

**Table: Proteins used in phylogenetic analysis**

Gene model	Putative function	<i>T. equi</i> length (aa)	Alignment length (aa)	PI <sup>A</sup>	# MPT <sup>B</sup>	Topology <sup>C</sup>
BEWA_028760 <sup>D</sup>	<i>myosin A</i>	835	847	409	1	A
BEWA_005330	<i>eukaryotic translation initiation factor</i>	733	789	401	1	A
BEWA_037430	<i>DNA replication licensing factor MCM5</i>	779	859	322	1	A
BEWA_049210	<i>adenosylhomocysteinase</i>	492	507	306	1	A
BEWA_009450	<i>heat shock protein 70kD</i>	654	671	301	1	A
BEWA_017580	<i>vacuolar ATP synthase subunit C</i>	406	453	263	1	A
BEWA_043900	<i>protein kinase domain containing protein</i>	503	542	239	1	A
BEWA_037580	<i>DnaJ domain containing protein</i>	420	455	230	1	A
BEWA_019520	<i>heat shock protein 90 (HSP90)</i>	717	766	220	1	A
BEWA_032130	<i>chaperonin-60kD, ch60</i>	534	559	208	1	A
BEWA_041190	<i>cell division cycle protein 48</i>	804	858	193	1	A
BEWA_037520	<i>clathrin-adaptor chain</i>	441	492	192	1	A
BEWA_034850	<i>conserved hypotheticalprotein</i>	202	254	152	1	A
BEWA_015100	<i>proteasome subunit alpha type</i>	260	274	150	1	A
BEWA_022370	<i>vacuolar ATP synthase subunit D</i>	237	259	139	1	A
BEWA_009590	<i>enolase</i>	443	479	135	1	A
BEWA_031590	<i>60S acidic ribosomal protein P0</i>	314	326	134	1	A
BEWA_017550	<i>histone deacetylase</i>	449	472	132	1	A
BEWA_045860	<i>adenylate kinase</i>	246	262	125	1	A
BEWA_010440	<i>vacuolar sorting protein 26</i>	272	330	124	1	A
BEWA_038400	<i>eukaryotic translation initiation factor 4A</i>	392	396	123	1	A
BEWA_045060	<i>protein transport protein Sec61</i>	477	481	122	1	A
BEWA_011020	<i>40S ribosomal protein S7</i>	193	217	113	1	A
BEWA_027970	<i>conserved hypothetical protein</i>	194	222	113	1	A
BEWA_019150	<i>proteasome regulatory subunit</i>	312	315	112	1	A
BEWA_010900	<i>vacuolar proton-translocating ATPase</i>	181	217	109	1	A
BEWA_010860	<i>proteasome subunit alpha type</i>	238	258	106	1	A
BEWA_052280	<i>Ras-related protein Rab1b (small GTP-binding protein)</i>	221	230	98	1	A
BEWA_052650	<i>40S ribosomal protein S19</i>	173	173	96	1	A
BEWA_052880	<i>40S ribosomal protein S3a</i>	263	265	94	1	A
BEWA_042640	<i>60S ribosomal protein L2/L8</i>	260	261	93	1	A
BEWA_031840	<i>translationally controlled tumor protein</i>	175	175	90	1	A
BEWA_027590	<i>60S ribosomal protein L18a</i>	190	193	89	1	A
BEWA_053410	<i>60S ribosomal protein L28</i>	138	168	88	1	A
BEWA_030290	<i>60S ribosomal protein L6</i>	190	190	87	1	A
BEWA_021630	<i>nucleoside diphosphate kinase</i>	150	175	86	1	A
BEWA_038020	<i>protein kinase domain containing protein</i>	290	302	81	1	A
BEWA_018030	<i>60S ribosomal protein L27e</i>	149	165	76	1	A
BEWA_024780	<i>eukaryotic translation initiation factor 2, beta subunit</i>	243	248	76	1	A
BEWA_032210	<i>DNA-directed RNA polymerase subunit rpb8</i>	146	151	73	1	A

BEWA_009670	60S acidic ribosomal protein P1	116	123	72	1	A
BEWA_044990	multiprotein bridging factor type	147	160	71	1	A
BEWA_020290	60S ribosomal protein L27a	145	158	56	1	A
BEWA_006560	60S ribosomal protein L22	123	45	55	1	A
BEWA_008940	40S ribosomal protein S3	219	236	55	1	A
BEWA_030910	60S ribosomal protein L11	172	175	48	1	A
BEWA_026740	translation initiation factor eIF-1A	154	176	44	1	A
BEWA_014410	60S ribosomal protein L37a	95	96	36	1	A
BEWA_005410	40S ribosomal protein S14	152	173	31	1	A
BEWA_028110	histone H2b	124	131	22	1	A
BEWA_025390	conserved hypothetical protein	165	198	115	1	B
BEWA_038070	ubiquitin-conjugating enzyme family member protein	198	219	76	1	B
BEWA_026400	eukaryotic peptide chain release factor	428	446	137	1	B
BEWA_009700	vacuolar ATP synthase catalytic subunit A	612	627	241	1	B
BEWA_027570	60S ribosomal protein L18	184	229	65	1	B
BEWA_009410	conserved hypothetical protein	248	278	180	1	B
BEWA_013610	40S ribosomal protein S4	184	206	79	1	B
BEWA_051440	40S ribosomal protein S8	191	223	76	1	B
BEWA_007100	pyruvate kinase	516	544	249	1	B
BEWA_045850	diphthinesynthase	271	320	131	1	B
BEWA_032470	prohibitin	279	318	85	1	B
BEWA_011610	importin alpha	532	583	301	1	B
BEWA_005460	60S ribosomal protein L12	166	169	57	1	B
BEWA_031600	60S ribosomal protein L38	79	101	53	1	B
BEWA_006190	LSM domain containing protein	122	161	64	1	B
BEWA_012260	60S ribosomal protein L34a	145	162	83	1	B
BEWA_020360	60S ribosomal protein L23	140	146	26	1	B
BEWA_009500	phosphoglycerate mutase	250	303	117	1	B
BEWA_016650	40S ribosomal protein S27	83	86	24	1	B
BEWA_007700	ADP-ribosylation factor family member protein	196	219	82	1	B
BEWA_027890	conserved hypothetical protein	199	211	144	1	B
BEWA_010040	40S ribosomal protein	280	296	113	1	B
BEWA_020160	60S ribosomal protein L30	109	111	43	1	B
BEWA_038930	actin	382	430	209	1	B
BEWA_011640	DNA-directed RNA polymerase	206	214	66	1	B
BEWA_031870	small GTP-binding protein domain containing protein	367	368	85	1	B
BEWA_019950	chaperonin containing t-complex protein 1, epsilon subunit	536	575	234	1	B
BEWA_040690	conserved hypothetical protein	76	113	52	1	B
BEWA_005070	60S ribosomal protein L36	117	120	63	1	B
BEWA_049420	60S ribosomal protein L19	180	201	74	1	C
BEWA_024880	1-acyl-sn-glycerol-3-phosphate acyltransferase	276	314	173	1	C
BEWA_018100	60S ribosomal protein L5e	307	326	152	1	C
BEWA_010270	60S ribosomal protein L26	138	175	51	1	C

BEWA_019170	conserved hypothetical protein	173	201	107	1	C
BEWA_008800	vacuolar ATP synthase subunit	385	430	206	1	C
BEWA_010850	proteasome subunit alpha type	256	272	104	1	C
BEWA_025460	60S ribosomal protein L17	188	209	87	1	C
BEWA_016270	60S ribosomal protein L24	178	212	100	1	C
BEWA_014640	glucose-6-phosphate isomerase	555	615	301	1	C
BEWA_005310	40S ribosomal protein S24	136	160	61	1	C
BEWA_011460	conserved hypothetical protein	130	145	58	1	C
BEWA_030920	40S ribosomal protein S18	155	156	49	1	C
BEWA_024030	proliferating cell nuclear antigen 2	268	305	134	1	D
BEWA_042550	ubiquitin domain containing protein	91	125	30	1	D
BEWA_001300	26S protease regulatory subunit	397	412	112	1	D
BEWA_003280	60S ribosomal protein L1	218	221	82	1	D
BEWA_043560	chaperonin containing t-complex protein1, theta subunit	539	591	329	1	D
BEWA_008860	conserved hypothetical protein	180	199	116	1	D
BEWA_026680	DNA-directed RNA polymerase I	316	385	172	1	D
BEWA_039360	U6 small nuclear ribonucleoprotein E	89	134	46	1	E
BEWA_050030	chaperonin containing t-complex protein 1, alpha subunit	547	574	226	1	E
BEWA_054840	60S ribosomal protein L35a	118	146	58	1	F
BEWA_018170	transcription factor btf3	162	227	95	1	F
BEWA_006940	N-acetyltransferase	153	192	104	1	G
BEWA_019530	ADP-ribosylation factor put.	182	189	65	1	G
BEWA_051470	chaperonin-60kD, ch60	540	573	279	1	G
BEWA_020790	signal peptide containing protein	412	466	258	1	G
BEWA_010610	conserved hypothetical protein	279	313	120	1	H
BEWA_027050	40S ribosomal protein S2	262	292	71	1	H
BEWA_007000	proteasome subunit beta type 3	218	244	101	1	I
BEWA_013620	40S ribosomal protein S28	68	68	13	1	J
BEWA_011470	S-adenosylmethionine synthetase	401	435	167	2	AB
BEWA_006110	proteasome subunit alpha type	277	301	136	2	AB
BEWA_052640	40S ribosomal protein S12	143	170	67	2	AB
BEWA_040030	eukaryotic translation initiation factor 2 alpha subunit	331	366	136	2	AB
BEWA_030470	conserved hypothetical protein	258	367	163	2	AB
BEWA_031760	conserved hypothetical protein	118	154	76	2	AB
BEWA_019430	60S ribosomal protein L37	92	103	32	2	AB
BEWA_037530	26S proteasome regulatory subunit 7	426	460	107	2	AC
BEWA_018280	U6 small nuclear ribonucleoprotein	94	98	50	2	AD
BEWA_039830	26S proteasome subunit 4	440	457	90	2	AC
BEWA_017900	40S ribosomal protein S8	131	137	31	2	AD
BEWA_020460	translation initiation factor 6	250	280	90	2	AC
BEWA_031130	bet3 transport protein	186	206	88	2	AD
BEWA_024530	splicing factor 3A subunit 2	238	256	124	2	AC
BEWA_010820	er lumen protein retaining receptor	224	223	88	2	AD

BEWA_013500	replication factor C subunit 4	325	357	147	2	AC
BEWA_042350	60S ribosomal protein L10e	229	235	152	2	AC
BEWA_017790	nuclear transport factor 2	125	169	74	2	BG
BEWA_000870	40S ribosomal protein S15	149	152	53	2	BC
BEWA_052490	60S ribosomal protein L7	259	268	111	2	BC
BEWA_010950	40S ribosomal protein S10	113	155	58	2	BO
BEWA_020010	conserved hypothetical protein	188	246	94	2	BC
BEWA_034410	DnaJ domain containing protein	388	409	244	2	BF
BEWA_041030	actin depolymerizing factor	120	136	92	2	EH
BEWA_052070	60S ribosomal protein L15	206	222	56	2	DE
BEWA_052600	small nuclear ribonucleoprotein G	105	111	50	2	CN
BEWA_014000	prohibitin	273	296	95	2	CD
BEWA_002990	60S ribosomal protein L32	133	137	69	2	DE
BEWA_041920	ribosomal protein S26	115	115	36	2	DF
BEWA_013830	U6 snRNA-associated Sm-like protein LSm8	95	115	53	2	CR
BEWA_044960	40S ribosomal protein S5	194	207	37	3	ABD
BEWA_018110	60S ribosomal protein L7a	270	289	134	3	ACD
BEWA_021800	vacuolar ATP synthase subunit f	123	141	56	3	ACE
BEWA_028610	40S ribosomal protein S13e	152	154	46	3	CPQ
BEWA_018190	60S ribosomal protein L10	229	228	62	3	CEI
BEWA_041010	60S ribosomal protein L31	119	120	59	3	CDF
BEWA_024170	histone H2a	153	164	24	3	DFG
BEWA_010100	ribosomal protein S27	165	168	90	3	DFG
BEWA_041310	small ribonucleoprotein D1	120	148	46	7	ADEHKLM

<sup>A</sup> Number of parsimony informative characters (calculated using PAUP\*).

<sup>B</sup> Number of equally parsimonious trees recovered.

<sup>C</sup> See Figure S3 for tree topologies A-D.

<sup>D</sup> Protein sequences producing most commonly recovered topology, sorted by parsimony informative characters are boxed.