAGGCGGAGGTGGAAGGATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGAAGAAGTAGGATA	10
M00764_CREB5_MIP216	AAAAGTGTAGGACAAGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGATTTTCCCTCCTT	10
M00764_CREB5_MIP29	CATCTTTATTGCCCTCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGTAAGTGTTTGATT	10
M00764_CREB5_MIP30	CACGAGTGTGTTGTGGGGAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGCCCCAGGGAAAG	10
M00764_CREB5_MIP37	CAAACTTTTACATCTAACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGAGTTAAGAACTTGT	10
M00764_DCLK2_MIP98	CCTTAAGAGTCCCCCTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTATTAAAGTGCTGTTTT	10
M00764_DMPK_MIP18	GGTCTTACATGGGAAGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAATAAAGGGCTTCTG	10
M00764_DMPK_MIP2	ATAAATATCCAAACCGCCGAAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTGGGGGTCCTA	10
M00764_DMPK_MIP25	GAGGTGACGCTGCGGGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGATTCCTAGCCTGGAAC	10
M00764_DMPK_MIP29	CAAACTACCTTTCAGGAACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACACTAACACAACCT	10
M00764_DMPK_MIP30	GCTTGCACGTGTGGCTCAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGGCTCTACAGTGCA	10
M00764_DMPK_MIP4	ATGCACAAGAAAGCTTTGCACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGCTCCGAGAGC	10
M00764_DMPK_MIP43	GGCCAGCGTGGCGAAACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCACAGTGGCTTATATTTG	10
M00764_DMPK_MIP51	CCTTCCTTGCTGAGTCAGGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAAGCATGCCATGAC	10
M00764_DMPK_MIP53	CACTGTCCTTACTCCAACTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTGTCTGAAGACTGC	10
M00764_DMPK_MIP55	GTCCCGGAGACCATCCCAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCAGCCGAGCAGGGGC	10
M00764_DMPK_MIP6	CACCCCCACCTATCGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGCTGCTGCTGCTGCTGG	10
M00764_DMPK_MIP64	GGTGAGCCAGTGCCCTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTTCATTTATCCCACCCT	10
M00764_DMPK_MIP65	GCTTCTACAGTTCTGACCCCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATGTCCCTGCACGG	10
M00764_DMPK_MIP67	GTCTATGGCCATGACAATCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGGTCCCTCTCCA	10
M00764_DMPK_MIP82	CAGAGGGACGACTTCGAGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGGGAGACAGACAGA	10
M00764_DMPK_MIP83	GCCCTCCCATAGAGGTGAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACAAGGGGGAAAGCC	10
M00764_DMPK_MIP89	GGAAGAAGTGGAGGCAGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGGCCTCTCAGAAGTC	10
M00764_DMPK_MIP91	CCTTTTAAGGCAGCAGGAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGAGAGGAGACAGT	10
M00764_DMPK_MIP93	AGGTTTTTCCAGAGGCTGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGGAGTGCTCCTCCC	10
M00764_DMPK_MIP94	CCCACAGCCCCTAATGACTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCTTGTGTCCATCT	10
M00764_DMPK_MIP96	GTGTGTAACAAACTGTGTGTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCCCACCTCCTC	10
M00764_EBF3_MIP2	GTAAAATCTACCATTTAGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTACCAAAAGTGAAA	10
M00764_EBF3_MIP30	GCTTCTTTTGGAAAAGGGAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGTCCACCAGCCTC	10
M00764_EBF3_MIP49	GTGGCATCCCACTGTCCCTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACGCTGTACAGCGCCT	10
M00764_EBF3_MIP63	CAAAGAAGTTGTCGCCAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTTGTGTCAATACACTA	10
M00764_EBF3_MIP76	GGAATCAGTTCATTTGGATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATATATGCTTTATTAAAT	10
M00764_EBF3_MIP81	GGCTTGCATTTCAAGGTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTCAGGACTGCTGCC	10
M00764_EBF3_MIP88	CCACTATAAACTCCAGTTATTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGGCCGAGAGCCT	10
M00764_EBF3_MIP92	GGAGGCAGGCGGTGCCGGTGCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTGCTGGCGCTCT	10
M00764_EYA2_MIP106	ACTTTCTCGCAGTAGACAGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACCTGGCTACAGC	10
M00764_EYA2_MIP26	GGGGGCCAGAGGGAGGGTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGAAGCTGCCCCTGC	10
M00764_EYA2_MIP30	CAGTGTCTACCTGGAATGAAACGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGAGGTGGGGAAG	10
M00764_EYA2_MIP96	GCCTGTAATCTCAACTACTTGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGGTATTTTGGGG	10
M00764_FAM114A1_MIP1	GAAGGCCTTCCTCAAATATGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAAGCCGGAGACAA	10
M00764_FAM114A1_MIP38	CTAAGGAGAAGGAGAAGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGAATCTCCCCCTCT	10
M00764_FAM114A1_MIP5	CAAATTCAGCTAAAGTTTGATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGCGGAAAGCCAGA	10
M00764_FAM114A1_MIP69	ATACTGAATTAGTATCAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGCATGGAAAGAAAAC	10
M00764_FAM114A1_MIP71	CACCTTTTTTAAGGGAAGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCAAGCTTTTTTTTT	10
M00764_FAM114A1_MIP88	CTGAGGCGGGCAGATCACGAGGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTGGGATAAGATC	10
M00764_FAM114A1_MIP89	CTGAGGTGGGCAGATCACGAGGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTGGGATAAGATC	10
M00764_FAM171A1_MIP100	CATTCCCTGCATCCCACCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTACCAAGAACCCTCC	10
M00764_FAM171A1_MIP33	ATAATATAAAAGGAGACACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAAAAAGTACTTCAAT	10
M00764_FAM171A1_MIP49	GCTGGAGTGCGATGGCACAATCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAGTAGTAATG	10
M00764_FAM171A1_MIP66	GAAAGTACCAAATATTTTAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGTTACAAGAAATCA	10
M00764_FAM171A1_MIP77	GTTTAAAAGTATAGAATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAGCCCAGGAGATCGA	10
M00764_FAM171A1_MIP96	CGTTGGGGGACACAACTACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGAACCATCCAAGTAC	10

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M00764_FTSJ2_MIP24	GCACTGCAGCCTGGGCAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAACAAAAAGAAAAAAT	10
M00764_FTSJ2_MIP34	GACTCACGGTCAGCAGTCAGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGGATTTCGCTTC	10
M00764_FTSJ2_MIP44	GAGAAGCGGGGCACTGAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCTAAACTGAAAGAGCA	10
M00764_GALNT12_MIP12	GCGGGGAGGCAAGAAAGTAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCCTCAGAGCCCC	10
M00764_GALNT12_MIP13	CATGTGAGCTCTTACACTATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCTCACCTTTTCAGG	10
M00764_GALNT12_MIP5	GCTGAATACACCCTGCAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCATTTCGGCAGGGTCT	10
M00764_GALNT12_MIP59	CTAATCGTGGCTTCCCCAACATACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGTTCGTGCAGCTG	10
M00764_GLO1_MIP1	CATTCTGAAGAGAGAACAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATAAAATGAAACTTCAA	10
M00764_GLO1_MIP3	GTGAGTGCTTTAAACAAATAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCAGTTTGTGGATGA	10
M00764_GLO1_MIP60	CCCTCTTCCCATCACACTCCCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTTCCAGCCACCGTC	10
M00764_GLO1_MIP61	GTTTGATGGGGCGATCGTGGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGGAACGGCTCCC	10
M00764_GRIN2B_MIP179	ATAACTTATTCCCAGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGAGGCTTAAATAAAA	10
M00764_GRIN2B_MIP207	AGGAAGATGAGGGGATGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATATTTACATATGAAATAA	10
M00764_GRIN2B_MIP21	AAATCAAAATGATCTGTCAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCACTCAGAGTCC	10
M00764_GRIN2B_MIP215	ACCTCCAGAGCTGCACTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGAAGGGCTTCTACCAAG	10
M00764_GRIN2B_MIP241	GACTTGGCCGAGGCAGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCCTTTGTTCGGAACTG	10
M00764_GRIN2B_MIP4	CAACATAAAAAAACAAGAAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTGGGGTCGGG	10
M00764_GRIN2B_MIP57	GCTGAATATTTGGGAGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGGGTTAATTATTATTTTT	10
M00764_IQCH_MIP40	GTTTCTTTTTAGGGATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATGCAAAGGATTAAGG	10
M00764_IQCH_MIP91	CACATTGGCACTGTCAAAGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGCTCCAGAAGACT	10
M00764_KCNA4_MIP38	GGCTGAAGAATGCTCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGAAAAGAGAAGGATGT	10
M00764_KCNA4_MIP50	GTTGGGAGCCGGGTGCATCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCAGTCCCGAAAATG	10
M00764_KCNA4_MIP53	GAGGCCCAACCCCGGCGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCAACCCTCCTCCCCT	10
M00764_KCNK13_MIP14	CCTCCGGGGGGCAGGACCGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCGCGTGGACAACG	10
M00764_LAMA1_MIP113	AGTCCATTAGGTGAAAAGGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTACATATTTAATTAG	10
M00764_LAMA1_MIP249	GAATAAAGTTTTATTGGAATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAAAGTCACTCTAC	10
M00764_LAMA1_MIP272	GAAGATGAAGGCATCAAAATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGATCTGCATTGAGC	10
M00764_LEO1_MIP20	CCTGCCTCCGCCTTCTCAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCATGTGAGGCAGAAA	10
M00764_LEO1_MIP21	CGGATTATGAGGTCAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTTTTATGGAGTTTT	10
M00764_LEO1_MIP22	CGGATGATGAGGTCAGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTTTTATGGAGTTTT	10
M00764_LEO1_MIP53	ATAAAGAGAAAGGAACGGAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATATTTACTAAAATCA	10
M00764_LEO1_MIP54	ATGAAGAGAAAGGAACGGAGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATATTTACTAAAATCA	10
M00764_LEO1_MIP55	GAACCCACCTTTACGCTCAGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGTGCAGGGGGCG	10
M00764_LEO1_MIP59	ATTAAACCTATCGCGAGTCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGCCATTTCGTCAAT	10
M00764_LEO1_MIP60	CAGTCACCGCCCACCCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACAATTTTTAAGAGGGTA	10
M00764_LEO1_MIP61	ATTCTAATTCCTCAGCCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGTTATTTCATCCCAA	10
M00764_LEO1_MIP62	GCTTGAACCCGGACAGTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCCTGAGTTTGCGAC	10
M00764_MAP2K5_MIP102	CAGAAGAAGTTGGAAATTTTACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGTTCTTAATAAATT	10
M00764_MAP2K5_MIP108	GATACCTTGATTTTTAAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTGTTTTCTTTTTCCTA	10
M00764_MAP2K5_MIP138	GCCCAGTGTTCACAATCTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGTGAGCAGACACTGG	10
M00764_MAP2K5_MIP154	GCAGGGGCCCCCGTGAGGCTGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGACTGCCTGTCA	10
M00764_MAP2K5_MIP155	CATTTCCATCATTGAACTGCACGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGACGGGTGGGTTGTT	10
M00764_MAP2K5_MIP157	CAGGCAAGGCCACCTGCTGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGTGGGCAGGGACC	10
M00764_MAP2K5_MIP9	CAGGGCGCGGCGCGCGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACTAGGAGAGGGTCCTC	10
M00764_MDGA1_MIP102	CGTAATGGTAGACGGAGTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATATATAATCTATTTC	10
M00764_MDGA1_MIP103	CGTAATGGTAGACGGAGTGACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATATATAATCTATTTC	10
M00764_MDGA1_MIP107	GGCTAACATGGCGAAACCTCGTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGATACTTTATCC	10
M00764_MDGA1_MIP108	GGCTAGCATGGCGAAACCTCGTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGATACTTTATCC	10
M00764_MDGA1_MIP111	GTAGAGGGGACTCACTAACCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGACCCCACTCCCC	10
M00764_MDGA1_MIP113	CACCCCACGCATCCTGCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAGCCTGCGGGGAATG	10
M00764_MDGA1_MIP114	GTTTGGGGTTCTGGGTGAGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCCCCAGTCTGGGG	10
M00764_MDGA1_MIP115	CCCCCAACACTGGTCCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATTCGCCCCATAAAAT	10
M00764_MDGA1_MIP119	AATTGAAAAATATTTTGACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTGTTCCAGATATCTC	10
M00764_MDGA1_MIP130	GTTCTGTGAGCAGTGCTGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATGGAATCAGACTGGG	10
M00764_MDGA1_MIP131	CAATTCTCAGAGCTGTGCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCCCCTGGATGAGAC	10
M00764_MDGA1_MIP141	CAGCTCTTCGAGGCATTCTCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGAAGACGCCCCT	10
M00764_MDGA1_MIP145	CAAACCAGGCCTAGACCCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCCTATGCCTATACC	10
M00764_MDGA1_MIP146	GCTGGGAGGCCCAGGTTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAGCGGGCTGAGCTG	10
M00764_MDGA1_MIP155	GTAGGACACGGAGGTCTGTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTACCTTCCCAGCTTT	10
M00764_MDGA1_MIP159	GATCGCCTGCCGAGCTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCCAGAAGGCAGAGC	10
M00764_MDGA1_MIP167	CCCCCTCACATTTCCGCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGTGCCTGGCATATT	10
M00764_MDGA1_MIP179	GGCACCCTCAGCATCCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACGAAACTCTGGTGGTGAA	10
M00764_MDGA1_MIP193	GTTCTCAGCCTTGCAGTAGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCACCTCACCTCAT	10
M00764_MDGA1_MIP222	TTTTCTCTAATTGGTCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAGGAGAGAGAGAGAA	10
M00764_MDGA1_MIP33	GGAAGGGGAGTGGCCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACACCTCTTTCTCATTCA	10
M00764_MDGA1_MIP42	GAGGGGAACAAGGGAGACAAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATCCCCCCATCCCC	10
M00764_MDGA1_MIP67	GCTGTTCCACTTGCACACACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACCAAAGACTGACCCCC	10
M00764_MDGA1_MIP71	CCACCCTCAGGCCCTCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACTGAGGTCAAGTAAAT	10
M00764_MDGA1_MIP76	GTCTGCTTCCGGGGACACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTCAGACATTCTGAACC	10
M00764_MDGA1_MIP78	CCTTAGCCCCCAGGAAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAATCTGGGGTGGGGTC	10
M00764_MDGA1_MIP98	GACAAAGTTCAAAAAAGAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCAGGTAGGACAA	10
M00764_MEIS1_MIP117	ATTACTTCCTTCTCTGCTCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGGAGTAAAGAACAG	10
M00764_MEIS1_MIP130	GTTAGATGCTGGAACAGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAACTGTGGGAACACAGT	10

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ID	**MIP**	***c***
M00764_MEIS1_MIP132	CAATCGTGAATTTTAAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTTAGTAGGAGATGGTT	10
M00764_MEIS1_MIP141	ATAGAGGCTGTGCCTCTAATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTTGCAGAGCCTGT	10
M00764_MEIS1_MIP162	ACTGGGGTTGCTGCCAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAAGTCACTGTATTCACT	10
M00764_MEIS1_MIP163	GTCAAGGAAGAAGCATGACTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGCTCTGGCACAGT	10
M00764_MEIS1_MIP170	ATCTAATATGTCCTCTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACTAGAATTCATACTGG	10
M00764_MEIS1_MIP189	CATAATTTAAAAACAAAACAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCACCCCTAGCAAATA	10
M00764_MEIS1_MIP200	GATGTACATTTATCCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCATTTTCTTATGTTCTCC	10
M00764_MEIS1_MIP46	ATGTCGCTTGTCTCAGCCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACATTCCCCTCCCTTC	10
M00764_MEIS1_MIP48	ATCCCAACCCCAAGGCCCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGCGGGTTCCTCCT	10
M00764_MEIS1_MIP52	CAGACCCAGGTGACCGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACAAACAACATAATGGT	10
M00764_MEIS1_MIP59	GCAGAGTGAGCTCTCCACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAATTAAATAAGCTGA	10
M00764_MEIS1_MIP67	GCAAAGTTTCTGCTGCCTTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCCCTTTCTCAGTC	10
M00764_MEIS1_MIP99	AAAACTCTCAAAAGATAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAATAAAACACTGGGAA	10
M00764_MEIS2_MIP143	GTATTTATTGTTGTGTTTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTAGCATCAGCTGCAA	10
M00764_MEIS2_MIP149	CAACCCTTTATTTTTATTTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAGGTATTCAGTTC	10
M00764_MEIS2_MIP189	GGATATGGAACTCGAGGCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCTACTTGAACAAG	10
M00764_MEIS2_MIP191	GTTTGTTTTCCCCCCCAGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGGAGCTTTACTTGA	10
M00764_MEIS2_MIP217	CGTTGGCTCGCTACGGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTATTAGCGTTTTTCTTC	10
M00764_MEIS2_MIP219	GAGGCACTGGCCCTAGTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGACTACTAGCCTGGG	10
M00764_MEIS2_MIP228	ACCGAACTGTCGTGTTTCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCTCTTTCTCTTCTC	10
M00764_MEIS2_MIP232	GCTCTCTTTCTCTCTCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATGAATAGTTTGCAAAA	10
M00764_MEIS2_MIP247	GGGTAGTTCCCTTCGTTTCCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTCCGGGCTCGTA	10
M00764_MEIS2_MIP69	CCATCAAATATTCATGTACAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGTGGTGGCTGAA	10
M00764_MEIS2_MIP98	GGAAGGGGAGGGGGAAAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGTTGCTACAATAAGGC	10
M00764_MICALL2_MIP100	GTTGCCCCCGGCAGGCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAACTGAAGCACCACAAG	10
M00764_MICALL2_MIP101	CCTCCCACCATCACCCGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTAACGGCTTGGCTAA	10
M00764_MICALL2_MIP107	GGCCCAGCCTCTGACAAAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTCACTCCTGGTGTG	10
M00764_MICALL2_MIP11	CCTTCCCTTCCACTGGCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCAGATCTTGGACAAG	10
M00764_MICALL2_MIP111	AACTGAGTGTGGTTTGAGGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGCCAGAAAGGCTG	10
M00764_MICALL2_MIP125	CCGGGGCTGTGCCAGAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTAGGGTTTAGAAATCC	10
M00764_MICALL2_MIP134	GCTGCTGGGCTGGACGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCAGCCTGGACAACAGAGTGA	10
M00764_MICALL2_MIP140	GTGGGCAGAGGCACCGGCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCACCACATGGGACC	10
M00764_MICALL2_MIP141	GTGGGCAGAGGCACCAGCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCACCACATGGGACC	10
M00764_MICALL2_MIP144	GTGCAGGGCCTGGGGGGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAGGGGACCAGTATGC	10
M00764_MICALL2_MIP147	CCAGAAACTTCAGTGCTCTCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACCTCATTCCTTC	10
M00764_MICALL2_MIP148	GTAGTACGACATCAGACGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCATCTTGCCCAAACAGA	10
M00764_MICALL2_MIP150	GACCAGGTGGGTCGCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCGCCCCTCACCAGTGC	10
M00764_MICALL2_MIP154	GAGTGCCTTCCCAGGTGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTGGAGCAGACACC	10
M00764_MICALL2_MIP156	GATACCCTGGGCAGAAAACACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCCCGGGAAGTTCC	10
M00764_MICALL2_MIP159	CCTTCTGCCTTGGCCTCCTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTGCTGTCCGGGAC	10
M00764_MICALL2_MIP166	GGCGCGGACTCCTCTCCGTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAATCTGCTGGGA	10
M00764_MICALL2_MIP169	CCACCCACGTGCCCTCGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGTCTGCAGAAGAGC	10
M00764_MICALL2_MIP177	CCCCTGAGCTCAGCTGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAATTGGAGGTTAGGGC	10
M00764_MICALL2_MIP178	CCTTTGGAGATAAGAGAATTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGACCCCACTCG	10
M00764_MICALL2_MIP180	GGACGTTGGCCTGCAGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATACAAACTGACAGGGGAA	10
M00764_MICALL2_MIP181	GATCTTCCCGGCCTCTCTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCTGCCCTTGCAAG	10
M00764_MICALL2_MIP182	GAGACGGCTGGAACTGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTTTCCGTTGTTGAAACC	10
M00764_MICALL2_MIP183	GGCAAGGACAGGGGTGTCCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACCTGCAGCCCCCAT	10
M00764_MICALL2_MIP184	CACACACCGTGGGCCAGGCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTGCAGGCTGTGG	10
M00764_MICALL2_MIP185	GGTATACCTGATTTTAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCAGCCAGTGTTGAAAG	10
M00764_MICALL2_MIP190	CCAGATGGCACAGTCGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCAGGAGAGAATCCCAC	10
M00764_MICALL2_MIP20	CAGGCCCTCCTGTCCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTCCACCTCTATGAGAC	10
M00764_MICALL2_MIP21	CCTCTGGGAGCGTGACGGGGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCCACGTGCGTCTC	10
M00764_MICALL2_MIP23	ACTTCCAAGGCCACGTGCGTCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTTCCCCATGTTAG	10
M00764_MICALL2_MIP40	GCTGCTACACTAAATGCCTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTGAGGCTCAGGGC	10
M00764_MICALL2_MIP42	AGTCAGGTGGCCTCACAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTTGCAGAGGATGAAAC	10
M00764_MICALL2_MIP48	ACTGAGGGTGTCTGTGGGAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCAGCAGAAGCTGCTT	10
M00764_MICALL2_MIP55	GGGGTGTTGCTGATCTGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGACCCAGCCCCGTG	10
M00764_MICALL2_MIP56	GGGGTGTTGCTGACCTGGAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGACCCAGCCCCGTG	10
M00764_MICALL2_MIP59	GGACGGCCAGTCTCCTGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTCTCTGGGGCTGACCT	10
M00764_MICALL2_MIP64	CATGCATCACATTCATGAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGTAACACAGGAAGT	10
M00764_MICALL2_MIP65	CATGCATCACATTCATGAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGTCACACAGGAAGT	10
M00764_MICALL2_MIP73	GTGTTCATGTATGTGATGCTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGGGACTGGACCT	10
M00764_MICALL2_MIP74	GTGTTCATGTATGTGATGCCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGGGACTGGACCT	10
M00764_MICALL2_MIP78	GGTGGTTCGGGTTCCGACCTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCAGGAGGGTCCCAG	10
M00764_MICALL2_MIP80	GCCTGGAATCTGCTTCGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCCTGGTTTGGGGG	10
M00764_MICALL2_MIP81	GATTACATACTCACTGCATTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTGAGACACGCAA	10
M00764_MICALL2_MIP82	GATTGACACGCCTATCCAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGATGGAGAGCGAAT	10
M00764_MICALL2_MIP86	GGGACACACAGCACAGGAGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTGGCTCAGGTGTT	10
M00764_MICALL2_MIP89	CATCAAAGCAGGGCCGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCTCGATAAAGCCAT	10
M00764_MICALL2_MIP91	AAAACACGTGAGGCCATAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGCACAGGGTTGG	10
M00764_MICALL2_MIP93	ACCGTCACCGGGACACCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCTCAGGTCATAGGG	10
M00764_MICALL2_MIP95	ATGTAACTGCCAGACCGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATGTGGTGACACAGGGT	10

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M00764_MICALL2_MIP99	CGGATGCCTGAGAGGTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTCACCCTGCGTTAAG	10
M00764_MPPED2_MIP147	GTCCAGCGGAGCCCGGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCGGGAGGCTGAGGTCG	10
M00764_MPPED2_MIP150	CAATTATACATTTTTCATGACCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAGCGAGCGTTGG	10
M00764_MPPED2_MIP161	GAAACCCTGGGGCTTCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTTCCCCTATCATTTT	10
M00764_MPPED2_MIP163	AGCTGGGTGTTCTCTTTGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCTAGGGTCGCCTTC	10
M00764_MPPED2_MIP3	TGACCTTGTGATCCACCCGCCTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGGGTTCAAGAA	10
M00764_MPPED2_MIP50	GTAGTTTCGTCCTGGGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATGAAATTTAGGAAAGC	10
M00764_MPPED2_MIP71	CCTTCTCCCTCACAATCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTCTATCAAAATCTT	10
M00764_MPPED2_MIP87	GTTCCATTTCTGATTTTCCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAATTAAGTCACTAC	10
M00764_MYT1_MIP104	GAAGCAGGAAACATGGTGAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTGGCCTGGGGAAG	10
M00764_MYT1_MIP105	GTAAGATGGAAATCACTGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCCTGGTTTTCTGA	10
M00764_MYT1_MIP106	GAGTCAGCCCATGTCTCCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCCCCTCAGGACAGA	10
M00764_MYT1_MIP108	GGCACTTCGAATCTCTCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGCAGAACCCCCTAC	10
M00764_MYT1_MIP2	GCTCCCTGCCAGGAGCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTGGAAGATACAAAGG	10
M00764_MYT1_MIP31	CCTCCCTTCCCCACAGACTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCTTCCTCTTCTTG	10
M00764_MYT1_MIP36	TGTAATCCCAGGACTTTGGGAGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAATCAGATAAAC	10
M00764_MYT1_MIP49	GTCAGTGACTGTTGACTTCCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGGCTCTGCTCGG	10
M00764_MYT1_MIP50	CAGACTCATCCTTTCACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGAGCCGGGCTGCCCGCCT	10
M00764_MYT1_MIP82	CAACCCAGTGGGCGAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTCAAAATTCTCTTCC	10
M00764_MYT1_MIP85	GGCCCCTCCTCCACTCAGTCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGGGACAGCTGGA	10
M00764_MYT1_MIP98	CCCCTCTGTGCAGTCAGTAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCGTCATTCTCCTG	10
M00764_NECAP1_MIP48	ACTCCCCACATAAAGCCCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGAGGTAGGAAGCTG	10
M00764_NECAP1_MIP6	GGGACCAGCCTGACTAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTTTCCAGATTTAACA	10
M00764_NECAP1_MIP8	GTAATCCCAGCATTTTTGGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGGTTGCCACCAGC	10
M00764_NENF_MIP3	AAGTGAACCATCCACCTCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGCCACCAGAGTAGT	10
M00764_NRG3_MIP12	GACCCCTTCTTCCTCTCCAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCGTGGTACCTCTGTT	10
M00764_NRG3_MIP151	ATTTGTAATGTCTAGATCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACACTTTGGTAAAAATG	10
M00764_NRG3_MIP16	CCCTGTCTCCCTTTCAGGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTCAGTAGCAGCACG	10
M00764_NRG3_MIP18	GCAGAGTGAGAGCTGATTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCAAATTTCGTAAGTA	10
M00764_NRG3_MIP43	GGTATTATTTTCCTTCTGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATATTTAAATAATTA	10
M00764_NRG3_MIP60	ACGCCACCGCACTCCAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGTCTCTACTAAAAAACTAC	10
M00764_NRG3_MIP83	TAAATGGGCTTCTCTGCTGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGAACCGGGGAGG	10
M00764_NRG3_MIP84	CAAAAGATACAAAAAATTAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAGACTACTGGCCG	10
M00764_NRSN2_MIP11	GAGTCCCTACCCATCCCTGGTACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGCTCCCATCTGTC	10
M00764_NRSN2_MIP47	CCTGTCGCCTGGCAGGCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCTTCTGCTGCTGGGT	10
M00764_NRSN2_MIP54	GTTTTGGGAGGACTTGAGGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGGCAGGAGCTGA	10
M00764_NRSN2_MIP61	CAGCTGGAGAGCAGCGCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACCTAGAAACCAAGCCC	10
M00764_NRSN2_MIP65	GGTAAAACCCCGTCTCCACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTACCGCATCTGTAAA	10
M00764_NTNG1_MIP10	ACAGCAACAGCGAGCGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGAGGAGTTACTGGAAAC	10
M00764_NTNG1_MIP139	GTGCCACAACAACGTGCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACATGATGTACCAGATG	10
M00764_NTNG1_MIP14	AGTGCTATGTGCAGTGACATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGGAGCAGGGTCCC	10
M00764_NTNG1_MIP140	GGAGCTCGTTGTCGCAGACATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCCAGAGTCGGAG	10
M00764_NTNG1_MIP20	GGAGGCGAAGGTAATTAAGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCCCTCATCTACCT	10
M00764_NTNG1_MIP81	GTTTAAAAAGGAAGATAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAATACTGTCATTTAGG	10
M00764_NTNG1_MIP86	GTAACAGCATATTCTGTGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGAGCACAACACTAC	10
M00764_NTNG1_MIP89	ACGTCTGGCTAATTTTTGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGAGTCTTGTCATCC	10
M00764_NTNG1_MIP90	ACGTCTGGCTAATCTTTGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGAGTCTTGTCATCC	10
M00764_OLFML2B_MIP56	CCCTCATGGCCAAGCCTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCCAGCTTTAGAAGGT	10
M00764_OLFML2B_MIP57	CGGACGCAAGGAAGAGGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAGTGGCTGCTGAGAG	10
M00764_OSBP_MIP13	GGTTTGATTTCCTTCCCATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGAGAGCAGAAGTTAA	10
M00764_OSBP_MIP24	AAAGAAGAGTAGAAGGGAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTTAACTCCTTGGTA	10
M00764_OSBP_MIP91	GTGAGAGCCTGGGGTGGGACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGGCCAGCCGCGGGGA	10
M00764_OSBP_MIP99	CTTTTCCAGCCCCTTCCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGCTTCTTGTTAGGAAG	10
M00764_OSGIN1_MIP15	CCCTCCAGACCCCCAAGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATATCAGCAAATCTTCA	10
M00764_OSGIN1_MIP16	GGGCTTCCCTGGACCCTGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGAGAGAGACAGGCA	10
M00764_OSGIN1_MIP17	CGTGGGATGGGGAAGTGGAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGGCCTTCTCAAGCCC	10
M00764_OSGIN1_MIP19	GTGTGCACATGTGCTCATGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGGGGCTGGGGC	10
M00764_OSGIN1_MIP20	GTGTGCACATATGCTCATGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCAGGGGCTGGGGC	10
M00764_OSGIN1_MIP29	ATACCCTCACTTCCCTCTGGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCAGGCAGCGTGA	10
M00764_OSGIN1_MIP39	GGTGTGGGTGGTGGCACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTGGAAGAATTCTGGAG	10
M00764_OSGIN1_MIP45	GATTCACTCCAGGCAGGTGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGGGCGCGGCTGCC	10
M00764_OSGIN1_MIP49	CCGAGGTGGTCCTTTCTGGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTGGACTTGCCCA	10
M00764_OSGIN1_MIP51	CAGAGCTCTGGGTAGTACATACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTACCTGCTCTCCG	10
M00764_OSGIN1_MIP55	ATGGCGTGCTCCTTCCGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGAGATGCCAGAGTCC	10
M00764_OSGIN1_MIP60	GGGGTTGGGGGGCTGGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGTTATGCCCCAGAC	10
M00764_OSGIN1_MIP65	GTGCTTCAAGGAAGACTGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGTTCAACCAGCTGC	10
M00764_OSGIN1_MIP67	CATTGACGTGGACCCCTTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGAGAAGGTGTTTGGGG	10
M00764_OSGIN1_MIP7	GACTCCATCTTAAAAAAAAAAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGCGGTCACCTGT	10
M00764_OSGIN1_MIP70	GCCGAGTGTTAGGGTGGCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTCCTCTTGACCCCAA	10
M00764_OSGIN1_MIP71	AAAGCTGCTGGTGTGACCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCCCACGTTGCTGG	10
M00764_OSGIN1_MIP9	ATACAGGCTGCCAGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAGATATTTTCCTTATT	10
M00764_PCDHB5_MIP35	GCTCGGTGCCCGAGGGCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCCGACTCGCTCACT	10
M00764_PCDHB5_MIP36	GAACAGGAGCACCGAAAAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAGTGGTAGCTCTGGG	10

continued table…

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M00764_PDE11A_MIP165	ATGAAATAGATGTATATAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTAAAACAGAACAGC	10
M00764_PDE11A_MIP18	GTATATTTGCAAATACATTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCTGATATCACACATAT	10
M00764_PDE11A_MIP212	GTTCCGGAAACCCGAGCTATCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGGAATCTGGGAGAT	10
M00764_PDE11A_MIP226	GTCATCAAGTTGAATCAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTCATTTTAATTTTAGGT	10
M00764_PDE11A_MIP43	AGAAACGTAAGAACACCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAGTCGAGATCACGTCACTGC	10
M00764_PDE11A_MIP7	CATTTGTGTACTAGCGTATACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAGAGTAAAAGAAAA	10
M00764_PIAS1_MIP15	CCCGGAATCAGAGAGAAAGAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCCCCAAAGGCTCC	10
M00764_PIK3R4_MIP89	ACTTTTGAAATGATCAGAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATACTGCTTGTTTTTC	10
M00764_PKP4_MIP115	AAGCCACTGCACTACAGCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTTCTCTACTAAAAAC	10
M00764_PKP4_MIP178	GGCCACAAGATAAATGTGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGTGGTAAGCAGAAGA	10
M00764_PKP4_MIP42	GCTCTGCCTCCTGGGCTCAAGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTATAACAGATATTC	10
M00764_PKP4_MIP79	CCTATATATGAGGGGAGGACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGTGATTGTCTCAGT	10
M00764_PKP4_MIP91	ATTAAAAAATGTTTTACCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTGCTAAAAAATTAACA	10
M00764_PLXNA2_MIP117	GGGCAACGTGGCTTCGCTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAGGAAACGGGCAGC	10
M00764_PLXNA2_MIP176	ACCTTCTTAAAGTTTTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTTACAGGTTCTAGGG	10
M00764_PLXNA2_MIP177	ACCTTCTTAAAGTTTTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTTACAGGTTTTAGGG	10
M00764_PLXNA2_MIP195	CATGCCTCAGTTCAGCACCTTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCTCCTCACCGCCG	10
M00764_PLXNA2_MIP60	GCCCGGCTGCCCAAGCTACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACACAAAGCCACCAGG	10
M00764_PLXNA2_MIP79	GAACCTATGCAAAGAGCTGCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGGCTTGAGGCAC	10
M00764_PLXNA2_MIP83	GGATGGGTCCAAGGCACCATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGAGAGATTCTTCCCC	10
M00764_PLXNA2_MIP96	GGTGACTGGAAGCGGCTCAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGACACTGGCTCACA	10
M00764_PTPRD_MIP123	CCTTATACAGGCAGTGTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGCATATATAGTCTGCTT	10
M00764_PTPRD_MIP185	ATTACTATATTGGTAAAACAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGATAATATGAA	10
M00764_PTPRD_MIP215	CCGCACGGATGCTGAGAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAATTTCAGATCGGACA	10
M00764_PTPRD_MIP220	ACACAATAATGGAAGCTGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGACCTAAAAAAGGA	10
M00764_PTPRD_MIP85	CAGTTCGGGTTGCTTTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAAAATAGAAATTTAAG	10
M00764_PTPRM_MIP167	CAGCTATAGTTATTCATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTATGATTGAGGATG	10
M00764_PTPRM_MIP168	CAGCTATAGTTATTCATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTATGACTGAGGATG	10
M00764_PTPRM_MIP176	GTATAATAAAAGGTGATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTGATAAGAGGGTTAATA	10
M00764_PTPRM_MIP184	AGCAGGAAGTTTGAGTTCGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCTACAGGAGACCCA	10
M00764_PTPRM_MIP187	ATTAAATCAGAGTATAAAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAACTCAGACTATAT	10
M00764_PTPRM_MIP218	CCTTTTATTATCTCTTTTAAACTACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAACAAACCAAA	10
M00764_PTPRM_MIP240	GATACCAAGAAAACTTAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAGAAGGAAGCTTGTGG	10
M00764_PTPRM_MIP258	GTTTTAACCGTATGATGGAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTAGGTGCTACGTCG	10
M00764_PTPRM_MIP272	GCTTTTCCCTTGGAAACAATACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATTTCTTTTAATGA	10
M00764_PTPRM_MIP39	AACTGTATGACCACAGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAATATAGGAATCTGA	10
M00764_PTPRM_MIP59	GCTTATATAAGCTTTAAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCTACATAAAGAAAA	10
M00764_PTPRM_MIP71	GTAACAAGTTTTCTGTATTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGTTTATTACTTCAT	10
M00764_PTPRM_MIP97	GTTAATACTAAGCAGATAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTGATATTTTACCCAGG	10
M00764_RASGRP4_MIP1	GGGACTCAGGAATAGGAGATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCTTCACAAACCCC	10
M00764_RASGRP4_MIP20	GGGTACAGTGGCTCATGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGGTTACCCATCCTAGG	10
M00764_RASGRP4_MIP30	ACACCAGACATTCCCTATATCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCACCCCACCCCAT	10
M00764_RASGRP4_MIP40	GTGTCTCCAGGACCAGGATAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCAAGGGCAGCA	10
M00764_RASGRP4_MIP45	GACAGCACCAAGGTGAATCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGTGCATGCTTCTC	10
M00764_RASGRP4_MIP49	CCCAACTTCTCGTACTTCCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCCTGCACCTTCTT	10
M00764_RASGRP4_MIP54	AGTACGAGGCTGCCCGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTAGGACATCAGAGAT	10
M00764_RASGRP4_MIP55	ACACTGGGGTAGGGGAGGGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGTGTCCTTGCTTT	10
M00764_RASGRP4_MIP68	GCAGGCCCAGGTTCATGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGAGGTGGAGAGAAG	10
M00764_RASGRP4_MIP71	CCTCCCCTTGCCCAGGACTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGCAGAGGGAGGCCTCA	10
M00764_RASGRP4_MIP72	GCTGAGCCCTACTCTTGCAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCAGCCTCTTCCTT	10
M00764_RASGRP4_MIP8	TTCCGCCTCCTGGGTTCAAGTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATACATTTAGACTCA	10
M00764_RIMS2_MIP101	ACTATGGTTTGACAAGGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACTAAGTAAAGTTTATA	10
M00764_RIMS2_MIP113	ACTACTTATTTTATTTGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTATCAGTGCCAGAAC	10
M00764_RIMS2_MIP145	GAAAGGTAATAAAAACTATCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCATGCTTATCCCCTTC	10
M00764_RIMS2_MIP161	CAGGAAAGCCACGTCTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCCTCCAGGATTCTC	10
M00764_RIMS2_MIP164	CCCGCGGTACAAGATACGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGTAGCCGGCCAGTG	10
M00764_RIMS2_MIP171	AATTCTATCAATAATATCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTAATGGAAGAAGGAA	10
M00764_RIMS2_MIP18	ACTAAGTTTTATAGATATGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAATACTAACAGCTAA	10
M00764_RIMS2_MIP43	GAATAATTGAAAAGAAGTTACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAGTGTCTAACCAA	10
M00764_RIMS2_MIP51	CATCATGTCTCCAACCCTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAACTGATTTGGCT	10
M00764_RIMS2_MIP53	ACCAACTATTATTCAGCAGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGTGCCTGCAACACT	10
M00764_RIMS2_MIP54	GCTATGCCTTTAAAATGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGGAATATCATATTA	10
M00764_RIMS2_MIP66	ACTTTGTCTGTAGCACTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCAACCAGTTGTAATCC	10
M00764_RIMS2_MIP84	ACTTTAGTAGTTATGAGTTATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGATGACTGAATCAG	10
M00764_SEMA6D_MIP27	CACTAAATGTAAGTGTTTCCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTGGATAGCTGA	10
M00764_SEMA6D_MIP6	CCTTTGGTCTCTGAGCAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCCTCTTTGACACTTC	10
M00764_SEMA6D_MIP79	GGTGAGGAGGAAGGTAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCCCCATCAATTATGGA	10
M00764_SEMA6D_MIP8	GGGTTCGTCCGCTCCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTATCGAGGACTGGAAAC	10
M00764_SEMA6D_MIP9	CCTTCGGCCCCCAAGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGAGGCCGGGCGGCAAGG	10
M00764_SETBP1_MIP100	GCCTGCGGTTTGTGTTTCCTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGACCCGCCCTA	10
M00764_SETBP1_MIP101	CCACGCCCTTCTCTCCAGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCGAGGGAGTGAGAG	10
M00764_SETBP1_MIP103	CAGGAGGAGCAGGCTGGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATCAGGAGCTCTTGG	10
M00764_SETBP1_MIP139	GTCCAAATGCCAGAGCTTACAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCAGAAGCTGAA	10

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M00764_SETBP1_MIP4	AAGAAAAAGCATTGATCGGAGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAAAAGCGCCCTCG	10
M00764_SETBP1_MIP5	GCTAAAATTAGCAGGGCTCGCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAAAAGCAAAAAAA	10
M00764_SKOR1_MIP22	CCCCTCAAAGAGGAAGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCAAAGTGCAAGGACC	10
M00764_SKOR1_MIP32	AATGAGTTTGGACTCCCCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGATTGGGTTCCTTGCAG	10
M00764_SKOR1_MIP34	GCAGCTCCTGCTTGGAGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGTGTTGGAGATCTGC	10
M00764_SKOR1_MIP38	AGAGCTGTTGTAACGCGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACGCCAGGAGTTGAAGT	10
M00764_SKOR1_MIP67	CGGCTCCACTTTCTCACTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTCTTACCTCTGACAAT	10
M00764_SKOR1_MIP72	GCCATGCTGCTCCTTGTAAATACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGCCCACGACGCC	10
M00764_SKOR1_MIP76	ATGTAGCAACTTCGCTGGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCCTCAAATCCCCCTA	10
M00764_SKOR1_MIP8	CCCACAGACTCCTTTGCCTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCCTTTTCCTCCACT	10
M00764_SLC14A2_MIP103	GATTTTTTAAAAATTTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTAGGCAGCAAACAGTGC	10
M00764_SLC14A2_MIP22	ATATATTCTTTCTTTCAATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGTTGCCCTGCATCA	10
M00764_SLC14A2_MIP30	ACCCAGGCTGGAGTACATTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTTTGGCCAATTTCTCCC	10
M00764_SLC14A2_MIP32	CTACTGGGAGGCTGAGACAGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGCCGAGTCGGGT	10
M00764_SLC14A2_MIP63	CACTACCCCAAAGTGCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGGCTTAGGGGGAAG	10
M00764_SLC39A11_MIP104	GATGTGCCTTTCGCTTTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGTAATTGAATCATGGGGG	10
M00764_SLC39A11_MIP139	GTGGGAAGGAAGTCCCCGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAAGAGTGTGGGACTTG	10
M00764_SLC39A11_MIP75	GTCTTTCTGGACTGGCCACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAAATAGGGGGCACT	10
M00764_SLC39A11_MIP79	GTTCTCTTGAGGCCAGCAGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCAGAGGTACTGCT	10
M00764_SLC39A11_MIP93	GGGACTGCCATCTTCACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTTTTTCTTTTTTGAG	10
M00764_SLC39A11_MIP94	GGCTTGAGCCCGGGAAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAATGAGAGAACACACA	10
M00764_STEAP4_MIP1	GTATAAAAATTTCTAAATCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCGTGTGTCAATT	10
M00764_STEAP4_MIP103	CCCAGGAGGCTGAGGCAGGATAATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCGAGGCAGGTGAA	10
M00764_STEAP4_MIP122	GCTCACCTCCAGTCCCTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGAAACTTCCCTCTA	10
M00764_STEAP4_MIP14	GTCTTGGAAGCATCTGTATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACCTCTACAAGCTGA	10
M00764_STEAP4_MIP51	CTTCCTCCAGGTTGTCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAATGCATAATATGCATT	10
M00764_STEAP4_MIP56	GGACTAAAAATACTTCCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATAAATGTGTATTCA	10
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M00764_SUN1_MIP100	GTAAAAATGCAAAAAATTAGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTTCTGGGTTGGG	10
M00764_SUN1_MIP101	GTAAAAATGCAAAAAATTAGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGTTCTGGGTTGTG	10
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M00764_SUN1_MIP118	GCCTCAGCCTCCCAAAGTAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGAAACTGCTCATGA	10
M00764_SUN1_MIP141	GTATTCATCACTGTACAAAGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTAAGAAGTATTT	10
M00764_SUN1_MIP146	GTAGCAAAGTGGTCAGCTCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTCACCATGGAGCCT	10
M00764_SUN1_MIP168	GGCCAGAGGCAGATGTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAACGTGGCTGCCTGGGC	10
M00764_SUN1_MIP206	GTGCTGTGGGGTGAACTCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGGAGGTGGCTGACG	10
M00764_SUN1_MIP213	GTTTAAAAAACAAAAGTAGCGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGGGCCGCAGGAA	10
M00764_SUN1_MIP219	CCTCCCACAGGCCCCCAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTTCAGTCCAGCTCGAT	10
M00764_SUN1_MIP220	GTTTCAGAGGCGAGTCCTGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACCAGCCTCATGGGC	10
M00764_SUN1_MIP224	CCCACTCTTGGGTCCCAGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGTGCTGCCCATCA	10
M00764_SUN1_MIP225	CCCACTCTTGGGTCCCAGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGTGCTGCCCATCA	10
M00764_SUN1_MIP227	CCGGCAAGGAGCGTGATGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCGTCCTGACTGCAGAA	10
M00764_SUN1_MIP230	CCTCCACCGAGCGTGAGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCCCTTTTTAAAGCG	10
M00764_SUN1_MIP235	CACTTTACAGTAAATAAAGCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGGCACAGCCCT	10
M00764_SUN1_MIP35	CCCTGACTTTCAAAAAGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTCCTCACCAAAAAAC	10
M00764_SUN1_MIP4	AGTGCATTTGCGCGATCTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAACCTCAACCTCCCC	10
M00764_SUN1_MIP90	GGAGACTGGACTGCGGAGTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTAACCCCCAGGGGA	10
M00764_SUN1_MIP91	GGAGACTGGACTGCAGAGTAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTAACCCCCAGGGGA	10
M00764_SYT5_MIP10	AGCGAAACTCCGTCTCAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGTACACAGAGAAACC	10
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M00764_SYT5_MIP16	AAAACAAGAGAAAAAGAAAGAAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGAACCCAGGAGGA	10
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M00764_SYT5_MIP34	CGCAACCGAGTCCTGAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTAAGAAAAAGAGACCT	10
M00764_SYT5_MIP40	GAGCCTCGAGGGTTTCTTCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCGTCATCGTCCTG	10
M00764_SYT5_MIP43	AGCTTGGGGACATCTGCTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACAACATCCTGAGCC	10
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M00764_SYT5_MIP85	GTCCAGACCACTCCACTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGGTCTCGGGTAGGC	10
M00764_SYT5_MIP87	CCTCTAAGTTCCCCTAACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTATAGCCCAAAGAACG	10
M00764_TANC1_MIP12	CACAAGGAAAACATTTTGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAGATATTTGGCACAG	10
M00764_TANC1_MIP13	ACAGTGAACTTCTGAGCACTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTGGGATTGGGAA	10
M00764_TANC1_MIP169	GACTGCGTGCTGAGAACACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGCTCTTCAGCACTC	10
M00764t_LRRN1_MIP12	GCTGGGGAAAATGACGAAGTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGGAGGTGTGGGAG	10
M00764t_LRRN1_MIP13	CCCCTCAGGCCCGCGATCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCAACTATCGCTCTCC	10
M00764t_LRRN1_MIP15	GCCCGCCACCTTCCTTGCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGAGTTCGGTAGAT	10
M00764t_LRRN1_MIP19	CAGGTGGCCTGGAATGTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTCAGCCCGTGAGCCT	10
M00764t_LRRN1_MIP2	AAGAGATGGGGCCCCATTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACACACAGCCCGAGGAC	10
M00764t_LRRN1_MIP23	CACTTGAAGCTCACAGGCAAAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCGGCCCGGATGC	10
M00764t_LRRN1_MIP26	GAAAACATTCAAAAAGTAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTGAAGGTTGGTA	10
M00764t_LRRN1_MIP28	GTCATATATGACTGTGTACATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCATTGAAGATAAC	10
M00764t_LRRN1_MIP29	ACATCTGTCCTAATCTAATTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTTAAAAGCTTATT	10
M00764t_LRRN1_MIP64	ATGATACATTATTGCAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCCTTAGAAAAAGAAT	10

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M00764t_NPBWR2_MIP13	GCAGTCTCTGCCAGAGAACCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCAGCTGCTCTCTG	10
M00764t_NPBWR2_MIP18	CCCCTTGCTGACGTGGAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCTCACTGACAGACCT	10
M00764t_NPBWR2_MIP20	GGGCACTGAAGGCATCTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCAGGGTCTCCTCAGC	10
M00764t_OPRL1_MIP11	GTCTGCGGTCCCCGACAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATATCTTTCCTACCCGA	10
M00764t_OPRL1_MIP23	GTGTGTGACTTGTGTCCCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGCAGCAAAGCAGG	10
M00764t_OPRL1_MIP26	AGACAGGGACTCACAGAACACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGCAGGCACATG	10
M00764t_OPRL1_MIP30	ATGGTGACCTTGAGCCCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCCCCTCTGCAGCCG	10
M00764t_OPRL1_MIP31	GTCAATCCTGAGGCCCTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGTCTGGTGAGTCC	10
M00764t_OPRL1_MIP32	GTCAGTCCTGAGGCCCTGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCTGTCTGGTGAGTCC	10
M00764t_OPRL1_MIP37	GTCAGTGGGGTGTCCCCTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCATCCGTGCCCTC	10
M00764t_OPRL1_MIP38	CGACCTGTGCCGAGCCCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTCTGCAGGGAGAGAAA	10
M00764t_OPRL1_MIP42	CAGCAGCCCACGAACACAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTAGAGGATGGGGTTGAG	10
M00764t_OPRL1_MIP43	GTCTGACCGCGTGCGCAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTGCACGGCCCTGG	10
M00764t_OPRL1_MIP44	CAGGGCAGATGCACAGCAGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGACAGGCACCATGG	10
M00764t_OPRL1_MIP49	GCCTTCAGCCCTGTGACGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGACTCTTGGCCTCTCT	10
M00764t_OPRL1_MIP50	GCTGGAGCCCTGCCATGCAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAAGTCCTCCAGGTGG	10
M00764t_OPRL1_MIP52	CCCCCACCTGGACACTTTCTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATGGGGGTTGGGC	10
M00764t_OPRL1_MIP55	AAGCTGTGTGGAAGGAGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCTGGTCTTGACTGCT	10
M00764t_OPRL1_MIP56	CAAGCAAAGGAGAGGCTGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTACACAGAGCCATCT	10
M00764_TOX3_MIP2	ATAACTCATAAAAAAGTATAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGTTTCTTTGTT	10
M00764_TOX3_MIP73	CGAGGCTTCACCTGGGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCAGCTAGGACCTTTTA	10
M00764_TOX3_MIP8	CATTATTTTTTTCATGACAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTTTGATTTGGAGA	10
M00764_TREM1_MIP21	CATCCTGATAATTCAGTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGGAAAAGAATAAAAACA	10
M00764_TUBB3_MIP10	GCCTCCTTCCATCTGGGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGCCATAGTCCTGTC	10
M00764_TUBB3_MIP100	CAGGCAGTCGCAGTTTTCACACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGGGCACGACGC	10
M00764_TUBB3_MIP106	CCTTCATGGACATGCGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGAAGGTGGAGGACATC	10
M00764_TUBB3_MIP110	GCCCTCTTCCTCGGCCGTGGCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGGCTCCGGGGGT	10
M00764_TUBB3_MIP111	GTGTGAGCTGCTCCTGTCTCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGAAGCCAGCAGT	10
M00764_TUBB3_MIP21	CATCTTCAAGAACTTCAACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGGCTTTGGCCTTA	10
M00764_TUBB3_MIP25	GAAAGCTTCATCCACAGCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCACCCCATCTTTG	10
M00764_TUBB3_MIP27	CAAATGCCTGACTCAGTGACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGGTTTGCAGGAGC	10
M00764_TUBB3_MIP32	GGACAGCGTCAAGAGTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGGGATGGTCCCATTC	10
M00764_TUBB3_MIP33	CAGGTGGGGAAGGGGTCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCTCCAGCCATGATGA	10
M00764_TUBB3_MIP38	GAGGCCGGCAGTCAGGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGTTTTGCAGCCTCAG	10
M00764_TUBB3_MIP39	GAACAGGGACAGGGAGGAACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGTCAGCCTTAAGC	10
M00764_TUBB3_MIP45	GGTGCTCTGAGCTTTTGCCGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCTACCCTCTCGG	10
M00764_TUBB3_MIP5	GTGTGAGGGACCCCCTGGGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGAAGGGTGGGGC	10
M00764_TUBB3_MIP65	CCTCAGGAGTGACTTTTAGATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACACGCTCTGATG	10
M00764_TUBB3_MIP69	CTGTGTGACCTTGCACAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTCTCTCCCCCTAGA	10
M00764_TUBB3_MIP79	GCTGGGATAGGGAGGCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCCTGACATCCAGTTAC	10
M00764_TUBB3_MIP8	ACCTCTGGACCGTCCTGGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCCAGTCCAGACAC	10
M00764_TUBB3_MIP91	GTGCTCCTGGACCCCGGAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACACAGACGTGGGAAC	10
M00764_TUBB3_MIP96	ATCAGCCCTCCTGCTCCAGCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCATACCCGCCGTGGCTT	10
M00764_TUBB3_MIP97	GATGTTCAGGCAGGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCAGAGCCCTCGTCCTGA	10
M00764_TUBB3_MIP98	CATGCCTGTTCTGTCTTCTGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCAGTTGTTGCCG	10
M00764_TUBB3_MIP99	GGCTTCCAGCTGACCCACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCTCCCTGTACAGGTCA	10
M00764t_ZNF804B_MIP22	CCTGGGGGCTTTGTATGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCTGTTTATCGGATA	10
M00764_UBL4B_MIP4	CACATTTTCTTTCCTAGTGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCAGGTGCTGGCACA	10
M00764_UNCX_MIP25	GTATGAATTCGGACCCAGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCGGCCGCTCGCTC	10
M00764_UNCX_MIP27	GGTCAAACGCAAGTTTTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCTCCTCCCAAGAGA	10
M00764_UNCX_MIP5	GGTGCAGGGAAACGTTTTCCATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACACATGCTTCGC	10
M00764_VAV3_MIP101	AATAGGAAGAACAATTCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGTGGCTATAACTTTT	10
M00764_VAV3_MIP104	CATGTCACTCATTTCTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGCACAATTAGAAAAATG	10
M00764_VAV3_MIP112	GGATGAGGTAGAAGCCATAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTAACTAGTAAAAATAAA	10
M00764_VAV3_MIP161	CAGGAAGACTGTAAACTATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGGGATTTCCTGAAGC	10
M00764_VAV3_MIP185	ATGCGGCTAATTTCTTTGTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCCAGCTGCTTAAC	10
M00764_VAV3_MIP186	GGTGGGCAGCACCTTGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGGTTGATCTCCTTCA	10
M00764_VAV3_MIP193	CGAGAGAAGACCCCAGGACGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCTCTGGGGAGTCTGG	10
M00764_VAV3_MIP67	ATTCTGTAAAATCTTGTAATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAGAATCGGTTGAA	10
M00764_VAV3_MIP83	GTTTCCAAATAGAAAACATTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTTCTTAGTGTTTT	10
M00764_ARFRP1_MIP60	CAGGGACCCCCCTAGGTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAGACATGAGGTGCAAG	11
M00764_ATP2C1_MIP113	CATCAGATTGCATTAGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTAATCATAGCAGTGTT	11
M00764_BBS7_MIP45	GGATATTACACAATTCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTGACTCCAAGAATTCA	11
M00764_BBS7_MIP56	GTTTATCACCTTTTAAAATGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTCTTCCTTACGGT	11
M00764_BBS7_MIP79	AATGTTAGTAAACTGTATACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATTGAGAAGCCCGAG	11
M00764_BBS7_MIP89	CAACACACCTCAGGAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTATTGTAAAGGAAAA	11
M00764_BTBD9_MIP46	GTGGCTACCAGAAAGTCCCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGAGGGGCCTTCTG	11
M00764_BTBD9_MIP9	ATGACTCCTGTAGTGGCTAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTATCCCCCAGCCTGGG	11
M00764_CACNG8_MIP32	ATGAGAAGAAGCCAGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCATTAATCGATCATGT	11
M00764_CACNG8_MIP45	CCTGAGCAACAGACTGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAAAAAATTAGCCGGG	11
M00764_CACNG8_MIP61	AAGTGCTTTAAAAATTAAGCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTGAGTGCCAACCTGT	11
M00764_CADM1_MIP67	ACATTTTCTGAATCACAGTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAGCGTAGGGTATC	11

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M00764_CCDC148_MIP13	ATAGAACACTTTATGCTAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAACATGGAACTAAATG	11
M00764_COL20A1_MIP103	GACACCTGGGCTCCAGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGAACAGGAACAGGC	11
M00764_COL20A1_MIP169	AAGAGCCTGCAGGTGGAAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTACATCTGTCCTCCCTTCTC	11
M00764_COL6A6_MIP8	GAGTATGCAGATGTTGTGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGGTTTATTGGGAAGGT	11
M00764_COLEC11_MIP12	CAATCTGCTGGCCTTGGCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGATGCTCCCACTTC	11
M00764_COLEC11_MIP14	ATCTTCGGCAAGTGAAGCTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGAGCCACTGTGACTT	11
M00764_COLEC11_MIP37	GTTGGGAGGGTCCTTCCCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATGTGGTGGGTGCCT	11
M00764_CREB5_MIP208	GGAATTTAAAAAACAACAACTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGGAAAGAATTTTGA	11
M00764_CREB5_MIP28	GTCAGAGAAGGAGGGAAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGCAGAGTTGCTTT	11
M00764_DMPK_MIP47	AATACAAAATTTAGCCAGGCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGGGTTGGGCAAG	11
M00764_DMPK_MIP60	GCTGGGTGTATTCGCCTATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTCCTTTTGGTCCAGG	11
M00764_EYA2_MIP97	GAGGGTGGATCACTTGAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACACTCTTCACCCAGATA	11
M00764_GALNT12_MIP77	GGCCAAAGAGCTCAAGACCAGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTAGAATCCAAGAA	11
M00764_GLO1_MIP27	GATATATGTAGATTTGTGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTAGGACATTGTAGC	11
M00764_LAMA1_MIP130	CAGATGAAGATGTTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTGGGAGGTGGAGGTTGCAG	11
M00764_LEO1_MIP50	GCGACAGAGTGAGACTTTGTCTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGCCAGGCATGGTT	11
M00764_MAP2K5_MIP90	AGTGACTGAATTATAATTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGAATATGAAGCATTC	11
M00764_MDGA1_MIP221	ACAGGAGAGCGAGCGACAACGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCTTCCCCCAGCCCT	11
M00764_MEIS1_MIP228	GTCTAATTCATTTACTCACCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATTAAAATAACTAT	11
M00764_MEIS1_MIP54	CAGTGCTAAGAGAGGGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATCTATTTTGCTGACCT	11
M00764_MEIS2_MIP183	GTTATTTCCTCTGTTTGCCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCGAGGAGCAGGATG	11
M00764_MEIS2_MIP231	CAAAGCTAAAAAAGGGGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATACCTACCAGGAAAGGGG	11
M00764_MICALL2_MIP146	ATAAAAACATGATGTCCAAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCCTCGGACGTGG	11
M00764_MICALL2_MIP155	CATGTAACCTCAGTGGGCTTGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCCGGGGACCTCAC	11
M00764_MICALL2_MIP157	CCCAAGGTGCCCATCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCATGATTTAACCAACCC	11
M00764_MICALL2_MIP173	GGGTGCTCTGATCTGCCTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAGCCCAGTTGAATAG	11
M00764_MICALL2_MIP203	CAGAATGGCAGGACCCCCAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGGTGTTCGAGCCT	11
M00764_MICALL2_MIP22	GACTTTGGCCGGGCACGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGCCGACCCAGAATGC	11
M00764_MICALL2_MIP71	CATCACACACATGCACACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATACATGAACAGACACA	11
M00764_MICALL2_MIP72	CATCACACACATGCACTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATACATGAACAGACACA	11
M00764_MICALL2_MIP8	GTGTTTGCCTCGGTGCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATTCGGACTTGGACTC	11
M00764_MICALL2_MIP97	GGCTGATGATGAAACCGCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTGCCGGCAAACA	11
M00764_MPPED2_MIP17	CAACTCATCTTCTATTGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTGTGAATTTTCCAAACT	11
M00764_NENF_MIP4	GCCTCAGCCACCAGAGTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGACATTTTATTTTATTTT	11
M00764_NRG3_MIP134	CCCTTAAAAAAATATTTTGTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGGGTCTGAATTG	11
M00764_NRG3_MIP145	GCTAAGGTGAACTGAAACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGTTAGTATGGGAAG	11
M00764_NRSN2_MIP8	CAGGGCAGAACTGGGGCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACTTTCCCAAGATCACAC	11
M00764_OLFML2B_MIP54	GCCCTTCTTGCCCTGGATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGTCCTCACAGGGACAA	11
M00764_PDE11A_MIP223	GGACTCTGGCCAGGTGGCTGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAATCAGCAGTGGGAC	11
M00764_PTPRD_MIP71	ATTTCTCTATTAACTTTGCTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGCTCCACAGTA	11
M00764_SEMA6D_MIP72	GGAGGGCCTCCAAGTCCACTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGCCCGGCAGAGAA	11
M00764_SKOR1_MIP37	CAAGTGCATCAAGTGCGGCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGCAAGTCGTTCCTGG	11
M00764_SLC39A11_MIP92	AGGGTCTTACTCTGTCACCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCATTCTCACTCTTGT	11
M00764_STEAP4_MIP47	GCACTTTGGGAGGCCAAGTCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAAAGAGTATAAG	11
M00764_SUN1_MIP177	GAGGAGTGAATTACAAATGCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACGACCAAGGAC	11
M00764_SUN1_MIP207	GTCCCACATTCCCCACAGAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCAGGGCTCTGGACAC	11
M00764_SUN1_MIP218	GTGTGGGGTCATCATCTCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGCCTTGCAGTACCT	11
M00764_SYT5_MIP80	CCAGGCGATAGGGAAGAGAGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCAGCAGCCTGA	11
M00764t_NPBWR2_MIP19	CAGCATCAGCACTGACACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGCCTGGGTAAGTGAA	11
M00764t_OPRL1_MIP24	CAGACACACAGAAATGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGAGACTCACACACAGG	11
M00764_TOX3_MIP71	CGGGGACAGGCACCCATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAATCCTACAGGTGAAC	11
M00764_TUBB3_MIP26	GGTCACAAAGCCCCTTCTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCGGCCCTCAGGAG	11
M00764_TUBB3_MIP28	CGACTGCTGCAGGAAAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACTTCAAGCACTTTCTG	11
M00764_ZNF175_MIP60	ATGCTCAACCAATAAATATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAATATACGTACATAC	11
M00764_PDE11A_MIP44	GCGACCAGCGAGACTCCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACAAATTAGCCAGGCGCGG	12
M00764_STEAP4_MIP46	AAATATAAAAAATTAGCCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGACTGGCCGGGCGC	12
M00764_CACNG8_MIP43	GTGGAGCACACCTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCATGCCTGTAATCCCAGCGCT	17.39
M00764_CACNG8_MIP44	GTGGAGCACACCTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCATGCCTGTAATCCCAGCACT	17.39
M00764_CACNG8_MIP65	GAGGCTGAGAAAGAAGGATCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCTGGTGGATCACTT	17.39
M00764_CACNG8_MIP82	AGAGGCTGAAGCAGGAGAATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGTGGGTGGATCACTT	17.39
M00764_LAMA1_MIP92	GCATGGTAGCATGCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAGTGGCTTATGCCTGTAATC	17.39
M00764_LEO1_MIP49	CGGGAGGCAGAAGTTGCAGTGAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGACCAGCCTGACA	17.39
M00764_MICALL2_MIP31	CTCCGTCTGCCGAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCGAGTAGCTGGGATTACAG	17.39
M00764_AAGAB_IQCH_MIP4	CCAGCTGGTCTCCTGAGAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGACTGGAGGAAGAAC	20
M00764_AAGAB_IQCH_MIP6	GAACAGGCCAGGTCGCGCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAGCCGCTTCCGCC	20
M00764_AAGAB_MIP30	AATATATCTTAAGAAATTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATATATAATTATAATAA	20
M00764_AAGAB_MIP40	ATCTAAAATTACAGCTATTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTACTGTACAACAAA	20
M00764_AAGAB_MIP77	AAAATTATGTATAATTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTCCTACTTTATCTTTA	20
M00764_ADAM22_MIP10	GCTCTGTGTCCTGGGGACCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCCCGGGGGCGCGGA	20
M00764_ADAM22_MIP106	AAAAAAAATCAAAGAAATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTAGTATGTTCTTCTTA	20
M00764_ADAM22_MIP118	AGAACATGAAAGTCTTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAATATTGATAAATTGTT	20
M00764_ADAM22_MIP149	ATATTTATATTAGCATACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATAGAAATGAGCATGC	20
M00764_ADAM22_MIP151	GGTAATGTAAATATAGTGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTATATGTAACATTTTTAA	20

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M00764_ADAM22_MIP166	ACTAGGAAGCATATTTACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCATTTGAAATAATAAT	20
M00764_ADAM22_MIP179	CATATCTACATAATTTAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAACATTAATAGGATTT	20
M00764_ADAM22_MIP18	ATCCCATGTCTTCTTGGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACGACGCGCTCGACACG	20
M00764_ADAM22_MIP182	AACAAACCTTATTTTAAAACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAATAATCTTTTCTTT	20
M00764_ADAM22_MIP19	GTAATGCAGTACCTATAACACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAATTTGATTATTTTTCA	20
M00764_ADAM22_MIP204	CAAGTTAAAAAAGGAGTACATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACCGTGGAAAACACT	20
M00764_ADAM22_MIP23	AATATAAAATTATAATTACAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTCCTGGACACTTT	20
M00764_ADAM22_MIP24	AAATATAAAATTATAATTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCTGGTCCTGGACACTT	20
M00764_ADAM22_MIP27	AGAATCTTTTAATACTACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTCATCATTTATTTTTGT	20
M00764_ADAM22_MIP55	GTTTAATTTTTCAAGATATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTACATAACACAATTAG	20
M00764_ADAM22_MIP56	ATAATAAAATAACTCAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTAACATTTAAAAGACA	20
M00764_ADAM22_MIP57	CATGCATATTTGACGTAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAATTATATTCTTTAAAGT	20
M00764_ADAM22_MIP59	ATACTACAAGGAAATTGCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATATATAGTAGAATTT	20
M00764_ADAM22_MIP7	GCAGGAGAGTCAGCTGGGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGGCTGTAGCTAAGTG	20
M00764_ADAM22_MIP72	GTACATGTGTGGTTAGTTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATATATTTTATTTTTGTTT	20
M00764_ADAM22_MIP9	CGGACGCTTCCGCTGGCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGCCGAGTCCGTTTCC	20
M00764_ALLC_MIP42	GAAGTTAAAAATAACTATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCATAGTTAAAATCAT	20
M00764_ARFRP1_MIP100	CCTTCCGAGCCGCCGTGGGCTCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCCACAGCCTGAGG	20
M00764_ARFRP1_MIP101	GGACGAGGAGAGCCTGGAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTCCCCGAGGGAAAGG	20
M00764_ARFRP1_MIP11	GGCTGTGGGCAGGAGCGGCCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGAGAACCTCCCG	20
M00764_ARFRP1_MIP14	AAGGCAAGATCAGCCCCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAGGGTGAGGTGAAGCC	20
M00764_ARFRP1_MIP15	GGAAGACCCAGGCCATGTTCCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGACCCCGTGGCT	20
M00764_ARFRP1_MIP16	CAATTCCCAACCAGGTCTCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCAGAAGCCAGATGGC	20
M00764_ARFRP1_MIP17	GCTCAGGCTGGCTTGGGCTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGAGTCTGGCAGC	20
M00764_ARFRP1_MIP18	AGAACCCCAAAGCAAAGCAAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGGAAAGGCTGCC	20
M00764_ARFRP1_MIP19	GTTTTCTCGAAGACAAACTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGTAGGCGCAGCCGCGC	20
M00764_ARFRP1_MIP2	GATCAGTGGGGAGTGCCACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTTGCACAGCTACTGG	20
M00764_ARFRP1_MIP20	CACTTCACCATCCACTCGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATCAGCAGCATGGGAG	20
M00764_ARFRP1_MIP21	GTCGTGCGGAATGTGCACCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCTCGGCCCTCACAG	20
M00764_ARFRP1_MIP22	GTCTTGATGTCAGGGATTGAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGAGGCGGGGGGT	20
M00764_ARFRP1_MIP23	GACTGCACCAGCAAGATCGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGGGCATACGCCCTT	20
M00764_ARFRP1_MIP26	GTCATGGTGGCTTCTGCTCACAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCCCCGAGGTGGG	20
M00764_ARFRP1_MIP28	AGAAGGCAGGAAGTGAAGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAAGCAGCCCTCCC	20
M00764_ARFRP1_MIP30	ATGCCACCTCCAAGGGTAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGACGCCGGGCTGCTTCT	20
M00764_ARFRP1_MIP31	CAAGACCCCTCTGAGGTGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACCCAGGTGAAACTCA	20
M00764_ARFRP1_MIP33	GCCCAGAGGCCTCTTCCTGCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGTGACTGCCCAG	20
M00764_ARFRP1_MIP34	AGGCTGGGGACTCGGGAAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTCTGGAGAGGAACCA	20
M00764_ARFRP1_MIP35	GGTGTGCACCCAGACACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGACCAGCGAGGCGCTGT	20
M00764_ARFRP1_MIP36	CAGGGGCCCACAGGCGTGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCTCCACATCCTGCT	20
M00764_ARFRP1_MIP37	GGTGGAGTCAATGACGTAGATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTGAGCCTGCCCC	20
M00764_ARFRP1_MIP4	CCTGCCAAAGACCTCCTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGGGAGGGTATCATT	20
M00764_ARFRP1_MIP51	ACTTCTCTGGCCTACAGACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACAGTGGAAAGGAGG	20
M00764_ARFRP1_MIP55	AGGAGGGGGAAGAGGGAGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAAGGTGCACAGCCC	20
M00764_ARFRP1_MIP6	ACACAGGGTCCCCTGGAGAGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTCTGAAGCCTCC	20
M00764_ARFRP1_MIP7	GTTCTGCAGGTTGGTTCCCAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTCCTGGGAGGAGC	20
M00764_ARFRP1_MIP8	CCACCTGGGGAGCCCCTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACTCCTGTGAGTCACAGCC	20
M00764_ARFRP1_MIP88	GACCTATGTTGGGGTGCCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGAGAGGGACGA	20
M00764_ARFRP1_MIP90	ATTGCTGTGAGCAGGACACAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGCGTGGGAGCG	20
M00764_ARFRP1_MIP91	CGGCGCGCTCCCCAGGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCGCCCTCCCCCGAGGCT	20
M00764_ARFRP1_MIP92	GGCTCGCTGCTCCCGGGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGGAGCAGCCGCGCCG	20
M00764_ARFRP1_MIP93	CCGCCAGGTCTGAGGCTCCCCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGCGGGTGAGCA	20
M00764_ARFRP1_MIP94	GGCGGCTTGGGGCGGACGTAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGCAGGTAGGCCGC	20
M00764_ARFRP1_MIP95	GGCCGGCCTCAGGGAATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGGGCCTCGCGCCTCAC	20
M00764_ARFRP1_MIP96	GCGTCCCGTCAGGCGCCGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCAGCAGCCGATCGGC	20
M00764_ARFRP1_MIP97	GGACCAGGTGGCCGCGGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGGCGCTCGGGAGGAAG	20
M00764_ARFRP1_MIP98	CGGCCGGGCACCTCCTCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGCCGCCTCACCCTCC	20
M00764_ARFRP1_MIP99	CCTGAGCGGGGGTACCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGGCGGCGGGCGCGGCGG	20
M00764_ASTN2_MIP159	AACAATCTCCGAGGGCTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCATCTGTGGACAATC	20
M00764_ASTN2_MIP162	ATCCCAAGGAACCCCGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCGCCGAGTCGCGCCTC	20
M00764_ASTN2_MIP163	GCCGATGTCGCTCTCCCGCAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACGCACAAAGAGCA	20
M00764_ASTN2_MIP164	GAGCGGCGCCCGCGCCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCTGCTGCCGCCGCCGC	20
M00764_ASTN2_MIP165	GCTGAGCCGGGCGCCGGCGGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCGCCGGCCAGCA	20
M00764_ASTN2_MIP166	CGGCCCCGGCTCGGGGCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTTCGCTTCGGCGTCCG	20
M00764_ASTN2_MIP167	GCCGCCTCCCGGGGCCCAGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCAGCTGCGGAGACG	20
M00764_ASTN2_MIP168	GGGGCGGTCCAGGGCCGATCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGATCTTGGGAAAGGGG	20
M00764_ASTN2_MIP169	CCCCCCTGACTCAACCCAGTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCCCAGTGGCTCCC	20
M00764_ASTN2_MIP170	CCCGAGGGGGCCCTAAGTATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTATCCCCAAGAAGGC	20
M00764_ASTN2_MIP52	ATTTTATCTAACAGGCATTTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAACATGATAAAACT	20
M00764_ASTN2_MIP59	GACATTTATTTGTATTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTGTTTATGACATTCC	20
M00764_ASTN2_MIP65	CGAGCTAACTATCCTAAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATCATATTAACAAATT	20
M00764_ASTN2_MIP92	CAGTTTTCCGTCTCCTTGGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCACTGAGCCCCGC	20
M00764_ASTN2_MIP93	CGGAGCCGCGGGCGGTCAGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGCATGCTGGGGA	20
M00764_ASTN2_MIP94	CCCTCTGCGCACGCGCCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCCCGCCTGGCCGCTGAG	20

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ID	**MIP**	***c***
M00764_ASTN2_MIP95	GGACTAGGGTGGGGGTGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGGTTGGGGACTGG	20
M00764_ASTN2_MIP96	GGTCCCCACACCCTGCCATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAATCTCTTCAGAGCCC	20
M00764_ASTN2_MIP98	GCCCCGACATTACCTCATACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCCAGATTTCCTCAA	20
M00764_ATP2C1_MIP100	CCTGAAAGATAATTAAATAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTATGTCCATTAGAGAA	20
M00764_ATP2C1_MIP104	GAAATTGATTATTCAATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTCTTTTTGTTCTCTGA	20
M00764_ATP2C1_MIP116	CATCTTCCTTTCTTTCACCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTTCTTTTTGAAAGACA	20
M00764_ATP2C1_MIP122	AATAATTCCTAGGGTGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAGAAAACTAAAGAATAA	20
M00764_ATP2C1_MIP134	ATCTTTTCAATCTTTTATATTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCAAAGAGAATGT	20
M00764_ATP2C1_MIP137	ACTTGTTATTTTTTAATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAAAAGTTGGTAATGG	20
M00764_ATP2C1_MIP154	ACAATTATTAATCTAAAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTACCCAAAAACTATAATGAG	20
M00764_ATP2C1_MIP159	ATTTCAGTATTACTGGTTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAAACAATACTCTAA	20
M00764_ATP2C1_MIP167	AACTAAACATAAATAAGTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACTTTTCATTTCCCAAAT	20
M00764_ATP2C1_MIP172	CCTGTTGAAAGTAGCTGCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAATGGAAAGATGAAG	20
M00764_ATP2C1_MIP2	ATTAATGTAAAGTATCTGGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTACATTCATAGTTTT	20
M00764_ATP2C1_MIP200	GTTAAAATACTCTTAGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTATCTTTTTCCAAAAGT	20
M00764_ATP2C1_MIP21	CCTCACGGTCTCCCTCTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTCCAATAATAACCCTAC	20
M00764_ATP2C1_MIP223	GTATGTTTTTAATCATATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATTATATTAACATGT	20
M00764_ATP2C1_MIP224	ACAGTAAAAATAATAAAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGAGCAAGACCAGCAA	20
M00764_ATP2C1_MIP244	GTAATTCTAGTAAAGTAAAGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAACAAAGTAATTGTT	20
M00764_ATP2C1_MIP254	ATTCAGATTATTGTGATGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGACTATATTACCATTAAC	20
M00764_ATP2C1_MIP31	ACTTTCTGTATTGTGATATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTAGCAATAAAGTAT	20
M00764_ATP2C1_MIP35	AGTCATGGCCGCTGTCCCCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCTTACCCCAGGGA	20
M00764_ATP2C1_MIP38	GCAGACCAGCACGGCCTCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGCCTGCGCGCACCTC	20
M00764_ATP2C1_MIP39	CCCGCCTCCGACTCCTGCGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGTGAGAAGAAGCGA	20
M00764_ATP2C1_MIP40	CGGCTGAGACCCCGCAGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCTCTCTCCCTCCCTT	20
M00764_ATP2C1_MIP41	GGAGAAGAGGAGCTGCTCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTCAGAACCTGGAAGTTT	20
M00764_ATP2C1_MIP42	ACGACGGGGCGGGTGCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTATTACCTCCTGCCCCC	20
M00764_ATP2C1_MIP43	CATCCAGGGGATACCCGAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGAAGGAGTTCCCC	20
M00764_ATP2C1_MIP60	GAAAGCATAACAGTACATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATTGTATTTTATGTGA	20
M00764_ATP2C1_MIP61	GAAAGCATAACAATACATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATTGTATTTTATGTGA	20
M00764_ATP2C1_MIP65	ACATAATATAATGTATTATCACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCCATGAAAGGCT	20
M00764_ATP2C1_MIP67	AGTTTATTTTATGTATCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGATTTTTAAACTGAAAG	20
M00764_ATP2C1_MIP89	GCTCTCAATAGTATATAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTATAAACAATGAGTAA	20
M00764_ATP2C1_MIP91	CAAATATACTAATTACTAATCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACTCATCTTTAATAC	20
M00764_ATP2C1_MIP96	GCTAAGTGCTTGACAAAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTAAAAGGAAAGTTGTTTT	20
M00764_BBS7_MIP105	GGCGCTGCTTAGCCCCTCCGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCGCCCCGCCTGTGC	20
M00764_BBS7_MIP13	GTCAAATCATATAAGAAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGGAAAATTAAAATATA	20
M00764_BBS7_MIP14	AAGACTCTTTTAGTTTTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCTTGTAATACATTTGA	20
M00764_BBS7_MIP17	ATGAAAAAATGTTAAAAGAGAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGTAAAAACTAAAG	20
M00764_BBS7_MIP19	CACTGATCTTTTCATAGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATGTTAAATCATGGA	20
M00764_BBS7_MIP20	CACTGATCTTTTCATAGACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTATGTTAAATCATGGA	20
M00764_BBS7_MIP22	GTTCATATATATAGATTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTTTGCCTTAAAAATTT	20
M00764_BBS7_MIP32	CATTAATATAAAGCAAATTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTATAAAATTAATAT	20
M00764_BBS7_MIP35	CATTTTATATATGTCTATATATGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAGCAGATGTCAC	20
M00764_BBS7_MIP50	ATTTCTATTATGCCATTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTAATATTGACTATAG	20
M00764_BBS7_MIP51	ATCTTTAAATTTGAGAGTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATCAAGTAAATCTATTG	20
M00764_BBS7_MIP60	CAGATATATTAAAATAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAATATGTGGACACCACG	20
M00764_BBS7_MIP62	AATTTTATTAAGTGAAAATATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATGGTGGAAGTGT	20
M00764_BBS7_MIP63	GTTATTAAGAAGACTAATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTGCATTATCAAAACT	20
M00764_BBS7_MIP67	AGATTACTACATCCAAACCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACAACATTTTAATTTT	20
M00764_BBS7_MIP7	GATATGCTATTATACTTATTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTAATTCATATTTATTA	20
M00764_BBS7_MIP81	ATTTTTTGATGTATTAATTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTACATTTTATTATTC	20
M00764_BBS7_MIP87	GGAAAATAAAATTAACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTGAAACAAACCTCACTG	20
M00764_BBS7_MIP91	AATTATTTCTATATAGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAACTGTACTTTGAATTA	20
M00764_BTBD9_MIP110	ATTATATCTTTTCCTATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCATTTATACTCTCAAAG	20
M00764_BTBD9_MIP13	CCACTGGCTTTCAAAGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATATCAACGTCTCCAGTGAC	20
M00764_BTBD9_MIP134	GCGGGGACGCGCGCCCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGTGGCGCAGAGAGGG	20
M00764_BTBD9_MIP135	GTCCGCTTTCACGCACTCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGCTCCTCTGAGACCAA	20
M00764_BTBD9_MIP136	CGCGCCGCAGCAGCCGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCGGAAGCTGCCTTAGGCG	20
M00764_BTBD9_MIP15	CCCAGACATTTATCATAAATTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTCTGTCAACCAG	20
M00764_BTBD9_MIP31	AATAAAACACTTTTAATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGCGACAGCATAATAC	20
M00764_BTBD9_MIP32	AATAAAACACTTTTAATGTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGCGACAGCATAATAC	20
M00764_BTBD9_MIP8	GTGACCTTCAGAGAGGCTGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCTGCCAGTAAGGTC	20
M00764_C15orf61_MIP12	GTAGAGTCCCGCGGGAGTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAACCGCTTCTTCACGG	20
M00764_C15orf61_MIP13	GGCCTGCGAGCGTTCGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCGCCCGCAGCAGGCGAAC	20
M00764_C15orf61_MIP14	GTTAACCAGAGTAGACCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGGGTCCTTTGTACTC	20
M00764_C15orf61_MIP21	ATACTTTTTTCTTTCTACAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCTCAATAAAGAAG	20
M00764_C15orf61_MIP22	GCAAAAGTTTTATTTTAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCTTCATGTGTTTGTAGT	20
M00764_C15orf61_MIP24	GATTTAAATTGTTAATTAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGGATTTGCCAATGA	20
M00764_C15orf61_MIP27	GTAACTGTTTATAAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTAATAATAACTGGTTAAT	20
M00764_C15orf61_MIP29	ATGGTAAATTTCAGACATTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTGGGCTGAAATTT	20
M00764_C15orf61_MIP31	GTAGCAAAACATTTTATAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAGAACTATTTAATT	20
M00764_C15orf61_MIP7	GCGCGAGGCGGAGGGTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGCGAGCGCCGGGAAGGC	20

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M00764_C15orf61_MIP8	GTCGCGCTCCGCCTGCTGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCACCCGCGCGGCGCC	20
M00764_C15orf61_MIP9	CGTGGGCCCTCCTCAGGGCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAGGAGGTCCAGTGC	20
M00764_C7orf62_MIP15	GTTAATAATGTTCCTTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAATGGTATTTTATG	20
M00764_C7orf62_MIP22	GTTAGTGTCTAAGTAGAACAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGACACAATTTTAAG	20
M00764_C7orf62_MIP23	GTTTATTCAATTTTTAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGATTTGGCTTACTTAAC	20
M00764_CACNG8_MIP10	GATCAATCATTTCCCGGAGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAGAAGGGGTTTGG	20
M00764_CACNG8_MIP13	CCGGCTGTGTTCTGGTTTATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTACAACTCCTGCGGGGG	20
M00764_CACNG8_MIP15	CGAGCAGCAGCAGGATGGCGCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCAGGTGGGCCGCC	20
M00764_CACNG8_MIP16	CATCGGCGTGATCGTGTACATCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCCTGGGGGTGG	20
M00764_CACNG8_MIP17	GGTCAGACGGGAGCCTCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGAAGTAGAAGGACCAG	20
M00764_CACNG8_MIP18	GGACCTGCTCAAGGCCGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAACCACTACTCGTACG	20
M00764_CACNG8_MIP19	GATGTAGATGTTGACGGCCAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTAGCGGAAGCGGT	20
M00764_CACNG8_MIP2	CCCACCATCCCACTAACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTGTCTTCTGCCCAAGA	20
M00764_CACNG8_MIP20	GACATCTCCATGTACACGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCCGTCTGCCCAG	20
M00764_CACNG8_MIP21	GTGGAGGCAAAGCCCGGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCCGGCGCCCCCGGC	20
M00764_CACNG8_MIP22	GGCGGCGGCGTCACGGTCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGCGTTCGGCGGCGC	20
M00764_CACNG8_MIP23	GCCTCCTTGGGGAAGGCGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGAGCGTGTTGGTGTT	20
M00764_CACNG8_MIP24	GTCGGGGGCGCCCCCGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAAGGAGGCCGCCGCCT	20
M00764_CACNG8_MIP25	GGCAGCCTCGATGCACGCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCCTCCCCTGCCCC	20
M00764_CACNG8_MIP26	CAGTTTCGAGATGTTTTCTTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCCCCTCCGAA	20
M00764_CACNG8_MIP27	ACACCATGGCCCTCCCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGTATTCGTGTATTATGG	20
M00764_CACNG8_MIP4	GGGGCTCCACTGCTTCTCTTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGGCGGCTGGTGGA	20
M00764_CACNG8_MIP5	CGCTTCTGCCTGCGCTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCCTCTAATGCGAGAT	20
M00764_CACNG8_MIP55	GAGACAGCAAATATTTGCTGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGCTGAGGTGAAAGG	20
M00764_CACNG8_MIP6	GGGGCCCGGGGCCGGCGGGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTTCCAGCGCTTC	20
M00764_CACNG8_MIP7	ACTGACTACTGGCTCTACACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGTCAAACTGGAGTC	20
M00764_CACNG8_MIP71	GAGAATCACTTGAACTTGGGAGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCCAGGAATTTCA	20
M00764_CACNG8_MIP77	ACGGCCTCTCTTTCCCCCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCTCCCCCAGATGTAGA	20
M00764_CACNG8_MIP8	GATGGCGATGGTCATGAGGCCGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCCGCCGGGGTCCT	20
M00764_CACNG8_MIP9	GCCTCCCGGGGCTGCCTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGCGGCGCCTCGGAGAAG	20
M00764_CADM1_MIP133	GTAAACATTAAAAAGAAAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGCATGTTAATAAAT	20
M00764_CADM1_MIP14	GGGTGGTGGGGGGGGACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGAAACAAAGTTTCCTGT	20
M00764_CADM1_MIP161	GGGCTTAACTGGGTTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAAGAAAAACTACCG	20
M00764_CADM1_MIP168	CATAAATCAAGATAGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGATTAGGTTACTGAGA	20
M00764_CADM1_MIP189	GAAGGCACCCCAGTAGCCTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTGCGGCGGCAGCGGC	20
M00764_CADM1_MIP190	CTAATGAGATGCTAATGACATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCCCGGGAGGCGCCG	20
M00764_CADM1_MIP191	GCCAACGCCGCCAGTCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGTGGGGGAGGGAGCGA	20
M00764_CADM1_MIP192	CGTATGCAAATATGTTTATGTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCAATCACAGCGC	20
M00764_CADM1_MIP193	GCGCGGGCGCGCCGCCGAACGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAGCCCGAGTCCTT	20
M00764_CADM1_MIP44	ACTTTGTAACATTAATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGTCCTAGCATCTACT	20
M00764_CADM1_MIP52	AATTCATAGAAAAAGGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTTTTTCTAAAAAGA	20
M00764_CADM1_MIP53	AATTCATTGAAAAAGGGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTTTTTTCTAAAAAGA	20
M00764_CADM1_MIP88	CATTGTCTTTTTTTTTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATTTTAATTTAGGAATGT	20
M00764_CALML4_MIP11	CCCCAGGCACCTCATGGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGCTTTTCACACCTCT	20
M00764_CALML4_MIP32	CCTTCCTCTCTCCACCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGAGGACTTTAAGGGTG	20
M00764_CALML4_PIAS1_MIP8	AATCTAAGCTTTGTATTTAATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAATCACAGATT	20
M00764_CCDC148_MIP10	GTAATTATTATTATCCATATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTACTATTAAATATAACTTA	20
M00764_CCDC148_MIP5	ATTATCTATTAAATATTTAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAGAAATTAGAAATAG	20
M00764_CCDC148_MIP57	CCATAATGTAATATTTCATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAAATCCTATTCAGCAG	20
M00764_CCDC148_MIP72	GCAAAGCTAAAGGTTAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTATTTTTATGACTAAT	20
M00764_CCDC148_MIP74	GACTTCCAATAACATGATATTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTATAATAATTTCTA	20
M00764_CCDC148_MIP9	GTTATCCTATAAAAAGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTTTATGCACTATATTTC	20
M00764_CCDC148_PKP4_MIP10	GCGGCACCCGAAAAAATTAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGCCGAGGGTCTC	20
M00764_CCDC148_PKP4_MIP11	GCTTTCCTGCCCCGCCTCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCGCGGAGACTCCTGC	20
M00764_CCDC148_PKP4_MIP12	GGGGACGCGGCAGCGGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGAGAGGAATCGCCGGG	20
M00764_CCDC148_PKP4_MIP13	GAGCCCTGCTGGACGCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGTTTCACCCTCCATTT	20
M00764_CCDC148_PKP4_MIP14	GCGCGGCGCTCAAGTTCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGCTAGAAGGACAGA	20
M00764_CCDC148_PKP4_MIP15	GTCCCCGAAGTCCTGTACTCCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGACACCACTGGGCG	20
M00764_CCDC148_PKP4_MIP16	AACGCAAGACCGCGCGGGCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCAGCGGCGAGGCT	20
M00764_CCDC148_PKP4_MIP17	GCTGCCGAGGCTGCCGGCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGCTCCACCCCTCCCGGC	20
M00764_CCDC148_PKP4_MIP18	GCTCCGCTTCAACTCCTGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTGTCGCACTCAGCCAA	20
M00764_CCDC148_PKP4_MIP19	GGTGTGTGTGTACAGCGGGGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCGCTACCCGGAGA	20
M00764_CCDC148_PKP4_MIP20	GACTACCGCTGCGCCCCGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGGAAGGCGCTAGGGC	20
M00764_CCDC148_PKP4_MIP6	CAGGTCGCCATAGAGACCGATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCGGGAACGTCAG	20
M00764_CCDC148_PKP4_MIP7	GCGTCGACGCCGGCCGCGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGCTGGCCCGGGGACG	20
M00764_CCDC148_PKP4_MIP8	ACTCAGCCCCGGAGCCCCCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCCCTCCCTCCCCC	20
M00764_CCDC148_PKP4_MIP9	CCGCTGCCTAAGCTGGAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCGGGGGCGGGGGCCGG	20
M00764_CNTN4_MIP12	GCCTGCTCTTAGGGAAGGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAGGAACAGGAGCCCG	20
M00764_CNTN4_MIP132	AATTAATTTAGCAATACAGTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTATAAGAGATACAATG	20
M00764_CNTN4_MIP138	ATACTGTATACACTGTTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAAATATTTTTTATATT	20
M00764_CNTN4_MIP14	ACTCACTCTCCTTCTGGAACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCATTCGTTTCCAG	20
M00764_CNTN4_MIP19	GTTTAATAGAAAATATATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGAAAAATCTACAATT	20
M00764_CNTN4_MIP2	GATCGTTAAGGCGCCCTGGCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTTCAGCGGCCAGG	20

continued table…

ID	**MIP**	***c***
M00764_CNTN4_MIP27	ATATTTTTCCCTGAAGAACTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTTGTTAGGTATA	20
M00764_CNTN4_MIP4	CAGGCAAGAGGAGATTATCAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCGCATGCTCAGTGC	20
M00764_CNTN4_MIP5	CCCGCGGCTAAGGAGCCGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGCCTCCTCCGGCCG	20
M00764_CNTN4_MIP6	CGGGGGAGACGCTCGGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTACTTGCAGCCAATCCTGG	20
M00764_CNTN4_MIP7	GAGGCGGCAGCTGTGCGGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGAGCCCGGGGTTCGAC	20
M00764_CNTN4_MIP8	CGCGGGTGTGGGGGGGAAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCCTCGGACTGTGCC	20
M00764_CNTN4_MIP93	ATTATTTTATTATATAGACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCACAGGTCCAAAATGT	20
M00764_COL20A1_MIP1	CGTGCTGTGACGTAAGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAACCAGAGCTTCAGCA	20
M00764_COL20A1_MIP10	AGCTCGCCCCTTGCCTCAGCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCGCTCCCCACTC	20
M00764_COL20A1_MIP100	ATCGTGTGCAGTGACACCTGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTCGGCCGCGGT	20
M00764_COL20A1_MIP104	CCAATGTATTGCTGCCACTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGATGGAGAGACCTGC	20
M00764_COL20A1_MIP105	ACGCCACTGGACTCACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGAGGCTCATGAAATA	20
M00764_COL20A1_MIP106	CGTATAGCTCCTGCTGCAGGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGCTGGAACCTTG	20
M00764_COL20A1_MIP107	GTGTCCACAGCCTTGTCTACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGAGGTCCTTGGACCT	20
M00764_COL20A1_MIP109	GCAAAGACCAGCCCCTGAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGGCTCCCCAAAACT	20
M00764_COL20A1_MIP11	CAATGTCTGATTGCTGGACATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAACAGGACCCCCAGC	20
M00764_COL20A1_MIP126	GCCTGTGTCTCCAGGGAGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCTCCTTTAATGGAG	20
M00764_COL20A1_MIP127	GGGTAGGGCCTGACAAGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGAGTGACACCTACC	20
M00764_COL20A1_MIP128	GGTCCACCAGGGGTCAAAGGAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCAGCAGGGCTCG	20
M00764_COL20A1_MIP129	AGATGGGCTGGACAGCGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCTCCATCCCTGTCCTTC	20
M00764_COL20A1_MIP130	CAGAGGTGGCCCTGCCTGTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGAACCCTCCAAGCCC	20
M00764_COL20A1_MIP131	GAGGCCAACTCTCCCGGGGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCCCAGGAGAAAGC	20
M00764_COL20A1_MIP132	CCTGCCTCACCTGCTGCACCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCAGGGACCAAAGGTG	20
M00764_COL20A1_MIP133	AGCAGCAAAGGTGAGGCAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCAGTTCCCTCCAGG	20
M00764_COL20A1_MIP134	GGGTGGGGTTTGTACCTGTACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACACAGGAACCCTGGG	20
M00764_COL20A1_MIP137	CAGCAAATCTGCTCCCACTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGTTGGAAATGCACTT	20
M00764_COL20A1_MIP143	CAGAACAGGCCTCCAACAACAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCCTCCATGGAGCCTG	20
M00764_COL20A1_MIP144	CCCCCCTTAGGTGGGCTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCAGGACAGACGTGG	20
M00764_COL20A1_MIP145	CCCATGGAGCTGCTGAAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGCCCAGAGAACAGAC	20
M00764_COL20A1_MIP152	ACTGTGTCCTGCTGACACCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTGCCTACCACAC	20
M00764_COL20A1_MIP153	CAGGCCACGCCAGGACACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGCTTCTGCTCCAAGAT	20
M00764_COL20A1_MIP154	CCGCCACCTTGAGGGCAGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTCCTTCCACGAGAACA	20
M00764_COL20A1_MIP155	CACGCCCCCATTCTCCAGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGCTGCTGTGCTGAC	20
M00764_COL20A1_MIP157	GTCCTCCCCACTCCCGCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTTCCAGGGCCCTCAAG	20
M00764_COL20A1_MIP158	GGGAGGAAGGATGGGAGGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGAGCACCAACAAG	20
M00764_COL20A1_MIP159	GAGAGGCTGATTCGGGGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTCCTGGCTGCTGC	20
M00764_COL20A1_MIP16	GAATGCGTGCTGAATTCACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAAGAGAGCAAGTT	20
M00764_COL20A1_MIP160	CCATCTCAGCGTCCAAGTCATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGCAGAGATGCCCCC	20
M00764_COL20A1_MIP161	ACTGGGGGCAACCTGGGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAACAGACGGGGGATGA	20
M00764_COL20A1_MIP162	CCTGAGACGTCTGTGGGATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCGTTTATTCTGAGT	20
M00764_COL20A1_MIP163	GAACTGTCATGGAGCCCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCAGATGAGGGGTA	20
M00764_COL20A1_MIP166	GGGCCCTGTTCTGACGGGGACACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCACCTGTCACTCCCAG	20
M00764_COL20A1_MIP167	CCTCATGCTGTCCAGGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCCCTGGGCAGCAGGGG	20
M00764_COL20A1_MIP179	CCATATCATTGAGGAGAGAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGCCTTGTGGCCC	20
M00764_COL20A1_MIP18	CAGGTGAGGACCTGCCCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCACTATGTCCTGTTTCT	20
M00764_COL20A1_MIP189	ACTTTATGCTGGAGGCCAATTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCCGGGGGGAAC	20
M00764_COL20A1_MIP19	CATGGGCTTCACCTGCACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGTGCTGACACTAAGG	20
M00764_COL20A1_MIP193	CCTTTACGGCCACAGCTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTGCACGTCTCCCAT	20
M00764_COL20A1_MIP196	GGCAGCACCTAAGGCCATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATGACCTTCCCACAAC	20
M00764_COL20A1_MIP2	GAGGGGAAGGGTGACCACATGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCCGTCGGGTCAG	20
M00764_COL20A1_MIP200	GCCTTCCTGGGCGCTGTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGCTTCCATTTCTGAC	20
M00764_COL20A1_MIP23	CATCTTTGCATGCCTCCCAGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGCTGGGGTCCCAC	20
M00764_COL20A1_MIP25	GCCAGAGGCCCCTCGGCTCTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGATGCGCCCTTGA	20
M00764_COL20A1_MIP28	AGGCCCATCCCTGGTCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTGCTGGAAGTGACTG	20
M00764_COL20A1_MIP29	CACCCGGGTGTGGTCCCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCCTGGAGCATTGGC	20
M00764_COL20A1_MIP3	CAGTATGCCCTCCCAGCCCATCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAGCCACTCAGATG	20
M00764_COL20A1_MIP34	CAACCGGACAGCAGAGATGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGGACGGAGGCCA	20
M00764_COL20A1_MIP36	CCCAGGTCCTTGAGGACACGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGTGGAAGCTGGGGCTC	20
M00764_COL20A1_MIP37	GCGGTGGGGGTCTCCATGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTGGACGGTGATGTC	20
M00764_COL20A1_MIP38	GGTGAGGGGCAGGGTCACCCGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCGTCCCCGCCGAG	20
M00764_COL20A1_MIP39	GGCAGATGAGACGGCTGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGGTACCACACGGGA	20
M00764_COL20A1_MIP4	GTGGGACCCTGCCCTGCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTGTCCAGCACCCACAC	20
M00764_COL20A1_MIP40	CCCCCTGGTGGCCACTCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGGAGGTCACCTGG	20
M00764_COL20A1_MIP41	CCCCAGGGAGGTGAGGGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACCCTCCCTGCCCCCA	20
M00764_COL20A1_MIP43	GACAGGAACTCCGTCAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACCAGGTACTCTGTG	20
M00764_COL20A1_MIP44	CCTGGTGACCACAGGTAGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCTGTTCCAGGTGG	20
M00764_COL20A1_MIP45	CGCCAACCCCGCCCTCATAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGAGCTGCTCGCTAT	20
M00764_COL20A1_MIP46	CAGCACCTCTGCCTCCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAAGTGCCACTTTGAATC	20
M00764_COL20A1_MIP47	CCATGCAGGGACACTTTAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAAGCAGGAGAACA	20
M00764_COL20A1_MIP48	ACGTCATGTCTCTGCAGGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCACTACCTGGTGC	20
M00764_COL20A1_MIP49	GGCCCAGCTCACCTCTCGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAGTCCCTGCCAGGTTC	20
M00764_COL20A1_MIP5	GGCTGCACGGCCCAACACTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCCTTTGCCCTCC	20
M00764_COL20A1_MIP50	CCCGGCTGCCTGCCCACAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGGGCGGCCCGAGGTGCT	20

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ID	**MIP**	***c***
M00764_COL20A1_MIP51	CCCGGCTGCCTGCCCACGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGGGCGGCCCGAGGTGCT	20
M00764_COL20A1_MIP52	GGAGCACTCACGGGTCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGCACGCGGCCTCCAT	20
M00764_COL20A1_MIP53	GAGACACCTGGGCTTCTCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGCCTTCCATGGCAT	20
M00764_COL20A1_MIP54	GGGTGGCTGCAAAGCACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGAGTGTCCACCCTCG	20
M00764_COL20A1_MIP55	GGGTGGCTGCAAAGCACAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGTGTCCACCCTCG	20
M00764_COL20A1_MIP57	AAACGGGGAAAATGGGCTTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCCAGGAGCCTCTG	20
M00764_COL20A1_MIP58	GCAGCAGGTGGGAGGGCGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGTCACCCGGCCAGTC	20
M00764_COL20A1_MIP6	CCTTTCATAAGCTCCAGCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGTTCTTGGAGAGAT	20
M00764_COL20A1_MIP60	CCGCAGCCCCGTCTGGCGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGAGGTGCCCAGGCT	20
M00764_COL20A1_MIP61	GGGAGCTTTCTCTGAAGGAAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGCCTTCCCCTCTC	20
M00764_COL20A1_MIP62	GTGCGCCCACCCTGTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTACCAGATCACGTGGAC	20
M00764_COL20A1_MIP64	GTCCCTCCGCTATACCCCCTGTACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCTCCTCTCCCTAGA	20
M00764_COL20A1_MIP65	GGGCCCCGTCCCTGTAGTAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTAGGGTCCTGGGC	20
M00764_COL20A1_MIP66	GTCATTGGAGTCTGCAGCACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCACTTCCCCTC	20
M00764_COL20A1_MIP67	GTCGTTGGAGTCTGCAGCACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCCACTTCCCCTC	20
M00764_COL20A1_MIP69	GGTTGTGCCAGGGGGGTGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAAACCACCTAGTGTC	20
M00764_COL20A1_MIP70	ACACCCCTGCCACTGCCCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGAAAGGAGGCACC	20
M00764_COL20A1_MIP71	CCACCCTCCAACCTGGCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGTGGAGGCATTACGC	20
M00764_COL20A1_MIP72	GAGCATGGGTTGTGTGGGGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGTAGGTGAGCCA	20
M00764_COL20A1_MIP73	GTGGGGCCTCCTGGAAGGGGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCTGCAGGTCAGCT	20
M00764_COL20A1_MIP74	GCCTCAGGCTCTACCAAGACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTTCCTGGGCAACTT	20
M00764_COL20A1_MIP77	CAGCCAACCCCAGACCTAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGAGGCTGTGTCTGC	20
M00764_COL20A1_MIP78	GCCCAGCCCTCCGCCCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTCCCACCTATACAGA	20
M00764_COL20A1_MIP79	GGCTGCTGAGAGGAGACAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTGGGTCCCAGGTCAC	20
M00764_COL20A1_MIP80	GTTTGACCTGATGGTGGCCTTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCACCCCTCCCTCC	20
M00764_COL20A1_MIP82	GCTGAAGATTAGGAGGACATGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGCCATGGAGCCC	20
M00764_COL20A1_MIP83	GACACCCTGAGGGGTGGGACCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCCGGCCCAGGACAC	20
M00764_COL20A1_MIP84	CCTCCAAGTACTTCTGTTGAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTGAGACTCCCCTGT	20
M00764_COL20A1_MIP88	CGAGACACCCCGTGAGGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCGTTCTGCCAGGTTTG	20
M00764_COL20A1_MIP89	GAAGTAGGCGCACAAGGAAGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCCTACTCCTCCTG	20
M00764_COL20A1_MIP9	GGGCCACTGGAGAGCTGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACCTGTGGAGGAGAGTG	20
M00764_COL20A1_MIP90	GTGTCCCGGGCAGGGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGACGTGGGCCCCGCGTC	20
M00764_COL20A1_MIP91	CCTCTGAAGGCCTCCCAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACGACAGGACAGGAGCA	20
M00764_COL20A1_MIP92	GAAGTCCCTGACCTACTTCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTCACCTCCAGCTTG	20
M00764_COL20A1_MIP94	CCTTCCTTGGGAGGGAACATTGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCTTCGGGAGCTT	20
M00764_COL20A1_MIP95	CCTGCTCTCCTAGGGAGAGGAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCAGGAGCCTCCCG	20
M00764_COL20A1_MIP96	GTTCCTGACCCCAGGTCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCTTTGGGACCCACAG	20
M00764_COL20A1_MIP97	GACCTCACCTCAGGTTTCGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTGCACCTGTGAGA	20
M00764_COL20A1_MIP98	GCTTCGTCACGCTGGGGAGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGAGAACCTCCCGT	20
M00764_COL20A1_MIP99	CGGCAGTCCACATAGAGCCTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGCAGGGCCCAACT	20
M00764_COL6A6_MIP138	GTTATTTTTTAATGTTTTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTTATATGATGTATGC	20
M00764_COL6A6_MIP164	ACTTAATCATATAATTATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAGAGACTAGAGCATCT	20
M00764_COL6A6_MIP40	CATTCTTGTCCTGGCTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACATGTTCACTGAAGCCC	20
M00764_COL6A6_MIP50	ATGTCTTATTTTAGACTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCTTAGATGAGTCCTT	20
M00764_COL6A6_MIP51	CATATAATGCTACTTATCAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAAAATCTGATGATT	20
M00764_COL6A6_MIP73	ATTATACAAATAAAGTTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACTATAACTGTCCTTTTAT	20
M00764_COL6A6_MIP82	CCTAAAAATAGAAAATAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTACCAACAAGAACTT	20
M00764_COL6A6_MIP89	CATAGAATTAAAGCATTATTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAGACATATCAAG	20
M00764_COLEC11_MIP10	GTGCAGAGGGGAGGCAGGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCATGAGGCGCCTGG	20
M00764_COLEC11_MIP15	ACTTAAATCCTACCTCTGTGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATGTCCGTTTCCACT	20
M00764_COLEC11_MIP2	CTTCTTATGATTGTAATTTTATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCAATAATACGTTTT	20
M00764_COLEC11_MIP26	GAAGCTGGTCATTTTCTTACTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCCACCCGACACT	20
M00764_COLEC11_MIP27	GAGGAGGGGGCGGGGGAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGGACAGCAGAGTGTGT	20
M00764_COLEC11_MIP28	GCACCCACGTGACTCCCCCGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCGGCACCCACG	20
M00764_COLEC11_MIP30	CAACCACGTGACTCCCCTCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGACCGCGGATGAGG	20
M00764_COLEC11_MIP33	CCTTTGTGCTTTTAATTGTGATAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGTCCGGACAGCT	20
M00764_COLEC11_MIP40	CCGTGGGGCCGACTCTTCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGACCCAGAGGGCAGGG	20
M00764_COLEC11_MIP52	GCCCCTGCTGCCTGTGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGAGCTCAAGTTCATCAA	20
M00764_COLEC11_MIP54	GCGTAGCGCTTCTCCTCCTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGTTGATGCCGATGAA	20
M00764_COLEC11_MIP9	GTTATCTCGGGGAGCTTCCTGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCGAGGACACTGCC	20
M00764_CORO6_MIP10	CGGGGCGGGGCCGAGCTTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCTGGAGCGACGTGGG	20
M00764_CORO6_MIP11	GTCCCGAACTCCGGACCCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCCAGGAGCAGCGCAT	20
M00764_CORO6_MIP13	GACACGGCCTCTCTGTCCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACATCCTGGACGTGC	20
M00764_CORO6_MIP14	GAAATGAGCACGGGTTCGGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTACCGACAAGGGGGC	20
M00764_CORO6_MIP15	CGCGAGCTCCGGGTCACGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTTCCAGGACGATCTGTA	20
M00764_CORO6_MIP23	CCTCCCGTGCTACTTCGGGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGACGATGCTGGAGTCG	20
M00764_CORO6_MIP24	CAGAACAACTTCGAGGAGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCAACTCTGGTCACT	20
M00764_CORO6_MIP25	AGCAAACCACCCCCAGGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAACCCTATGCCCCAAAC	20
M00764_CORO6_MIP26	GGTATATGTGCAGGGGAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCCATTCTCACACCC	20
M00764_CORO6_MIP27	CGAGGCACACACCCCAAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAACTGGGCAGAGGGG	20
M00764_CORO6_MIP28	CAGGGCATGCCCACCTGGACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCACCACGGGCTTCACC	20
M00764_CORO6_MIP30	CCCCCTCCCCCCAGGAGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGCTTAGGCCCCAT	20
M00764_CORO6_MIP33	GCGCGGCCTGGCCTACCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTCCCCGGAGTCGCAGC	20

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M00764_CORO6_MIP34	GCGCGCTAGCTCGCTCCTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCCTCACGAGGGCGCC	20
M00764_CORO6_MIP35	GGCCCACGCACCCGCACCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAGCCCGCAGCGGGC	20
M00764_CORO6_MIP36	CGTGCATGTCTGCGTGGAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGTGGACCCGCTGGGC	20
M00764_CORO6_MIP40	GCCCTAAGTAAGCCCCCAGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGACCAGTGGCCAGCT	20
M00764_CORO6_MIP57	ACCGCAGCCAGCGGAGCGGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCTCCTTCGCCCT	20
M00764_CORO6_MIP58	CAGCTGCCGCTGCCATCAACCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGCCGAGGAAGGCT	20
M00764_CORO6_MIP59	GGACACCCGGGTCCCAGATACTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGGGCAACTTGGGC	20
M00764_CORO6_MIP6	CAGTGAGCTGATTAGGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAGAGTTCTCTACCA	20
M00764_CORO6_MIP60	GCTAGGTGCGCACGCTGCTTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATAGGGGCGGGGCC	20
M00764_CORO6_MIP61	CAGCTGCACATTTATTTCGATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTCTAGGGGCGCAC	20
M00764_CRBN_MIP10	GCCATATCCTTTTAATTAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAATAAATTATGAAAT	20
M00764_CRBN_MIP100	GAAAAATTTTTAATCATTTATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAGAATGTGAGGTT	20
M00764_CRBN_MIP108	ATCGGGAGGCTGAGGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGCCGAGGTAGGCGGAT	20
M00764_CRBN_MIP11	GTAATATTTCTAAGAGGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGCTGCTATAATTTCAGC	20
M00764_CRBN_MIP112	CACATACAGTATGTAATTTAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTTTTCTTACAATAT	20
M00764_CRBN_MIP119	GCAGACGGCGGCGCGTACCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCGCCGGCCATGTCTG	20
M00764_CRBN_MIP25	GTTTCACATTGTAGGAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTAGAATAATTAATATAC	20
M00764_CRBN_MIP30	GTAAACATAACATTAATACCTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATGAAATAAGTCC	20
M00764_CRBN_MIP5	CATAAAATGTGAATACTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACGTTTATTGTTTGTTTGC	20
M00764_CRBN_MIP65	GATAGTTACATTTAGAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGTGAGCTGAGATTGTGT	20
M00764_CRBN_MIP88	CATAGACTACAAGTATTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAACTGGACTTTTTTGTGT	20
M00764_CREB5_MIP10	AAAGACTTTGCAAACAGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATGGTTTCAGACAAGACC	20
M00764_CREB5_MIP11	GGCTCTGCAAGCTGTTGCTTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCCATCAGGCCCTCC	20
M00764_CREB5_MIP12	GCGCCGTGTGACACGGCTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGCGTCGAGGGGGCA	20
M00764_CREB5_MIP13	GTTCAGGAATCCCACGTGACGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGGTGCACCAGG	20
M00764_CREB5_MIP140	GTTTTTAAACACACCGTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAATTTTACCTTTTTTT	20
M00764_CREB5_MIP141	GTTTTTAAACACACCGTCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAATTTTTCCTTTTTTT	20
M00764_CREB5_MIP158	GTCATTGTTTTATTTTATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTTGTTTGATTAAGTGA	20
M00764_CREB5_MIP18	CCTCTGGTCCGCCAAAATGTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGCATCCCTCCAGGC	20
M00764_CREB5_MIP19	GTTATGAATCGGGGGTGTGTGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAGTGCCGGAGCGC	20
M00764_CREB5_MIP20	GGTCCCCGCGTCAGGGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACGCTGGGAAGCTGGGGA	20
M00764_CREB5_MIP204	CCTTTTGTAAAATACTGTTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACTAGTTATATAAA	20
M00764_CREB5_MIP21	GGCTCGCTCTCCCCGGTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAGGAACCTCCCCCCGC	20
M00764_CREB5_MIP210	ACATAAAAATTAAAAATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTGTAGTGACAGTCACT	20
M00764_CREB5_MIP22	GCGCGCGCGCCCACCCGCCCCCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGCGAAAGCCAA	20
M00764_CREB5_MIP223	CATCTAAGAAAATATATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAAAATCATAAACCAGCT	20
M00764_CREB5_MIP224	CCTTTTTTTAACCAGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAATAACATTTATTAAT	20
M00764_CREB5_MIP226	AAAATACACATAACTATAGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGTTCAGAATGTTGA	20
M00764_CREB5_MIP23	GTTACCTCTTCCCGGCCGCTGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGTCGCCCTCGG	20
M00764_CREB5_MIP238	GTTTTTTGTTTTTTAAATTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAAAATATATAAAC	20
M00764_CREB5_MIP241	ATATTTTACAATAGAATAATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACCAACTGTTGTATTT	20
M00764_CREB5_MIP242	CAATCCTATAAAGTTCTATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTATTCTAAAGGAGAAAA	20
M00764_CREB5_MIP31	GTATTATTTAAGAAAGGCACCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCACTCTAGCCCCGC	20
M00764_CREB5_MIP62	AATAAGTGTTTAAATGAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAACTTTGTATTTAAGG	20
M00764_CREB5_MIP64	ACTATATATTTCTTTAGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATCTGGCTGAGTACTG	20
M00764_DCLK2_MIP10	GACTTGTGAGGCGTGGCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTTCCTTCCTTCCTCC	20
M00764_DCLK2_MIP11	GTTGGGCCGCCCGAGGCTCGCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGTCATTGTCCAGT	20
M00764_DCLK2_MIP110	GACTGAGCCTCCTGCAGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCTCAGTGGAGGAGAT	20
M00764_DCLK2_MIP111	GCGGCGCCAGGTTCCTGCCCGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAACTCAGGCGCAGG	20
M00764_DCLK2_MIP112	AAGGCTGCATCCGTTCTGCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTCCCTCTCTTCAC	20
M00764_DCLK2_MIP12	CCAGAGCCAGGTGTCCCGGCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACGGAGCAAGTCG	20
M00764_DCLK2_MIP13	CCCGCCCTCTCCGCGCAGGTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCATCGCGGCTG	20
M00764_DCLK2_MIP14	GCAGCTCGGGCCCCAAGGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGCGGACGCCCTCGGA	20
M00764_DCLK2_MIP15	GCCTTTTGTCCCGTTCCTCAAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCGCGTGCGGTAG	20
M00764_DCLK2_MIP19	CCAGGCTGGTGACCTTCCGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCAATTCCCGTGCGGCT	20
M00764_DCLK2_MIP5	AAAACTACAAAGGAAGGAGATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGGAGCAGCTCC	20
M00764_DCLK2_MIP6	GCTGACAGCCTGTCGGCGGCGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCCCGGGACCCGC	20
M00764_DCLK2_MIP7	GGGGATGCCAAACCGCGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCTAGCGGGAAATAA	20
M00764_DCLK2_MIP8	CGGCGCTGCACCCCGGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTGGGAGGCGGGCTGC	20
M00764_DCLK2_MIP9	ATCCCGCCCGCCGGGCAGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGCTCCCGGGAGCGCCG	20
M00764_DMPK_MIP1	CCAATCCGGAGGCGTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTATTTATTGTCTGTCCCC	20
M00764_DMPK_MIP10	GAAAGCGCCTCCGATAGGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTAGGGTTCAGGGAGC	20
M00764_DMPK_MIP100	GGCCCTGTGACAGGAGGACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCAAGGGGTGGGGAGA	20
M00764_DMPK_MIP101	GAACCCTTCAGTGCTAGAGTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACTTCTCTCTGCGGCC	20
M00764_DMPK_MIP104	GGAGCAAGGGGGTGGTTGCTACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAATCCATCTCTGAGTC	20
M00764_DMPK_MIP106	GCAGAGAGCCTGAGGGCTAAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCAGCCTTTGGGCA	20
M00764_DMPK_MIP11	CCTGTTCGCCGTTGTTCTGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGCGGGCCCACCTAT	20
M00764_DMPK_MIP12	GTCATTGGCTGCTTCCTAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTGGCTCCTGGGACTC	20
M00764_DMPK_MIP13	AGTGGACTAACAACAGCTGTAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCACCCGCTTAGCT	20
M00764_DMPK_MIP14	GTACCCTGGCAGGGAGCAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTTGATTGGCTGCCCG	20
M00764_DMPK_MIP15	CCGGCTGCCCACGCCCCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCGATCGGGTCACCTG	20
M00764_DMPK_MIP17	CCCTAGATAACCTCCCCAACCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCTCCTGGTCTCC	20
M00764_DMPK_MIP19	CCCCTGCCTCAGACCTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCACGCCGCGCCACCGC	20

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M00764_DMPK_MIP21	GGCGTGTATAGACACCTGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTAGAGGCACACGTC	20
M00764_DMPK_MIP22	CACCGGCCCGCATCCCGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATCCGCTCCTGCAACTGCC	20
M00764_DMPK_MIP23	CCCCTCTCGTCCGGCCCGGACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGTGCTCACCCGGC	20
M00764_DMPK_MIP24	CGCTGGAACTGCCACTTCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTTCTGGTTGTCCGTGC	20
M00764_DMPK_MIP26	CCCTCAGCCCCATCCCTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAGACTCAGGACTTGG	20
M00764_DMPK_MIP27	CCCTCAGACCCATCCCTGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAGACTCAGGACTTGG	20
M00764_DMPK_MIP3	CCGACTCGCTGACAGGCTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTACTCGGGAAATTTGCTTTT	20
M00764_DMPK_MIP31	GAAACAGTAAGTTGGTGGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCCCTCCTCCTCT	20
M00764_DMPK_MIP45	CATCTAAAAAAAAAAAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGCGTATGCCTGTAATGC	20
M00764_DMPK_MIP5	ACGCCCTGCTCTGGGGAGCGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGAGGCCCTGACGT	20
M00764_DMPK_MIP57	GTGCTCCTGCTCAGAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAGAAGGGATGTGTCC	20
M00764_DMPK_MIP61	CCCTCTGCCTGGTCTAATACTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGGGGTGCCCACAG	20
M00764_DMPK_MIP63	ACAGCGGTCCAGCAGGATGTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTCCCACACTCTGTG	20
M00764_DMPK_MIP69	GACAACCCCTCCCAGAGACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCCAAACTTGCTCA	20
M00764_DMPK_MIP7	CACAGACCATTTCTTTCTTTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGAGGGGCCGGGTC	20
M00764_DMPK_MIP71	GAAAGAGAACCCAGAGGCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATAGAGATCTGCCGGG	20
M00764_DMPK_MIP73	CACACCCTCTTACCGCACACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTATCCCATTCCAGGTAA	20
M00764_DMPK_MIP75	GTCCCTCTCCTCACGGAAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCGTCCAGTGACAGCAC	20
M00764_DMPK_MIP76	GTTGGTGAATGGGGACCGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACATGCTGAAGAGGGG	20
M00764_DMPK_MIP77	GTGGAGACGGCGGGAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACGTCCGCCCAGCCCC	20
M00764_DMPK_MIP78	GCCTCCAGCCCAGCCCTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGAGATAGTAAGACAGA	20
M00764_DMPK_MIP79	GCCTCCAGCCCAGCCCTAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGAGATAGTGAGACAGA	20
M00764_DMPK_MIP8	GGTGGGCGCGGCTTCTGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGACCCTTCGAGCCCCGT	20
M00764_DMPK_MIP80	GGGCTTGGGACCAATGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTTCAGCGAGGTAAGCCG	20
M00764_DMPK_MIP81	CCTTAAGCCTCACCACGATGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCCCAACCCCTATG	20
M00764_DMPK_MIP86	GGAGTCAGGGTGGAAGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTGTGGTTCAAGAACCA	20
M00764_DMPK_MIP9	GCCAGTTCACAACCGCTCCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAACTCACCGCAGTCTGG	20
M00764_DMPK_MIP90	CCCCACAGTCCCTGAGCCACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAACCCCCCGGAACCC	20
M00764_DMPK_MIP92	CAATGTCTTGGCTCTCTCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTGGGGTAGGGGTCTG	20
M00764_DMPK_MIP97	CTCCTGGTGGACGCCCAGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCCTCTGTGCCCAGA	20
M00764_DMPK_MIP98	AACTGGCCCAGGACAAGTACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTGTCCAACATGTCA	20
M00764_DMPK_MIP99	GTCTGCCTGTCCCTGGCTGTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTCAGCCGCACCTC	20
M00764_EBF3_MIP100	GTTTATTTGTCTTTGGAGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGGGAAAGGGTCCAT	20
M00764_EBF3_MIP101	CGCCCCTCGCCGCCGCCGCCGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTCTCCCCGAGG	20
M00764_EBF3_MIP102	GGCGAGGGGCGGCCGCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGGGCGGCGGCGGCGC	20
M00764_EBF3_MIP103	CAATTGCAGTTTGGCCCCTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGCCGAGCGCCACCG	20
M00764_EBF3_MIP104	GCAGTGGCTGCGTTTGTTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTTGCATTTATTGCATG	20
M00764_EBF3_MIP105	GAGGAGCGGGCAACGGACTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGTAAAATGCTGAGGC	20
M00764_EBF3_MIP28	CCCCCTATTCAACTGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAAACAGAAGTCCCTCAC	20
M00764_EBF3_MIP40	GGCCTTTCTCCTGGCACCTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAGCCTCTCCTCCT	20
M00764_EBF3_MIP43	GCACGAAAACAAAACATGACATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGAGGCTGCCATGG	20
M00764_EBF3_MIP56	GGTGGAAGCCTTATACGGAATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACTGGTCTCCACA	20
M00764_EBF3_MIP74	GGGACAAGCAGAGGCTGGGGTTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCCGAGGCAGCCCG	20
M00764_EBF3_MIP75	CCAGGACAAGAACCCGGAGATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTCGAGCGTGGTG	20
M00764_EBF3_MIP89	GAAGCCCAGCGTTCTCCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATTGCATTTAGTGCGAT	20
M00764_EBF3_MIP90	GCAGGAAAGTGACATCACCGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGCGGCGGGCTCGGC	20
M00764_EBF3_MIP91	GCTTCTAGAAAGAGAGAGGGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGAAGTTGCCCAGC	20
M00764_EBF3_MIP93	GAAAGAGACAGCGGCCCGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCAATCTCCACCGGCTG	20
M00764_EBF3_MIP94	CCCGCAGCGGCGTGGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGTGGACGCCAACACGGCC	20
M00764_EBF3_MIP95	CCTGAATCCCAAACATGAAAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTACGTACCTCTGG	20
M00764_EBF3_MIP96	GAATATTCCGCGCGGGGGGACGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCCGAGCAGGGCGA	20
M00764_EBF3_MIP97	GGCTCCACCGGCGGCGGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCTGCCCTGGCCGCC	20
M00764_EBF3_MIP98	GCCCGGCCGCTGGTGTATGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGACACCACGTTGAG	20
M00764_EBF3_MIP99	GTGAGTGCTGCGGCGCAGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTGTTGTTGTTGTTTGCAG	20
M00764_EYA2_MIP10	GCTGTCTCTGCCGTTGCCGCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGCCTGGGGTGGGC	20
M00764_EYA2_MIP11	CCTCCGCAGCTGTCGGGACGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCACTGCGCGCGGTGA	20
M00764_EYA2_MIP36	ATCAAAGGGAAATGAGAAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTATTCATTAATTATG	20
M00764_EYA2_MIP6	GGACCTCAATAGTGACACTAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGTCCTGGAGGCCAG	20
M00764_EYA2_MIP7	GTGTGTGCGCCCGCGTAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGGGAGGAGGCTGGGC	20
M00764_EYA2_MIP8	CGGCGGCTGGACGCAGGGCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGGGAGGACCGGCCC	20
M00764_EYA2_MIP9	AGCCCGGCCTCGTCGGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGGGGCAGAGGGAGGG	20
M00764_EYA2_MIP95	TACCTCCAGCCTGGACAACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTGTTTCTACTAAAAATAC	20
M00764_FAM114A1_MIP36	GAGTGATTAACTTTCTTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCTACTTCACATTTTAC	20
M00764_FAM114A1_MIP49	GTTAAAGATTACAATCTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAATGATTTATTAATACA	20
M00764_FAM114A1_MIP6	CCTCGTGGGGCGGGGCGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGGAGAGGCGGCGCG	20
M00764_FAM114A1_MIP66	CCATTTTATATAGATGGAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGACGGCTGGTTTCCAGCTT	20
M00764_FAM114A1_MIP7	GCGCCGCGGGGACGCCCGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCCGAGTACGCGCGG	20
M00764_FAM114A1_MIP8	CATACCTTGGCGCCTCGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGACCCGCTGGGCACT	20
M00764_FAM114A1_MIP84	GTATTACTTTAAATCAATTCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAAATTTATTTACAA	20
M00764_FAM114A1_MIP9	GGTCCCACTCCCTACCGCAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCAGGCCTTGACCTC	20
M00764_FAM171A1_MIP89	CCTTGGGCTCCGGCGCCGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCCGATGCGGCTCGG	20
M00764_FAM171A1_MIP90	CAGTGGGCGGCGGCGGGGCCGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGAGCCGCCGCCGG	20

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M00764_FAM171A1_MIP91	GATTGGCCCGGCCCCGCCGCCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATCTCCGCCGCGGG	20
M00764_FAM171A1_MIP92	GGCGGCGGGCCCGGCGCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGCAGGAAGGGGTTAA	20
M00764_FAM171A1_MIP93	GCTGCGTCGCGCCCCCAGCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCTGCTGCTCCGCCAGC	20
M00764_FAM171A1_MIP94	GCGCCGGGCGGGGGCGCCCTCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGGTGACCTGGTG	20
M00764_FAM171A1_MIP95	ATTTCACACCCAGTGTTAAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGACCTGCCTTTCAGG	20
M00764_FTSJ2_MIP35	CCCTGCCCCTGGAGACCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGGAGCTACCCGGCCC	20
M00764_FTSJ2_MIP36	CGGCGGGGCCGTGGGGAGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGCCTCGGGGCTGGGT	20
M00764_FTSJ2_MIP37	GCCATTGGTGTTCCCCGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGCTGAGTGCGGGGAC	20
M00764_FTSJ2_MIP38	GCTGCTGCGCGTGCAGACAGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCGCGCGCTTTTCG	20
M00764_FTSJ2_MIP39	CCGGGAGCTCGAAGGAGACCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGCGGCGGTGCAGGT	20
M00764_FTSJ2_MIP40	AGCTCCCCTAGTCTCCTGCCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCCCGCTCTCCTT	20
M00764_GALNT12_MIP10	GCTGGAACCCGCTGTGAGTGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGGGCGAGGCGGTG	20
M00764_GALNT12_MIP11	GAGGTAGATGTTAATCTGGTGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCTGCCACTGCTCT	20
M00764_GALNT12_MIP6	GCGGCACGGCGGTTCCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAGATGCAAGTCTCAG	20
M00764_GALNT12_MIP65	GTCTGTATGTTTTATATTCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATATAAAAAGTAGAAG	20
M00764_GALNT12_MIP7	CGCCCCCGGCCCGCCCCACCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTTCCCGCGGGCAG	20
M00764_GALNT12_MIP72	CCTAAATATATATATATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGAAGTTTGTTCAGGAG	20
M00764_GALNT12_MIP8	GGCTGCCGAGCCGGGACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGCACGGCGCGGCGGC	20
M00764_GALNT12_MIP9	GGCCCCGGCCCCACGCTGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCTGCAGCTGCAGCC	20
M00764_GALNT12_MIP91	AAATAAAATCTTTATCTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGACAGTCTCTCTATACTGG	20
M00764_GLO1_MIP10	ACTTTTTCTATCAGTATCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTATTAAATGAGATAAAG	20
M00764_GLO1_MIP34	ATTTCTTTACATTGTTTATCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTATTTTGCTACATTTT	20
M00764_GLO1_MIP35	GTCTTATATTCTCTTATCTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATGATATCACATTTCTG	20
M00764_GLO1_MIP42	GTGAGTATGAGTTTCTATATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTGATTTTCCCATTA	20
M00764_GLO1_MIP43	CATAACTTAATATTCAAGTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTCATAAGCCAAGAA	20
M00764_GLO1_MIP62	GGGCTGCGGTTCTGCCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAATGCGGCCCGGTCCC	20
M00764_GRIN2B_MIP16	AGGAAGAGGGAAGCAAAGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCCCCAAAAGATTAA	20
M00764_GRIN2B_MIP166	GGTTAAATATGTGAGTTTAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTATTTTAAAGATT	20
M00764_GRIN2B_MIP5	GTAATTATTTTTTTCAAGTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTACAAAAAAGCCCTCCACC	20
M00764_GRIN2B_MIP6	AGTATATATATAAGCAAATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTCTTATTTTGGACA	20
M00764_GRIN2B_MIP91	ATATCATTCATAAGTGAACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTACATTAAGCAGGACACTA	20
M00764_GRIN2B_MIP98	GTAAGATATTGTGAATAATTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCACATACATCTACAGA	20
M00764_IQCH_MIP1	CAGATTGTGAAAAATTATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGTCTCAAACTACTGTC	20
M00764_IQCH_MIP116	CCTCTAGAATTTGGAGTAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGAAATAGTATATTAT	20
M00764_IQCH_MIP15	ATTACAATTTGAAAAGCTTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTATGCTTAATAAA	20
M00764_IQCH_MIP32	CATTTATTAGTAGTGTAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAAAACATCCACCACAG	20
M00764_IQCH_MIP37	GTTGAATTTAATACTATTATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAATCATAAAAACATTTTTC	20
M00764_IQCH_MIP38	GTAAACAATAAATAAAGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGAGAAGATGGCAGAA	20
M00764_IQCH_MIP78	CCATCTGCTCGTAATTAGAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTACATTAGTGCTAATT	20
M00764_KCNA4_MIP10	GCAAATCTATCTTTATATTTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATGAAATATGCAAATGA	20
M00764_KCNA4_MIP29	CCGCTCCCGGGCCCGGGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGTACAGGCCCCGC	20
M00764_KCNA4_MIP43	AAAAACAAGCCAGCCGGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGGCAACAGAACTTGTT	20
M00764_KCNA4_MIP46	GGTGTGGCGTTCGCGACGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACTTGTTAAGCCCGAA	20
M00764_KCNA4_MIP47	CGCCCCCGCCCAGAGCGCGTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCTGGGAGTCGGGGG	20
M00764_KCNA4_MIP6	CCTTTAGAAATTGATTATATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAATTGTAAGAAATACTGT	20
M00764_KCNA4_MIP7	GTAAATACTTCAAAATGCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAATTTACTTTCTTTTTT	20
M00764_KCNK13_MIP1	CCGCCCGGACCAAGCGCGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTGGAACAGGGAGC	20
M00764_KCNK13_MIP10	GGGGCCCGGCCATGGCTGGCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGGCGGTCATGGGC	20
M00764_KCNK13_MIP11	GGGGGCAGCCCCCAGGCCCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAAGACGGCGGCGC	20
M00764_KCNK13_MIP12	AGCGCCTGGCCAACTTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCTGAACGAGGACAAC	20
M00764_KCNK13_MIP13	CCCAGCGCTGCTTGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGTCCCAGCGCGGGCGG	20
M00764_KCNK13_MIP17	GAAGAACAAGATGGTGCTGGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCACCTCACACTGCC	20
M00764_KCNK13_MIP2	CGGACGCCGCTCAGCACAGCCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCTAACTTCCTT	20
M00764_KCNK13_MIP3	GGGCTGCGGCGTCCGAGGGCTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTTGTGGTCGTGGT	20
M00764_KCNK13_MIP5	CGCAGGCCGCCGACGGCTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTCCCGCAAAGAGACG	20
M00764_KCNK13_MIP6	CCCTATCTGAGCCGGACAGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTACCCGCAGACCTCCG	20
M00764_KCNK13_MIP7	GCGTCTTCAGGGCAAGCTCGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTCGGAGTTCTCCTTAA	20
M00764_KCNK13_MIP9	GCTTTGTCGCCGCCGTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGCGCCCCACCGCCGGCT	20
M00764_KRTAP19-5_MIP1	GCATAATTTATTCTAAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATTTTGTTATATATAATA	20
M00764_KRTAP19-5_MIP3	CATGTTAGGTTGTCAGGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGAATTATGGAATGA	20
M00764_LAMA1_MIP218	GTTATTTCATAGAATCATTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGGAGCTTGGTGTGA	20
M00764_LAMA1_MIP271	AATAAAATAAAAAGATTCATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTATATTCGCCTTCGCT	20
M00764_LAMA1_MIP284	GGAGTGGGTGTCTCGGCCACGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGAGAGGTGAGCCC	20
M00764_LAMA1_MIP285	GCGCCCGCCTGGAACGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGACCCTAGGACCCGGGC	20
M00764_LAMA1_MIP286	ACCGAGTGGCGGCGGAGGCGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGGGGTGTGTCCG	20
M00764_LAMA1_MIP287	CGCGGACCCCAAGTCGGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCTCCAGCCGCCC	20
M00764_LAMA1_MIP288	GCGCCGGGACCCAGAGGCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGGAATCCACCCTCCCGG	20
M00764_LAMA1_MIP289	GGCGAGAGGCGACCCCTCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGAGAAACTGGGCTG	20
M00764_LAMA1_MIP290	GTGGGTCCTGGCCCGGGGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAACAAGTTGCAACTCA	20
M00764_LAMA1_MIP68	CATAAGATGAAAGTTTTCTAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAATGCAGAATATAA	20
M00764_LAMA1_MIP69	GTAATTTGTCTTTTTATCAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAATCTCTGTTCATAT	20
M00764_LAMA1_MIP70	ATATATCTACTTATTGGTATCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGTTTAATTCTA	20
M00764_LEO1_MIP1	ACTGTACAATAAAATATATACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCGCGCCTGGCCGGAAAA	20

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ID	MIP	*c*
M00764_LEO1_MIP15	AAGTTTTGAAATACTTTTTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGATACGCCGAGATGA	20
M00764_LEO1_MIP28	ATATTTTATAAAGAATATTACTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAATGGTACCTTTA	20
M00764_LEO1_MIP38	CAAACTTTTCTAACTCTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCATAAATCAGGTAATAC	20
M00764_MAP2K5_MIP104	ATAAATTTCTAGATGTAGTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATAAATGTGAAATATG	20
M00764_MAP2K5_MIP107	GAGACAGGGTGTCACCCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTTAAACTCCACAAATA	20
M00764_MAP2K5_MIP111	GAAAGATATTAATTTTAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACTCTCTTACCCTATAACA	20
M00764_MAP2K5_MIP12	CCTCCCCCTCATCCTCCATTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTCCGCTAGTTCCTG	20
M00764_MAP2K5_MIP152	GTTATCTGTGTCATTTGTATACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTAAACATAAATATAT	20
M00764_MAP2K5_MIP161	GTCGCTGCATATGGCTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTATACCTAAAGACACCA	20
M00764_MAP2K5_MIP4	GTCATTAAGCAGGGTCAGGAAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCGGGAGCTGCAGC	20
M00764_MAP2K5_MIP55	ATACTAATATAAAGTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGCCCAATGTGAAGCTT	20
M00764_MAP2K5_MIP56	ATACTAATATAAAGTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGCCCAGTGTGAAGCTT	20
M00764_MAP2K5_MIP57	GAAATATTTGAAAATGATATATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCCCTACTGGCACA	20
M00764_MAP2K5_MIP6	CTGCTGCCCTTTTCCAACATGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTCTGTGGGCGATGA	20
M00764_MAP2K5_MIP61	ATTAATATTCTTTTTTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGGCACTATAGTTTTCAA	20
M00764_MAP2K5_MIP7	GAGGATGCGCCCCCGGCGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGGAGGAGGAGGAAGGC	20
M00764_MAP2K5_MIP8	GTCTCCGGGTGGGGCAGAAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGAGTAACAGTGTCGCC	20
M00764_MAP2K5_MIP80	CAGTCTGTAGCTGAAGGCCTGAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAGGAGTATTGACT	20
M00764_MAP2K5_MIP94	CCTATGGTATTGACTTGCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAATATTAATACCTTTC	20
M00764_MAP2K5_MIP95	AAAAAATTACCTTATAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTTTTCTACAAAAAATG	20
M00764_MAP2K5_MIP96	GGTTTTGATATAGATATCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATCATTGGATTTTATGGA	20
M00764_MDGA1_MIP134	GCCCGGAGTTTTACTTCGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTCCGTCCCCTCTCT	20
M00764_MDGA1_MIP136	CCCATCCTCGTTTTCCCCAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCCTTTTCTGTGTCT	20
M00764_MDGA1_MIP138	CCCTCCTCTCCCTTCTCTTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGGCCCTTTCCCC	20
M00764_MDGA1_MIP143	GCTCGTCCTTGACCCCTGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCTTTCAGCTCGGT	20
M00764_MDGA1_MIP147	CCCTCCACTCACACCTTCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCCCACCTACTCCA	20
M00764_MDGA1_MIP148	GTGGTAGGTGGGGCGGGACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGGCGTGGGCGGGTCTT	20
M00764_MDGA1_MIP149	CCCAATCCCAGCCCGGGTGATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCAGCGGCAGCTAC	20
M00764_MDGA1_MIP150	CCTTTGAAACGCCACACAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCACATCGTTGGAGAC	20
M00764_MDGA1_MIP151	CAGCTGCTGCCGCCGCCGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCCCGCCGGAGGTGGA	20
M00764_MDGA1_MIP152	GTGAGCCCCCGCCAGGAAAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGTCCTGGGAACTGG	20
M00764_MDGA1_MIP157	CAACGTGCGCCCCCGTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGACAAGGAGGCTGCACTGC	20
M00764_MDGA1_MIP158	CCTACCCTTGGGCACACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGGGGCAGCCCCGAGG	20
M00764_MDGA1_MIP162	GTATTTAAATTATATTTAATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAAATACAAAGAAAC	20
M00764_MDGA1_MIP164	CATGGAAGTGTCTTAAGGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAAAGGGAGAGACTAC	20
M00764_MDGA1_MIP170	CATGTCCAAGCGGCTGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACTCCTGACGTGATCA	20
M00764_MDGA1_MIP195	GCGCTGAGTGCCCTGCAACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCGTCTCGTTGAACAC	20
M00764_MDGA1_MIP207	GGAAACTTTGCAAGAGGCGCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCACCGGCCGTG	20
M00764_MDGA1_MIP208	ACGCCCCTATGTCCCCCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGGCAGTGGAAGGGGA	20
M00764_MDGA1_MIP209	CCCCCCGCCGCCTCTCGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGCCGGAGGAGAAACAC	20
M00764_MDGA1_MIP210	CCCGGCCGCCGAGCCGCCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGAGGTGGCGGCGACC	20
M00764_MDGA1_MIP211	CCTCGGGTCGGGGCGCTGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACGACAAGTTTGTCA	20
M00764_MDGA1_MIP212	AGTTAATCAATCTGCTGTTTCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGACCTCTCGGCGG	20
M00764_MDGA1_MIP213	GGAGCCCCGGCCTCCCCGACTCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCAGGAGGGCCGGG	20
M00764_MDGA1_MIP214	CCGATAAACCCGGGGGAAGAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGAAAGCACTCGC	20
M00764_MDGA1_MIP216	CCCGGGCTCCGAGCTCTCGGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGAAAGTTTGAG	20
M00764_MDGA1_MIP217	GCTACGGCCGCGGCCAGACGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCCGGAGCCCGGCC	20
M00764_MDGA1_MIP218	CAACTTGGGCTTTGCTGTGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAGTTGGTCGTCCCCG	20
M00764_MDGA1_MIP219	GAGCGAGCGGAGCGCTCCCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGAGCGAGAGACC	20
M00764_MDGA1_MIP220	AAAAGGAGCCAATTAAAGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCATTCCGCGCTCC	20
M00764_MDGA1_MIP224	GGAGAGGAAGGGAGAGAGAGCGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTCGGGATAGATGG	20
M00764_MDGA1_MIP225	GGTTGGGGGGGAATGTTAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAAGGCTGGAGAACAG	20
M00764_MDGA1_MIP226	ACTGCACACTTCGTAAATGTTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGCTCGCACACTC	20
M00764_MDGA1_MIP227	GCACTCCTGCTCCGCGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAGGTGGAGCAGGTGAG	20
M00764_MDGA1_MIP228	CGAACCCCCCCTCCCTTCGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCCGGGTCCTGCTAA	20
M00764_MDGA1_MIP23	CCATGCATTCTTCCTGCCCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTTGCCTGCACTCATTT	20
M00764_MDGA1_MIP231	CAGGAAATGGGCCTGGGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGAAAGGAAGGTGGAA	20
M00764_MDGA1_MIP68	ATCTCTGCAACGCCAAGAGGAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCCCCTCCCTGGC	20
M00764_MDGA1_MIP69	GCTGTGTGGCCACCCCCCCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCCTGTCTCCTCTT	20
M00764_MEIS1_MIP131	GTTAAAAGATTTAGGTGTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAAATATTTAATAAAT	20
M00764_MEIS1_MIP144	ATATTAATAAAAGATTATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAATTATCATCTGTGCAT	20
M00764_MEIS1_MIP172	ACAAAACTATCTTATTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATTTTTAATATTATGCA	20
M00764_MEIS1_MIP232	GTATTATTGCAATTTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTTAATATGTTGACTT	20
M00764_MEIS1_MIP239	AGAATAATTTCACTGATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAATTAGATTTTGAAGT	20
M00764_MEIS1_MIP5	AGGGGGTGTAGGTAGGGAAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAACTGCCAGTCCCTA	20
M00764_MEIS1_MIP62	ACCCCCTACCTCCCACCTCCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTCTCCCCTCCCTCTC	20
M00764_MEIS1_MIP63	CCGCTCTTACCAAGTTATCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACAGAAACATTTGCAGC	20
M00764_MEIS1_MIP7	CATTGGCTGCGGGGAAAATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTCCAGCTGAAACCT	20
M00764_MEIS1_MIP89	GAACCCTCGAGTAGCTGCTGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGGCCCCACAGAAGT	20
M00764_MEIS2_MIP14	GATTAAGTAATCTTTTAAAGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCATTTTGTTTTGTT	20
M00764_MEIS2_MIP151	AAGAGGAAGCAGAAGAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTAGGTTTCTAATGCA	20
M00764_MEIS2_MIP155	ATAGGGTTAGAAACAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTTCTCTTTGCTT	20
M00764_MEIS2_MIP156	ATAGGATTAGAAACAGAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTTCTTCTCTTTGCTT	20

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M00764_MEIS2_MIP167	CGTTCTAGGTCCACGAACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGTTAGTTTGGAAGACA	20
M00764_MEIS2_MIP174	GTTTAATCAACACGGGGAGCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGAGCCCCTGTGTT	20
M00764_MEIS2_MIP181	AAGTACTTAAATCCGCTTTCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGGATGTAACCACT	20
M00764_MEIS2_MIP182	ACTTCTCGCAGTTTACTCCTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCCTGCCCCTCA	20
M00764_MEIS2_MIP207	CACACTCACACACAGTAAGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGCAGAAGAGCAGG	20
M00764_MEIS2_MIP209	GTTCAGGTGGTGAACCGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTACCCATAGATCGCGT	20
M00764_MEIS2_MIP210	GCTCCACGCCACACAGCACTACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCTGACAGTACGATG	20
M00764_MEIS2_MIP211	AGCTGCCCCATTACGGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCATCTTTATCCCTTCCT	20
M00764_MEIS2_MIP216	GGAGTTAGTGTGAGGAGGAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCATGAACCAAGAGC	20
M00764_MEIS2_MIP220	CGGCGGCAGCGGCGCAGCAGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAGACAAAACAAGCA	20
M00764_MEIS2_MIP221	GGCTCGCGCGGCTCGGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGAGTGCGTGTGAGTGG	20
M00764_MEIS2_MIP222	AGGGAAAGAAGCCGATGAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATTGCACACGCACACAC	20
M00764_MEIS2_MIP227	AAAGAGAAAAAGAAGAAATATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCAACTGAGGGGA	20
M00764_MEIS2_MIP230	CCCCGCGGTATCTATAATACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAATGAATGATGGTTGATG	20
M00764_MEIS2_MIP235	ACGACTTCCGGGTTCCGTCATTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCCCCCCAGCCGG	20
M00764_MEIS2_MIP236	GGGGGGAGGAAAAGGAGAGTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGCGATCGGACAGC	20
M00764_MEIS2_MIP237	CCGTCCCCCATCCCCGTGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCCTCTTCTCTCTCCC	20
M00764_MEIS2_MIP243	CCTCCTCACTTCCTCCCTCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCACTTTGGAGACGCA	20
M00764_MEIS2_MIP245	CCCCCACTCTCTCCGTCTTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAATCGCCCCTGTGTAA	20
M00764_MEIS2_MIP248	AAGCGCGTCCTCTCCCCAACTTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCGCGCGTCAATCA	20
M00764_MEIS2_MIP40	ACATCTTATCATATCTATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGATAAATGCAATAAGAA	20
M00764_MEIS2_MIP73	GAGGAAGCTGAAGTCCCTTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTTCAGATCTTAAGC	20
M00764_MEIS2_MIP8	AGCATTATTTCTATGTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTAAAAATAGGCAAATA	20
M00764_MICALL2_MIP10	CATGGGCTTGGCCCGGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAGAGGAAGAAGTCCAA	20
M00764_MICALL2_MIP102	CTGTGCCTGATGCCTGCGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGTGGGGGAGGTGG	20
M00764_MICALL2_MIP103	CTGTGCCTGATGCCTGCCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGGTGGGGGAGGTGG	20
M00764_MICALL2_MIP104	CCTGCAGCTCGCTCCCAATGACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCACTCCCAATGCCCA	20
M00764_MICALL2_MIP106	CATGTGACACAGTCTCTCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTCCCCTGTGAAATC	20
M00764_MICALL2_MIP108	CCCCCTCGACAACCAGTTTCCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCAGACACAAGGCC	20
M00764_MICALL2_MIP109	AGGGCCTGCTTGAGGAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGCAGCGCCCCCAACCC	20
M00764_MICALL2_MIP110	CAGCGCTGGAAGAGGCTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAATAAGTTTTTCCAAACA	20
M00764_MICALL2_MIP112	AAGCTCCACATCTGCAGCCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCCCCGTGCACAG	20
M00764_MICALL2_MIP113	GGGCTCCTCACGTGGACGGACGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGAGGCAGCCGC	20
M00764_MICALL2_MIP114	GCCAGGCCCTCTGAGAGCCGCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGAGGCAAACAAGGC	20
M00764_MICALL2_MIP115	AACTTGGGGCTTGCAGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGCGAGTTGCCCGCAGC	20
M00764_MICALL2_MIP116	GGGTCTGGTCCCCCGACAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTCCTCCCCCAGGTGTA	20
M00764_MICALL2_MIP117	ACTCCTGTGTCCACTTGCGAGGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGCCCCCGAGTGC	20
M00764_MICALL2_MIP118	CCTCGTTCCTCTCCCCTCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGGAGGCTTTACCACC	20
M00764_MICALL2_MIP119	GATGCCAGCACCTCTCTGAGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCTGAAGCAGCTC	20
M00764_MICALL2_MIP12	GTTTCTGGCAGGGGGACTTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGTGTGGTCATGGTG	20
M00764_MICALL2_MIP120	GCAGCTTGGTCAGCAGCACCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTGGCCAGTTCTCC	20
M00764_MICALL2_MIP121	CAGAAGGGGCTTGTGGGACTACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTATCTCCAGCCCA	20
M00764_MICALL2_MIP122	GGCCCTCTTCACGCCTGCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTCCTCTGGACCACAG	20
M00764_MICALL2_MIP123	GAGGACTCTGAGGAGGAGCCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACCAAGGCCTGTGCT	20
M00764_MICALL2_MIP124	CACTCCTTCCCTCCCCACTCACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGGGTCTAGTCCCTCCA	20
M00764_MICALL2_MIP126	CCCTCCCCTGCCCAGTTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTGTTTCTCCAGCAGG	20
M00764_MICALL2_MIP127	GGCCCGGCCTTTGTGTGTGTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGGTGGCTTGGCTG	20
M00764_MICALL2_MIP128	GCTGGTGCACCTGGCACCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCAAAATCAGGACAGAT	20
M00764_MICALL2_MIP129	GCTCCTGCCGCCCTGCCCCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCCCCATCCCCAACC	20
M00764_MICALL2_MIP13	GTCCTGTCACCAAGGCTGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCACGTGAGAACCTG	20
M00764_MICALL2_MIP130	CATGGACCCCAAAAAGTCCACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACAGCCTGGGGCTT	20
M00764_MICALL2_MIP131	CCCTGGCATGGGCACCGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCCGCTCCCCCAGTG	20
M00764_MICALL2_MIP132	ACCATGTCCTCGGCATCCAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGGGGCCTGGTCC	20
M00764_MICALL2_MIP133	GGCTGAGCATCTTGACCTACGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGGGGCTCCCAGCT	20
M00764_MICALL2_MIP135	GTCTCCAAAAACATAATAATACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGTGGTGGTGCGCAC	20
M00764_MICALL2_MIP136	AGGTTGCAGTGAGCTGACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTACAAGTTCATGGTGA	20
M00764_MICALL2_MIP138	GGGACAATTTGAACTTAAGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATGTCCTGTGCTGT	20
M00764_MICALL2_MIP139	GCTTATTCTGCAGCAGGCAAACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTGTCCCCGCTGA	20
M00764_MICALL2_MIP14	GGCAGGTTCACCCTGAGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTGGGCTGGCTGGCTGG	20
M00764_MICALL2_MIP142	CAGTGAAGTAGGGTCCCCAGCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCAGGGCCGGAAGG	20
M00764_MICALL2_MIP145	GGGAATCGGGGGCTCCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAACAATAAACTGGTGAG	20
M00764_MICALL2_MIP149	GCCTCTGCCCACCTGTGGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTGACTGTGGCAGG	20
M00764_MICALL2_MIP15	CCATGAGCGACAATGGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCACTCAGCATCCCCGGC	20
M00764_MICALL2_MIP151	CCAAGCGTTGTGATGGGAAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTCCTGCCCTCGGGG	20
M00764_MICALL2_MIP161	GTGGGGCCAGGAAGCTTCTAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATTCGCCACCAGGAG	20
M00764_MICALL2_MIP162	CCTAGTTCTGAGCCCAGCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTCTGGGAGGACAACC	20
M00764_MICALL2_MIP163	GGTCTCGGCCCCCACTTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCCCCATCTGTGAAACAG	20
M00764_MICALL2_MIP164	CCTCTCTCCTTAGGAAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCCCATAAGAATGCTC	20
M00764_MICALL2_MIP165	CCCACTGCCCCCACCCCACCGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGGGGTCCAAGC	20
M00764_MICALL2_MIP167	CAGAAGCTCCGCCTGTGCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAGACAGAGGCATC	20
M00764_MICALL2_MIP168	GCAGCCATGCTGGGCGTCAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGCTCAGTGGCAGCGA	20
M00764_MICALL2_MIP17	CCAGCCCCTCAACAGTGACATGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGTCTCCAGCAGTG	20
M00764_MICALL2_MIP170	GTCACAAGTCTGTTTTTTCTCTACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTCCCTCCCTCTC	20

continued table…

ID	**MIP**	***c***
M00764_MICALL2_MIP172	ACACCAGAGCCAGTGCCCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCGTCCACCCCAGG	20
M00764_MICALL2_MIP174	CAGACCATGGCTCCACTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCAGGATGAGGTTCAAGC	20
M00764_MICALL2_MIP176	CCAGAACCGTCTCGCAAGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGCTTTTCCCACACTCC	20
M00764_MICALL2_MIP186	ACCCCTCTAACTGACCCACGACCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGTGGCAGTAACTTAT	20
M00764_MICALL2_MIP187	GGTGGAGAGTTGGCCAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGTATACATTCCCAAGA	20
M00764_MICALL2_MIP188	GGTGCAGGACTTGGAAGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCCGGCCTCTGCCCCGG	20
M00764_MICALL2_MIP189	CCAGGAAGTAAACAGTGTGATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCCACTCCCTCTGC	20
M00764_MICALL2_MIP19	ACCAGTGACCTGGGACAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCACACCAGTGACCTG	20
M00764_MICALL2_MIP191	GTCTTCCTCTCTCTCTCCAGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGCTCTGCCTGGCC	20
M00764_MICALL2_MIP192	AAGTGTGGGGCCCTGGGCAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAAACCTCAGAGACAG	20
M00764_MICALL2_MIP193	GTGTGCAAGGTGGGGGCTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGCCTGTAGCCAGAC	20
M00764_MICALL2_MIP194	GGAAGTGAGGGCACTGCCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGAGGCGGCCACAGA	20
M00764_MICALL2_MIP195	GACACGGGCGGGGAAACTGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAATATCTGCAACATGACC	20
M00764_MICALL2_MIP196	GCGCGCCCGCCGCGCGGCGGAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGATGGCGCAGAA	20
M00764_MICALL2_MIP197	CCCACATGGCGGCCATCAGGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGGCTGGGCGCC	20
M00764_MICALL2_MIP198	CAGCCGCCAAGTCCTGCCTCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGAACCGCCAGACCC	20
M00764_MICALL2_MIP199	GGGCGGGGCCTACAAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTATCAGGAGGCAGGACCC	20
M00764_MICALL2_MIP2	ATTATCTTAATTAATAATCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAGAGGAATGTGATAT	20
M00764_MICALL2_MIP200	GCCTCCCGAGAGGCCCCGCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCGCCCCCAGCCGC	20
M00764_MICALL2_MIP201	AAACCTGGAGGCTGGGGGCGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTGGGGCGGGGCCT	20
M00764_MICALL2_MIP202	ACCCCTGCGGAGACCTGGAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGGTCCCGCCCGA	20
M00764_MICALL2_MIP24	ATCTAAAAAAATTAGCCGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTAAGACTTTGGCCGGG	20
M00764_MICALL2_MIP3	ATTATCTTTATTAATAATCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAAGAGGAATGTGATAT	20
M00764_MICALL2_MIP33	GAGGGGCCCCCGGCACCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGATGGCCACATGTGGC	20
M00764_MICALL2_MIP34	AGGGTCAGCCAGCCCCGTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTACGTGAGCACCGTGAA	20
M00764_MICALL2_MIP35	CCTCTGTGGGGATGGCTCGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCACCTGCCCCTCAC	20
M00764_MICALL2_MIP36	GGGAGCAGGAGCTGCTGGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAAAAGAGGAGCCTGG	20
M00764_MICALL2_MIP37	CATCAGAGCCCGTGTGCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCTCACAGGACACAA	20
M00764_MICALL2_MIP38	CGTCAGAGCCCGTGTGCTGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCTCACAGGACACAA	20
M00764_MICALL2_MIP39	ATTCACTTATTCACTCATTCATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGCTGTGCTGCAGG	20
M00764_MICALL2_MIP41	GTCAGGGCGAGCCATAGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCAAGGTACTTAACCTTG	20
M00764_MICALL2_MIP43	CCTGGTGGTGAGACCTTCCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGGCGAGCTGCGCC	20
M00764_MICALL2_MIP44	CCCGCCCAGCCCGCAACGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCGGGCTTGGCCATGAGC	20
M00764_MICALL2_MIP45	CAGGCGGGGGACAGGGCGGCAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATGTCTGTGCGGCAG	20
M00764_MICALL2_MIP46	GCTCTCACTTGTACATCAGCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCAACGAGGTCC	20
M00764_MICALL2_MIP49	GGGGCTGGGGGCCATGAACTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCGAGAGGCGGCTGGAC	20
M00764_MICALL2_MIP50	CCCTGCCCGGCTCCCCACCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCCGCGGAGCTCCAG	20
M00764_MICALL2_MIP51	CATCCTCACCGCCCCTCCGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCACCCTGCTCCTTC	20
M00764_MICALL2_MIP52	GAAGGAGCCTGACCTCAGCACACTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGGAGGTCACCGTC	20
M00764_MICALL2_MIP53	CTGTGTCCTGGTCACGTTGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGGCTGGGCCTGGA	20
M00764_MICALL2_MIP54	CCCCAGTCCCTCAAGCTGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCTGCCTCCCTAATG	20
M00764_MICALL2_MIP6	CCTCAGAGGAGACGTCGGTACAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGCCTCCCAGCTCTT	20
M00764_MICALL2_MIP60	GGAGCCCCCTGGCCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCCCAGTGGCCCTGCTCT	20
M00764_MICALL2_MIP61	ACAAGCCCTACACCCACGTCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGACAGAGCCACGCT	20
M00764_MICALL2_MIP62	CAGTCGGGAGGCCCAGGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATATCCAGCTCTCGTG	20
M00764_MICALL2_MIP63	CAGTCGGGAGGCCCAGGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATATCCAGCTCTCATG	20
M00764_MICALL2_MIP7	GTTTCTTTATTGAGACCACAGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCACAGAGCACGT	20
M00764_MICALL2_MIP75	GTCCAGGAGTACCTGGGAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGACTACCAGCTTCTCTG	20
M00764_MICALL2_MIP76	GGACCCAGGGGCCCCCGGGTTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGGCCCCCAGGA	20
M00764_MICALL2_MIP77	GGCCCACCTGGAGGGGCTCCCAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCTGCCTGAGACC	20
M00764_MICALL2_MIP79	CACACATGGGGAGACTCCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGAGCAAATGCCACC	20
M00764_MICALL2_MIP84	CATGAGCACCAGCCTCCAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGCTGTGGGGGTGT	20
M00764_MICALL2_MIP85	CCTGCCTCTGGGCCTCAACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATAGCCACTCCACCCT	20
M00764_MICALL2_MIP9	GTCCAAGTCCGGATGCCAGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGTCCACATGCCCCTT	20
M00764_MICALL2_MIP90	ACGGCTCTGTCTCCCAACCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCTTAGGGCTTGTGAG	20
M00764_MICALL2_MIP94	CCGCTGGTGTCCCAGTATGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCCTGCCTGTCGCTTTG	20
M00764_MICALL2_MIP96	GGCCTGGCTTGGCCGTGGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATGTCCTCAGGGCTATG	20
M00764_MICALL2_MIP98	GCCCGCCTTCCTCTCCGTCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGGGTAAAAGCACCA	20
M00764_MPPED2_MIP105	CATTATTTTGTATTATTGTTGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAAAGGAGTAACAG	20
M00764_MPPED2_MIP123	ACTAATTTATTCCTTCTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTATAACCCAGGAAACTGATAG	20
M00764_MPPED2_MIP143	CGAAAGAATGTGTCACCCGGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCCACCACCCTAGATT	20
M00764_MPPED2_MIP146	CCTATCTTTTTTCTCTCCCTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTTCCTTCCTGAAA	20
M00764_MPPED2_MIP148	CCTGGAACGGCGGAGAAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCATCACAGCCCCACGTC	20
M00764_MPPED2_MIP154	GGAGAGTGAGGTTGGGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCTGTAGAGAAGAAATCC	20
M00764_MPPED2_MIP155	GTCAGAGGCGCGTGCGAGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAATCCGCCCCGGGA	20
M00764_MPPED2_MIP156	GCTGGGGGCGCGCGGGGGCGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCCGCCCTCCGCCTC	20
M00764_MPPED2_MIP157	CCTCCAGCCGGCTCGGGCCGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTTCTCCCCCCGCC	20
M00764_MPPED2_MIP158	ACAGGGACTGCCACTGGGGTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGCGGCGCTAGAGGG	20
M00764_MPPED2_MIP159	ACTGCACCGCTCGCTCTCCCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGGGCAGGGACTGC	20
M00764_MPPED2_MIP160	CCGGGTCAAGCAGGCGGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGACCCCGCGCCCCTG	20
M00764_MPPED2_MIP23	GAGACTGGGTATTTTATAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGATTTGAGTTCTGTTCA	20
M00764_MPPED2_MIP40	CCTTGGCTCCCGGAGGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGATAATAAGCTTTGGTGG	20
M00764_MPPED2_MIP83	ATATAATTATTCTCCTCATATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCCTCATTGTAAAG	20

continued table…

ID	**MIP**	***c***
M00764_MYT1_MIP10	AAGTACTTTACAATATTTATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAAAAGGGCAGAGAGCAT	20
M00764_MYT1_MIP128	ATTTCTCTATTTTTAAATACTACTTCAGCTTCCCGATATCCGACGGTAGTGTATAAAAATGTTAAATAAA	20
M00764_MYT1_MIP130	AAATAGTTATTTTTGCTTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTACAAAATACTTTTTAA	20
M00764_MYT1_MIP45	GACACAGGTCCTGGGAGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCTCTTCCTCTTCTTCA	20
M00764_MYT1_MIP56	GCGTGTTGCGGTTGCTGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACCACGGCCCCCACCCT	20
M00764_MYT1_MIP74	AGGAGGTGGGTGCAGGCGCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCCACAGCAGCACCAGC	20
M00764_MYT1_MIP91	AGGAAAGCCTTCTGGGCTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGAAGCGTAGTTCCCTGT	20
M00764_NECAP1_MIP16	ACTAACCCCGAGGCGCTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTCGCCCCCGGCAGCGCC	20
M00764_NECAP1_MIP31	CATTTATTTAAGTCTACATACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATTTTCAGTAGCGACAG	20
M00764_NECAP1_MIP39	ATAGGGAGCTCATAACCTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATTGTAATGTATAATGAA	20
M00764_NECAP1_MIP83	GCTTATTTGATTACCTTTTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAATATATTATGTATTTGA	20
M00764_NENF_MIP11	GCGAAGGGCGGGAGTTCTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGTGACATTTTTTGGTAA	20
M00764_NENF_MIP12	GAACCTGGAAATTAGGATTGGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCGTCCCGGAGT	20
M00764_NENF_MIP13	GCTGGCAGCGCTGGCCCTGGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTGGGCGCGGGGC	20
M00764_NENF_MIP14	GCCGCAGCCGCCGCCGCGGCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGGCCAGCTCCTCC	20
M00764_NENF_MIP15	GGCGGCCCAGGAAGCTCTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTGCGGCTTTTCACCG	20
M00764_NENF_MIP18	ATCTCTGTAGGTGGAAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATGAGGACTGAGAAAA	20
M00764_NENF_MIP5	CCATCTCGGCCCACTGCAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTAAATACTAGGGAGAAAA	20
M00764_NRG3_MIP1	GGAAATCACGCCCCGGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGGAGAGTCAAACTCCA	20
M00764_NRG3_MIP10	GAGTTACGCTGTAGCGACTGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCGCCACCTGGTGC	20
M00764_NRG3_MIP11	GGCCGCCCCTTCGCCGCCGCCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCATTTGAGAAGCA	20
M00764_NRG3_MIP115	ATTAAAAGTTGTTAATTTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAAATAAAATATATAATC	20
M00764_NRG3_MIP13	GGCCCATCCCCTTGGAGTCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTGGGCGTCCTGGAG	20
M00764_NRG3_MIP14	ACGGAACACTGCGGCCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCGCCGGGGGTGCCGCCT	20
M00764_NRG3_MIP143	ATTACCATTTATTTTATAGCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTAATGATATCAGTAT	20
M00764_NRG3_MIP15	GATGGGCACCCGGTGCCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGTACTTGGAGTTCCTG	20
M00764_NRG3_MIP2	AGAGTGCTGGCCGAGGGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGACAGCGGCGCTGTTCG	20
M00764_NRG3_MIP3	GGAGAGACCAATCCCAGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCACCCGCATTCCGACA	20
M00764_NRG3_MIP35	CACCATCTCTAATAAAAATGCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATATTATGTACCAATT	20
M00764_NRG3_MIP4	GGCGCGGTGCCCCGAGGATGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCAGGCAGGCCCTCT	20
M00764_NRG3_MIP5	GCCCGCTCCCTGGGGCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGCGGCGGGGCGCGTCTG	20
M00764_NRG3_MIP6	CCTCTCCTCCCCGCCCGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCAGGAGGCGGCTTGGAG	20
M00764_NRG3_MIP7	GCGGGGGAGGGGACGGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGGGCGCGGGCTCCGG	20
M00764_NRG3_MIP75	ACTTGTTCATTTGAGTATAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCTTTTTGTTGTTGTTC	20
M00764_NRG3_MIP8	GAAGACCGGCTCCTAGGATGAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTGCATGCGGCCGC	20
M00764_NRG3_MIP9	GGGCCGCGGCAGAGGCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGCCGCCGCCGCAGCCG	20
M00764_NRG3_MIP93	CATAAATAGGGAAAAAACAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAACTTCTTCACTCTCTGTG	20
M00764_NRSN2_MIP13	GAGCCCCACCCCAGCGTAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGACTCCTCACCGAAGCT	20
M00764_NRSN2_MIP14	AACTCTGGAAGGGGACAGGAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGGGGTGGGGAAC	20
M00764_NRSN2_MIP15	CCTGCTCGCTCGGACACCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAAAGGCGGGTCCGGTTCG	20
M00764_NRSN2_MIP16	GCCCGCATCCTCAGCCCGGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAACTGCGGCGCAGGC	20
M00764_NRSN2_MIP17	GGTTCTCCAGGGGCTGGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGGCTGTTTCTGTCT	20
M00764_NRSN2_MIP18	AAAAACCCATTCCTACCCCTCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGAGGTGGGGGTCC	20
M00764_NRSN2_MIP20	GGAGGGCGCCCCTTCTCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAAAGGACGCAGTTGGTG	20
M00764_NRSN2_MIP21	GGGGGGGATGGGTAGGGGGTGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGGCCCGAAGATGGA	20
M00764_NRSN2_MIP22	GTCTCCCCACGTCGGACAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTCTGAGGGTCTGGGAA	20
M00764_NRSN2_MIP23	GCGGCGGAGGGAGGAGGCGAGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGCACCCGGGACG	20
M00764_NRSN2_MIP24	CCTCTCCAGTAGCAGCAGGACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTCCCATGGCAACCC	20
M00764_NRSN2_MIP26	GTCCCCCAGGCCCCATTTCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATCTATTTGGAGTCGC	20
M00764_NRSN2_MIP27	GTAGGAGCCTCCGTGCGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCTGGAGAGGAGGGCTCG	20
M00764_NRSN2_MIP28	CCTTTCCTTCCCCGCTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCGCCCCGCCCGCCTCCT	20
M00764_NRSN2_MIP51	CATAACCCCCTCTCAGTGTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTCATGGTTCTCGCC	20
M00764_NRSN2_MIP63	CCTTCCCTTTCAATAAACAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTAACCCTTACCTTCAGT	20
M00764_NRSN2_MIP66	GCTGGAGTGCAGTGGCACGAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGACTTATTGTCTT	20
M00764_NTNG1_MIP13	CGGAAAGAGGAGCGGCAAAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTTCTGGATTGCGGCT	20
M00764_NTNG1_MIP141	CCCCCTGGTGTTCTAGGTGTCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGGCATCCTCTGCG	20
M00764_NTNG1_MIP164	CATAAATAGAAAATTATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTCTATTGAATGTTTGTT	20
M00764_NTNG1_MIP18	GAGATCTCATTATTAATATCACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAATAGAAAAAAGAA	20
M00764_NTNG1_MIP2	ATTTAGCTTGCCCCCCAAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCTCCTGCCTTAATTGT	20
M00764_NTNG1_MIP21	GAGGGGGAATTCCTTCCCGTTGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGCGGGAGAGGACC	20
M00764_NTNG1_MIP22	GGAGGCTCCGCGGGAGCTGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGTTCTCGGTCCTCG	20
M00764_NTNG1_MIP23	CCCCAGGCGGGAGCGGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGAGCCGAGCCGACGG	20
M00764_NTNG1_MIP24	GGTTTCCCCACCCCCCGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCAGGGCCGCCGCCCCGC	20
M00764_NTNG1_MIP71	ATTCTATTTTAACAGTAAGAACCTTCAGCTTCCCGATATCCGACGGTAGTGTATAATGTGATTTAATGTA	20
M00764_NTNG1_MIP77	ATTTTTATTCCTCCCATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATAAATAGGGATTTTTTTG	20
M00764_NTNG1_MIP78	ATTTTTATTCCTCCCATATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTATACATAGGGATTTTTTTG	20
M00764_NTNG1_MIP9	CAAACCGTTCCCAAGCACACCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGGCCCCCTCCCT	20
M00764_NTNG1_MIP92	GGAGAAAAAGAAAACAATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATCAGAAATGGACACTGGG	20
M00764_OLFML2B_MIP45	GCATCATTTACATAGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTAATGAAAGAGGGGCTT	20
M00764_OLFML2B_MIP46	GTATCATTTACATAGAAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTAATGAAAGAGGGGCTT	20
M00764_OLFML2B_MIP58	GTCGGGAAGGAGATGCCCAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTCCAGCCACCTGAGC	20
M00764_OLFML2B_MIP59	GGGGAGGGAAGAGGCGGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCGGGCACGGGCTAGCT	20
M00764_OLFML2B_MIP60	GTCCGGTCCCCGTGCGTCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTGGCTGCATCTCCGC	20

continued table…

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M00764_OLFML2B_MIP61	CAGCTGCCGCGCGCCGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGAGGGCGGAGCCTCT	20
M00764_OLFML2B_MIP62	CCTGTGCGCTTCCAGGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGTAACTTCTCTTCACTC	20
M00764_OSBP_MIP2	ACTTCTTCCATTAGCGGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATGACTTTTAAAAAATTAT	20
M00764_OSBP_MIP39	CTAATTTTTTTGTATTCTTAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAGTCCAGGCTGGA	20
M00764_OSBP_MIP60	ATTCTCCAGAGATACTTAAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAATTGTCAATGTTG	20
M00764_OSBP_MIP61	ATTCTCCAGAGATACTTAAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATAATTGTCAATATTG	20
M00764_OSBP_MIP87	CCACTCCCCCGGCCCCCGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCATCGCCGCTGGTAGCCT	20
M00764_OSBP_MIP88	GGCGGCTGGCCCGGCCCCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCGCCGGTCCCCCAG	20
M00764_OSBP_MIP89	ACCGGAACCGCCTACGAGAGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGCCTCCTCCCACC	20
M00764_OSBP_MIP90	GTATCTCCAGGCGGCGGCGGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGGCCGAGCCCTC	20
M00764_OSGIN1_MIP1	AGAAGCCAGGGAAAAGTGGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTGAAGGAAGGGG	20
M00764_OSGIN1_MIP10	GTTGTAAATGTAAAATACATGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTCAGATAAATAAGAA	20
M00764_OSGIN1_MIP11	CAAGCTCTCAATAGCCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAATATTGAAGATACACT	20
M00764_OSGIN1_MIP2	AGAAGCCAGGGAAAAGCGGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCTGAAGGAAGGGG	20
M00764_OSGIN1_MIP21	GTGAGGAGGGGGAGGCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTCTACCAGGAACCAG	20
M00764_OSGIN1_MIP22	GTGAGGAGGGGGAGGCATCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTTTCTACCAGGACCCAG	20
M00764_OSGIN1_MIP27	GCCCAGCAGGGGCCCTTTAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATGGCAAAGGCCAGGCT	20
M00764_OSGIN1_MIP28	ACCCCCATCCCTGGGGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATGAATGAACTTGCACA	20
M00764_OSGIN1_MIP31	CCAGCTGGACCGGAGGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCCCTGACCCTCCTAG	20
M00764_OSGIN1_MIP48	CCCCTCCCGGTCATCATTGTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACCCAGGCCTCACCC	20
M00764_OSGIN1_MIP54	CCCCACGTGGTTCTGGGCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGGCCTCGAAGGCCG	20
M00764_OSGIN1_MIP61	GCTTCCTGACCAGGAACCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTACGTGGTCAAGAAG	20
M00764_OSGIN1_MIP62	GCTCACCTGGAAGAGGGGGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGATGAAGGGCAGGG	20
M00764_OSGIN1_MIP63	CCGACGCGGTCCTCTACGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGGGCATCCCCGGGGAG	20
M00764_OSGIN1_MIP64	GACAGCCCCGCGCCAATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTGTGGTACTCGGGGTA	20
M00764_OSGIN1_MIP68	GGTTCCTCTTGGCGCTCAGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGGGAGCTGGCCACA	20
M00764_OSGIN1_MIP69	GCTCCCAGGCCCTGAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTGTACGCCATGGGGCCG	20
M00764_PCDHB5_MIP24	GCCACAGACCACGGCTCCCCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGCCGCCCCAGAA	20
M00764_PCDHB5_MIP25	GCCACAGACCGCGGCTCCCCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGCTGCCGCCCCAGAA	20
M00764_PCDHB5_MIP26	CCTGCAGGGCCTCGTAGTCCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGTTCTGCAGCGGA	20
M00764_PCDHB5_MIP27	CCTGCAGGGCCTCGTAGTCCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGTTCTGCAGCGGA	20
M00764_PCDHB5_MIP28	GGCTACCTGGTGACCAAGGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGAGCAGCGAGGC	20
M00764_PCDHB5_MIP29	GGCTACCTGGTGACCAAGGTGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTGAGCAGCGAGGC	20
M00764_PCDHB5_MIP30	GCCCAGGGCACCAGCTCGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATTGTGCGCCCACAT	20
M00764_PCDHB5_MIP31	GCCCGGGGCACCAGCTCGGTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCATTGTGCGCCCACAT	20
M00764_PCDHB5_MIP32	GCTGAACAGCCCGGGCTCCGTGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCAGCGTGGCGGTGG	20
M00764_PCDHB5_MIP33	GGAGGCTCGCCATTGTCCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGCCACCACCAGGTA	20
M00764_PCDHB5_MIP34	GGAGACTCGCCATTGTCCTTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGCCACCACCAGGTA	20
M00764_PCDHB5_MIP42	GCAGAATATATAGAAAATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTCATTTGTTAGCATATG	20
M00764_PDE11A_MIP111	GAGAGTTACCCATGTTGTTATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTATATCCTTATAATTT	20
M00764_PDE11A_MIP13	CATTTTTCTTTATATTTAAATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAAGCAGATAATGAA	20
M00764_PDE11A_MIP185	CATACCTCTAATGCAGTACTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATCTCAATAAAATCT	20
M00764_PDE11A_MIP187	CAATGGGCTATGATTGTGCCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCATTTAATTTTT	20
M00764_PDE11A_MIP24	GACATAATAAAACTTACATATATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATTCAGTCCCCA	20
M00764_PDE11A_MIP92	GAAATAATTTTGGCATATAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATTTCAGTCTACACAA	20
M00764_PIAS1_MIP10	GTTAGCCTCCCTGCCCCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGGGCGCTGACGGGTCGT	20
M00764_PIAS1_MIP11	GGAAGGTGAAAAAGCCGAGCCCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGCCTGACAGGAGC	20
M00764_PIAS1_MIP12	GCTTGTCAGGAAGCGCCTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTTCCTCCTTTGCAGTCC	20
M00764_PIAS1_MIP13	GAGTCCGGGGCGGGGGCTACTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCCCGGGGCTCGCT	20
M00764_PIAS1_MIP22	CACTCATAGTAACTTTTATAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATGAATAAACTATCAGAT	20
M00764_PIAS1_MIP32	CATATTTCAAAGATAGAATTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGTTTTCTTATTATGG	20
M00764_PIAS1_MIP37	CAAATTATCATAAATATAACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGACCTGTACTGTGAAGT	20
M00764_PIAS1_MIP42	AAACATTTTTATTTTGGATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGTGAAAGTGAATACA	20
M00764_PIAS1_MIP5	GAGCCCCATCTCTCTGCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCACGTTCCATTTAAATA	20
M00764_PIAS1_MIP53	AATAAACAAATTCTAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTAATAATATTCTTCCATGTTT	20
M00764_PIAS1_MIP6	GGGGCGGGGCCAGGCCGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCTCGCCGCTTGGCGCCA	20
M00764_PIAS1_MIP66	GTATATTAATTTTTGTCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCTTCTAAGTTTAAAACT	20
M00764_PIAS1_MIP7	CCACCTTCCCAGCCCGCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGCGCTTTACCTTTAG	20
M00764_PIAS1_MIP8	ACCCGGGCCTGGAGTTGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGATGGCGGACAGTGCGGA	20
M00764_PIAS1_MIP9	GAGTCAGGCCCGAGAGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCACAACAATAACACGCC	20
M00764_PIAS1_MIP92	ATTTATATACAAAAGTAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAAATAATGAAAAATCT	20
M00764_PIK3R4_MIP122	ATCACTATAATCTGATTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGGAAAACTAATATAT	20
M00764_PIK3R4_MIP123	ATCGCTATAATCTGATTTTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAGGAAAACTAATATAT	20
M00764_PIK3R4_MIP3	GGGATTTTTATTGTATATGTTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCAAAATTATGTCT	20
M00764_PIK3R4_MIP51	AATACTTTTTCTCAAATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCATATATATGCATTCT	20
M00764_PIK3R4_MIP58	ATTCAATAAATACAACTTGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCATAATCAAATAT	20
M00764_PIK3R4_MIP71	GAAATTTATTAGCTTTTAATTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGATTTCTTTGTTTTCC	20
M00764_PIK3R4_MIP74	CATATTTCTAATTCTATGAATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATCCAGTGTGAAA	20
M00764_PIK3R4_MIP77	ATTTTTGCAAAACTATATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTACTTCTATCCTAAGAAA	20
M00764_PIK3R4_MIP78	ATTTTTGCAAAACTATATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGTTCTATCCTAAGAAA	20
M00764_PIK3R4_MIP79	CCCTTTTGGATATTTAAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCAAATTTTATTATTTCTTA	20
M00764_PKP4_MIP14	GCCTTTAAAAAATTAATCTTTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCGCCAGGAAGCT	20
M00764_PKP4_MIP154	GCATTCTGCTCATCATTTGTCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACAGTCCCCACCCC	20

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M00764_PKP4_MIP27	ATTCTATTCACTAAGAAGTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATATACTTTATGCCTT	20
M00764_PKP4_MIP31	AAAACAGGAAAAGCTAAGTACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTAAAAATAATAAAATAC	20
M00764_PKP4_MIP41	CGTCTCAAAACAAAAAAAAAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCGGGCGCCTGTAATCT	20
M00764_PKP4_MIP69	ATAGTTAAAAATGTAAAGATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCTTGGCCAAACT	20
M00764_PKP4_MIP83	ATATTTCTTTGTAATTCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTACCTTAGTACATTCTAA	20
M00764_PKP4_MIP89	CAATGAACATACTATATAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGATGGTTTTAATTACTTA	20
M00764_PKP4_MIP9	AAGAATCTGATTATTCAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAAAAAAAGAGTTTAAAAC	20
M00764_PLXNA2_MIP124	CATACAGACGCACATGGATGCACTTCAGCTTCCCGATATCCGACGGTAGTGTATGATGAGGAGGAGGCTG	20
M00764_PLXNA2_MIP185	GCCATCTTCTCCAAAGGGCAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTGTCCCTGCCCTTCGG	20
M00764_PLXNA2_MIP216	CGGCTTGGCCGCGGCGGGCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCTGGGTAAGCGGCGG	20
M00764_PLXNA2_MIP217	CTCGGAATCAGGGAGACGACCAAACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGAGCGCCCGGCCCA	20
M00764_PLXNA2_MIP219	GCTCTCAGGGGGCACCCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAATTCATTAAAATCCA	20
M00764_PLXNA2_MIP220	GGCGACAGCGCCCAGCCGGGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCAGAGGAGCCCGGAA	20
M00764_PLXNA2_MIP223	GCAGCTCTGGCTCCCGCGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTCGCACGCCCTACCGCTC	20
M00764_PLXNA2_MIP224	CAGACTGGAGCGGGAGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGCCTCTATGATAATGAG	20
M00764_PLXNA2_MIP225	CCCCTCCCCCGCCCGCGCGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTCCCTATTTCACCAT	20
M00764_PLXNA2_MIP226	CAGGGTGCTGGCGGTGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTAAGGTGGCCGATGGGT	20
M00764_PLXNA2_MIP61	GCTCCGAGGCTGAGCCTGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGGGGAGAGTCATGAA	20
M00764_PTPRD_MIP133	CATAATTTGTCATTAGAATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGGTAATTTTATTTGA	20
M00764_PTPRD_MIP139	CATACTAATAAAAAGCAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGATATCTATTGTATAATT	20
M00764_PTPRD_MIP17	CAGAACATCCATGAAGCTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATATATTTTCTTTTTTTTC	20
M00764_PTPRD_MIP176	ACTAAATAAATAATTCTGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATGTATATGTTTTTGTG	20
M00764_PTPRD_MIP177	CAATGAAATGAGGAAAGGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGCTACATTCATTTCA	20
M00764_PTPRD_MIP18	ATTTTTGTTTTCCACATTTTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCATAAGTTTGCCACA	20
M00764_PTPRD_MIP188	CATGTGAATAATTAATTCTTCATCTTCAGCTTCCCGATATCCGACGGTAGTGTACTTACCAATAGATTCT	20
M00764_PTPRD_MIP19	CCTAATGGAATATCAAATATACTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATTATTTAAAATCATG	20
M00764_PTPRD_MIP193	CACTAATACATAAAAACACACTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAATAAAATGTTCATAT	20
M00764_PTPRD_MIP222	CCTTCGCGCCCCGCCACGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATTCCGGAGCAGCAAGAGG	20
M00764_PTPRD_MIP223	GCTGGAGGAAAGTGTTGGCGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACTGGGCTGGCCGCACG	20
M00764_PTPRD_MIP224	ACCCGAAATCCAGCATCCAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAATTTAATCCCGCGGA	20
M00764_PTPRD_MIP225	GCTGACTCTCTTCCACTTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAGGGCCAAGAGGAC	20
M00764_PTPRD_MIP226	GTCTCCTCCCCCTCCTCCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTCCTCCTCTTCCCG	20
M00764_PTPRD_MIP227	ACAGCGGCGGCGGCGGCAGCGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGGAGGAAAGAGGAG	20
M00764_PTPRD_MIP228	AAAGTGAAGCGCACGCGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTCTCCTCCCTCCGCC	20
M00764_PTPRD_MIP235	ACACATAAAATTTAAAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAACAAATACTTACCAGGT	20
M00764_PTPRD_MIP237	GAGAAATGTTATTATATGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTCACAGGTTAGGAATTC	20
M00764_PTPRD_MIP241	GTAAATGCATAGATTGAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTATACTTCATTTATGGA	20
M00764_PTPRD_MIP247	ATCTTGTAGGGGGAAGCTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATCTGATCAATTGACT	20
M00764_PTPRD_MIP250	ATAAGAAAAAACTATTCTAAAATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTATAATATTTAAAG	20
M00764_PTPRD_MIP254	GTGAACTAGAAATAGATAATACTTCAGCTTCCCGATATCCGACGGTAGTGTAACCAATACTTTTAAAAAT	20
M00764_PTPRD_MIP259	CCCCCTCCCTCCGGAAAAGAAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGCCTCCTCCCCTC	20
M00764_PTPRD_MIP26	CAATCGTATATTGTCTATAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACACTCTAGTGCAATAAAAA	20
M00764_PTPRD_MIP260	GGTTGGGGAGGCCGATGAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAATTATTCTGAAGGCAAAGT	20
M00764_PTPRD_MIP261	GCGCTCCCCTCCCAGCCCGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCGCGCCCGCAGCCGG	20
M00764_PTPRD_MIP262	CGTCTCCAGCAGCTGCCGCTCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCACGCGCTCCGGCC	20
M00764_PTPRD_MIP263	GTGCGAGCGAGACGAGGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCGCCCCGGCCCCCGCCC	20
M00764_PTPRD_MIP264	GGGAGACCCGGCACCCACCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGTGGGCCCCGCTCCGG	20
M00764_PTPRD_MIP265	CCTCCCGCCCCATCTGGCGCGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCATATCCTCCTGTTCC	20
M00764_PTPRD_MIP29	GTCTATATATACATAGACACCTTCAGCTTCCCGATATCCGACGGTAGTGTAATACCAATATGTCAAAAAA	20
M00764_PTPRD_MIP3	GTTATTTGTTTTAATTTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCATACAGACTTCTTT	20
M00764_PTPRD_MIP33	AAGTTTACACAGTTAGAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTCTACAGCAAGATATT	20
M00764_PTPRD_MIP51	ATTTAAAGTATCTGACACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTACTTTGTAATAAATAT	20
M00764_PTPRM_MIP10	CGCTCCCTTCAGCCGGCCTGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGTAGTGGCTGTGGC	20
M00764_PTPRM_MIP109	AAATATCTTCTCTTCAAAGGTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTAAATACTAGATAG	20
M00764_PTPRM_MIP11	CACGTCACGGCCGCCCGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCACAGGCAGCCCCA	20
M00764_PTPRM_MIP12	GAGGCGGCGAGCTCAGCAACCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCGCCCGGGGCTGGGC	20
M00764_PTPRM_MIP13	CCCCTGCCCGGGACCCGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGGGTCCTCCTCCCCT	20
M00764_PTPRM_MIP130	GTTTTCTTTAAGACAAATAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAATAAACTTTTAAGG	20
M00764_PTPRM_MIP131	GTATTATATATACATATATATATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGTCCAAGTGGCCACA	20
M00764_PTPRM_MIP135	GAAAGAGTGTAATATTCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTATTCTTTTCCAACCAAT	20
M00764_PTPRM_MIP14	GTCTCTCCTCGCTGCCTCGGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGAGTGGGGCCAGGG	20
M00764_PTPRM_MIP15	GGTAAACAGCAGAGCGCTAAGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGCCAGGCAAGTCCC	20
M00764_PTPRM_MIP16	CGCCCGGGACGCCGACAGCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACCATGAGGGGACT	20
M00764_PTPRM_MIP239	ACTATTATTCTGCAGAGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAGTAAAGTTAAATTTTC	20
M00764_PTPRM_MIP48	GAAACATAACAGTTTTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTTATTACCCAGCATTGACATC	20
M00764_PTPRM_MIP5	CATGCCTCGGTGTCCCGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGGGAGCCGGGAGCGCC	20
M00764_PTPRM_MIP6	CCGCAGCCGCCGAGCAGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTGGCGATCGCGGGGCT	20
M00764_PTPRM_MIP7	AAAAGCGAGCCAGGAGATCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCGGGACCAGCGGCCTGC	20
M00764_PTPRM_MIP8	GCTACCAAAATAGAAGACGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGGCCGCGCCCGCGGGGT	20
M00764_PTPRM_MIP9	GGCTCTGGGGAGGGTGACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCTGGGGGCGGCCCCGC	20
M00764_RASGRP4_MIP22	CAAAATAAATAAAGGAAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGAGACGCCAAGGTGGGAG	20
M00764_RASGRP4_MIP38	GTGCTCCTCTGTCCCCGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGACGAGATCTATGAG	20

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M00764_RASGRP4_MIP42	CACAGCCCGACAGGTTGCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGAGCTCACTGAGCTC	20
M00764_RASGRP4_MIP47	ACCTCAACTGGGATGCTGTCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCGGCTCAGATAG	20
M00764_RASGRP4_MIP52	CACCTGGTCCTTCCCCTTCCAGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCTGGGTGCAGGTG	20
M00764_RASGRP4_MIP57	CCAATACCCTGCCCCTCTTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAACTCAGCCCAGAGA	20
M00764_RASGRP4_MIP59	GATGCGACACCCTGAGGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCCCACACACATTTAG	20
M00764_RASGRP4_MIP64	GTGGAAGGAGGGGTACTCTGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACAGTCCTGGAGGATA	20
M00764_RASGRP4_MIP73	GCTCTCTATCTCCCCCATCTTTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCACCCTCAGGCCA	20
M00764_RIMS2_MIP1	GACCCCAACCCCACCCACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACGGTTTCCCGGAGAA	20
M00764_RIMS2_MIP106	ATACTTTTATTTATATAACTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGAATTTCGGGAACG	20
M00764_RIMS2_MIP138	GCATATCTTCTCCTTGTAGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAGATTTAATATTTT	20
M00764_RIMS2_MIP151	GAAAATGCATTTTAGATAAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTGATGCTGGTGCTTT	20
M00764_RIMS2_MIP159	CATCAGCGGCATCTCCCTGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAGGAAACAGCAGGAGC	20
M00764_RIMS2_MIP16	CCATTCTTAAAACAAGTAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTATAACAACAATAAGGAAAAA	20
M00764_RIMS2_MIP160	GCGGTCCCCGCCAATCAGCGGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGGCGGGCGGAGCG	20
M00764_RIMS2_MIP163	AAAGCGGGTCCTCGTCCAAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCAGGGAGGCAGGGG	20
M00764_RIMS2_MIP19	CCTTAATGATAAAATAGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAGAGGCATTGTGTAATAC	20
M00764_RIMS2_MIP190	CATAAGATTTGTATATTTAACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCAGATCAAAACTTGT	20
M00764_RIMS2_MIP195	ATTATATTTCTAAAGAAATATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATTTAAAGCAATTTCTT	20
M00764_RIMS2_MIP2	CCCGGGGGCTTGTTCGCAGGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGCCGGCGGGACG	20
M00764_RIMS2_MIP21	GTTCATTTGTATTATTTAATCTTCAGCTTCCCGATATCCGACGGTAGTGTCATAATCCTAATTCACTGCT	20
M00764_RIMS2_MIP3	AGCGCCCGGAGGCGGAGTACTGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGGCGGGAGGGC	20
M00764_RIMS2_MIP4	CCCTTTCCCTTGAACCGCTCACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCGCCCCGGTCCGCC	20
M00764_RIMS2_MIP5	GGGGAGGGTGGTGGAGTAAGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGTGGGGAAGGAGGGCT	20
M00764_RIMS2_MIP6	AGGCCATTGATTTGTATGTATTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACAGCCCTTCGCCC	20
M00764_RIMS2_MIP7	CAATCCAAGGCGACAGCCCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGACATGTTTGGTGGA	20
M00764_RIMS2_MIP75	GGGTGTACTATATTATGCTTACTTCAGCTTCCCGATATCCGACGGTAGTGTTACAAAATAAATAAATGAT	20
M00764_RIMS2_MIP78	GTTTCTAAAAGATTATCAATGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTAATAGAAACATAAA	20
M00764_RIMS2_MIP79	GATAATGTGCTTAATGATGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTACAGTATCATTAAT	20
M00764_RIMS2_MIP8	GGAGGAGAGGAAAATCATCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCCTAGGGTGGTTCGG	20
M00764_RIMS2_MIP80	ATTATGGATTAAATGGCAAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTAGAAATGTTTATA	20
M00764_RIMS2_MIP97	AAACACTATTTGATATTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATAAATGAAGCAGTATGAT	20
M00764_SEMA6D_MIP120	CCTATCTTTAATAAGTAAGAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCTCTTATCTTGCA	20
M00764_SEMA6D_MIP151	CAGTGATCAAGCAGATATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTAACTAATACATAGTATGT	20
M00764_SEMA6D_MIP153	ACTATTTTTTAGATAGAAACTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATATGTTTATGCTAA	20
M00764_SEMA6D_MIP194	AGTTTACAAGGTATCTATTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTAAAAATATAACATGTT	20
M00764_SEMA6D_MIP21	CATTAATACAATATAATGGACCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCATAAATGTATACACC	20
M00764_SEMA6D_MIP59	GTATTTTATAAAGATAAAGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTCATTTCTCCCACA	20
M00764_SEMA6D_MIP60	AAATCCCATTTCTACTTTGAATGACTTCAGCTTCCCGATATCCGACGGTAGTGTCTTTACAAACCCGCCC	20
M00764_SEMA6D_MIP64	GAGTAGCTGCTCCTTCTAGCAACTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGGTGAACCGTGGC	20
M00764_SEMA6D_MIP65	GCTCCGGCTCGCCTGATGGATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGCCTCCAGGCGGCGC	20
M00764_SEMA6D_MIP73	ACGCTGGGACGCCCGGGGTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGTTAGCAGGGGTTG	20
M00764_SEMA6D_MIP74	CGCTCTGGGGCCAACGGGCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTACGCCCGCGAGGGG	20
M00764_SEMA6D_MIP75	GGTGACTTGGCCATCCCCATCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCTGGAGAAGGGGCG	20
M00764_SEMA6D_MIP76	GAGCTCCCGCCCCTCGCCGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGTGGCCGGTGGGCT	20
M00764_SEMA6D_MIP77	GTTCCCCGACTGGAAATGCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCTCCCCTTACTGGCAG	20
M00764_SEMA6D_MIP80	GCTGCAGAACGCCTCTCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTACTGTATCAGTTTCTG	20
M00764_SETBP1_MIP1	GATCGGAGCGGCAGCGCGGCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGCCCGCCCGCGTC	20
M00764_SETBP1_MIP10	CACACACGTCGCCCCCGGTTCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGAATCGCGCCCAT	20
M00764_SETBP1_MIP11	CTTATTGAGTTTCGCCTAATCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCGGGCGAGGTTG	20
M00764_SETBP1_MIP112	AAAGATCAGGTACCAAGGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTCCAGATAAGAACACT	20
M00764_SETBP1_MIP113	ACTAAAACATTATTGTACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTCTTAAAAGCAAATGGGA	20
M00764_SETBP1_MIP12	CCCTCCAGCCCAAAGCTTCCACCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCCGAGTCCACTCCAC	20
M00764_SETBP1_MIP13	GTTAAGTGGAGCTAGAGAGCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCGGTCCTGCAGC	20
M00764_SETBP1_MIP14	CCTGCCTTCCCACCCCTTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCCTGTTCTTCTTTCTAT	20
M00764_SETBP1_MIP145	AATGTATTTGTATTTTATTGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCACAAGATTGTCTTACAA	20
M00764_SETBP1_MIP2	CGAGCGGGCGGGCAGGGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACTCCAGCGCTCACCGG	20
M00764_SETBP1_MIP3	GCCCGCGGTCGCTAGTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGATGGGTTGGAGCGTTAAAA	20
M00764_SETBP1_MIP6	ACATTCACACACACACGCCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCGGCGGGCGCCCCGGCC	20
M00764_SETBP1_MIP7	CAGATGCTCATCGCCATGGAGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGGCGGCAGAGTCG	20
M00764_SETBP1_MIP8	CAAACGGCGAGCCGCGAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCGCGTGCTCACCCATGT	20
M00764_SETBP1_MIP9	CCTGCATGCAAAAGTTCACGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGCGGAGCCGGAGC	20
M00764_SETBP1_MIP98	GCGGCGGGCTCCAGCACCAGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGTGGCGGGGGCAG	20
M00764_SETBP1_MIP99	CAGGAAGAGGAGGTGAAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCCACCGCCGCCACCACC	20
M00764_SGCZ_MIP28	GAAATAATATATATATTGTGGACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTGGTGGGGACATAGA	20
M00764_SKOR1_MIP10	GGCTACCGGGTATGGTCCCCTTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACGGCGACTACCGGC	20
M00764_SKOR1_MIP11	GTAATTGTTCAAACTTGGGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTTCCAAGGACAGGCTG	20
M00764_SKOR1_MIP12	ACTTTATGGCCCCAGGGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTGAAGTACTCCTCCCT	20
M00764_SKOR1_MIP13	AAGTGGGGAGGGCCCAGTGCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGGCCTGCACGCCCC	20
M00764_SKOR1_MIP14	CGGCTCTCAGCTGTCAGGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGTGCGGCCGCTTACC	20
M00764_SKOR1_MIP15	GGCGCCACACCCACCGCCCGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCCGTTGACCCCGAGGC	20
M00764_SKOR1_MIP16	AGCACGGCTGTGCGCGCGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCTCTTCTTCCGGCCAGT	20
M00764_SKOR1_MIP17	CCTGGTTCTCCGCGCTCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGCGGCTGGAGCCGGGC	20
M00764_SKOR1_MIP18	CTTTTTTTTCGTTTAGTTCTGATTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCGGACTCCCGCC	20

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ID	**MIP**	***c***
M00764_SKOR1_MIP20	CATAGTTGCCGATTTCGAGAAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGACCCCCTTCTTCTGAC	20
M00764_SKOR1_MIP26	GCTAGGTCCGGGTGCGCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTTATCCAGCCGAAATCTTTCT	20
M00764_SKOR1_MIP27	GCACCCAGCTTGGTGCCCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGAGGAGAAGGAGGAGG	20
M00764_SKOR1_MIP28	CCCCGCCCGCCCGCGTGCATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCTTCCCTGGCAGACACGG	20
M00764_SKOR1_MIP29	GGGGTGGGGAGGGGGGAGGGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCGTGCGCCTTCGG	20
M00764_SKOR1_MIP30	GTATCTGGGTTTCACTTCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCGGGCTTCAGGAC	20
M00764_SKOR1_MIP33	GTACTCGGGCTCCAGCGCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGAAAATGGCTCATCT	20
M00764_SKOR1_MIP36	GGCGTGCACTGCACGCACGTGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTTGGGTGGTTTGTG	20
M00764_SKOR1_MIP40	CAGTTCGTCTGTGGCCGACTTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGCACCACCCTTCC	20
M00764_SKOR1_MIP41	GGCCTCCGGGGCCACCTCCACCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGTCGGGTGGGCAG	20
M00764_SKOR1_MIP42	CCTCATCTTCGCCACAGCGCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGATCACCGGGTAGCTT	20
M00764_SKOR1_MIP43	CATCCTTACGGCTTCCCTACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGGAGCTAGTGGCCC	20
M00764_SKOR1_MIP44	GGGAAAAGTGGTGGGGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCACCCCCGCCTGTCCCCGC	20
M00764_SKOR1_MIP45	GCCAAGGACGCAGCGGCAGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGGAGCGGCGGCGGCGG	20
M00764_SKOR1_MIP46	GATGCCCCCAGAACATGGCGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGCAGCGGGGTAGGAC	20
M00764_SKOR1_MIP47	GTGCCGAGCCAGCCAAAGAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCAGCCTCCCGGTA	20
M00764_SKOR1_MIP48	GTCCAGGGGCTCTGGGGCACCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGGCAACGGGGCCA	20
M00764_SKOR1_MIP49	GAGCATCGCTAAGCTCTACGGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCTGGACGAAGACG	20
M00764_SKOR1_MIP50	AAGGCCGACACGTAGGAGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGTCCGGGCTCACGTA	20
M00764_SKOR1_MIP51	GACGACGAGGACGCCCAAGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCTGGGAGCGGCGG	20
M00764_SKOR1_MIP52	GGGAAGCGGTTGGATTCCACGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGAGTTTGCGGGACC	20
M00764_SKOR1_MIP53	ACTTGGCAGCCGAAGACTTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACAGCCCACTGGACCC	20
M00764_SKOR1_MIP54	CCCAAATGCGGGCCGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGGGCGCGGGGCTCACCT	20
M00764_SKOR1_MIP55	AACGGGAATTTTGTTCCGCGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTACGAGCTGCGAGAGC	20
M00764_SKOR1_MIP56	GGGCCCGCGGCCTCCTACGTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGCGGGGTAGGGCTG	20
M00764_SKOR1_MIP57	GCTCTTCACGTGCTCATCCCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCCTTCCTTGACCC	20
M00764_SKOR1_MIP66	CCCCCCCTTTCACCCCTACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCTGTTGCACCATTTCTT	20
M00764_SKOR1_MIP74	GTTTCCAAGTGTAAATACCGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGAGCGAGGAACAA	20
M00764_SKOR1_MIP75	CCGGGGAGCCCGGGAGGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAGTTAACCCCTTGAGGTC	20
M00764_SKOR1_MIP81	AAACGAAAGTCACGGGTACACTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCAGAACCCGCGGGGC	20
M00764_SLC39A11_MIP105	GTGCTGACTCAGAAGGGGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGCACAGGAAACACCCG	20
M00764_SLC39A11_MIP106	GAATTGTGGCTCCCACAATTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTAATCTTTACAATAAT	20
M00764_SLC39A11_MIP140	GAAAAGCCAACTCACTAGGGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCAAACCCCTCCTCTC	20
M00764_SLC39A11_MIP142	GAAGAATAGATTCTCTGGTTCACACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCATCAGCCCCCGCT	20
M00764_SLC39A11_MIP147	AATGACGGAACCAGAGCCTCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTACATAGGAGGCAGAGGCT	20
M00764_STEAP4_MIP123	GATTTCGCAAGAGAAGCGGAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAGCGCCAACGGTG	20
M00764_STEAP4_MIP29	CCATTACCTATAGCTGTAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGAACTTATTTGTTTTTG	20
M00764_STEAP4_MIP3	CAATGTCACTATGTACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTGTTAACAATAATATATATTC	20
M00764_STEAP4_MIP57	AAACATATCAGCAGTAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTAATTAAACAAAACTAGGAAA	20
M00764_STEAP4_MIP6	ATTAAAAGCAAATACACATACTTCAGCTTCCCGATATCCGACGGTAGTGTCCTACTCATGTAATTTAAAA	20
M00764_STEAP4_MIP75	AATGATTAAAATATATTAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTTATGCATGATCTTCCC	20
M00764_STEAP4_MIP78	ATATAGAAGCTACTTATTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATAATGATGAATCTTCACAC	20
M00764_STEAP4_MIP79	GTCTTAGTCTATTATAATTGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCACTATATTAGGTT	20
M00764_STEAP4_MIP8	CATATTCTACTTTTACAATGCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTGGACATCTTTCCATA	20
M00764_STEAP4_MIP80	CAATGCAAGTGAAATCCAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTATAATACCTAAATAATAC	20
M00764_STEAP4_MIP96	ACTAACTAATAATTTTTGAGACTCTTCAGCTTCCCGATATCCGACGGTAGTGTATATAATACATCAGTCT	20
M00764_SUN1_MIP1	ATAAGGCCTTTATTTATTTACTCTTCAGCTTCCCGATATCCGACGGTAGTGTTATATTTTTGTAAACATG	20
M00764_SUN1_MIP10	GGCAGACCCCTCCCCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAACCTCTCCCCAAGAT	20
M00764_SUN1_MIP11	TGCAGACCCCTCCCCCAGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCAAACCTCTCCCCAAGAT	20
M00764_SUN1_MIP119	AAAATATTAGCCTTTAGAATAACTTCAGCTTCCCGATATCCGACGGTAGTGTAACTGGAACAAAACAGAT	20
M00764_SUN1_MIP12	CAGATACGCGGTCTACGTTGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGGGGGGGTTTGCATCT	20
M00764_SUN1_MIP13	GTCCCCCTCCTCCAGGTGCAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCCCCCAGGTGCAGAT	20
M00764_SUN1_MIP14	CATTCGGGGGAAAGGCCTGCATCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGAGGACTCCAGGC	20
M00764_SUN1_MIP142	GTTTTTAAAATTAAAACTAACCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACGGCACACGAATGGAG	20
M00764_SUN1_MIP15	CCTCGGCCCGGGGCGCGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTCCCCCTCCCCTTCC	20
M00764_SUN1_MIP16	CGGGAGCAACGCAGGCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTGCCCTTGGCCCGGCCCG	20
M00764_SUN1_MIP165	GGGGGTGTTGCAGCCAAACGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGCCGTCTTCTACCG	20
M00764_SUN1_MIP169	GCAGATGTGACCGGAGAGCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAAATGCACGTTCTAACC	20
M00764_SUN1_MIP17	GCTGCGCCAGGGCCTCCTGGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGCAGGTGAGCTCC	20
M00764_SUN1_MIP170	GTGTTGGTCGGATGGGGGGGCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTGCCAGGCTGTGCTTCT	20
M00764_SUN1_MIP171	CCCCCCATCCGACCAACATCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAACCAGCACTGCCC	20
M00764_SUN1_MIP172	GTGGTGTTGGTCGGATTGGGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGTGCTGGTTCCCTGT	20
M00764_SUN1_MIP173	GATGCGGGGGCAGTGCTGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGGTGTTGGTCGGA	20
M00764_SUN1_MIP174	GATGGGGGGGCAGTGCTGGTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTGTGGTGTTGGTCGGA	20
M00764_SUN1_MIP175	CCCCCCATCCGACCAACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAAGGTGAAGGTCAAT	20
M00764_SUN1_MIP176	CCCCCAATCCGACCAACACCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAAAGGTGAAGGTCAAT	20
M00764_SUN1_MIP18	CGCGCTGAGGGCGCCCAGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGGAGCAGGACCCCTG	20
M00764_SUN1_MIP19	AGGAGCGTCCTCCCCGCGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGACCCTGGCGGTCGTGGC	20
M00764_SUN1_MIP203	CCTGCTCTTCTTCAGCCATGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCTGACCTGAAGATGAGC	20
M00764_SUN1_MIP204	GTGTGCTTGCTCTGGGACATGTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGTGGGAGGTCATTCCC	20
M00764_SUN1_MIP208	GGCGTGGGCACCTCTCTGCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTCTCCTGAGCGCGTGACCTT	20
M00764_SUN1_MIP21	CATGGAGAGACCACAACCCTACACTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTTATTTGCACC	20
M00764_SUN1_MIP217	CCGCCGGAGGGATGGCTGGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAAGAACAGCTGTCCTATG	20

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ID	**MIP**	***c***
M00764_SUN1_MIP221	GATGTCTCCACGTGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTGAGCCGCCGCACAGA	20
M00764_SUN1_MIP222	GGTGTCTCCACGTGGCCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCCTGAGCCGCCGCACAGA	20
M00764_SUN1_MIP223	CCCCGAGATTGACCCACAATAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGAGGCTGGCGGTGG	20
M00764_SUN1_MIP226	ACCTGAGAGCCCAGCCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTTTGTTCTGGGTCCTTTC	20
M00764_SUN1_MIP228	ACTTGCAGCTGTGTCCCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTTTTGAACACGGGG	20
M00764_SUN1_MIP229	ACTTGCAGCTGTGTCCCATGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTTTTTGAACACGGGG	20
M00764_SUN1_MIP65	ATCTATAAACTTGCTGTTTTTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTATATTAACAGTTG	20
M00764_SUN1_MIP8	GAGGTCTCCTGCAGGGCCCCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCTGGCCGCCGCC	20
M00764_SUN1_MIP85	AATTTATAGAATTTCAAATACTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAGCCACTCCTTCAG	20
M00764_SUN1_MIP87	GGGGTAACCCCCAGGGGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGACTGTGGAGTAACCC	20
M00764_SUN1_MIP9	ACGCGGACGCCCTCCTGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGGGGAATTGGGGTGG	20
M00764_SYT5_MIP11	CGCCTGTAATCCTAGCACATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGATTGCACCATTGCC	20
M00764_SYT5_MIP12	CGCCTGTAATCCCAGCACATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGATTGCACCATTGCC	20
M00764_SYT5_MIP13	AAATGCCGTCTCTACTAAAAATACACTTCAGCTTCCCGATATCCGACGGTAGTGTATAGAAAAGAAAAGAAA	20
M00764_SYT5_MIP26	GTCTGCTCTCCTCTCTCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGACAACTTTCCAGCACACT	20
M00764_SYT5_MIP27	AAGCTTAAGGGTGGGGCTGGCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGGGTGTGTCCGCGA	20
M00764_SYT5_MIP28	CCACCCCAACCATCTGAACCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGACTCCCACCCCA	20
M00764_SYT5_MIP29	CAGGCCAGCCCCGCCGGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCCAGGCTTGGCCGGGGG	20
M00764_SYT5_MIP30	GGCACTGGGCGGACATGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCTCTTCCTCCCGCGC	20
M00764_SYT5_MIP32	GTGAAAACGGACACCGCCCCTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGCAGGAAGAAAGGC	20
M00764_SYT5_MIP44	GCCGCCCCAGGTCCACGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGGAAAGCCTATGATCTGAT	20
M00764_SYT5_MIP45	GGCCTGGCGGGAGCTGCAGGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTACGTGGAGCTGG	20
M00764_SYT5_MIP63	GTAACTCTGGCCCAGCCCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGATGAGCCAGTAAGGTG	20
M00764_SYT5_MIP64	GACAAGGTGTGGCCCAGCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGCCTCCTCATCTTCAG	20
M00764_SYT5_MIP66	GGGATCCCAGCCGGATTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAAGATCCCATTCCATGCAA	20
M00764_SYT5_MIP67	GTCTTGCTCACCTGGGCCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCAGTCCAGGATGAC	20
M00764_SYT5_MIP68	GTCTTGCTCACTTGGGCCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCATTCCAGTCCAGGATGAC	20
M00764_SYT5_MIP69	GGGGTGGGGGGCCGAGCAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTGAGTGTCTCTGCAGAAAAG	20
M00764_SYT5_MIP70	AACTCCAACTCCCATGAGGCCTTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGCCCCGGGGTTGG	20
M00764_SYT5_MIP72	CGTCCTCGCCCCTCCGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCGCGAGTCATGCTGGGA	20
M00764_SYT5_MIP74	CAGGCTCGCTCCGGGGCCCACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCGTTGCCCAGAG	20
M00764_SYT5_MIP75	CAGGCTTGCTCCGGGGCCCACCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCGCGTTGCCCAGAG	20
M00764_SYT5_MIP76	CCCGCCGGGACTCCGCGTCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGGAGGGAGCAGTCG	20
M00764_SYT5_MIP77	CCCCTCATCCTTCTTGGCCTGTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTCCGAGCGCCCACA	20
M00764_SYT5_MIP79	GTCTCCAGGGTCTCTCCCTCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCTCCACGCATCCGT	20
M00764_SYT5_MIP81	GGATGCGGATGGGCTGAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCTTTGTCTTCTCCATA	20
M00764_SYT5_MIP82	GAGTGGGGGCTGGGGCACTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGGGTCCGGGCGGGGCTG	20
M00764_SYT5_MIP83	CGCGTGTGTGCCCGTGTGCGTGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGACGCCGAGGCG	20
M00764_SYT5_MIP84	ATCCTGCTCCGCTCCGCGGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGGTTCCCGGGTGGAG	20
M00764_SYT5_MIP89	GCAGCTACTCTAGAGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTAACCTCAGCACTTTGGGAG	20
M00764_TANC1_MIP10	CCACTCTTTCTCCTGAGAGACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCTTTGAGTCACTAC	20
M00764_TANC1_MIP126	GTTTCCCTCCTGGGAAACAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGTACCTGCTGACTTG	20
M00764_TANC1_MIP141	CCCTGAATGCTTCAGAAGCAATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAAGAGGGAAGCTGGAG	20
M00764_TANC1_MIP182	CCTAATTTTTAATATCTATTAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGAGAAGGTTCCTCAGCC	20
M00764_TANC1_MIP199	CGGATAGGAGCTGTTTCCCACACTTCAGCTTCCCGATATCCGACGGTAGTGTAACAGTGTTGGGAAGCTG	20
M00764_TANC1_MIP224	ATAAATATGTCTATTGTTCAACTTCAGCTTCCCGATATCCGACGGTAGTGTAAATTATATCAACTTAAAA	20
M00764_TANC1_MIP241	GAAATTATAAAACGAAATTACTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAGATGTCTTGAAACAGA	20
M00764_TANC1_MIP5	CGGCGCCAGGTCCGGGCCTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCGCCCGCCCCGGCCG	20
M00764_TANC1_MIP6	CCGGAGCGGAGGCTTTGCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGAGGGGCGCGGGAGG	20
M00764_TANC1_MIP7	CCGTCCCCCCGCCTTGCTCGGCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGGTTCCCCACAC	20
M00764_TANC1_MIP8	GGAGAGGTCGAGAGGGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCCGAGGCCCGGCCCTG	20
M00764_TANC1_MIP94	AAAGAAGAAAAAAAAAATTTTACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTTTTCTTCTATCTGGTG	20
M00764t_LRRN1_MIP1	GAAGTCGCTTCCCATTGGAGGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACCCTGCGTCTTAAAAT	20
M00764t_LRRN1_MIP10	GCCGCCGCCGTGGGTGCCGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTCCGGTCTTGGTGCTCT	20
M00764t_LRRN1_MIP11	CAGCAGCAGGAGGAGGAGAAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTTCGACTTCCCCTCGCTG	20
M00764t_LRRN1_MIP16	ACCTCAGCCCGTGAGCCTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCAGAACCTTGGGAAG	20
M00764t_LRRN1_MIP17	ACCTCAGCCCGTGAGCCTTGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGTCAGAGCCTTGGGAAG	20
M00764t_LRRN1_MIP18	CTCAAGGCTCACGGGCTGAGGTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCCCCGCGTGGAGCT	20
M00764t_LRRN1_MIP21	AAGTCCAGCAGCGAGAGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCAGAAGCGAGGAAAGTTT	20
M00764t_LRRN1_MIP22	CTTGCCAGGCAGGGACTCCCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGCGAGGTCCCCTTCTC	20
M00764t_LRRN1_MIP3	GGGGCTGTGGGAGCCAAGTTCTTCAGCTTCCCGATATCCGACGGTAGTGTGGTTTTTAGCAAAAGACAGA	20
M00764t_LRRN1_MIP4	CCCGCCGCGCTGCGCCTTTGTTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCACGGACGTGTATT	20
M00764t_LRRN1_MIP5	CGGGTGGCCGGGCCGCGGTCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGGCTGCTCCGCCGT	20
M00764t_LRRN1_MIP6	CGAGCCGGTGAACGAGGCGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTCGGGCGGGAGGGGAGGA	20
M00764t_LRRN1_MIP61	GTTATCTTATTCTTTTTATCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACAATGAATTTTCTTT	20
M00764t_LRRN1_MIP67	CACATTCTTCATCAAAGTACAACTTCAGCTTCCCGATATCCGACGGTAGTGTCAATATATTCATATATAC	20
M00764t_LRRN1_MIP7	CGGTGCGCCCCGCTTTGTGCTCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCGCCCCAGGCGCCT	20
M00764t_LRRN1_MIP8	AGCCGACTGAGCCCAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCGGGCGGCGGCATCCC	20
M00764t_LRRN1_MIP9	GGGAAGGAGGGTCGGAGAAGTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCACTGGCTCCTTGGGG	20
M00764t_NPBWR2_MIP1	CCCATCATCATCATGCCCACACCTTCAGCTTCCCGATATCCGACGGTAGTGTGAACCCCTTCCTCTACGC	20
M00764t_NPBWR2_MIP3	CAGACCCCACTGGTCATCAGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCCAAGGCTCTAGG	20
M00764t_NPBWR2_MIP4	GTGTAGACACGGCTGGCCTTGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTCACCTTCCGCCTGGC	20
M00764t_NPBWR2_MIP6	GTATCGGTCCACGCTCATCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCAGCGAAAGAGAAGA	20

continued table…

ID	MIP	*c*
M00764t_NPBWR2_MIP7	GGTGGTGCTGGCCACCGTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCAACATCGCGGAGCACCTGC	20
M00764t_OPRL1_MIP1	CCACTCAGCCCTTCGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAGTGATTGCTCAAAGGTG	20
M00764t_OPRL1_MIP13	GTGCCAGAGGCAGAGCCACGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTAGATGGTTGTGGGGAGC	20
M00764t_OPRL1_MIP14	CAAGGTGGCAGCTGTAGGCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGGGTGTAGGGACCAA	20
M00764t_OPRL1_MIP15	CCCTCCCTCGACCAGGTGGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGAGGCCCAGCCCCCAC	20
M00764t_OPRL1_MIP16	GCGTCAACAAGCCCAAAGAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAATGACCCCTATGAGGGG	20
M00764t_OPRL1_MIP2	CCAGGGTCCACGTGGACCTGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGAAACCTGGGTTCTTCCGG	20
M00764t_OPRL1_MIP20	GGGAAGGTGGGTCACCGCACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCTCAGCAGACGCC	20
M00764t_OPRL1_MIP22	GGAGCTGGGACCACCGTGGAGACTTCAGCTTCCCGATATCCGACGGTAGTGTGACACACCCAGAAACGCC	20
M00764t_OPRL1_MIP27	CGTACAGAGTGGATTTGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCTCAGTGTCTGTGGCTG	20
M00764t_OPRL1_MIP29	AGGGCTCCTGGGGAACTGCCTTCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTGTCCCTCCTGAGCC	20
M00764t_OPRL1_MIP3	GGGTTCCCCTTTTTCTGGAGCTCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGGGAGCTTCGGGAGC	20
M00764t_OPRL1_MIP4	CGCCGCCGCCGGCCCGCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTCGAGTCCCGTGCGCC	20
M00764t_OPRL1_MIP41	ACGCCTGTCCAGGTCTTCGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTCTGCTACAGCCTCATGAT	20
M00764t_OPRL1_MIP48	GCATGTCAGCTGCTTCCAGGTAGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACACAGCTGCTGCTCC	20
M00764t_OPRL1_MIP5	GAGTGGCTCGGGAGCGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGACCGCCGGCGCGAGGAAG	20
M00764t_OPRL1_MIP51	CCTGGGCCAGCCGCACCTCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTTGCCCTGAGCTTGGAG	20
M00764t_OPRL1_MIP58	CATGCTGGCTCTGCTGTGAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGATTCTCTGGGTGACCAC	20
M00764t_OPRL1_MIP6	CCTGGGGGTGGCCCGGAGAGTCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAAAGCCAGGGGCCG	20
M00764t_OPRL1_MIP7	GGCCGACGCGCGGGCGGGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACGGCCCCGCCGAGCAGAG	20
M00764t_OPRL1_MIP8	GGGAAAGAGGAGGCTGCTGCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGTAGTAGATGGGGGTGTG	20
M00764t_OPRL1_MIP9	AGCTGGGCAAGCAGCATATGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTTGGGAACCCCCCACAG	20
M00764_TOX3_MIP5	AATGTAAATATTTTCTTTCACTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTAAAAGGGAAATGCAC	20
M00764_TOX3_MIP61	GCCTGCTGCACTTTTCTTTGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTGCCAGCCTGGACT	20
M00764_TOX3_MIP62	CCTCCTCGCCGCCGCTAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGTACCCCAGGCACTGCGC	20
M00764_TOX3_MIP63	GGGTCCCGGCCCCGGCGAACCCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCTTTGTGTGCGGC	20
M00764_TOX3_MIP64	CGCGGGGCGCGGCGCTGGGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCTCGGGAGCCGCGGC	20
M00764_TOX3_MIP65	CCCCGGCGCCCGGCCCGCGCGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCGTCTCCTCAGTCCGCC	20
M00764_TOX3_MIP66	CCCCTCCCACCGCGGGCAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCCCGCTCCTCCTCCTCC	20
M00764_TOX3_MIP67	CGGGGAGGGGACCGGCGGCTGAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGGCGGGGGTGATGG	20
M00764_TOX3_MIP68	CCCTCCTTTCCTCGGCCGAAGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCACCCCGCCCCGCCGGC	20
M00764_TOX3_MIP69	GCTCCGAGGCAGTGGGGACAAACTTCAGCTTCCCGATATCCGACGGTAGTGTACAGGAAGGGAGCAGACG	20
M00764_TOX3_MIP70	CCTTTCGAATGTCCCCTGCGTCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGACCACAGCTTCCCC	20
M00764_TREM1_MIP19	ATTATATTTATGAAATTTAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGAAGAAAAATATATCTG	20
M00764_TREM1_MIP23	ATTCTATTTATCTATAATTGCTTCAGCTTCCCGATATCCGACGGTAGTGTAAATCAACATTTAATAACTG	20
M00764_TREM1_MIP57	AGACAGGAAGTAACCAAAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGTTAAGAGGGAAGCT	20
M00764_TREM1_MIP59	CTAGATTAATAAAGAAAAAAGCTTCAGCTTCCCGATATCCGACGGTAGTGTTGAACTGAAGGAAAGTGAG	20
M00764_TUBB3_MIP1	CCTCTCCAGGGCTCACTAGCATTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAGCGACACCCCC	20
M00764_TUBB3_MIP103	CCCGGCTTCGCCCCCCTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGACCTCAACCACCTGGTATC	20
M00764_TUBB3_MIP104	AGGGCACCATGTTGACGGCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGCGGCCATCATGTTC	20
M00764_TUBB3_MIP105	GAGCAAGAACAGCAGCTACTTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCAGATGTTCGATGCCA	20
M00764_TUBB3_MIP15	GTTGCTCCTGCTCACCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAGCAGAGGCTGGACA	20
M00764_TUBB3_MIP16	GTTGCTCCCGCTCACCAGCACTTCAGCTTCCCGATATCCGACGGTAGTGTCAGGAAGCAGAGGCTGGACA	20
M00764_TUBB3_MIP17	AAGATGGAGATGTAGTGGTCCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGACGGCCACGTG	20
M00764_TUBB3_MIP18	AAGATGGAGATGTAGCGGTCCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCAGGACGGCCACGTG	20
M00764_TUBB3_MIP19	CATCGCCCGGCTCCACAAGACTTCAGCTTCCCGATATCCGACGGTAGTGTCACGCTCTTCATCGCCTACT	20
M00764_TUBB3_MIP20	GCATGTGGACGTACAGCACGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCAGCAGAGGAAGAAAATG	20
M00764_TUBB3_MIP29	AAACGTGGCTGCCTCCCCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGGTAATAAATGTGACTCA	20
M00764_TUBB3_MIP34	CCTGCACTGAGCCCCCTTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCAGAAGCCTCACATC	20
M00764_TUBB3_MIP37	GGGAGCTGCTTCCTGGCAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGACTGAGCACTCAGTCAGC	20
M00764_TUBB3_MIP4	GAGCAGCAACTCAGCTGTCAACGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGCCCCTCTAGGAGT	20
M00764_TUBB3_MIP41	ACAGGCAAGTTCGCAGCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTATCTCTTGAGAACAAAAGAT	20
M00764_TUBB3_MIP43	GGCACCCGACCTCCTCCACCAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCCTGAACCCACTGAG	20
M00764_TUBB3_MIP44	GTCTGCCAAAAGACAGGGAGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCACCCCTCTGTGTTC	20
M00764_TUBB3_MIP46	CTCCTCTGGGAGACAGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAAAAAGACCCTCCGTACAAA	20
M00764_TUBB3_MIP47	GGCTGTGGGGGCGCCGGGCTCCACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCGCGCGTCCCCGCC	20
M00764_TUBB3_MIP48	CCGCGGCTATAAGAGCGCGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGGGGCGCCGCATT	20
M00764_TUBB3_MIP49	CCTTCGCATCGGCTGATGTCACCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCCTGGATGTGCACGAT	20
M00764_TUBB3_MIP50	GAGGCGCCGTGCCCCGCGGGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCCGCCCGCCAGACGC	20
M00764_TUBB3_MIP53	GTTTCTATTTATTTATTATTATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGAGAGATGGAGTTTCA	20
M00764_TUBB3_MIP6	GATCTCCTTTACGTTAAAAAACACTTCAGCTTCCCGATATCCGACGGTAGTGTTGCGTTTTAAAAAGTCG	20
M00764_TUBB3_MIP9	CATGGGGGACACCCAAGGCCCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGAATCCCTGAGCCCAGG	20
M00764_TUBB3_MIP92	CCACGTTCCCACGCCTGTGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGGATGCCACGTTCCCA	20
M00764_TUBB3_MIP93	GAGGGCCTCGCTTCACTTCTGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCATGCCTGTGTCCTGG	20
M00764_TUBB3_MIP94	CCCGCCCCAGGACACAGACATGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCAAACAGCCACCCCAGA	20
M00764t_ZNF804B_MIP11	ACAGAGCACGGAGGGGACCCGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCTCCCGAGAAGACG	20
M00764t_ZNF804B_MIP18	CTTCTAAGTCATGGAAAGATGCTTCAGCTTCCCGATATCCGACGGTAGTGTTAGGATAAAGAATAATAAG	20
M00764t_ZNF804B_MIP5	AGCCAACTTTCTACTGTTTGGGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCTGTGGGGCGAGGCCA	20
M00764t_ZNF804B_MIP6	CGTCCCCAACTCCCTGTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCCCCCCGCGGCTGCAGCG	20
M00764t_ZNF804B_MIP7	GAGGAGGGCAGTTAGCGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTGTGGGGAGAGTGGCGGG	20
M00764t_ZNF804B_MIP8	AGCATCCCCCGGGCAGGCGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTGGCGCTCCCAAGGACT	20
M00764t_ZNF804B_MIP9	GCGTCCTGGGCTGCTGGCTGCTTCAGCTTCCCGATATCCGACGGTAGTGTTATTTAAGGACAACTTCCAG	20
M00764_UBL4B_MIP12	GCACGGCCTCAGAGCTCCTGTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGCTGCTAAGGCAGGAGCA	20

continued table…

ID	**MIP**	***c***
M00764_UNCX_MIP10	ATCCGGGGGGGGGGGCGCAGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGCTTGCAGCCCGGGCT	20
M00764_UNCX_MIP11	ACTATCCCGACGTGTTCATGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGTCCTGTGACTGCCC	20
M00764_UNCX_MIP12	CGTTGAACGCCTTCTCCAGCTCCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCCAGAGCCTGGGG	20
M00764_UNCX_MIP13	GAAGAAGGAGAACACGAAAAAGGGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGCAGGCCCCTCTGG	20
M00764_UNCX_MIP14	GGCGGTTTTGGAACCAGACCTACTTCAGCTTCCCGATATCCGACGGTAGTGTATCTTCTCCAGCTCCTTG	20
M00764_UNCX_MIP15	CAGCTCCGACAGCGACAGCGGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCGGAGGAGATCGCGC	20
M00764_UNCX_MIP16	GCGCGCTGTGCAGGGACAGGCCCTTCAGCTTCCCGATATCCGACGGTAGTGTTCGCCGGGAGGGGCGGGC	20
M00764_UNCX_MIP17	GCGGACAAGGACGCGGCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCACGCCTCGGGCGCCGC	20
M00764_UNCX_MIP18	CCGCTTCTTTGGCTCGGGTAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACGCTGAATGGGCT	20
M00764_UNCX_MIP19	GTGCGCGCCGCGGACCCTGACTTCAGCTTCCCGATATCCGACGGTAGTGTCGCCGCGGGGCTGCCCAAGG	20
M00764_UNCX_MIP2	AGTGAAGTGGGGGGCTAGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTGAGAGTACAGCATTTCTGGT	20
M00764_UNCX_MIP20	GCAGCCCGGGCGCGAAGTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCGCGTCCTTGGGCGCCGGC	20
M00764_UNCX_MIP21	GCGTCGCAGCCCCGACGCCGTCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCGGCGCGGGCCTGG	20
M00764_UNCX_MIP22	CGAAGGCCGAGTCCGGGGCGCCGCTTCAGCTTCCCGATATCCGACGGTAGTGTCGGCGGTCCCCGCGTCC	20
M00764_UNCX_MIP23	CCTGGCGCGGCGGCCGGACCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGGGCGGCGGCGGGGACTG	20
M00764_UNCX_MIP24	CGGGAACCCCGCAGGTGGCCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTCGTTGCGTGAGTCGGA	20
M00764_UNCX_MIP26	AAGAAAGAAAACAAAAGAAAAGAACTTCAGCTTCCCGATATCCGACGGTAGTGTGGGTTTTTTGGGGGCC	20
M00764_UNCX_MIP3	GGGGCCGGCCCCGAGCCCGCGCTTCAGCTTCCCGATATCCGACGGTAGTGTACAAGACGGGCTGGGGGCG	20
M00764_UNCX_MIP4	GACGTCAGAGCCGATTAGCGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTCCCTCCGGCTCCCC	20
M00764_UNCX_MIP6	GCCGGCCCCCCGCGCGAGATCTTCAGCTTCCCGATATCCGACGGTAGTGTAAGTAAAGCGCCGGAGTGCG	20
M00764_UNCX_MIP7	GGGCCGGTGGCGGGGCGCGGCTTCAGCTTCCCGATATCCGACGGTAGTGTCCGGCCAGCTCGTACACGTG	20
M00764_UNCX_MIP8	GTCAACCCCACGCCGCTGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCTACCCGCTGGGCCACCA	20
M00764_UNCX_MIP9	ACCGAGGCGGCGGCGGCGCACGAGCTTCAGCTTCCCGATATCCGACGGTAGTGTACCAGGGCCCCCGCCC	20
M00764_VAV3_MIP1	ACTATTTATTATATTGACATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTCTGGACTGCTGG	20
M00764_VAV3_MIP105	CCTTAATTATGTTTAGCAAATCTTCAGCTTCCCGATATCCGACGGTAGTGTATTTTAAATAATTTAAAAC	20
M00764_VAV3_MIP114	GTAATTTACTTATAATCTTGCTTCAGCTTCCCGATATCCGACGGTAGTGTGTGATCGTATGTAAGAGAAA	20
M00764_VAV3_MIP134	ATTTTATAAAATATTTAAACCTTCAGCTTCCCGATATCCGACGGTAGTGTAAACTGAAATTAGAGGTGCC	20
M00764_VAV3_MIP146	GAAGATGAAGAAGATCTCTATCTTCAGCTTCCCGATATCCGACGGTAGTGTTCCACTAATTCCATTTTAT	20
M00764_VAV3_MIP17	CATGATTTCATAGGATTATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCATAAGTGAGCTATCCCTG	20
M00764_VAV3_MIP178	GACTTTATATGATTTAATAAGTATCTTCAGCTTCCCGATATCCGACGGTAGTGTAACCAAACTGCTTTCA	20
M00764_VAV3_MIP187	CGGCTCAGGTGTTCGACCTTGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGCATCCTTGCCGCCCG	20
M00764_VAV3_MIP188	ATCGAGGGAGCAGGAGCCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGCTCCATGCCCGACGGCTC	20
M00764_VAV3_MIP189	CCGCGCGGGGAAAGGGCCGGCGGCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCGCACGGAGAGC	20
M00764_VAV3_MIP190	GTCCGCAAGTCCCCAGACGCGCCTTCAGCTTCCCGATATCCGACGGTAGTGTCGCTGCAGCGAGTCCCGC	20
M00764_VAV3_MIP191	ACCGGCCGGCGTGCTGGGCATGCTCTTCAGCTTCCCGATATCCGACGGTAGTGTATCCCCTTTCTGGCCG	20
M00764_VAV3_MIP192	GCTGAATACTGTAATACGATCTTCAGCTTCCCGATATCCGACGGTAGTGTGGGGCCGGCGGAGGGGGGCG	20
M00764_VAV3_MIP194	CATTCTCTATAGCTGATTCCTCCTTCAGCTTCCCGATATCCGACGGTAGTGTGGAGCGACGGATTAATTG	20
M00764_VAV3_MIP2	ACTATTTATTACATTGACATATTCTTCAGCTTCCCGATATCCGACGGTAGTGTTCACTCTGGACTGCTGG	20
M00764_VAV3_MIP39	GAAAAGTTATTTAAAGATAATCCTTCAGCTTCCCGATATCCGACGGTAGTGTATTGCAGAAAATAGAAAA	20
M00764_VAV3_MIP40	GTTTTTAATCAGTAGAAATCACTTCAGCTTCCCGATATCCGACGGTAGTGTAATGCTTACCATTAAACTT	20
M00764_VAV3_MIP46	CAATCTCTAAAACTATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTCAACCAGAAGCAGTG	20
M00764_VAV3_MIP47	CCATCTCTAAAACTATAAAACTTCAGCTTCCCGATATCCGACGGTAGTGTAGTGTCAACCAGAAGCAGTG	20
M00764_VAV3_MIP72	GTAAAGTTTATCTTAAAATACTTCAGCTTCCCGATATCCGACGGTAGTGTTGGCTTTTGGATAACTGCAG	20
M00764_VAV3_MIP82	ATATAAAATTTCTCTATTGAACATCTTCAGCTTCCCGATATCCGACGGTAGTGTTAAAACCTTCAGGAAT	20
M00764_VAV3_MIP89	CCAAACTCAATTCTATAAGCACTTCTTCAGCTTCCCGATATCCGACGGTAGTGTCCCCTGGAGCTCTCAG	20
M00764_VAV3_MIP90	GATCAAAGGAGACTGAGAAGGCTTCAGCTTCCCGATATCCGACGGTAGTGTTTTTTAGAGGGAAAGAAAG	20
M00764_ZNF175_MIP23	GTATAATAAATATGTGTGTTACTTCAGCTTCCCGATATCCGACGGTAGTGTATTCTGTGTATCTCTTGAT	20
M00764_ZNF175_MIP3	CCTAGAAATATATATACACAAGTCTTCAGCTTCCCGATATCCGACGGTAGTGTCAGAAAGATAACATTTT	20
M00764_ZNF175_MIP53	GTCTAATTATATGTTATTGAATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGACAAATCTTACAAATG	20
M00764_ZNF175_MIP59	AAATCCAAGATTAAATGCTCCCTTCAGCTTCCCGATATCCGACGGTAGTGTAGCATATTATTATATACAG	20
M00764_ZNF175_MIP64	GTATAATAAAGGAGTTAATCATCTTCAGCTTCCCGATATCCGACGGTAGTGTAGATGGTGGAGATGGAAA	20
M00764_ZNF175_MIP8	CCAATCACTTCAGCGTCCAGTAACTTCAGCTTCCCGATATCCGACGGTAGTGTCACCTCACAGCCTCGTC	20
M00764_CACNG8_MIP1	GACTTTCTTGGGCAGAAGACACTTCAGCTTCCCGATATCCGACGGTAGTGTGAGTGGGGTTAGTGGGATG	21

Appendix F – Script for Reviewing the Mapping of MIPs’ Reads

The following shell script can extract the mapping of the MIPs’ targets’ reads and was used to visualize the off-target effects of MIPs. The script uses samtools [408, 409].

```
#!/bin/sh

PROBE_FILE_PATH=$1
#NOTE: The probe file has 5 columns with header:
#column 1 = MIP name
#column 2 = extension probe sequence
#column 3 = reverse-complement of the extension probe sequence
#column 4 = ligation probe sequence
#column 5 = reverse-complement of the ligation probe sequence
MIP_TARGET_FILE=$2
#NOTE: The target file has two columns:
#column 1 = MIP name
#column 2 = target position of format chr*:*-*
ALIGNED_FASTQ_PATH=$3
#NOTE: contains the path to the aligned fastq file
OUTPUT_FOLDER=$4
JOBS=$5


#go through each supplied MIP in the probe file and get the reads with the
#probes of that MIP into a new sam file
echo Getting reads...
INDEX_VECTOR=$(seq 2 $(wc -l ${PROBE_FILE_PATH}|awk ‘{print $1}’))
for INDEX in ${INDEX_VECTOR}
do
echo -e -n "\r MIP ${INDEX}"
EXT_PROBE=$(awk -v REIHE=${INDEX} ‘NR==REIHE{print $2}’ \
${PROBE_FILE_PATH})
RC_EXT_PROBE=$(awk -v REIHE=${INDEX} ‘NR==REIHE{print $3}’ \
${PROBE_FILE_PATH})
LIG_PROBE=$(awk -v REIHE=${INDEX} ‘NR==REIHE{print $4}’ \
${PROBE_FILE_PATH})
RC_LIG_PROBE=$(awk -v REIHE=${INDEX} ‘NR==REIHE{print $5}’ \
${PROBE_FILE_PATH})
MIP=$(awk -v REIHE=${INDEX} ‘NR==REIHE{print $1}’ ${PROBE_FILE_PATH})
grep ‘^@’ ${ALIGNED_FASTQ_PATH} > \
${OUTPUT_FOLDER}/${MIP}.at_least_one_probe_match.sam
awk -v EXT=${EXT_PROBE} -v EXT_RV=${RC_EXT_PROBE} -v LIG=${LIG_PROBE} \
-v LIG_RV=${RC_LIG_PROBE} ‘{if ((substr($10,1,30) ~ LIG_RV || \
substr($10, length($10)-29, length($10)) ~ EXT_RV) || \
(substr($10,1,30) ~ EXT || substr($10, length($10)-29, length($10)) ~ \
LIG)) print $0}’ ${ALIGNED_FASTQ_PATH} >> \
${OUTPUT_FOLDER}/${MIP}.at_least_one_probe_match.sam &
#job handler
NUMBEROFJOBS=$(jobs -p | wc -l)
while [ $NUMBEROFJOBS -ge ${JOBS} ]
do
sleep 1
NUMBEROFJOBS=$(jobs -p | wc -l)
done
#end job handler
done
echo

#sort and index the new mip-wise sam files
echo Sorting and indexing reads...
NEW_RESULT_FOLDER=${OUTPUT_FOLDER}/
#for DATEI in $(ll ${NEW_RESULT_FOLDER}| awk ‘NR!=1 {print $9}’)
for DATEI in $(ls ${NEW_RESULT_FOLDER}*at_least_one_probe_match.sam)
do
echo ${DATEI}
samtools view -b ${DATEI} > ${DATEI}.bam
samtools sort -O bam -T ${DATEI}.partialsorted -o ${DATEI}.sorted.bam \
```

```
${DATEI}.bam
samtools sort -O sam -T ${DATEI}.partialsorted -o ${DATEI}.sorted.sam \
${DATEI}.sorted.bam &
#job handler
NUMBEROFJOBS=$(jobs -p | wc -l)
while [ $NUMBEROFJOBS -ge ${JOBS} ]
do
sleep 1
NUMBEROFJOBS=$(jobs -p | wc -l)
done
#end job handler
done
echo

#get summary stats and number of on-target reads for each sorted bam file
echo Creating statistics...
for DATEI in $(ls ${NEW_RESULT_FOLDER}*sorted.bam)
do
samtools index ${DATEI} &
#job handler
NUMBEROFJOBS=$(jobs -p | wc -l)
while [ $NUMBEROFJOBS -ge ${JOBS} ]
do
sleep 1
NUMBEROFJOBS=$(jobs -p | wc -l)
done
#end job handler
done
#create index stats
for DATEI in $(ls ${NEW_RESULT_FOLDER}*sorted.bam)
do
samtools idxstats ${DATEI} > ${DATEI}.idxstats
#NOTE: the idxstats output can be used to visualize the mappings of a MIP
done
#create a summary about how often reads of a MIP’s probe map into the
#actual target region of that mip
for MIP in $(seq 1 $(wc -l  ${MIP_TARGET_FILE} | awk ‘{print $1}’))
do
MIP_NAME=$(awk -v REIHE=${MIP} ‘NR==REIHE{print $1}’ ${MIP_TARGET_FILE})
MIP_TARGET=$(awk -v REIHE=${MIP} ‘NR==REIHE {print $2}’ \
${MIP_TARGET_FILE})
echo ${MIP_NAME} >> ${OUTPUT_FOLDER}/on_target_summary_count.txt
samtools view -c \
${OUTPUT_FOLDER}/${MIP_NAME}.at_least_one_probe_match.sam.sorted.bam \
${MIP_TARGET} >> ${OUTPUT_FOLDER}/on_target_summary_count.txt
done
echo done
```

Appendix G – Script for Counting MIPs’ Reads in a Fastq File

The following shell script counts MIPs’ reads in a fastq file based on a supplied list of MIP probes.

```
#!/bin/sh

FASTQ_FOLDER=$1
FW_FASTQ_GZ=$2
RV_FASTQ_GZ=$3
PROBE_FILE_PATH=$4
JOBS=$5
#NOTE: The probe file has 5 columns with header:
#column 1 = MIP name
#column 2 = extension probe sequence
#column 3 = reverse-complement of the extension probe sequence
#column 4 = ligation probe sequence
#column 5 = reverse-complement of the ligation probe sequence



#get the reads
echo Getting reads...
zcat ${FASTQ_FOLDER}/${FW_FASTQ_GZ} | awk ‘NR % 4 == 2’ > \
${FASTQ_FOLDER}/${FW_FASTQ_GZ}.reads
zcat ${FASTQ_FOLDER}/${RV_FASTQ_GZ} | awk ‘NR % 4 == 2’ > \
${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads
#get read lengths
echo Counting read length...
awk ‘{print length($0)}’ ${FASTQ_FOLDER}/${FW_FASTQ_GZ}.reads > \
${FASTQ_FOLDER}/${FW_FASTQ_GZ}.reads.nchar
awk ‘{print length($0)}’ ${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads > \
${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads.nchar
#get the first 30 characters from the unmerged reads
echo Getting first bases...
cat ${FASTQ_FOLDER}/${FW_FASTQ_GZ}.reads | cut -c -30 > \
${FASTQ_FOLDER}/${FW_FASTQ_GZ}.reads.fw_start
cat ${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads | cut -c -30 > \
${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads.rv_start

#count the extension probes in the R2 reads = RV reads
echo Counting MIPs in RV reads...
READ_PATH=${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads.rv_start
RESULT_PATH=${READ_PATH}.mip_counts
rm ${RESULT_PATH}
INDICES=$(seq 2 $(wc -l ${PROBE_FILE_PATH} | awk ‘{print $1}’))
for INDEX in ${INDICES}
do
echo -e -n "\r MIP ${INDEX}"
echo $(head -${INDEX} ${PROBE_FILE_PATH} | tail -1 | awk ‘{print $1}’) \
$(grep -c -e $(head -${INDEX} ${PROBE_FILE_PATH} | tail -1 | awk ‘{print \
$2}’) ${READ_PATH}) >> ${RESULT_PATH} &
#job handler
NUMBEROFJOBS=$(jobs -p | wc -l)
while [ $NUMBEROFJOBS -ge ${JOBS} ]
do
sleep 1
NUMBEROFJOBS=$(jobs -p | wc -l)
done
done
#end job handler
done

echo

#count reverse complement ligation probes in the R1 reads = FW reads
echo Counting MIPs in FW reads...
READ_PATH=${FASTQ_FOLDER}/${RV_FASTQ_GZ}.reads.fw_start
RESULT_PATH=${READ_PATH}.mip_counts
```

```
rm ${RESULT_PATH}
INDICES=$(seq 2 $(wc -l ${PROBE_FILE_PATH} | awk ‘{print $1}’))
for INDEX in ${INDICES}
do
echo -e -n "\r MIP ${INDEX}"
echo $(head -${INDEX} ${PROBE_FILE_PATH} | tail -1 | awk ‘{print $1}’) \
$(grep -c -e $(head -${INDEX} ${PROBE_FILE_PATH} | tail -1 | awk ‘{print \
$5}’) ${READ_PATH}) >> ${RESULT_PATH} &
#job handler
NUMBEROFJOBS=$(jobs -p | wc -l)
while [ $NUMBEROFJOBS -ge ${JOBS} ]
do
sleep 1
NUMBEROFJOBS=$(jobs -p | wc -l)
done
done
#end job handler
done
```

Appendix H – Age Distributions of Individuals Used for MIPseq

The following histograms illustrate the age and sex distribution for RLS cases and population based controls during the QC of the MIPseq data.

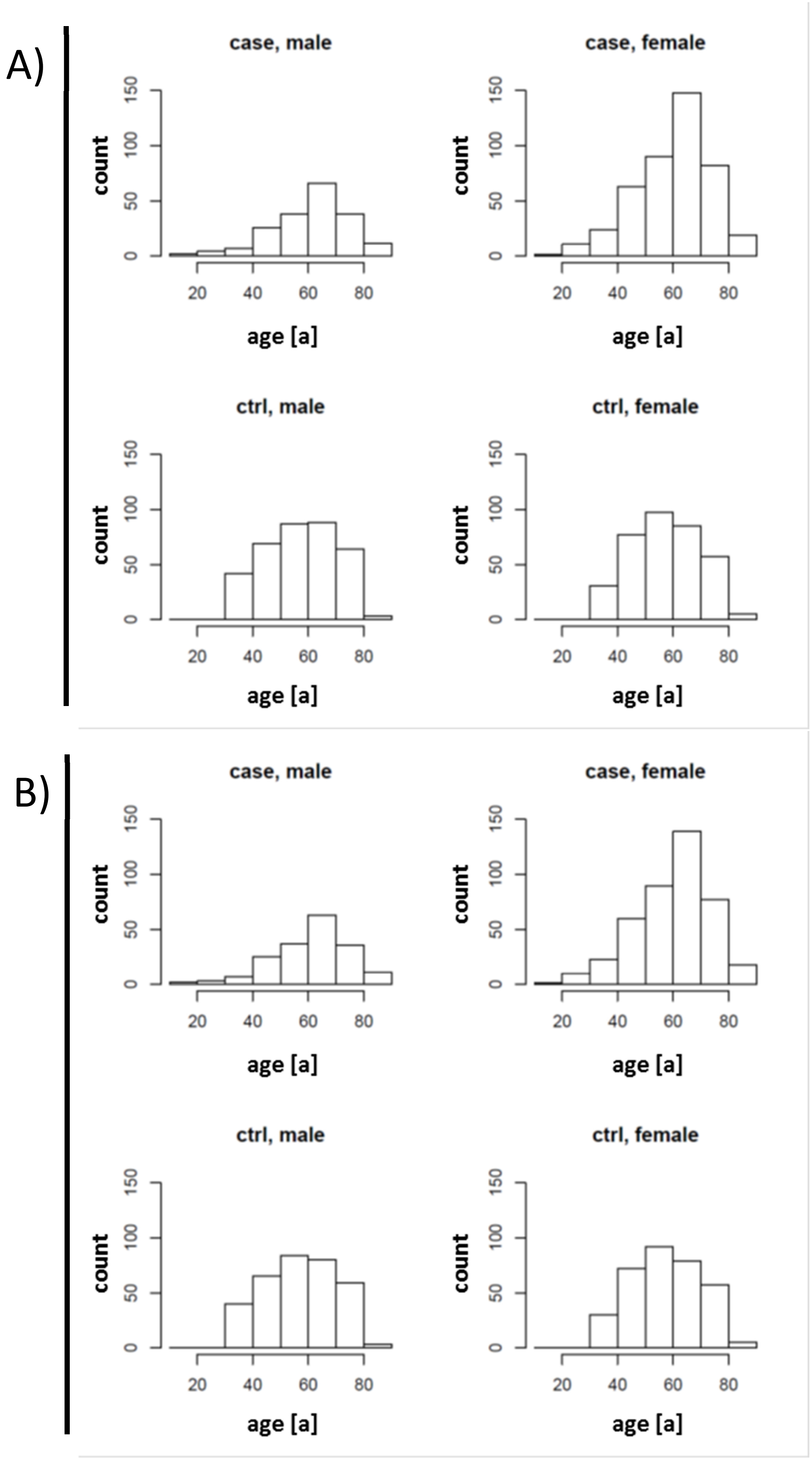

Figure 18: Age distributions of individuals used in MIPseq: The histograms are shown for cases and controls, stratified by sex, before (A) and after (B) removal of related individuals and population outliers.

.

Appendix I – Sizes of RLS Pedigrees

The families' sizes, number of affected and unaffected individuals of this study are listed in the following Table 34.

Table 34: Sample sizes in the RLS affected pedigrees: The numbers indicate the sample size after QC and removal of individuals with unknown phenotypes. Ped = pedigree identifier, n = sum of RLS affected and unaffected individuals in the pedigree, n_{cases} *= RLS affected individuals,* n_{ctrls} *= unaffected individuals (age ≥ 40 years). The families are listed in alphabetical order.*

Pedigree	n	n_{cases}	n_{ctrls}
b002	9	5	4
b005	9	5	4
b006	14	7	7
b008	16	11	5
b010	6	5	1
b015	6	5	1
b020	6	4	2
b027	8	6	2
b029	7	5	2
b030	8	6	2
d006	3	2	1
d010	5	4	1
dau_a	4	4	0
dau_b	0	0	0
i001	9	5	4
i002	22	17	5
i003	6	6	0
i004	4	3	1
i014	2	1	1
k4827	17	17	0
k5006	17	15	2
k5301	9	6	3
k5332	22	16	6
k7150	45	35	10
m007	4	4	0
p001	8	7	1
p002	5	2	3
p004	7	5	2
p015	6	4	2
p018	6	4	2
r017	9	8	1
rls0001	19	11	8
rls0002	53	32	21
rls0164	13	9	4
rls0263	8	8	0
rls0327	2	1	1
rls0330	1	1	0
rls0378	11	8	3
rls0411a	14	7	7
rls0721	4	2	2
rls0722	4	4	0
rls0760	4	3	1
rls0777	3	3	0
rls0874	3	3	0
rls0900	6	4	2
rls0961	4	4	0
rls1194	4	3	1
rls1372	11	9	2
rls1727/g167	9	4	5
rls1789	3	3	0
rls-k086	5	3	2
t001	21	15	6
t003	11	11	0
t004	12	8	4
t005	14	10	4
t006	8	6	2
t007	13	9	4
t008	8	4	4
t009	8	5	3
t010	6	4	2
t012	9	6	3
t014	11	6	5
t015	9	5	4
t017	8	3	5
t019	7	4	3
t020	7	4	3
t021	4	3	1
t023	4	4	0
t025	11	9	2
t026	7	5	2
t033	7	5	2
t035	6	6	0
t037	5	5	0
t038	7	5	2
t040	10	5	5
t052	4	3	1
t059	13	10	3
t060	4	4	0
ZD	10	8	2

References

1. Hammer, A., H. Hammer, and K. Hammer, *Physikalische Formeln und Tabellen*. 6 ed. 1994, München: J. Lindauer Verlag (Schaefer).
2. HUGO Gene Nomenclature Committee (HGNC). *HGNC Database*. 2017 [cited 2017 March 1]; Available from: www.genenames.org.
3. Scholze-Stubenrecht, W., et al., *Duden*, M. Wermke, K. Kunkel-Razum, and W. Scholze-Stubenrecht, Editors. 2006, Bibliographisches Institut & F. A. Brockhaus AG: Mannheim. p. 165.
4. R Core Team, *R: A language and environment for statistical computing.* 2013.
5. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 50.
6. Dietz and Kowalczyk, *CHEMIKALIENKUNDE*. 2 ed. 1962, Leipzig: VEB Fachbuchverlag Leipzig.
7. Garcia-Borreguero, D., et al., *Validation of the Augmentation Severity Rating Scale (ASRS): a multicentric, prospective study with levodopa on restless legs syndrome.* Sleep Med, 2007. **8**(5): p. 455-63.
8. Han, F. and W. Pan, *A data-adaptive sum test for disease association with multiple common or rare variants.* Hum Hered, 2010. **70**(1): p. 42-54.
9. Alberts, B., et al., *Molecular Biology of the Cell*. 2002, Garland Science: New York.
10. Szatkiewicz, J.P., et al., *Copy number variation in schizophrenia in Sweden.* Mol Psychiatry, 2014. **19**(7): p. 762-73.
11. Dear, P.H., *Basepair (bp)*, in *eLS*. 2001, John Wiley & Sons, Ltd.
12. Auer, P.L., G. Wang, and S.M. Leal, *Testing for rare variant associations in the presence of missing data.* Genet Epidemiol, 2013. **37**(6): p. 529-38.
13. Agency for Administrative Simplification (ASA/DAV). 2017 [cited 2017 March 3]; Available from: https://www.business.belgium.be/en/managing_your_business/setting_up_your_business/company_types/private_limited_liability_company.
14. USPS. 2017 [cited 2017 March 1]; Available from: http://pe.usps.gov/text/pub28/28apb.htm#ep19305.
15. Kircher, M., et al., *A general framework for estimating the relative pathogenicity of human genetic variants.* Nat Genet, 2014. **46**(3): p. 310-5.
16. Morgenthaler, S. and W.G. Thilly, *A strategy to discover genes that carry multi-allelic or mono-allelic risk for common diseases: a cohort allelic sums test (CAST).* Mutat Res, 2007. **615**(1-2): p. 28-56.
17. Reich, D.E. and E.S. Lander, *On the allelic spectrum of human disease.* Trends Genet, 2001. **17**(9): p. 502-10.
18. Frohman, M.A., *Polymerase Chain Reaction (PCR): Specialised Applications*, in *eLS*. 2001, John Wiley & Sons, Ltd.
19. Schork, N.J., et al., *Common vs. Rare Allele Hypotheses for Complex Diseases.* Curr Opin Genet Dev, 2009. **19**(3): p. 212-9.
20. Ashcroft, R.E., et al., *Front Matter*, in *Handbook of Statistical Genetics*, D.J. Balding, M. Bishop, and C. Cannings, Editors. 2008, John Wiley & Sons, Ltd: Chichester. p. i-lii.
21. Li, B. and S.M. Leal, *Methods for detecting associations with rare variants for common diseases: application to analysis of sequence data.* Am. J. Hum. Genet., 2008. **83**: p. 311-321.
22. McKusick-Nathans Institute of Genetic Medicine. *Online Mendelian Inheritance in Man, OMIM®*. 2017 [cited 2017 March 2]; Available from: https://www.omim.org.
23. Eisel, D., et al., *Lab FAQS*. 4 ed. 2011, Mannheim: Roche Diagnostics GmbH.
24. Trenkwalder, C., et al., *Restless legs syndrome-current therapies and management of augmentation.* Nat Rev Neurol, 2015. **11**(8): p. 434-45.
25. Szentkiralyi, A., et al., *Incidence of restless legs syndrome in two population-based cohort studies in Germany.* Sleep Med, 2011. **12**(9): p. 815-20.

26. Xiong, L., et al., *Molecular genetic studies of DMT1 on 12q in French-Canadian restless legs syndrome patients and families.* Am J Med Genet B Neuropsychiatr Genet, 2007. **144b**(7): p. 911-7.
27. Komor, A.C., et al., *Programmable editing of a target base in genomic DNA without double-stranded DNA cleavage.* Nature, 2016. **533**(7603): p. 420-4.
28. Desai, A.V., et al., *Genetic influences in self-reported symptoms of obstructive sleep apnoea and restless legs: a twin study.* Twin Res, 2004. **7**(6): p. 589-95.
29. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 403.
30. QIAGEN. *What is the composition of Buffer EB?* 2017 [cited 2017 March 3]; Available from: https://www.qiagen.com/dk/resources/faq?id=d8ef773f-6a37-4993-908b-8bbc7bc5c8d6&lang=en.
31. Chen, L.S., et al., *An exponential combination procedure for set-based association tests in sequencing studies.* Am J Hum Genet, 2012. **91**(6): p. 977-86.
32. Spieler, D., et al., *Restless legs syndrome-associated intronic common variant in Meis1 alters enhancer function in the developing telencephalon.* Genome Res, 2014. **24**(4): p. 592-603.
33. Lin, D.Y. and Z.Z. Tang, *A general framework for detecting disease associations with rare variants in sequencing studies.* Am J Hum Genet, 2011. **89**(3): p. 354-67.
34. Winkelman, J.W., G.M. Chertow, and J.M. Lazarus, *Restless legs syndrome in end-stage renal disease.* Am J Kidney Dis, 1996. **28**(3): p. 372-8.
35. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 427.
36. Panier, S. [cited 2017 February 28]; Available from: www.eurlssg.org.
37. Lippert, C., et al., *FaST linear mixed models for genome-wide association studies.* Nat Methods, 2011. **8**(10): p. 833-5.
38. Allen, R.P., et al., *Clinical efficacy and safety of IV ferric carboxymaltose (FCM) treatment of RLS: a multi-centred, placebo-controlled preliminary clinical trial.* Sleep Med, 2011. **12**(9): p. 906-13.
39. U.S. Food and Drug Administration. [cited 2017 February 28]; Available from: www.fda.gov.
40. Affimetrix. *OncoScan® FFPE Assay Kit*. [cited 2016 May 16]; Available from: http://media.affymetrix.com/support/technical/brochures/oncoscan_ffpe_kit_brochure.pdf.
41. Eichacker, S., et al. [cited 2017 February 28]; Available from: www.helmholtz-muenchen.de/kora.
42. Chang, C.C., et al., *Second-generation PLINK: rising to the challenge of larger and richer datasets.* Gigascience, 2015. **4**: p. 7.
43. Rosani, U., et al., *Target Capture and Massive Sequencing of Genes Transcribed in Mytilus galloprovincialis.* BioMed Research International, 2014. **2014**: p. 538549.
44. Zhou, X. and M. Stephens, *Genome-wide efficient mixed-model analysis for association studies.* Nat Genet, 2012. **44**(7): p. 821-4.
45. Scholze-Stubenrecht, W., et al., *Duden*, M. Wermke, K. Kunkel-Razum, and W. Scholze-Stubenrecht, Editors. 2006, Bibliographisches Institut & F. A. Brockhaus AG: Mannheim. p. 461.
46. Scholze-Stubenrecht, W., et al., *Duden*, M. Wermke, K. Kunkel-Razum, and W. Scholze-Stubenrecht, Editors. 2006, Bibliographisches Institut & F. A. Brockhaus AG: Mannheim. p. 290.
47. Scholze-Stubenrecht, W., et al., *Duden*, M. Wermke, K. Kunkel-Razum, and W. Scholze-Stubenrecht, Editors. 2006, Bibliographisches Institut & F. A. Brockhaus AG: Mannheim. p. 573.
48. Chen, H., et al., *Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models.* Am J Hum Genet, 2016. **98**(4): p. 653-66.

49. Belonogova, N.M., et al., *Region-based association analysis of human quantitative traits in related individuals.* PLoS One, 2013. **8**(6): p. e65395.
50. Bagos, P.G., *Genetic model selection in genome-wide association studies: robust methods and the use of meta-analysis.* Stat Appl Genet Mol Biol, 2013. **12**(3): p. 285-308.
51. Shim, S., et al., *Meta-analysis for genome-wide association studies using case-control design: application and practice.* Epidemiol Health, 2016. **38**: p. e2016058.
52. Engelmann, C., et al. *Towards high availability for high-performance computing system services: Accomplishments and limitations*. in *Los Alamos Computer Science Institute (LACSI) Symposium 2006*. 2006. Santa Fe.
53. Bio-Rad Laboratories. *iProof™ High-Fidelity Master Mix* [cited 2017 March 3]; Available from: http://www.bio-rad.com/webroot/web/pdf/lsr/literature/10002299.pdf.
54. Erbel, R., et al., *Signs of subclinical coronary atherosclerosis in relation to risk factor distribution in the Multi-Ethnic Study of Atherosclerosis (MESA) and the Heinz Nixdorf Recall Study (HNR).* Eur Heart J, 2008. **29**(22): p. 2782-91.
55. Schmermund, A., et al., *Assessment of clinically silent atherosclerotic disease and established and novel risk factors for predicting myocardial infarction and cardiac death in healthy middle-aged subjects: rationale and design of the Heinz Nixdorf RECALL Study. Risk Factors, Evaluation of Coronary Calcium and Lifestyle.* Am Heart J, 2002. **144**(2): p. 212-8.
56. Applied Biosystems. 2009 [cited 2017 March 3]; Available from: http://www.gene-quantification.de/ab-hrm-guide.pdf.
57. Thermo Fisher Scientific Inc. 2015 [cited 2017 March 3]; Available from: https://tools.thermofisher.com/content/sfs/manuals/Qubit_dsDNA_HS_Assay_UG.pdf.
58. Powell, J.E., P.M. Visscher, and M.E. Goddard, *Reconciling the analysis of IBD and IBS in complex trait studies.* Nat Rev Genet, 2010. **11**(11): p. 800-5.
59. Purcell, S., et al., *PLINK: a tool set for whole-genome association and population-based linkage analyses.* Am J Hum Genet, 2007. **81**(3): p. 559-75.
60. World Health Organisation. *International Statistical Classification of Diseases and Related Health Problems 10th Revision (ICD-10)-WHO Version for ;2016* 2016 [cited 2016 May 27]; Available from: http://apps.who.int/classifications/icd10/browse/2016/en#/G25.8.
61. Allen, R.P., et al., *The prevalence and impact of restless legs syndrome on patients with iron deficiency anemia.* Am J Hematol, 2013. **88**(4): p. 261-4.
62. Eichacker, S., et al. [cited 2017 Febraury 28]; Available from: www.helmholtz-muenchen.de/ihg.
63. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 655.
64. Rinaldi, F., et al., *Defining the phenotype of restless legs syndrome/Willis-Ekbom disease (RLS/WED): a clinical and polysomnographic study.* J Neurol, 2016. **263**(2): p. 396-402.
65. Walters, A.S., et al., *Validation of the International Restless Legs Syndrome Study Group rating scale for restless legs syndrome.* Sleep Med, 2003. **4**(2): p. 121-32.
66. International Restless Legs Syndrome Study Group. [cited 2017 February 28]; Available from: irlssg.org.
67. Freeman, A., et al., *Sleep fragmentation and motor restlessness in a Drosophila model of Restless Legs Syndrome.* Curr Biol, 2012. **22**(12): p. 1142-8.
68. Allen, R.P. and C.J. Earley, *Validation of the Johns Hopkins restless legs severity scale.* Sleep Med, 2001. **2**(3): p. 239-242.
69. Liu, D.J. and S.M. Leal, *A novel adaptive method for the analysis of next-generation sequencing data to detect complex trait associations with rare variants due to gene main effects and interactions.* PLoS Genet, 2010. **6**(10): p. e1001156.
70. Xiong, L., et al., *MEIS1 intronic risk haplotype associated with restless legs syndrome affects its mRNA and protein expression levels.* Hum Mol Genet, 2009. **18**(6): p. 1065-74.

71. Whitfield, A.C., B.T. Moore, and R.N. Daniels, *Classics in chemical neuroscience: levodopa.* ACS Chem Neurosci, 2014. **5**(12): p. 1192-7.
72. Weigend, B., *Die US-amerikanische Limited Liability Company im Vergleich zu deutschen Gesellschaftsformen unter Berücksichtigung steuerlicher Aspekte*, in *Rechtswissenschaft*. 2004, Universität Hamburg: Berlin.
73. Minica, C.C., et al., *The Weighting is the Hardest Part: On the Behavior of the Likelihood Ratio Test and the Score Test Under a Data-Driven Weighting Scheme in Sequenced Samples.* Twin Res Hum Genet, 2017: p. 1-11.
74. Lee, S., L. Miropolsky, and M. Wu. *Package 'SKAT'*. 2016 [cited 2016 May 16]; Available from: https://cran.r-project.org/web/packages/SKAT/SKAT.pdf.
75. Karas, M., et al., *Matrix Dependence of Metastable Fragmentation of Glycoproteins in MALDI TOF Mass Spectrometry.* Analytical Chemistry, 1995. **67**(3): p. 675-679.
76. de Vlaming, R., et al., *Meta-GWAS Accuracy and Power (MetaGAP) Calculator Shows that Hiding Heritability Is Partially Due to Imperfect Genetic Correlations across Studies.* PLoS Genet, 2017. **13**(1): p. e1006495.
77. Suzuki, T., et al., *MICAL, a novel CasL interacting molecule, associates with vimentin.* J Biol Chem, 2002. **277**(17): p. 14933-41.
78. O'Roak, B.J., et al., *Multiplex targeted sequencing identifies recurrently mutated genes in autism spectrum disorders.* Science, 2012. **338**(6114): p. 1619-22.
79. Broad Institute. *RMSMappingQuality*. 2017 [cited 2017 Mar 19]; Available from: https://software.broadinstitute.org/gatk/documentation/tooldocs/current/org_broadinstitute_gatk_tools_walkers_annotator_RMSMappingQuality.php.
80. Janning, W. and E. Knust, *Genetik*. 2004, Stuttgart: Georg Thieme Verlag.
81. Wheeler, D.L., et al., *Database resources of the National Center for Biotechnology Information.* Nucleic Acids Res, 2000. **28**(1): p. 10-4.
82. Ritter, B., et al., *Identification of a family of endocytic proteins that define a new alpha-adaptin ear-binding motif.* EMBO Rep, 2003. **4**(11): p. 1089-95.
83. Endrullat, C., et al., *Standardization and quality management in next-generation sequencing.* Appl Transl Genom, 2016. **10**: p. 2-9.
84. National Human Genome Research Institute. [cited 2017 March 1]; Available from: www.genome.gov.
85. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 860.
86. Garcia-Borreguero, D., et al., *Treatment of restless legs syndrome with pregabalin: a double-blind, placebo-controlled study.* Neurology, 2010. **74**(23): p. 1897-904.
87. Hornyak, M., et al., *Periodic leg movements in sleep and periodic limb movement disorder: prevalence, clinical significance and treatment.* Sleep Med Rev, 2006. **10**(3): p. 169-77.
88. Ramensky, V., P. Bork, and S. Sunyaev, *Human non-synonymous SNPs: server and survey.* Nucleic Acids Res, 2002. **30**(17): p. 3894-900.
89. Majewsky, M., et al., *Determination of microplastic polyethylene (PE) and polypropylene (PP) in environmental samples using thermal analysis (TGA-DSC).* Sci Total Environ, 2016. **568**: p. 507-11.
90. Davidson, S., et al., *A remote and highly conserved enhancer supports amygdala specific expression of the gene encoding the anxiogenic neuropeptide substance-P.* Mol Psychiatry, 2006. **11**(4): p. 323, 410-21.
91. Ng, P.C. and S. Henikoff, *Predicting deleterious amino acid substitutions.* Genome Res, 2001. **11**(5): p. 863-74.
92. Wu, M.C., et al., *Rare-variant association testing for sequencing data with the sequence kernel association test.* Am J Hum Genet, 2011. **89**(1): p. 82-93.
93. Lee, S., M.C. Wu, and X. Lin, *Optimal tests for rare variant effects in sequencing association studies.* Biostatistics, 2012. **13**(4): p. 762-75.

94. Liu, X., et al., *dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Nonsynonymous and Splice-Site SNVs.* Hum Mutat, 2016. **37**(3): p. 235-41.
95. Pan, W., *Asymptotic tests of association with multiple SNPs in linkage disequilibrium.* Genet Epidemiol, 2009. **33**(6): p. 497-507.
96. Spielman, R.S., R.E. McGinnis, and W.J. Ewens, *Transmission test for linkage disequilibrium: the insulin gene region and insulin-dependent diabetes mellitus (IDDM).* Am. J. Hum. Genet., 1993. **52**: p. 506-516.
97. Kent, W.J., et al., *The human genome browser at UCSC.* Genome Res, 2002. **12**(6): p. 996-1006.
98. Bloom, L. and H.R. Horvitz, *The Caenorhabditis elegans gene unc-76 and its human homologs define a new gene family involved in axonal outgrowth and fasciculation.* Proc Natl Acad Sci U S A, 1997. **94**(7): p. 3414-9.
99. Danecek, P., et al., *The variant call format and VCFtools.* Bioinformatics, 2011. **27**(15): p. 2156-8.
100. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 1450.
101. Price, A.L., et al., *Pooled association tests for rare variants in exon-resequencing studies.* Am J Hum Genet, 2010. **86**(6): p. 832-8.
102. Walters, A.S., et al., *Review of diagnostic instruments for the restless legs syndrome/Willis-Ekbom Disease (RLS/WED): critique and recommendations.* J Clin Sleep Med, 2014. **10**(12): p. 1343-9.
103. Hornby, A.S., *Oxford Advanced Learner's Dictionary of Current English*, S. Wehmeier and M. Ashby, Editors. 2000, Oxford University Press: Oxford. p. 1478.
104. Madsen, B.E. and S.R. Browning, *A groupwise association test for rare mutations using a weighted sum statistic.* PLoS Genet, 2009. **5**(2): p. e1000384.
105. Willis, T., *The London practice of physic*. 1685, London: Bassett and Crooke.
106. Ekbom, K.-A., *PREFACE.* Acta Medica Scandinavica, 1945. **121**(S158): p. 7-8.
107. Ekbom, K.-A., *CHAPTER 1: Introduction.* Acta Medica Scandinavica, 1945. **121**(S158): p. 9-11.
108. Ekbom, K.-A., *CHAPTER 2: Historical Review.* Acta Medica Scandinavica, 1945. **121**(S158): p. 12-15.
109. Ekbom, K.-A., *CHAPTER 3: Source and Nature of my Cases.* Acta Medica Scandinavica, 1945. **121**(S158): p. 16-17.
110. Ekbom, K.-A., *CHAPTER 4: The Paresthetic Form of Restless Legs (Asthenia Crurum Paraesthetica).* Acta Medica Scandinavica, 1945. **121**(S158): p. 18-59.
111. Ekbom, K.-A., *CHAPTER 5: The Painful Form of Restless Legs (Asthenia Crurum Dolorosa).* Acta Medica Scandinavica, 1945. **121**(S158): p. 60-65.
112. Ekbom, K.-A., *CHAPTER 6: Brief Survey of Paresthesia in General.* Acta Medica Scandinavica, 1945. **121**(S158): p. 66-73.
113. Ekbom, K.-A., *CHAPTER 7: Case Reports.* Acta Medica Scandinavica, 1945. **121**(S158): p. 74-118.
114. Ekbom, K.-A., *Summary.* Acta Medica Scandinavica, 1945. **121**(S158): p. 119-121.
115. Ekbom, K.-A., *References.* Acta Medica Scandinavica, 1945. **121**(S158): p. 122-123.
116. Ekbom, K.-A., *Asthenia Crurum Paraesthetica («Irritable legs«).* Acta Medica Scandinavica, 1944. **118**(1-3): p. 197-209.
117. Allen, R.P., et al., *Restless legs syndrome/Willis-Ekbom disease diagnostic criteria: updated International Restless Legs Syndrome Study Group (IRLSSG) consensus criteria--history, rationale, description, and significance.* Sleep Med, 2014. **15**(8): p. 860-73.
118. Walters, A.S., *Toward a better definition of the restless legs syndrome. The International Restless Legs Syndrome Study Group.* Mov Disord, 1995. **10**(5): p. 634-42.

119. Allen, R.P., et al., *Restless legs syndrome: diagnostic criteria, special considerations, and epidemiology. A report from the restless legs syndrome diagnosis and epidemiology workshop at the National Institutes of Health.* Sleep Med, 2003. **4**(2): p. 101-19.
120. Walters, A.S., et al., *Review of Severity Rating Scales for Restless Legs Syndrome: Critique and Recommendations.* Movement Disorders Clinical Practice, 2014. **1**(4): p. 317-324.
121. Allen, R.P. and C.J. Earley, *Augmentation of the restless legs syndrome with carbidopa/levodopa.* Sleep, 1996. **19**(3): p. 205-13.
122. Garcia-Borreguero, D., et al., *Diagnostic standards for dopaminergic augmentation of restless legs syndrome: report from a World Association of Sleep Medicine-International Restless Legs Syndrome Study Group consensus conference at the Max Planck Institute.* Sleep Med, 2007. **8**(5): p. 520-30.
123. Koo, B.B., *Restless Leg Syndrome Across the Globe: Epidemiology of the Restless Legs Syndrome/Willis-Ekbom Disease.* Sleep Med Clin, 2015. **10**(3): p. 189-205, xi.
124. Ohayon, M.M., R. O'Hara, and M.V. Vitiello, *Epidemiology of restless legs syndrome: a synthesis of the literature.* Sleep Med Rev, 2012. **16**(4): p. 283-95.
125. Carlos, K., et al., *Willis–Ekbom Disease or Restless Legs Syndrome?* Sleep Medicine, 2015. **16**(9): p. 1156-1159.
126. Allen, R.P., et al., *Restless legs syndrome prevalence and impact: REST general population study.* Arch Intern Med, 2005. **165**(11): p. 1286-92.
127. Ohayon, M.M. and T. Roth, *Prevalence of restless legs syndrome and periodic limb movement disorder in the general population.* J Psychosom Res, 2002. **53**(1): p. 547-54.
128. Tan, E.K., et al., *Restless legs syndrome in an Asian population: A study in Singapore.* Mov Disord, 2001. **16**(3): p. 577-9.
129. Kim, J., et al., *Prevalence of restless legs syndrome and associated factors in the Korean adult population: the Korean Health and Genome Study.* Psychiatry Clin Neurosci, 2005. **59**(3): p. 350-3.
130. Rangarajan, S., S. Rangarajan, and G.A. D'Souza, *Restless legs syndrome in an Indian urban population.* Sleep Med, 2007. **9**(1): p. 88-93.
131. Tsuboi, Y., et al., *Prevalence of restless legs syndrome in a Japanese elderly population.* Parkinsonism Relat Disord, 2009. **15**(8): p. 598-601.
132. Mizuno, S., et al., *Prevalence of restless legs syndrome in non-institutionalized Japanese elderly.* Psychiatry Clin Neurosci, 2005. **59**(4): p. 461-5.
133. Nomura, T., et al., *Prevalence of restless legs syndrome in a rural community in Japan.* Mov Disord, 2008. **23**(16): p. 2363-9.
134. Szentkiralyi, A., et al., *Multimorbidity and the risk of restless legs syndrome in 2 prospective cohort studies.* Neurology, 2014. **82**(22): p. 2026-33.
135. Comella, C.L., *Treatment of Restless Legs Syndrome.* Neurotherapeutics, 2014. **11**(1): p. 177-87.
136. Trenkwalder, C., et al., *Restless legs syndrome associated with major diseases: A systematic review and new concept.* Neurology, 2016. **86**(14): p. 1336-43.
137. Knovich, M.A., et al., *Ferritin for the clinician.* Blood Rev, 2009. **23**(3): p. 95-104.
138. Gigli, G.L., et al., *Restless legs syndrome in end-stage renal disease.* Sleep Med, 2004. **5**(3): p. 309-15.
139. Collado-Seidel, V., et al., *Clinical and biochemical findings in uremic patients with and without restless legs syndrome.* Am J Kidney Dis, 1998. **31**(2): p. 324-8.
140. Kavanagh, D., S. Siddiqui, and C.C. Geddes, *Restless legs syndrome in patients on dialysis.* Am J Kidney Dis, 2004. **43**(5): p. 763-71.
141. Lee, K.A., M.E. Zaffke, and K. Baratte-Beebe, *Restless legs syndrome and sleep disturbance during pregnancy: the role of folate and iron.* J Womens Health Gend Based Med, 2001. **10**(4): p. 335-41.

142. Pantaleo, N.P., et al., *Pregnancy accounts for most of the gender difference in prevalence of familial RLS.* Sleep Med, 2010. **11**(3): p. 310-3.
143. Hening, W.A., et al., *The four diagnostic criteria for Restless Legs Syndrome are unable to exclude confounding conditions ("mimics").* Sleep Med, 2009. **10**(9): p. 976-81.
144. Allen, R.P., et al., *Validation of the self-completed Cambridge-Hopkins questionnaire (CH-RLSq) for ascertainment of restless legs syndrome (RLS) in a population survey.* Sleep Med, 2009. **10**(10): p. 1097-100.
145. Hoque, R. and A.L. Chesson, Jr., *Pharmacologically induced/exacerbated restless legs syndrome, periodic limb movements of sleep, and REM behavior disorder/REM sleep without atonia: literature review, qualitative scoring, and comparative analysis.* J Clin Sleep Med, 2010. **6**(1): p. 79-83.
146. Winkelmann, J., et al., *"Anxietas tibiarum". Depression and anxiety disorders in patients with restless legs syndrome.* J Neurol, 2005. **252**(1): p. 67-71.
147. Szentkiralyi, A., et al., *Restless legs syndrome and all-cause mortality in four prospective cohort studies.* BMJ Open, 2012. **2**(6).
148. Stefanidis, I., et al., *Restless legs syndrome does not affect 3-year mortality in hemodialysis patients.* Sleep Med, 2015. **16**(9): p. 1131-8.
149. Ambrosetto, C., et al., *Clinical and polygraphic remarks in the syndrome of restless legs.* Riv Patol Nerv Ment, 1965. **86**(2): p. 244-52.
150. Montplaisir, J., et al., *Clinical, polysomnographic, and genetic characteristics of restless legs syndrome: a study of 133 patients diagnosed with new standard criteria.* Mov Disord, 1997. **12**(1): p. 61-5.
151. Bixler, E.O., et al., *Nocturnal myoclonus and nocturnal myoclonic activity in the normal population.* Res Commun Chem Pathol Pharmacol, 1982. **36**(1): p. 129-40.
152. Eisensehr, I., B.L. Ehrenberg, and S. Noachtar, *Different sleep characteristics in restless legs syndrome and periodic limb movement disorder.* Sleep Med, 2003. **4**(2): p. 147-52.
153. Li, J., et al., *Association of low ferritin with PLM in the Wisconsin Sleep Cohort.* Sleep Med, 2015. **16**(11): p. 1413-8.
154. Sun, E.R., et al., *Iron and the restless legs syndrome.* Sleep, 1998. **21**(4): p. 371-7.
155. Akpinar, S., *Treatment of restless legs syndrome with levodopa plus benserazide.* Arch Neurol, 1982. **39**(11): p. 739.
156. Thorpe, A.J., et al., *Possible sites of therapeutic action in restless legs syndrome: focus on dopamine and alpha2delta ligands.* Eur Neurol, 2011. **66**(1): p. 18-29.
157. Reichmann, H., et al., *Ergoline and non-ergoline derivatives in the treatment of Parkinson's disease.* J Neurol, 2006. **253 Suppl 4**: p. Iv36-8.
158. Earley, C.J. and R.P. Allen, *Pergolide and carbidopa/levodopa treatment of the restless legs syndrome and periodic leg movements in sleep in a consecutive series of patients.* Sleep, 1996. **19**(10): p. 801-10.
159. Stiasny, K., et al., *Treatment of idiopathic restless legs syndrome (RLS) with the D2-agonist cabergoline--an open clinical trial.* Sleep, 2000. **23**(3): p. 349-54.
160. Walters, A.S., et al., *A double-blind randomized crossover trial of bromocriptine and placebo in restless legs syndrome.* Ann Neurol, 1988. **24**(3): p. 455-8.
161. Hogl, B., et al., *Efficacy and augmentation during 6 months of double-blind pramipexole for restless legs syndrome.* Sleep Med, 2011. **12**(4): p. 351-60.
162. Walters, A.S., et al., *Ropinirole is effective in the treatment of restless legs syndrome. TREAT RLS 2: a 12-week, double-blind, randomized, parallel-group, placebo-controlled study.* Mov Disord, 2004. **19**(12): p. 1414-23.
163. Trenkwalder, C., et al., *Ropinirole in the treatment of restless legs syndrome: results from the TREAT RLS 1 study, a 12 week, randomised, placebo controlled study in 10 European countries.* J Neurol Neurosurg Psychiatry, 2004. **75**(1): p. 92-7.

164. Oertel, W., et al., *Long-term safety and efficacy of rotigotine transdermal patch for moderate-to-severe idiopathic restless legs syndrome: a 5-year open-label extension study.* Lancet Neurol, 2011. **10**(8): p. 710-20.

165. Kvernmo, T., S. Hartter, and E. Burger, *A review of the receptor-binding and pharmacokinetic properties of dopamine agonists.* Clin Ther, 2006. **28**(8): p. 1065-78.

166. Cotter, P.E. and S.T. O'Keeffe, *Restless leg syndrome: is it a real problem?* Ther Clin Risk Manag, 2006. **2**(4): p. 465-75.

167. Trenkwalder, C., et al., *One-year treatment with standard and sustained-release levodopa: appropriate long-term treatment of restless legs syndrome?* Mov Disord, 2003. **18**(10): p. 1184-9.

168. Collado-Seidel, V., et al., *A controlled study of additional sr-L-dopa in L-dopa-responsive restless legs syndrome with late-night symptoms.* Neurology, 1999. **52**(2): p. 285-90.

169. Crevoisier, C., et al., *Bioavailability of L-dopa after Madopar HBS administration in healthy volunteers.* Eur Neurol, 1987. **27 Suppl 1**: p. 36-46.

170. Trenkwalder, C., et al., *Augmentation in restless legs syndrome is associated with low ferritin.* Sleep Med, 2008. **9**(5): p. 572-4.

171. Garcia-Borreguero, D., et al., *Systematic evaluation of augmentation during treatment with ropinirole in restless legs syndrome (Willis-Ekbom disease): results from a prospective, multicenter study over 66 weeks.* Mov Disord, 2012. **27**(2): p. 277-83.

172. Trenkwalder, C., et al., *Cabergoline compared to levodopa in the treatment of patients with severe restless legs syndrome: results from a multi-center, randomized, active controlled trial.* Mov Disord, 2007. **22**(5): p. 696-703.

173. Pritchett, A.M., et al., *Valvular Heart Disease in Patients Taking Pergolide.* Mayo Clinic Proceedings, 2002. **77**(12): p. 1280-1286.

174. Van Camp, G., et al., *Heart valvular disease in patients with Parkinson's disease treated with high-dose pergolide.* Neurology, 2003. **61**(6): p. 859-861.

175. Schade, R., et al., *Dopamine Agonists and the Risk of Cardiac-Valve Regurgitation.* New England Journal of Medicine, 2007. **356**(1): p. 29-38.

176. Zanettini, R., et al., *Valvular Heart Disease and the Use of Dopamine Agonists for Parkinson's Disease.* New England Journal of Medicine, 2007. **356**(1): p. 39-46.

177. Tran, T., et al., *Risks of Cardiac Valve Regurgitation and Heart Failure Associated with Ergot- and Non-Ergot-Derived Dopamine Agonist Use in Patients with Parkinson's Disease: A Systematic Review of Observational Studies.* CNS Drugs, 2015. **29**(12): p. 985-98.

178. Danoff, S.K., et al., *Pleuropulmonary disease due to pergolide use for restless legs syndrome.* Chest, 2001. **120**(1): p. 313-6.

179. Moore, T.J., J. Glenmullen, and D.R. Mattison, *Reports of pathological gambling, hypersexuality, and compulsive shopping associated with dopamine receptor agonist drugs.* JAMA Intern Med, 2014. **174**(12): p. 1930-3.

180. Jones, H.B. and S. George, *'You never told me I would turn into a gambler': a first person account of dopamine agonist--induced gambling addiction in a patient with restless legs syndrome.* BMJ Case Rep, 2011. **2011**.

181. Garcia-Borreguero, D., et al., *The long-term treatment of restless legs syndrome/Willis-Ekbom disease: evidence-based guidelines and clinical consensus best practice guidance: a report from the International Restless Legs Syndrome Study Group.* Sleep Med, 2013. **14**(7): p. 675-84.

182. Stiasny, K., et al., *Restless legs syndrome and its treatment by dopamine agonists.* Parkinsonism Relat Disord, 2000. **7**(1): p. 21-25.

183. Manconi, M., et al., *Preferential D2 or preferential D3 dopamine agonists in restless legs syndrome.* Neurology, 2011. **77**(2): p. 110-7.

184. Takahashi, M., et al., *Subunit structure of dihydropyridine-sensitive calcium channels from skeletal muscle.* Proc Natl Acad Sci U S A, 1987. **84**(15): p. 5478-82.

185. De Jongh, K.S., C. Warner, and W.A. Catterall, *Subunits of purified calcium channels. Alpha 2 and delta are encoded by the same gene.* J Biol Chem, 1990. **265**(25): p. 14738-41.
186. Jay, S.D., et al., *Structural characterization of the dihydropyridine-sensitive calcium channel alpha 2-subunit and the associated delta peptides.* J Biol Chem, 1991. **266**(5): p. 3287-93.
187. Gurnett, C.A., M. De Waard, and K.P. Campbell, *Dual function of the voltage-dependent Ca2+ channel alpha 2 delta subunit in current stimulation and subunit interaction.* Neuron, 1996. **16**(2): p. 431-40.
188. Gee, N.S., et al., *The novel anticonvulsant drug, gabapentin (Neurontin), binds to the alpha2delta subunit of a calcium channel.* J Biol Chem, 1996. **271**(10): p. 5768-76.
189. Field, M.J., et al., *Identification of the alpha2-delta-1 subunit of voltage-dependent calcium channels as a molecular target for pain mediating the analgesic actions of pregabalin.* Proc Natl Acad Sci U S A, 2006. **103**(46): p. 17537-42.
190. Sommer, M., et al., *Pregabalin in restless legs syndrome with and without neuropathic pain.* Acta Neurol Scand, 2007. **115**(5): p. 347-50.
191. Adler, C.H., *Treatment of restless legs syndrome with gabapentin.* Clin Neuropharmacol, 1997. **20**(2): p. 148-51.
192. Mellick, G.A. and L.B. Mellick, *Management of restless legs syndrome with gabapentin (Neurontin).* Sleep, 1996. **19**(3): p. 224-6.
193. Garcia-Borreguero, D., et al., *Treatment of restless legs syndrome with gabapentin: a double-blind, cross-over study.* Neurology, 2002. **59**(10): p. 1573-9.
194. Saletu, M., et al., *Comparative placebo-controlled polysomnographic and psychometric studies on the acute effects of gabapentin versus ropinirole in restless legs syndrome.* J Neural Transm (Vienna), 2010. **117**(4): p. 463-73.
195. Kushida, C.A., et al., *Randomized, double-blind, placebo-controlled study of XP13512/GSK1838262 in patients with RLS.* Neurology, 2009. **72**(5): p. 439-46.
196. Kushida, C.A., et al., *A randomized, double-blind, placebo-controlled, crossover study of XP13512/GSK1838262 in the treatment of patients with primary restless legs syndrome.* Sleep, 2009. **32**(2): p. 159-68.
197. Inoue, Y., et al., *Gabapentin enacarbil in Japanese patients with restless legs syndrome: a 12-week, randomized, double-blind, placebo-controlled, parallel-group study.* Curr Med Res Opin, 2013. **29**(1): p. 13-21.
198. Ellenbogen, A.L., et al., *A 52-week study of gabapentin enacarbil in restless legs syndrome.* Clin Neuropharmacol, 2011. **34**(1): p. 8-16.
199. CENTER FOR DRUG EVALUATION AND RESEARCH. *APPLICATION NUMBER: 022399Orig1s000 SUMMARY REVIEW*. 2011 [cited 2016 May 25]; Available from: http://www.accessdata.fda.gov/drugsatfda_docs/nda/2011/022399Orig1s000SumR.pdf.
200. Allen, R.P., et al., *Comparison of pregabalin with pramipexole for restless legs syndrome.* N Engl J Med, 2014. **370**(7): p. 621-31.
201. Allen, R., et al., *A randomized, double-blind, 6-week, dose-ranging study of pregabalin in patients with restless legs syndrome.* Sleep Med, 2010. **11**(6): p. 512-9.
202. Papazisis, G. and D. Tzachanis, *Pregabalin's abuse potential: a mini review focusing on the pharmacological profile.* Int J Clin Pharmacol Ther, 2014. **52**(8): p. 709-16.
203. Trenkwalder, C., et al., *Prolonged release oxycodone-naloxone for treatment of severe restless legs syndrome after failure of previous treatment: a double-blind, randomised, placebo-controlled trial with an open-label extension.* Lancet Neurol, 2013. **12**(12): p. 1141-50.
204. Ondo, W.G., *Methadone for refractory restless legs syndrome.* Mov Disord, 2005. **20**(3): p. 345-8.
205. Silver, N., et al., *A 10-year, longitudinal assessment of dopamine agonists and methadone in the treatment of restless legs syndrome.* Sleep Med, 2011. **12**(5): p. 440-4.

206. Connor, J.R., et al., *Profile of altered brain iron acquisition in restless legs syndrome.* Brain, 2011. **134**(Pt 4): p. 959-68.
207. Grote, L., et al., *A randomized, double-blind, placebo controlled, multi-center study of intravenous iron sucrose and placebo in the treatment of restless legs syndrome.* Mov Disord, 2009. **24**(10): p. 1445-52.
208. Mehmood, T., et al., *Response to intravenous iron in patients with iron deficiency anemia (IDA) and restless leg syndrome (Willis-Ekbom disease).* Sleep Med, 2014. **15**(12): p. 1473-6.
209. Cho, Y.W., R.P. Allen, and C.J. Earley, *Lower molecular weight intravenous iron dextran for restless legs syndrome.* Sleep Med, 2013. **14**(3): p. 274-7.
210. Garcia-Borreguero, D., et al., *Guidelines for the first-line treatment of restless legs syndrome/Willis–Ekbom disease, prevention and treatment of dopaminergic augmentation: a combined task force of the IRLSSG, EURLSSG, and the RLS-foundation.* Sleep Medicine, 2016. **21**: p. 1-11.
211. Visscher, P.M., W.G. Hill, and N.R. Wray, *Heritability in the genomics era--concepts and misconceptions.* Nat Rev Genet, 2008. **9**(4): p. 255-66.
212. Ondo, W. and J. Jankovic, *Restless legs syndrome: clinicoetiologic correlates.* Neurology, 1996. **47**(6): p. 1435-41.
213. Winkelmann, J., et al., *Clinical characteristics and frequency of the hereditary restless legs syndrome in a population of 300 patients.* Sleep, 2000. **23**(5): p. 597-602.
214. Winkelmann, J., et al., *Complex segregation analysis of restless legs syndrome provides evidence for an autosomal dominant mode of inheritance in early age at onset families.* Ann Neurol, 2002. **52**(3): p. 297-302.
215. Mathias, R.A., et al., *Segregation analysis of restless legs syndrome: possible evidence for a major gene in a family study using blinded diagnoses.* Hum Hered, 2006. **62**(3): p. 157-64.
216. Ondo, W.G., K.D. Vuong, and Q. Wang, *Restless legs syndrome in monozygotic twins: clinical correlates.* Neurology, 2000. **55**(9): p. 1404-6.
217. Lazzarini, A., et al., *Studies of penetrance and anticipation in five autosomal-dominant restless legs syndrome pedigrees.* Mov Disord, 1999. **14**(1): p. 111-6.
218. Desautels, A., et al., *Identification of a major susceptibility locus for restless legs syndrome on chromosome 12q.* Am J Hum Genet, 2001. **69**(6): p. 1266-70.
219. Bonati, M.T., et al., *Autosomal dominant restless legs syndrome maps on chromosome 14q.* Brain, 2003. **126**(Pt 6): p. 1485-92.
220. Chen, S., et al., *Genomewide linkage scan identifies a novel susceptibility locus for restless legs syndrome on chromosome 9p.* Am J Hum Genet, 2004. **74**(5): p. 876-85.
221. Pichler, I., et al., *Linkage analysis identifies a novel locus for restless legs syndrome on chromosome 2q in a South Tyrolean population isolate.* Am J Hum Genet, 2006. **79**(4): p. 716-23.
222. Levchenko, A., et al., *A novel autosomal dominant restless legs syndrome locus maps to chromosome 20p13.* Neurology, 2006. **67**(5): p. 900-1.
223. Kemlink, D., et al., *Suggestive evidence for linkage for restless legs syndrome on chromosome 19p13.* Neurogenetics, 2008. **9**(2): p. 75-82.
224. Levchenko, A., et al., *Autosomal-dominant locus for Restless Legs Syndrome in French-Canadians on chromosome 16p12.1.* Mov Disord, 2009. **24**(1): p. 40-50.
225. Winkelmann, J., et al., *New loci for restless legs syndrome map to chromosome 4q and 17p.* Akt Neurol, 2006. **33**(S 1): p. V57.
226. Desautels, A., et al., *Restless legs syndrome: confirmation of linkage to chromosome 12q, genetic heterogeneity, and evidence of complexity.* Arch Neurol, 2005. **62**(4): p. 591-6.
227. Winkelmann, J., et al., *Evidence for further genetic locus heterogeneity and confirmation of RLS-1 in restless legs syndrome.* Mov Disord, 2006. **21**(1): p. 28-33.
228. Levchenko, A., et al., *The 14q restless legs syndrome locus in the French Canadian population.* Ann Neurol, 2004. **55**(6): p. 887-91.

229. Kemlink, D., et al., *Family-based association study of the restless legs syndrome loci 2 and 3 in a European population.* Mov Disord, 2007. **22**(2): p. 207-12.

230. Ray, A. and D.E. Weeks, *No convincing evidence of linkage for restless legs syndrome on chromosome 9p.* Am J Hum Genet, 2005. **76**(4): p. 705-7; author reply 707-10.

231. Liebetanz, K.M., et al., *RLS3: fine-mapping of an autosomal dominant locus in a family with intrafamilial heterogeneity.* Neurology, 2006. **67**(2): p. 320-1.

232. Lohmann-Hedrich, K., et al., *Evidence for linkage of restless legs syndrome to chromosome 9p: are there two distinct loci?* Neurology, 2008. **70**(9): p. 686-94.

233. Pichler, I., et al., *Fine-mapping of restless legs locus 4 (RLS4) identifies a haplotype over the SPATS2L and KCTD18 genes.* J Mol Neurosci, 2013. **49**(3): p. 600-5.

234. Sas, A.M., et al., *Autosomal dominant restless legs syndrome maps to chromosome 20p13 (RLS-5) in a Dutch kindred.* Mov Disord, 2010. **25**(11): p. 1715-22.

235. Skehan, E.B., et al., *A novel locus for restless legs syndrome maps to chromosome 19p in an Irish pedigree.* Neurogenetics, 2012. **13**(2): p. 125-32.

236. Balaban, H., et al., *A novel locus for restless legs syndrome on chromosome 13q.* Eur Neurol, 2012. **68**(2): p. 111-6.

237. Young, J.E., et al., *Clinical and genetic description of a family with a high prevalence of autosomal dominant restless legs syndrome.* Mayo Clin Proc, 2009. **84**(2): p. 134-8.

238. Desautels, A., et al., *Mutational analysis of neurotensin in familial restless legs syndrome.* Mov Disord, 2004. **19**(1): p. 90-4.

239. Xiong, L., et al., *Genetic association studies of neurotensin gene and restless legs syndrome in French Canadians.* Sleep Med, 2008. **9**(3): p. 273-82.

240. Winkelmann, J., et al., *Variants in the neuronal nitric oxide synthase (nNOS, NOS1) gene are associated with restless legs syndrome.* Mov Disord, 2008. **23**(3): p. 350-8.

241. Weissbach, A., et al., *Exome sequencing in a family with restless legs syndrome.* Mov Disord, 2012. **27**(13): p. 1686-9.

242. Stefansson, H., et al., *A genetic risk factor for periodic limb movements in sleep.* N Engl J Med, 2007. **357**(7): p. 639-47.

243. Winkelmann, J., et al., *Genome-wide association study of restless legs syndrome identifies common variants in three genomic regions.* Nat Genet, 2007. **39**(8): p. 1000-6.

244. Schormair, B., et al., *PTPRD (protein tyrosine phosphatase receptor type delta) is associated with restless legs syndrome.* Nat Genet, 2008. **40**(8): p. 946-8.

245. Winkelmann, J., et al., *Genome-wide association study identifies novel restless legs syndrome susceptibility loci on 2p14 and 16q12.1.* PLoS Genet, 2011. **7**(7): p. e1002171.

246. Kim, M.K., et al., *Association of restless legs syndrome variants in Korean patients with restless legs syndrome.* Sleep, 2013. **36**(12): p. 1787-91.

247. Lin, C.H., et al., *Association of candidate genetic variants with restless legs syndrome in end stage renal disease: a multicenter case-control study in Taiwan.* Eur J Neurol, 2014. **21**(3): p. 492-8.

248. Schormair, B., et al., *MEIS1 and BTBD9: genetic association with restless leg syndrome in end stage renal disease.* J Med Genet, 2011. **48**(7): p. 462-6.

249. Vavrova, J., et al., *Restless legs syndrome in Czech patients with multiple sclerosis: an epidemiological and genetic study.* Sleep Med, 2012. **13**(7): p. 848-51.

250. Yang, Q., et al., *Association studies of variants in MEIS1, BTBD9, and MAP2K5/SKOR1 with restless legs syndrome in a US population.* Sleep Med, 2011. **12**(8): p. 800-4.

251. Yang, Q., et al., *Family-based and population-based association studies validate PTPRD as a risk factor for restless legs syndrome.* Mov Disord, 2011. **26**(3): p. 516-9.

252. Moore, H.t., et al., *Periodic leg movements during sleep are associated with polymorphisms in BTBD9, TOX3/BC034767, MEIS1, MAP2K5/SKOR1, and PTPRD.* Sleep, 2014. **37**(9): p. 1535-42.

253. Kemlink, D., et al., *Replication of restless legs syndrome loci in three European populations.* J Med Genet, 2009. **46**(5): p. 315-8.
254. Szentkiralyi, A., et al., *Lack of Association between Genetic Risk Loci for Restless Legs Syndrome and Multimorbidity.* Sleep, 2016. **39**(1): p. 111-5.
255. Oexle, K., et al., *Dilution of candidates: the case of iron-related genes in restless legs syndrome.* Eur J Hum Genet, 2013. **21**(4): p. 410-4.
256. Jimenez-Jimenez, F.J., et al., *Association Between Vitamin D Receptor rs731236 (Taq1) Polymorphism and Risk for Restless Legs Syndrome in the Spanish Caucasian Population.* Medicine (Baltimore), 2015. **94**(47): p. e2125.
257. Jung, J.S., et al., *Association between restless legs syndrome and CLOCK and NPAS2 gene polymorphisms in schizophrenia.* Chronobiol Int, 2014. **31**(7): p. 838-44.
258. Garcia-Martin, E., et al., *Heme Oxygenase-1 and 2 Common Genetic Variants and Risk for Restless Legs Syndrome.* Medicine (Baltimore), 2015. **94**(34): p. e1448.
259. Hennessy, M.D., et al., *Polymorphisms of interleukin-1 Beta and interleukin-17Alpha genes are associated with restless legs syndrome.* Biol Res Nurs, 2014. **16**(2): p. 143-51.
260. Lahut, S., et al., *The PD-associated alpha-synuclein promoter Rep1 allele 2 shows diminished frequency in restless legs syndrome.* Neurogenetics, 2014. **15**(3): p. 189-92.
261. Jimenez-Jimenez, F.J., et al., *Neuronal nitric oxide synthase (nNOS, NOS1) rs693534 and rs7977109 variants and risk for restless legs syndrome.* J Neural Transm (Vienna), 2015. **122**(6): p. 819-23.
262. Cho, C.H., et al., *Association between Antipsychotics-Induced Restless Legs Syndrome and Tyrosine Hydroxylase Gene Polymorphism.* Psychiatry Investig, 2009. **6**(3): p. 211-5.
263. Desautels, A., et al., *Evidence for a genetic association between monoamine oxidase A and restless legs syndrome.* Neurology, 2002. **59**(2): p. 215-9.
264. Sorensen, E., et al., *Genetic factors influencing ferritin levels in 14,126 blood donors: results from the Danish Blood Donor Study.* Transfusion, 2016. **56**(3): p. 622-7.
265. Gan-Or, Z., et al., *Analysis of functional GLO1 variants in the BTBD9 locus and restless legs syndrome.* Sleep Med, 2015. **16**(9): p. 1151-5.
266. Vilarino-Guell, C., et al., *MEIS1 p.R272H in familial restless legs syndrome.* Neurology, 2009. **73**(3): p. 243-5.
267. Schulte, E.C., et al., *Targeted resequencing and systematic in vivo functional testing identifies rare variants in MEIS1 as significant contributors to restless legs syndrome.* Am J Hum Genet, 2014. **95**(1): p. 85-95.
268. Vetrugno, R., et al., *"Phantom" restless legs syndrome.* J Neurol Neurosurg Psychiatry, 2010. **81**(1): p. 122-3.
269. Skidmore, F.M., et al., *Bilateral restless legs affecting a phantom limb, treated with dopamine agonists.* J Neurol Neurosurg Psychiatry, 2009. **80**(5): p. 569-70.
270. Giummarra, M.J. and J.L. Bradshaw, *The phantom of the night: restless legs syndrome in amputees.* Med Hypotheses, 2010. **74**(6): p. 968-72.
271. Freeman, A.A. and D.B. Rye, *The molecular basis of restless legs syndrome.* Curr Opin Neurobiol, 2013. **23**(5): p. 895-900.
272. Nagatsu, T., *Tyrosine hydroxylase: human isoforms, structure and regulation in physiology and pathology.* Essays Biochem, 1995. **30**: p. 15-35.
273. Lewis, D.A., D.S. Melchitzky, and J.W. Haycock, *Four isoforms of tyrosine hydroxylase are expressed in human brain.* Neuroscience, 1993. **54**(2): p. 477-92.
274. Yamada, K., et al., *Detection of tyrosine hydroxylase and phenylethanolamine-N-methyltransferase messenger RNAs in the mouse adrenal gland and the brain by in situ hybridization.* Histochemistry, 1992. **97**(3): p. 201-6.
275. Erikson, K.M., et al., *Iron deficiency decreases dopamine D1 and D2 receptors in rat brain.* Pharmacol Biochem Behav, 2001. **69**(3-4): p. 409-18.

276. Bianco, L.E., et al., *Iron deficiency alters dopamine uptake and response to L-DOPA injection in Sprague-Dawley rats.* J Neurochem, 2008. **106**(1): p. 205-15.
277. Connor, J.R., et al., *Altered dopaminergic profile in the putamen and substantia nigra in restless leg syndrome.* Brain, 2009. **132**(Pt 9): p. 2403-12.
278. Dowling, P., et al., *Dopamine D3 receptor specifically modulates motor and sensory symptoms in iron-deficient mice.* J Neurosci, 2011. **31**(1): p. 70-7.
279. Casares, F. and R.S. Mann, *Control of antennal versus leg development in Drosophila.* Nature, 1998. **392**(6677): p. 723-6.
280. Kurant, E., et al., *Dorsotonals/homothorax, the Drosophila homologue of meis1, interacts with extradenticle in patterning of the embryonic PNS.* Development, 1998. **125**(6): p. 1037-48.
281. Maeda, R., et al., *Xmeis1, a protooncogene involved in specifying neural crest cell fate in Xenopus embryos.* Oncogene, 2001. **20**(11): p. 1329-42.
282. Azcoitia, V., et al., *The homeodomain protein Meis1 is essential for definitive hematopoiesis and vascular patterning in the mouse embryo.* Dev Biol, 2005. **280**(2): p. 307-20.
283. Minehata, K., A. Kawahara, and T. Suzuki, *meis1 regulates the development of endothelial cells in zebrafish.* Biochem Biophys Res Commun, 2008. **374**(4): p. 647-52.
284. Catoire, H., et al., *Restless legs syndrome-associated MEIS1 risk variant influences iron homeostasis.* Ann Neurol, 2011. **70**(1): p. 170-5.
285. Argiropoulos, B., E. Yung, and R.K. Humphries, *Unraveling the crucial roles of Meis1 in leukemogenesis and normal hematopoiesis.* Genes Dev, 2007. **21**(22): p. 2845-9.
286. Samaniego, F., et al., *Molecular characterization of a second iron-responsive element binding protein, iron regulatory protein 2. Structure, function, and post-translational regulation.* J Biol Chem, 1994. **269**(49): p. 30904-10.
287. DeAndrade, M.P., et al., *Motor restlessness, sleep disturbances, thermal sensory alterations and elevated serum iron levels in Btbd9 mutant mice.* Hum Mol Genet, 2012. **21**(18): p. 3984-92.
288. Hashimoto, Y., et al., *Uncovering genes required for neuronal morphology by morphology-based gene trap screening with a revertible retrovirus vector.* Faseb j, 2012. **26**(11): p. 4662-74.
289. Drgonova, J., et al., *Mouse model for PTPRD associations with WED/RLS and addiction: reduced expression alters locomotion, sleep behaviors and cocaine-conditioned place preference.* Mol Med, 2015.
290. Uetani, N., et al., *Mammalian motoneuron axon targeting requires receptor protein tyrosine phosphatases sigma and delta.* J Neurosci, 2006. **26**(22): p. 5872-80.
291. Naciff, J.M., et al., *Gene expression profile induced by 17 alpha-ethynyl estradiol in the prepubertal female reproductive system of the rat.* Toxicol Sci, 2003. **72**(2): p. 314-30.
292. Dinev, D., et al., *Extracellular signal regulated kinase 5 (ERK5) is required for the differentiation of muscle cells.* EMBO Rep, 2001. **2**(9): p. 829-34.
293. Cavanaugh, J.E., et al., *Neuroprotective role of ERK1/2 and ERK5 in a dopaminergic cell line under basal conditions and in response to oxidative stress.* J Neurosci Res, 2006. **84**(6): p. 1367-75.
294. Rick, C.E., et al., *Differentiated dopaminergic MN9D cells only partially recapitulate the electrophysiological properties of midbrain dopaminergic neurons.* Dev Neurosci, 2006. **28**(6): p. 528-37.
295. Arndt, S., et al., *Fussel-15, a novel Ski/Sno homolog protein, antagonizes BMP signaling.* Mol Cell Neurosci, 2007. **34**(4): p. 603-11.
296. Mizuhara, E., et al., *Corl1, a novel neuronal lineage-specific transcriptional corepressor for the homeodomain transcription factor Lbx1.* J Biol Chem, 2005. **280**(5): p. 3645-55.
297. Yuan, S.H., Z. Qiu, and A. Ghosh, *TOX3 regulates calcium-dependent transcription in neurons.* Proc Natl Acad Sci U S A, 2009. **106**(8): p. 2909-14.

298. Dittmer, S., et al., *TOX3 is a neuronal survival factor that induces transcription depending on the presence of CITED1 or phosphorylated CREB in the transcriptionally active complex.* J Cell Sci, 2011. **124**(Pt 2): p. 252-60.
299. Sahu, S.K., et al., *TOX3 regulates neural progenitor identity.* Biochim Biophys Acta, 2016. **1859**(7): p. 833-840.
300. Fisher, R.A., *The correlation between relatives on the supposition of mendelian inheritance.* Philosophical Transactions of the Royal Society of Edinburgh in 1918, 1918(52): p. 399-433.
301. Pritchard, J.K., *Are rare variants responsible for susceptibility to complex diseases?* Am J Hum Genet, 2001. **69**(1): p. 124-37.
302. Risch, N. and K. Merikangas, *The future of genetic studies of complex human diseases.* Science, 1996. **273**: p. 1516-1517.
303. Hindorff, L.A., et al. *A Catalog of Published Genome-Wide Association Studies*. [cited 2015 March 7]; Available from: www.genome.gov/gwastudies.
304. Welter, D., et al., *The NHGRI GWAS Catalog, a curated resource of SNP-trait associations.* Nucleic Acids Res, 2014. **42**(Database issue): p. D1001-6.
305. Maher, B., *Personal genomes: The case of the missing heritability.* Nature, 2008. **456**(7218): p. 18-21.
306. Kathiresan, S., *Common variants at 30 loci contribute to polygenic dyslipidemia.* Nature Genet., 2009. **41**: p. 56-65.
307. Berge, K.E., et al., *Accumulation of dietary cholesterol in sitosterolemia caused by mutations in adjacent ABC transporters.* Science, 2000. **290**(5497): p. 1771-5.
308. Funke, H., et al., *A molecular defect causing fish eye disease: an amino acid exchange in lecithin-cholesterol acyltransferase (LCAT) leads to the selective loss of alpha-LCAT activity.* Proc Natl Acad Sci U S A, 1991. **88**(11): p. 4855-9.
309. Manolio, T.A., et al., *Finding the missing heritability of complex diseases.* Nature, 2009. **461**(7265): p. 747-53.
310. Rivas, M.A., et al., *Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease.* Nat Genet, 2011. **43**(11): p. 1066-73.
311. Balding, D.J., *A tutorial on statistical methods for population association studies.* Nat Rev Genet, 2006. **7**(10): p. 781-91.
312. Clayton, D.G., *Population structure, differential bias and genomic control in a large-scale, case–control association study.* Nature Genet., 2005. **37**: p. 1243-1246.
313. Devlin, B. and K. Roeder, *Genomic control for association studies.* Biometrics, 1999. **55**(4): p. 997-1004.
314. Pritchard, J.K. and N.A. Rosenberg, *Use of unlinked genetic markers to detect population stratification in association studies.* Am. J. Hum. Genet., 1999. **65**: p. 220-228.
315. Reich, D.E. and D.B. Goldstein, *Detecting association in a case–control study while correcting for population stratification.* Genet. Epidemiol., 2001. **20**: p. 4-16.
316. Clarke, G.M., et al., *Basic statistical analysis in genetic case-control studies.* Nat Protoc, 2011. **6**(2): p. 121-33.
317. Pritchard, J.K., M. Stephens, and P. Donnelly, *Inference of population structure using multilocus genotype data.* Genetics, 2000. **155**: p. 945-959.
318. Rosenberg, N.A., *Genetic structure of human populations.* Science, 2002. **298**: p. 2381-2385.
319. Pritchard, J.K., et al., *Association mapping in structured populations.* Am. J. Hum. Genet., 2000. **67**: p. 170-181.
320. Alexander, D.H., J. Novembre, and K. Lange, *Fast model-based estimation of ancestry in unrelated individuals.* Genome Res., 2009. **19**: p. 1655-1664.
321. Jolliffe, I.T., *Principal Components Analysis*. 2 ed. 2002, New York: Springer-Verlag New York, Inc.
322. Patterson, N., A.L. Price, and D. Reich, *Population structure and eigenanalysis.* PLoS Genet., 2006. **2**: p. e190.

323. Tian, C., *Analysis and application of European genetic substructure using 300 K SNP information.* PLoS Genet., 2008. **4**: p. e4.
324. Won, S., *On the analysis of genome-wide association studies in family-based designs: a universal, robust analysis approach and an application to four genome-wide association studies.* PLoS Genet., 2009. **5**: p. e1000741.
325. Henderson, C.R., *Best linear unbiased estimation and prediction under a selection model.* Biometrics, 1975. **31**(2): p. 423-47.
326. Yu, J., et al., *A unified mixed-model method for association mapping that accounts for multiple levels of relatedness.* Nat Genet, 2006. **38**(2): p. 203-8.
327. Kang, H.M., et al., *Variance component model to account for sample structure in genome-wide association studies.* Nat Genet, 2010. **42**(4): p. 348-54.
328. Hardy, G.H., *MENDELIAN PROPORTIONS IN A MIXED POPULATION.* Science, 1908. **28**(706): p. 49-50.
329. Nielsen, D.M., M.G. Ehm, and B.S. Weir, *Detecting marker-disease association by testing for Hardy-Weinberg disequilibrium at a marker locus.* Am J Hum Genet, 1998. **63**(5): p. 1531-40.
330. Laurie, C.C., et al., *Quality control and quality assurance in genotypic data for genome-wide association studies.* Genet Epidemiol, 2010. **34**(6): p. 591-602.
331. Sasieni, P.D., *From genotypes to genes: doubling the sample size.* Biometrics, 1997. **53**: p. 1253-1261.
332. Armitage, P., *Tests for Linear Trends in Proportions and Frequencies.* Biometrics, 1955. **11**(3): p. 375-386.
333. Cochran, W.G., *Some Methods for Strengthening the Common X^2 Tests.* Biometrics, 1954. **10**(4): p. 417-451.
334. Zheng, G., et al., *Choice of Scores in Trend Tests for Case-Control Studies of Candidate-Gene Associations.* Biometrical Journal, 2003. **45**(3): p. 335-348.
335. Aickin, M. and H. Gensler, *Adjusting for multiple testing when reporting research results: the Bonferroni vs Holm methods.* Am J Public Health, 1996. **86**(5): p. 726-8.
336. Sidak, Z., *Rectangular Confidence Regions for the Means of Multivariate Normal Distributions.* Journal of the American Statistical Association, 1967. **62**(318): p. 626-633.
337. Pe'er, I., et al., *Estimation of the multiple testing burden for genomewide association studies of nearly all common variants.* Genet Epidemiol, 2008. **32**(4): p. 381-5.
338. Dudbridge, F. and A. Gusnanto, *Estimation of significance thresholds for genomewide association scans.* Genet Epidemiol, 2008. **32**(3): p. 227-34.
339. Benjamini, Y. and Y. Hochberg, *Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing.* Journal of the Royal Statistical Society. Series B (Methodological), 1995. **57**(1): p. 289-300.
340. 1000 Genomes Project Consortium, et al., *A global reference for human genetic variation.* Nature, 2015. **526**(7571): p. 68-74.
341. Asimit, J. and E. Zeggini, *Rare variant association analysis methods for complex traits.* Annu Rev Genet, 2010. **44**: p. 293-308.
342. Xing, G., et al., *Blindly using Wald's test can miss rare disease-causal variants in case-control association studies.* Ann Hum Genet, 2012. **76**(2): p. 168-77.
343. Lee, S., et al., *Rare-variant association analysis: study designs and statistical tests.* Am J Hum Genet, 2014. **95**(1): p. 5-23.
344. Neale, B.M., et al., *Testing for an unusual distribution of rare variants.* PLoS Genet, 2011. **7**(3): p. e1001322.
345. Basu, S. and W. Pan, *Comparison of statistical tests for disease association with rare variants.* Genet Epidemiol, 2011. **35**(7): p. 606-19.
346. Derkach, A., J.F. Lawless, and L. Sun, *Robust and powerful tests for rare variants using Fisher's method to combine evidence of association from two or more complementary tests.* Genet Epidemiol, 2013. **37**(1): p. 110-21.

347. Lee, S., et al., *Optimal unified approach for rare-variant association testing with application to small-sample case-control whole-exome sequencing studies.* Am J Hum Genet, 2012. **91**(2): p. 224-37.

348. Illumina. *Infinium® Assay Workflow*. 2012 [cited 2016 May 26]; Available from: http://www.illumina.com/content/dam/illumina-marketing/documents/products/workflows/workflow_infinium_ii.pdf.

349. Steemers, F.J., et al., *Whole-genome genotyping with the single-base extension assay.* Nat Methods, 2006. **3**(1): p. 31-3.

350. Abecasis Lab. *Exome Chip Design*. 2013 6th August 2013 [cited 2016 May 27]; Available from: http://genome.sph.umich.edu/wiki/Exome_Chip_Design#Content_Contributors.

351. Illumina. *An Introduction to Next-Generation Sequencing Technology*. 2016 [cited 2016 May 26]; Available from: http://www.illumina.com/content/dam/illumina-marketing/documents/products/illumina_sequencing_introduction.pdf.

352. Illumina. *Illumina Sequencing Technology*. 2010 [cited 2016 May 27]; Available from: http://www.illumina.com/documents/products/techspotlights/techspotlight_sequencing.pdf.

353. Illumina. *Multiplexed Sequencing with the Illumina Genome Analyzer System*. 2008 [cited 2016 May 27]; Available from: http://www.illumina.com/documents/products/datasheets/datasheet_sequencing_multiplex.pdf.

354. Holle, R., et al., *KORA--a research platform for population based health research.* Gesundheitswesen, 2005. **67 Suppl 1**: p. S19-25.

355. Wichmann, H.E., C. Gieger, and T. Illig, *KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes.* Gesundheitswesen, 2005. **67 Suppl 1**: p. S26-30.

356. Erbel, R., et al., *[The Heinz Nixdorf Recall study].* Bundesgesundheitsblatt Gesundheitsforschung Gesundheitsschutz, 2012. **55**(6-7): p. 809-15.

357. Grove, M.L., et al., *Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium.* PLoS One, 2013. **8**(7): p. e68095.

358. Frazer, K.A., et al., *A second generation human haplotype map of over 3.1 million SNPs.* Nature, 2007. **449**(7164): p. 851-61.

359. Altshuler, D.M., et al., *Integrating common and rare genetic variation in diverse human populations.* Nature, 2010. **467**(7311): p. 52-8.

360. International HapMap Consortium, *Integrating ethics and science in the International HapMap Project.* Nat Rev Genet, 2004. **5**(6): p. 467-75.

361. International HapMap Consortium, *A haplotype map of the human genome.* Nature, 2005. **437**(7063): p. 1299-320.

362. International HapMap Consortium, *The International HapMap Project.* Nature, 2003. **426**(6968): p. 789-96.

363. Thorisson, G.A., et al., *The International HapMap Project Web site.* Genome Res, 2005. **15**(11): p. 1592-3.

364. Price, A.L., et al., *Long-range LD can confound genome scans in admixed populations.* Am J Hum Genet, 2008. **83**(1): p. 132-5; author reply 135-9.

365. Purcell, S. and C. Chang. *PLINK 1.9 v1.90b3.32*. 2014 [cited 2016 March 1]; Available from: https://www.cog-genomics.org/plink2.

366. Listgarten, J., C. Lippert, and D. Heckerman, *FaST-LMM-Select for addressing confounding from spatial structure and rare variants.* Nat Genet, 2013. **45**(5): p. 470-1.

367. Listgarten, J., et al., *Improved linear mixed models for genome-wide association studies.* Nat Methods, 2012. **9**(6): p. 525-6.

368. Aulchenko, Y.S., et al., *GenABEL: an R library for genome-wide association analysis.* Bioinformatics, 2007. **23**(10): p. 1294-6.

369. Illumina Inc. *HumanExome-12v1_A_Gene_Annotation.txt*. Available from: ftp://ussd-ftp.illumina.com/MyIllumina/6ce9dc2c-b552-4a3e-a9c1-33649ed61373/HumanExome-12v1_A_Gene_Annotation.txt.
370. Illumina Inc. *HumanExome-12v1_A*. 2014 [cited 2017 March 3]; Available from: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL18544; ftp://ftp.ncbi.nlm.nih.gov/geo/platforms/GPL18nnn/GPL18544/suppl/GPL18544_humanexome-12v1_a.csv.gz; ftp://ftp.ncbi.nlm.nih.gov/geo/platforms/GPL18nnn/GPL18544/suppl/GPL18544_humanexome-12v1_a_gene_annotation.txt.gz.
371. San Lucas, F.A., et al., *Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools.* Bioinformatics, 2012. **28**(3): p. 421-2.
372. Li, B., D.J. Liu, and S.M. Leal, *Identifying rare variants associated with complex traits via sequencing.* Curr Protoc Hum Genet, 2013. **Chapter 1**: p. Unit 1 26.
373. Schormair, B., et al., *RLS meta-GWAS*. 2014.
374. Ramasamy, A., et al., *Genetic variability in the regulation of gene expression in ten regions of the human brain.* Nat Neurosci, 2014. **17**(10): p. 1418-28.
375. Clayton, D., *SnpMatrix and XSnpMatrix classes and methods*. 2013.
376. GTEx Consortium, *The Genotype-Tissue Expression (GTEx) project.* Nat Genet, 2013. **45**(6): p. 580-5.
377. GTEx Consortium, *Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.* Science, 2015. **348**(6235): p. 648-60.
378. GTEx Consortium. [cited 2014 December 4]; Available from: www.gtexportal.org.
379. Johnson, A.D., et al., *SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap.* Bioinformatics, 2008. **24**(24): p. 2938-9.
380. 1000 Genomes Project Consortium, et al., *A map of human genome variation from population-scale sequencing.* Nature, 2010. **467**(7319): p. 1061-73.
381. Westra, H.J., et al., *Systematic identification of trans eQTLs as putative drivers of known disease associations.* Nat Genet, 2013. **45**(10): p. 1238-43.
382. Montgomery, S.B., et al., *Transcriptome genetics using second generation sequencing in a Caucasian population.* Nature, 2010. **464**(7289): p. 773-7.
383. Schadt, E.E., et al., *Mapping the genetic architecture of gene expression in human liver.* PLoS Biol, 2008. **6**(5): p. e107.
384. Gibbs, J.R., et al., *Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain.* PLoS Genet, 2010. **6**(5): p. e1000952.
385. Stranger, B.E., et al., *Population genomics of human gene expression.* Nat Genet, 2007. **39**(10): p. 1217-24.
386. Karolchik, D., et al., *The UCSC Table Browser data retrieval tool.* Nucleic Acids Res, 2004. **32**(Database issue): p. D493-6.
387. Karolchik, D., et al., *The UCSC Genome Browser database: 2014 update.* Nucleic Acids Res, 2014. **42**(Database issue): p. D764-70.
388. Pruitt, K.D., T. Tatusova, and D.R. Maglott, *NCBI reference sequences (RefSeq): a curated non-redundant sequence database of genomes, transcripts and proteins.* Nucleic Acids Res, 2007. **35**(Database issue): p. D61-5.
389. Pruitt, K.D., et al., *RefSeq: an update on mammalian reference sequences.* Nucleic Acids Res, 2014. **42**(Database issue): p. D756-63.
390. Hsu, F., et al., *The UCSC Known Genes.* Bioinformatics, 2006. **22**(9): p. 1036-46.
391. Thierry-Mieg, D. and J. Thierry-Mieg, *AceView: a comprehensive cDNA-supported gene and transcripts annotation.* Genome Biol, 2006. **7 Suppl 1**: p. S12.1-14.
392. Hubbard, T., et al., *The Ensembl genome database project.* Nucleic Acids Res, 2002. **30**(1): p. 38-41.

393. Harrow, J., et al., *GENCODE: producing a reference annotation for ENCODE.* Genome Biol, 2006. **7 Suppl 1**: p. S4.1-9.
394. Sharp, P.A., *Speculations on RNA splicing.* Cell, 1981. **23**(3): p. 643-6.
395. Breathnach, R. and P. Chambon, *Organization and expression of eucaryotic split genes coding for proteins.* Annu Rev Biochem, 1981. **50**: p. 349-83.
396. Cech, T.R., *RNA splicing: three themes with variations.* Cell, 1983. **34**(3): p. 713-6.
397. Cooper, S.J., et al., *Comprehensive analysis of transcriptional promoter structure and function in 1% of the human genome.* Genome Res, 2006. **16**(1): p. 1-10.
398. Konarska, M.M., et al., *Characterization of the branch site in lariat RNAs produced by splicing of mRNA precursors.* Nature, 1985. **313**(6003): p. 552-7.
399. Boyle, E.A., et al., *MIPgen: optimized modeling and design of molecular inversion probes for targeted resequencing.* Bioinformatics, 2014. **30**(18): p. 2670-2.
400. Li, H., *Toward better understanding of artifacts in variant calling from high-coverage samples.* Bioinformatics, 2014. **30**(20): p. 2843-51.
401. Genovese, G., et al., *Mapping the human reference genome's missing sequence by three-way admixture in Latino genomes.* Am J Hum Genet, 2013. **93**(3): p. 411-21.
402. Database of Single Nucleotide Polymorphisms (dbSNP). Bethesda (MD). *National Center for Biotechnology Information, National Library of Medicine. (dbSNP Build ID: 141).* [cited 2014 August 13]; Available from: http://www.ncbi.nlm.nih.gov/SNP/.
403. Sherry, S.T., et al., *dbSNP: the NCBI database of genetic variation.* Nucleic Acids Res, 2001. **29**(1): p. 308-11.
404. Illumina. *MiSeq® System*. 2015 [cited 2016 May 15]; Available from: http://www.illumina.com/documents/products/datasheets/datasheet_miseq.pdf.
405. Bronner, I.F., et al., *Improved Protocols for Illumina Sequencing.* Curr Protoc Hum Genet, 2014. **80**: p. 18.2.1-42.
406. Zhang, J., et al., *PEAR: a fast and accurate Illumina Paired-End reAd mergeR.* Bioinformatics, 2014. **30**(5): p. 614-20.
407. Li, H. and R. Durbin, *Fast and accurate short read alignment with Burrows-Wheeler transform.* Bioinformatics, 2009. **25**(14): p. 1754-60.
408. Li, H., *A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data.* Bioinformatics, 2011. **27**(21): p. 2987-93.
409. Li, H., et al., *The Sequence Alignment/Map format and SAMtools.* Bioinformatics, 2009. **25**(16): p. 2078-9.
410. McKenna, A., et al., *The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data.* Genome Res, 2010. **20**(9): p. 1297-303.
411. Wang, G.T., et al., *Power analysis and sample size estimation for sequence-based association studies.* Bioinformatics, 2014. **30**(16): p. 2377-8.
412. Gazave, E., et al., *Neutral genomic regions refine models of recent rapid human population growth.* Proc Natl Acad Sci U S A, 2014. **111**(2): p. 757-62.
413. Gazave, E., et al., *Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect.* Genetics, 2013. **195**(3): p. 969-78.
414. Wang, G., et al. *SEQPower*. 2015 [cited 2016 June 17]; Available from: http://www.bioinformatics.org/spower/mlogit.
415. Illumina. *HiSeq® 3000/HiSeq 4000 Sequencing Systems*. 2015 [cited 2016 May 15]; Available from: http://www.illumina.com/content/dam/illumina-marketing/documents/products/datasheets/hiseq-3000-4000-specification-sheet-770-2014-057.pdf.
416. Beckmann Coulter Inc. *Agencourt AMPure XP*. 2013 [cited 2015; Available from: https://www.beckmancoulter.com/wsrportal/techdocs?docname=B37419AA.

417. Nakazawa, M. *fmsb: Functions for Medical Statistics Book with some Demographic Data*. 2015 [cited 2016 May 11]; Available from: https://cran.r-project.org/web/packages/fmsb/index.html.
418. Hinrichs, A.S., et al., *The UCSC Genome Browser Database: update 2006.* Nucleic Acids Res, 2006. **34**(Database issue): p. D590-8.
419. Carson, A.R., et al., *Effective filtering strategies to improve data quality from population-based whole exome sequencing studies.* BMC Bioinformatics, 2014. **15**: p. 125.
420. Database of Single Nucleotide Polymorphisms (dbSNP). Bethesda (MD). *National Center for Biotechnology Information, National Library of Medicine. (dbSNP Build ID: 142)*. 2016 [cited 2016 May 16]; Available from: http://www.ncbi.nlm.nih.gov/SNP/.
421. Fuchsberger, C., et al., *Imputation server: next generation genotype imputation service*, in *ASHG 2014 Annual Meeting*. 2014: San Diego.
422. Howie, B., J. Marchini, and M. Stephens, *Genotype imputation with thousands of genomes.* G3 (Bethesda), 2011. **1**(6): p. 457-70.
423. Vazquez, A.I., et al., *Technical note: an R package for fitting generalized linear mixed models in animal breeding.* J Anim Sci, 2010. **88**(2): p. 497-504.
424. Bates, D., et al., *Fitting Linear Mixed-Effects Models Using lme4.* 2015, 2015. **67**(1): p. 48.
425. Zeileis, A. and T. Hothorn, *Diagnostic Checking in Regression Relationships.* R News, 2002. **2**(3): p. 7-10.
426. NAGELKERKE, N.J.D., *A note on a general definition of the coefficient of determination.* Biometrika, 1991. **78**(3): p. 691-692.
427. Sun, G., et al., *Variation explained in mixed-model association mapping.* Heredity (Edinb), 2010. **105**(4): p. 333-40.
428. Adzhubei, I.A., et al., *A method and server for predicting damaging missense mutations.* Nat Methods, 2010. **7**(4): p. 248-9.
429. Kumar, P., S. Henikoff, and P.C. Ng, *Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm.* Nat Protoc, 2009. **4**(7): p. 1073-81.
430. Ng, P.C. and S. Henikoff, *Predicting the effects of amino acid substitutions on protein function.* Annu Rev Genomics Hum Genet, 2006. **7**: p. 61-80.
431. Ng, P.C. and S. Henikoff, *SIFT: Predicting amino acid changes that affect protein function.* Nucleic Acids Res, 2003. **31**(13): p. 3812-4.
432. Ng, P.C. and S. Henikoff, *Accounting for human polymorphisms predicted to affect protein function.* Genome Res, 2002. **12**(3): p. 436-46.
433. Shah, T.S., et al., *optiCall: a robust genotype-calling algorithm for rare, low-frequency and common variants.* Bioinformatics, 2012. **28**(12): p. 1598-603.
434. Goldstein, J.I., et al., *zCall: a rare variant caller for array-based genotyping: genetics and population analysis.* Bioinformatics, 2012. **28**(19): p. 2543-5.
435. Zhou, J., et al., *iCall: a genotype-calling algorithm for rare, low-frequency and common variants on the Illumina exome array.* Bioinformatics, 2014. **30**(12): p. 1714-20.
436. Yang, J., et al., *Genomic inflation factors under polygenic inheritance.* Eur J Hum Genet, 2011. **19**(7): p. 807-12.
437. Bulik-Sullivan, B.K., et al., *LD Score regression distinguishes confounding from polygenicity in genome-wide association studies.* Nat Genet, 2015. **47**(3): p. 291-5.
438. Kinnersley, B., et al., *Search for new loci and low-frequency variants influencing glioma risk by exome-array analysis.* Eur J Hum Genet, 2015.
439. Wessel, J., et al., *Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility.* Nat Commun, 2015. **6**: p. 5897.
440. Dankowski, T., et al., *Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array.* Genet Epidemiol, 2015. **39**(8): p. 601-8.
441. Eicher, J.D., et al., *Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals.* Am J Hum Genet, 2016. **99**(1): p. 40-55.

442. Li, D., et al., *A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohn's Disease and Human Gut Microbiome Composition.* Gastroenterology, 2016. **151**(4): p. 724-32.

443. Li, M., et al., *SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function.* J Am Soc Nephrol, 2017. **28**(3): p. 981-994.

444. CHARGE Consortium Hematology Working Group, *Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits.* Nat Genet, 2016. **48**(8): p. 867-76.

445. Iossifov, I., et al., *The contribution of de novo coding mutations to autism spectrum disorder.* Nature, 2014. **515**(7526): p. 216-21.

446. O'Roak, B.J., et al., *Recurrent de novo mutations implicate novel genes underlying simplex autism risk.* Nat Commun, 2014. **5**: p. 5595.

447. Wilson, K.D., et al., *A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases.* Circ Res, 2015. **117**(7): p. 603-11.

448. Wu, B. and J.S. Pankow, *On Sample Size and Power Calculation for Variant Set-Based Association Tests.* Ann Hum Genet, 2016. **80**(2): p. 136-43.

449. Ng, S.B., et al., *Targeted capture and massively parallel sequencing of 12 human exomes.* Nature, 2009. **461**(7261): p. 272-6.

450. Voight, B.F. and J.K. Pritchard, *Confounding from cryptic relatedness in case-control association studies.* PLoS Genet, 2005. **1**(3): p. e32.

451. Gross, A., et al., *Population-genetic comparison of the Sorbian isolate population in Germany with the German KORA population using genome-wide SNP arrays.* BMC Genet, 2011. **12**: p. 67.

452. Zawistowski, M., et al., *Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests.* Eur J Hum Genet, 2014. **22**(9): p. 1137-44.

453. Mathieson, I. and G. McVean, *Differential confounding of rare and common variants in spatially structured populations.* Nat Genet, 2012. **44**(3): p. 243-6.

454. Wang, S., et al., *Loss of Myt1 function partially compromises endocrine islet cell differentiation and pancreatic physiological function in the mouse.* Mech Dev, 2007. **124**(11-12): p. 898-910.

455. Nielsen, J.A., et al., *Myelin transcription factor 1 (Myt1) modulates the proliferation and differentiation of oligodendrocyte lineage cells.* Mol Cell Neurosci, 2004. **25**(1): p. 111-23.

456. Passer, B.J., et al., *The p53-inducible TSAP6 gene product regulates apoptosis and the cell cycle and interacts with Nix and the Myt1 kinase.* Proc Natl Acad Sci U S A, 2003. **100**(5): p. 2284-9.

457. Zhang, F., et al., *Metalloreductase Steap3 coordinates the regulation of iron homeostasis and inflammatory responses.* Haematologica, 2012. **97**(12): p. 1826-35.

458. Nagase, T., et al., *Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.* DNA Res, 2000. **7**(2): p. 143-50.

459. Jansen, G., et al., *Characterization of the myotonic dystrophy region predicts multiple protein isoform-encoding mRNAs.* Nat Genet, 1992. **1**(4): p. 261-6.

460. Yang, Y., et al., *RasGRP4, a new mast cell-restricted Ras guanine nucleotide-releasing protein with calcium- and diacylglycerol-binding motifs. Identification of defective variants of this signaling protein in asthma, mastocytosis, and mast cell leukemia patients and demonstration of the importance of RasGRP4 in mast cell development and function.* J Biol Chem, 2002. **277**(28): p. 25756-74.

461. Giehl, K.A., et al., *Nonsense mutations in AAGAB cause punctate palmoplantar keratoderma type Buschke-Fischer-Brauer.* Am J Hum Genet, 2012. **91**(4): p. 754-9.

462. Pohler, E., et al., *Haploinsufficiency for AAGAB causes clinically heterogeneous forms of punctate palmoplantar keratoderma.* Nat Genet, 2012. **44**(11): p. 1272-6.

463. Bigdeli, T.B., B.M. Neale, and M.C. Neale, *Statistical properties of single-marker tests for rare variants.* Twin Res Hum Genet, 2014. **17**(3): p. 143-50.
464. Pirie, A., et al., *The effect of rare variants on inflation of the test statistics in case-control analyses.* BMC Bioinformatics, 2015. **16**: p. 53.
465. Nevanlinna, H.R., *The Finnish population structure. A genetic and genealogical study.* Hereditas, 1972. **71**(2): p. 195-236.
466. Peltonen, L., A. Jalanko, and T. Varilo, *Molecular genetics of the Finnish disease heritage.* Hum Mol Genet, 1999. **8**(10): p. 1913-23.
467. Chamary, J.V., J.L. Parmley, and L.D. Hurst, *Hearing silence: non-neutral evolution at synonymous sites in mammals.* Nat Rev Genet, 2006. **7**(2): p. 98-108.
468. Plotkin, J.B. and G. Kudla, *Synonymous but not the same: the causes and consequences of codon bias.* Nat Rev Genet, 2011. **12**(1): p. 32-42.
469. Cartegni, L., S.L. Chew, and A.R. Krainer, *Listening to silence and understanding nonsense: exonic mutations that affect splicing.* Nat Rev Genet, 2002. **3**(4): p. 285-98.
470. Nackley, A.G., et al., *Human catechol-O-methyltransferase haplotypes modulate protein expression by altering mRNA secondary structure.* Science, 2006. **314**(5807): p. 1930-3.
471. Segre, A.V., et al., *Common inherited variation in mitochondrial genes is not enriched for associations with type 2 diabetes or related glycemic traits.* PLoS Genet, 2010. **6**(8).

Publications

1. Bessette, D. C., Tilch, E., Seidens, T., Quinn, M. C., Wiegmans, A. P., Shi, W., Cocciardi, S., McCart-Reed, A., Saunus, J. M., Simpson, P. T., Grimmond, S. M., Lakhani, S. R., Khanna, K. K., Waddell, N., Al-Ejeh, F., Chenevix-Trench, G., *Using the MCF10A/MCF10CA1a Breast Cancer Progression Cell Line Model to Investigate the Effect of Active, Mutant Forms of EGFR in Breast Cancer Development and Treatment Using Gefitinib.* PLoS One, 2015. **10**(5): p. e0125232.
2. Brenndörfer, J., Altmann, A., Widner-Andrä, R., Pütz, B., Czamara, D., Tilch, E., Kam-Thong, T., Weber, P., Rex-Haffner, M., Bettecken, T., Bultmann, A., Müller-Myhsok, B., Binder, E. E., Landgraf, R., Czibere, L., *Connecting Anxiety and Genomic Copy Number Variation: A Genome-Wide Analysis in CD-1 Mice.* PLoS One, 2015. **10**(5): p. e0128465.
3. Tilch, E., Schormair, B., Pütz, B., Czamara, D., Müller-Nurasyid, M., Lichtner, P., Trenkwalder, C., Paulus, W., Högl, B., Berger, K., Fietze, I., Oertel, W., Meitinger, T., Gieger, C., Müller-Myhsok, B., Winkelmann, J., *Rare variant stratification in a German/Austrian sample set*; (Abstract/Program 2030M). Presented at the 64th Annual Meeting of The American Society of Human Genetics, October 20, 2014 in San Diego, CA
4. Schulte, E. C., Kousi, M., Tan, P. L., Tilch, E., Knauf, F., Lichtner, P., Trenkwalder, C., Högl, B., Frauscher, B., Berger, K., Fietze, I., Hornyak, M., Oertel, W. H., Bachmann, C. G., Zimprich, A., Peters, A., Gieger, C., Meitinger, T., Müller-Myhsok, B., Katsanis, N., Winkelmann, J., *Targeted resequencing and systematic in vivo functional testing identifies rare variants in MEIS1 as significant contributors to restless legs syndrome.* Am J Hum Genet, 2014. **95**(1): p. 85-95.
5. Spieler, D., Kaffe, M., Knauf, F., Bessa, J., Tena, J. J., Giesert, F., Schormair, B., Tilch, E., Lee, H., Horsch, M., Czamara, D., Karbalai, N., von Toerne, C., Waldenberger, M., Gieger, C., Lichtner, P., Claussnitzer, M., Naumann, R., Müller-Myhsok, B., Torres M, Garrett L, Rozman J, Klingenspor M, Gailus-Durner, V., Fuchs, H., Hrabě de Angelis, M., Beckers, J., Hölter, S. M., Meitinger, T., Hauck, S. M., Laumen, H., Wurst, W., Casares, F., Gómez-Skarmeta, J. L., Winkelmann, J., *Restless legs syndrome-associated intronic common variant in Meis1 alters enhancer function in the developing telencephalon.* Genome Res, 2014. **24**(4): p. 592-603.
6. Tilch, E., Seidens, T., Cocciardi, S., Reid, L. E., Byrne, D., Simpson, P. T., Vargas, A. C., Cummings, M. C., Fox, S. B., Lakhani, S. R., Chenevix Trench, G., *Mutations in EGFR, BRAF and RAS are rare in triple-negative and basal-like breast cancers from Caucasian women.* Breast Cancer Res Treat, 2014. **143**(2): p. 385-92.