

Supplementary Tables

Key: * low numbers of sequences hit this gene. a longer contigs had a greater success than shorter ones (i.e a contig from contigs36 could distinguish the tRNA and map when the equivalent contig from contig20 did not.

Table s1 Mapping of trimmed contigs and sequences against rRNAs of Giardia Assemblage A

rRNA	# of Annotated genes	# found contigs20	# found contigs36	# found contigs50	# found sequences
5 S rRNA	1	1	0	0	1
5.8S rRNA	1	1	0	0	1
18 S rRNA	4	4	2	2	4
28 S rRNA	4	3	1	0	4

Table s2 Mapping of trimmed contigs and sequences against tRNAs of Giardia Assemblage A

tRNA	# of Annotated genes	# found contigs20	# found contigs36	# found contigs50	# found sequences
Ser	4	4	4	2	4
Val	4	2	1	1	4
Asn	2	2	2	2	2
Arg	6	3	4a	3a	6
Trp	1	0	0	0	1*
Met	3	1	1	0	3
Ala	4	2	1	1	4
Gly	4	2	1	1	4
Glu	3	2	1	1	3
Gln	4	2	2	2	4
Pro	3	1	1a	1a	3
Ile	4	3	2	1	4
Thr	3	3	2	1	3
Leu	6	3	4a	4a	6
Cys	1	0	1a	1a	1
Tyr	1	1	1	1	1
Phe	1	0	1a	1a	1
Lys	3	2	1	1	3
His	1	0	1a	1a	1
Asp	1	2	2	2	1

Table s3 Mapping of trimmed contigs and sequences against tRNAs of Trichomonas

tRNA	# of Annotated genes	# found contigs20	# found contigs36	# found contigs50	# found sequences
Ala AGC	19	13	0	0	17
CGC	2	2	0	0	2
TGC	7	6	0	0	5
Arg ACG	16	14	3	2	16
CCG	2	1	1	1	2
CCT	4	4	2	1	4
TCG	1	1	1	1	1
TCT	8	5	1	0	8
Asn GTT	17	12	9	12	17
Asp GTC	26	17	1	1	25
Cys GCA	12	9	0	0	11
Gln CTG	9	6	5	6	9
TTG	9	6	5	3	9
Glu CTC	14	9	5	2	14
TTC	24	16	6	5	24
Gly CCC	3	1	0	0	2
GCC	18	10	11	9	18
TCC	8	5	0	0	7
His GTG	10	6	7	7	10
Ile GAT	20	18	3	2	20
TAT	10	8	2	1	9
Leu AAG	19	11	0	0	19
CAA	5	2	0	0	3
CAG	2	2	1	1	2
TAA	9	5	2	0	7
TAG	2	2	0	0	2
Lys CTT	20	14	13	13	20
TTT	19	17	9	5	19
Met CAT	22	14	2	1	22
Phe AAA	2	2	1	1	2
GAA	15	12	6	6	15
Pro AGG	3	3	0	0	3
CGG	2	2	2	1	2
TGG	11	9	0	0	11

Ser ACT	2	1	1	1	1
AGA	12	8	1	1	1
CGA	3	3	1	1	1
GCT	5	3	3	4	5
GGA	1	1	0	1	1
TGA	7	5	1	2	6
Thr AGT	5	4	2	2	5
CGT	2	2	0	0	2
TGT	18	11	2	1	18
Trp CCA	5	5	0	0	5
Tyr GTA	13	11	6	5	13
Val CAC	1	1	1	1	1
GAC	21	10	7	7	21
TAC	3	3	3	2	3