**Supplementary Table S3:** Functional roles of each of the 400 putative gene products used for inferring *Bradyrhizobium* phylogeny.

			Kyoto Encyclopedia of Genes and Genomes (KEGG)					
Gene number	Gene identifier <sup>a</sup>	KEGG Orthology	KEGG Annotation	Functional class	Definition	Amino Acid model		
1	BJ6T_00940		Uncharacterised	Unclassified		JTT		
2	BJ6T_00960	K02050	NitT/TauT family transport system permease protein  NitT/TauT family transport system ATP-	Mineral and organic ion transport system  Mineral and organic ion transport	ABC.SN.P	LG		
3	BJ6T_00970	K02049	binding protein	system	ABC.SN.A	JTT		
4	BJ6T_01730	K05524	ferredoxin	Energy metabolism	fdxA	Dayhoff		
5	BJ6T_01770	K02902	large subunit ribosomal protein L28	Translation	RP-L28	DCMut		
6	BJ6T_01900		Uncharacterised	Unclassified		JTT		
7	BJ6T_01930	K09882	cobaltochelatase CobS	Metabolism of cofactors and vitamins	cobS	LG		
8	BJ6T_01980		Uncharacterised	Unclassified		DCMut		
9	BJ6T_02010	K01735	3-dehydroquinate synthase	Amino acid metabolism	aroB	JTT		
10	BJ6T_02040	K04763	integrase/recombinase XerD	Chromosome and associated proteins	xerD	JTT		
11	BJ6T_02180	K03574	8-oxo-dGTP diphosphatase	DNA repair and recombination proteins	mutT	LG		
12	BJ6T_02220	K11206	deaminated glutathione amidase	Unclassified metabolism	NIT1	CpREV		
13	BJ6T_02230		Uncharacterised	Unclassified		JTT		
14	BJ6T_02290	K02835	peptide chain release factor 1	Translation factors	prfA	JTT		
15	BJ6T_02440	K00023	acetoacetyl-CoA reductase	Carbohydrate metabolism	phbB	JTT		
16	BJ6T_02460		Uncharacterised	Unclassified		JTT		
17	BJ6T_02900	K01087	trehalose 6-phosphate phosphatase	Carbohydrate metabolism	otsB	WAG		
18	BJ6T_02910		Uncharacterised	Unclassified		JTT		
19	BJ6T_03810		Uncharacterised	Unclassified		JTT		
20	BJ6T_03820	K02888	large subunit ribosomal protein L21	Translation	RP-L21	LG		
21	BJ6T_03830	K02899	large subunit ribosomal protein L27	Translation	RP-L27	Dayhoff		
22	BJ6T_03960	K09710	ribosome-associated protein	Ribosome biogenesis	ybeB	JTT		

23	BJ6T_04010	K08311	putative (di)nucleoside polyphosphate hydrolase	Folding, sorting and degradation	nudH	JTT
			F-type H+-transporting ATPase subunit			
24	BJ6T_04040	K02114	epsilon F-type H+-transporting ATPase subunit	Energy metabolism	ATPF1E	LG
25	BJ6T_04050	K02112	beta	Energy metabolism	ATPF1B	LG
	_			Energy metabolism		
26	BJ6T_04240	K01903	succinyl-CoA synthetase beta subunit	Carbohydrate metabolism	sucC	Dayhoff
27	BJ6T_04270	K01975	RNA 2',3'-cyclic 3'-phosphodiesterase	Transfer RNA biogenesis	thpR	LG
28	BJ6T_04330		Uncharacterised	Unclassified		JTT
29	BJ6T_04340		Uncharacterised	Unclassified		LG
30	BJ6T_04410	K06190	intracellular septation protein	Cell growth	ispZ	LG
				Cellular processes		
31	BJ6T_04420	K03110	fused signal recognition particle receptor	Membrane Transport	ftsY	JTT
32	BJ6T_04470		Uncharacterised	Unclassified		JTT
33	BJ6T_04510	K02959	small subunit ribosomal protein S16	Translation	RP-S16	JTT
34	BJ6T_04540	K02884	large subunit ribosomal protein L19	Translation	RP-L19	LG
35	BJ6T_04690	K01673	carbonic anhydrase	Energy metabolism	cynT	WAG
				Metabolism of other secondary metabolites		
36	BJ6T_04700	K00133	aspartate-semialdehyde dehydrogenase	Amino acid metabolism	asd	LG
37	BJ6T_04740	K00052	3-isopropylmalate dehydrogenase	Amino acid metabolism	leuB	LG
38	BJ6T_04800	K18661	malonyl-CoA/methylmalonyl-CoA synthetase	Amino acid metabolism	matB	JTT
39	BJ6T_04830	K00242	succinate dehydrogenase / fumarate reductase, membrane anchor subunit	Energy metabolism	sdhD	LG
40	BJ6T_04990	1100272	Uncharacterised	Unclassified	30110	LG
		K06207			turo A	LG
41	BJ6T_05100	K06207	GTP-binding protein	Signaling proteins	typA	
42	BJ6T_05160		Uncharacterised	Unclassified		JTT
43	BJ6T_05170	K01507	inorganic pyrophosphatase methylenetetrahydrofolate	Energy metabolism	ppa	LG
44	BJ6T_05180	K01491	dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase	Metabolism of cofactors and vitamins	folD	JTT
45	BJ6T_05200	K02221	YggT family protein	Secretion system	yggT	LG

46	BJ6T_05640	K07157	Uncharacterised	Unclassified		JTT
47	BJ6T_05880		Uncharacterised	Unclassified		LG
48	BJ6T_05890		Uncharacterised	Unclassified		JTT
49	BJ6T_05900		Uncharacterised	Unclassified		JTT
50	BJ6T_05990	K03496	chromosome partitioning protein	Chromosome and associated proteins	parA	JTT
51	BJ6T_06030	K03628	transcription termination factor Rho	Folding, sorting and degradation	rho	LG
52	BJ6T_06060	K06287	septum formation protein	Cell growth	maf	JTT
53	BJ6T_06070	K00859	dephospho-CoA kinase	Metabolism of cofactors and vitamins	coaE	WAG
54	BJ6T_06090	K03071	preprotein translocase subunit SecB	Cellular processes	secB	JTT
55	BJ6T_06100		Uncharacterised	Unclassified		JTT
56	BJ6T_06120		Uncharacterised	Unclassified		JTT
57	BJ6T_06140	K03667	ATP-dependent HsIUV protease ATP-binding subunit HsIU	Chaperones and folding catalysts	hslU	LG
58	BJ6T_06170	K01419	ATP-dependent HsIUV protease, peptidase subunit HsIV	Peptidases	hsIV	LG
59	BJ6T_06200	K02501	glutamine amidotransferase	Amino acid metabolism	hisH	WAG
60	BJ6T_06230	K01523	phosphoribosyl-ATP pyrophosphohydrolase	Amino acid metabolism	hisE	Dayhoff
61	BJ6T_06240	K00867	type I pantothenate kinase	Metabolism of cofactors and vitamins	coaA	LG
62	BJ6T_06350	K01920	glutathione synthase	Amino acid metabolism	gshB	WAG
63	BJ6T_06360	K07460	putative endonuclease	Unclassified	yraN	LG
64	BJ6T_06370	K07056	16S rRNA (cytidine1402-2'-O)- methyltransferase	Ribosome biogenesis	rsml	JTT
65	BJ6T_06390		Uncharacterised	Unclassified		JTT
66	BJ6T_06400	K02428	XTP/dITP diphosphohydrolase	Nucleotide metabolism	rdgB	JTT
67	BJ6T_06410	K00989	ribonuclease PH	Transfer RNA biogenesis	rph	JTT
68	BJ6T_06430	K03687	molecular chaperone GrpE	Folding, sorting and degradation	GRPE	JTT
69	BJ6T_06460	K04043	molecular chaperone DnaK	Folding, sorting and degradation	dnaK	JTT
70	BJ6T_06470	K03686	molecular chaperone DnaJ	Folding, sorting and degradation	dnaJ	JTT
71	BJ6T_06570	K00215	4-hydroxy-tetrahydrodipicolinate reductase	Metabolism of other secondary metabolites	dapB	WAG

	T.			T	T	1
72	BJ6T_06600		Uncharacterised	Unclassified		LG
73	BJ6T_06640		Uncharacterised	Unclassified		LG
74	BJ6T_06700	K21600	CsoR family transcriptional regulator, copper-sensing transcriptional repressor	Unclassified	csoR	JTT
75	BJ6T_06740	K01890	phenylalanyl-tRNA synthetase beta chain	Translation	FARSB	JTT
76	BJ6T_06760	K01889	phenylalanyl-tRNA synthetase alpha chain	Translation	FARSA	JTT
77	BJ6T_06780	K02887	large subunit ribosomal protein L20	Translation	RP-L20	LG
78	BJ6T_06820		Uncharacterised	Unclassified		WAG
79	BJ6T_07070	K03684	ribonuclease D	Transfer RNA biogenesis	rnd	Dayhoff
80	BJ6T_07230		Uncharacterised	Unclassified		JTT
81	BJ6T_07240		Uncharacterised	Unclassified		JTT
82	BJ6T_07340		Uncharacterised	Unclassified		JTT
83	BJ6T_07350	K00800	3-phosphoshikimate 1- carboxyvinyltransferase	Amino acid metabolism	aroA	WAG
84	BJ6T_07430	K01695	tryptophan synthase alpha chain	Amino acid metabolism	trpA	WAG
85	BJ6T_07440	K01963	acetyl-CoA carboxylase carboxyl transferase subunit beta	Lipid metabolism	accD	LG
86	BJ6T_07450	K11754	dihydrofolate synthase / folylpolyglutamate synthase	Metabolism of cofactors and vitamins	folC	JTT
87	BJ6T_07500	K00992	N-acetyl-alpha-D-muramate 1-phosphate uridylyltransferase	Carbohydrate metabolism	murU	WAG
88	BJ6T_07600	K03688	ubiquinone biosynthesis protein	Unclassified metabolism	ubiB	JTT
89	BJ6T_07620	K10563	formamidopyrimidine-DNA glycosylase	Replication and repair	mutM	JTT
90	BJ6T_07730	K01716	3-hydroxyacyl-	Lipid metabolism	fabA	JTT
				Metabolism of cofactors and vitamins		
91	BJ6T_07740	K00647	3-oxoacyl-	Lipid metabolism	fabB	LG
92	BJ6T_07810	K04761	LysR family transcriptional regulator, hydrogen peroxide-inducible genes activator	Cellular processes	oxyR	JTT
93	BJ6T_07840	K04761	small subunit ribosomal protein S15	Translation	RP-S15	JTT
93	BJ6T_07860	K02930	ribosome-binding factor A	Ribosome biogenesis	rbfA	LG
95	BJ6T_07890	K02600	N utilization substance protein A	Transcription machinery	nusA	LG
			phosphate starvation-inducible protein			
96	BJ6T_07980	K06217	PhoH and related proteins	Signaling proteins	phoH	JTT

97	BJ6T_08010	K03711	Fur family transcriptional regulator, ferric uptake regulator	Transcription factors	fur	JTT
98	BJ6T_08020	K03789	Uncharacterised	Ribosome biogenesis	riml	JTT
99	BJ6T_08030	K14742	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB	Transfer RNA biogenesis	tsaB	JTT
100	BJ6T_08050		Uncharacterised	Unclassified		Dayhoff
101	BJ6T_08070	K01867	tryptophanyl-tRNA synthetase	Translation	WARS	JTT
102	BJ6T_08350	K02338	DNA polymerase III subunit beta	Replication and repair	dnaN	Dayhoff
103	BJ6T_08360	K02313	chromosomal replication initiator protein	Cellular processes	dnaA	JTT
104	BJ6T_08370	K02968	small subunit ribosomal protein S20	Translation	RP-S20	LG
105	BJ6T_08380		Uncharacterised	Unclassified		LG
106	BJ6T_09160		Uncharacterised	Unclassified		JTT
107	BJ6T_09170	K15012	two-component system, response regulator RegA	Signal Transduction	regA	JTT
108	BJ6T_09490	K09823	Fur family transcriptional regulator, zinc uptake regulator	Cellular processes	zur	JTT
109	BJ6T_09630	K00795	farnesyl diphosphate synthase	Metabolism of terpenoids and polyketides	ispA	WAG
110	BJ6T_09640	K03814	monofunctional glycosyltransferase	Glycan biosynthesis and metabolism	mtgA	JTT
111	BJ6T_09830		Uncharacterised	Unclassified		JTT
112	BJ6T_11680		Uncharacterised	Unclassified		JTT
113	BJ6T_11720		Uncharacterised	Unclassified		LG
114	BJ6T_11740	K07577	putative mRNA 3-end processing factor	Translation		JTT
115	BJ6T_11850		Uncharacterised	Unclassified		JTT
116	BJ6T_11880	K06985	aspartyl protease family protein	Cellular processes		LG
117	BJ6T_11920	K05800	Lrp/AsnC family transcriptional regulator	Transcription factors	ybaO	JTT
118	BJ6T_11950		Uncharacterised	Unclassified		JTT
119	BJ6T_12060	K06187	recombination protein RecR	Replication and repair	recR	Dayhoff
120	BJ6T_12100	K01462	peptide deformylase	Unclassified metabolism	PDF	LG
121	BJ6T_12190	K00930	acetylglutamate kinase	Amino acid metabolism	argB	LG
			YidC/Oxa1 family membrane protein	Cellular processes		
122	BJ6T_12220	K03217	insertase	Membrane Transport	yidC	LG
123	BJ6T_13280	K00013	histidinol dehydrogenase	Amino acid metabolism	hisD	WAG

124	BJ6T_13290		Uncharacterised	Unclassified		JTT
125	BJ6T_13300		Uncharacterised	Unclassified		JTT
126	BJ6T_13750		Uncharacterised	Unclassified		LG
120	D301_13730		cell division transport system ATP-	Officiassified		
127	BJ6T_14940	K09812	binding protein	Membrane Transport	ftsE	LG
128	BJ6T_15010	K00817	histidinol-phosphate aminotransferase	Metabolism of other secondary metabolites	hisC	LG
129	BJ6T_15440	K03088	RNA polymerase sigma-70 factor, ECF subfamily	Transcription machinery	rpoE	Dayhoff
130	BJ6T_16040	K04564	superoxide dismutase, Fe-Mn family	Cellular processes	SOD2	LG
131	BJ6T_16080	K02074	zinc/manganese transport system ATP- binding protein	Transporters	ABC.ZM.A	JTT
132	BJ6T_16100	K02077	zinc/manganese transport system substrate-binding protein	Transporters	ABC.ZM.S	JTT
133	BJ6T_16160	K00808	homospermidine synthase	Metabolism of other secondary metabolites	hss	LG
134	BJ6T_16250	K01772	protoporphyrin/coproporphyrin ferrochelatase	Metabolism of cofactors and vitamins	hemH	JTT
135	BJ6T_16320	K06041	arabinose-5-phosphate isomerase	Glycan biosynthesis and metabolism	kdsD	JTT
				Signal Transduction  Metabolism of other secondary metabolites		
136	BJ6T_16480	K01092	myo-inositol-1(or 4)-monophosphatase	Carbohydrate metabolism		JTT
137	BJ6T_16500	K13589	two-component system, cell cycle response regulator CpdR	Signal Transduction	cpdR	LG
138	BJ6T_17410		Uncharacterised	Unclassified		LG
139	BJ6T_17560		Uncharacterised	Unclassified		JTT
140	BJ6T_17570		Uncharacterised	Unclassified		JTT
141	BJ6T_17600		Uncharacterised	Unclassified		LG
142	BJ6T_17770		Uncharacterised	Unclassified		LG
143	BJ6T_17840		Uncharacterised	Unclassified		LG
144	BJ6T_17910	K01945	phosphoribosylamineglycine ligase	Nucleotide metabolism	purD	WAG
145	BJ6T_18050	K07263	zinc protease	Peptidases	pqqL	JTT
146	BJ6T_18110		Uncharacterised	Unclassified		WAG
147	BJ6T_18180	K03635	molybdopterin synthase catalytic subunit	Folding, sorting and degradation	MOCS2B	JTT

148	BJ6T_18200	K08744	cardiolipin synthase (CMP-forming)	Lipid metabolism	CRLS	LG
149	BJ6T_18230	K07115	23S rRNA (adenine2030-N6)- methyltransferase	Ribosome biogenesis	rlmJ	JTT
150	BJ6T_18250	KU/115	Uncharacterised	Unclassified	TITIO	LG
151	BJ6T_18300		Uncharacterised	Unclassified		JTT
152	BJ6T_18330	K01892		Translation	HARS	WAG
	_	KU1092	histidyl-tRNA synthetase		ПАКО	
153	BJ6T_18540 BJ6T_18550	K13292	Uncharacterised phosphatidylglycerol:prolipoprotein diacylglycerol transferase	Unclassified Unclassified metabolism	lgt	JTT LG
155	BJ6T_18570	K09806	uncharacterized protein	Unclassified	<u> </u>	LG
156	BJ6T_18660		Uncharacterised	Unclassified		JTT
157	BJ6T_18870	K00799	glutathione S-transferase	Metabolism of other secondary metabolites	GST	JTT
158	BJ6T_18890		Uncharacterised	Unclassified		LG
159	BJ6T_19060	K00831	phosphoserine aminotransferase	Metabolism of cofactors and vitamins	serC	LG
160	BJ6T_19330		Uncharacterised	Unclassified		Dayhoff
161	BJ6T_19430	K09117	uncharacterized protein	Unclassified		Dayhoff
162	BJ6T_22800	K00873	pyruvate kinase	Nucleotide metabolism	PK	JTT
163	BJ6T_22830		Uncharacterised	Unclassified		LG
164	BJ6T_22870		Uncharacterised	Unclassified		JTT
165	BJ6T_23030	K01588	5-(carboxyamino)imidazole ribonucleotide mutase	Nucleotide metabolism	purE	JTT
166	BJ6T_23120		Uncharacterised	Unclassified		JTT
				Amino acid metabolism		
167	BJ6T_23570	K01939	adenylosuccinate synthase	Nucleotide metabolism	purA	WAG
168	BJ6T_24030	K02417	flagellar motor switch protein FliN/FliY	Cell motility	fliNY	JTT
169	BJ6T_24050	K02410	flagellar motor switch protein FliG	Cell motility	fliG	LG
170	BJ6T_26890		Uncharacterised	Unclassified		LG
171	BJ6T_27370		Uncharacterised	Unclassified		JTT
172	BJ6T_27670	K03147	phosphomethylpyrimidine synthase	Metabolism of cofactors and vitamins	thiC	WAG
173	BJ6T_28220	K01000	phospho-N-acetylmuramoyl- pentapeptide-transferase	Glycan biosynthesis and metabolism	mraY	LG

174	BJ6T_28320	K02535	UDP-3-O-	Glycan biosynthesis and metabolism	lpxC	JTT
174	D301_20320	102333	ABC-2 type transport system permease	Giycan biosynthesis and metabolism	ірхС	311
175	BJ6T_28480	K01992	protein	Transporters	ABC-2.P	LG
176	D ICT 20400	K04000	ABC-2 type transport system ATP-	Transportare	ABC 2 A	JTT
176	BJ6T_28490	K01990	binding protein	Transporters	ABC-2.A	JII
				Energy metabolism		
177	BJ6T_29130	K01679	fumarate hydratase, class II	Carbohydrate metabolism  Metabolism of cofactors and		JTT
				vitamins		
178	BJ6T_29220	K00560	thymidylate synthase	Nucleotide metabolism	thyA	JTT
179	BJ6T_29260	K04087	membrane protease subunit HflC	Unclassified	hflC	LG
179	D301_29200	1104007	membrane protease subunit rino	Metabolism of cofactors and	TIIIC	LG
				vitamins		
180	BJ6T_29310	K01652	acetolactate synthase I/II/III large subunit	Carbohydrate metabolism		LG
				Metabolism of cofactors and		
				vitamins		
181	BJ6T_29330	K01653	acetolactate synthase I/III small subunit	Carbohydrate metabolism  Metabolism of other secondary		LG
				metabolism of other secondary		
182	BJ6T_34860	K00121	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	Carbohydrate metabolism	frmA	WAG
183	BJ6T_37590	K01251	adenosylhomocysteinase	Amino acid metabolism		LG
184	BJ6T_37880		Uncharacterised	Unclassified		JTT
185	BJ6T_38080		Uncharacterised	Unclassified		JTT
186	BJ6T_38260	K04755	ferredoxin, 2Fe-2S	Unclassified	fdx	Dayhoff
187	BJ6T_38280	K00384	thioredoxin reductase (NADPH)	Metabolism of other amino acids	trxB	LG
188	BJ6T_38540	K02396	flagellar hook-associated protein 1 FlgK	Cell motility	flgK	LG
189	BJ6T_38600	K06601	flagellar protein FlbT	Unclassified	flbT	LG
190	BJ6T_38660		Uncharacterised	Unclassified		LG
191	BJ6T_38770	K02392	flagellar basal-body rod protein FlgG	Cell motility	flgG	LG
192	BJ6T_38780	K02391	flagellar basal-body rod protein FlgF	Cell motility	flgF	LG
193	BJ6T_38790	K02415	flagellar FliL protein	Bacterial motility proteins	fliL	LG
194	BJ6T_38930	K02388	flagellar basal-body rod protein FlgC	Cell motility	flgC	JTT
195	BJ6T_38940	K02408	flagellar hook-basal body complex protein FliE	Cell motility	fliE	JTT

196	BJ6T_38950	K02420	flagellar biosynthetic protein FliQ	Cell motility	fliQ	LG
197	BJ6T_38960	K02421	flagellar biosynthetic protein FliR	Cell motility	fliR	LG
198	BJ6T_38990	1102121	Uncharacterised	Unclassified		LG
199	BJ6T_39800	K03553	recombination protein RecA	Replication and repair	recA	LG
200	BJ6T_39850	K01872	alanyl-tRNA synthetase	Translation	AARS	JTT
201	BJ6T_40000	K01952	phosphoribosylformylglycinamidine synthase	Nucleotide metabolism	purL	JTT
202	BJ6T_40020	K01952	phosphoribosylformylglycinamidine synthase	Nucleotide metabolism	purL	WAG
203	BJ6T_40140		Uncharacterised	Unclassified		LG
204	BJ6T_40170		Uncharacterised	Unclassified		JTT
205	BJ6T_40180	K07390	monothiol glutaredoxin	Chaperones and folding catalysts	grxD	JTT
206	BJ6T_40930		Uncharacterised	Unclassified		JTT
207	BJ6T_41290		Uncharacterised	Unclassified		WAG
208	BJ6T_41620		Uncharacterised	Unclassified		JTT
209	BJ6T_41640		Uncharacterised	Unclassified		JTT
210	BJ6T_41650		Uncharacterised	Unclassified		LG
211	BJ6T_42020		Uncharacterised	Unclassified		JTT
212	BJ6T_42130		Uncharacterised	Unclassified		LG
213	BJ6T_42250	K08998	uncharacterized protein	Unclassified		JTT
214	BJ6T_42270		Uncharacterised	Unclassified		Dayhoff
215	BJ6T_42280	K01495	GTP cyclohydrolase IA	Metabolism of cofactors and vitamins	GCH1	LG
216	BJ6T_42290	K01496	phosphoribosyl-AMP cyclohydrolase	Amino acid metabolism	hisl	JTT
217	BJ6T_42310		Uncharacterised	Unclassified		JTT
218	BJ6T_43710	K02601	transcriptional antiterminator NusG	Ribosome biogenesis	nusG	LG
219	BJ6T_43720	K02867	large subunit ribosomal protein L11	Translation	RP-L11	LG
220	BJ6T_43750	K02864	large subunit ribosomal protein L10	Translation	RP-L10	LG
221	BJ6T_43870	K02906	large subunit ribosomal protein L3	Translation	RP-L3	LG
222	BJ6T_43890	K02892	large subunit ribosomal protein L23	Translation	RP-L23	LG
223	BJ6T_43920	K02890	large subunit ribosomal protein L22	Translation	RP-L22	LG
224	BJ6T_43930	K02982	small subunit ribosomal protein S3	Translation	RP-S3	LG

225	BJ6T_43940	K02878	large subunit ribosomal protein L16	Translation	RP-L16	LG
226	BJ6T_43960	K02961	small subunit ribosomal protein S17	Translation	RP-S17	Dayhoff
227	BJ6T_43970	K02874	large subunit ribosomal protein L14	Translation	RP-L14	LG
228	BJ6T_43980	K02895	large subunit ribosomal protein L24	Translation	RP-L24	LG
229	BJ6T_43990	K02931	large subunit ribosomal protein L5	Translation	RP-L5	LG
230	BJ6T_44000	K02954	small subunit ribosomal protein S14	Translation	RP-S14	DCMut
231	BJ6T_44010	K02994	small subunit ribosomal protein S8	Translation	RP-S8	LG
232	BJ6T_44020	K02933	large subunit ribosomal protein L6	Translation	RP-L6	JTT
233	BJ6T_44030	K02881	large subunit ribosomal protein L18	Translation	RP-L18	Dayhoff
234	BJ6T_44060	K02876	large subunit ribosomal protein L15	Translation	RP-L15	LG
				Cellular processes		
235	BJ6T_44070	K03076	preprotein translocase subunit SecY	Membrane Transport	secY	LG
236	BJ6T_44090	K02952	small subunit ribosomal protein S13	Translation	RP-S13	LG
237	BJ6T_44100	K02948	small subunit ribosomal protein S11	Translation	RP-S11	JTT
238	BJ6T_44120	K02879	large subunit ribosomal protein L17	Translation	RP-L17	LG
239	BJ6T_44200	K07478	putative ATPase	Replication and repair	ycaJ	LG
240	BJ6T_44230		Uncharacterised	Unclassified		JTT
241	BJ6T_45560	K06891	ATP-dependent Clp protease adaptor protein ClpS	Protein processing	clpS	RtREV
242	BJ6T_45800	K11443	two-component system, cell cycle response regulator DivK	Signal Transduction	divK	JTT
243	BJ6T_45810	K02488	two-component system, cell cycle response regulator	Signal Transduction	pleD	LG
244	BJ6T_46190	K00609	aspartate carbamoyltransferase catalytic subunit	Amino acid metabolism	pyrB	LG
245	BJ6T_46300	K02435	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C	Translation	gatC	JTT
246	BJ6T_46340	K02434	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B	Translation	gatB	JTT
247	BJ6T_46470	K03060	DNA-directed RNA polymerase subunit omega	Transcription	rpoZ	LG
248	BJ6T_46490	K03474	pyridoxine 5-phosphate synthase	Metabolism of cofactors and vitamins	pdxJ	WAG
249	BJ6T_46500	K00997	holo-	Metabolism of cofactors and vitamins	acpS	WAG

250	BJ6T_46520	K03685	ribonuclease III	Translation	rnc	JTT
251	BJ6T_46530	K03595	GTPase	Ribosome biogenesis	era	WAG
252	BJ6T_46740		Uncharacterised	Unclassified		JTT
253	BJ6T_46780	K07738	transcriptional repressor NrdR	Transcription factors	nrdR	JTT
054	D.IOT. 40000	1/00700		Metabolism of cofactors and		177
254	BJ6T_46800	K00793	riboflavin synthase	vitamins  Metabolism of cofactors and	ribE	JTT
255	BJ6T_46810	K00794	6,7-dimethyl-8-ribityllumazine synthase	vitamins	ribH	LG
256	BJ6T_46840	K15987	K(+)-stimulated pyrophosphate-energized sodium pump	Energy metabolism	hppA	LG
257	BJ6T_46870	K17662	cytochrome b pre-mRNA-processing protein 3	Uncharacterised	CBP3	JTT
258	BJ6T_46910	K04764	integration host factor subunit alpha	Chromosome and associated proteins	ihfA	LG
259	BJ6T_47120		Uncharacterised	Unclassified		LG
260	BJ6T_47130		Uncharacterised	Unclassified		LG
261	BJ6T_47180		Uncharacterised	Unclassified		LG
262	BJ6T_47210	K01740	O-acetylhomoserine (thiol)-lyase	Amino acid metabolism	metY	LG
263	BJ6T_47250	K02871	large subunit ribosomal protein L13	Translation	RP-L13	LG
264	BJ6T_47260	K02996	small subunit ribosomal protein S9	Translation	RP-S9	Dayhoff
265	BJ6T_47690	K00330	NADH-quinone oxidoreductase subunit A	Energy metabolism	nuoA	LG
266	BJ6T_47720	K00333	NADH-quinone oxidoreductase subunit D	Energy metabolism	nuoD	LG
267	BJ6T_47740	K00334	NADH-quinone oxidoreductase subunit E	Energy metabolism	nuoE	WAG
268	BJ6T_47790	K00338	NADH-quinone oxidoreductase subunit I	Energy metabolism	nuol	LG
269	BJ6T_47800	K00339	NADH-quinone oxidoreductase subunit J	Energy metabolism	nuoJ	LG
270	BJ6T_47810	K00340	NADH-quinone oxidoreductase subunit K	Energy metabolism	nuoK	MtArt
271	BJ6T_47830	K00342	NADH-quinone oxidoreductase subunit M	Energy metabolism	nuoM	LG
272	BJ6T_47840	K00343	NADH-quinone oxidoreductase subunit N	Energy metabolism	nuoN	LG
273	BJ6T_47880		Uncharacterised	Unclassified		LG
274	BJ6T_48260	K09810	lipoprotein-releasing system ATP-binding protein	Membrane Transport	lolD	LG
275	BJ6T_48520	K09903	uridylate kinase	Nucleotide metabolism	pyrH	JTT
276	BJ6T_48530	K02838	ribosome recycling factor	Translation factors	frr	LG

277	BJ6T_48550	K00981	phosphatidate cytidylyltransferase	Signal Transduction		LG
278	BJ6T_48570	K11749	regulator of sigma E protease	Cellular processes	rseP	LG
279	BJ6T_48600	K02372	3-hydroxyacyl- UDP-N-acetylglucosamine	Metabolism of cofactors and vitamins	fabZ	LG
280	BJ6T_48620	K00677	acyltransferase	Glycan biosynthesis and metabolism	lpxA	LG
281	BJ6T_48730	K01885	glutamyl-tRNA synthetase	Translation  Metabolism of cofactors and vitamins	EARS	Dayhoff
282	BJ6T_48740	K01886	glutaminyl-tRNA synthetase	Translation	QARS	LG
283	BJ6T_48850	K01356	repressor LexA	DNA repair and recombination proteins	lexA	JTT
284	BJ6T_48970	K03637	cyclic pyranopterin monophosphate synthase	Folding, sorting and degradation  Metabolism of cofactors and vitamins	moaC	WAG
285	BJ6T_49010	K01803	triosephosphate isomerase (TIM)	Energy metabolism  Carbohydrate metabolism	TPI	JTT
				Amino acid metabolism		
286	BJ6T_49340	K00382	dihydrolipoamide dehydrogenase	Carbohydrate metabolism	DLD	LG
287	BJ6T_49600		Uncharacterised	Unclassified		Dayhoff
288	BJ6T_49670	K03116	sec-independent protein translocase protein TatA	Membrane Transport	tatA	LG
289	BJ6T_49680	K03117	sec-independent protein translocase protein TatB	Membrane Transport	tatB	LG
				Metabolism of cofactors and vitamins		
290	BJ6T_49720	K03787	5'-nucleotidase	Nucleotide metabolism	surE	WAG
291	BJ6T_49740	K00573	protein-L-isoaspartate(D-aspartate) O-methyltransferase	Unclassified metabolism		JTT
				Cellular processes		
292	BJ6T_49840	K03210	preprotein translocase subunit YajC	Membrane Transport	yajC	LG
293	BJ6T_49860	K03074	preprotein translocase subunit SecF	Membrane Transport	secF	LG
294	BJ6T_50300	K00954	pantetheine-phosphate adenylyltransferase	Metabolism of cofactors and vitamins		JTT
295	BJ6T_50330		Uncharacterised	Unclassified		WAG
296	BJ6T_50750		Uncharacterised	Unclassified		JTT

297	BJ6T_50810		Uncharacterised	Unclassified		LG
298	BJ6T_50950	K11940	heat shock protein HspQ	Chromosome and associated proteins	hspQ	JTT
299	BJ6T_50970	K03185	2-octaprenyl-6-methoxyphenol hydroxylase	Metabolism of cofactors and vitamins	ubiH	JTT
300	BJ6T_52050	K03642	rare lipoprotein A	Structural proteins	rlpA	LG
301	BJ6T_52130	K00943	dTMP kinase	Nucleotide metabolism	tmk	JTT
302	BJ6T_52170	K06167	phosphoribosyl 1,2-cyclic phosphate phosphodiesterase	Metabolism of other amino acids	phnP	WAG
				Cellular processes		
303	BJ6T_52510	K03666	host factor-I protein	Folding, sorting and degradation	hfq	Blosum62
304	BJ6T_53350	K01738	cysteine synthase A	Amino acid metabolism	cysK	LG
305	BJ6T_53360	K09972	general L-amino acid transport system ATP-binding protein	Membrane Transport	aapP	JTT
306	BJ6T_53380	K09970	general L-amino acid transport system permease protein	Membrane Transport	aapQ	LG
307	BJ6T_53420		Uncharacterised	Unclassified		LG
308	BJ6T_53720		Uncharacterised	Unclassified		JTT
309	BJ6T_54220	K02356	elongation factor P	Translation factors	efp	LG
			fructose-1,6-bisphosphatase II /	Energy metabolism	glpX-	
310	BJ6T_54480	K11532	sedoheptulose-1,7-bisphosphatase	Carbohydrate metabolism	SEBP	LG
311	BJ6T_54590		Uncharacterised	Unclassified		LG
312	BJ6T_54740	K13628	iron-sulfur cluster assembly protein	Transfer RNA biogenesis	iscA	LG
313	BJ6T_54750		Uncharacterised	Unclassified		JTT
314	BJ6T_55160		Uncharacterised	Unclassified		LG
315	BJ6T_55240	K00684	leucyl/phenylalanyl-tRNAprotein transferase	Unclassified metabolism	aat	JTT
316	BJ6T_56870	K11175	phosphoribosylglycinamide formyltransferase 1	Metabolism of cofactors and vitamins	purN	JTT
317	BJ6T_56890	K08744	cardiolipin synthase (CMP-forming)	Lipid metabolism	CRLS	JTT
318	BJ6T_56900		Uncharacterised	Unclassified		JTT
				Signal Transduction		
319	BJ6T_56970	K00940	nucleoside-diphosphate kinase	Nucleotide metabolism	ndk	JTT
320	BJ6T_57080	K07091	lipopolysaccharide export system permease protein	Membrane Transport	lptF	LG

321	BJ6T_57260		Uncharacterised	Unclassified		JTT
322	BJ6T_57290	K02078	acyl carrier protein	Fatty acid biosynthesis	acpP	Dayhoff
323	BJ6T_57350	K02963	small subunit ribosomal protein S18	Translation	RP-S18	Dayhoff
324	BJ6T_57370	K02939	large subunit ribosomal protein L9	Translation	RP-L9	LG
325	BJ6T_57690		Uncharacterised	Unclassified		JTT
326	BJ6T_57750	K03306	inorganic phosphate transporter, PiT family	Transporters	TC.PIT	LG
327	BJ6T_57760	K07220	uncharacterized protein	Unclassified		JTT
328	BJ6T_57830		Uncharacterised	Unclassified		JTT
329	BJ6T_58650	K02427	23S rRNA (uridine2552-2'-O)- methyltransferase	Ribosome biogenesis	rlmE	LG
330	BJ6T_58790	K00020	3-hydroxyisobutyrate dehydrogenase	Amino acid metabolism	mmsB	JTT
331	BJ6T_60520		Uncharacterised	Unclassified		LG
332	BJ6T_60530	K02372	3-hydroxyacyl-	Lipid metabolism	fabZ	LG
333	BJ6T_60540	K09458	3-oxoacyl-	Metabolism of cofactors and vitamins	fabF	JTT
334	BJ6T_60560	K02517	Kdo2-lipid IVA lauroyltransferase	Glycan biosynthesis and metabolism	lpxL	LG
335	BJ6T_60570	K11073	putrescine transport system substrate- binding protein	Membrane Transport	potF	JTT
336	BJ6T_60620	K02557	chemotaxis protein MotB	Cell motility	motB	LG
337	BJ6T_60630	K02556	chemotaxis protein MotA	Cell motility	motA	LG
			CDP-diacylglycerolserine O-	Amino acid metabolism		
338	BJ6T_60670	K17103	phosphatidyltransferase	Lipid metabolism	CHO1	LG
339	BJ6T_60700	K06966	pyrimidine/purine-5'-nucleotide nucleosidase	Nucleotide metabolism	ppnN	LG
340	BJ6T_60730	K03830	putative acetyltransferase	Unclassified metabolism	yafP	LG
341	BJ6T_61250	K00383	glutathione reductase (NADPH)	Metabolism of other amino acids	GSR	LG
342	BJ6T_61260	K09924	uncharacterized protein	Unclassified		LG
343	BJ6T_61450		Uncharacterised	Unclassified		LG
344	BJ6T_66370	K02483	two-component system	Signal Transduction		JTT
345	BJ6T_66450		Uncharacterised	Unclassified		JTT
346	BJ6T_66930	K11357	two-component system, cell cycle sensor histidine kinase DivJ	Signal Transduction	divJ	JTT

347	BJ6T_66950	K02426	cysteine desulfuration protein SufE	Poorly characterized	sufE	Dayhoff
348	BJ6T_67000		Uncharacterised	Unclassified		WAG
349	BJ6T_67040		Uncharacterised	Unclassified		JTT
350	BJ6T_67050	K00796	dihydropteroate synthase	Metabolism of cofactors and vitamins	folP	JTT
351	BJ6T_67060	K01633	7,8-dihydroneopterin aldolase/epimerase/oxygenase	Metabolism of cofactors and vitamins	folB	JTT
352	BJ6T_67620		Uncharacterised	Unclassified		WAG
353	BJ6T_67650	K21678	presqualene diphosphate synthase	Unclassified metabolism	hpnD	WAG
354	BJ6T_67660	K21679	hydroxysqualene synthase	Unclassified metabolism	hpnC	JTT
355	BJ6T_69770	K06196	cytochrome c-type biogenesis protein	Transporters	ccdA	JTT
356	BJ6T_71470		Uncharacterised	Unclassified		WAG
357	BJ6T_71480	K03602	exodeoxyribonuclease VII small subunit	Replication and repair	xseB	LG
358	BJ6T_71770		Uncharacterised	Unclassified		LG
359	BJ6T_72570		Uncharacterised	Unclassified		Dayhoff
360	BJ6T_72580		Uncharacterised	Unclassified		JTT
361	BJ6T_72650	K01246	DNA-3-methyladenine glycosylase I	Replication and repair	tag	JTT
362	BJ6T_72680		Uncharacterised	Unclassified		JTT
363	BJ6T_72740		Uncharacterised	Unclassified		LG
364	BJ6T_72770	K03517	quinolinate synthase	Metabolism of cofactors and vitamins	nadA	WAG
365	BJ6T_72790	K00767	nicotinate-nucleotide pyrophosphorylase (carboxylating)	Metabolism of cofactors and vitamins	nadC	JTT
366	BJ6T_73150	K13581	modification methylase	Cellular processes	ccrM	LG
367	BJ6T_73300		Uncharacterised	Unclassified		JTT
368	BJ6T_73430	K03216	tRNA (cytidine/uridine-2'-O-)- methyltransferase	Transfer RNA biogenesis	trmL	JTT
369	BJ6T_73460	K00228	coproporphyrinogen III oxidase	Metabolism of cofactors and vitamins	CPOX	Dayhoff
370	BJ6T_73660	K03924	MoxR-like ATPase	Unclassified metabolism	moxR	JTT
371	BJ6T_73770		Uncharacterised	Unclassified		JTT
372	BJ6T_74000	K00111	glycerol-3-phosphate dehydrogenase	Lipid metabolism	glpA	WAG
373	BJ6T_76480		Uncharacterised	Unclassified		JTT

374	BJ6T_76590	K13588	histidine phosphotransferase ChpT	Cellular processes	chpT	JTT
375	BJ6T_83160	K01934	5-formyltetrahydrofolate cyclo-ligase	Metabolism of cofactors and vitamins	MTHFS	WAG
373	B301_83100	K01954	5-iomylietranyurorolate cyclo-iigase	Energy metabolism	WITTES	WAG
376	BJ6T_83210	K00927	phosphoglycerate kinase	Carbohydrate metabolism	PGK	Dayhoff
370	B301_83210	N00921	priospriogrycerate kinase	Signal Transduction	FGR	Dayrion
				Metabolism of other secondary metabolites		
377	BJ6T_83270	K01092	myo-inositol-1(or 4)-monophosphatase	Carbohydrate metabolism		LG
378	BJ6T_83370	K02909	large subunit ribosomal protein L31	Translation	RP-L31	LG
379	BJ6T_83530	K07735	putative transcriptional regulator	Transcription factors	algH	Dayhoff
380	BJ6T_83540		Uncharacterised	Unclassified		JTT
381	BJ6T_83570	K00019	3-hydroxybutyrate dehydrogenase	Lipid metabolism		LG
382	BJ6T_83590		Uncharacterised	Unclassified		LG
383	BJ6T_83640	K00390	phosphoadenosine phosphosulfate reductase	Energy metabolism	cysH	JTT
384	BJ6T_84000	K02518	translation initiation factor IF-1	Translation factors	infA	CpREV
385	BJ6T_84060	K02278	prepilin peptidase CpaA	Secretion system	сраА	JTT
386	BJ6T_84130	K12511	tight adherence protein C	Secretion system	tadC	LG
387	BJ6T_84180		Uncharacterised	Unclassified		JTT
388	BJ6T_84210	K13894	microcin C transport system permease protein	Membrane Transport	yejB	LG
389	BJ6T_86740		Uncharacterised	Unclassified		JTT
390	BJ6T_86770	K02108	F-type H+-transporting ATPase subunit a	Energy metabolism	ATPF0A	LG
391	BJ6T_86790	K02109	F-type H+-transporting ATPase subunit b	Energy metabolism	ATPF0B	Dayhoff
392	BJ6T_86880	K14998	surfeit locus 1 family protein	Unclassified	SURF1	JTT
393	BJ6T_86910	K02258	cytochrome c oxidase assembly protein subunit 11	Energy metabolism	COX11	Dayhoff
394	BJ6T_86940	K02274	cytochrome c oxidase subunit I	Energy metabolism	coxA	CpREV
395	BJ6T_86960		Uncharacterised	Unclassified		Dayhoff
396	BJ6T_87190		Uncharacterised	Unclassified		JTT
397	BJ6T_87250	K07226	heme iron utilization protein	Unclassified	hugZ	JTT
398	BJ6T_87290	K02793		Membrane Transport		Dayhoff

			PTS system, mannose-specific IIA component	Carbohydrate metabolism	PTS-Man- EIIA	
399	BJ6T_87300	K11189	phosphocarrier protein	Transporters	PTS-HPR	JTT
400	BJ6T_87680	K01265	methionyl aminopeptidase	Peptidases	map	WAG

 $<sup>^{\</sup>mathrm{a}}$  The highlighted text in the "Gene identifier" column refers to the genes used in the 128 Maximum likelihood dataset.