

Supplementary File 1 – Best similarity match to each of the 68 genes present in all five previously sequenced *Ca. Kinetoplastibacterium* spp. genomes, but absent from the *Ca. Kinetoplastibacterium sorsogonicusi* genome.

Representative protein	Description	EC number(s)	BLAST E-value
AGF49874.1	acetyl-CoA synthetase	6.2.1.1	0E+00
AGF49875.1	heme-degrading domain-containing protein (GlcG)		6.64E-40
AGF49876.1	NlpC/P60 family protein (NLPC_P60)		4.36E-32
AGF49889.1	3-oxoacyl-ACP reductase FabG	1.1.1.100	6.73E-110
AGF49890.1	[acyl-carrier-protein] S-malonyltransferase (FabD)	2.3.1.39	2.42E-119
AGF49891.1	3-oxoacyl-[acyl-carrier-protein] synthase III	2.3.1.180	3.47E-174
AGF49892.1	glycerol-3-phosphate acyltransferase PlsX	2.3.1.15	4.16E-165
AGF49910.1	peptidyl-prolyl cis-trans isomerase C	5.2.1.8	6.72E-22
AGF49912.1	conserved hypothetical membrane protein (ZipA C_terminal domain)		2.84E-04
AGF49946.1	DNA translocase FtsK		0.00E+00
AGF49977.1	flavin reductase		9.92E-41
AGF49988.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	2.3.1.51	5.95E-46
AGF50000.1	ABC transporter ATP-binding protein		1.00E-174
AGF50018.1	lytic transglycosylase	4.2.2.-	2.11E-92
AGF50019.1	enoyl-ACP reductase (FabI)	1.3.1.9 / 1.3.1.10	2.97E-135
AGF50032.1	GNAT family N-acetyltransferase		4.70E-09
AGF50037.1	acetyl-CoA carboxylase biotin carboxylase subunit	6.4.1.2 / 6.3.4.14	0.00E+00
AGF50038.1	acetyl-CoA carboxylase, biotin carboxyl carrier protein		4.62E-65
AGF50046.1	glutamate-1-semialdehyde-2,1-aminomutase	5.4.3.8	0.00E+00
AGF50048.1	DUF3460 domain-containing protein		2.71E-25
AGF50053.1	boxy-terminal processing protease (S41 family peptidase)	3.4.21.102	2.90E-119
AGF50056.1	protein-export chaperone SecB		5.52E-53
AGF50077.1	HPr kinase/phosphorylase	2.7.11.- / 2.7.4.-	1.83E-135
AGF50083.1	lactate dehydrogenase	1.1.1.27	4.82E-113
AGF50094.1	lysine transporter LysE		5.76e-45
AGF50104.1	tyrosine recombinase XerC		9.05E-127
AGF50105.1	GTP-binding protein		6.71E-110
AGF50112.1	biotin--[acetyl-CoA-carboxylase] ligase	6.3.4.15	1.09E-42
AGF50125.1	iron donor protein CyaY		1.08E-30
AGF50129.1	porphobilinogen synthase	4.2.1.24	1.28E-166
AGF49457.1	cysteine hydrolases superfamily protein		1E-10
AGF49475.1	histidinol-phosphate transaminase (HisC)	2.6.1.9	1E-170
AGF49487.1	monovalent cation:H ⁺ antiporter of the CPA1 family		1E-62

AGF49508.1	uroporphyrinogen decarboxylase (hemE)	4.1.1.37	0
AGF49511.1	glutamate--cysteine ligase	6.3.2.2	0
AGF49513.1	Tim44 domain-containing protein		1.04E-16
AGF49520.1	glutamyl-tRNA reductase	1.2.1.70	4.68E-148
AGF49526.1	phosphoenolpyruvate carboxylase	4.1.1.31	0.00E+00
AGF49559.1	inositol monophosphatase	3.1.3.25	9.67E-92
AGF49561.1	magnesium and cobalt transporter		1.86E-88
AGF49581.1	site-specific tyrosine recombinase XerD		5.91E-147
AGF49611.1	DUF1178 domain-containing protein		8.14E-49
AGF49622.1	MFS transporter		1.34E-23
AGF49626.1	squalene synthase HpnD (Isoprenoid Biosynthesis enzymes, Class 1)	2.5.1.32 / 2.5.1.99	2.56E-22
AGF49627.1	NA repair protein RadA		0.00E+00
AGF49628.1	TRAP transporter substrate-binding protein DctP		1.92E-135
AGF49636.1	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	2.1.1.177	4.07E-60
AGF49643.1	recombination regulator RecX		4.84E-25
AGF49646.1	hydroxymethylbilane synthase	2.5.1.61	1.33E-149
AGF49647.1	uroporphyrinogen-III synthase hemD	4.2.1.75	5.93E-31
AGF49648.1	uroporphyrin-III C-methyltransferase (hemX family)		1.72E-05
AGF49661.1	glutathione synthase	6.3.2.3	1.72E-151
AGF49662.1	HPr family phosphocarrier protein		3.02E-21
AGF49667.1	bifunctional riboflavin kinase/FAD synthetase	2.7.1.26 / 2.7.7.2	8.32E-122
AGF49674.1	cold-shock protein		1.34E-03
AGF49681.1	low molecular weight phosphotyrosine protein phosphatase	3.1.3.48	4.56e-66
AGF49696.1	glycerol-3-phosphate 1-O-acyltransferase PlsY	2.3.1.15	6.79E-52
AGF49700.1	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	2.1.1.190	1.37E-172
AGF49720.1	exodeoxyribonuclease VII large subunit	3.1.11.6	1.20E-168
AGF49728.1	integration host factor subunit alpha		3.79E-46
AGF49729.1	MerR family transcriptional regulator		6.60E-23
AGF49760.1	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	4.2.1.59	4.00E-83
AGF49770.1	endolytic transglycosylase MltG		1.28E-103
AGF49793.1	aminopeptidase N	3.4.11.2	0.00E+00
AGF49802.1	primosomal replication protein N		2.00E-19
AGF49807.1	exodeoxyribonuclease VII small subunit	3.1.11.6	1.03E-16
AGF49850.1	Histone deacetylase		9.80E-158
AGF49851.1	integration host factor subunit beta		4.39E-38