

Table S1. *T.brucei* Gene ID of 597 mitochondrial proteins used as positive samples.

Index	Gene ID	Index	Gene ID	Index	Gene ID
1	Tb09.160.0760	200	Tb11.03.0260	399	Tb927.8.7530
2	Tb09.160.1820	201	Tb11.03.0475	400	Tb927.8.8170
3	Tb09.160.2250	202	Tb11.03.0870	401	Tb927.8.8180
4	Tb09.160.2970	203	Tb11.03.0950	402	Tb04.24M18.150
5	Tb09.160.3110	204	Tb11.0400	403	Tb09.160.0370
6	Tb09.160.3800	205	Tb11.46.0006	404	Tb09.160.1020
7	Tb09.160.4090	206	Tb11.47.0004	405	Tb09.160.2060
8	Tb09.160.4130	207	Tb11.47.0012	406	Tb09.160.2160
9	Tb09.160.4300	208	Tb11.47.0017	407	Tb09.160.2220
10	Tb09.160.4310	209	Tb11.47.0022	408	Tb09.160.2380
11	Tb09.160.4380	210	Tb11.47.0024	409	Tb09.160.4840
12	Tb09.160.4750	211	Tb11.55.0009	410	Tb09.160.5050
13	Tb09.160.5240	212	Tb11.55.0016	411	Tb09.160.5110
14	Tb09.160.5260	213	Tb11.55.0026	412	Tb09.211.0760
15	Tb09.160.5280	214	Tb927.1.1160	413	Tb09.211.0950
16	Tb09.211.0230	215	Tb927.1.1200	414	Tb09.211.1240
17	Tb09.211.0330	216	Tb927.1.1580	415	Tb09.211.1880
18	Tb09.211.1380	217	Tb927.1.1690	416	Tb09.211.1940
19	Tb09.211.1600	218	Tb927.1.2990	417	Tb09.211.2530
20	Tb09.211.1750	219	Tb927.1.3030	418	Tb09.211.2600
21	Tb09.211.1900	220	Tb927.1.4100	419	Tb09.211.3720
22	Tb09.211.2370	221	Tb927.1.4230	420	Tb10.26.0100
23	Tb09.211.2430	222	Tb927.1.730	421	Tb10.26.0390
24	Tb09.211.2580	223	Tb927.2.1860	422	Tb10.26.1020
25	Tb09.211.3000	224	Tb927.2.2470	423	Tb10.389.1910
26	Tb09.211.3200	225	Tb927.2.2940	424	Tb10.406.0100
27	Tb09.211.3800	226	Tb927.2.2970	425	Tb10.61.3070
28	Tb09.211.4400	227	Tb927.2.3030	426	Tb10.6k15.0120
29	Tb09.211.4510	228	Tb927.2.3610	427	Tb10.6k15.0160
30	Tb09.211.4511	229	Tb927.2.3800	428	Tb10.6k15.0310
31	Tb09.211.4580	230	Tb927.2.4110	429	Tb10.6k15.0480
32	Tb09.211.4700	231	Tb927.2.4380	430	Tb10.6k15.0500
33	Tb09.211.4740	232	Tb927.2.4400	431	Tb10.6k15.1120
34	Tb09.244.2620	233	Tb927.2.4590	432	Tb10.6k15.1280
35	Tb09.244.2670	234	Tb927.2.4610	433	Tb10.6k15.1430
36	Tb09.244.2840	235	Tb927.2.4890	434	Tb10.6k15.1450
37	Tb09.v1.0420	236	Tb927.2.5930	435	Tb10.6k15.1800
38	Tb10.05.0050	237	Tb927.2.6070	436	Tb10.6k15.1910
39	Tb10.05.0070	238	Tb927.3.1000	437	Tb10.6k15.1930

40	Tb10.100.0070	239	Tb927.3.1380	438	Tb10.6k15.2640
41	Tb10.100.0160	240	Tb927.3.1410	439	Tb10.70.0660
42	Tb10.100.0220	241	Tb927.3.1590	440	Tb10.70.1120
43	Tb10.26.0050	242	Tb927.3.1690	441	Tb10.70.1460
44	Tb10.26.0600	243	Tb927.3.1710	442	Tb10.70.2350
45	Tb10.26.0750	244	Tb927.3.1790	443	Tb10.70.2670
46	Tb10.26.0860	245	Tb927.3.1890	444	Tb10.70.2970
47	Tb10.26.1000	246	Tb927.3.1940	445	Tb10.70.3010
48	Tb10.389.0130	247	Tb927.3.2180	446	Tb10.70.3190
49	Tb10.389.0340	248	Tb927.3.2230	447	Tb10.70.3590
50	Tb10.389.0690	249	Tb927.3.2260	448	Tb10.70.3820
51	Tb10.389.0890	250	Tb927.3.2880	449	Tb10.70.4120
52	Tb10.389.1140	251	Tb927.3.2980	450	Tb10.70.4980
53	Tb10.389.1710	252	Tb927.3.3660	451	Tb10.70.5430
54	Tb10.389.1785	253	Tb927.3.5240	452	Tb10.70.5880
55	Tb10.389.1880	254	Tb927.3.5610	453	Tb10.70.5900
56	Tb10.406.0050	255	Tb927.3.5630	454	Tb10.70.6260
57	Tb10.406.0490	256	Tb927.3.750	455	Tb10.70.7440
58	Tb10.406.0510	257	Tb927.3.770	456	Tb10.70.7450
59	Tb10.61.0090	258	Tb927.3.820	457	Tb10.70.7900
60	Tb10.61.0190	259	Tb927.3.860	458	Tb10.v4.0053
61	Tb10.61.0610	260	Tb927.3.970	459	Tb11.01.0880
62	Tb10.61.1530	261	Tb927.4.1070	460	Tb11.01.0890
63	Tb10.61.1790	262	Tb927.4.1500	461	Tb11.01.1500
64	Tb10.61.1820	263	Tb927.4.1660	462	Tb11.01.2490
65	Tb10.61.2510	264	Tb927.4.1810	463	Tb11.01.2740
66	Tb10.61.3110	265	Tb927.4.2720	464	Tb11.01.3190
67	Tb10.6k15.0150	266	Tb927.4.3300	465	Tb11.01.3290
68	Tb10.6k15.0490	267	Tb927.4.3450	466	Tb11.01.3490
69	Tb10.6k15.0960	268	Tb927.4.3690	467	Tb11.01.3970
70	Tb10.6k15.1300	269	Tb927.4.4160	468	Tb11.01.4740
71	Tb10.6k15.1460	270	Tb927.4.4300	469	Tb11.01.5110
72	Tb10.6k15.1600	271	Tb927.4.440	470	Tb11.01.5280
73	Tb10.6k15.2180	272	Tb927.4.4600	471	Tb11.01.5460
74	Tb10.6k15.2310	273	Tb927.4.4610	472	Tb11.01.6320
75	Tb10.6k15.2510	274	Tb927.4.4620	473	Tb11.01.6710
76	Tb10.6k15.3030	275	Tb927.4.4910	474	Tb11.01.7900
77	Tb10.6k15.3040	276	Tb927.4.720	475	Tb11.01.8225
78	Tb10.6k15.3080	277	Tb927.5.1060	476	Tb11.01.8230
79	Tb10.6k15.3250	278	Tb927.5.1510	477	Tb11.01.8500
80	Tb10.6k15.3290	279	Tb927.5.1550	478	Tb11.02.0180

81	Tb10.6k15.3640	280	Tb927.5.1710	479	Tb11.02.0430
82	Tb10.6k15.3900	281	Tb927.5.1790	480	Tb11.02.1860
83	Tb10.70.0430	282	Tb927.5.2070	481	Tb11.02.1880
84	Tb10.70.0530	283	Tb927.5.2580	482	Tb11.02.2420
85	Tb10.70.0625	284	Tb927.5.2780	483	Tb11.02.3310
86	Tb10.70.1410	285	Tb927.5.2930	484	Tb11.02.3570
87	Tb10.70.1520	286	Tb927.5.3010	485	Tb11.02.3720
88	Tb10.70.1580	287	Tb927.5.3040	486	Tb11.02.4330
89	Tb10.70.1640	288	Tb927.5.3090	487	Tb11.02.4500
90	Tb10.70.1750	289	Tb927.5.3110	488	Tb11.02.4660
91	Tb10.70.1890	290	Tb927.5.3300	489	Tb11.02.5100
92	Tb10.70.2090	291	Tb927.5.3350	490	Tb11.02.5820
93	Tb10.70.2155	292	Tb927.5.3360	491	Tb11.03.0510
94	Tb10.70.2190	293	Tb927.5.3410	492	Tb11.03.0900
95	Tb10.70.2290	294	Tb927.5.3640	493	Tb11.12.0014
96	Tb10.70.2320	295	Tb927.5.3870	494	Tb11.46.0012
97	Tb10.70.2630	296	Tb927.5.3980	495	Tb11.47.0009
98	Tb10.70.3150	297	Tb927.5.4040	496	Tb11.47.0020
99	Tb10.70.3280	298	Tb927.5.4120	497	Tb11.55.0010
100	Tb10.70.3680	299	Tb927.5.450	498	Tb11.55.0017
101	Tb10.70.3840	300	Tb927.6.1250	499	Tb927.1.1330
102	Tb10.70.3850	301	Tb927.6.1410	500	Tb927.1.1610
103	Tb10.70.4220	302	Tb927.6.1440	501	Tb927.1.1730
104	Tb10.70.4280	303	Tb927.6.1680	502	Tb927.1.3010
105	Tb10.70.4380	304	Tb927.6.2010	503	Tb927.1.3800
106	Tb10.70.4500	305	Tb927.6.2080	504	Tb927.1.5000
107	Tb10.70.4850	306	Tb927.6.2180	505	Tb927.1.740
108	Tb10.70.5110	307	Tb927.6.2420	506	Tb927.1.790
109	Tb10.70.5380	308	Tb927.6.2790	507	Tb927.1.840
110	Tb10.70.5510	309	Tb927.6.3600	508	Tb927.2.2210
111	Tb10.70.5970	310	Tb927.6.3740	509	Tb927.2.2510
112	Tb10.70.6930	311	Tb927.6.3930	510	Tb927.2.3180
113	Tb10.70.7550	312	Tb927.6.4040	511	Tb927.2.4700
114	Tb10.70.7650	313	Tb927.6.4080	512	Tb927.2.4830
115	Tb10.70.7760	314	Tb927.6.4130	513	Tb927.3.1720
116	Tb10.70.7840	315	Tb927.6.4200	514	Tb927.3.1730
117	Tb10.70.7960	316	Tb927.6.4540	515	Tb927.3.1820
118	Tb11.01.0610	317	Tb927.6.4560	516	Tb927.3.2010
119	Tb11.01.0640	318	Tb927.6.4580	517	Tb927.3.2080
120	Tb11.01.1130	319	Tb927.6.4930	518	Tb927.3.2130
121	Tb11.01.1160	320	Tb927.6.4990	519	Tb927.3.2300

122	Tb11.01.1440	321	Tb927.6.590	520	Tb927.3.2370
123	Tb11.01.1600	322	Tb927.7.1070	521	Tb927.3.2670
124	Tb11.01.1690	323	Tb927.7.1340	522	Tb927.3.3680
125	Tb11.01.1740	324	Tb927.7.1550	523	Tb927.3.3890
126	Tb11.01.1810	325	Tb927.7.2570	524	Tb927.3.4030
127	Tb11.01.1840	326	Tb927.7.2620	525	Tb927.3.4210
128	Tb11.01.1900	327	Tb927.7.2760	526	Tb927.3.4260
129	Tb11.01.1910	328	Tb927.7.2990	527	Tb927.3.4420
130	Tb11.01.1930	329	Tb927.7.3050	528	Tb927.3.4920
131	Tb11.01.2000	330	Tb927.7.3240	529	Tb927.3.940
132	Tb11.01.2170	331	Tb927.7.3460	530	Tb927.3.950
133	Tb11.01.2340	332	Tb927.7.3470	531	Tb927.4.1130
134	Tb11.01.3300	333	Tb927.7.3510	532	Tb927.4.1440
135	Tb11.01.3500	334	Tb927.7.3590	533	Tb927.4.1540
136	Tb11.01.3550	335	Tb927.7.3910	534	Tb927.4.1760
137	Tb11.01.3710	336	Tb927.7.3940	535	Tb927.4.2360
138	Tb11.01.3860	337	Tb927.7.3950	536	Tb927.4.2440
139	Tb11.01.4702	338	Tb927.7.3960	537	Tb927.4.2580
140	Tb11.01.4860	339	Tb927.7.3990	538	Tb927.4.330
141	Tb11.01.4870	340	Tb927.7.4140	539	Tb927.4.3660
142	Tb11.01.5040	341	Tb927.7.4710	540	Tb927.4.600
143	Tb11.01.5180	342	Tb927.7.5260	541	Tb927.4.630
144	Tb11.01.5390	343	Tb927.7.6350	542	Tb927.4.830
145	Tb11.01.5480	344	Tb927.7.6800	543	Tb927.5.1130
146	Tb11.01.5960	345	Tb927.7.6990	544	Tb927.5.2150
147	Tb11.01.6620	346	Tb927.7.7010	545	Tb927.5.2810
148	Tb11.01.6680	347	Tb927.7.7080	546	Tb927.5.3340
149	Tb11.01.7090	348	Tb927.7.7330	547	Tb927.5.4080
150	Tb11.01.7110	349	Tb927.7.7410	548	Tb927.5.510
151	Tb11.01.7140	350	Tb927.7.7420	549	Tb927.5.530
152	Tb11.01.7290	351	Tb927.7.7440	550	Tb927.5.740
153	Tb11.01.7300	352	Tb927.7.800	551	Tb927.6.1200
154	Tb11.01.7480	353	Tb927.7.840	552	Tb927.6.1590
155	Tb11.01.7510	354	Tb927.8.1060	553	Tb927.6.1860
156	Tb11.01.8090	355	Tb927.8.1240	554	Tb927.6.1890
157	Tb11.01.8200	356	Tb927.8.1420	555	Tb927.6.2140
158	Tb11.01.8470	357	Tb927.8.1430	556	Tb927.6.2230
159	Tb11.01.8620	358	Tb927.8.1490	557	Tb927.6.2380
160	Tb11.01.8630	359	Tb927.8.1860	558	Tb927.6.2490
161	Tb11.02.0130	360	Tb927.8.1880	559	Tb927.6.2510
162	Tb11.02.0250	361	Tb927.8.1890	560	Tb927.6.2630

163	Tb11.02.0290	362	Tb927.8.1990	561	Tb927.6.3360
164	Tb11.02.0440	363	Tb927.8.2530	562	Tb927.6.4070
165	Tb11.02.0490	364	Tb927.8.2540	563	Tb927.7.1080
166	Tb11.02.0770	365	Tb927.8.2740	564	Tb927.7.2200
167	Tb11.02.1110	366	Tb927.8.2760	565	Tb927.7.2390
168	Tb11.02.1440	367	Tb927.8.3110	566	Tb927.7.2410
169	Tb11.02.1480	368	Tb927.8.3170	567	Tb927.7.2690
170	Tb11.02.2070	369	Tb927.8.3300	568	Tb927.7.3100
171	Tb11.02.2250	370	Tb927.8.3320	569	Tb927.7.3520
172	Tb11.02.2280	371	Tb927.8.3330	570	Tb927.7.3750
173	Tb11.02.2300	372	Tb927.8.3580	571	Tb927.7.3770
174	Tb11.02.2390	373	Tb927.8.3690	572	Tb927.7.3810
175	Tb11.02.2460	374	Tb927.8.3830	573	Tb927.7.4440
176	Tb11.02.2480	375	Tb927.8.4040	574	Tb927.7.5110
177	Tb11.02.2700	376	Tb927.8.4250	575	Tb927.7.5280
178	Tb11.02.2710	377	Tb927.8.4440	576	Tb927.7.5440
179	Tb11.02.2740	378	Tb927.8.4550	577	Tb927.7.640
180	Tb11.02.2960	379	Tb927.8.4810	578	Tb927.7.910
181	Tb11.02.3130	380	Tb927.8.4860	579	Tb927.8.1740
182	Tb11.02.3180	381	Tb927.8.5120	580	Tb927.8.1770
183	Tb11.02.3530	382	Tb927.8.5200	581	Tb927.8.2470
184	Tb11.02.3670	383	Tb927.8.5280	582	Tb927.8.2670
185	Tb11.02.3800	384	Tb927.8.5560	583	Tb927.8.2880
186	Tb11.02.3810	385	Tb927.8.5640	584	Tb927.8.3090
187	Tb11.02.4120	386	Tb927.8.5690	585	Tb927.8.4000
188	Tb11.02.4480	387	Tb927.8.580	586	Tb927.8.4240
189	Tb11.02.4800	388	Tb927.8.5860	587	Tb927.8.4380
190	Tb11.02.4810	389	Tb927.8.6060	588	Tb927.8.4930
191	Tb11.02.4890	390	Tb927.8.6080	589	Tb927.8.5100
192	Tb11.02.5160	391	Tb927.8.620	590	Tb927.8.5220
193	Tb11.02.5280	392	Tb927.8.630	591	Tb927.8.5420
194	Tb11.02.5390	393	Tb927.8.6580	592	Tb927.8.5660
195	Tb11.02.5530	394	Tb927.8.680	593	Tb927.8.6110
196	Tb11.02.5660	395	Tb927.8.6960	594	Tb927.8.6560
197	Tb11.02.5670	396	Tb927.8.6970	595	Tb927.8.6640
198	Tb11.02.5770	397	Tb927.8.7170	596	Tb927.8.6800
199	Tb11.03.0180	398	Tb927.8.7260	597	Tb927.8.7040

Table S2. *T.brucei* Gene ID of 1290 non-mitochondrial proteins used as negative samples.

Index	Gene ID	Index	Gene ID	Index	Gene ID
1	Tb09.142.0100	431	Tb11.02.2830	861	Tb927.8.7840
2	Tb09.142.0230	432	Tb11.02.2930	862	Tb927.8.7900
3	Tb09.142.0240	433	Tb11.02.2940	863	Tb927.8.7920
4	Tb09.142.0450	434	Tb11.02.3160	864	Tb927.8.7930
5	Tb09.160.0110	435	Tb11.02.3200	865	Tb927.8.7940
6	Tb09.160.0160	436	Tb11.02.3270	866	Tb927.8.8020
7	Tb09.160.0260	437	Tb11.02.3390	867	Tb927.8.8040
8	Tb09.160.0280	438	Tb11.02.3400	868	Tb927.8.8090
9	Tb09.160.0580	439	Tb11.02.3595	869	Tb927.8.8100
10	Tb09.160.0700	440	Tb11.02.3610	870	Tb927.8.8220
11	Tb09.160.0710	441	Tb11.02.3740	871	Tb927.8.8230
12	Tb09.160.0815	442	Tb11.02.3920	872	Tb927.8.8240
13	Tb09.160.2010	443	Tb11.02.3990	873	Tb927.8.8250
14	Tb09.160.2050	444	Tb11.02.4040	874	Tb927.8.8260
15	Tb09.160.2150	445	Tb11.02.4050	875	Tb927.8.8300
16	Tb09.160.2420	446	Tb11.02.4070	876	Tb927.8.8330
17	Tb09.160.2540	447	Tb11.02.4100	877	Tb927.8.900
18	Tb09.160.2600	448	Tb11.02.4140	878	Tb927.8.920
19	Tb09.160.2990	449	Tb11.02.4200	879	Tb927.8.980
20	Tb09.160.3150	450	Tb11.02.4220	880	Tb927.7.2640
21	Tb09.160.3210	451	Tb11.02.4350	881	Tb10.61.2870
22	Tb09.160.3410	452	Tb11.02.4360	882	Tb927.3.4680
23	Tb09.160.3470	453	Tb11.02.4470	883	Tb927.8.1710
24	Tb09.160.3520	454	Tb11.02.4520	884	Tb927.6.160
25	Tb09.160.3630	455	Tb11.02.4570	885	Tb11.01.2570
26	Tb09.160.3670	456	Tb11.02.4580	886	Tb927.6.2270
27	Tb09.160.3690	457	Tb11.02.4640	887	Tb927.3.4090
28	Tb09.160.3820	458	Tb11.02.5060	888	Tb09.211.0900
29	Tb09.160.4220	459	Tb11.02.5110	889	Tb10.61.2745
30	Tb09.160.4430	460	Tb11.02.5180	890	Tb10.70.7230
31	Tb09.160.4680	461	Tb11.02.5210	891	Tb927.6.4320
32	Tb09.160.5020	462	Tb11.02.5250	892	Tb927.1.3070
33	Tb09.160.5030	463	Tb11.02.5270	893	Tb09.160.0770
34	Tb09.160.5160	464	Tb11.02.5310	894	Tb927.1.1710
35	Tb09.160.5380	465	Tb11.02.5320	895	Tb11.01.4390
36	Tb09.160.5390	466	Tb11.02.5410	896	Tb927.6.1290
37	Tb09.160.5400	467	Tb11.02.5470	897	Tb11.03.0530
38	Tb09.160.5550	468	Tb11.02.5610	898	Tb927.7.7130
39	Tb09.160.5580	469	Tb11.02.5620	899	Tb927.6.4500

40	Tb09.160.5590	470	Tb11.02.5640	900	Tb11.01.6200
41	Tb09.211.0050	471	Tb11.02.5790	901	Tb10.70.5870
42	Tb09.211.0110	472	Tb11.02.5810	902	Tb927.8.820
43	Tb09.211.0120	473	Tb11.03.0050	903	Tb927.7.4500
44	Tb09.211.0130	474	Tb11.03.0140	904	Tb10.389.1040
45	Tb09.211.0210	475	Tb11.03.0170	905	Tb927.6.630
46	Tb09.211.0430	476	Tb11.03.0290	906	Tb927.7.4460
47	Tb09.211.0790	477	Tb11.03.0410	907	Tb11.01.2390
48	Tb09.211.0860	478	Tb11.03.0500	908	Tb927.8.1840
49	Tb09.211.0865	479	Tb11.03.0670	909	Tb927.3.1110
50	Tb09.211.1000	480	Tb11.03.0815	910	Tb927.8.4080
51	Tb09.211.1010	481	Tb11.03.0890	911	Tb927.3.5430
52	Tb09.211.1020	482	Tb11.03.0935	912	Tb927.4.4700
53	Tb09.211.1030	483	Tb11.03.0970	913	Tb10.61.1340
54	Tb09.211.1190	484	Tb11.09.0003	914	Tb09.211.2960
55	Tb09.211.1210	485	Tb11.12.0006	915	Tb09.211.0890
56	Tb09.211.1510	486	Tb11.12.0013	916	Tb927.5.1250
57	Tb09.211.1530	487	Tb11.12.0016	917	Tb10.70.1080
58	Tb09.211.1695	488	Tb11.14.0007	918	Tb10.70.0980
59	Tb09.211.1760	489	Tb11.14.0008	919	Tb11.01.6600
60	Tb09.211.1820	490	Tb11.14.0015	920	Tb927.7.6640
61	Tb09.211.2310	491	Tb11.14.0019	921	Tb927.1.3250
62	Tb09.211.2590	492	Tb11.17.0002	922	Tb927.7.2120
63	Tb09.211.2650	493	Tb11.18.0004	923	Tb10.406.0550
64	Tb09.211.2730	494	Tb11.18.0013	924	Tb927.6.400
65	Tb09.211.2900	495	Tb11.18.0017	925	Tb927.4.5340
66	Tb09.211.2920	496	Tb11.22.0012	926	Tb927.8.910
67	Tb09.211.3040	497	Tb11.24.0007	927	Tb10.70.3570
68	Tb09.211.3270	498	Tb11.24.0012	928	Tb927.7.2680
69	Tb09.211.3280	499	Tb11.27.0001	929	Tb10.70.5170
70	Tb09.211.3620	500	Tb11.39.0006	930	Tb927.4.3810
71	Tb09.211.3650	501	Tb11.46.0001	931	Tb927.4.3590
72	Tb09.211.3770	502	Tb11.46.0002	932	Tb09.160.1100
73	Tb09.211.3870	503	Tb11.47.0001	933	Tb927.3.4160
74	Tb09.211.3920	504	Tb11.50.0005	934	Tb927.3.5010
75	Tb09.211.4240	505	Tb11.50.0006	935	Tb927.4.3510
76	Tb09.211.4350	506	Tb11.51.0005	936	Tb927.2.5970
77	Tb09.211.4550	507	Tb11.55.0020	937	Tb927.7.6610
78	Tb09.211.4760	508	Tb11.55.0027	938	Tb11.02.1000
79	Tb09.211.4840	509	Tb11.57.0004	939	Tb10.70.1130
80	Tb09.211.4850	510	Tb11.57.0008	940	Tb10.6k15.1820

81	Tb09.211.4870	511	Tb11.57.0019	941	Tb927.7.2780
82	Tb09.244.0050	512	Tb11.57.0024	942	Tb09.244.2800
83	Tb09.244.0200	513	Tb11.57.0035	943	Tb11.02.2040
84	Tb09.244.0250	514	Tb11.57.0052	944	Tb927.3.2680
85	Tb09.244.0470	515	Tb11.57.0084	945	Tb927.5.2620
86	Tb09.244.0910	516	Tb927.1.05	946	Tb927.8.5830
87	Tb09.244.1000	517	Tb927.1.120	947	Tb11.01.1350
88	Tb09.244.1570	518	Tb927.1.1240	948	Tb11.02.0460
89	Tb09.244.1580	519	Tb927.1.1270	949	Tb927.5.3450
90	Tb09.244.1600	520	Tb927.1.1370	950	Tb927.4.2030
91	Tb09.244.1740	521	Tb927.1.1380	951	Tb927.2.3990
92	Tb09.244.1830	522	Tb927.1.180	952	Tb10.6k15.2450
93	Tb09.244.2060	523	Tb927.1.2100	953	Tb927.7.3370
94	Tb09.244.2120	524	Tb927.1.2120	954	Tb927.5.1280
95	Tb09.244.2200	525	Tb927.1.2150	955	Tb11.02.1320
96	Tb09.244.2280	526	Tb927.1.2160	956	Tb927.4.4350
97	Tb09.244.2310	527	Tb927.1.2260	957	Tb09.160.0350
98	Tb09.244.2330	528	Tb927.1.2430	958	Tb927.5.1300
99	Tb09.244.2380	529	Tb927.1.2450	959	Tb927.8.1960
100	Tb09.244.2400	530	Tb927.1.2470	960	Tb11.03.0700
101	Tb09.244.2410	531	Tb927.1.2490	961	Tb11.02.1500
102	Tb09.244.2420	532	Tb927.1.2510	962	Tb927.7.2400
103	Tb09.244.2440	533	Tb927.1.2550	963	Tb927.7.4680
104	Tb09.244.2450	534	Tb927.1.2600	964	Tb09.160.0460
105	Tb09.244.2460	535	Tb927.1.2820	965	Tb11.01.7070
106	Tb09.244.2470	536	Tb927.1.2850	966	Tb11.01.3850
107	Tb09.244.2480	537	Tb927.1.2880	967	Tb927.3.1740
108	Tb09.244.2500	538	Tb927.1.290	968	Tb11.02.1810
109	Tb09.244.2510	539	Tb927.1.3110	969	Tb927.3.4880
110	Tb09.244.2520	540	Tb927.1.3120	970	Tb927.3.1680
111	Tb09.244.2530	541	Tb927.1.3180	971	Tb11.01.2310
112	Tb09.244.2540	542	Tb927.1.3200	972	Tb927.7.6980
113	Tb09.244.2725	543	Tb927.1.3220	973	Tb927.8.4270
114	Tb09.244.2730	544	Tb927.1.3280	974	Tb927.7.6260
115	Tb09.244.2740	545	Tb927.1.3320	975	Tb927.8.2030
116	Tb09.244.2790	546	Tb927.1.3820	976	Tb927.6.4020
117	Tb09.354.0060	547	Tb927.1.420	977	Tb927.5.3030
118	Tb09.354.0090	548	Tb927.1.480	978	Tb927.7.3860
119	Tb09.354.0180	549	Tb927.1.4870	979	Tb11.01.1250
120	Tb09.v1.0310	550	Tb927.1.4900	980	Tb927.4.3350
121	Tb09.v1.0320	551	Tb927.1.5030	981	Tb11.02.1260

122	Tb09.v1.0350	552	Tb927.1.5080	982	Tb10.389.1320
123	Tb09.v1.0640	553	Tb927.1.5110	983	Tb927.6.3650
124	Tb10.05.0010	554	Tb927.1.5120	984	Tb927.4.2000
125	Tb10.05.0020	555	Tb927.1.5170	985	Tb927.7.3760
126	Tb10.05.0120	556	Tb927.1.5200	986	Tb10.70.3670
127	Tb10.05.0220	557	Tb927.1.5220	987	Tb09.211.3140
128	Tb10.100.0080	558	Tb927.1.5240	988	Tb11.02.4230
129	Tb10.100.0100	559	Tb927.1.5300	989	Tb927.8.540
130	Tb10.100.0155	560	Tb927.1.5330	990	Tb927.3.2490
131	Tb10.20.0130	561	Tb927.1.540	991	Tb927.3.4750
132	Tb10.26.0070	562	Tb927.1.630	992	Tb927.6.4440
133	Tb10.26.0200	563	Tb927.1.700	993	Tb10.70.7350
134	Tb10.26.0320	564	Tb927.1.870	994	Tb927.4.4040
135	Tb10.26.0370	565	Tb927.2.1080	995	Tb927.1.750
136	Tb10.26.0510	566	Tb927.2.1170	996	Tb11.01.7750
137	Tb10.26.0590	567	Tb927.2.1180	997	Tb11.02.0210
138	Tb10.389.0060	568	Tb927.2.1380	998	Tb11.02.2670
139	Tb10.389.0110	569	Tb927.2.170	999	Tb927.6.3000
140	Tb10.389.0120	570	Tb927.2.1780	1000	Tb927.8.3710
141	Tb10.389.0270	571	Tb927.2.1890	1001	Tb927.5.1340
142	Tb10.389.0330	572	Tb927.2.1920	1002	Tb10.70.5050
143	Tb10.389.0350	573	Tb927.2.2020	1003	Tb10.05.0170
144	Tb10.389.0470	574	Tb927.2.2060	1004	Tb927.3.3130
145	Tb10.389.0480	575	Tb927.2.2180	1005	Tb927.4.1680
146	Tb10.389.0710	576	Tb927.2.2190	1006	Tb10.70.1570
147	Tb10.389.0730	577	Tb927.2.2240	1007	Tb927.5.840
148	Tb10.389.1330	578	Tb927.2.240	1008	Tb927.5.1700
149	Tb10.389.1450	579	Tb927.2.2440	1009	Tb927.8.2770
150	Tb10.389.1530	580	Tb927.2.2460	1010	Tb927.6.4520
151	Tb10.389.1550	581	Tb927.2.2670	1011	Tb10.61.2430
152	Tb10.389.1570	582	Tb927.2.280	1012	Tb09.211.4780
153	Tb10.406.0240	583	Tb927.2.2900	1013	Tb927.4.4760
154	Tb10.406.0260	584	Tb927.2.3080	1014	Tb927.6.3220
155	Tb10.406.0320	585	Tb927.2.3370	1015	Tb11.02.0230
156	Tb10.406.0330	586	Tb927.2.340	1016	Tb927.6.2340
157	Tb10.406.0340	587	Tb927.2.3440	1017	Tb09.211.4200
158	Tb10.406.0360	588	Tb927.2.3460	1018	Tb10.70.1770
159	Tb10.406.0370	589	Tb927.2.3580	1019	Tb11.24.0011
160	Tb10.406.0380	590	Tb927.2.370	1020	Tb927.4.360
161	Tb10.406.0390	591	Tb927.2.3720	1021	Tb927.6.4850
162	Tb10.406.0400	592	Tb927.2.380	1022	Tb10.100.0210

163	Tb10.406.0410	593	Tb927.2.3930	1023	Tb10.389.0830
164	Tb10.406.0420	594	Tb927.2.4020	1024	Tb927.6.5080
165	Tb10.406.0430	595	Tb927.2.4060	1025	Tb11.01.4620
166	Tb10.406.0440	596	Tb927.2.4280	1026	Tb927.7.5910
167	Tb10.406.0450	597	Tb927.2.4370	1027	Tb09.211.3400
168	Tb10.406.0460	598	Tb927.2.4390	1028	Tb927.7.5990
169	Tb10.406.0500	599	Tb927.2.470	1029	Tb11.01.2330
170	Tb10.406.0615	600	Tb927.2.4870	1030	Tb10.70.2750
171	Tb10.61.0060	601	Tb927.2.4930	1031	Tb927.8.3410
172	Tb10.61.0210	602	Tb927.2.5060	1032	Tb927.7.930
173	Tb10.61.0420	603	Tb927.2.510	1033	Tb927.5.2130
174	Tb10.61.0600	604	Tb927.2.5250	1034	Tb927.7.5580
175	Tb10.61.0740	605	Tb927.2.560	1035	Tb927.4.2410
176	Tb10.61.0770	606	Tb927.2.5750	1036	Tb927.2.5810
177	Tb10.61.0890	607	Tb927.2.5850	1037	Tb927.6.5130
178	Tb10.61.1030	608	Tb927.2.5910	1038	Tb927.7.4820
179	Tb10.61.1040	609	Tb927.2.6000	1039	Tb11.01.0510
180	Tb10.61.1090	610	Tb927.2.6090	1040	Tb11.01.7010
181	Tb10.61.1330	611	Tb927.2.6150	1041	Tb927.2.5130
182	Tb10.61.1360	612	Tb927.2.6200	1042	Tb927.7.5660
183	Tb10.61.1380	613	Tb927.2.6220	1043	Tb09.160.0430
184	Tb10.61.1390	614	Tb927.2.6240	1044	Tb927.7.3330
185	Tb10.61.1590	615	Tb927.2.6280	1045	Tb927.7.2240
186	Tb10.61.1630	616	Tb927.2.6320	1046	Tb927.7.3310
187	Tb10.61.1920	617	Tb927.2.6410	1047	Tb927.8.7090
188	Tb10.61.1950	618	Tb927.2.690	1048	Tb927.7.6910
189	Tb10.61.1980	619	Tb927.3.150	1049	Tb927.7.2190
190	Tb10.61.2040	620	Tb927.3.1500	1050	Tb927.5.1880
191	Tb10.61.2090	621	Tb927.3.1510	1051	Tb927.4.3790
192	Tb10.61.2180	622	Tb927.3.1780	1052	Tb927.6.2220
193	Tb10.61.2530	623	Tb927.3.180	1053	Tb11.01.4850
194	Tb10.61.2610	624	Tb927.3.190	1054	Tb927.5.890
195	Tb10.61.2640	625	Tb927.3.210	1055	Tb11.01.0320
196	Tb10.61.2650	626	Tb927.3.2190	1056	Tb09.211.0180
197	Tb10.61.2750	627	Tb927.3.2340	1057	Tb927.7.2720
198	Tb10.61.2970	628	Tb927.3.2960	1058	Tb11.02.0352
199	Tb10.61.3050	629	Tb927.3.3310	1059	Tb10.70.0640
200	Tb10.61.3190	630	Tb927.3.3320	1060	Tb09.211.3955
201	Tb10.6k15.0020	631	Tb927.3.340	1061	Tb927.2.2950
202	Tb10.6k15.0030	632	Tb927.3.3480	1062	Tb11.02.0990
203	Tb10.6k15.0040	633	Tb927.3.370	1063	Tb11.01.4370

204	Tb10.6k15.0050	634	Tb927.3.4220	1064	Tb11.01.3960
205	Tb10.6k15.0060	635	Tb927.3.4290	1065	Tb10.70.2620
206	Tb10.6k15.0070	636	Tb927.3.4310	1066	Tb927.4.1850
207	Tb10.6k15.0270	637	Tb927.3.4320	1067	Tb927.4.1310
208	Tb10.6k15.0410	638	Tb927.3.4330	1068	Tb10.6k15.2760
209	Tb10.6k15.0450	639	Tb927.3.5030	1069	Tb927.8.6940
210	Tb10.6k15.0540	640	Tb927.3.5280	1070	Tb927.4.2770
211	Tb10.6k15.0890	641	Tb927.3.5530	1071	Tb927.2.4980
212	Tb10.6k15.0900	642	Tb927.3.5540	1072	Tb927.8.2860
213	Tb10.6k15.0910	643	Tb927.3.580	1073	Tb927.4.3130
214	Tb10.6k15.0920	644	Tb927.3.590	1074	Tb11.02.1190
215	Tb10.6k15.0990	645	Tb927.4.1220	1075	Tb927.3.5620
216	Tb10.6k15.1000	646	Tb927.4.1930	1076	Tb10.70.0310
217	Tb10.6k15.1100	647	Tb927.4.2710	1077	Tb09.211.0610
218	Tb10.6k15.1160	648	Tb927.4.3190	1078	Tb927.4.420
219	Tb10.6k15.1180	649	Tb927.4.3550	1079	Tb927.7.570
220	Tb10.6k15.1520	650	Tb927.4.3930	1080	Tb927.8.6050
221	Tb10.6k15.1570	651	Tb927.4.3990	1081	Tb927.6.4750
222	Tb10.6k15.1770	652	Tb927.4.4000	1082	Tb927.8.1190
223	Tb10.6k15.1790	653	Tb927.4.4010	1083	Tb11.39.0004
224	Tb10.6k15.1950	654	Tb927.4.4020	1084	Tb927.3.1200
225	Tb10.6k15.2050	655	Tb927.4.4250	1085	Tb10.6k15.0380
226	Tb10.6k15.2060	656	Tb927.4.4270	1086	Tb11.01.1450
227	Tb10.6k15.2190	657	Tb927.4.4290	1087	Tb927.8.1500
228	Tb10.6k15.2500	658	Tb927.4.430	1088	Tb927.4.2990
229	Tb10.6k15.2610	659	Tb927.4.4330	1089	Tb927.1.1670
230	Tb10.6k15.2620	660	Tb927.4.4470	1090	Tb11.02.3410
231	Tb10.6k15.2770	661	Tb927.4.4730	1091	Tb10.61.1560
232	Tb10.6k15.2890	662	Tb927.4.4820	1092	Tb927.4.920
233	Tb10.6k15.2930	663	Tb927.4.4830	1093	Tb927.3.1150
234	Tb10.6k15.3160	664	Tb927.4.4840	1094	Tb10.26.0670
235	Tb10.6k15.3170	665	Tb927.4.4850	1095	Tb10.6k15.3800
236	Tb10.6k15.3190	666	Tb927.4.4860	1096	Tb09.160.5620
237	Tb10.6k15.3340	667	Tb927.4.4870	1097	Tb927.3.2750
238	Tb10.6k15.3350	668	Tb927.4.5260	1098	Tb11.02.4300
239	Tb10.6k15.3500	669	Tb927.4.5270	1099	Tb927.8.2460
240	Tb10.6k15.3510	670	Tb927.4.5300	1100	Tb11.02.0270
241	Tb10.6k15.3540	671	Tb927.4.5400	1101	Tb10.70.6570
242	Tb10.6k15.3600	672	Tb927.4.5410	1102	Tb927.7.2380
243	Tb10.6k15.3680	673	Tb927.4.5420	1103	Tb927.6.1900
244	Tb10.6k15.3780	674	Tb927.4.5430	1104	Tb927.7.6090

245	Tb10.70.0070	675	Tb927.4.5460	1105	Tb927.3.5180
246	Tb10.70.0090	676	Tb927.4.5530	1106	Tb10.389.1290
247	Tb10.70.0300	677	Tb927.4.5560	1107	Tb10.61.2260
248	Tb10.70.0480	678	Tb927.4.5580	1108	Tb927.6.1530
249	Tb10.70.0520	679	Tb927.4.5700	1109	Tb10.70.4540
250	Tb10.70.0720	680	Tb927.4.5790	1110	Tb927.8.7490
251	Tb10.70.0790	681	Tb927.4.890	1111	Tb11.01.1730
252	Tb10.70.0800	682	Tb927.5.1000	1112	Tb10.6k15.2630
253	Tb10.70.0820	683	Tb927.5.1610	1113	Tb927.8.5580
254	Tb10.70.1100	684	Tb927.5.230	1114	Tb927.4.1270
255	Tb10.70.1170	685	Tb927.5.2760	1115	Tb927.5.2260
256	Tb10.70.1310	686	Tb927.5.2900	1116	Tb927.1.2210
257	Tb10.70.1380	687	Tb927.5.320	1117	Tb11.01.7740
258	Tb10.70.1440	688	Tb927.5.350	1118	Tb11.01.4030
259	Tb10.70.1540	689	Tb927.5.360	1119	Tb927.7.4520
260	Tb10.70.1560	690	Tb927.5.370	1120	Tb927.3.5060
261	Tb10.70.1690	691	Tb927.5.380	1121	Tb10.6k15.3460
262	Tb10.70.1880	692	Tb927.5.3860	1122	Tb10.6k15.0710
263	Tb10.70.2140	693	Tb927.5.390	1123	Tb927.5.1460
264	Tb10.70.2170	694	Tb927.5.400	1124	Tb927.5.3230
265	Tb10.70.2420	695	Tb927.5.4030	1125	Tb10.70.5030
266	Tb10.70.2440	696	Tb927.5.4170	1126	Tb10.6k15.0255
267	Tb10.70.2465	697	Tb927.5.4670	1127	Tb11.01.0620
268	Tb10.70.2470	698	Tb927.5.4690	1128	Tb11.18.0014
269	Tb10.70.2490	699	Tb927.5.4730	1129	Tb09.160.0860
270	Tb10.70.2520	700	Tb927.5.4810	1130	Tb11.02.2130
271	Tb10.70.2610	701	Tb927.5.4840	1131	Tb10.389.0150
272	Tb10.70.2680	702	Tb927.5.4950	1132	Tb11.02.2030
273	Tb10.70.2700	703	Tb927.5.5240	1133	Tb927.1.1540
274	Tb10.70.2720	704	Tb927.5.650	1134	Tb927.5.4310
275	Tb10.70.2800	705	Tb927.6.1460	1135	Tb11.01.1090
276	Tb10.70.3160	706	Tb927.6.190	1136	Tb10.61.2050
277	Tb10.70.3360	707	Tb927.6.220	1137	Tb927.7.1430
278	Tb10.70.3370	708	Tb927.6.2700	1138	Tb927.3.800
279	Tb10.70.3440	709	Tb927.6.2850	1139	Tb927.3.4490
280	Tb10.70.3480	710	Tb927.6.300	1140	Tb927.6.1430
281	Tb10.70.3510	711	Tb927.6.330	1141	Tb10.70.0830
282	Tb10.70.3600	712	Tb927.6.3490	1142	Tb927.3.1550
283	Tb10.70.3660	713	Tb927.6.3540	1143	Tb10.26.0880
284	Tb10.70.3950	714	Tb927.6.4340	1144	Tb927.3.2100
285	Tb10.70.4060	715	Tb927.6.450	1145	Tb10.389.0210

286	Tb10.70.4070	716	Tb927.6.460	1146	Tb927.5.1680
287	Tb10.70.4155	717	Tb927.6.480	1147	Tb10.6k15.1410
288	Tb10.70.4300	718	Tb927.6.490	1148	Tb11.02.2840
289	Tb10.70.4350	719	Tb927.6.4960	1149	Tb10.389.1340
290	Tb10.70.4400	720	Tb927.6.4980	1150	Tb927.3.3560
291	Tb10.70.4510	721	Tb927.6.510	1151	Tb11.55.0024
292	Tb10.70.4570	722	Tb927.6.520	1152	Tb11.01.7670
293	Tb10.70.4700	723	Tb927.6.5260	1153	Tb11.03.0810
294	Tb10.70.4750	724	Tb927.6.530	1154	Tb11.01.5820
295	Tb10.70.4880	725	Tb927.6.5370	1155	Tb09.160.3710
296	Tb10.70.5250	726	Tb927.6.5450	1156	Tb11.02.4540
297	Tb10.70.5260	727	Tb927.6.5550	1157	Tb11.22.0004
298	Tb10.70.5360	728	Tb927.6.5740	1158	Tb927.5.760
299	Tb10.70.5460	729	Tb927.6.640	1159	Tb10.70.3750
300	Tb10.70.5480	730	Tb927.7.100	1160	Tb09.211.1690
301	Tb10.70.5520	731	Tb927.7.1590	1161	Tb927.3.2220
302	Tb10.70.5840	732	Tb927.7.1730	1162	Tb927.6.4370
303	Tb10.70.6010	733	Tb927.7.1740	1163	Tb927.8.6460
304	Tb10.70.6300	734	Tb927.7.1750	1164	Tb10.05.0100
305	Tb10.70.6325	735	Tb927.7.1780	1165	Tb09.244.2830
306	Tb10.70.6360	736	Tb927.7.1920	1166	Tb927.2.3020
307	Tb10.70.6650	737	Tb927.7.230	1167	Tb927.5.1230
308	Tb10.70.6960	738	Tb927.7.240	1168	Tb09.211.3340
309	Tb10.70.7480	739	Tb927.7.2540	1169	Tb927.8.5040
310	Tb10.70.7570	740	Tb927.7.290	1170	Tb927.8.8280
311	Tb11.01.0420	741	Tb927.7.300	1171	Tb927.6.4120
312	Tb11.01.0625	742	Tb927.7.3120	1172	Tb11.v4.0005
313	Tb11.01.0700	743	Tb927.7.3260	1173	Tb927.2.2230
314	Tb11.01.0725	744	Tb927.7.3450	1174	Tb10.70.0510
315	Tb11.01.0730	745	Tb927.7.3490	1175	Tb927.5.2850
316	Tb11.01.0760	746	Tb927.7.4060	1176	Tb927.7.2170
317	Tb11.01.0920	747	Tb927.7.4070	1177	Tb10.70.1030
318	Tb11.01.1230	748	Tb927.7.4160	1178	Tb927.7.1670
319	Tb11.01.1280	749	Tb927.7.4170	1179	Tb11.01.5680
320	Tb11.01.1465	750	Tb927.7.4180	1180	Tb11.01.4920
321	Tb11.01.1470	751	Tb927.7.4670	1181	Tb09.160.3890
322	Tb11.01.1475	752	Tb927.7.4790	1182	Tb927.3.1290
323	Tb11.01.1480	753	Tb927.7.5000	1183	Tb10.70.5350
324	Tb11.01.1650	754	Tb927.7.5020	1184	Tb10.389.0680
325	Tb11.01.1750	755	Tb927.7.5230	1185	Tb11.02.1910
326	Tb11.01.1760	756	Tb927.7.6040	1186	Tb927.6.3140

327	Tb11.01.1770	757	Tb927.7.6050	1187	Tb10.6k15.3810
328	Tb11.01.1790	758	Tb927.7.6060	1188	Tb11.01.5780
329	Tb11.01.1920	759	Tb927.7.6070	1189	Tb927.4.4660
330	Tb11.01.2140	760	Tb927.7.6080	1190	Tb11.02.1720
331	Tb11.01.2190	761	Tb927.7.6500	1191	Tb09.211.0690
332	Tb11.01.2220	762	Tb927.7.6540	1192	Tb09.211.2700
333	Tb11.01.2420	763	Tb927.7.6960	1193	Tb10.70.1490
334	Tb11.01.2440	764	Tb927.7.7380	1194	Tb927.5.1900
335	Tb11.01.2510	765	Tb927.7.7520	1195	Tb927.8.1140
336	Tb11.01.2780	766	Tb927.7.7530	1196	Tb11.01.1300
337	Tb11.01.2820	767	Tb927.7.880	1197	Tb10.389.1760
338	Tb11.01.2886	768	Tb927.8.1020	1198	Tb11.02.4390
339	Tb11.01.3020	769	Tb927.8.1110	1199	Tb09.211.1910
340	Tb11.01.3260	770	Tb927.8.130	1200	Tb927.3.1030
341	Tb11.01.3350	771	Tb927.8.1330	1201	Tb11.01.6770
342	Tb11.01.3380	772	Tb927.8.1340	1202	Tb927.4.3320
343	Tb11.01.3420	773	Tb927.8.1610	1203	Tb927.3.5520
344	Tb11.01.3675	774	Tb927.8.1620	1204	Tb09.211.0410
345	Tb11.01.3676	775	Tb927.8.1630	1205	Tb11.01.8770
346	Tb11.01.3900	776	Tb927.8.1640	1206	Tb927.6.5030
347	Tb11.01.4070	777	Tb927.8.170	1207	Tb11.01.7120
348	Tb11.01.4520	778	Tb927.8.1810	1208	Tb10.6k15.0140
349	Tb11.01.4600	779	Tb927.8.1940	1209	Tb927.3.1920
350	Tb11.01.4660	780	Tb927.8.2050	1210	Tb927.8.4480
351	Tb11.01.4750	781	Tb927.8.2100	1211	Tb927.8.3020
352	Tb11.01.5300	782	Tb927.8.2200	1212	Tb927.7.6620
353	Tb11.01.5350	783	Tb927.8.2410	1213	Tb10.389.1360
354	Tb11.01.5450	784	Tb927.8.2480	1214	Tb11.47.0008
355	Tb11.01.5500	785	Tb927.8.2560	1215	Tb927.3.3440
356	Tb11.01.5510	786	Tb927.8.2610	1216	Tb927.8.670
357	Tb11.01.5535	787	Tb927.8.2640	1217	Tb927.6.3290
358	Tb11.01.5560	788	Tb927.8.2810	1218	Tb11.01.0720
359	Tb11.01.5570	789	Tb927.8.2910	1219	Tb927.7.7460
360	Tb11.01.5590	790	Tb927.8.2920	1220	Tb927.7.4220
361	Tb11.01.5600	791	Tb927.8.2930	1221	Tb927.5.3210
362	Tb11.01.5660	792	Tb927.8.2940	1222	Tb11.02.4460
363	Tb11.01.5720	793	Tb927.8.3310	1223	Tb927.7.7070
364	Tb11.01.5730	794	Tb927.8.3370	1224	Tb927.7.5340
365	Tb11.01.5790	795	Tb927.8.3620	1225	Tb927.3.5340
366	Tb11.01.5890	796	Tb927.8.3650	1226	Tb927.8.1270
367	Tb11.01.5900	797	Tb927.8.3750	1227	Tb927.7.1060

368	Tb11.01.5915	798	Tb927.8.3800	1228	Tb927.8.6240
369	Tb11.01.5940	799	Tb927.8.4010	1229	Tb927.3.4810
370	Tb11.01.6030	800	Tb927.8.4060	1230	Tb927.6.620
371	Tb11.01.6060	801	Tb927.8.4110	1231	Tb927.5.900
372	Tb11.01.6090	802	Tb927.8.4180	1232	Tb927.4.2180
373	Tb11.01.6210	803	Tb927.8.4280	1233	Tb927.3.3200
374	Tb11.01.6220	804	Tb927.8.4410	1234	Tb927.7.3170
375	Tb11.01.6230	805	Tb927.8.4430	1235	Tb10.26.0800
376	Tb11.01.6240	806	Tb927.8.460	1236	Tb927.5.3260
377	Tb11.01.6250	807	Tb927.8.4700	1237	Tb927.8.4500
378	Tb11.01.6530	808	Tb927.8.4710	1238	Tb11.01.1880
379	Tb11.01.6800	809	Tb927.8.4720	1239	Tb927.6.1190
380	Tb11.01.6870	810	Tb927.8.4730	1240	Tb927.7.6360
381	Tb11.01.6880	811	Tb927.8.4740	1241	Tb927.7.7050
382	Tb11.01.6930	812	Tb927.8.480	1242	Tb11.02.0340
383	Tb11.01.6980	813	Tb927.8.4890	1243	Tb11.01.8400
384	Tb11.01.7130	814	Tb927.8.5030	1244	Tb11.01.0870
385	Tb11.01.7170	815	Tb927.8.5090	1245	Tb927.7.1820
386	Tb11.01.7390	816	Tb927.8.5210	1246	Tb927.8.4220
387	Tb11.01.7500	817	Tb927.8.5260	1247	Tb11.01.0790
388	Tb11.01.7520	818	Tb927.8.5450	1248	Tb927.4.470
389	Tb11.01.7535	819	Tb927.8.5600	1249	Tb11.01.4280
390	Tb11.01.7545	820	Tb927.8.5630	1250	Tb11.01.4703
391	Tb11.01.7680	821	Tb927.8.570	1251	Tb927.8.2330
392	Tb11.01.7690	822	Tb927.8.5710	1252	Tb927.6.2940
393	Tb11.01.7825	823	Tb927.8.5740	1253	Tb10.61.0330
394	Tb11.01.7880	824	Tb927.8.5880	1254	Tb11.01.2020
395	Tb11.01.7950	825	Tb927.8.5970	1255	Tb927.3.4000
396	Tb11.01.7970	826	Tb927.8.5980	1256	Tb10.70.4840
397	Tb11.01.8085	827	Tb927.8.6030	1257	Tb927.4.1740
398	Tb11.01.8280	828	Tb927.8.6090	1258	Tb11.02.4950
399	Tb11.01.8320	829	Tb927.8.6150	1259	Tb927.6.1470
400	Tb11.01.8420	830	Tb927.8.6160	1260	Tb11.02.4650
401	Tb11.01.8460	831	Tb927.8.6180	1261	Tb927.5.1020
402	Tb11.01.8520	832	Tb927.8.6200	1262	Tb10.61.2440
403	Tb11.02.0330	833	Tb927.8.6210	1263	Tb09.211.3160
404	Tb11.02.0500	834	Tb927.8.6450	1264	Tb927.3.5420
405	Tb11.02.0530	835	Tb927.8.6510	1265	Tb927.3.2350
406	Tb11.02.0580	836	Tb927.8.6540	1266	Tb10.100.0150
407	Tb11.02.0730	837	Tb927.8.6680	1267	Tb927.4.2040
408	Tb11.02.0740	838	Tb927.8.6950	1268	Tb927.7.5760

409	Tb11.02.0815	839	Tb927.8.7120	1269	Tb11.01.0160
410	Tb11.02.0820	840	Tb927.8.7140	1270	Tb10.6k15.2350
411	Tb11.02.0870	841	Tb927.8.7150	1271	Tb927.5.1820
412	Tb11.02.1040	842	Tb927.8.730	1272	Tb09.211.2450
413	Tb11.02.1090	843	Tb927.8.7350	1273	Tb10.61.2370
414	Tb11.02.1105	844	Tb927.8.740	1274	Tb09.211.4360
415	Tb11.02.1106	845	Tb927.8.7450	1275	Tb11.01.6690
416	Tb11.02.1120	846	Tb927.8.750	1276	Tb09.160.3980
417	Tb11.02.1135	847	Tb927.8.7520	1277	Tb927.3.2470
418	Tb11.02.1280	848	Tb927.8.7570	1278	Tb927.5.2530
419	Tb11.02.1564	849	Tb927.8.7590	1279	Tb927.4.2240
420	Tb11.02.1600	850	Tb927.8.760	1280	Tb10.70.5060
421	Tb11.02.1680	851	Tb927.8.7600	1281	Tb11.03.0690
422	Tb11.02.1830	852	Tb927.8.7610	1282	Tb927.4.1890
423	Tb11.02.1840	853	Tb927.8.7620	1283	Tb927.6.1870
424	Tb11.02.2110	854	Tb927.8.7630	1284	Tb927.5.1270
425	Tb11.02.2240	855	Tb927.8.7640	1285	Tb11.01.1640
426	Tb11.02.2410	856	Tb927.8.7650	1286	Tb10.70.5010
427	Tb11.02.2430	857	Tb927.8.7670	1287	Tb09.211.3930
428	Tb11.02.2600	858	Tb927.8.7680	1288	Tb927.3.3710
429	Tb11.02.2640	859	Tb927.8.7700	1289	Tb927.6.5070
430	Tb11.02.2800	860	Tb927.8.7740	1290	Tb927.6.2210

Table S3. A list of initial features collected for distinguishing mitochondrial proteins from non-mitochondrial proteins in *T.brucei*. (The number in parentheses indicates the dimension of each property.)

Type of properties	Features (dimension)	Sources
Basic sequence attributes	Sequence length (1) Split amino acid composition (40) Di-peptide composition (400)	Locally calculated
Physicochemical properties	Secondary structural content (4) Radius of Gyration (1)	SSCP: http://coot.embl.de/SSCP Radius of Gyration: http://www.scfbio-iitd.res.in/software/proteomics/rg.jsp
	Composition, transition and distribution of: hydrophobicity (21) normalized Van der Waals volume (21) polarity (21) polarizability (21) charge (21) secondary structure (21) solvent accessibility (21)	PROFEAT: http://jing.cz3.nus.edu.sg/cgi-bin/prof/prof.cgi
	Unfoldability (1) Disordered regions (3) Global charge (1) Hydrophobicity (1)	FoldIndex: http://bioportal.weizmann.ac.il/fldbin/findex
Signal peptide and transmembrane topology	Signal peptide (3) Transmembrane domains (alpha-helix and beta-barrel) (3)	SignalP: http://www.cbs.dtu.dk/services/SignalP Phobius: http://phobius.cbr.su.se TMB-Hunt: http://bmbpcu36.leeds.ac.uk/~andy/betaBarrel/AACompPred//aaTMB_Hunt.cgi

Table S4. Features selected from initial feature list by feature selection program, and their discriminative power calculated with ANOVA based on the 597 mitochondrial proteins and 1290 non-mitochondrial proteins.

Rank	Feature Description	$\mu^+(\sigma^+)$	$\mu^-(\sigma^-)$	F	P-value
1	R% in 30NT residues	0.109(0.054)	0.068(0.055)	227.46	0.000
2	E% in 30NT residues	0.025(0.035)	0.059(0.051)	210.64	0.000
3	W% in remaining residues	0.016(0.013)	0.011(0.008)	128.32	0.000
4	Distribution of charge 3	7.914(7.390)	4.349(6.135)	120.61	0.000
5	Distribution of charge 6	28.967(8.164)	24.829(8.559)	98.21	0.000
6	D% in 30NT residues	0.023(0.030)	0.042(0.043)	96.56	0.000
7	Composition of Normalized vdw volumns 3	27.011(4.665)	24.741(5.055)	86.36	0.000
8	Dipeptide MR%	0.291(0.334)	0.167(0.238)	84.78	0.000
9	Signal peptide	0.136(0.179)	0.265(0.325)	81.09	0.000
10	Y% in remaining residues	0.033(0.016)	0.027(0.014)	73.06	0.000
11	Dipeptide RW%	0.145(0.242)	0.070(0.149)	69.35	1.110e-16
12	Dipeptide YR%	0.276(0.356)	0.165(0.246)	62.05	5.551e-15
13	Composition of solvent accessibility 3	26.025(3.246)	24.652(3.741)	59.64	1.843e-14
14	beta-barrel transmembrane (bbtm) score	-0.462(0.337)	-0.329(0.366)	57.21	6.073e-14
15	Distribution of Normalized vdw volumns 5	26.616(4.020)	25.110(4.113)	55.45	1.449e-13
16	Dipeptide PW%	0.090(0.190)	0.040(0.105)	53.36	4.087e-13
17	Dipeptide WW%	0.046(0.154)	0.011(0.050)	52.95	4.997e-13
18	log P BBTM/Non-BBTM protein ratio	-2.076(1.825)	-1.370(2.113)	49.6	2.632e-12
19	Distribution of hydrophobicity 2	1.352(1.027)	1.010(0.993)	47.31	8.208e-12
20	Distribution of charge 1	2.032(2.693)	3.230(3.973)	44.77	2.909e-11
21	Composition of Normalized vdw volumns 2	34.330(3.489)	35.693(4.537)	42.26	1.022e-10
22	Dipeptide KK%	0.317(0.441)	0.530(0.748)	41.55	1.456e-10
23	F% in 30NT residues	0.049(0.041)	0.036(0.040)	41.24	1.701e-10
24	Distribution of Normalized vdw volumns 1	1.328(1.015)	1.005(1.020)	41.22	1.719e-10
25	Transition of polarizability 3	21.963(3.851)	20.727(3.936)	40.83	2.088e-10
26	Distribution of charge 11	52.566(9.064)	49.566(9.680)	40.78	2.139e-10
27	Dipeptide WR%	0.149(0.259)	0.084(0.180)	39.92	3.290e-10
28	Transition of Normalized vdw volumns 1	26.171(3.815)	27.531(4.601)	39.59	3.881e-10
29	P% in remaining residues	0.050(0.018)	0.043(0.024)	38.82	5.719e-10
30	Transition of polarizability 1	25.733(3.921)	26.970(4.075)	38.47	6.828e-10
31	Distribution of charge 4	21.784(6.317)	23.879(7.294)	36.53	1.805e-09
32	Dipeptide ML%	0.321(0.375)	0.228(0.273)	36.45	1.884e-09
33	Transition of Normalized	19.480(3.146)	18.439(3.663)	35.97	2.390e-09

	vdw volumes 2				
34	Composition of polarizability 1	31.780(4.405)	33.165(4.819)	35.57	2.937e-09
35	Distribution of secondary structure 3	1.857(1.864)	1.386(1.467)	35.27	3.413e-09
36	Dipeptide YP%	0.168(0.268)	0.106(0.189)	34.03	6.381e-09
37	H% in remaining residues	0.026(0.012)	0.023(0.011)	33.33	9.087e-09
38	I% in remaining residues	0.040(0.014)	0.045(0.017)	33.31	9.163e-09
39	Number of predicted transmembrane segments	0.323(0.848)	1.021(2.909)	33.03	1.057e-08
40	W% in 30NT residues	0.013(0.022)	0.008(0.017)	32.01	1.767e-08
41	Dipeptide CK%	0.113(0.233)	0.064(0.141)	31.71	2.055e-08
42	Dipeptide RF%	0.302(0.323)	0.218(0.294)	31.08	2.839e-08
43	Dipeptide RH%	0.248(0.316)	0.173(0.252)	30.98	2.974e-08
44	C% in remaining residues	0.016(0.011)	0.020(0.013)	30.89	3.119e-08
45	Transition of polarity 2	23.137(3.667)	21.918(4.788)	30.47	3.867e-08
46	Dipeptide RY%	0.275(0.311)	0.196(0.278)	30.3	4.210e-08
47	Dipeptide RM%	0.206(0.283)	0.141(0.219)	30.2	4.418e-08
48	Distribution of hydrophobicity 5	23.237(3.637)	24.271(3.882)	30.11	4.623e-08
49	K% in 30NT residues	0.040(0.041)	0.054(0.058)	30.03	4.832e-08
50	Distribution of polarity 2	1.421(1.047)	1.108(1.205)	29.89	5.176e-08
51	Transition of polarity 3	20.096(3.050)	21.253(4.741)	29.82	5.369e-08
52	Dipeptide PL%	0.530(0.460)	0.417(0.397)	29.8	5.432e-08
53	Dipeptide EW%	0.116(0.217)	0.070(0.144)	29.39	6.679e-08
54	M% in remaining residues	0.026(0.012)	0.023(0.012)	29.06	7.900e-08
55	Dipeptide HR%	0.221(0.297)	0.153(0.233)	29.04	7.991e-08
56	Charge	0.026(0.026)	0.037(0.049)	28.67	9.609e-08
57	N% in remaining residues	0.036(0.012)	0.039(0.015)	28.48	1.062e-07
58	Dipeptide HV%	0.289(0.309)	0.385(0.396)	27.48	1.770e-07
59	Dipeptide FR%	0.283(0.363)	0.203(0.286)	26.93	2.337e-07
60	Dipeptide RR%	0.808(0.628)	0.617(0.798)	26.73	2.588e-07
61	Distribution of polarizability 4	25.859(3.426)	24.950(3.622)	26.61	2.757e-07
62	Dipeptide KT%	0.234(0.288)	0.327(0.396)	26.39	3.073e-07
63	Dipeptide WT%	0.083(0.194)	0.047(0.115)	26.13	3.523e-07
64	Dipeptide LP%	0.525(0.425)	0.424(0.391)	26.01	3.746e-07
65	Dipeptide CK%	0.065(0.149)	0.120(0.244)	25.97	3.809e-07
66	Dipeptide DD%	0.269(0.440)	0.426(0.693)	25.87	4.022e-07

The μ^+ , μ^- and σ^+ , σ^- are the means and standard deviations of each feature element in positive and negative datasets, respectively.

Table S5. Five-fold cross validation accuracy of various kinds of amino acid composition (AAC), based on 597 mitochondrial proteins and 1290 non-mitochondrial proteins.

	AAC in whole sequences	AAC in the first n N-terminal residues and in the remaining residues				
		$n = 15$	$n = 20$	$n = 25$	$n = 30$	$n = 35$
Accuracy (%)	78.4831	85.1746	85.2042	85.4532	85.5731	85.4625

Table S6. Frequency of signal peptide (SP), alpha-helical transmembrane domain (TM) and beta-barrel TM in mitochondrial proteins (mp) and non-mitochondrial proteins (non-mp) in *T.brucei*, yeast, mouse and human. Data in the table indicates the percentage of proteins with SP, alpha-helical TM or beta-barrel TM.

Organisms	SP (%)		Alpha-helical TM (%)		Beta-barrel TM (%)	
	mp	non-mp	mp	non-mp	mp	non-mp
<i>T.brucei</i>	6.87	21.01	20.10	21.55	9.38	18.06
Yeast	9.55	16.24	26.09	26.28	19.28	30.18
Mouse	9.89	27.17	22.76	27.63	14.18	14.42
Human	8.86	26.88	22.61	27.66	13.63	16.85

Table S7. Thirteen prediction programs used for comparison.

Program	URL
WoLF PSORT	http://wolfsort.org/
Predotar v1.03	http://urgi.versailles.inra.fr/predotar/predotar.html
MitoProt II	http://ihg2.helmholtz-muenchen.de/ihg/mitoprot.html
PredSL	http://hannibal.biol.uoa.gr/PredSL/input.html
PSORT II	http://psort.ims.u-tokyo.ac.jp/form2.html
TargetP v1.1	http://www.cbs.dtu.dk/services/TargetP/
MitPred	http://www.imtech.res.in/raghava/mitpred/submit.html
MITOPRED	http://bioapps.rit.albany.edu/MITOPRED/
iPSORT	http://hc.ims.u-tokyo.ac.jp/iPSORT/
Proteome Analyst	http://pasub.cs.ualberta.ca:8080/pa/Subcellular
ESLpred	http://www.imtech.res.in/raghava/eslpred/submit.html
PLOC	http://www.genome.jp/SIT/plocdir/
SubLoc v1.0	http://www.bioinfo.tsinghua.edu.cn/SubLoc/eu_predict.htm

Table S8. Reciprocal best blast list between T.brucei mitocarta proteins and human or yeast mitocarta proteins.

Gene ID	RBB pair partner ID
Tb09.160.2210	YPL059W
Tb09.160.3110	YLR163C
Tb09.160.4300	YBR003W
Tb09.160.4380	YLL041C
Tb09.160.4440	YGR029W
Tb09.160.5260	YBR026C
Tb09.211.0510	YBR024W
Tb09.211.1380	YAL044C
Tb09.211.1610	YNL169C
Tb09.211.1750	YER053C
Tb09.211.1880	YKR070W
Tb09.211.1960	YOL096C
Tb09.211.2580	YMR188C
Tb09.211.3030	YKR066C
Tb09.211.3200	YIL006W
Tb09.211.3420	YDR236C
Tb09.211.4700	YEL024W
Tb10.05.0150	YNR001C
Tb10.100.0070	YBR039W
Tb10.100.0160	YLR038C
Tb10.389.0890	YER178W
Tb10.61.0340	YPL224C
Tb10.61.0510	YLL018C-A
Tb10.61.1530	YOR196C
Tb10.61.1810	YBL030C
Tb10.6k15.0960	YMR145C
Tb10.6k15.3030	YPR024W
Tb10.6k15.3080	YNL071W
Tb10.6k15.3140	YOR241W
Tb10.6k15.3250	YGR244C
Tb10.70.0280	YLR259C
Tb10.70.2155	YPL271W
Tb10.70.2190	YLR069C
Tb10.70.2290	YPR011C
Tb10.70.2630	YMR150C
Tb10.70.2970	YDR529C
Tb10.70.4280	YHR037W
Tb10.70.4380	YPL132W
Tb10.70.4600	YLR289W
Tb10.70.5110	YKL085W
Tb10.70.5510	YDR376W
Tb10.70.7960	YPL005W
Tb11.01.0710	YJL102W
Tb11.01.1130	YNR041C
Tb11.01.1160	YLR239C
Tb11.01.1440	YDR019C

Tb11.01.1740	YIL125W
Tb11.01.2280	YML110C
Tb11.01.3550	YDR148C
Tb11.01.3780	YER141W
Tb11.01.4870	YJL143W
Tb11.01.5180	YDR204W
Tb11.01.7090	YER048W-A
Tb11.01.7110	YBL013W
Tb11.01.8470	YFL018C
Tb11.01.8700	YMR301C
Tb11.02.1520	YDR511W
Tb11.02.2280	YGR112W
Tb11.02.2960	YOR100C
Tb11.02.3130	YKL029C
Tb11.02.3530	YFL036W
Tb11.02.4020	YER154W
Tb11.02.5280	YIL155C
Tb11.02.5670	YPL013C
Tb11.03.0870	YOR130C
Tb11.03.0950	YGR207C
Tb11.47.0012	YDR513W
Tb927.1.1000	YIL042C
Tb927.1.2990	YLR067C
Tb927.2.2970	YDL198C
Tb927.2.3030	YDR258C
Tb927.2.4110	YHR024C
Tb927.2.4400	YKR042W
Tb927.2.4700	YKR065C
Tb927.2.4890	YNL185C
Tb927.2.5210	YKL055C
Tb927.3.1000	YDL120W
Tb927.3.1380	YJR121W
Tb927.3.1790	YBR221C
Tb927.3.2230	YOR142W
Tb927.3.2300	YNL310C
Tb927.3.2980	YJL133W
Tb927.3.4890	YOR125C
Tb927.3.860	YKL192C
Tb927.4.1810	YML009C
Tb927.4.2480	YML060W
Tb927.4.3300	YMR089C
Tb927.5.1030	YPR067W
Tb927.5.1310	YPL172C
Tb927.5.1520	YBR227C
Tb927.5.3980	YNL284C
Tb927.5.4080	YMR060C
Tb927.5.500	YOR266W
Tb927.6.2170	YOR232W

Tb927.6.2420	YIL070C
Tb927.6.2510	YOL071W
Tb927.6.4040	YMR193W
Tb927.6.4990	YDL004W
Tb927.7.1340	YOR020C
Tb927.7.1640	YMR023C
Tb927.7.1720	YKL040C
Tb927.7.1910	YMR189W
Tb927.7.3960	YBL038W
Tb927.7.4940	YNL221C
Tb927.7.5120	YOR201C
Tb927.7.5820	YGR255C
Tb927.7.890	YPL252C
Tb927.8.1030	YGL018C
Tb927.8.1240	YOR356W
Tb927.8.1860	YDR430C
Tb927.8.1890	YOR065W
Tb927.8.3560	YML061C
Tb927.8.3580	YDR375C
Tb927.8.3690	YDL066W
Tb927.8.4810	YGR132C
Tb927.8.5120	YEL039C
Tb927.8.5540	YLL027W
Tb927.8.6580	YKL148C
Tb09.160.2210	Q86SX6 GLRX5_HUMAN
Tb09.160.3110	O75439 MPPB_HUMAN
Tb09.160.4300	Q5T2R2-3 DPS1_HUMAN
Tb09.160.4310	P49448 DHE4_HUMAN
Tb09.160.4380	P21912 DHSB_HUMAN
Tb09.160.4910	O15229 KMO_HUMAN
Tb09.160.5240	Q9HD33-2 RM47_HUMAN
Tb09.160.5260	Q9BV79 MECR_HUMAN
Tb09.211.0330	Q96EY1 DNJA3_HUMAN
Tb09.211.1380	P23434 GCSH_HUMAN
Tb09.211.1750	Q00325-2 MPCP_HUMAN
Tb09.211.1960	Q9NZJ6 COQ3_HUMAN
Tb09.211.2580	Q9Y2R5 RT17_HUMAN
Tb09.211.4580	P54886 P5CS_HUMAN
Tb09.211.4700	P47985 UCRI_HUMAN
Tb09.244.2620	Q16795 NDUA9_HUMAN
Tb10.05.0150	O75390 CISY_HUMAN
Tb10.100.0070	P36542 ATPG_HUMAN
Tb10.389.0690	Q02978 M2OM_HUMAN
Tb10.389.1140	P28331 NDUS1_HUMAN
Tb10.61.0510	Q49B96 COX19_HUMAN
Tb10.61.1530	O43766 LIAS_HUMAN
Tb10.61.1790	P56556 NDUA6_HUMAN
Tb10.61.1810	Q9H0C2 ADT4_HUMAN

Tb10.61.2510	Q70HW3-2 SAMC_HUMAN
Tb10.61.3070	Q8N5M1 ATPF2_HUMAN
Tb10.6k15.0490	Q99797 MIPEP_HUMAN
Tb10.6k15.0960	Q9BRQ8-2 AIFM2_HUMAN
Tb10.6k15.3030	Q96TA2 YMEL1_HUMAN
Tb10.6k15.3080	P10515 ODP2_HUMAN
Tb10.6k15.3140	Q05932 FOLC_HUMAN
Tb10.6k15.3250	Q96I99 SUCB2_HUMAN
Tb10.70.0280	P10809 CH60_HUMAN
Tb10.70.2155	P56381 ATP5E_HUMAN
Tb10.70.2190	Q96RP9 EFGM_HUMAN
Tb10.70.2290	Q86VD7 S2542_HUMAN
Tb10.70.2630	Q96LU5 IMP1L_HUMAN
Tb10.70.2970	P14927 QCR7_HUMAN
Tb10.70.3280	Q13825 AUHM_HUMAN
Tb10.70.3850	Q9Y2Z2-5 MTO1_HUMAN
Tb10.70.4280	P30038 AL4A1_HUMAN
Tb10.70.4380	Q9Y6N1 COX11_HUMAN
Tb10.70.4980	Q9Y6N5 SQRD_HUMAN
Tb10.70.5110	P40926 MDHM_HUMAN
Tb10.70.5510	P22570 ADRO_HUMAN
Tb10.70.7550	P12694 ODBA_HUMAN
Tb10.v4.0043	P21953 ODBB_HUMAN
Tb11.01.0640	Q9P0J0 NDUAD_HUMAN
Tb11.01.0710	Q969S9 RRF2M_HUMAN
Tb11.01.1130	Q96H96-2 COQ2_HUMAN
Tb11.01.1320	Q8NE62 CHDH_HUMAN
Tb11.01.1440	P48728 GCST_HUMAN
Tb11.01.3550	P36957 ODO2_HUMAN
Tb11.01.3760	Q9Y3D2 MSRB2_HUMAN
Tb11.01.3780	Q7KZN9 COX15_HUMAN
Tb11.01.4870	Q9Y584 TIM22_HUMAN
Tb11.01.5180	Q9Y3A0 COQ4_HUMAN
Tb11.01.7110	Q96DP5 FMT_HUMAN
Tb11.01.7460	Q9Y6M9 NDUB9_HUMAN
Tb11.01.8200	Q6NVY1 HIBCH_HUMAN
Tb11.01.8470	P09622 DLDH_HUMAN
Tb11.01.8700	O75027 ABCB7_HUMAN
Tb11.02.0250	Q12931 TRAP1_HUMAN
Tb11.02.0290	P55809 SCOT1_HUMAN
Tb11.02.2280	Q15526 SURF1_HUMAN
Tb11.02.2740	P00505 AATM_HUMAN
Tb11.02.2960	Q9Y619 ORNT1_HUMAN
Tb11.02.3530	O00411 RPOM_HUMAN
Tb11.02.3810	Q9BYD3 RM04_HUMAN
Tb11.02.4020	Q8N8Q8 COX18_HUMAN
Tb11.02.4480	Q9HCC0 MCCB_HUMAN

Tb11.02.5280	P43304 GPDM_HUMAN
Tb11.02.5530	P13804 ETFA_HUMAN
Tb11.03.0260	Q16540 RM23_HUMAN
Tb11.03.0950	P38117 ETFB_HUMAN
Tb11.47.0009	Q8IXM3 RM41_HUMAN
Tb11.47.0012	Q9NS18-2 GLRX2_HUMAN
Tb11.47.0017	O75251 NDUS7_HUMAN
Tb11.55.0026	P26440 IVD_HUMAN
Tb927.1.1000	Q16654 PDK4_HUMAN
Tb927.2.4890	Q9Y3B7 RM11_HUMAN
Tb927.3.1000	Q16595 FRDA_HUMAN
Tb927.3.1380	P06576 ATPB_HUMAN
Tb927.3.1710	Q96A35 RM24_HUMAN
Tb927.3.1790	P11177-2 ODPB_HUMAN
Tb927.3.2230	P53597 SUCA_HUMAN
Tb927.3.2980	Q9NYZ2 MFRN1_HUMAN
Tb927.3.4890	Q99807 COQ7_HUMAN
Tb927.3.5610	P09001 RM03_HUMAN
Tb927.3.860	O14561 ACPM_HUMAN
Tb927.4.1070	Q9BYD1 RM13_HUMAN
Tb927.4.1660	Q6KCM7-6 SCMC2_HUMAN
Tb927.4.2480	O15527 OGG1_HUMAN
Tb927.4.2700	P35914 HMGCL_HUMAN
Tb927.4.3300	Q9Y4W6 AFG32_HUMAN
Tb927.4.4910	P42126 D3D2_HUMAN
Tb927.4.4980	P10109 ADX_HUMAN
Tb927.5.1310	Q12887 COX10_HUMAN
Tb927.5.1520	O76031 CLPX_HUMAN
Tb927.5.1550	Q9BSK2 S2533_HUMAN
Tb927.5.3410	Q9BYD2 RM09_HUMAN
Tb927.5.3980	Q9P015 RM15_HUMAN
Tb927.5.4330	P11182 ODB2_HUMAN
Tb927.5.450	P49821-2 NDUV1_HUMAN
Tb927.6.1250	P51398 RT29_HUMAN
Tb927.6.2170	Q9HAV7 GRPE1_HUMAN
Tb927.6.4990	P30049 ATPD_HUMAN
Tb927.7.1340	P61604 CH10_HUMAN
Tb927.7.1910	P23378 GCSP_HUMAN
Tb927.7.2200	Q9Y5J7 TIM9_HUMAN
Tb927.7.3470	Q07021 C1QBP_HUMAN
Tb927.7.3770	Q8NCW5 AIBP_HUMAN
Tb927.7.4710	Q9H2W6 RM46_HUMAN
Tb927.7.5820	Q9Y2Z9 COQ6_HUMAN
Tb927.7.6350	P19404 NDUV2_HUMAN
Tb927.8.1060	O95822 DCMC_HUMAN
Tb927.8.1240	Q16134 ETFD_HUMAN
Tb927.8.1860	Q5JRX3 PREP_HUMAN

Tb927.8.1890	P08574 CY1_HUMAN
Tb927.8.1990	P30048 PRDX3_HUMAN
Tb927.8.2540	P22307 NLTP_HUMAN
Tb927.8.3580	Q9Y276 BCS1_HUMAN
Tb927.8.3690	P48735 IDHP_HUMAN
Tb927.8.4810	P35232 PHB_HUMAN
Tb927.8.5120	P99999 CYC_HUMAN
Tb927.8.5540	Q9BUE6 ISCA1_HUMAN
Tb927.8.5810	Q8N8R3 MCATL_HUMAN
Tb927.8.6060	O75600 KBL_HUMAN
Tb927.8.6110	P54868 HMCS2_HUMAN
Tb927.8.6580	P31040 DHSA_HUMAN
Tb927.8.6970	Q96RQ3 MCCA_HUMAN

Table S9. Expression profile of the mitocarta from long slender (LS), short stumpy (SS) and procyclic (PC) trypanosomes.

Gene ID	LS	SS	PC	Description
Tb927.2.1860	159	164	98	hypothetical protein, conserved
Tb927.2.2210	16	17	30	hypothetical protein, conserved
Tb927.2.2220	4	9	3	hypothetical protein, conserved
Tb927.2.2400	48	29	3	hypothetical protein, conserved
Tb927.2.2470	8	7	34	RNA-editing complex protein; KREPA1
Tb927.2.2510	3	1	48	hypothetical protein, conserved
Tb927.2.2940	3	7	31	hypothetical protein, conserved
Tb927.2.2970	55	56	84	mitochondrial carrier protein, putative
Tb927.2.3030	13	14	92	ATP-dependent Clp protease subunit, heat shock protein 78 (HSP78), putative
Tb927.2.3180	0	0	0	hypothetical protein, conserved
Tb927.2.3330	43	11	1	hypothetical protein
Tb927.2.3420	32	41	12	hypothetical protein, conserved
Tb927.2.3610	106	93	209	hypothetical protein, conserved
Tb927.2.3800	1	1	9	hypothetical protein, conserved
Tb927.2.4110	4	5	3	mitochondrial processing peptidase alpha subunit, putative
Tb927.2.4130	23	25	23	enoyl-CoA hydratase/Enoyl-CoA isomerase/3-hydroxyacyl-CoA dehydrogenase, putative
Tb927.2.4380	38	16	26	hypothetical protein, conserved
Tb927.2.4400	50	90	26	hypothetical protein, conserved
Tb927.2.4590	18	14	56	branched-chain amino acid aminotransferase, putative
Tb927.2.4610	13	13	61	branched-chain amino acid aminotransferase, putative
Tb927.2.4700	9	13	12	hypothetical protein, conserved
Tb927.2.4740	1	1	9	ribosomal protein L11, putative
Tb927.2.4830	4	3	3	TFIIF-stimulated CTD phosphatase, putative
Tb927.2.4890	1	2	7	ribosomal protein L11, putative
Tb927.2.4990	3	2	5	hypothetical protein, conserved
Tb927.2.5020	43	29	32	hypothetical protein, conserved
Tb927.2.5140	15	9	12	hypothetical protein, conserved
Tb927.2.5180	26	21	45	aldo-keto reductase, putative
Tb927.2.5210	51	41	51	3-oxoacyl-(acyl-carrier protein) reductase, putative
Tb927.2.5720	0	0	0	hypothetical protein
Tb927.2.5900	13	8	7	hypothetical protein, conserved
Tb927.2.5930	4	6	5	hypothetical protein, conserved
Tb927.2.6070	116	150	79	hypothetical protein, conserved
Tb927.3.750	0	0	0	hypothetical protein, conserved
Tb927.3.770	2	2	6	hypothetical protein, conserved
Tb927.3.820	9	6	6	hypothetical protein, conserved
Tb927.3.860	491	432	377	acyl carrier protein, mitochondrial precursor, putative
Tb927.3.940	16	21	40	hypothetical protein, conserved
Tb927.3.950	209	210	20	hypothetical protein, conserved
Tb927.3.970	750	736	465	hypothetical protein, conserved
Tb927.3.1000	23	18	92	frataxin-like, mitochondrial precursor, putative
Tb927.3.1100	20	11	61	hypothetical protein, conserved
Tb927.3.1160	21	15	32	hypothetical protein, conserved
Tb927.3.1180	35	36	7	hypothetical protein, conserved

Tb927.3.1380	13	33	174	ATP synthase beta chain, mitochondrial precursor
Tb927.3.1410	94	80	65	cytochrome oxidase subunit VII
Tb927.3.1590	448	470	635	hypothetical protein, conserved
Tb927.3.1690	38	17	33	hypothetical protein, conserved
Tb927.3.1710	9	14	15	hypothetical protein, conserved
Tb927.3.1720	14	2	3	hypothetical protein, conserved
Tb927.3.1730	150	218	122	hypothetical protein, conserved
Tb927.3.1760	35	31	32	chaperone protein DNAJ, putative
Tb927.3.1790	10	21	15	pyruvate dehydrogenase E1 beta subunit, putative
Tb927.3.1810	19	17	54	hypothetical protein, conserved
Tb927.3.1820	1	1	1	hypothetical protein, conserved
Tb927.3.1890	84	113	552	hypothetical protein, conserved
Tb927.3.1940	61	130	145	hypothetical protein, conserved
Tb927.3.2010	28	22	28	hypothetical protein, conserved
Tb927.3.2080	98	36	176	hypothetical protein, conserved
Tb927.3.2130	26	17	19	hypothetical protein, conserved
Tb927.3.2180	78	46	252	hypothetical protein, conserved
Tb927.3.2230	33	22	110	succinyl-CoA synthetase alpha subunit, putative
Tb927.3.2260	36	31	29	hypothetical protein, conserved
Tb927.3.2300	20	17	15	hypothetical protein, conserved
Tb927.3.2370	265	411	254	hypothetical protein, conserved
Tb927.3.2390	4	11	143	hypothetical protein, conserved
Tb927.3.2630	6	4	13	hypothetical protein, conserved
Tb927.3.2670	18	19	77	hypothetical protein, conserved
Tb927.3.2860	17	18	19	hypothetical protein, conserved
Tb927.3.2880	325	673	1436	hypothetical protein, conserved
Tb927.3.2920	1	2	0	hypothetical protein, conserved
Tb927.3.2970	11	14	64	hypothetical protein, conserved
Tb927.3.2980	16	27	18	mitochondrial carrier protein, putative
Tb927.3.3050	7	3	1	hypothetical protein, conserved
Tb927.3.3330	83	92	345	heat shock protein 20, putative
Tb927.3.3620	66	62	39	hypothetical protein, conserved
Tb927.3.3660	64	94	32	hypothetical protein, conserved
Tb927.3.3680	3	1	0	hypothetical protein, conserved
Tb927.3.3890	28	63	101	hypothetical protein, conserved
Tb927.3.3990	0	0	1	RNA-editing complex protein; KREPB6
Tb927.3.4030	25	41	84	hypothetical protein, conserved
Tb927.3.4130	15	20	67	hypothetical protein, conserved
Tb927.3.4140	19	20	7	hypothetical protein, conserved
Tb927.3.4210	2	2	1	hypothetical protein, conserved
Tb927.3.4260	92	80	38	hypothetical protein, conserved
Tb927.3.4420	25	24	12	hypothetical protein, conserved
Tb927.3.4530	41	54	9	hypothetical protein, conserved
Tb927.3.4700	31	34	20	hypothetical protein, conserved
Tb927.3.4740	106	112	36	hypothetical protein, conserved
Tb927.3.4780	96	100	35	hypothetical protein, conserved
Tb927.3.4890	18	22	18	ubiquinone biosynthesis protein COQ7 homolog, putative
Tb927.3.4920	19	70	37	hypothetical protein, conserved

Tb927.3.4950	120	93	85	hypothetical protein, conserved
Tb927.3.5000	7	4	6	hypothetical protein, conserved
Tb927.3.5240	36	37	26	hypothetical protein, conserved
Tb927.3.5360	83	107	73	hypothetical protein, conserved
Tb927.3.5600	19	22	28	hypothetical protein, conserved
Tb927.3.5610	77	100	89	ribosomal protein L3 mitochondrial, putative
Tb927.3.5630	4	2	1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative
Tb927.4.330	8	11	18	hypothetical protein, conserved
Tb927.4.340	8	2	9	hypothetical protein, conserved
Tb927.4.440	53	95	47	hypothetical protein, conserved
Tb927.4.480	5	2	3	hypothetical protein, conserved
Tb927.4.600	67	124	50	hypothetical protein, conserved
Tb927.4.630	12	11	11	hypothetical protein, conserved
Tb927.4.650	12	14	7	chaperone protein DNAJ, putative
Tb927.4.700	2	4	5	hypothetical protein, conserved
Tb927.4.720	69	135	142	hypothetical protein, conserved
Tb927.4.830	16	21	219	hypothetical protein, conserved
Tb927.4.940	44	49	81	hypothetical protein, conserved
Tb927.4.950	17	23	32	hypothetical protein, conserved
Tb927.4.1070	17	14	30	50S ribosomal protein L13, putative
Tb927.4.1130	18	14	5	hypothetical protein, conserved
Tb927.4.1260	33	47	8	hypothetical protein, conserved
Tb927.4.1440	11	18	22	hypothetical protein, conserved
Tb927.4.1470	19	32	26	hypothetical protein, conserved
Tb927.4.1500	6	6	15	hypothetical protein, conserved
Tb927.4.1540	40	51	89	hypothetical protein, conserved
Tb927.4.1660	54	80	92	mitochondrial carrier protein, putative
Tb927.4.1750	6	3	17	hypothetical protein, conserved
Tb927.4.1760	12	17	15	hypothetical protein, conserved
Tb927.4.1810	47	50	87	hypothetical protein, conserved
Tb927.4.2150	13	6	10	hypothetical protein, conserved
Tb927.4.2250	1	3	8	hypothetical protein, conserved
Tb927.4.2260	28	15	38	centrin, putative
Tb927.4.2310	18	22	82	asparaginyl-tRNA synthetase, putative
Tb927.4.2360	55	89	55	hypothetical protein, conserved
Tb927.4.2440	51	80	31	hypothetical protein, conserved
Tb927.4.2480	8	9	12	8-oxoguanine DNA glycosylase, putative
Tb927.4.2550	42	49	85	hypothetical protein, conserved
Tb927.4.2560	0	2	0	cardiolipin synthetase, putative
Tb927.4.2580	28	42	15	hypothetical protein, conserved
Tb927.4.2700	0	0	0	hydroxymethylglutaryl-CoA lyase, putative; 3-hydroxy-3-methylglutarate-CoA lyase, putative
Tb927.4.2720	3	3	3	hypothetical protein, conserved
Tb927.4.2790	35	59	31	hypothetical protein, conserved
Tb927.4.2900	10	12	3	hypothetical protein, conserved
Tb927.4.2910	154	107	36	hypothetical protein, conserved
Tb927.4.2940	64	110	26	hypothetical protein, conserved
Tb927.4.3010	397	439	99	hypothetical protein, conserved
Tb927.4.3040	7	6	0	hypothetical protein, conserved

Tb927.4.3070	162	75	29	hypothetical protein, conserved
Tb927.4.3080	25	36	15	hypothetical protein, conserved
Tb927.4.3150	8	8	9	hypothetical protein, conserved
Tb927.4.3300	20	14	26	mitochondrial ATP-dependent zinc metallopeptidase, putative
Tb927.4.3390	25	15	22	tuzin, putative
Tb927.4.3450	210	277	167	hypothetical protein, conserved
Tb927.4.3660	20	15	44	hypothetical protein, conserved
Tb927.4.3680	35	37	126	protein phosphatase 2C, putative
Tb927.4.3690	10	8	29	hypothetical protein, conserved
Tb927.4.3960	56	51	17	hypothetical protein, conserved
Tb927.4.4140	3	1	6	hypothetical protein, conserved
Tb927.4.4150	2	3	5	hypothetical protein, conserved
Tb927.4.4160	35	2	56	hypothetical protein, conserved
Tb927.4.4300	131	163	44	hypothetical protein, conserved
Tb927.4.4600	6	1	3	hypothetical protein, conserved
Tb927.4.4610	70	47	20	hypothetical protein, conserved
Tb927.4.4620	24	18	395	cytochrome oxidase subunit VIII
Tb927.4.4680	0	0	0	hypothetical protein, conserved
Tb927.4.4910	373	350	330	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative
Tb927.4.4980	86	122	69	adrenodoxin precursor, putative
Tb04.24M18.150	0	0	0	hypothetical protein, conserved
Tb927.5.450	34	39	231	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.5.500	76	51	37	hypothetical protein, conserved
Tb927.5.510	10	22	51	hypothetical protein, conserved
Tb927.5.530	0	1	0	hypothetical protein, conserved
Tb927.5.560	8	9	25	hypothetical protein, conserved
Tb927.5.680	148	151	36	hypothetical protein, conserved
Tb927.5.740	21	22	37	hypothetical protein, conserved
Tb927.5.1030	11	15	16	hypothetical protein, conserved
Tb927.5.1060	19	25	136	mitochondrial processing peptidase, beta subunit, putative
Tb927.5.1130	298	293	144	hypothetical protein, conserved
Tb927.5.1240	95	100	173	hypothetical protein, conserved
Tb927.5.1310	33	49	29	protoheme IX farnesyltransferase, putative
Tb927.5.1510	79	79	80	hypothetical protein, conserved
Tb927.5.1520	15	29	32	heat shock protein HslVU, ATPase subunit HslU, putative
Tb927.5.1530	5	4	1	hypothetical protein, conserved
Tb927.5.1550	148	62	124	mitochondrial carrier protein, putative
Tb927.5.1710	13	6	34	ribonucleoprotein p18, mitochondrial precursor, putative
Tb927.5.1720	20	21	26	hypothetical protein, conserved
Tb927.5.1790	20	16	13	hypothetical protein, conserved
Tb927.5.1940	4	8	15	hypothetical protein, conserved
Tb927.5.2000	57	30	25	hypothetical protein
Tb927.5.2070	46	58	38	hypothetical protein, conserved
Tb927.5.2100	36	34	40	hypothetical protein, conserved
Tb927.5.2150	51	32	26	hypothetical protein, conserved
Tb927.5.2550	84	36	98	hypothetical protein, conserved
Tb927.5.2580	1	6	9	hypothetical protein, conserved
Tb927.5.2780	6	7	15	mitochondrial DNA polymerase beta

Tb927.5.2810	13	22	3	hypothetical protein, conserved
Tb927.5.2830	4	5	11	hypothetical protein, conserved
Tb927.5.2930	100	132	138	hypothetical protein, conserved
Tb927.5.3000	64	53	61	hypothetical protein, conserved
Tb927.5.3010	32	17	28	hypothetical protein, conserved
Tb927.5.3040	11	12	22	hypothetical protein, conserved
Tb927.5.3060	1	1	1	hypothetical protein, conserved
Tb927.5.3090	33	50	182	hypothetical protein, conserved
Tb927.5.3110	26	26	35	hypothetical protein, conserved
Tb927.5.3140	12	8	8	hypothetical protein, conserved
Tb927.5.3300	155	198	255	hypothetical protein, conserved
Tb927.5.3340	1	3	17	hypothetical protein, conserved
Tb927.5.3350	20	14	44	iron superoxide dismutase, putative
Tb927.5.3360	85	70	194	50S ribosomal protein L2, putative
Tb927.5.3410	0	0	0	hypothetical protein, conserved
Tb927.5.3420	33	34	52	hypothetical protein, conserved
Tb927.5.3440	49	46	26	hypothetical protein, conserved
Tb927.5.3640	22	21	55	hypothetical protein, conserved
Tb927.5.3690	185	145	179	hypothetical protein, conserved
Tb927.5.3770	68	47	24	hypothetical protein, conserved
Tb927.5.3870	7	17	23	hypothetical protein, conserved
Tb927.5.3910	4	6	13	hypothetical protein, conserved
Tb927.5.3980	9	14	8	hypothetical protein, conserved
Tb927.5.4040	8	10	24	hypothetical protein, conserved
Tb927.5.4070	26	13	15	hypothetical protein, conserved
Tb927.5.4080	93	94	76	hypothetical protein, conserved
Tb927.5.4120	2	4	11	hypothetical protein, conserved
Tb927.5.4130	17	9	21	hypothetical protein, conserved
Tb927.5.4330	6	7	34	dihydrolipoamide branched chain transacylase, putative
Tb927.6.590	4	4	85	hypothetical protein, conserved
Tb927.6.610	117	81	126	hypothetical protein, conserved
Tb927.6.680	8	4	4	hypothetical protein, conserved
Tb927.6.1200	73	46	46	hypothetical protein, conserved
Tb927.6.1250	37	41	53	hypothetical protein, conserved
Tb927.6.1410	126	255	43	hypothetical protein, conserved
Tb927.6.1440	48	53	116	hypothetical protein, conserved
Tb927.6.1510	19	32	61	lysyl-tRNA synthetase, putative
Tb927.6.1590	7	33	3	hypothetical protein, conserved
Tb927.6.1680	13	17	20	zinc finger protein, putative
Tb927.6.1710	24	31	51	hypothetical protein, conserved
Tb927.6.1840	100	106	65	hypothetical protein, conserved
Tb927.6.1860	44	47	39	hypothetical protein, conserved
Tb927.6.1890	7	3	1	hypothetical protein, conserved
Tb927.6.2010	613	747	303	hypothetical protein, conserved
Tb927.6.2070	91	117	94	hypothetical protein, conserved
Tb927.6.2080	26	18	62	hypothetical protein, conserved
Tb927.6.2140	23	16	31	hypothetical protein, conserved
Tb927.6.2160	26	21	28	hypothetical protein, conserved

Tb927.6.2170	65	80	215	co-chaperone GrpE, putative
Tb927.6.2180	127	142	38	hypothetical protein, conserved
Tb927.6.2230	60	56	108	hypothetical protein, conserved
Tb927.6.2290	21	25	14	hypothetical protein, conserved
Tb927.6.2350	20	16	12	hypothetical protein, conserved
Tb927.6.2380	1	4	7	hypothetical protein, conserved
Tb927.6.2420	1168	1232	674	p22 protein precursor
Tb927.6.2470	5	4	4	hypothetical protein, conserved
Tb927.6.2480	101	137	139	chaperone protein DNAJ, putative
Tb927.6.2490	20	4	40	hypothetical protein, conserved
Tb927.6.2510	4	0	2	hypothetical protein, conserved
Tb927.6.2540	26	8	5	DREV methyltransferase, putative
Tb927.6.2590	16	34	16	hypothetical protein, conserved
Tb927.6.2610	160	141	66	hypothetical protein, conserved
Tb927.6.2630	3	1	3	hypothetical protein, conserved
Tb927.6.2790	73	99	1032	L-threonine 3-dehydrogenase, putative
Tb927.6.3360	13	11	34	hypothetical protein, conserved
Tb927.6.3420	141	231	105	hypothetical protein, conserved
Tb927.6.3600	9	5	15	hypothetical protein, conserved
Tb927.6.3610	1	1	1	hypothetical protein, conserved
Tb927.6.3730	4	2	0	chaperone protein DNAJ, putative
Tb927.6.3740	3	2	17	heat shock 70 kDa protein, mitochondrial precursor, putative
Tb927.6.3850	3	3	1	chaperone protein DNAJ, putative
Tb927.6.3930	8	12	10	hypothetical protein, conserved
Tb927.6.4030	17	6	13	superoxide dismutase, putative
Tb927.6.4040	16	16	9	hypothetical protein, conserved
Tb927.6.4070	110	158	56	hypothetical protein, conserved
Tb927.6.4080	14	14	14	hypothetical protein, conserved
Tb927.6.4130	220	84	575	hypothetical protein, conserved
Tb927.6.4150	82	71	29	hypothetical protein, conserved
Tb927.6.4200	12	30	351	hypothetical protein, conserved
Tb927.6.4270	8	6	7	hypothetical protein, conserved
Tb927.6.4400	7	7	9	hypothetical protein, conserved
Tb927.6.4450	6	4	6	hypothetical protein, conserved
Tb927.6.4540	4	5	17	3-hydroxy-3-methylglutaryl-CoA reductase, putative
Tb927.6.4560	7	6	15	hypothetical protein, conserved
Tb927.6.4580	10	11	4	hypothetical protein, conserved
Tb927.6.4700	112	150	160	hypothetical protein, conserved
Tb927.6.4790	9	8	3	hypothetical protein, conserved
Tb927.6.4930	16	24	7	hypothetical protein, conserved
Tb927.6.4990	62	83	325	ATP synthase, epsilon chain, putative
Tb927.7.340	91	78	9	hypothetical protein, conserved
Tb927.7.560	21	18	28	hypothetical protein, conserved
Tb927.7.600	114	180	31	DNA ligase, putative
Tb927.7.610	8	1	19	DNA ligase, putative
Tb927.7.630	34	26	32	hypothetical protein, conserved
Tb927.7.640	240	444	78	hypothetical protein, conserved
Tb927.7.740	79	54	53	chaperone protein DNAJ, putative

Tb927.7.800	25	24	38	hypothetical protein, conserved
Tb927.7.840	215	160	515	hypothetical protein, conserved
Tb927.7.870	4	9	16	hypothetical protein, conserved
Tb927.7.890	16	41	43	electron transfer protein, putative
Tb927.7.910	31	26	50	hypothetical protein, conserved
Tb927.7.1000	47	29	9	hypothetical protein, conserved
Tb927.7.1010	131	60	338	hypothetical protein, conserved
Tb927.7.1070	3	9	32	RNA-editing complex protein; exonuclease; KREX1
Tb927.7.1080	39	37	20	hypothetical protein, conserved
Tb927.7.1250	4	0	9	hypothetical protein, conserved
Tb927.7.1270	58	71	24	hypothetical protein, conserved
Tb927.7.1340	119	98	68	10 kDa heat shock protein, putative
Tb927.7.1350	35	76	20	hypothetical protein, conserved
Tb927.7.1370	18	9	0	spliced leader RNA PSE-promoter transcription factor, putative
Tb927.7.1440	46	44	137	DNA polymerase sigma-like protein
Tb927.7.1490	82	82	47	hypothetical protein, conserved
Tb927.7.1550	14	21	32	RNA-editing complex protein; RNA-editing 3' terminal uridylyl transferase 2; KRET2
Tb927.7.1640	28	31	34	GTP-binding protein, putative
Tb927.7.1720	23	29	75	HIRA-interacting protein 5, putative
Tb927.7.1900	0	1	0	protein kinase, putative
Tb927.7.1910	18	43	21	glycine dehydrogenase, putative
Tb927.7.2090	7	4	0	hypothetical protein, conserved
Tb927.7.2200	81	112	409	hypothetical protein, conserved
Tb927.7.2210	29	55	63	hypothetical protein, conserved
Tb927.7.2220	13	4	9	hypothetical protein, conserved
Tb927.7.2280	26	12	13	hypothetical protein, conserved
Tb927.7.2390	40	42	49	hypothetical protein, conserved
Tb927.7.2410	53	46	81	hypothetical protein, conserved
Tb927.7.2490	27	13	31	hypothetical protein, conserved
Tb927.7.2560	12	19	10	hypothetical protein, conserved
Tb927.7.2570	15	26	20	hypothetical protein, conserved
Tb927.7.2620	6	6	2	hypothetical protein, conserved
Tb927.7.2690	151	251	122	hypothetical protein, conserved
Tb927.7.2700	21	9	79	NADH-cytochrome b5 reductase, putative
Tb927.7.2760	33	48	86	hypothetical protein, conserved
Tb927.7.2960	30	20	28	hypothetical protein, conserved
Tb927.7.2990	28	19	33	hypothetical protein, conserved
Tb927.7.3050	24	32	90	hypothetical protein, conserved
Tb927.7.3100	36	45	82	hypothetical protein, conserved
Tb927.7.3240	131	235	61	hypothetical protein, conserved
Tb927.7.3270	10	8	20	hypothetical protein, conserved
Tb927.7.3460	15	9	9	hypothetical protein, conserved
Tb927.7.3470	27	44	5	p22 protein precursor, putative
Tb927.7.3510	3	1	4	hypothetical protein, conserved
Tb927.7.3520	4	3	4	hypothetical protein, conserved
Tb927.7.3590	31	11	32	hypothetical protein, conserved
Tb927.7.3750	13	11	29	TFIIF-stimulated CTD phosphatase, putative
Tb927.7.3770	23	13	12	hypothetical protein, conserved

Tb927.7.3800	2	1	3	hypothetical protein, conserved
Tb927.7.3810	259	173	449	hypothetical protein, conserved
Tb927.7.3910	10	9	41	hypothetical protein, conserved
Tb927.7.3940	128	178	611	mitochondrial carrier protein, putative; ADP/ATP mitochondrial translocase, putative; adenine nucleotide mitochondrial translocator, putative
Tb927.7.3950	12	12	14	RNA-editing complex protein; RNA-editing 3' terminal uridylyl transferase 1; KRET1
Tb927.7.3960	51	54	61	50S ribosomal protein L16, putative
Tb927.7.3970	257	134	57	hypothetical protein, conserved
Tb927.7.3990	9	9	9	mitochondrial DNA polymerase I protein C
Tb927.7.4050	24	36	24	hypothetical protein, conserved
Tb927.7.4140	84	90	46	hypothetical protein, conserved
Tb927.7.4200	20	29	72	hypothetical protein, conserved
Tb927.7.4210	8	13	8	hypothetical protein, conserved
Tb927.7.4430	69	49	50	hypothetical protein, conserved
Tb927.7.4440	4	3	11	hypothetical protein, conserved
Tb927.7.4710	20	16	20	hypothetical protein, conserved
Tb927.7.4940	129	94	117	oligopeptidase B protein, putative; serine peptidase, clan SC, family S9A-like protein
Tb927.7.5110	8	11	17	hypothetical protein, conserved
Tb927.7.5120	34	17	22	hypothetical protein, conserved
Tb927.7.5130	80	72	84	hypothetical protein, conserved
Tb927.7.5260	31	50	31	hypothetical protein, conserved
Tb927.7.5280	48	26	56	hypothetical protein, conserved
Tb927.7.5440	43	51	94	hypothetical protein, conserved
Tb927.7.5510	15	11	0	hypothetical protein, conserved
Tb927.7.5550	71	119	29	hypothetical protein, conserved
Tb927.7.5720	13	13	29	hypothetical protein, conserved
Tb927.7.5820	12	11	63	monooxygenase, putative
Tb927.7.6100	66	22	3	hypothetical protein
Tb927.7.6200	7	3	9	chaperone protein DNAJ, putative
Tb927.7.6350	25	19	14	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.7.6410	92	119	92	hypothetical protein, conserved
Tb927.7.6660	1	1	1	chaperone protein DNAJ, putative
Tb927.7.6800	55	62	26	hypothetical protein, conserved
Tb927.7.6940	14	7	5	glutaminyl cyclase, putative
Tb927.7.6990	346	679	447	hypothetical protein, conserved
Tb927.7.7010	18	30	4	hypothetical protein, conserved
Tb927.7.7080	303	306	111	mitochondrial glycoprotein-like protein
Tb927.7.7090	3	2	9	hypothetical protein, conserved
Tb927.7.7230	28	13	10	nitroreductase, putative
Tb927.7.7330	13	14	25	hypothetical protein, conserved
Tb927.7.7360	0	0	0	cell division control protein 2 homolog 2
Tb927.7.7410	41	48	3	oxidoreductase, putative
Tb927.7.7420	24	59	135	ATP synthase alpha chain, mitochondrial precursor
Tb927.7.7440	11	6	25	hypothetical protein, conserved
Tb927.8.580	5	3	3	hypothetical protein, conserved
Tb927.8.620	229	228	86	RNA-editing complex protein MP42

Tb927.8.630	20	24	60	lipoate-protein ligase, putative
Tb927.8.680	20	27	20	RNA-editing complex protein
Tb927.8.1010	10	22	16	chaperone protein DNAJ, putative
Tb927.8.1030	120	109	46	chaperone protein DNAJ, putative
Tb927.8.1060	41	51	6	malonyl-CoA decarboxylase, mitochondrial precursor, putative
Tb927.8.1240	10	12	9	electron transfer flavoprotein-ubiquinone oxidoreductase, putative
Tb927.8.1420	19	8	17	acyl-CoA dehydrogenase, mitochondrial precursor, putative
Tb927.8.1430	2	2	7	hypothetical protein, conserved
Tb927.8.1440	18	18	24	maoC-like dehydratase, putative
Tb927.8.1490	114	104	52	hypothetical protein, conserved
Tb927.8.1700	277	165	44	hypothetical protein, conserved
Tb927.8.1740	42	51	56	hypothetical protein, conserved
Tb927.8.1770	10	30	20	hypothetical protein, conserved
Tb927.8.1850	5	4	20	hypothetical protein, conserved
Tb927.8.1860	15	17	36	pitrilysin-like metalloprotease
Tb927.8.1880	111	118	84	hypothetical protein, conserved
Tb927.8.1890	78	46	338	cytochrome c1, heme protein, mitochondrial precursor
Tb927.8.1990	89	53	47	tryparedoxin peroxidase
Tb927.8.2110	44	18	61	hypothetical protein, conserved
Tb927.8.2170	25	12	21	hypothetical protein, conserved
Tb927.8.2180	17	16	4	hypothetical protein, conserved
Tb927.8.2190	21	10	29	hypothetical protein, conserved
Tb927.8.2240	4	6	1	tryptophanyl-tRNA synthetase, putative
Tb927.8.2300	12	15	9	hypothetical protein, conserved
Tb927.8.2340	7	2	3	hypothetical protein, conserved
Tb927.8.2470	34	55	50	hypothetical protein, conserved
Tb927.8.2530	39	56	136	hypothetical protein, conserved
Tb927.8.2540	11	2	62	3-ketoacyl-CoA thiolase, putative
Tb927.8.2650	15	19	26	hypothetical protein, conserved
Tb927.8.2670	23	21	44	hypothetical protein, conserved
Tb927.8.2700	265	249	50	hypothetical protein, conserved
Tb927.8.2740	50	71	263	mitochondrial RNA binding protein
Tb927.8.2750	231	250	68	hypothetical protein, conserved
Tb927.8.2760	10	14	3	hypothetical protein, conserved
Tb927.8.2880	8	17	28	hypothetical protein, conserved
Tb927.8.2970	109	25	59	hypothetical protein, conserved
Tb927.8.2990	5	10	9	hypothetical protein, conserved
Tb927.8.3040	229	188	65	hypothetical protein, conserved
Tb927.8.3070	20	16	61	hypothetical protein, conserved
Tb927.8.3090	2	1	3	hypothetical protein, conserved
Tb927.8.3110	101	49	183	hypothetical protein, conserved
Tb927.8.3130	6	9	4	S-adenosyl-methyltransferase mraW-like protein, putative
Tb927.8.3160	24	8	23	hypothetical protein, conserved
Tb927.8.3170	183	206	76	hypothetical protein, conserved
Tb927.8.3230	4	11	20	hypothetical protein, conserved
Tb927.8.3300	67	156	10	hypothetical protein, conserved
Tb927.8.3320	77	130	24	hypothetical protein, conserved
Tb927.8.3330	55	122	27	mitochondrial carrier protein, putative

Tb927.8.3560	41	29	117	DNA repair and recombination helicase protein PIF1, putative
Tb927.8.3580	9	10	13	ATP-dependent chaperone, putative
Tb927.8.3690	8	12	48	isocitrate dehydrogenase [NADP], mitochondrial precursor, putative
Tb927.8.3740	19	6	9	hypothetical protein, conserved
Tb927.8.3810	48	54	39	hypothetical protein, conserved
Tb927.8.3830	9	6	15	ATP-dependent DEAD/H RNA helicase, putative
Tb927.8.3960	1	2	6	hypothetical protein, conserved
Tb927.8.4000	119	125	69	hypothetical protein, conserved
Tb927.8.4040	4	4	1	endonuclease G, putative
Tb927.8.4150	4	8	17	hypothetical protein, conserved
Tb927.8.4240	2	5	14	hypothetical protein, conserved
Tb927.8.4250	45	56	21	hypothetical protein, conserved
Tb927.8.4380	166	113	277	hypothetical protein, conserved
Tb927.8.4440	12	13	3	mitochondrial carrier protein, putative
Tb927.8.4470	31	39	16	chaperone protein DNAJ, putative
Tb927.8.4550	52	78	72	hypothetical protein, conserved
Tb927.8.4810	40	34	45	prohibitin
Tb927.8.4860	78	65	141	hypothetical protein, conserved
Tb927.8.4920	390	302	232	hypothetical protein, conserved
Tb927.8.4930	210	216	44	hypothetical protein, conserved
Tb927.8.4960	28	48	64	hypothetical protein, conserved
Tb927.8.5100	80	57	43	hypothetical protein, conserved
Tb927.8.5120	1	2	1	cytochrome c
Tb927.8.5130	4	4	2	hypothetical protein, conserved
Tb927.8.5200	282	311	172	hypothetical protein, conserved
Tb927.8.5220	3	5	4	hypothetical protein, conserved
Tb927.8.5280	109	97	51	hypothetical protein, conserved
Tb927.8.5420	34	39	34	hypothetical protein, conserved
Tb927.8.5480	227	236	130	hypothetical protein, conserved
Tb927.8.5540	55	25	32	hypothetical protein, conserved
Tb927.8.5560	74	51	24	hypothetical protein, conserved
Tb927.8.5640	9	13	27	hypothetical protein, conserved
Tb927.8.5660	9	6	15	hypothetical protein, conserved
Tb927.8.5690	64	12	32	hypothetical protein, conserved
Tb927.8.5790	0	0	0	hypothetical protein
Tb927.8.5810	30	31	8	mitochondrial carrier protein, putative
Tb927.8.5860	60	38	67	50S ribosomal protein L17, putative
Tb927.8.6040	8428	11155	9191	hypothetical protein, conserved
Tb927.8.6060	47	96	434	2-amino-3-ketobutyrate coenzyme A ligase, putative
Tb927.8.6080	17	21	103	hypothetical protein, conserved
Tb927.8.6110	14	14	38	hypothetical protein, conserved
Tb927.8.6400	12	9	19	hypothetical protein, conserved
Tb927.8.6410	88	191	112	short-chain dehydrogenase, putative
Tb927.8.6560	460	621	96	hypothetical protein, conserved
Tb927.8.6580	120	279	297	succinate dehydrogenase flavoprotein, putative
Tb927.8.6620	352	245	59	hypothetical protein, conserved
Tb927.8.6640	47	54	49	hypothetical protein, conserved
Tb927.8.6800	64	57	126	hypothetical protein, conserved

Tb927.8.6820	23	10	42	hypothetical protein, conserved
Tb927.8.6890	0	0	0	hypothetical protein, conserved
Tb927.8.6960	26	24	19	hypothetical protein, conserved
Tb927.8.6970	35	17	21	3-methylcrotonyl-CoA carboxylase alpha subunit, putative
Tb927.8.7040	30	14	22	hypothetical protein, conserved
Tb927.8.7170	1	4	16	inositol polyphosphate 1-phosphatase, putative
Tb927.8.7260	216	340	122	kinetoplast-associated protein, putative
Tb927.8.7290	4	7	20	hypothetical protein, conserved
Tb927.8.7380	45	9	50	dihydrolipoamide dehydrogenase, point mutation
Tb927.8.7530	120	172	287	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative
Tb927.8.7770	120	101	32	hypothetical protein, conserved
Tb927.8.8170	261	329	108	hypothetical protein, conserved
Tb927.8.8180	6	4	4	hypothetical protein, conserved
Tb927.8.8190	9	1	9	hypothetical protein, conserved
Tb927.8.8360	17	14	56	receptor-type adenylate cyclase GRESAG 4, putative
Tb09.160.0360	15	14	91	hypothetical protein, conserved
Tb09.160.0370	7	9	33	hypothetical protein, conserved
Tb09.160.0410	177	215	61	hypothetical protein, conserved
Tb09.160.0470	7	2	3	hypothetical protein, conserved
Tb09.160.0540	6	3	3	hypothetical protein, conserved
Tb09.160.0550	15	37	55	hypothetical protein, conserved
Tb09.160.0760	8	7	10	hypothetical protein, conserved
Tb09.160.0890	132	139	31	hypothetical protein, conserved
Tb09.160.1020	42	33	35	hypothetical protein, conserved
Tb09.160.1280	14	12	12	hypothetical protein, conserved
Tb09.160.1370	1	2	1	hypothetical protein, conserved
Tb09.160.1760	46	34	59	hypothetical protein, conserved
Tb09.160.1820	6	4	213	cytochrome oxidase subunit V
Tb09.160.2000	3	2	10	pseudouridylate synthase, putative
Tb09.160.2060	3	1	9	hypothetical protein, conserved
Tb09.160.2100	6	9	9	low molecular weight protein tyrosine phosphatase, putative
Tb09.160.2160	30	39	67	hypothetical protein, conserved
Tb09.160.2210	137	240	127	glutaredoxin-like protein
Tb09.160.2220	73	51	32	hypothetical protein, conserved
Tb09.160.2250	58	84	50	hypothetical protein, conserved
Tb09.160.2280	198	125	57	hypothetical protein, conserved
Tb09.160.2380	142	143	94	hypothetical protein, conserved
Tb09.160.2970	18	35	21	mitochondrial RNA editing ligase 1; RNA-editing complex protein; RNA editing ligase; KREL1
Tb09.160.3050	36	41	25	hypothetical protein, conserved
Tb09.160.3110	37	40	39	mitochondrial processing peptide beta subunit, putative; metallo-peptidase, Clan ME, Family M16
Tb09.160.3370	26	30	20	hypothetical protein, conserved
Tb09.160.3800	372	240	217	hypothetical protein, conserved
Tb09.160.3880	0	0	0	hypothetical protein, conserved
Tb09.160.4090	236	209	109	DNA topoisomerase II
Tb09.160.4130	12	18	60	RNA-editing complex protein; KREPB7
Tb09.160.4150	369	389	923	hypothetical protein, conserved
Tb09.160.4300	25	47	134	farnesyl pyrophosphate synthetase, putative

Tb09.160.4310	101	67	75	glutamate dehydrogenase
Tb09.160.4380	24	7	180	succinate dehydrogenase, putative
Tb09.160.4440	28	18	41	hypothetical protein, conserved
Tb09.160.4460	76	126	72	TFIIF-stimulated CTD phosphatase, putative
Tb09.160.4480	72	117	71	TFIIF-stimulated CTD phosphatase, putative
Tb09.160.4660	175	174	67	hypothetical protein, conserved
Tb09.160.4670	30	26	11	hypothetical protein, conserved
Tb09.160.4750	20	34	32	hypothetical protein, conserved
Tb09.160.4840	150	159	43	hypothetical protein, conserved
Tb09.160.4900	2	7	2	hypothetical protein, unlikely
Tb09.160.4910	91	75	26	flavoprotein monooxygenase, putative
Tb09.160.5000	0	0	0	hypothetical protein, unlikely
Tb09.160.5050	38	36	16	hypothetical protein, conserved
Tb09.v1.0280	0	0	0	hypothetical protein, unlikely
Tb09.160.5110	33	16	45	hypothetical protein, conserved
Tb09.160.5240	54	72	25	hypothetical protein, conserved
Tb09.160.5260	15	14	52	oxidoreductase, putative
Tb09.160.5270	25	16	21	hypothetical protein, conserved
Tb09.160.5280	11	11	9	mitochondrial exoribonuclease DSS; exoribonuclease DSS (EMBL:AY233297)
Tb09.160.5320	44	32	33	hypothetical protein, conserved
Tb09.v1.0420	10	14	38	hypothetical protein, conserved
Tb09.211.0040	28	44	61	hypothetical protein, conserved
Tb09.211.0070	71	110	4	hypothetical protein, conserved
Tb09.211.0190	9	11	13	metalloprotease-like protein; peptide deformylase, putative
Tb09.211.0220	29	14	129	rhomboid-like protein; serine peptidase, Clan S- , family S54, putative
Tb09.211.0230	52	33	11	hypothetical protein, conserved
Tb09.211.0330	34	30	85	chaperone protein DNAJ, putative
Tb09.211.0510	2	4	12	cytochrome c oxidase assembly factor, putative
Tb09.211.0530	35	32	108	hypothetical protein, conserved
Tb09.211.0760	9	7	10	hypothetical protein, conserved
Tb09.211.0950	63	67	50	hypothetical protein, conserved
Tb09.211.1240	103	228	157	hypothetical protein, conserved
Tb09.211.1280	250	189	65	hypothetical protein, conserved
Tb09.211.1320	13	10	10	AMP deaminase, putative
Tb09.211.1380	118	26	64	glycine cleavage system H protein, putative
Tb09.211.1600	12	11	21	hypothetical protein, conserved
Tb09.211.1610	10	12	3	phosphatidylserine decarboxylase, putative
Tb09.211.1750	217	279	950	mitochondrial carrier protein, putative; mitochondrial phosphate transporter, putative
Tb09.211.1880	24	6	8	hypothetical protein, conserved
Tb09.211.1900	50	56	337	hypothetical protein, conserved
Tb09.211.1940	2	5	10	hypothetical protein, conserved
Tb09.211.1960	11	7	17	3-demethylubiquinone-9 3-methyltransferase, putative
Tb09.211.2370	31	20	45	mitochondrial carrier protein, putative
Tb09.211.2430	80	48	45	hypothetical protein, conserved
Tb09.211.2530	10	7	28	hypothetical protein, conserved
Tb09.211.2580	95	102	65	30S Ribosomal protein S17, putative

Tb09.211.2600	64	44	56	hypothetical protein, conserved
Tb09.211.2620	15	9	44	hypothetical protein, conserved
Tb09.211.2670	272	347	88	hypothetical protein, conserved
Tb09.211.2780	19	14	6	hypothetical protein, conserved
Tb09.211.3000	10	12	90	hypothetical protein, conserved
Tb09.211.3030	14	13	5	hypothetical protein, conserved
Tb09.211.3050	4	6	1	hypothetical protein, conserved
Tb09.211.3080	15	6	11	hypothetical protein, conserved
Tb09.211.3170	10	11	3	hypothetical protein, conserved
Tb09.211.3200	10	35	52	mitochondrial carrier protein, putative
Tb09.211.3230	8	6	84	hypothetical protein, conserved
Tb09.211.3420	300	343	886	riboflavin kinase, putative
Tb09.211.3470	13	16	11	hypothetical protein, conserved
Tb09.211.3500	67	57	18	hypothetical protein, conserved
Tb09.211.3530	1	1	4	hypothetical protein, conserved
Tb09.211.3630	3	11	33	hypothetical protein, conserved
Tb09.211.3680	8	13	15	chaperone protein DNAJ, putative
Tb09.211.3720	1	0	0	hypothetical protein, conserved
Tb09.211.3800	26	36	10	hypothetical protein, conserved
Tb09.211.3900	61	85	26	hypothetical protein, conserved
Tb09.211.4370	3	14	8	hypothetical protein, conserved
Tb09.211.4380	7	6	1	hypothetical protein, conserved
Tb09.211.4400	4	4	1	hypothetical protein, conserved
Tb09.211.4510	17	22	4	hypothetical protein, conserved
Tb09.211.4511	2	1	4	kinetoplastid membrane protein KMP1
Tb09.211.4512	297	171	1102	kinetoplastid membrane protein KMP1
Tb09.211.4513	274	170	1059	kinetoplastid membrane protein KMP1
Tb09.211.4580	6	8	11	hypothetical protein, conserved
Tb09.211.4700	12	7	9	reiske iron-sulfur protein , mitochondrial precursor
Tb09.211.4740	0	0	0	hypothetical protein, conserved
Tb09.211.4880	6	12	10	cyclophilin-like protein, putative
Tb09.244.2860	2472	4587	1475	hypothetical protein, conserved
Tb09.244.2840	89	72	49	hypothetical protein, conserved
Tb09.244.2670	13	6	4	hypothetical protein, conserved
Tb09.244.2640	16	15	2	hypothetical protein, conserved
Tb09.244.2620	3	3	11	NADH-ubiquinone oxidoreductase complex I subunit, putative
Tb09.v4.0018	8	1	3	expression site-associated gene (ESAG) protein, putative; expression site-associated gene 3 (ESAG3) protein, putative
Tb10.100.0070	76	100	167	ATP synthase F1 subunit gamma protein, putative
Tb10.100.0160	44	36	362	cytochrome oxidase subunit VI
Tb10.100.0220	14	12	9	mitochondrial structure specific endonuclease I (SSE), putative
Tb10.70.7960	4	4	9	hypothetical protein, conserved
Tb10.70.7900	0	2	7	hypothetical protein, conserved
Tb10.70.7840	37	41	199	choline dehydrogenase, putative
Tb10.70.7760	249	239	500	hypothetical protein, conserved
Tb10.70.7650	26	30	19	hypothetical protein, conserved
Tb10.70.7640	3	4	3	hypothetical protein, conserved
Tb10.70.7550	14	14	71	2-oxoisovalerate dehydrogenase alpha subunit, putative
Tb10.70.7540	19	42	15	hypothetical protein, conserved

Tb10.70.7530	2	5	0	hypothetical protein, conserved
Tb10.70.7500	11	3	0	hypothetical protein, conserved
Tb10.70.7450	20	12	69	hypothetical protein, conserved
Tb10.70.7440	2	0	3	hypothetical protein, conserved
Tb10.70.7250	7	8	32	hypothetical protein, conserved
Tb10.70.6930	159	124	338	hypothetical protein, conserved
Tb10.70.6820	57	98	102	hypothetical protein, conserved
Tb10.70.6800	163	223	106	aspartyl-tRNA synthetase, putative
Tb10.70.6690	125	140	17	hypothetical protein, conserved
Tb10.70.6640	28	20	21	hypothetical protein, conserved
Tb10.70.6350	33	51	39	hypothetical protein, conserved
Tb10.70.6340	4	9	100	ATPase subunit 9, putative
Tb10.70.6260	4	3	4	hypothetical protein, conserved
Tb10.70.6150	80	85	48	hypothetical protein, conserved
Tb10.70.5970	180	160	41	hypothetical protein, conserved
Tb10.70.5960	58	34	50	hypothetical protein, conserved
Tb10.70.5900	29	27	27	hypothetical protein, conserved
Tb10.70.5880	29	14	31	hypothetical protein, conserved; leucine-rich repeat protein (LRRP), putative
Tb10.70.5830	15	12	16	actin-like protein, putative
Tb10.70.5780	1	2	3	hypothetical protein, conserved
Tb10.70.5720	25	16	94	hypothetical protein, conserved
Tb10.70.5510	1	1	3	adrenodoxin reductase, putative; ferredoxin NADP ⁺ reductase-like protein
Tb10.70.5430	8	6	3	hypothetical protein, conserved
Tb10.70.5380	164	100	52	pyruvate dehydrogenase complex E3 binding protein, putative
Tb10.70.5130	207	94	44	adenylate kinase, putative
Tb10.70.5120	68	54	79	malate dehydrogenase, putative
Tb10.70.5110	170	74	493	mitochondrial malate dehydrogenase
Tb10.70.5080	28	23	10	hypothetical protein, conserved
Tb10.70.4980	47	59	100	hypothetical protein, conserved
Tb10.70.4850	6	5	2	hypothetical protein, conserved
Tb10.70.4600	50	59	4	GTP-binding protein, putative; elongation factor, putative
Tb10.70.4500	13	16	21	hypothetical protein, conserved
Tb10.70.4380	4	6	12	cytochrome C oxidase assembly protein, putative
Tb10.70.4280	46	19	30	delta-pyrroline-5-carboxylate dehydrogenase, putative
Tb10.70.4220	157	143	224	hypothetical protein, conserved
Tb10.70.4120	4	14	3	hypothetical protein, conserved
Tb10.70.3850	0	0	1	RNA-editing complex protein; RNA editing 3' exouridylylase; KREX2
Tb10.70.3840	181	142	45	hypothetical protein, conserved
Tb10.70.3820	18	34	4	hypothetical protein, conserved
Tb10.70.3790	1	3	2	hypothetical protein, conserved
Tb10.70.3680	18	16	32	rRNA dimethyltransferase, putative
Tb10.70.3590	21	58	130	hypothetical protein, conserved; predicted TPR repeat protein
Tb10.70.3280	164	119	217	methylglutaconyl-CoA hydratase, mitochondrial precursor, putative
Tb10.70.3260	0	0	0	hypothetical protein, conserved
Tb10.70.3190	270	288	306	hypothetical protein, conserved
Tb10.70.3150	9	15	98	NADH-ubiquinone oxidoreductase complex I subunit, putative

Tb10.70.3010	4	11	71	hypothetical protein, conserved
Tb10.70.2970	687	712	1485	hypothetical protein, conserved
Tb10.70.2900	21	15	8	2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor, putative
Tb10.70.2670	12	7	23	hypothetical protein, conserved
Tb10.70.2630	61	80	43	mitochondrial inner membrane signal peptidase, putative; serine peptidase clan SF, family S26B, putative
Tb10.70.2350	87	63	58	hypothetical protein, conserved
Tb10.70.2320	34	7	103	hypothetical protein, conserved
Tb10.70.2290	114	136	27	mitochondrial carrier protein, putative
Tb10.70.2210	19	11	65	cell division related protein kinase 2, putative; CDC2-related protein kinase
Tb10.70.2190	15	15	56	Mitochondrial elongation factor G, putative
Tb10.70.2155	30	58	662	hypothetical protein, conserved
Tb10.70.2150	57	51	24	hypothetical protein, conserved
Tb10.70.2100	207	144	140	RNA-editing complex protein; RNA-binding protein; KREPA4
Tb10.70.2090	6	15	26	RNA-editing complex protein; KREPA6
Tb10.70.1890	9	21	17	hypothetical protein, conserved
Tb10.70.1750	7	8	10	RNA editing endoribonuclease
Tb10.70.1640	41	32	50	hypothetical protein, conserved
Tb10.70.1580	1	7	20	RNA editing endoribonuclease
Tb10.70.1520	13	24	73	hypothetical protein, conserved
Tb10.70.1460	40	40	38	hypothetical protein, conserved
Tb10.70.1430	69	59	21	hypothetical protein, conserved
Tb10.70.1410	13	11	9	protein phosphatase 2C, putative
Tb10.70.1330	5	9	16	heat shock protein, putative
Tb10.70.1120	21	39	123	hypothetical protein, conserved; predicted RanGDP binding protein
Tb10.70.1000	422	571	228	hypothetical protein, conserved
Tb10.70.0850	39	42	70	proteasome alpha 1 subunit, putative; 20S proteasome subunit alpha-6, putative
Tb10.70.0660	30	39	15	hypothetical protein, conserved
Tb10.70.0625	12	18	67	hypothetical protein, conserved
Tb10.70.0530	24	14	32	hypothetical protein, conserved
Tb10.70.0430	105	87	95	chaperonin Hsp60, mitochondrial precursor
Tb10.70.0380	14	7	3	hypothetical protein
Tb10.70.0280	235	106	322	chaperonin Hsp60, mitochondrial precursor
Tb10.6k15.3900	24	29	29	hypothetical protein, conserved
Tb10.6k15.3700	130	94	11	hypothetical protein, conserved
Tb10.6k15.3640	489	88	20	alternative oxidase
Tb10.6k15.3290	12	12	124	hypothetical protein, conserved
Tb10.6k15.3250	4344	4019	3501	succinyl-CoA ligase [GDP-forming] beta-chain, putative
Tb10.6k15.3140	17	7	29	folylpolyglutamate-dihydrofolate synthetase, putative
Tb10.6k15.3080	63	6	158	dihydrolipoamide acetyltransferase E2 subunit, putative
Tb10.6k15.3040	122	124	80	hypothetical protein, conserved
Tb10.6k15.3030	307	224	539	mitochondrial ATP-dependent zinc metallopeptidase, putative; metallo-peptidase, Clan MA(E) Family M41
Tb10.6k15.2875	1	0	0	hypothetical protein, conserved
Tb10.6k15.2800	33	42	26	hypothetical protein
Tb10.6k15.2640	119	85	249	hypothetical protein, conserved
Tb10.6k15.2530	41	31	9	hypothetical protein, conserved

Tb10.6k15.2510	10	21	238	hypothetical protein, conserved
Tb10.6k15.2490	8	4	23	TFIIF-stimulated CTD phosphatase, putative
Tb10.6k15.2410	117	104	145	hypothetical protein, conserved
Tb10.6k15.2360	54	66	17	hypothetical protein, conserved
Tb10.6k15.2310	146	92	87	RNA-editing complex protein; KREPA2
Tb10.6k15.2180	63	43	167	cytochrome oxidase subunit IX
Tb10.6k15.1930	2	1	6	hypothetical protein, conserved
Tb10.6k15.1920	20	19	32	hypothetical protein, conserved
Tb10.6k15.1910	85	24	142	hypothetical protein, conserved
Tb10.6k15.1800	16	36	25	hypothetical protein, conserved
Tb10.6k15.1600	10	5	9	kinetoplast DNA-associated protein, putative
Tb10.6k15.1460	52	2	14	kinetoplast DNA-associated protein, putative
Tb10.6k15.1450	130	66	162	hypothetical protein, conserved
Tb10.6k15.1430	287	197	123	hypothetical protein, conserved
Tb10.6k15.1310	10	21	13	hypothetical protein, conserved
Tb10.6k15.1300	127	142	24	hypothetical protein, conserved
Tb10.6k15.1280	217	276	86	hypothetical protein, conserved
Tb10.6k15.1220	104	86	186	isoleucyl-tRNA synthetase, putative
Tb10.6k15.1130	4	11	10	hypothetical protein, conserved
Tb10.6k15.1120	14	9	16	hypothetical protein, conserved
Tb10.6k15.0980	2	2	3	ATP-dependent chaperone, putative; mitochondrial chaperone BCS1, putative
Tb10.6k15.0960	150	109	44	NADH dehydrogenase
Tb10.6k15.0550	5	10	30	hypothetical protein, conserved
Tb10.6k15.0520	107	77	38	hypothetical protein, conserved
Tb10.6k15.0500	11	7	30	hypothetical protein, conserved
Tb10.6k15.0490	42	25	39	mitochondrial intermediate peptidase, putative; metallo-peptidase, Clan MA(E) Family M3
Tb10.6k15.0480	69	9	67	hypothetical protein, conserved
Tb10.6k15.0440	4	5	3	hypothetical protein, conserved
Tb10.6k15.0340	26	14	9	hypothetical protein, conserved
Tb10.6k15.0310	14	18	13	hypothetical protein, conserved
Tb10.6k15.0170	20	26	26	hypothetical protein, conserved
Tb10.6k15.0160	25	31	7	hypothetical protein, conserved
Tb10.6k15.0150	22	7	10	hypothetical protein, conserved
Tb10.6k15.0120	138	176	35	hypothetical protein, conserved
Tb10.406.0630	2	1	2	hypothetical protein, conserved
Tb10.406.0620	2	6	9	hypothetical protein, conserved
Tb10.406.0510	53	28	83	hypothetical protein, conserved
Tb10.406.0490	31	41	37	monothiol glutaredoxin, putative
Tb10.406.0230	47	52	11	hypothetical protein, conserved
Tb10.406.0140	68	84	30	hypothetical protein, conserved
Tb10.406.0100	10	5	6	hypothetical protein, conserved
Tb10.406.0050	172	90	216	RNA-binding protein, putative; HNRNPA
Tb10.26.1020	29	53	256	hypothetical protein, conserved
Tb10.26.1000	334	459	178	hypothetical protein, conserved
Tb10.26.0860	34	41	15	HIRA-interacting protein 5, putative
Tb10.26.0750	13	9	7	hypothetical protein, conserved
Tb10.26.0700	0	5	4	hypothetical protein

Tb10.26.0600	16	14	14	hypothetical protein, conserved
Tb10.26.0585	38	22	32	hypothetical protein, conserved
Tb10.26.0530	4	5	3	hypothetical protein, conserved
Tb10.26.0410	0	0	0	hypothetical protein, conserved
Tb10.26.0390	45	53	112	hypothetical protein, conserved
Tb10.26.0100	126	155	340	hypothetical protein, conserved
Tb10.26.0050	2	4	30	hypothetical protein, conserved
Tb10.389.1910	6	12	17	hypothetical protein, conserved
Tb10.389.1890	67	117	49	hypothetical protein, conserved
Tb10.389.1880	4	8	10	hypothetical protein, conserved
Tb10.389.1840	37	67	4	ABC1 protein, putative
Tb10.389.1785	15	24	21	hypothetical protein, conserved
Tb10.389.1710	8	14	21	hypothetical protein, conserved
Tb10.389.1670	36	69	13	hypothetical protein, conserved
Tb10.389.1490	15	14	19	hypothetical protein, conserved
Tb10.389.1440	109	78	22	hypothetical protein, conserved
Tb10.389.1160	19	34	4	hypothetical protein, conserved
Tb10.389.1140	46	18	26	electron transfer protein, putative; ferredoxin, putative
Tb10.389.1130	172	117	52	hypothetical protein, conserved
Tb10.389.1110	1	1	0	hypothetical protein
Tb10.389.0900	21	22	20	hypothetical protein, conserved
Tb10.389.0890	6	7	13	pyruvate dehydrogenase E1 alpha subunit, putative
Tb10.389.0690	2	11	28	mitochondrial carrier protein, putative; mitochondrial 2-oxoglutarate/malate carrier protein, putative
Tb10.389.0650	40	39	89	hypothetical protein, conserved
Tb10.389.0630	193	110	201	bifunctional aminoacyl-tRNA synthetase, putative
Tb10.389.0610	64	53	37	hypothetical protein, conserved
Tb10.389.0590	7	6	6	hypothetical protein, conserved
Tb10.389.0340	6	13	9	mitochondrial carrier protein, putative
Tb10.389.0130	11	16	17	30S ribosomal protein S8, putative
Tb10.05.0150	52	4	9	citrate synthase, putative
Tb10.05.0200	22	13	32	protein kinase, putative
Tb10.05.0050	36	42	23	hypothetical protein, conserved; hypothetical protein
Tb10.05.0070	194	313	476	NADH-ubiquinone oxidoreductase complex I subunit,FT putative
Tb10.389.0020	7	3	6	phosphatidic acid phosphatase alpha, putative
Tb10.61.3115	7	5	8	hypothetical protein, conserved
Tb10.61.3110	367	377	258	hypothetical protein, conserved
Tb10.61.3100	50	74	40	chaperone protein DNAJ, putative
Tb10.61.3070	35	32	24	hypothetical protein, conserved
Tb10.61.3000	9	6	17	hypothetical protein, conserved
Tb10.61.2990	117	92	181	hypothetical protein, conserved
Tb10.61.2830	0	0	0	hypothetical protein
Tb10.61.2600	327	531	143	hypothetical protein, conserved
Tb10.61.2540	12	27	18	hypothetical protein, conserved
Tb10.61.2510	45	52	10	mitochondrial carrier protein, putative
Tb10.61.2420	41	35	33	hypothetical protein, conserved
Tb10.61.1830	218	294	666	mitochondrial carrier protein, putative; ADP/ATP translocase 1, putative

Tb10.61.1820	203	303	656	mitochondrial carrier protein, putative; ADP/ATP translocase 1, putative
Tb10.61.1810	251	333	668	mitochondrial carrier protein, putative; ADP/ATP translocase 1, putative
Tb10.61.1790	14	21	37	hypothetical protein, conserved
Tb10.61.1530	584	707	304	lipoic acid synthetase, mitochondrial precursor, putative
Tb10.61.1300	7	3	8	hypothetical protein, conserved
Tb10.61.1290	30	24	27	hypothetical protein, conserved
Tb10.61.1260	53	27	132	hypothetical protein, conserved
Tb10.61.0690	215	185	143	tRNA pseudouridine synthase A-like protein
Tb10.61.0610	68	59	33	mitochondrial carrier protein, putative
Tb10.61.0510	56	129	140	hypothetical protein, conserved
Tb10.61.0460	11	21	79	hypothetical protein, conserved
Tb10.61.0395	24	13	26	hypothetical protein, conserved
Tb10.61.0340	26	23	32	cation transporter, putative
Tb10.61.0280	47	11	9	receptor-type adenylate cyclase GRESAG 4, putative; expression site-associated gene 4 (ESAG4) protein, putative
Tb10.61.0270	3	4	2	hypothetical protein
Tb10.61.0200	7	12	31	hypothetical protein, conserved
Tb10.61.0190	38	47	55	hypothetical protein, conserved
Tb10.61.0110	30	21	32	ATP-dependent zinc metallopeptidase, putative; metallo-peptidase, Clan MA(E) Family M41
Tb10.61.0090	15	13	18	potassium voltage-gated channel, putative
Tb10.v4.0043	17	13	6	branched-chain alpha-keto acid dehydrogenase e1-beta subunit precursor, putative
Tb10.v4.0053	7	6	10	hypothetical protein
Tb11.03.0960	4	5	13	hypothetical protein, conserved
Tb11.03.0950	251	323	850	electron transfer flavoprotein, putative
Tb11.03.0900	9	10	3	hypothetical protein, conserved
Tb11.03.0870	77	88	342	mitochondrial carrier protein, putative
Tb11.03.0660	24	16	4	hypothetical protein, conserved
Tb11.03.0510	5	7	15	hypothetical protein, conserved
Tb11.03.0490	232	233	108	hypothetical protein, conserved
Tb11.03.0475	96	38	56	hypothetical protein, conserved
Tb11.03.0440	9	11	19	hypothetical protein, conserved
Tb11.03.0260	113	86	88	hypothetical protein, conserved
Tb11.03.0180	18	15	8	RNA-editing complex protein; KREPB5
Tb11.03.0110	10	3	10	chaperone protein DNAJ, putative
Tb11.47.0024	3	6	3	hypothetical protein, unknown function
Tb11.47.0022	25	26	34	hypothetical protein, conserved
Tb11.47.0020	40	35	23	hypothetical protein, conserved
Tb11.47.0018	120	72	66	NADH-cytochrome b5 reductase, putative
Tb11.47.0017	51	34	38	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor
Tb11.47.0014	372	404	34	hypothetical protein, conserved
Tb11.47.0012	25	36	53	glutaredoxin, putative
Tb11.47.0009	32	49	25	hypothetical protein, conserved
Tb11.47.0004	79	123	237	transketolase:dehydrogenase-like protein
Tb11.55.0026	185	198	58	Isovaleryl Coenzyme A dehydrogenase, putative
Tb11.55.0017	9	14	17	hypothetical protein, unknown function

Tb11.55.0016	5	3	5	hypothetical protein, conserved
Tb11.55.0030	12	12	22	hypothetical protein, conserved
Tb11.55.0010	23	9	32	hypothetical protein, conserved
Tb11.55.0009	307	319	384	mitochondrial RNA binding protein 1; gBP21, MRP1
Tb11.46.0012	45	19	30	hypothetical protein, conserved
Tb11.46.0007	82	100	44	hypothetical protein, conserved
Tb11.46.0006	31	38	48	hypothetical protein, conserved
Tb11.57.0002	77	92	40	hypothetical protein, conserved
Tb11.02.0130	56	72	44	hypothetical protein, conserved
Tb11.02.0180	12	9	38	hypothetical protein, conserved
Tb11.02.0250	19	14	367	heat shock protein 84, putative
Tb11.02.0290	20	6	15	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative
Tb11.02.0320	57	82	53	hypothetical protein, conserved
Tb11.02.0355	49	33	17	hypothetical protein, conserved
Tb11.02.0430	12	9	11	hypothetical protein, conserved
Tb11.02.0440	48	55	24	glycerolphosphate mutase, putative
Tb11.02.0445	23	20	63	hypothetical protein, conserved
Tb11.02.0490	12	11	32	RNA-editing complex protein; KREPB4
Tb11.02.0510	20	19	22	hypothetical protein, conserved
Tb11.02.0540	201	133	91	hypothetical protein
Tb11.02.0770	6	4	15	mitochondrial DNA polymerase I protein D, putative
Tb11.02.1110	5	9	15	hypothetical protein, conserved
Tb11.02.1150	42	47	42	hypothetical protein, conserved
Tb11.02.1180	21	14	19	hypothetical protein, conserved
Tb11.02.1350	10	7	11	hypothetical protein, conserved
Tb11.02.1440	94	82	60	hypothetical protein, conserved
Tb11.02.1480	41	44	208	mitochondrial processing peptidase alpha subunit, putative; metallo-peptidase, Clan ME, Family M16
Tb11.02.1520	81	66	105	hypothetical protein, conserved
Tb11.02.1610	123	155	207	hypothetical protein, conserved
Tb11.02.1860	35	37	70	hypothetical protein, conserved
Tb11.02.1880	30	37	18	hypothetical protein, conserved
Tb11.02.2070	287	208	144	long-chain-fatty acid-CoA ligase protein, putative; acyl-CoA synthetase, putative; fatty acid thiokinase (long chain), putative
Tb11.02.2250	89	86	128	hypothetical protein, conserved
Tb11.02.2280	23	40	80	hypothetical protein, conserved
Tb11.02.2300	82	54	37	mitochondrial DNA polymerase I protein B, putative; DNA polymerase I-like protein B
Tb11.02.2390	10	9	12	pyruvate dehydrogenase (lipoamide) kinase, putative
Tb11.02.2420	104	95	104	hypothetical protein, conserved
Tb11.02.2460	17	14	47	hypothetical protein, conserved
Tb11.02.2480	28	31	13	hypothetical protein, conserved
Tb11.02.2680	1	3	16	hypothetical protein, conserved
Tb11.02.2700	21	12	14	fumarate hydratase class I, putative
Tb11.02.2710	31	39	22	hypothetical protein, conserved
Tb11.02.2740	55	78	26	aspartate aminotransferase, mitochondrial
Tb11.02.2910	27	25	28	hypothetical protein, conserved
Tb11.02.2960	46	39	111	mitochondrial carrier protein, putative

Tb11.02.3060	13	21	9	hypothetical protein, conserved
Tb11.02.3130	2	17	28	malic enzyme, putative
Tb11.02.3180	5	8	44	hypothetical protein, conserved
Tb11.02.3230	10	6	6	hypothetical protein, conserved
Tb11.02.3310	373	413	430	hypothetical protein, conserved
Tb11.02.3470	2	4	3	formin, putative; formin-like protein
Tb11.02.3510	1	1	2	hypothetical protein, conserved
Tb11.02.3530	23	21	10	mitochondrial DNA-directed RNA polymerase
Tb11.02.3570	255	190	140	hypothetical protein, conserved
Tb11.02.3670	24	27	9	hypothetical protein, conserved
Tb11.02.3720	8	3	2	hypothetical protein, conserved
Tb11.02.3800	13	12	19	hypothetical protein, conserved
Tb11.02.3810	80	100	77	hypothetical protein, conserved
Tb11.02.3830	13	11	33	hypothetical protein, conserved
Tb11.02.3930	3	1	2	hypothetical protein, conserved
Tb11.02.4020	19	11	173	hypothetical protein, conserved
Tb11.02.4120	365	470	880	hypothetical protein, conserved
Tb11.02.4330	20	12	19	hypothetical protein, conserved
Tb11.02.4400	260	87	119	hypothetical protein, conserved
Tb11.02.4480	6	8	12	3-methylcrotonoyl-CoA carboxylase beta subunit, putative
Tb11.02.4500	75	55	72	hypothetical protein, conserved
Tb11.02.4535	12	4	31	hypothetical protein, conserved
Tb11.02.4600	4	4	3	hypothetical protein, conserved
Tb11.02.4660	4	4	6	hypothetical protein, conserved
Tb11.02.4730	9	14	21	DNA repair and recombination helicase protein PIF1, putative; DNA repair and recombination protein, mitochondrial precursor, putative
Tb11.02.4800	51	20	30	NADH-cytochrome b5 reductase-like protein
Tb11.02.4810	6	10	53	hypothetical protein, conserved
Tb11.02.4890	594	509	307	pterin-4-alpha-carbinolamine dehydratase, putative
Tb11.02.5100	4	7	38	hypothetical protein, conserved
Tb11.02.5160	2	51	33	hypothetical protein, conserved
Tb11.02.5280	46	16	22	glycerol-3-phosphate dehydrogenase, putative
Tb11.02.5290	2	7	4	hypothetical protein, conserved
Tb11.02.5390	21	21	20	hypothetical protein, conserved
Tb11.02.5530	3	8	15	electron-transfer-flavoprotein, alpha polypeptide, putative
Tb11.02.5580	6	9	11	hypothetical protein, conserved
Tb11.02.5660	28	18	34	hypothetical protein, conserved
Tb11.02.5670	23	23	15	hypothetical protein, conserved
Tb11.02.5770	87	85	113	mitochondrial RNA binding protein; RBP16; RNA- binding protein of 16 kDa
Tb11.02.5780	39	44	45	hypothetical protein, conserved
Tb11.02.5820	6	14	23	hypothetical protein, conserved
Tb11.01.0500	280	295	279	hypothetical protein, conserved
Tb11.01.0430	17	9	44	hypothetical protein, conserved
Tb11.01.0150	12	20	7	hypothetical protein, conserved
Tb11.12.0014	28	37	42	hypothetical protein, conserved
Tb11.01.0610	222	198	227	mitochondrial DEAD box protein; KREH1
Tb11.01.0640	35	29	76	NADH-ubiquinone oxidoreductase complex I subunit, putative

Tb11.01.0710	11	21	11	elongation factor G2-like protein
Tb11.01.0880	31	40	155	hypothetical protein, conserved
Tb11.01.0890	36	65	15	hypothetical protein, conserved
Tb11.01.1040	39	55	17	hypothetical protein, conserved
Tb11.01.1080	4	6	2	tRNA pseudouridine synthase, putative
Tb11.01.1100	31	31	25	helicase-like protein
Tb11.01.1130	20	12	12	prenyltransferase, putative
Tb11.01.1160	3	2	3	lipoate-protein ligase, putative; lipoyltransferase, putative
Tb11.01.1320	6	4	2	oxidoreductase, putative
Tb11.01.1360	38	47	3	hypothetical protein, conserved
Tb11.01.1440	4	4	20	aminomethyltransferase, putative
Tb11.01.1500	97	85	59	hypothetical protein, conserved
Tb11.01.1600	138	95	195	hypothetical protein, conserved
Tb11.01.1660	17	22	15	hypothetical protein, conserved
Tb11.01.1690	26	19	26	hypothetical protein, conserved
Tb11.01.1740	1027	1142	893	2-oxoglutarate dehydrogenase E1 component, putative
Tb11.01.1810	14	10	90	hypothetical protein, conserved
Tb11.01.1840	104	102	102	hypothetical protein, conserved
Tb11.01.1900	17	20	67	hypothetical protein, conserved
Tb11.01.1910	5	8	11	hypothetical protein, conserved
Tb11.01.1930	6	3	20	hypothetical protein, conserved
Tb11.01.2000	1147	754	810	hslVU complex proteolytic subunit, putative; hslVU complex proteolytic subunit, threonine peptidase, Clan T(1), family T1B
Tb11.01.2170	21	24	38	hypothetical protein, conserved
Tb11.01.2280	13	9	20	ubiquinone biosynthesis methyltransferase, putative
Tb11.01.2340	20	39	22	hypothetical protein, conserved
Tb11.01.2360	7	15	66	hypothetical protein, conserved
Tb11.01.2370	22	29	75	hypothetical protein, conserved
Tb11.01.2460	19	8	9	hypothetical protein, conserved
Tb11.01.2490	160	168	156	hypothetical protein, conserved
Tb11.01.2740	3	4	26	hypothetical protein, conserved
Tb11.01.2910	34	39	15	hypothetical protein, conserved
Tb11.01.2920	1	1	10	hypothetical protein, conserved
Tb11.01.3070	50	26	213	hypothetical protein, conserved
Tb11.01.3190	8	12	73	hypothetical protein, conserved
Tb11.01.3200	187	192	45	hypothetical protein, conserved
Tb11.01.3290	118	132	67	hypothetical protein, conserved
Tb11.01.3300	10	13	9	hypothetical protein, conserved
Tb11.01.3340	131	81	127	2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like protein, putative
Tb11.01.3490	26	40	49	hypothetical protein, conserved
Tb11.01.3500	3	3	25	hypothetical protein, conserved
Tb11.01.3550	85	129	82	2-oxoglutarate dehydrogenase E2 component, putative
Tb11.01.3710	53	92	26	hypothetical protein, conserved
Tb11.01.3760	126	86	21	hypothetical protein, conserved
Tb11.01.3780	231	296	134	cytochrome oxidase assembly protein, putative
Tb11.01.3860	101	99	947	hypothetical protein, conserved
Tb11.01.3970	61	66	73	hypothetical protein, conserved
Tb11.01.4170	8	12	4	DNA photolyase, putative

Tb11.01.4590	5	7	22	hypothetical protein, conserved
Tb11.01.4702	30	39	81	cytochrome oxidase subunit X
Tb11.01.4740	57	186	231	hypothetical protein, conserved
Tb11.01.4860	153	73	92	mitochondrial RNA binding protein 2
Tb11.01.4870	37	27	46	inner membrane preprotein translocase Tim17, putative
Tb11.01.5040	300	318	41	mitochondrial carrier protein, putative
Tb11.01.5110	5	8	4	hypothetical protein, conserved
Tb11.01.5180	17	10	62	ubiquinone biosynthesis protein-like protein
Tb11.01.5185	7	5	6	hypothetical protein, conserved
Tb11.01.5200	30	25	11	hypothetical protein, conserved
Tb11.01.5280	196	251	255	hypothetical protein, conserved
Tb11.01.5330	10	13	67	hypothetical protein, conserved
Tb11.01.5390	45	34	15	hypothetical protein, conserved
Tb11.01.5400	57	34	44	hypothetical protein, conserved
Tb11.01.5460	53	62	83	hypothetical protein, conserved
Tb11.01.5480	13	17	6	hypothetical protein, conserved
Tb11.01.5960	19	6	15	mitochondrial carrier protein, putative
Tb11.01.5980	1	5	7	hypothetical protein, conserved
Tb11.01.6080	10	9	3	ubiquitin carboxyl-terminal hydrolase, putative
Tb11.01.6180	4	13	3	hypothetical protein, conserved
Tb11.01.6320	67	112	74	hypothetical protein, conserved
Tb11.01.6580	3	4	5	hypothetical protein, conserved
Tb11.01.6620	599	624	206	hypothetical protein, conserved
Tb11.01.6680	69	7	35	chaperonin Hsp60, mitochondrial precursor, putative; heat shock protein 60
Tb11.01.6710	2	2	3	hypothetical protein, conserved
Tb11.01.6950	19	8	8	hypothetical protein, conserved
Tb11.01.7090	154	192	74	hypothetical protein, conserved
Tb11.01.7110	58	54	23	methionyl-trna formyltransferase
Tb11.01.7140	206	209	214	hypothetical protein, conserved
Tb11.01.7260	13	19	9	hypothetical protein, conserved
Tb11.01.7290	14	59	19	NUDIX hydrolase, conserved
Tb11.01.7300	8	12	10	poly(A) polymerase, putative
Tb11.01.7340	9	7	18	hypothetical protein, conserved
Tb11.01.7370	63	85	35	hypothetical protein, conserved
Tb11.01.7460	45	84	58	NADH-ubiquinone oxidoreductase complex I subunit, putative
Tb11.01.7480	5	17	32	superoxide dismutase, putative
Tb11.01.7510	134	52	22	hypothetical protein, conserved
Tb11.01.7900	0	1	3	hypothetical protein, conserved
Tb11.01.8050	18	14	3	hypothetical protein, conserved
Tb11.01.8070	10	7	14	hypothetical protein, conserved
Tb11.01.8090	9	6	26	kinetoplast DNA-associated protein, putative
Tb11.01.8110	10	12	55	hypothetical protein, conserved
Tb11.01.8120	1	2	0	hypothetical protein, conserved
Tb11.01.8200	104	100	333	enoyl-CoA hydratase/isomerase family protein, putative
Tb11.01.8225	137	122	430	hypothetical protein, conserved
Tb11.01.8230	7	13	4	hypothetical protein, conserved
Tb11.01.8470	163	219	273	dihydrolipoyl dehydrogenase
Tb11.01.8500	312	623	99	hypothetical protein, conserved

Tb11.01.8620	32	41	20	hypothetical protein, conserved
Tb11.01.8630	134	134	110	hypothetical protein, conserved
Tb11.01.8700	6	4	3	ABC transporter, putative
Tb11.01.8710	3	4	2	hypothetical protein, conserved
Tb927.1.730	10	12	12	hypothetical protein, conserved
Tb927.1.740	7	2	9	hypothetical protein, conserved
Tb927.1.790	28	22	10	hypothetical protein, conserved
Tb927.1.840	6	6	21	hypothetical protein, conserved
Tb927.1.1000	15	11	43	developmentally regulated phosphoprotein
Tb927.1.1130	20	10	16	glycerol-3-phosphate dehydrogenase (FAD-dependent), putative
Tb927.1.1160	28	24	6	hypothetical protein, conserved
Tb927.1.1200	6	8	0	hypothetical protein, conserved
Tb927.1.1210	9	6	6	hypothetical protein, conserved
Tb927.1.1330	20	32	38	hypothetical protein, conserved
Tb927.1.1580	173	193	265	cytochrome c oxidase assembly factor, putative; electron transport protein SCO1/2, putative
Tb927.1.1610	117	129	66	hypothetical protein, conserved
Tb927.1.1690	6	12	10	RNA-editing complex protein; RNA editing endoribonuclease
Tb927.1.1730	8	11	67	hypothetical protein, conserved
Tb927.1.2320	47	42	10	hypothetical protein, conserved
Tb927.1.2730	10	6	2	hypothetical protein, conserved
Tb927.1.2990	23	24	8	hypothetical protein, conserved
Tb927.1.3010	26	22	26	hypothetical protein, conserved
Tb927.1.3030	606	516	185	RNA editing ligase; RNA-editing complex protein; KREL2
Tb927.1.3040	7	7	11	hypothetical protein, conserved
Tb927.1.3800	14	14	73	hypothetical protein, conserved
Tb927.1.4100	0	0	0	cytochrome oxidase subunit IV
Tb927.1.4230	72	110	57	hypothetical protein, conserved
Tb927.1.4970	12	20	4	hypothetical protein
Tb927.1.5000	18	10	104	hypothetical protein, conserved
Tb11.0400	-	-	-	
Tb927.5.295b	-	-	-	
Tb927.5.450b	-	-	-	Alternative version (resequencing) of Tb927.5.450
Tb11.1220	-	-	-	
Tb11.0420	-	-	-	
Tb11.0300	-	-	-	
Tb11.0550	-	-	-	
Tb11.0320	-	-	-	
Tb927.5.500b	-	-	-	

Table S10A. Alternatively spliced transcripts from the long slender bloodstream form.

Gene ID	LS TPM (1)	LS UTR length	Description
Tb927.3.3050	4,1,2	-52,-38,1893	hypothetical protein, conserved
Tb10.26.0750	4,6,1,2	12,16,25,80	hypothetical protein, conserved
Tb11.01.8070	1,1,2,1,1,6	112,137,156,423,739,746	hypothetical protein, conserved
Tb927.4.1130	2,1,1,6,7,1	3,14,15,16,38,39	hypothetical protein, conserved
Tb927.8.2670	5,1,2,2,1,1,7,6	2722,2718,2652,1743,1352,221,14,-459	hypothetical protein, conserved
Tb10.70.5130	49,60,1,98,1	258,255,43,32,-118	adenylate kinase, putative
Tb927.2.5930	2,2	375,315	hypothetical protein, conserved
Tb09.160.2060	1,1,1,1	172,170,157,146	hypothetical protein, conserved
Tb10.70.1330	2,2,1	59,46,27	heat shock protein, putative
Tb11.01.1910	2,1,1,1,1	311,292,268,266,79	hypothetical protein, conserved
Tb11.02.5820	1,1,2,2	-806,-9,6,52	hypothetical protein, conserved
Tb11.02.5670	1,2,13,7,1	16,50,193,242,1018	hypothetical protein, conserved
Tb927.7.3520	1,1,2,1	52,62,75,139	hypothetical protein, conserved
Tb10.70.6690	1,1,32,1,3,74,14	143,155,168,279,282,779,784	hypothetical protein, conserved
Tb927.6.3600	1,1,4,1,1,1,1,1	- 175,71,84,94,113,136,137,160	hypothetical protein, conserved
Tb10.26.0600	6,7,3,1	1144,534,79,30	hypothetical protein, conserved
Tb927.6.4580	3,2,...	137,1683,...	hypothetical protein, conserved
Tb927.8.4470	7,14,1,8,1,1,1	-40,-35,-29,47,49,57,110	chaperone protein DNAJ, putative
Tb927.3.4420	6,7,10,3	54,62,72,73	hypothetical protein, conserved
Tb09.211.4880	1,1,3,1	-416,59,185,331	cyclophilin-like protein, putative
Tb927.7.910	15,1,1,14,1	91,266,268,281,595	hypothetical protein, conserved
Tb927.2.4890	1,1	21,48	ribosomal protein L11, putative
Tb927.1.1330	1,7,10,3	22,20,19,16	hypothetical protein, conserved
Tb927.7.1370	4,1,3,1,9,1	3219,2889,2237,1469,1401,6	spliced leader RNA PSE-promoter transcription factor, putative
Tb10.6k15.1220	2,49,2,2,46,3,1,1	903,334,-41,-142,-154,-163,-173,-175	isoleucyl-tRNA synthetase, putative
Tb927.7.4200	2,2,10,1,6	767,78,75,4,-235	hypothetical protein, conserved
Tb927.8.5640	3,1,5,1,1	854,152,112,39,-840	hypothetical protein, conserved
Tb10.v4.0043	1,9,8	17,24,689	branched-chain alpha-keto acid dehydrogenase e1-beta subunit precursor, putative
Tb927.3.770	1,1	57,488	hypothetical protein, conserved
Tb10.389.0590	2,1,1,3	181,204,214,234	hypothetical protein, conserved
Tb927.6.3740	1,1,2	22,43,58	heat shock 70 kDa protein, mitochondrial precursor, putative
Tb927.6.4540	1,1,1,1,1	33,50,431,489,522	3-hydroxy-3-methylglutaryl-CoA reductase, putative
Tb09.211.2600	15,1,13,1,27,7,1	883,881,880,868,93,69,-216	hypothetical protein, conserved
Tb10.6k15.1130	1,2,2	184,144,139	hypothetical protein, conserved
Tb10.6k15.1310	5,1,3,1,1,1	26,12,-143,-148,-154,-211	hypothetical protein, conserved
Tb927.7.2990	1,1,16,1,9	869,846,203,200,126	hypothetical protein, conserved
Tb927.8.1700	5,11,131,2,7,1,120	-201,-198,-196,-84,-38,101,114	hypothetical protein, conserved

Tb927.3.3680	2,1,1	90,52,49	hypothetical protein, conserved
Tb927.7.560	1,2,7,1,10	-1367,-682,60,96,195	hypothetical protein, conserved
Tb927.1.3010	1,7,10,9	127,63,39,22	hypothetical protein, conserved
Tb09.211.3680	4,1,3,1	439,111,-61,-64	chaperone protein DNAJ, putative
Tb11.01.6710	1,1,1	-5,35,40	hypothetical protein, conserved
Tb11.02.4020	8,10	16,36	hypothetical protein, conserved
Tb11.02.1480	1,1,6,18,1,2,12,1	1148,1145,1117,1093,1075,1001,132,57	mitochondrial processing peptidase alpha subunit, putative; metallo-peptidase, Clan ME, Family M16
Tb10.61.0200	1,2,1,1,3,1	138,135,129,119,86,72	hypothetical protein, conserved
Tb927.4.700	1,1	2,313	hypothetical protein, conserved
Tb927.6.680	1,1,1,1,2,1,3,1	142,151,157,177,191,210,292,1209	hypothetical protein, conserved
Tb927.7.5720	1,1,8,4	163,162,145,106	hypothetical protein, conserved
Tb11.01.8700	3,2,1	47,51,83	ABC transporter, putative
Tb11.01.3190	1,4,2,2	43,41,36,33	hypothetical protein, conserved
Tb927.8.2530	1,1,6,21,4,1,7	1444,1400,953,936,915,844,113	hypothetical protein, conserved
Tb927.2.4700	1,1,1,1,2,3,2	438,501,506,508,2036,2042,2292	hypothetical protein, conserved
Tb927.7.2560	1,1,2,2,3,4	-2248,-1321,-1281,-51,298,311	hypothetical protein, conserved
Tb11.02.2460	1,2,4,1,7,1,1	1507,1506,1502,1490,32,23,20	hypothetical protein, conserved
Tb11.01.3200	109,1,45,1,31,1	751,672,584,571,101,88	hypothetical protein, conserved
Tb927.6.2140	1,1,7,1,14	60,62,78,690,693	hypothetical protein, conserved
Tb927.3.1940	1,26,32,1,1	-181,4,13,2077,2202	hypothetical protein, conserved
Tb11.01.3300	3,3,4	55,41,39	hypothetical protein, conserved
Tb927.7.5550	1,10,1,1,40,13,4,2	333,314,295,253,-58,-61,-101,-278	hypothetical protein, conserved
Tb09.160.4750	1,1,1,7,11,1	115,89,85,66,-7,-23	hypothetical protein, conserved
Tb10.v4.0053	1,3,3	57,125,146	hypothetical protein
Tb10.70.7840	1,22,13,1,1	224,194,176,173,142	choline dehydrogenase, putative
Tb09.160.0360	1,2,2,1,1,2,3,4,1,1	248,252,298,425,466,471,481,998,1038,1550	hypothetical protein, conserved
Tb11.02.1350	2,1,1,1,6,1,1	292,282,268,256,234,215,179	hypothetical protein, conserved
Tb11.02.5100	2,1,1	4,1,-6	hypothetical protein, conserved
Tb927.8.4960	2,2,9,4,1,7,3,2	610,608,600,128,49,30,10,-76	hypothetical protein, conserved
Tb11.01.6950	1,1,1,1,1,1,5,2,1,6	-133,-85,-77,-52,-49,-47,-27,-18,-6,37	hypothetical protein, conserved
Tb927.6.1590	2,2,3	-745,-742,172	hypothetical protein, conserved
Tb927.8.8360	3,3,1,3,1,2,1,3	2076,1113,1108,757,729,688,687,33	receptor-type adenylate cyclase GRESAG 4, putative
Tb11.01.5980	1,1	126,92	hypothetical protein, conserved
Tb10.6k15.3900	6,5,12,1	691,119,116,82	hypothetical protein, conserved
Tb10.70.7250	4,3	48,37	hypothetical protein, conserved
Tb11.02.4810	1,3,2	70,93,97	hypothetical protein, conserved
Tb10.6k15.0520	46,61,1	34,28,17	hypothetical protein, conserved
Tb927.8.6040	1,2451,2,2397,3244,18	1777,1754,1732,1207,697,	hypothetical protein, conserved

	2,12,140,1	693,690,10,9	
Tb927.4.4620	7,11,6	20,25,43	cytochrome oxidase subunit VIII
Tb927.3.4890	1,4,1,...	2,10,889,...	ubiquinone biosynthesis protein COQ7 homolog, putative
Tb927.6.4450	1,1,1,1,1,2	-743,21,29,84,91,162	hypothetical protein, conserved
Tb927.7.3770	1,6,3,1,13	-815,62,93,124,130	hypothetical protein, conserved
Tb11.01.8710	1,1,1	796,981,985	hypothetical protein, conserved
Tb11.12.0014	12,1,15,1	389,385,12,-407	hypothetical protein, conserved
Tb927.1.740	4,2,1	25,73,80	hypothetical protein, conserved
Tb927.5.1520	8,7	229,282	heat shock protein HslVU, ATPase subunit HslU, putative
Tb11.02.0430	3,2,7,1	-324,-153,91,116	hypothetical protein, conserved
Tb927.4.3660	3,10,8	36,74,115	hypothetical protein, conserved
Tb11.55.0016	2,1,1,1	82,112,117,135	hypothetical protein, conserved
Tb927.7.2220	6,3,1,1,2,1	90,93,95,97,309,386	hypothetical protein, conserved
Tb09.v1.0420	1,1,4,1,1,3	- 120,27,60,1547,1559,1568	hypothetical protein, conserved
Tb11.02.3060	6,2,4,1	28,-5,-11,-29	hypothetical protein, conserved
Tb09.211.4580	1,3,2,1	151,213,242,248	hypothetical protein, conserved
Tb10.61.1260	23,1,29,1	125,116,110,104	hypothetical protein, conserved
Tb10.389.0900	1,10,9,2	36,43,158,716	hypothetical protein, conserved
Tb11.01.5185	1,3,2	30,36,109	hypothetical protein, conserved
Tb927.1.3800	1,1,5,7	336,115,73,63	hypothetical protein, conserved
Tb927.5.1790	2,1,1,1,1,1,3,1,1,10,1,1	513,482,473,127,117,106,9 8,81,64,46,37,-1259	hypothetical protein, conserved
Tb927.1.5000	10,6,1,1	36,21,19,6	hypothetical protein, conserved
Tb11.01.5960	8,9,1,1	72,67,13,0	mitochondrial carrier protein, putative
Tb10.70.6340	2,1,1	89,124,150	ATPase subunit 9, putative
Tb927.2.5900	6,6,1,1,1	-28,-31,-34,-2595,-2794	hypothetical protein, conserved
Tb10.389.1140	19,1,24,1,1,1	39,43,813,1700,1714,1745	electron transfer protein, putative; ferredoxin, putative
Tb09.160.1280	1,1,4,1,3,3	-344,-191,9,36,39,52	hypothetical protein, conserved
Tb11.02.3470	1,1	240,237	formin, putative; formin-like protein
Tb927.7.6350	1,1,3,13,1,3,3	158,185,308,315,706,709,1 357	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.7.4440	1,2,1	270,314,2176	hypothetical protein, conserved
Tb11.55.0030	1,1,2,1,7,1	-28,-9,83,233,238,261	hypothetical protein, conserved
Tb927.5.3870	3,1,2,1	1682,1676,69,65	hypothetical protein, conserved
Tb927.7.3270	6,4,1	24,38,40	hypothetical protein, conserved
Tb927.8.6060	17,1,18,12	191,162,146,132	2-amino-3-ketobutyrate coenzyme A ligase, putative
Tb927.5.2070	2,1,11,4,3,1,1,4,2,1,17	36,42,43,52,60,66,72,80,84 ,85,88	hypothetical protein, conserved
Tb09.211.3470	7,4,1,1	693,688,679,47	hypothetical protein, conserved
Tb927.7.7330	2,4,1,2,2,1,1	13,74,91,92,103,108,158	hypothetical protein, conserved
Tb927.4.2940	34,3,21,6,1	1413,137,55,38,-86	hypothetical protein, conserved
Tb11.47.0020	1,19,5,1,15,1	4349,724,719,712,64,62	hypothetical protein, conserved
Tb11.02.0320	4,20,25,2,1,5	106,109,111,151,719,1051	hypothetical protein, conserved
Tb927.6.1840	4,46,39,3,2,1,5	226,245,248,253,254,257,2 59	hypothetical protein, conserved

Tb927.5.4040	3,4,1	68,71,107	hypothetical protein, conserved
Tb10.389.0340	1,2,3	171,175,194	mitochondrial carrier protein, putative
Tb11.01.3860	57,44,1	-136,-139,-170	hypothetical protein, conserved
Tb11.01.6080	2,2,2,5	54,52,48,-400	ubiquitin carboxyl-terminal hydrolase, putative
Tb927.4.3150	3,1,3,1	212,191,155,149	hypothetical protein, conserved
Tb927.6.4040	1,1,7,6,2	-9,8,36,38,87	hypothetical protein, conserved
Tb927.5.2150	14,1,1,23,1,1,1,5,...	-1120,-805,9,11,151,700,707,729,.. ..	hypothetical protein, conserved
Tb927.7.2490	6,4,1,11,1,4	56,65,77,81,87,479	hypothetical protein, conserved
Tb927.7.3950	6,3,3	271,217,202	RNA-editing complex protein; RNA-editing 3' terminal uridylyl transferase 1; KRET1
Tb10.406.0100	1,1,2,2,2,3	-32,8,13,19,21,29	hypothetical protein, conserved
Tb10.6k15.2490	1,3,4	126,135,330	TFIIF-stimulated CTD phosphatase, putative
Tb10.70.7960	1,2,1,1,1	27,25,22,13,-14	hypothetical protein, conserved
Tb927.3.1690	1,23,4,1,10	62,70,75,177,185	hypothetical protein, conserved
Tb927.3.5600	1,1,1,1,10,6	78,72,62,31,14,5	hypothetical protein, conserved
Tb11.01.4740	1,22,3,6,11,14,1	33,38,46,242,252,260,279	hypothetical protein, conserved
Tb927.8.5560	1,29,1,1,44	137,120,-22,-122,-150	hypothetical protein, conserved
Tb11.02.2700	7,1,3,1,10	164,144,106,47,-88	fumarate hydratase class I, putative
Tb11.02.0290	3,6,2,1,8	60,74,76,78,79	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative
Tb10.70.4380	2,2	80,46	cytochrome C oxidase assembly protein, putative
Tb09.160.4310	37,61,3,1,1	236,154,143,139,-1512	glutamate dehydrogenase
Tb927.8.3830	1,1,4,1,1,1,1	100,111,118,208,212,232,233	ATP-dependent DEAD-H RNA helicase, putative
Tb927.6.4930	5,9,2	21,-27,-31	hypothetical protein, conserved
Tb11.02.2280	4,12,7	263,202,196	hypothetical protein, conserved
Tb10.61.2990	3,45,70	22,45,1002	hypothetical protein, conserved
Tb927.7.3970	1,1,154,1,99,1,1	513,498,493,491,457,453,-218	hypothetical protein, conserved
Tb927.2.4110	1,1,1,1,1	157,160,221,224,533	mitochondrial processing peptidase alpha subunit, putative
Tb927.3.1790	3,3,4	121,128,130	pyruvate dehydrogenase E1 beta subunit, putative
Tb09.211.0510	1,1	51,78	cytochrome c oxidase assembly factor, putative
Tb11.01.0150	1,2,3,3,1,1,2	481,429,425,421,389,238,-982	hypothetical protein, conserved
Tb11.01.0880	13,15,3	74,30,17	hypothetical protein, conserved
Tb09.211.4700	3,1,7,1	-69,174,177,191	reiske iron-sulfur protein, mitochondrial precursor
Tb11.01.6180	2,1,1	95,92,-194	hypothetical protein, conserved
Tb09.211.0760	2,1,2,6	-34,42,48,51	hypothetical protein, conserved
Tb927.2.5210	1,3,10,1,28,8,1	102,101,65,61,30,26,-31	3-oxoacyl-(acyl-carrier protein) reductase, putative
Tb927.2.3420	1,1,7,2,18,5	92,175,178,382,389,391	hypothetical protein, conserved

Tb11.01.7480	1,3,1	113,116,121	superoxide dismutase, putative
Tb927.3.4210	1,1	-113,-52	hypothetical protein, conserved
Tb11.02.5290	1,1,1	111,38,-178	hypothetical protein, conserved
Tb10.6k15.2510	2,6,3	15,18,21	hypothetical protein, conserved
Tb11.01.0890	9,2,5,1,20	-142,-145,-176,-191,-203	hypothetical protein, conserved
Tb927.7.5110	3,4,1	83,14,6	hypothetical protein, conserved
Tb927.8.7290	1,2,2	109,106,36	hypothetical protein, conserved
Tb11.02.4800	3,28,20	-65,-59,47	NADH-cytochrome b5 reductase-like protein
Tb927.7.3750	1,4,1,6,1	370,414,417,425,475	TFIIF-stimulated CTD phosphatase, putative
Tb11.01.2920	1,1	102,70	hypothetical protein, conserved
Tb927.6.4400	1,4,1,2	19,29,92,162	hypothetical protein, conserved
Tb09.244.2860	...,17,1,122,2	...,1982,1979,41,39	hypothetical protein, conserved
Tb927.8.2760	5,6	49,45	hypothetical protein, conserved
Tb10.61.0460	6,3,2	176,167,147	hypothetical protein, conserved
Tb927.8.2190	4,1,11,1,1,1,1,1	567,561,27,9,6,-3,-5,-6	hypothetical protein, conserved
Tb927.3.4700	1,1,1,18,1,2,1,7	-59,-52,31,36,101,102,103,106	hypothetical protein, conserved
Tb927.5.450	14,19	708,714	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.8.3690	3,4	235,258	isocitrate dehydrogenase [NADP], mitochondrial precursor, putative
Tb927.7.3990	2,4,1,1,1	1128,471,459,42,-784	mitochondrial DNA polymerase I protein C
Tb927.8.5280	52,2,53,1,1	42,39,37,14,0	hypothetical protein, conserved
Tb10.100.0220	8,1,5,1	16,15,11,-12	mitochondrial structure specific endonuclease I (SSE-1), putative
Tb10.70.0660	9,2,2,1,15,1	-3546,-545,94,104,107,124	hypothetical protein, conserved
Tb11.01.1040	9,20,1,1,1,1,6,1	166,90,75,69,67,-1251,-1254,-1260	hypothetical protein, conserved
Tb927.3.4140	7,9,1,1,1,2	16,18,46,47,48,583	hypothetical protein, conserved

(1) TPM (tags per million) represents the linear normalization of sequence tags to 1 million tags.

Table S10B. Alternatively spliced transcripts from the short stumpy life stage

Gene ID	SS TPM	SS UTR length	Description
Tb10.26.0750	5,1,3	16,25,80	hypothetical protein, conserved
Tb11.01.1690	1,10,5,4	1054,110,108,102	hypothetical protein, conserved
Tb927.6.4080	5,1,7,1	48,109,114,143	hypothetical protein, conserved
Tb11.01.8070	1,4,1,1,1,1	112,137,140,156,764,1622	hypothetical protein, conserved
Tb10.70.1580	3,3,1	32,12,8	RNA editing endoribonuclease
Tb927.7.1910	23,1,1,16,1,2	72,44,-1478,-1648,-1667,-2499	glycine dehydrogenase, putative
Tb927.4.1130	1,1,2,8,1,1,1	3,14,16,38,39,62,63	hypothetical protein, conserved
Tb11.55.0010	5,1,1,2	81,155,306,307	hypothetical protein, conserved
Tb09.211.3000	6,7	271,268	hypothetical protein, conserved
Tb927.7.1550	7,1,9,2,1	329,323,232,-987,-989	RNA-editing complex protein; RNA-editing 3%27 terminal uridylyl transferase 2; KRET2
Tb927.8.2670	7,1,1,1,2,9	2722,2718,2652,221,14,-459	hypothetical protein, conserved
Tb10.70.5130	1,29,37,27,1	1822,258,255,32,15	adenylate kinase, putative
Tb927.2.5930	1,1,3,1	402,375,315,-55	hypothetical protein, conserved
Tb927.3.1820	1,1	376,627	hypothetical protein, conserved
Tb927.3.2130	1,8,5,3	-370,-192,-176,-175	hypothetical protein, conserved
Tb927.8.3090	1,1	83,55	hypothetical protein, conserved
Tb09.160.2060	1,1	170,146	hypothetical protein, conserved
Tb927.8.3130	4,4	41,21	S-adenosyl-methyltransferase mraW-like protein, putative
Tb10.70.1330	5,2,1,1	59,46,27,2	heat shock protein, putative
Tb927.8.4040	2,1,1,1,1	-92,-80,118,119,145	endonuclease G, putative
Tb11.02.4600	2,2	280,289	hypothetical protein, conserved
Tb927.8.4150	1,3,1,1,2	122,257,276,311,352	hypothetical protein, conserved
Tb927.7.3510	1,1	9,41	hypothetical protein, conserved
Tb10.70.6690	42,1,1,2,73,21	168,229,279,282,779,784	hypothetical protein, conserved
Tb927.6.3600	1,2,1,1,1	71,84,120,136,137	hypothetical protein, conserved
Tb927.6.4580	1,3,2,2,...	113,137,1683,3319,...	hypothetical protein, conserved
Tb927.7.3800	1,1	29,32	hypothetical protein, conserved
Tb927.8.4470	1,10,12,1,11,1,3,1	-53,-40,-35,38,47,49,57,114	chaperone protein DNAJ, putative
Tb927.3.4420	3,5,9,6,1	54,62,72,73,76	hypothetical protein, conserved
Tb09.211.4880	1,2,1,7,1,1	-416,59,152,185,306,331	cyclophilin-like protein, putative
Tb927.7.910	11,1,14	91,268,281	hypothetical protein, conserved
Tb927.1.1330	7,16,9	20,19,16	hypothetical protein, conserved
Tb927.7.1370	2,1,1,1,2,2	3219,2237,1469,1418,1401,6	spliced leader RNA PSE-promoter transcription factor, putative
Tb10.6k15.1220	1,42,1,2,1,32,7	903,334,246,-41,-142,-154,-163	isoleucyl-tRNA synthetase, putative
Tb10.70.4280	9,2,1,4,1,1,1,1	950,942,228,79,74,60,52,-705	delta-1-pyrroline-5-carboxylate dehydrogenase, putative
Tb927.7.4200	1,1,12,1,2,10,1	767,105,75,50,4,-235,-238	hypothetical protein, conserved
Tb927.3.770	1,1,1	57,484,488	hypothetical protein, conserved
Tb10.389.0590	3,1,2	181,214,234	hypothetical protein, conserved
Tb927.6.4540	1,1,1,1,2	25,50,67,484,522	3-hydroxy-3-methylglutaryl-CoA reductase, putative

Tb09.211.2600	9,8,1,18,8	883,880,868,93,69	hypothetical protein, conserved
Tb10.6k15.1310	7,2,2,1,6,1,1	26,12,5,-93,-143,-148,-154	hypothetical protein, conserved
Tb927.7.2990	2,10,1,1,6	869,203,200,165,126	hypothetical protein, conserved
Tb09.211.0330	1,1,11,1,16,1	574,582,593,595,596,632	chaperone protein DNAJ, putative
Tb927.1.4970	11,6,2	-63,-71,-102	hypothetical protein
Tb927.2.4990	1,1,1	-44,-26,10	hypothetical protein, conserved
Tb927.7.6660	1,1	12,339	chaperone protein DNAJ, putative
Tb927.3.3680	1,1	52,49	hypothetical protein, conserved
Tb09.160.4130	10,2,5,1,1	188,185,183,159,-652	RNA-editing complex protein; KREPB7
Tb927.6.4070	2,64,92,1	12,33,34,54	hypothetical protein, conserved
Tb927.7.560	1,1,4,2,9	-1367,-682,60,96,195	hypothetical protein, conserved
Tb927.5.3640	1,11,7,1	100,69,-473,-545	hypothetical protein, conserved
Tb09.211.3680	6,1,6,1	439,111,-61,-64	chaperone protein DNAJ, putative
Tb11.02.1480	2,1,1,12,1,9,1,6,12	1186,1159,1148,1117, 1108,1093,1075,1001,132	mitochondrial processing peptidase alpha subunit, putative; metallo- peptidase, Clan ME, Family M16
Tb10.61.0200	2,3,1,6	138,135,129,86	hypothetical protein, conserved
Tb927.7.5720	7,6	145,106	hypothetical protein, conserved
Tb11.01.3190	1,6,3,1,1,1	48,41,36,33,27,-172	hypothetical protein, conserved
Tb927.8.2530	1,1,10,21,13,9,1	2713,1962,953,936,915,113,10 1	hypothetical protein, conserved
Tb927.2.4700	1,1,1,6,3,2	384,438,490,2036,2042,2292	hypothetical protein, conserved
Tb927.7.2560	5,8,2,4	-1281,-51,298,311	hypothetical protein, conserved
Tb11.02.2460	1,2,3,3,4,1	1533,1507,1506,1502,32,20	hypothetical protein, conserved
Tb11.02.2390	4,1,4,1	10136,10132,16,3	pyruvate dehydrogenase(lipoamide) kinase, putative
Tb10.26.0700	1,1,1,1,1,1	88672,87554,77586,9780,853,8 47	hypothetical protein
Tb927.8.3330	54,67	-37,-43	mitochondrial carrier protein, putative
Tb927.2.2940	1,1,2,1,2,1	338,44,32,24,-16,-61	hypothetical protein, conserved
Tb927.3.1940	58,71,1	4,13,1749	hypothetical protein, conserved
Tb11.01.3300	1,4,7	55,41,39	hypothetical protein, conserved
Tb11.02.5530	1,4,3	162,163,189	electron-transfer-flavoprotein, alpha polypeptide, putative
Tb927.8.5130	2,1,1	618,615,245	hypothetical protein, conserved
Tb10.70.7840	1,24,16	224,194,176	choline dehydrogenase, putative
Tb09.160.0360	2,1,1,8,1,1	298,481,975,998,1579,1620	hypothetical protein, conserved
Tb11.02.1350	2,1,1,2,1	292,278,257,234,209	hypothetical protein, conserved
Tb927.8.4960	1,2,2,8,1,8,15,8,3	2108,610,608,600,562,128,30,1 0,-76	hypothetical protein, conserved
Tb11.01.6950	1,2,1,1,3	-49,-27,-18,-6,37	hypothetical protein, conserved
Tb927.6.1590	9,15,1,8	-745,-742,141,172	hypothetical protein, conserved
Tb927.8.8360	1,1,1,1,5,1,1,4	2092,2076,1113,1108,757,729, 687,33	receptor-type adenylate cyclase GRESAG 4, putative
Tb09.160.0550	17,1,4,16	-737,-721,19,23	hypothetical protein, conserved
Tb11.01.8120	1,1,1	21,26,246	hypothetical protein, conserved
Tb10.70.7250	4,4	48,37	hypothetical protein, conserved

Tb10.6k15.0520	34,43	34,28	hypothetical protein, conserved
Tb927.8.6040	1,1,1,1, 3449,1,1,3448, 1,1,3898,1, 226,13,1,114	1789,1777,1772,1761, 1754,1753,1732,1207 ,1151,71 6,697,696, 693,690,674,10	hypothetical protein, conserved
Tb10.70.5380	1,46,32,2,18,1	154,115,112,109,-74,-96	pyruvate dehydrogenase complex E3 binding protein, putative
Tb927.4.4620	3,7,8	20,25,43	cytochrome oxidase subunit VIII
Tb927.3.4890	6,7,1,1,...	10,889,2109,6636,...	ubiquinone biosynthesis protein COQ7 homolog, putative
Tb927.6.4450	1,2,1,1,1	-743,29,66,91,162	hypothetical protein, conserved
Tb11.12.0014	2,21,3,11,1	430,389,385,12,-388	hypothetical protein, conserved
Tb10.389.0690	4,6	67,93	mitochondrial carrier protein, putative; mitochondrial 2- oxoglutarate/malate carrier protein, putative
Tb11.55.0016	1,1,1,1,1	-1276,82,117,135,138	hypothetical protein, conserved
Tb927.7.2220	1,1,1,1,1,1	-801,90,93,95,309,374	hypothetical protein, conserved
Tb927.8.6400	4,1,4	147,14,-18	hypothetical protein, conserved
Tb10.70.6350	1,1,1,1,16,1,1,1,30	85,207,270,275,279,338,1161,1 519,1521	hypothetical protein, conserved
Tb09.v1.0420	1,1,4,3,6	-108,-93,27,60,1568	hypothetical protein, conserved
Tb11.02.3060	11,6,5	28,-5,-11	hypothetical protein, conserved
Tb927.8.3070	9,7	65,45	hypothetical protein, conserved
Tb09.211.4580	1,4,3	208,213,242	hypothetical protein, conserved
Tb10.61.1260	14,4,9	125,116,110	hypothetical protein, conserved
Tb927.8.6820	4,5,1	99,138,1085	hypothetical protein, conserved
Tb10.6k15.3080	1,1,1,1,1,3	-132,-105,-102,-61,31,38	dihydrolipoamide acetyltransferase E2 subunit, putative
Tb11.01.5185	1,2,2,1	2,30,36,109	hypothetical protein, conserved
Tb927.1.3800	6,7,1	73,63,52	hypothetical protein, conserved
Tb927.5.1790	1,1,3,2,1,7,1	513,109,98,81,64,46,37	hypothetical protein, conserved
Tb09.160.1370	1,1,1	236,245,789	hypothetical protein, conserved
Tb11.02.3180	3,2,1,1,1	139,47,40,-468,-1177	hypothetical protein, conserved
Tb11.01.5960	2,3,1	72,67,13	mitochondrial carrier protein, putative
Tb10.70.6340	4,2,1,1	89,124,150,158	ATPase subunit 9, putative
Tb927.2.5900	4,3,1	-28,-31,-2082	hypothetical protein, conserved
Tb10.6k15.0500	3,3,1	722,182,138	hypothetical protein, conserved
Tb09.v4.0018	1,1	85,30	expression site-associated gene (ESAG) protein, putative; expression site-associated gene 3(ESAG3) protein, putative
Tb11.02.3510	1,1	113,62	hypothetical protein, conserved
Tb09.160.1280	1,2,1,1,1,2,1,4	-344,-191,-36,9,38,39,45,52	hypothetical protein, conserved
Tb927.2.4740	1,1	21,48	ribosomal protein L11, putative
Tb11.02.3470	1,2,1	240,237,-14	formin, putative; formin-like protein
Tb927.7.6350	1,1,2,8,2,1,4,1	152,158,308,315,709,725, 1357,2006	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.7.4440	1,1,1	270,285,314	hypothetical protein, conserved

Tb11.02.2710	11,23,1,4,1	202,121,112,-1821,-1827	hypothetical protein, conserved
Tb927.5.2830	1,1,1,1,2	67,84,102,104,106	hypothetical protein, conserved
Tb927.7.3270	4,3,1	24,38,40	hypothetical protein, conserved
Tb927.8.3960	1,1,1	2,38,41	hypothetical protein, conserved
Tb10.61.1300	1,1,1,1	202,186,184,175	hypothetical protein, conserved
Tb927.8.6060	26,1,24,41,5	191,162,146,132,118	2-amino-3-ketobutyrate coenzyme A ligase, putative
Tb927.5.2070	1,9,7,4,2,1,1,9,2,22	42,43,52,60,66,72,74,80,84,88	hypothetical protein, conserved
Tb09.211.3470	9,6,1,1,1	693,688,679,33,8	hypothetical protein, conserved
Tb927.4.2560	1,1,1	214,211,-1442	cardiolipin synthetase, putative
Tb927.8.2240	1,3,2	82,79,26	tryptophanyl-tRNA synthetase, putative
Tb927.7.7330	1,1,4,4,2,2,1	13,69,74,92,103,108,158	hypothetical protein, conserved
Tb927.4.2940	49,4,1,52,4	1413,137,119,55,38	hypothetical protein, conserved
Tb11.02.0320	1,11,22,44,4	84,106,109,111,1051	hypothetical protein, conserved
Tb927.6.1840	1,49,45,2,3,1,1,4	226,245,248,253,254,257,258,259	hypothetical protein, conserved
Tb09.160.0370	4,1,1,1,4	80,93,129,130,134	hypothetical protein, conserved
Tb927.5.4040	6,4,1	68,71,110	hypothetical protein, conserved
Tb10.389.0340	1,3,3,5,1	124,171,175,194,255	mitochondrial carrier protein, putative
Tb11.01.6080	1,2,1,1,2,2,1,1	110,54,52,48,-371, -400, -405, -416	ubiquitin carboxyl-terminal hydrolase, putative
Tb927.4.3150	4,1,1,1,1,1,1	212,191,188,155,149,0,-990	hypothetical protein, conserved
Tb927.6.4040	1,7,7,1	-16,36,38,87	hypothetical protein, conserved
Tb10.70.5830	5,1,7	83,79,-146	actin-like protein, putative
Tb927.5.2150	10,1,1,15,1,1,1,2,...	-1120,-805,9,11,28,151,700,729,...	hypothetical protein, conserved
Tb927.7.2490	1,2,1,7,2	-1188,56,65,81,479	hypothetical protein, conserved
Tb927.4.3300	1,1,4,1,1,6,1	-759,-754,-734,23,47,52,91	mitochondrial ATP-dependent zinc metallopeptidase, putative
Tb927.7.3950	1,2,7,1,1	704,271,217,202,-1121	RNA-editing complex protein; RNA-editing 3' terminal uridylyl transferase 1; KRET1
Tb10.406.0100	1,2,2	13,19,21	hypothetical protein, conserved
Tb11.01.4860	35,1,2,6,29,1	4,12,215,219,225,639	mitochondrial RNA binding protein 2
Tb10.6k15.2490	2,2	135,330	TFIIF-stimulated CTD phosphatase, putative
Tb11.01.4740	1,101,23,6,21,32,1,1	33,38,46,242,252,260,279,283	hypothetical protein, conserved
Tb927.8.5560	21,1,1,28,1	120,6,-22,-150,-159	hypothetical protein, conserved
Tb927.6.2490	1,1,2	42,-8,-11	hypothetical protein, conserved
Tb11.02.2700	5,4,1,3	164,106,-54,-88	fumarate hydratase class I, putative
Tb11.02.0290	3,1,1,1	60,74,76,79	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative
Tb09.160.4310	26,34,6,1	236,154,143,-1512	glutamate dehydrogenase
Tb927.4.1540	2,18,1,2,9,1,17,1	-48,168,740,750,765,779,781,1629	hypothetical protein, conserved

Tb10.70.5430	1,2,1,1,1,1	669,228,215,101,59,-82	hypothetical protein, conserved
Tb927.8.3830	1,2,2,1	100,118,208,212	ATP-dependent DEAD%2FH RNA helicase, putative
Tb10.389.0020	1,1,1,1	212,261,395,417	phosphatidic acid phosphatase alpha, putative
Tb927.4.830	1,10,11	-201,-181,-176	hypothetical protein, conserved
Tb11.02.2280	12,17,11	263,202,196	hypothetical protein, conserved
Tb11.02.5390	1,10,5,5	56,28,-11,-898	hypothetical protein, conserved
Tb10.61.2990	1,5,46,41	17,22,45,1002	hypothetical protein, conserved
Tb927.2.4110	1,2,1,1,1	160,224,315,526,533	mitochondrial processing peptidase alpha subunit, putative
Tb927.3.1790	6,4,11	121,128,130	pyruvate dehydrogenase E1 beta subunit, putative
Tb09.211.0510	1,2,1,1	43,51,78,110	cytochrome c oxidase assembly factor, putative
Tb11.01.0150	6,2,2,1,1,8	481,429,425,421,389,-982	hypothetical protein, conserved
Tb11.01.0880	2,1,24,13,1	190,187,74,30,-383	hypothetical protein, conserved
Tb927.4.2250	1,1,1,1	272,232,166,162	hypothetical protein, conserved
Tb11.01.7480	4,6,6,1	113,116,121,139	superoxide dismutase, putative
Tb927.3.4210	1,1,1	-4311,-113,-52	hypothetical protein, conserved
Tb11.02.5290	1,4,1,1,1	711,111,38,34,7	hypothetical protein, conserved
Tb10.6k15.2510	3,11,7	15,18,21	hypothetical protein, conserved
Tb11.01.0890	1,1,13,14,1,34,1,1	145,136,-142,-176,-199,-203,-210,-215	hypothetical protein, conserved
Tb927.8.7290	2,2,1,2	109,106,102,36	hypothetical protein, conserved
Tb927.7.3750	1,1,2,6,2	30,344,417,425,475	TFIIF-stimulated CTD phosphatase, putative
Tb927.8.3160	4,4	702,683	hypothetical protein, conserved
Tb10.70.4120	1,6,1,4,1	127,6,-642,-675,-680	hypothetical protein, conserved
Tb09.211.3080	1,3,2	84,81,0	hypothetical protein, conserved
Tb11.01.2360	8,7	156,134	hypothetical protein, conserved
Tb927.6.4400	1,2,1,1,3	-67,29,38,91,162	hypothetical protein, conserved
Tb09.244.2860	...,4,10,1,175,1	...,3810,1982,1979,41,35	hypothetical protein, conserved
Tb927.5.680	64,1,85,1,1	41,10,-996,-1002,-1006	hypothetical protein, conserved
Tb927.8.2190	5,3,1,1	567,27,6,-6	hypothetical protein, conserved
Tb927.5.450	2,18,19	608,708,714	NADH-ubiquinone oxidoreductase, mitochondrial, putative
Tb927.8.1860	1,1,9,7,1	84,92,94,98,106	pitrilysin-like metalloprotease
Tb927.7.3990	1,3,1,2,1	1133,1128,1123,471,42	mitochondrial DNA polymerase I protein C
Tb11.01.6580	1,2,1,1	-267,131,158,878	hypothetical protein, conserved
Tb927.8.5280	1,1,51,44,1	58,55,42,37,14	hypothetical protein, conserved
Tb10.100.0220	5,7,1	16,11,5	mitochondrial structure specific endonuclease I (SSE-1), putative
Tb11.02.0130	21,42,7,1,1	-1288,396,427,450,455	hypothetical protein, conserved
Tb10.70.0660	14,3,19,1,1,1,1	-3546,94,107,124,135,162,722	hypothetical protein, conserved
Tb11.01.1040	26,12,2,1,14	166,90,75,-1251,-1254	hypothetical protein, conserved
Tb927.3.4140	9,10,1	16,18,583	hypothetical protein, conserved

Table S10C. Alternatively spliced transcripts from the procyclic life stage.

Gene ID	PC TPM	PC UTR length	Description
Tb10.26.0750	2,2,2,2	1,12,16,25	hypothetical protein, conserved
Tb11.01.1690	1,1,15,3,7	1054,187,110,108,102	hypothetical protein, conserved
Tb927.6.4080	4,2,4,1,2,1	48,109,114,143,254,265	hypothetical protein, conserved
Tb11.01.8070	1,5,2,1,2,3,1	-220,137,140,716,746,764,1447	hypothetical protein, conserved
Tb927.7.1910	11,9,2	72,44,-1648	glycine dehydrogenase, putative
Tb10.389.1880	5,3,2	110,32,2	hypothetical protein, conserved
Tb927.8.2170	11,9,2	71,22,0	hypothetical protein, conserved
Tb927.4.1130	1,2,3	-8,3,16	hypothetical protein, conserved
Tb09.211.3000	50,40	271,268	hypothetical protein, conserved
Tb927.8.2670	1,12,2,3,1,3,22,1	2790,2722,2714,1743, 1352,221,14,-459	hypothetical protein, conserved
Tb10.70.5130	3,1,15,20,6	768,544,258,255,32	adenylate kinase, putative
Tb927.7.2700	38,41	13,42	NADH-cytochrome b5 reductase, putative
Tb09.160.2060	5,4	170,146	hypothetical protein, conserved
Tb927.8.3130	2,1,1,1	41,21,15,-6	S-adenosyl-methyltransferase mraW-like protein, putative
Tb11.02.4600	1,2,1	224,280,289	hypothetical protein, conserved
Tb927.8.4150	9,9	276,352	hypothetical protein, conserved
Tb927.6.2510	1,1	119,15	hypothetical protein, conserved
Tb11.02.5670	2,5,9	50,193,242	hypothetical protein, conserved
Tb927.1.730	7,1,2,2,1	15,616,642,643,644	hypothetical protein, conserved
Tb10.389.1910	5,4,7,1	194,167,151,102	hypothetical protein, conserved
Tb10.70.6690	6,1,1,6,3	168,279,282,779,784	hypothetical protein, conserved
Tb10.26.0600	1,5,6,2	1144,534,79,66	hypothetical protein, conserved
Tb927.7.3800	2,2	29,32	hypothetical protein, conserved
Tb927.8.4470	4,9,1,2,1	-40,-35,38,47,57	chaperone protein DNAJ, putative
Tb927.3.4420	3,5,3,1	23,62,72,73	hypothetical protein, conserved
Tb09.211.4880	2,6,2,1	51,152,185,331	cyclophilin-like protein, putative
Tb10.70.2900	1,2,4,1	681,64,24,17	2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor, putative
Tb927.1.1210	2,3,1	798,194,-43	hypothetical protein, conserved
Tb927.1.1330	11,15,11,1	20,19,16,0	hypothetical protein, conserved
Tb10.v4.0043	3,3	24,64	branched-chain alpha-keto acid dehydrogenase e1-beta subunit precursor, putative
Tb927.3.770	2,2,1,2	54,57,72,488	hypothetical protein, conserved
Tb10.389.0590	1,1,3,1	87,94,181,204	hypothetical protein, conserved
Tb927.6.3740	1,8,3,5	27,37,43,58	heat shock 70 kDa protein, mitochondrial precursor, putative
Tb927.6.4540	1,1,9,1,1,1,1,3,1	2,8,33,48,50,52,486,489,522	3-hydroxy-3-methylglutaryl-CoA reductase, putative
Tb09.211.2600	20,10,21,3,1	883,880,93,69,38	hypothetical protein, conserved
Tb927.5.2810	1,1,2	47,132,1004	hypothetical protein, conserved
Tb927.3.950	6,12,1,2	2144,258,249,-38	hypothetical protein, conserved
Tb927.8.1420	8,1,1,5,2,1	196,181,96,88,80,-1460	acyl-CoA dehydrogenase, mitochondrial precursor, putative

Tb927.7.2990	1,3,8,17,3,2	1124,873,869,203,200,126	hypothetical protein, conserved
Tb09.211.0330	2,9,46,29	574,582,593,596	chaperone protein DNAJ, putative
Tb927.8.1700	2,4,14,2,22	-201,-198,-196,-38,114	hypothetical protein, conserved
Tb11.01.6320	16,15,43	65,626,629	hypothetical protein, conserved
Tb11.01.8230	1,1,1,1,1	-1109,8,198,217,284	hypothetical protein, conserved
Tb09.160.3370	8,11,1,1	366,361,342,19	hypothetical protein, conserved
Tb927.6.4070	4,25,26	12,33,34	hypothetical protein, conserved
Tb927.4.2550	4,2,2,1,1,2,3,1,29,37,4	482,364,343,317,296,284,264,259,235,224,221	hypothetical protein, conserved
Tb927.1.3010	2,7,9,9	127,63,39,22	hypothetical protein, conserved
Tb10.6k15.0490	1,4,23,5,6	98,97,80,77,65	mitochondrial intermediate peptidase, putative; metallo-peptidase, Clan MA(E) Family M3
Tb11.02.0355	1,5,8,2,1,1	-195,339,364,392,393,404	hypothetical protein, conserved
Tb11.01.6710	1,1,1,1	-8,-5,36,37	hypothetical protein, conserved
Tb927.6.680	2,2,1	191,246,4946	hypothetical protein, conserved
Tb927.5.3140	3,2,3	121,208,289	hypothetical protein, conserved
Tb927.8.2530	1,65,58,3,9,1	1400,953,936,915,113,101	hypothetical protein, conserved
Tb927.2.4700	1,3,1,1,3,2,1	429,438,529,885,2036,2042,2292	hypothetical protein, conserved
Tb927.7.2560	5,5	298,311	hypothetical protein, conserved
Tb11.01.7900	1,1,1	26,42,73	hypothetical protein, conserved
Tb11.02.2460	6,10,8,2,20,1	1507,1506,1502,1490,32,20	hypothetical protein, conserved
Tb10.26.0700	1,1,1,2	86605,77676,853,847	hypothetical protein
Tb11.01.3200	17,6,22	751,584,101	hypothetical protein, conserved
Tb927.8.3330	10,16,1	-37,-43,-50	mitochondrial carrier protein, putative
Tb927.7.5550	7,1,1,2,5,4,5,4	314,295,278,265,0,-58,-61,-101	hypothetical protein, conserved
Tb09.160.4750	3,1,12,6,9,1	89,85,66,52,-7,-23	hypothetical protein, conserved
Tb11.02.3810	1,3,40,32	384,403,413,425	hypothetical protein, conserved
Tb10.70.2090	14,12,1	241,238,210	RNA-editing complex protein; KREPA6
Tb10.v4.0053	6,4	125,146	hypothetical protein
Tb927.3.820	1,1,1,3	42,49,75,81	hypothetical protein, conserved
Tb11.02.1350	2,1,1,4,3	292,268,263,234,215	hypothetical protein, conserved
Tb927.7.800	19,20	27,42	hypothetical protein, conserved
Tb927.8.8170	1,26,1,28,1,7,44	1230,1229,1210,1034,1029,168,53	hypothetical protein, conserved
Tb927.8.4960	20,9,12,1,1,3,1,1,3,11,3	610,608,600,562,146,128,62,49,30,10,-76	hypothetical protein, conserved
Tb927.8.1060	3,3	171,203	malonyl-CoA decarboxylase, mitochondrial precursor, putative
Tb927.8.6040	2,3,1,2073,1,1,2072,4883,107,12,37	1794,1789,1784,1754,1752,1209,1207,697,693,690,10	hypothetical protein, conserved
Tb927.6.4450	3,1,1,2	29,84,91,162	hypothetical protein, conserved
Tb11.01.8710	1,1	981,985	hypothetical protein, conserved
Tb11.12.0014	19,1,1,20,1	389,385,370,12,-125	hypothetical protein, conserved
Tb10.70.5960	9,29,11	77,71,60	hypothetical protein, conserved
Tb11.55.0016	2,1,3	82,112,117	hypothetical protein, conserved
Tb927.7.2220	1,1,1,3,3	90,95,309,365,707	hypothetical protein, conserved

Tb11.01.0500	137,3,139	772,767,45	hypothetical protein, conserved
Tb09.211.4580	1,1,3,4,2	172,208,213,242,247	hypothetical protein, conserved
Tb10.61.1260	59,32,42	125,116,110	hypothetical protein, conserved
Tb10.389.0900	1,7,11,1	31,43,158,716	hypothetical protein, conserved
Tb927.2.4130	1,1,3,5,13	-316,-311,22,75,83	enoyl-CoA hydratase/Enoyl-CoA isomerase/3-hydroxyacyl-CoA dehydrogenase, putative
Tb927.5.1790	1,2,3,1,7	482,98,81,64,46	hypothetical protein, conserved
Tb09.v4.0018	2,2	85,41	expression site-associated gene (ESAG) protein, putative; expression site-associated gene 3 (ESAG3) protein, putative
Tb09.160.1280	2,3,1,3,3	-12,-9,0,9,52	hypothetical protein, conserved
Tb927.7.2620	1,1	151,182	hypothetical protein, conserved
Tb11.02.3470	1,1,1	252,240,237	formin, putative; formin-like protein
Tb927.5.2780	1,1,1,7,5	52,86,125,128,409	mitochondrial DNA polymerase beta
Tb927.8.620	2,4,1,42,1,37	95,102,113,122,129,150	RNA-editing complex protein MP42
Tb11.02.2710	13,9	202,121	hypothetical protein, conserved
Tb10.61.1300	4,1,2,1	202,188,186,175	hypothetical protein, conserved
Tb11.55.0009	1,140,21,185,36,1	2,7,148,151,159,515	mitochondrial RNA binding protein 1; gBP21, MRP1
Tb927.5.2070	1,2,9,3,8,8,1,6	9,42,43,52,60,80,84,88	hypothetical protein, conserved
Tb927.2.4830	1,2,1	65,73,96	TFIIF-stimulated CTD phosphatase, putative
Tb927.7.7440	3,8,2,13	175,205,1832,1836	hypothetical protein, conserved
Tb927.4.2940	7,3,14,1,2	1413,137,55,25,13	hypothetical protein, conserved
Tb09.160.2220	3,15,1,3,7,1,1,1	52,35,34,27,24,19,-47,-79	hypothetical protein, conserved
Tb11.47.0020	1,7,2,11,3	726,724,719,64,62	hypothetical protein, conserved
Tb11.02.0320	2,11,15,9,16	84,106,109,111,151	hypothetical protein, conserved
Tb927.6.1840	5,32,22,1,2,3	226,245,248,253,254,259	hypothetical protein, conserved
Tb09.160.0370	15,10,1,1,7	80,93,129,130,134	hypothetical protein, conserved
Tb927.5.4040	14,9,1	68,71,107	hypothetical protein, conserved
Tb09.160.0760	6,1,3	0,70,82	hypothetical protein, conserved
Tb11.01.6080	1,1,1,1	110,54,48,17	ubiquitin carboxyl-terminal hydrolase, putative
Tb927.2.2400	2,2	65,144	hypothetical protein, conserved
Tb927.5.2150	1,15,1,1,3,...	-1120,11,21,151,729,...	hypothetical protein, conserved
Tb10.406.0100	1,3,2	19,21,29	hypothetical protein, conserved
Tb927.5.2100	1,1,1,15,1,21,1	-157,69,94,96,100,101,118	hypothetical protein, conserved
Tb11.01.4740	1,18,3,3,126,78,2,1	-94,38,46,242,252,260,275,279	hypothetical protein, conserved
Tb10.70.5780	1,1,1	55,51,15	hypothetical protein, conserved
Tb927.6.2490	1,9,23,8	42,-8,-11,-33	hypothetical protein, conserved
Tb11.02.2700	3,8,1,3	164,106,47,-88	fumarate hydratase class I, putative
Tb11.02.0290	3,7,6	74,76,79	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative
Tb10.70.4380	6,6	80,46	cytochrome C oxidase assembly protein, putative
Tb927.4.1540	14,1,1,1,32,3,38	168,566,590,750,765,779,781	hypothetical protein, conserved
Tb927.8.3830	3,2,5,6	111,118,208,212	ATP-dependent DEAD/H RNA helicase,

			putative
Tb10.389.0020	3,3	261,322	phosphatidic acid phosphatase alpha, putative
Tb927.7.7230	1,5,3,1	65,69,461,465	nitroreductase, putative
Tb11.02.2280	20,46,14	263,202,196	hypothetical protein, conserved
Tb927.3.1410	37,19,7,3	941,116,94,79	cytochrome oxidase subunit VII
Tb11.01.7340	2,6,10	146,152,155	hypothetical protein, conserved
Tb927.7.3970	1,30,3,23	498,493,475,457	hypothetical protein, conserved
Tb11.01.0150	2,2,2,1,1	429,425,421,389,238	hypothetical protein, conserved
Tb11.01.6180	1,1,1	95,60,-194	hypothetical protein, conserved
Tb927.2.3420	3,6,2,1	178,389,391,497	hypothetical protein, conserved
Tb927.8.7260	22,3,2,2,1,50,6,5,1,30,1	1850,1845,1335,982,981,958,913,54,47,6,-87	kinetoplast-associated protein, putative
Tb927.4.2250	1,3,3,1	272,186,175,166	hypothetical protein, conserved
Tb11.01.0710	5,5,1	-5,-15,-28	elongation factor G2-like protein
Tb11.01.4702	1,1,10,38,1,11,20	1,8,30,35,1738,1744,3777	cytochrome oxidase subunit X
Tb10.389.0890	3,5,5	168,184,210	pyruvate dehydrogenase E1 alpha subunit, putative
Tb09.160.0890	1,10,15,4	-242,-238,-208,-136	hypothetical protein, conserved
Tb927.8.7290	1,11,7,1	131,109,106,36	hypothetical protein, conserved
Tb11.02.4800	4,13,13	-65,-59,47	NADH-cytochrome b5 reductase-like protein
Tb927.7.3470	1,1,1,3	15,67,795,1078	p22 protein precursor, putative
Tb11.01.2920	5,5	32,4	hypothetical protein, conserved
Tb927.2.3800	2,1,1,1,4	9,600,603,629,4817	hypothetical protein, conserved
Tb927.6.4400	4,1,1,2,1	29,66,67,91,162	hypothetical protein, conserved
Tb09.244.2860	...,14,1,120,3,1	...,3810,1982,1979,41,39,35	hypothetical protein, conserved
Tb927.2.5140	6,5,1	24,14,5	hypothetical protein, conserved
Tb927.8.2760	2,2	49,45	hypothetical protein, conserved
Tb927.8.2190	3,1,16,3,6	567,32,27,9,6	hypothetical protein, conserved
Tb927.3.4700	1,9,4,2,3,2,1	31,36,54,81,106,107,2093	hypothetical protein, conserved
Tb11.02.3230	3,2,1	239,222,174	hypothetical protein, conserved
Tb09.211.1610	1,1,2	79,87,125	phosphatidylserine decarboxylase, putative
Tb11.01.2340	10,1,11	196,195,166	hypothetical protein, conserved
Tb927.8.680	2,1,8,9	-150,-20,49,714	RNA-editing complex protein
Tb927.7.3990	2,3,4	1133,1128,471	mitochondrial DNA polymerase I protein C
Tb11.01.6580	2,1,3	131,134,158	hypothetical protein, conserved
Tb927.8.5280	1,26,1,21,1,2	55,42,39,37,5,0	hypothetical protein, conserved
Tb10.100.0220	4,4,1	16,11,5	mitochondrial structure specific endonuclease I(SSE-1), putative
Tb10.70.0660	4,8,3	-3546,94,107	hypothetical protein, conserved
Tb11.01.1040	3,9,3,3	166,90,75,69	hypothetical protein, conserved
Tb927.3.4140	2,3,2	16,18,583	hypothetical protein, conserved

Table S11. Alternative splice variants that potentially change N-terminus of the corresponding protein and the corresponding localization signal (M, mitochondrial; S, secretory)

	Canonical		Alternative	
Gene ID	Size (aa)	Loc.	Size (aa)	Loc.
Tb927.2.4130	803	M	367	-
			350	
Tb927.4.3300	719	M	393	-
			324	
			314	
Tb927.5.1790	631	M	549	-
Tb927.5.2150	529	-	398	M
Tb927.5.3640	270	M	229	-
			188	
Tb927.5.680	585	M	517	-
			417	
			363	
Tb927.6.4450	603	M	384	-
			368	S
Tb927.7.1910	970	M	828	-
			776	
			746	
			711	
Tb927.7.2220	669	M	419	-
Tb927.7.2490	703	M	561	S
Tb927.7.2560	1205	M	971	S
			817	S
			762	-
Tb927.7.3990	1649	M	803	-
Tb927.7.560	773	M	684	-
			455	
Tb927.8.2670	428	M	295	S
			244	-
			190	-
Tb927.8.2880	1131	M	640	-
Tb09.160.4130	411	M	332	-
Tb09.160.4310	992	M	807	-
			775	
Tb09.211.4880	384	M	243	-
			236	
Tb10.70.0660	1508	M	1469	-
			646	
			637	
Tb10.70.4120	556	-	371	M
Tb10.70.4280	561	M	348	-
Tb10.70.5430	192	M	87	-
Tb10.70.5510	600	M	417	-
Tb11.01.1040	668	M	613	-
			585	

			523	
			434	
			420	
Tb11.01.1660	553	M	466	-
Tb11.01.6080	442	M	269	-
Tb11.01.8230	1068	M	712	-
Tb11.02.0130	747	M	654	-
Tb11.02.0355	271	M	133	-
Tb11.02.0430	383	M	166	-
Tb11.02.5820	527	M	441	-
Tb11.12.0014	277	M	124	-
Tb11.55.0016	831	M	698	-
Tb09.160.0360	204	M	337	-
Tb10.26.0860	243	-	337	M
Tb11.02.3810	351	-	459	M
Tb927.4.4910	400	M	470	S
Tb927.7.7090	152	M	308	S
Tb927.7.7090	152		312	