


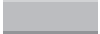



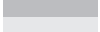

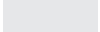

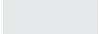

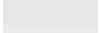

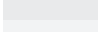

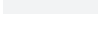












































































Supplementary Table S1

Gene	Intron1	Top Hit	Api ²	Group ³	Group ⁴	Api ⁵
tRNA syn asn	y	<i>Plasmodium</i>	7	Ap		
tRNA syn ser	y	<i>Cryptosporidium</i>	4	F, Ap		
tRNA syn glu	y	<i>Ashbya</i>	4	F, Ap		
tRNA syn val 1	y	<i>Strongylocentrotus</i>	3	A		
tRNA syn phe-A1	y	<i>Gibberella</i>	2	E		
tRNA syn asp	y	<i>Cryptosporidium</i>	2	F		
tRNA syn trp	y	<i>Cryptosporidium</i>	2	A		
tRNA syn lys	y	<i>Cryptosporidium</i>	2	A		
tRNA syn ala	y	<i>Bombyx</i>	2	F		
tRNA syn val 2		<i>Aedes</i>	1	A		
tRNA syn lys		<i>Rhizobium</i>	0	B		
tRNA syn phe-B1		<i>Anopheles</i>	0	A		
S15 mito	y	<i>Theileria</i>	5 ⁶	Ap		
S16	y	<i>Theileria</i>	4 ⁶	Ap		
L21 50S	y	<i>Theileria</i>	2 ⁶	Ap		
S17	y	<i>Plasmodium</i>	2 ⁶	Ap		
P1		<i>Neospora</i>	9	Ap		
S7		<i>Theileria</i>	8	Ap		
L12	y	<i>Plasmodium</i>	8	Ap		
S5	y	<i>Theileria</i>	7	Ap		
L23		<i>Cryptosporidium</i>	6	Ap, F		
L3		<i>Micromalthus</i>	6	Ap, A		
L5	y	<i>Eimeria</i>	6	Ap		
S2	y	<i>Plasmodium</i>	5	Ap, A		
L7A 1	y	<i>Theileria</i>	4	Ap, A		
L40		<i>Theileria</i>	4	F, Ap		
L7A 2	y	<i>Cryptosporidium</i>	4	A, Ap		
L21		<i>Cryptosporidium</i>	4	Ap, F, P		
S9		<i>Cyanophora</i>	3	F, Ap		
L4		<i>Oryza</i>	3	P, Ap		
L7	y	<i>Ashbya</i>	3	Ap, P		
S27	y	<i>Coprinopsis</i>	2	E		
S3A	y	<i>Oryza</i>	2	P		
S8	y	<i>Cryptosporidium</i>	2	P, Ap		
S13		<i>Cryptosporidium</i>	2	E		
S18		<i>Theileria</i>	2	E		
S29		<i>Plasmodium</i>	1	A		
L13		<i>Schizosaccharomyces</i>	1	E		
L1 Bacterial	y	<i>Nocardioides</i>	0	B		
S4		<i>Pan</i>	0	A		
L7/L12						
glutamate dehydrogenase		<i>Plasmodium</i>	9	Ap, B		
glutamate dehydrogenase		<i>Theileria</i>	7	Ap		
splicing factor 3b subunit 3	y	<i>Plasmodium</i>	7	Ap		
glycerol-3-phosphate dehydrogenase	y	<i>Theileria</i>	6	Ap		
sec61	y	<i>Plasmodium</i>	6	Ap		

Supplementary Table S1 continued.

Gene	Intron ¹	Top Hit	Api ²	Group ³	Group ⁴	Api ⁵
formate/nitrite transporter	y	<i>Toxoplasma</i>	6	Ap, B		
nitrate reductase		<i>Plasmodium</i>	4	Ap, P		
dihydrolipoamide branched chain transacetylase	y	<i>Leishmania</i>	4	P, Ap		
enolase 2		<i>Plasmodium</i>	3	Ap, P		
glycine cleavage system H protein	y	<i>Thermotoga</i>	1	B, E		
tat interactive protein 2		<i>Danio</i>	0	A		
glyceraldehyde 3-phosphate dehydrogenase		<i>Lithobius</i>	0	A		
proline oxidase		<i>Canis</i>	0	A		
polyethylene glycol dehydrogenase		<i>Apis</i>	0	A, B		
probable NADH-dependent dehydrogenase		<i>Blastopirellula</i>	0	B		
saccharopine dehydrogenase		<i>Rhodococcus</i>	0	B		
short chain dehydrogenase	y	<i>Photobacterium</i>	0	B		
acyl-CoA dehydrogenase		<i>Mycobacterium</i>	0	B		
10 kDa inner membrane protein		<i>Xanthobacter</i>	0	B		
oxidoreductase		<i>Bradyrhizobium</i>	0	B		
cysteine synthase		<i>Rhodobacter</i>	0	B		
D-3-phosphoglycerate dehydrogenase		<i>Synechococcus</i>	0	B		
histidinol dehydrogenase		<i>Methanosarcina</i>	0	B		
alpha/beta hydrolase		<i>Rhodofera</i>	0	B		
beta-ketoacyl synthase		<i>Herpetosiphon</i>	0	B		
formylmethanofuran dehydrogenase		<i>Rubrivivax</i>	0	B		
2-oxoglutarate dehydrogenase		<i>Acidovorax</i>	0	B		
3-hydroxyacyl-CoA dehydrogenase		<i>Polaromonas</i>	0	B		
D-lactate dehydrogenase		<i>Photobacterium</i>	0	B		
male sterility-like		<i>Polaromonas</i>	0	B		
DTDP-4-hydroxymannose 3,5-epimerase		<i>Azoarcus</i>	0	B		
aldehyde reductase	y	<i>Pseudoalteromonas</i>	0	B, E		
dihydroorotate dehydrogenase		<i>Rattus</i>	0	B, E		
17-beta-hydroxysteroid dehydrogenase	y	<i>Tetrahymena</i>	0	E		
electron-transferring-flavoprotein dehydrogenase	y	<i>Acidiphilium</i>	0	E		
phosphoglycerate dehydrogenase		<i>Burkholderia</i>	0	E, B		
methylmalonate-semialdehyde dehydrogenase		<i>Tetrahymena</i>	0	E, B		
FAD-binding oxidase	y	<i>Aspergillus</i>	0	E, B		
MaoC like domain-containing protein		<i>Tetrahymena</i>	0	F		
dihydrolipoyl dehydrogenase	y	<i>Aspergillus</i>	0	F		
translation initiation factor eIF-6	y	<i>Candida</i>	0	F		
glycine dehydrogenase	y	<i>Magnaporthe</i>	0	F, B		
1,3-beta-glucan synthase		<i>Arabidopsis</i>	0	P		
alcohol dehydrogenase class 3	y	<i>Oryza</i>	0	P		
acyl carrier protein reductase		<i>Tetrahymena</i>	0	P		
aspartokinase-homoserine dehydrogenase		<i>Ostreococcus</i>	0	PcP, B		
aspartokinase-homoserine dehydrogenase	y	<i>Ostreococcus</i>	0	PcP, B		
aspartokinase-homoserine dehydrogenase		<i>Salinibacter</i>	0	PcP, B		
aspartokinase-homoserine dehydrogenase		<i>Salinibacter</i>	0	PcP, B		
histidinol-phosphate aminotransferase	y	<i>Chloroflexus</i>	0	PcP, B		

¹Genes in which introns were detected. Because many of the genes are fragments, there might be introns which were not detected due to the incompleteness of the nucleotide sequence information.

²Number of apicomplexans in the top 10 hits.

³Predominant group of the top hits: A, Animal; B, bacteria; F, Fungi; Ap, Apicomplexa; P, Plant; E, eukaryote; Pcp, chloroplast.

⁴Predominant group of the top hits: red, Bikonts; green, Unikonts; blue, bacteria; purple, eukaryote; brown, all organisms; white, suspected contaminant.







































⁵Number of apicomplexans in the top 10 hits in gray scale with darker boxes indicating higher number of hits.

⁶Of these hits all were apicomplexan.

⁷Only 6 hits, of which 4 were apicomplexan, 1 chloroplast, and 1 bacterial.

⁸This hit spanned a very short region of good homology.

Supplementary Table S1 continued.

Gene	Intron1	Top Hit	Api ²	Group ³	Group ⁴	Api ⁵
polyketide synthase	y	<i>Cryptosporidium</i>	5	Ap, B		
type I fatty acid synthase		<i>Toxoplasma</i>	7	Ap		
type I fatty acid synthase		<i>Toxoplasma</i>	8	Ap		
type I fatty acid synthase		<i>Toxoplasma</i>	8	Ap		
type I fatty acid synthase		<i>Toxoplasma</i>	8	Ap		
type I fatty acid synthase		<i>Toxoplasma</i>	8	Ap		
type I fatty acid synthase		<i>Toxoplasma</i>	5	Ap, B		
type I fatty acid synthase	y	<i>Toxoplasma</i>	6	Ap, B		
type I fatty acid synthase	y	<i>Toxoplasma</i>	5	Ap, B		
type I fatty acid synthase		<i>Toxoplasma</i>	4	Ap, B		
type I fatty acid synthase		<i>Toxoplasma</i>	4	Ap, B		
type I fatty acid synthase		<i>Toxoplasma</i>	4	Ap, B		
glucosamine-fructose-6-phosphate aminotransferase	y	<i>Plasmodium</i>	6	Ap, B		
ribulose phosphate isomerase		<i>Pavlova</i>	5	Pcp, Ap		
ribose-5-phosphate isomerase		<i>Arabidopsis</i>	4	Pcp, Ap		
glucosamine-fructose-6-phosphate aminotransferase		<i>Cryptosporidium</i>	3	B, E		
peptidylprolyl isomerase		<i>Arabidopsis</i>	1	E		
ketol-acid reductoisomerase		<i>delta proteobacterium</i>	0	Pcp		
6-phosphogluconolactonase	y	<i>Yersina</i>	0	B		

¹Genes in which introns were detected. Because many of the genes are fragments, there might be introns which were not detected due to the incompleteness of the nucleotide sequence information.

²Number of apicomplexans in the top 10 hits.

³Predominant group of the top hits: A, Animal; B, bacteria; F, Fungi; Ap, Apicomplexa; P, Plant; E, eukaryote; Pcp, chloroplast.

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