

Persistent inhibition of pore-based cell migration by sub-toxic doses of miuraenamamide, an actin filament stabilizer

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Supplement Table 1: Red cluster of proteome analysis (downregulated at 56 h, log2 scale).

			Gene symbol	Ctrl	56h
			ATP1A1	0,414	-0,244
			ATP2C1	-0,200	-2,498
Gene symbol	Ctrl	56h	ATP5I	0,147	-2,707
AAMDC	-0,193	-2,333	ATP6V1B2	0,391	-1,910
ABCC1	1,086	-1,780	ATP6V1G1	-0,175	-2,365
BHD10	0,986	-0,932	ATXN2	0,991	-1,356
ABHD5	1,362	-1,824	B3GAT1	0,581	-2,459
ABLIM1	-0,570	-1,542	BAX	0,874	-2,472
ABT1	0,569	-1,713	BBS2	0,340	-1,495
ABTB1	-0,807	-1,652	BCAS2	0,732	-2,550
ACP6	0,347	-2,505	BIN3	0,519	-2,203
ADD2	0,626	-2,356	BLMH	0,850	-2,248
ADHFE1	1,332	-1,549	BMP2K	0,165	-1,443
AGO3	0,168	-2,320	BMS1	1,518	-1,379
AIDA	0,922	-0,862	BOD1L1	-0,014	-0,799
AIM1	0,353	-1,290	BOLA3	1,007	-2,021
AKAP10	0,248	-2,165	BRCC3	0,473	-1,891
AKR7A2	0,956	-1,231	BUD13	0,877	-2,566
ALDH2	-0,092	-0,352	C14orf2;MP68	0,830	-1,952
ALG1	0,388	-1,339	C17orf49;BAP18;RNASEK-C17orf49	0,383	-0,878
AMBRA1	1,643	-0,982	C2orf49	0,950	-1,333
ANAPC2	1,149	-2,066	C6orf106	-0,711	-0,877
ANAPC7	1,364	-2,336	C9orf41	1,075	-2,068
ANKS1A	1,399	-0,645	CABLES1	0,477	-2,432
ANKS3	0,736	-2,426	CAMK1	0,460	-1,887
AOC1	0,958	-2,085	CASP10	0,805	-1,676
AP3M2	1,241	-1,988	CCDC138	1,957	-1,080
AP3S1	1,301	-1,912	CCDC18	2,239	-1,285
AP4B1	0,704	-1,396	CCDC53	0,602	-2,713
APIP	0,809	-1,576	CCNDBP1	0,336	-2,220
APOA1BP	-0,432	-1,541	CDIPT	0,482	-1,023
APP	0,251	-1,553	CDK11A	-0,148	-1,463
ARF5	0,858	-1,476	CDYL	1,578	-1,923
ARHGAP23	0,615	-1,712	CENPT	1,744	-1,360
ARHGEF7	0,471	-2,350	CEP162	-0,437	-1,395
ARIH2	0,461	-2,099	CES1	-0,228	-1,572
ARL14EP	1,121	-1,852	CFLAR	-0,471	-1,617
ARL6IP5	1,142	-2,394	CHD6	0,664	-2,318
ASMTL	-0,253	-1,692	CHD8	0,549	-2,500
ATE1	0,110	-2,319	CHMP5	0,075	-2,266
ATG10	0,877	-1,445	CIR1	0,974	-2,223
ATG101	1,774	-2,012	CLK2	-1,377	-1,817
ATG12	0,415	-2,428	CMC1	0,738	-2,445
ATG16L1	0,361	-1,480	CMPK1	-0,029	-2,412

Gene symbol	Ctrl	56h	Gene symbol	Ctrl	56h
CMTR2	1,755	-1,596	EPB41L1	-1,002	-0,683
CNN3	0,785	-1,600	EPG5	0,067	-1,429
COA6	-1,263	-1,727	EPN1	0,374	-1,474
COMMD6	0,087	-2,588	EPN2	0,736	-0,897
COPS3	1,863	-1,770	ERCC4	1,310	-1,747
CPEB2	-0,289	-2,399	EVL	0,347	-1,883
CPSF6	1,551	-1,569	EXOC8	1,848	-1,848
CRELD2	0,560	-1,957	FAHD2A;FAHD2B	1,116	-0,817
CREM	0,495	-2,144	FAM109A	2,574	-1,171
CRKL	1,017	-2,462	FAM111A	1,860	-2,017
CROT	0,504	-2,205	FAM114A1	-0,217	-1,996
CSNK1A1	1,030	-2,068	FAM168B	0,673	-2,337
CSNK1D	1,141	-1,936	FAM174B	0,585	-1,697
CSNK1E	-1,380	-0,968	FAM193A	0,472	-2,188
CSNK2A2	1,081	-1,736	FAM20B	0,300	-1,896
CSRP2	1,363	-1,909	FAM219A	1,162	-2,320
CTNNBIP1	0,344	-2,751	FAM96B	1,294	-2,439
CTSH	-0,086	-2,422	FANCM	-0,571	-1,703
CUTC	0,537	-2,427	FBXL8	-0,243	-2,166
CYB5R4	0,507	-2,463	FBXO42	0,924	-1,230
DCAF6	0,531	-1,581	FCHSD2	0,967	-1,363
DCTN4	-0,129	-1,121	FKBP2	-0,518	-2,011
DCUN1D5	1,061	-2,448	FLII	1,130	0,402
DDAH1	1,175	-1,448	FLNC	-0,881	-1,821
DDI2	1,421	-2,028	FOXE1	0,674	-1,002
DESI1	1,224	-2,311	FOXO6;FOXO4;FOXO1	0,569	-2,433
DHRS4;DHRS4L2	0,480	-1,493	GALNT7	0,659	-2,595
DHRS7B	0,746	-1,865	GAMT	-0,660	-1,857
DNAJC8	1,480	-1,129	GCC2	0,537	-2,080
DNPEP	0,386	-2,578	GEMIN2	0,870	-1,955
DOCK11	0,263	-2,345	GIT1	1,806	-0,713
DPYD	0,189	-2,403	GLCC11	-0,336	-1,760
DTX2	0,528	-2,211	GLG1	1,105	-1,947
DUSP12	1,316	-1,989	GLS	1,104	0,675
DVL3	1,324	-1,681	GM2A	0,393	-0,557
E2F7	2,028	-1,963	GNB1L	-0,762	-1,806
EAPP	0,967	-2,338	GNB5	0,929	-2,596
ECI2	0,942	-0,600	GOLGA1	1,913	-1,460
EED	1,606	-1,826	GORASP2	0,430	-2,430
EFHC1	0,749	-1,840	GOSR1	0,168	-2,055
EHD3	0,327	-2,480	GPCPD1	1,123	-2,319
EIF3I	1,250	-1,716	GPHN	0,357	-1,906
EIF4E2	0,668	-2,519	GPN3	0,034	-2,249
ELMO1	0,507	-2,349	GSN	-1,456	0,107
EP300	1,169	-2,379	GSTK1	0,282	-1,427

Gene symbol	Ctrl	56h	Gene symbol	Ctrl	56h
GSTZ1	0,446	-2,046	MAP1LC3A	0,352	-2,146
GTDC1	0,998	-1,463	MAP2K4	2,171	-1,272
HARS	-0,610	-0,463	MAPK11	-0,057	-2,468
HCCS	1,260	-1,099	MAPK14	1,009	0,497
HDAC2	0,960	-1,726	MAPK9	0,701	-2,360
HDHD1	1,535	-0,940	MARCKSL1	0,896	-1,341
HIPK3	1,186	-1,894	MARK2	0,860	-1,417
HLA-C;HLA-B	-0,621	-0,714	MATN3	0,831	-1,202
HLA-E	1,268	-2,038	MCM8	1,583	-1,176
HMG20A	0,907	-2,484	MED1	0,825	-1,752
HMOX2	1,422	-1,910	MED17	0,755	-1,391
HNRNPUL2;HNRNPUL2- BSCL2	1,136	-1,796	METTTL2B;METTL2A	0,879	-2,192
HOMER1	0,669	-2,476	METTTL5	1,213	-2,059
HOXB6	-0,371	-2,262	MINPP1	0,752	-0,694
HRSP12	1,277	-1,542	MITD1	1,507	-2,155
HSPA4	1,025	-1,939	MLEC	0,516	0,051
HYI	1,743	-1,538	MLLT6	0,421	-2,408
IFT22	0,700	-1,389	MMS22L	1,631	-1,463
IFT57	0,757	-1,842	MOB3A	0,715	-1,474
IKBKKG	-0,085	-1,924	MRPL33	0,236	-1,356
ILK	0,187	-2,227	MSI2	0,319	-1,831
IMPA1	0,691	-1,555	MTA2	1,706	-1,319
IMPAD1	2,185	-1,634	MTERF3	1,288	-1,765
INPP4B	1,355	-2,209	MTFR1L	0,708	-2,552
ISG20L2	1,524	-1,762	MTHFR	0,043	-1,439
ISYNA1	-0,174	-1,288	MTM1	1,455	-1,609
IWS1	0,376	-2,738	MTMR2	1,097	-2,460
JMY	-0,370	-1,198	MTPN	0,190	-1,877
KBTBD11	0,199	-1,692	MVB12A	0,296	-1,934
KCT2	0,795	-1,392	MYL1;MYL3	0,682	-2,169
KCTD1	0,379	-1,552	NAB1	1,538	-1,900
KCTD14	0,775	-2,243	NADSYN1	1,044	-1,631
KIAA0586	0,355	-1,788	NAGA	0,967	-1,867
KIAA0930	1,351	-1,976	NAPB	0,296	-2,451
KIF1B	0,664	1,930	NDUFB8	1,340	-2,358
KIF3A	1,184	-1,290	NFAT5	0,064	-0,931
KLHL11	0,290	-1,751	NFKB1	1,841	-0,385
LDB1	1,228	-2,439	NFKBIE	-0,238	-2,176
LEO1	0,472	-2,131	NFYB	1,273	-1,776
LMAN2L	0,887	-1,575	NFYC	0,978	-2,048
LPXN	0,908	-2,152	NGEF	1,336	-1,816
LRRC14	-0,142	-1,720	NIPSNAP1	0,920	-0,821
LZTS3	-1,080	-0,952	NLRC5	-0,089	-2,501
MAN2A1	1,515	-1,476	NMD3	0,931	-1,995
			NME2	1,131	-1,421

Gene symbol	Ctrl	56h	Gene symbol	Ctrl	56h
NMI	0,432	-1,094	PMM1	0,465	-1,732
NMT1	0,620	-2,125	POGK	-0,587	-1,861
NOP10	1,035	-2,327	POLG2	-0,626	-2,173
NOV	-0,070	-1,423	POLR3K	0,588	-2,699
NR2C2AP	0,990	-1,684	PPAT	0,291	-0,983
NSL1	0,282	-1,692	PPP1R12C	-0,019	-1,133
NSMAF	1,101	-2,230	PPP1R3B	0,529	-1,915
NSUN2	1,742	-1,666	PPP2R1B	1,494	-1,453
NUDT14	0,454	-2,330	PPP2R5C	0,759	-1,000
NUDT5	1,233	-1,997	PPP3R1	0,614	-1,877
NXT1;NXT2	0,856	-1,269	PPP5C	1,036	-1,847
OARD1	1,675	-2,133	PRAME	0,890	-1,388
OCIAD1	1,462	-1,468	PRKCH;PRKCE	1,035	-1,948
OGFR	1,479	-1,200	PRNP	0,778	-2,597
OIP5	1,101	-2,362	PRPF31	0,965	-1,962
OLA1	0,423	-1,393	PRPF38B	1,326	-1,585
OPA3	0,546	-1,673	PRPS1	1,847	-1,651
OPLAH	-1,146	-1,992	PRPSAP2	0,305	-2,154
OSCP1	0,543	-2,381	PRR14	0,566	-1,075
PALM3	1,313	-1,934	PRR14L	1,218	-1,998
PAN2	0,115	-1,902	PRRC2B	0,102	-2,002
PARP2	0,907	-1,866	PSMA1	0,594	-1,395
PAXBP1	2,150	-1,731	PSMC4	0,372	-1,438
PCBD1	0,067	-2,184	PSME3	1,489	-2,329
PCBP2	-0,754	-1,851	PTMA	0,171	-2,268
PCCA	1,247	-1,705	PTPN2	1,409	-2,442
PCDHGA4	0,340	-1,634	PTRH1	1,458	-1,977
PCTP	1,672	-1,259	PTRH2	0,217	-1,803
PDXP	1,330	-2,040	QDPR	0,734	-2,356
PFKL	0,685	-1,822	RAB43	0,829	-1,427
PGM2	0,667	-2,320	RABIF	-0,322	-1,588
PHC3	0,591	-2,223	RAC2	0,897	-1,895
PHF20L1	0,702	-1,597	RAC3	0,792	-1,863
PHF3	1,523	-1,778	RASSF2	0,777	-1,278
PIP4K2A	-0,008	-2,577	RBBP5	0,842	-2,128
PIP4K2C	0,537	-1,998	RBM27	1,246	-2,105
PIPSL	1,310	-1,959	RBMX2	0,986	-1,590
PIR	0,392	-2,192	RC3H1	0,040	-0,475
PITPNA	1,319	-1,550	RCOR3	-0,284	-2,423
PLAUR	0,558	-1,837	REXO2	1,097	-2,042
PLCB3	1,805	-1,512	RFXANK	0,248	-1,092
PLEKHA3	1,154	-1,662	RHOA	0,926	-1,682
PLEKHB2	0,661	-1,425	RILPL2	0,930	-2,243
PLEKHF2	0,754	-0,970	RIPK1	1,067	-2,118
PLEKHG5	1,269	-1,379	RNF138	1,298	-1,795

Gene symbol	Ctrl	56h	Gene symbol	Ctrl	56h
RNF20	0,969	-1,819	SPTY2D1	1,141	-2,286
RNF7	0,165	-2,600	SQSTM1	0,288	-1,725
RNMT	0,789	-2,455	SRPX	1,840	-0,997
RNPS1	0,547	-2,034	SS18	1,122	-2,039
RPE	-0,014	-1,571	SSH1	0,453	-2,207
RPRD1A	-0,104	-2,376	STAU2	1,194	-1,884
RPS27L;RPS27	1,229	-1,802	STK3	1,757	-1,779
RPS29	0,444	-2,671	STK38L	0,219	-2,464
RSRC2	0,588	-2,644	STXBP1	1,307	-2,124
RUFY2	0,938	-2,367	STYX	1,115	-1,670
RUVBL1	1,190	-1,343	SULT1C2	0,905	-2,216
SAMD4A	-0,052	-0,749	SURF4	1,153	-2,451
SAMD4B	1,150	-2,361	SUZ12	1,688	-1,179
SAP130	0,067	-2,232	SVIL	0,162	-1,642
SCFD1	0,830	-1,969	SYNE1	1,520	-1,359
SCRN2	0,939	-1,174	TADA1	0,214	-1,899
SDE2	0,143	-2,096	TAF9B	1,448	-1,783
SDF2	0,559	-2,542	TAGLN2	1,078	-1,238
SDSL	0,031	-1,406	TAOK1	1,171	-1,660
SEC61B	0,752	-2,304	TBC1D10B	1,443	-1,144
SECISBP2	0,329	-1,595	TBC1D25	1,076	-1,808
SECISBP2L	0,839	-2,251	TBC1D5	0,859	-2,105
SEH1L	1,247	-2,066	TBCEL	0,903	-1,448
SEPHS1	-0,681	-1,448	TBX15	2,744	-0,913
SEPHS2	0,678	-2,290	TCEB1	0,990	-1,815
SEPN1	1,261	-1,549	TDP2	2,292	-1,203
SERPINB5	0,874	-1,621	TEN1	0,717	-2,298
SET	0,556	-1,837	TGFBRAP1	-0,115	-1,971
SF1	-0,131	-0,288	TH1L;NELFCD	0,897	-1,752
SFMBT1	1,222	-2,058	THAP11	1,046	-1,954
SH3KBP1	0,265	-2,451	THG1L	0,901	-2,418
SHB	1,112	-1,490	THOC5	0,815	-1,148
SIMC1	1,498	-1,860	THOC7	0,384	-2,262
SIPA1L1	0,789	-2,112	THUMPD2	-0,044	-1,121
SIPA1L2	0,869	-2,061	TIMM10B	0,621	-2,681
SIX4	0,647	-2,703	TMED10	0,875	-1,165
SLC27A3	1,297	-1,332	TNIK	0,919	-2,281
SLC38A10	1,711	-1,217	TNK2	0,922	-1,608
SLC7A1	0,142	-2,366	TNRC6B	0,516	-1,905
SMARCA4	1,031	-1,729	TOM1L2	0,659	-1,483
SMYD3	1,342	-1,481	TOMM22	1,010	-1,176
SNRNP27	0,800	-2,669	TOR3A	0,780	-1,431
SON	1,202	-2,455	TPMT	1,175	-1,994
SOX13	0,721	-2,711	TRAPPC13	1,423	-1,984
SP140L	0,248	-2,136	TRAPPC2B;TRAPPC2	0,921	-2,210

Gene symbol	Ctrl	56h	Gene symbol	Ctrl	56h
TRDMT1	1,776	-1,472	WASF2	0,442	-1,719
TRIP4	-0,273	-2,121	WBSCR22	1,108	-2,367
TRMT11	-0,019	-2,506	WDFY2	0,275	-1,435
TRMT44	1,046	-1,888	WDR37	0,465	-2,114
TSEN2	0,250	-2,468	WDR55	1,389	-2,302
TSTA3	0,535	-1,318	WDR77	0,385	-0,952
TTC26	1,890	-1,402	WEE1	1,397	-1,269
TTC27	1,583	-1,383	WHAMM	0,066	-2,677
TUBB8	-0,309	-1,869	WHSC2;NELFA	0,752	-1,296
TUBG2;TUBG1	0,890	-1,750	WIZ	0,586	-1,546
TXNRD3	0,145	-1,098	WRN	1,186	-2,378
UBA5	0,527	-2,719	WTIP	0,713	-2,026
UBE2I	0,419	-1,716	YBX3	1,071	-2,458
UBE2Z	1,121	-2,353	YTHDC1	1,233	-1,954
UBP1	1,076	-2,178	ZC3H7B	0,990	-1,996
UBQLN1	0,707	-1,820	ZDHHC7	0,628	-2,320
UBQLN4	1,332	-1,718	ZFP36L2	0,916	-1,428
UBXN1	0,310	-2,356	ZFYVE19	0,150	-1,772
UCC1;EPDR1	0,154	-1,108	ZFYVE21	0,441	-2,581
UCKL1	0,472	-1,804	ZFYVE9	0,913	-2,026
UPF3A	1,064	-2,400	ZNF131	0,841	-1,858
UPRT	0,968	-2,108	ZNF274	1,223	-1,700
USB1	1,342	-1,969	ZNF408	1,291	-2,015
USP16	0,528	-2,201	ZNF616;ZNF480	2,312	-0,891
USP47	1,135	-2,094	ZNF618	0,272	-2,139
VPS36	1,437	-2,158	ZNF622	0,566	-1,787
VTA1	1,022	-2,194	ZNF696	1,265	-1,449

Supplement Table 2: Yellow cluster of proteome analysis (upregulated at 56 h, log₂ scale).

Gene symbol	Ctrl	56h
AARS	0,571	2,421
AATF	1,056	2,026
ABCC3	0,898	0,457
ACBD6	0,320	1,859
ACLY	0,306	2,349
ACTG1;ACTB;ACTA1	-1,773	1,490
ACTL6A	1,022	1,895
ACTR10	-0,210	2,082
ACTR3	0,393	1,996
ADA	-0,246	1,825
ADAM10	-0,070	1,720
ADAT1	0,473	1,705
ADAT3	-0,118	1,044
ADI1	0,625	1,106
ADNP	0,772	2,037
AES	0,191	0,389
AFF1	-0,726	2,486
AGL	-0,720	1,723
AHCY	0,696	1,827
AHCYL1	-0,061	1,784
AK2	-0,289	1,311
AKAP9	1,286	0,918
AKR1B1	0,288	1,186
ALDH1A2	-0,689	1,215
ALDH3A1	-0,542	1,833
ALPPL2;ALPP	-0,129	0,416
AMZ2	0,034	2,305
ANKZF1	-0,343	2,263
ANXA1	-0,625	1,625
APLF	-1,209	0,874
APOC3	-0,780	1,511
ARFGAP2	1,459	0,992
ARFGAP2	1,459	0,992
ARHGAP31	1,221	1,410
ARHGEF12	0,742	1,165
ARHGEF26	1,069	1,841
ARID4A	-0,022	0,791
ARL2	-0,969	2,519
ARL8A;ARL8B	-0,385	2,558
ARPC1B	0,757	0,706

Gene symbol	Ctrl	56h
ASH2L	1,580	1,023
ASPCR1	0,191	1,353
ASS1	-0,252	1,958
ATAT1	0,137	1,141
ATF2	-1,198	2,062
ATF7IP	0,867	0,514
ATL2	-0,628	2,188
ATXN3	0,384	2,445
AVL9	1,144	1,337
BAG6	0,666	2,154
BBS1	-0,601	1,504
BLOC1S3	-0,733	2,254
BLOC1S4	-0,579	2,071
BMP1	-0,242	-0,496
BRAF	0,269	0,427
BRD1	0,615	-0,506
BRD2	1,137	0,849
BRE	-0,082	1,974
C10orf35	1,134	1,989
C12orf43	1,122	1,447
C15orf52	1,634	0,354
C1orf122	-0,088	1,946
C5orf45	0,191	1,545
C6orf203	0,202	1,405
CAAP1	0,595	2,365
CALB1	-0,528	1,665
CALD1	-1,690	0,333
CAPRIN1	0,576	2,048
CAPRIN2	-0,096	1,712
CAPZA2	-0,076	2,179
CARKD;FLJ10769	0,783	-0,121
CARS	-0,069	1,557
CASK	-0,666	1,623
CASKIN1	-1,135	1,285
CASP2	0,130	2,339
CASP6	-0,548	2,652
CBX1;CBX3	-0,579	2,699
CBX5	-0,096	2,095
CBX6	-0,568	1,331
CC2D1A	-0,330	1,905
CCAR2	0,927	2,063
CCBL1	0,391	2,091
CCDC47	0,169	2,303
CCDC6	-1,431	1,464

Gene symbol	Ctrl	56h
CCDC9	-0,474	2,595
CCT2	0,570	1,503
CCT8	-0,037	1,923
CD46	-0,032	-0,076
CD70	-0,592	0,582
CDC37	-0,235	2,638
CDH13	0,763	1,387
CDH6	-0,880	1,392
CDK12	0,012	2,130
CDK13	1,410	1,528
CDK20	-0,409	1,788
CEP104	0,911	2,285
CFDP1	-0,920	1,917
CHAC2	0,574	2,130
CHCHD7	-1,217	1,031
CHEK2	-0,021	2,635
CHFR	1,988	1,234
CHM	0,479	2,375
CHMP2B	-1,496	1,424
CHN1	-1,476	2,028
CHRAC1	-0,041	1,120
CHURC1-FNTB;FNTB	-1,084	2,394
CINP	0,560	1,706
CKB	-0,426	2,336
CLEC16A	-0,085	2,518
CLIC4	-1,506	2,069
CLK3	-0,486	1,687
CLOCK	-0,742	1,563
CMC4	-0,303	2,699
CNIH4	1,269	2,220
CNOT11	0,917	2,052
CNOT2	1,441	1,231
CNRIP1	-1,042	2,530
COL4A3BP	0,721	2,162
COL5A2	-0,637	1,921
COMMD1	-0,003	2,053
COMMD3-BMI1;BMI1;PCGF2	0,658	2,237
COQ7	0,745	1,985
CPOX	0,638	1,287
CPQ	-0,997	1,979
CRTC1	-1,051	1,283
CSF1	-1,352	0,976

Gene symbol	Ctrl	56h
CTNBL1	0,866	2,212
CTSB	-1,124	2,130
CTSL	0,930	2,101
CXCL8	-0,086	1,418
CXXC5	-0,365	1,926
DARS2	0,911	1,720
DAZAP1	-0,072	2,335
DBNL	-0,975	2,342
DCAF15	0,670	2,523
DCLK1	-0,038	1,556
DCP2	0,517	2,041
DCTN6	-0,218	2,572
DDX1	0,613	2,087
DDX39A	0,335	2,379
DDX39B;DDX39A;hCG_2005638	-0,106	2,330
DDX3X;DDX3Y	0,863	1,532
DEK	1,146	1,464
DEPDC7	1,286	0,633
DES	-0,076	2,594
DHX36	0,654	1,867
DLST	1,152	1,538
DMAP1	1,139	2,245
DNAJC11	0,570	1,944
DNAJC7	0,936	1,786
DNTTIP2	0,871	1,486
DPH5	-0,254	2,626
DSC1	0,820	1,862
DSCC1	1,034	2,210
DSG1	0,242	2,558
DST	-0,566	2,047
DTNB;DTNA	-0,198	0,780
DYNC2LI1	-0,135	1,680
E2F4	0,829	2,071
E2F8	0,702	0,885
ECHS1	0,320	2,389
EHBP1	-0,116	2,692
EIF2A	-0,289	1,559
EIF2S1	0,668	2,430
EIF3B	0,672	2,189
ELOF1	-0,391	2,185
EMD	0,760	1,643
EML1	0,447	0,627

Gene symbol	Ctrl	56h
EMSY;C11orf30	1,564	1,685
ENAH	-0,082	1,834
ENO3	-1,121	2,282
EP400	0,473	1,830
EPS15L1	-0,124	1,251
ERBB2	0,148	0,989
ERCC6	-1,057	1,191
ERF	0,272	0,452
EVI5L	0,465	0,461
EXOC6	0,520	1,338
FABP3	0,569	0,792
FAM136A	0,195	2,337
FAM168A	0,350	1,584
FAM175B	-0,213	2,538
FAM188B	-0,333	1,319
FAM83G	1,329	2,005
FAM96A	-0,255	2,209
FAM98B	0,149	1,861
FBL	1,262	1,529
FBRSL1	-1,333	1,210
FBXO3	-0,344	2,347
FH	0,787	2,050
FKBP11	1,410	1,188
FKBP1A;FKBP12-Exp2	-0,686	1,474
FLOT2	0,738	1,448
FOXK2	0,131	1,187
FTO	0,422	2,391
FUS	-0,041	1,464
FXR2	1,135	1,592
FZD6	-1,353	0,265
GAB1	-0,167	2,131
GALNS	0,470	0,960
GALNT1	0,218	1,004
GAN	-0,472	0,654
GATSL3	0,463	0,497
GBE1	-0,347	1,134
GCAT	0,734	2,076
GCC1	1,683	1,587
GCDH	0,276	2,495
GDF15	-0,788	1,404
GDI1	-0,180	1,841
GFPT2	0,923	2,140
GLB1	-0,546	1,445

Gene symbol	Ctrl	56h
GLDC	0,231	1,591
GLIPR2	0,044	1,995
GLRX	0,588	0,836
GNAI2;GNAT1;GNAI1;GNAT2;GNAT3	-0,148	2,183
GNG11;GNGT1;GNGT2	1,197	0,411
GORAB	0,455	1,835
GPATCH1	0,313	1,375
GPI	0,087	2,120
GPN1	0,253	2,067
GPR108	-1,024	1,967
GPS2	0,070	2,673
GPX1	-0,688	2,299
GRN	-1,171	1,013
GRSF1	0,860	1,385
GSE1	-0,424	1,766
HAPLN3	-0,921	1,669
HAUS7	1,132	0,818
HAX1	0,368	1,240
HBA1	0,262	1,856
HBA2	0,028	1,933
HBG2;HBG1	-1,741	1,073
HBZ	-0,720	0,538
HCLS1	-0,932	1,829
HDDC2	-0,417	0,645
HDDC3	-0,792	1,789
HEBP1	-0,271	1,319
HIBADH	0,133	2,506
HIP1	-0,079	2,425
HIST1H1E;HIST1H1D	1,012	1,148
HMGB2	-0,881	2,379
HMG5	0,343	0,201
HMGXB3	-0,569	1,858
HN1	-0,395	2,259
HNF1A;HNF1B;HMBOX1	0,430	2,418
HOXB4	-1,236	0,900
HP1BP3	-0,383	2,298
HPX	0,000	1,475
HR	0,002	2,470
HS1BP3	0,472	1,255
HSBP1	1,106	1,700
HSD17B8	-0,414	1,640

Gene symbol	Ctrl	56h
HSPA1A	-0,839	2,078
HSPA2	-0,859	2,271
HSPA4L	0,045	1,564
HSPBAP1	0,798	0,994
IAH1	-0,439	2,622
ICAM1	-1,009	1,545
IDH3A	0,790	1,901
IDI1	1,880	0,905
IFT52	-0,074	2,035
IL18	0,010	1,466
INVS	0,725	1,730
IQSEC2	0,013	2,069
IRF5	-0,170	1,609
IRS1	0,155	2,021
ITFG2	1,738	1,822
ITFG3	-0,490	1,191
ITGB4	1,264	1,042
ITGB8	0,500	1,028
ITPKA	-1,254	1,589
ITPKB	-0,268	1,554
KANK1	0,690	1,814
KCTD17	-0,081	2,554
KDM8	-0,709	1,326
KHNYN	-0,228	1,808
KIAA1161	0,100	1,905
KIAA1522	-0,753	1,771
KIAA1598	-1,031	1,516
KIDINS220	0,057	0,869
KIT	-0,303	0,178
KLC4	-1,229	1,186
L3HYPDH	0,079	1,676
L3MBTL3	0,305	1,677
LANCL2	0,135	2,325
LASP1	-0,798	1,628
LCORL	0,252	2,300
LCP1	-1,329	0,651
LDHB	-0,056	1,792
LDLR	0,420	0,565
LENG1	-0,290	2,388
LMAN1	-0,164	2,224
LMNB2	0,313	1,852
LPP	-1,443	1,350
LRRN1	-1,232	0,516
LSM12	1,603	1,157

Gene symbol	Ctrl	56h
LSM2	-0,306	2,699
MAK16	0,833	1,398
MAL2	1,332	1,283
MAN1A2	0,588	1,656
MAPRE1	0,162	2,234
MASP1	-0,293	2,096
MCTS1	-0,056	2,463
MED10	0,132	1,610
MED20	0,460	2,519
MED25	0,371	1,777
METRNL	0,953	0,987
MEX3D	-0,129	1,207
MGMT	-0,099	1,338
MIF4GD	-0,218	2,544
MISP	1,001	0,722
MKNK1;DKFZ p686E14208	0,359	1,554
MMGT1	-0,489	1,667
MMP21	-0,500	1,740
MOB2	0,604	1,808
MPG	0,749	0,803
MPHOSPH8	-0,019	1,683
MPRIP	1,495	0,106
MPST	1,647	1,253
MRE11A	0,614	1,575
MRPS25	0,840	2,099
MRTO4	0,098	2,248
MTAP	1,402	1,074
MTDH	0,571	2,156
MVD	-0,589	2,358
MYDGF	-0,290	1,792
MYH14	0,480	1,700
MYH9	-0,991	1,893
MYL12A;MYL 12B	-0,206	2,407
MYO1D	0,415	1,937
NAA10;NAA1 1	-0,152	2,451
NACA	-0,923	0,879
NAMPT	1,384	1,662
NAP1L4	-0,275	2,435
NAPG	-0,287	2,631
NCAPH	1,483	1,291
NCDN	0,508	1,712
NCK1	0,374	2,031

Gene symbol	Ctrl	56h
NCKAP5L	-1,032	1,932
NCOA1	0,307	2,477
NDUFB3	1,070	0,595
NEO1	0,491	1,259
NFKB2	0,187	2,183
NME1- NME2;NME2; NME1;NME2P 1	-0,200	1,478
NOL3	1,014	1,219
NOVA1	-1,066	1,741
NPNT	-0,327	1,302
NRF1	0,534	2,021
NUDT12	0,518	0,380
NUDT18	-0,468	1,462
NUDT9	-0,926	2,042
NUMB	0,534	1,197
NUMBL	0,430	1,956
NUP43	0,013	2,447
OGDH	0,685	1,952
OGDHL	1,061	1,375
P2RX4	0,727	2,191
PANK3	0,674	-0,240
PAPOLA	0,661	1,288
PARD6B	-0,859	2,663
PCDHGA10	-0,983	2,028
PCMT1	-0,355	1,744
PDAP1	0,580	2,280
PDCD10	0,780	2,245
PDCD6	-0,055	1,698
PDCD7	0,408	0,872
PDHB	0,443	2,173
PDIA6	-0,875	2,323
PDLIM1	-1,027	1,490
PDXK	-0,147	2,152
PDZD8	1,301	1,015
PDZK1;PDZK 1P1	0,221	1,529
PEF1	0,780	1,618
PFKFB3	-0,491	1,876
PHF21A	-0,172	0,912
PHPT1	-1,456	1,631
PKD2	-0,246	1,512
PKM	0,138	1,293
PLCG1	0,034	1,449

Gene symbol	Ctrl	56h
PLEC	1,559	0,039
PLEKHM1	-0,373	1,861
PLXDC2	0,342	-0,227
PLXNA1	0,536	0,606
PMM2	0,019	1,522
PNPO	0,295	2,429
POLR1D	0,474	2,045
POLR2F	-0,163	2,321
POLR2H	0,297	2,326
POU2F1;POU 2F3;POU2F2	-0,375	2,177
PPME1	0,544	2,051
PPP1CC	0,896	1,752
PPP3CA	-0,262	2,397
PPT1	-0,535	2,366
PRDX1	-0,598	1,301
PRDX6	0,149	1,530
PREP	0,203	1,927
PRKAR1A	0,539	1,580
PRKRA	-0,459	2,321
PRMT3	0,758	1,935
PROSER2;C1 0orf47	0,482	1,469
PROSER3	0,404	1,906
PRPF3	-0,386	1,869
PRR5- ARHGAP8;PR R5;LOC55315 8;ARHGAP8	0,904	2,058
PSMA5	-0,163	2,648
PSMC3	-0,330	2,551
PSMC5	1,116	1,496
PSMD10	-0,405	1,478
PSMD11	0,455	2,363
PSMD3	0,314	2,374
PSME1	-0,406	2,347
PSTPIP2	0,919	1,186
PTMS	-1,837	1,717
PTPN6	-0,893	2,308
PTRF	-0,664	2,277
PUS3	0,495	1,721
PVRL2	0,192	2,230
PYCRL	0,469	2,356
RAB14	1,175	1,716
RAB1B;RAB1 C	-0,686	2,764

Gene symbol	Ctrl	56h
RAB28	1,095	2,052
RAB30	-0,365	2,099
RAB5B	-0,259	2,586
RABEP2	-0,262	2,094
RABEPK	0,130	1,922
RALGAPB	1,440	0,638
RASSF8	0,580	1,788
RBBP4;RBBP7	0,211	2,080
RBM5	0,050	1,740
REEP3	0,228	2,230
RGL3	-0,142	1,915
RMDN1	0,290	1,127
RMND5A	-0,542	2,443
RNF135	-0,075	2,251
RNF146	-0,375	2,051
RPL10A	-0,081	1,516
RPL14	-0,184	1,415
RPL32	0,252	2,423
RPL5	-0,157	1,169
RPS15	0,216	2,002
RPS17L;RPS17	-0,420	2,015
RRAS2	0,196	2,329
RRNAD1	0,639	0,788
RTCB	1,063	0,821
RTN1	-1,366	1,458
RUFY1	0,690	-1,218
SCAMP1	-0,072	2,538
SCAMP2	1,237	1,034
SCAPER	-0,529	1,721
SCP2	0,016	0,012
SCYL3	-1,495	1,908
SEMA3B	-0,208	1,080
SERPINB9	0,312	1,387
SETD1A	-1,252	1,032
SETX	0,666	2,414
SF3A1	1,126	1,612
SF3A2	-0,433	2,023
SH2D4A	-0,666	0,532
SHPK	-0,092	1,255
SIN3A	0,395	2,073
SLC12A2	-0,054	0,758
SLC16A3	0,852	1,635
SLC34A3;SLC	-0,483	2,187

Gene symbol	Ctrl	56h
34A1		
SLTM	-0,978	1,891
SLX4	1,331	0,754
SMCR8	0,924	1,148
SND1	-0,104	1,758
SNIP1	-0,607	2,304
SNRPE	-0,163	2,487
SNRPF	0,949	0,940
SNRPG;SNRPGP15	-0,543	2,365
SNRPN;SNRPNPB	0,313	2,138
SNTA1	0,583	1,158
SNX2	-0,121	2,432
SORBS2	-0,337	2,685
SORBS3	-0,128	2,191
SPATS2	0,090	2,200
SPICE1	0,567	0,593
SRP19	-0,682	2,400
SRRM1	-0,053	2,677
SRRM2	0,846	0,631
SSBP1	-1,153	0,328
SSH2	-1,243	1,576
ST13P5;ST13	-0,876	1,497
STAM	0,127	2,151
STAMBP	-0,285	2,018
STK38	0,408	2,228
STXBP4	0,403	1,978
SUB1	-0,516	2,467
SUMO1	-0,264	1,654
SUV420H1	0,330	2,082
TACSTD2	-1,104	0,944
TAP1	-0,054	0,983
TARS	0,495	2,110
TATDN2	0,768	0,871
TBC1D16	-1,283	1,420
TBC1D20	0,341	2,068
TBC1D23	0,128	2,550
TBC1D4	0,854	0,536
TECR	0,841	0,502
TET2	0,434	2,176
TFE3	-0,379	1,469
TICAM1	-1,322	1,921
TIMP2	0,153	1,917
TK2	1,295	1,463

Gene symbol	Ctrl	56h
TLDC1	0,593	1,714
TLN1	-0,560	1,892
TMEM106B	-0,727	1,288
TMEM55B	0,009	1,605
TMOD3	-1,261	2,450
TMUB1	1,385	0,071
TOB2	-0,526	1,178
TOE1	1,122	1,580
TOM1	-1,190	2,269
TOM1L1	0,391	2,476
TOR1A	-0,074	2,548
TPD52L2	-1,007	1,689
TPM1	-0,646	0,046
TRAF3IP1	0,130	2,668
TRAPPC2L	-0,467	2,228
TRIM2	-0,813	1,330
TRIM22	-0,751	0,892
TRIM37	0,680	1,358
TRPT1	0,606	0,728
TSC22D3	-1,109	1,867
TSC22D4	0,139	1,813
TSSK4	-0,339	2,216
TTC9	-0,288	2,447
TUBA1C	0,404	2,132
TUBB4B	0,094	2,606
TUBB6	-0,211	2,774
TULP4	0,128	1,911
TWF1	0,761	1,584
UBA3	1,410	1,009
UBE2H	0,800	1,574
UBE2K	0,410	1,905
UBE2M	0,596	1,836
UBE2V2	0,070	2,477
UBE4A	0,812	1,317
UBL5	-0,259	1,103
UBL7	-0,870	0,599
UBXN2B	-0,710	1,436
UCHL3	0,535	2,586
USP20	0,391	2,231
USP48	0,639	2,132
UTP11L	0,517	1,394
VBP1	0,126	1,316
VGLL4	-0,827	1,605
VPS54	1,299	1,533

Gene symbol	Ctrl	56h
VRK1	0,573	2,119
VWF	0,514	0,814
WARS	-0,522	2,004
WTAP	-0,858	2,437
WWC3	-0,129	0,987
WWOX	0,474	2,152
XPC	-0,405	2,469
XPNPEP1	0,450	1,607
XRCC6BP1	-0,703	2,111
YAP1	-0,228	2,015
YEATS2	-0,210	1,208
YWHAB	-0,029	2,494
ZBTB45	-0,686	1,252
ZDBF2	0,514	2,357
ZFAND1	1,018	1,980
ZHX2	0,141	1,867
ZNF574	1,240	-0,151
ZNF579	-0,170	1,690
ZNF703	-0,186	2,233
ZNRF2	-0,024	1,826

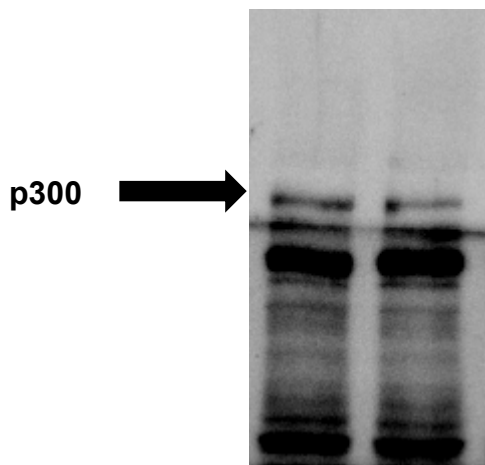
Supplement Table 3: Cluster genes of Wnt-signaling pathway enrichment at 56 h (log2 scale).

Gene symbol	Description	Ctrl	56 h
EP300	Histone acetyltransferase p300	1,169	-2,379
PLCB3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	1,805	-1,512
CSNK1A1	Casein kinase I isoform alpha	1,030	-2,068
CTNNBIP1	Beta-catenin-interacting protein 1	0,344	-2,751
MAPK9	Mitogen-activated protein kinase 9	0,701	-2,360
CHD8	Chromodomain-helicase-DNA-binding protein 8	0,549	-2,500
DVL3	Segment polarity protein dishevelled homolog DVL-3	1,324	-1,681
PPP2R1B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	1,494	-1,453
CSNK2A2	Casein kinase II subunit alpha	1,081	-1,736
RAC2	Ras-related C3 botulinum toxin substrate 2	0,897	-1,895
RAC3	Ras-related C3 botulinum toxin substrate 3	0,792	-1,863
RHOA	Transforming protein RhoA	0,926	-1,682
RUVBL1	RuvB-like 1	1,190	-1,343
PPP3R1	Calcineurin subunit B type 1	0,614	-1,877
PPP2R5C	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	0,759	-1,000
NFAT5	Nuclear factor of activated T-cells 5	0,064	-0,931
CSNK1E	Casein kinase I isoform epsilon	-1,380	-0,968

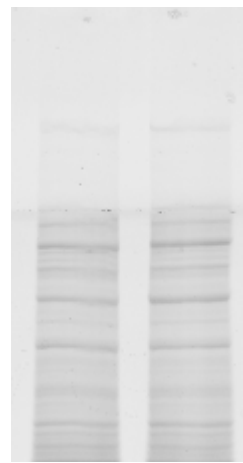
Supplement Table 4: Proteome analysis of MRTF-associated genes after 56 h (log2 scale). #NV: not detected in proteome

Gene symbol	Description	Ctrl	56 h
MYOCD	Myocardin	#NV	#NV
CDH5	Cadherin 5	#NV	#NV
MYL9	Myosin Light Chain 9	#NV	#NV
MIR206	MicroRNA 206	#NV	#NV
EP300	E1A Binding Protein P300	1,17	-2,38
SMYD3	SET And MYND Domain Containing 3	1,34	-1,48
RHOA	Ras Homolog Family Member A	0,93	-1,68
MICAL2	Microtubule Associated Monooxygenase, Calponin And LIM Domain Containing 2	1,82	-0,67
ATE1	Arginyltransferase 1	0,11	-2,32
KPNA3	Karyopherin Subunit Alpha 3	1,83	-0,40
MKL1	Megakaryoblastic Leukemia (Translocation) 1	1,28	-0,72
BRMS1L	BRMS1, Breast Cancer Metastasis Suppressor 1	0,50	-0,88
DNMT1	DNA Methyltransferase 1	0,61	-0,40
MKL2	MKL1/Myocardin Like 2	1,18	0,41
LIMA1	LIM Domain And Actin Binding 1	-0,71	-1,33
KPNB1	Karyopherin Subunit Beta 1	1,44	1,09
C1QTNF6	C1q And Tumor Necrosis Factor Related Protein 6	0,65	0,41
STAT3	Signal Transducer And Activator Of Transcription 3	0,83	0,64
TRIM27	Tripartite Motif Containing 27	0,47	0,73
CYR61	Cysteine Rich Angiogenic Inducer 61	-0,58	0,00
SRF	Serum Response Factor	-0,09	0,54
PALLD	Palladin, Cytoskeletal Associated Protein	-0,68	0,28

Supplementary Figure 1: Full versions of the cropped Western blot in Fig. 6B

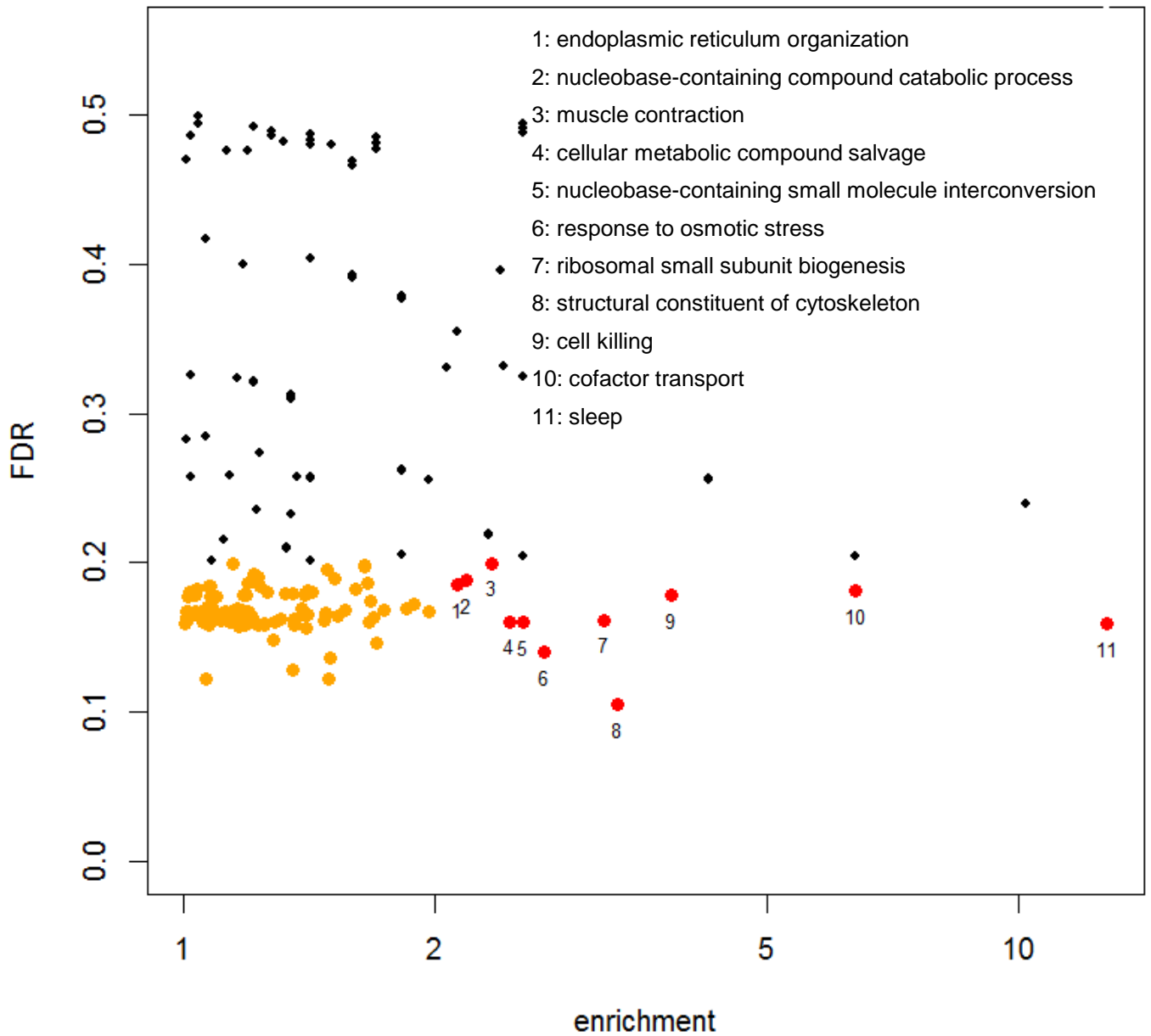


Complete blot for Figure 6B



Loading control by stain-free gel
for Figure 6B

Supplementary Figure 2: Dot plot of enriched pathways for up-regulated proteins

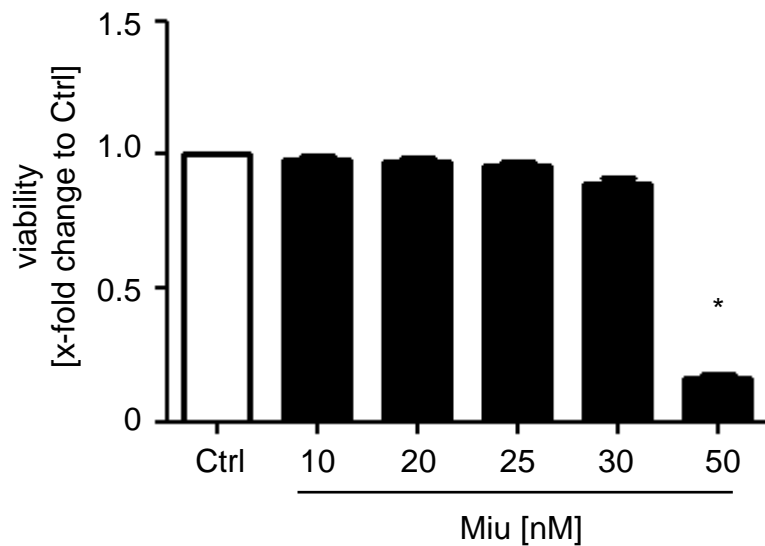


orange dots: FDR < 0.2 and enrichment value > 2.

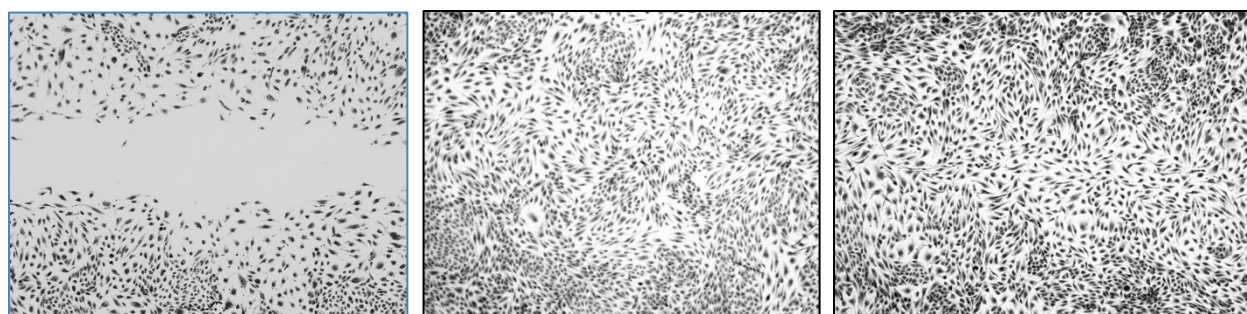
red dots: FDR < 0.2 and enrichment value > 2.

Supplementary Figure 3: Viability, 2D and 3D migration of primary endothelial cells (HUVECs)

a: Viability



b: Scratch assay



Negative control
(minimal medium)

Positive control
(ECGM)

Pretreatment with
20 nM Miu for 72 h

c: Boyden chamber

