

S3 Table. Complete list of the 384 single copy genes.

Protein accession	Gene	RFD	Branch congruence measure	π	Description
number in	name		(%)		
<i>N. abscessus</i>					
NBRC 100374					
WP_083899681.1	NA	34	0.76	0.309	prolyl oligopeptidase family serine peptidase
WP_043696244.1	<i>mngC</i>	34	0.76	0.276	Acyl-CoA dehydrogenase
WP_043695513.1	<i>ppk</i>	36	0.77	0.305	Polyphosphate kinase
WP_043685774.1	<i>topA</i>	36	0.77	0.295	DNA topoisomerase
WP_043699045.1	<i>cysG</i>	36	0.77	0.283	Siroheme synthase
WP_043700493.1	NA	36	0.74	0.33	putative ABC transporter
WP_043699130.1	<i>metE</i>	38	0.88	0.313	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
WP_051169005.1	<i>ndh</i>	40	0.72	0.32	NADH dehydrogenase
WP_043686035.1	NA	42	0.73	0.338	trehalose-phosphatase
WP_043694756.1	<i>ftsK</i>	42	0.73	0.303	DNA translocase
WP_051169366.1	<i>hemL</i>	42	0.73	0.303	Glutamate-1-semialdehyde 2,1-aminomutase
WP_043700199.1	<i>leuS</i>	42	0.73	0.285	Leucine--tRNA ligase
WP_051168648.1	<i>folC</i>	42	0.72	0.303	Dihydrofolate synthase
WP_043685249.1	NA	42	0.71	0.309	Fatty acid ABC transporter
WP_043692156.1	<i>mshC</i>	42	0.7	0.316	L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase
WP_157229694.1	<i>nuoG</i>	42	0.7	0.313	NADH-quinone oxidoreductase subunit G
WP_043689770.1	<i>menE</i>	44	0.86	0.325	2-succinylbenzoate--CoA ligase
WP_043697332.1	<i>glgC</i>	44	0.72	0.31	Glucose-1-phosphate adenylyltransferase
WP_043685900.1	<i>lysSI</i>	44	0.71	0.312	Lysine--tRNA ligase 1
WP_043685154.1	NA	44	0.71	0.31	cysteine desulfurase-like protein
WP_043699618.1	NA	44	0.71	0.31	HAD-IB family hydrolase
WP_043699464.1	<i>pta</i>	44	0.7	0.319	Phosphate acetyltransferase
WP_043695811.1	NA	44	0.7	0.315	Glycogen synthase
WP_043694528.1	NA	44	0.69	0.304	DEAD/DEAH box helicase
WP_174377743.1	NA	46	0.84	0.306	HAMP domain-containing protein
WP_051169086.1	<i>hflX</i>	46	0.71	0.302	GTPase HflX
WP_174377687.1	<i>uvrB</i>	46	0.71	0.296	UvrABC system protein B
WP_043689634.1	<i>uvrA</i>	46	0.71	0.293	UvrABC system protein A
WP_043685381.1	NA	46	0.71	0.288	Putative aminotransferase
WP_043697701.1	<i>cbs</i>	46	0.71	0.281	Putative cystathionine beta-synthase
WP_086006697.1	NA	46	0.7	0.311	acyltransferase
WP_043688567.1	<i>pepN</i>	46	0.7	0.301	Aminopeptidase N
WP_043687657.1	<i>glmS</i>	46	0.7	0.285	Glutamine--fructose-6-phosphate aminotransferase
WP_043687634.1	NA	46	0.69	0.326	ABC transporter
WP_043685622.1	<i>mtgA</i>	46	0.69	0.318	Biosynthetic peptidoglycan transglycosylase
WP_043697400.1	<i>fbiC</i>	46	0.69	0.313	FO synthase

WP_043697624.1	<i>fumC</i>	46	0.68	0.328	Fumarate hydratase class II
WP_043688748.1	NA	46	0.68	0.318	HlyC/CorC family transporter
WP_043692891.1	<i>cobN</i>	46	0.68	0.306	Aerobic cobaltochelatae subunit CobN
WP_043689536.1	<i>ilvA</i>	46	0.68	0.298	L-threonine dehydratase biosynthetic IlvA
WP_043684896.1	<i>embB</i>	46	0.67	0.309	putative arabinosyltransferase B
WP_043688262.1	<i>glgE</i>	46	0.67	0.306	Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase
WP_043686561.1	<i>dapB1</i>	48	0.85	0.261	Dipeptidyl aminopeptidase BI
WP_083899718.1	<i>lon</i>	48	0.84	0.287	Lon protease
WP_043693099.1	<i>metH</i>	48	0.7	0.285	Methionine synthase
WP_043688201.1	<i>argS</i>	48	0.69	0.305	Arginine--tRNA ligase
WP_043697784.1	<i>mfd</i>	48	0.69	0.3	Transcription-repair-coupling factor
WP_043696400.1	<i>pgm</i>	48	0.69	0.299	Phosphoglucomutase
WP_043695237.1	<i>yhgF</i>	48	0.69	0.288	Protein YhgF
WP_043685835.1	<i>dltA</i>	48	0.68	0.333	D-alanine--D-alanyl carrier protein ligase
WP_043699061.1	<i>sasA</i>	48	0.68	0.312	Adaptive-response sensory-kinase
WP_043696736.1	<i>pdtaS</i>	48	0.67	0.323	putative sensor histidine kinase
WP_174377666.1	<i>deoA</i>	48	0.67	0.321	Thymidine phosphorylase
WP_043688990.1	NA	48	0.67	0.32	helix-turn-helix domain-containing protein
WP_043685247.1	NA	48	0.67	0.318	putative ABC transporter
WP_043688272.1	<i>dinG</i>	48	0.67	0.315	putative ATP-dependent helicase
WP_043697950.1	<i>moeA1</i>	48	0.67	0.307	Molybdopterin molybdenumtransferase 1
WP_043699575.1	<i>dnaJ1</i>	48	0.67	0.297	Chaperone protein DnaJ 1
WP_043688260.1	<i>glgB</i>	48	0.66	0.316	1,4-alpha-glucan branching enzyme
WP_043697629.1	NA	48	0.66	0.315	PhoH family protein
WP_043693849.1	<i>pyrC</i>	48	0.66	0.303	Dihydroorotase
WP_043688778.1	<i>dnaG</i>	48	0.66	0.3	DNA primase
WP_043700394.1	NA	48	0.66	0.268	ABC transporter substrate-binding protein
WP_043695332.1	<i>frr</i>	50	0.83	0.296	Ribosome-recycling factor
WP_043696697.1	<i>moeZ</i>	50	0.83	0.278	adenylyltransferase/sulfurtransferase
WP_043696894.1	<i>algC</i>	50	0.68	0.316	Phosphomannomutase/phosphoglucomutase
WP_083899274.1	<i>polA</i>	50	0.68	0.313	DNA polymerase I
WP_043697326.1	<i>mrp</i>	50	0.68	0.292	Iron-sulfur cluster carrier protein
WP_043693088.1	<i>arc</i>	50	0.68	0.286	Proteasome-associated ATPase
WP_043686502.1	<i>purL</i>	50	0.68	0.269	Phosphoribosylformylglycinamide synthase
WP_043688202.1	<i>lysA</i>	50	0.67	0.294	Diaminopimelate decarboxylase
WP_043684743.1	<i>serS</i>	50	0.67	0.29	Serine--tRNA ligase
WP_174377697.1	<i>dapE</i>	50	0.67	0.285	Succinyl-diaminopimelate desuccinylase
WP_043686010.1	<i>radA</i>	50	0.66	0.32	DNA repair protein RadA
WP_043697651.1	NA	50	0.66	0.32	hypothetical protein
WP_043694444.1	<i>kimA</i>	50	0.66	0.31	Potassium transporter KimA
WP_043698038.1	<i>uvrD1</i>	50	0.66	0.303	ATP-dependent DNA helicase UvrD1
WP_043689746.1	<i>argJ</i>	50	0.66	0.294	Arginine biosynthesis bifunctional protein

WP_174377695.1	<i>nuoD</i>	50	0.65	0.288	NADH-quinone oxidoreductase subunit D
WP_169334193.1	<i>gmk</i>	52	0.82	0.322	Guanylate kinase
WP_043697370.1	<i>dapD</i>	52	0.82	0.305	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
WP_043685134.1	<i>glfT2</i>	52	0.67	0.32	Galactofuranosyltransferase GlfT2
WP_043697614.1	<i>glpX</i>	52	0.67	0.281	Fructose-1,6-bisphosphatase class 2
WP_043692966.1	<i>dop</i>	52	0.67	0.275	Pup deamidase/depupylase
WP_157229688.1	<i>secA1</i>	52	0.67	0.26	Protein translocase subunit SecA 1
WP_051168438.1	NA	52	0.66	0.312	FAD-binding oxidoreductase
WP_043699206.1	<i>ramB</i>	52	0.66	0.311	HTH-type transcriptional regulator
WP_043693670.1	<i>tkt</i>	52	0.66	0.271	Transketolase
WP_043684435.1	<i>pknB</i>	52	0.65	0.35	Serine/threonine-protein kinase
WP_043687599.1	<i>eccC</i>	52	0.65	0.322	ESX secretion system protein
WP_043689046.1	<i>glnE</i>	52	0.65	0.307	Bifunctional glutamine synthetase adenylyltransferase
WP_051169285.1	NA	52	0.64	0.324	EAL domain-containing protein
WP_043697695.1	<i>metB</i>	52	0.64	0.313	Cystathionine gamma-synthase
WP_043695755.1	<i>ligA</i>	52	0.64	0.301	DNA ligase A
WP_043699448.1	<i>btuD</i>	52	0.63	0.312	Vitamin B12 import ATP-binding protein
WP_040865365.1	NA	52	0.63	0.304	TetR family transcriptional regulator
WP_043685860.1	<i>gltC</i>	52	0.63	0.299	HTH-type transcriptional regulator
WP_051168722.1	<i>pheS</i>	52	0.63	0.286	Phenylalanine--tRNA ligase alpha subunit
WP_086006622.1	<i>pyk</i>	54	0.65	0.304	Pyruvate kinase
WP_043686458.1	<i>purB</i>	54	0.65	0.288	Adenylosuccinate lyase
WP_043699502.1	<i>purA</i>	54	0.65	0.282	Adenylosuccinate synthetase
WP_083899251.1	<i>ctaC</i>	54	0.65	0.279	Cytochrome c oxidase subunit 2
WP_043699749.1	NA	54	0.65	0.274	Acyl-CoA dehydrogenase fadE12
WP_043690243.1	NA	54	0.64	0.321	HlyC/CorC family transporter
WP_043689852.1	<i>der</i>	54	0.64	0.314	GTPase Der
WP_043694562.1	NA	54	0.64	0.31	DEAD/DEAH box helicase
WP_051168778.1	<i>gcvP</i>	54	0.64	0.309	putative glycine dehydrogenase
WP_043697796.1	<i>glmU</i>	54	0.64	0.308	Bifunctional protein
WP_043690683.1	NA	54	0.64	0.294	SDR family oxidoreductase
WP_043693348.1	NA	54	0.64	0.292	coenzyme F420-dependent oxidoreductase
WP_043687596.1	<i>eccD5</i>	54	0.63	0.306	ESX-5 secretion system protein
WP_051168435.1	<i>tgt</i>	54	0.61	0.292	Queuine tRNA-ribosyltransferase
WP_043684840.1	NA	56	0.81	0.295	Putative peptide transport permease protein
WP_043685876.1	<i>ftsH</i>	56	0.65	0.257	ATP-dependent zinc metalloprotease
WP_043698046.1	<i>pgi</i>	56	0.64	0.3	Glucose-6-phosphate isomerase
WP_051168485.1	<i>otsA</i>	56	0.64	0.297	Trehalose-6-phosphate synthase
WP_043687877.1	NA	56	0.64	0.291	hypothetical protein
WP_043689564.1	<i>trpC</i>	56	0.64	0.29	Indole-3-glycerol phosphate synthase
WP_043688667.1	<i>tig</i>	56	0.64	0.272	Trigger factor
WP_043688724.1	<i>fprB</i>	56	0.63	0.329	putative ferredoxin

WP_169334154.1	<i>fadD3</i>	56	0.63	0.325	CoA ligase
WP_043689786.1	<i>tyrS</i>	56	0.63	0.324	Tyrosine--tRNA ligase
WP_043700485.1	<i>sdhA</i>	56	0.63	0.315	Succinate dehydrogenase flavoprotein
WP_043686516.1	<i>purF</i>	56	0.63	0.312	Amidophosphoribosyltransferase
WP_043700203.1	NA	56	0.63	0.312	hypothetical protein
WP_043686050.1	NA	56	0.63	0.309	lipid-transfer protein
WP_043689562.1	<i>trpE</i>	56	0.63	0.303	Anthranilate synthase component 1
WP_043688232.1	<i>murA</i>	56	0.62	0.336	UDP-N-acetylglucosamine 1- carboxyvinyltransferase
WP_043684354.1	<i>yidC</i>	56	0.62	0.31	Membrane protein insertase
WP_043689172.1	<i>pepA</i>	56	0.62	0.307	putative cytosol aminopeptidase
WP_043686047.1	NA	56	0.62	0.284	Acyl-CoA dehydrogenase FadE29
WP_083899478.1	<i>aftC</i>	56	0.61	0.322	Alpha-(1->3)-arabinofuranosyltransferase
WP_043685625.1	NA	56	0.61	0.316	ArsA family ATPase
WP_043688017.1	<i>scmP</i>	56	0.61	0.312	N-acetylcysteine deacetylase
WP_043694282.1	NA	56	0.61	0.306	Phosphatidylinositol phosphate synthase
WP_086006729.1	NA	56	0.61	0.286	hypothetical protein
WP_043689398.1	NA	56	0.6	0.319	putative RNA pseudouridine synthase
WP_043686215.1	NA	58	0.81	0.316	Putative acyl-CoA dehydrogenase FadE17
WP_043699247.1	<i>lpdC</i>	58	0.81	0.256	Dihydrolipoyl dehydrogenase
WP_051168500.1	NA	58	0.8	0.339	DUF3071 domain-containing protein
WP_043684511.1	<i>gltD</i>	58	0.63	0.259	Glutamate synthase [NADPH] small chain
WP_043694934.1	<i>pnp</i>	58	0.63	0.253	Polyribonucleotide nucleotidyltransferase
WP_043691023.1	<i>nuoL</i>	58	0.62	0.323	NADH-quinone oxidoreductase subunit L
WP_086006780.1	<i>nuoM</i>	58	0.62	0.313	NADH-quinone oxidoreductase subunit M
WP_174377710.1	<i>rnj</i>	58	0.62	0.294	Ribonuclease J
WP_039798216.1	NA	58	0.62	0.288	DUF3090 domain-containing protein
WP_043693674.1	<i>zwf2</i>	58	0.62	0.288	Glucose-6-phosphate 1-dehydrogenase 2
WP_043693840.1	<i>carB</i>	58	0.62	0.279	Carbamoyl-phosphate synthase large chain
WP_043688075.1	<i>accD5</i>	58	0.62	0.249	putative propionyl-CoA carboxylase beta chain 5
WP_043694034.1	<i>aroC</i>	58	0.61	0.316	Chorismate synthase
WP_043695388.1	NA	58	0.61	0.314	chromosome segregation protein SMC
WP_043689835.1	<i>pyrG</i>	58	0.61	0.309	CTP synthase
WP_043688210.1	<i>prfA</i>	58	0.61	0.298	Peptide chain release factor 1
WP_086006598.1	<i>purK</i>	58	0.6	0.317	N5-carboxyaminoimidazole ribonucleotide synthase
WP_043690194.1	NA	58	0.6	0.314	acyl-CoA dehydrogenase family protein
WP_086006663.1	NA	58	0.6	0.314	putative AAA domain-containing protein
WP_043688744.1	<i>dnaJ2</i>	58	0.6	0.3	Chaperone protein
WP_043689528.1	<i>hisF</i>	58	0.6	0.296	Imidazole glycerol phosphate synthase subunit
WP_051169357.1	<i>hepT</i>	58	0.6	0.285	Heptaprenyl diphosphate synthase component

WP_043699333.1	<i>nuoL</i>	58	0.59	0.344	NADH-quinone oxidoreductase subunit L
WP_043694274.1	<i>tesB</i>	58	0.59	0.311	Acyl-CoA thioesterase 2
WP_174377696.1	<i>nuoC</i>	58	0.59	0.308	NADH-quinone oxidoreductase subunit C
WP_043688530.1	<i>orn</i>	58	0.59	0.297	Oligoribonuclease
WP_043689177.1	<i>ilvE</i>	58	0.59	0.296	Branched-chain-amino-acid aminotransferase
WP_043686360.1	NA	58	0.59	0.291	3-oxocholest-4-en-26-oate--CoA ligase
WP_043693706.1	<i>pgk</i>	58	0.59	0.281	Phosphoglycerate kinase
WP_043685144.1	<i>tagH</i>	60	0.81	0.315	Teichoic acids export ATP-binding protein
WP_043697127.1	<i>deaD</i>	60	0.62	0.304	ATP-dependent RNA helicase
WP_043692933.1	<i>hely</i>	60	0.62	0.303	putative helicase
WP_043694117.1	<i>alaS</i>	60	0.62	0.282	Alanine--tRNA ligase
WP_043689044.1	<i>glnA2</i>	60	0.62	0.281	Glutamine synthetase
WP_086006710.1	<i>metG</i>	60	0.62	0.274	Methionine--tRNA ligase
WP_043685491.1	<i>leuA</i>	60	0.62	0.254	2-isopropylmalate synthase
WP_086006727.1	<i>tldD</i>	60	0.61	0.308	Metalloprotease
WP_043695061.1	<i>mgo</i>	60	0.61	0.302	putative malate:quinone oxidoreductase
WP_083899255.1	<i>qcrC</i>	60	0.61	0.294	Cytochrome bc1 complex cytochrome c subunit
WP_043685439.1	NA	60	0.61	0.29	putative fatty acid methyltransferase
WP_043695674.1	<i>gata</i>	60	0.61	0.287	Glutamyl-tRNA(Gln) amidotransferase subunit A
WP_083899151.1	<i>guaB</i>	60	0.61	0.284	Inosine-5'-monophosphate dehydrogenase
WP_043695018.1	<i>nusA</i>	60	0.61	0.281	Transcription termination/ antitermination protein
WP_043696645.1	<i>nasD</i>	60	0.61	0.26	Nitrite reductase
WP_043695541.1	<i>leuB</i>	60	0.6	0.269	3-isopropylmalate dehydrogenase
WP_043687896.1	<i>lpdA</i>	60	0.58	0.313	NAD(P)H dehydrogenase
WP_043686520.1	<i>purM</i>	60	0.58	0.305	Phosphoribosylformylglycinamidine cyclo-ligase
WP_043691073.1	<i>nuoB</i>	60	0.58	0.304	NADH-quinone oxidoreductase subunit B
WP_043686699.1	NA	62	0.8	0.32	DEAD/DEAH box helicase
WP_043700026.1	<i>hcaB</i>	62	0.8	0.276	3-phenylpropionate-dihydrodiol/cinnamic acid-dihydrodiol dehydrogenase
WP_043688750.1	<i>era</i>	62	0.79	0.279	GTPase Era
WP_086006615.1	<i>aceE</i>	62	0.61	0.28	Pyruvate dehydrogenase E1 component
WP_043688253.1	NA	62	0.6	0.313	hypothetical protein
WP_043698004.1	<i>purH</i>	62	0.6	0.309	Bifunctional purine biosynthesis protein
WP_043684864.1	<i>glfT2</i>	62	0.6	0.286	Galactofuranosyltransferase
WP_043684752.1	NA	62	0.6	0.278	Putative Rieske 2Fe-2S iron-sulfur protein
WP_043698893.1	<i>rpoC</i>	62	0.6	0.24	DNA-directed RNA polymerase subunit beta
WP_043688692.1	<i>proA</i>	62	0.59	0.303	Gamma-glutamyl phosphate reductase
WP_043685537.1	<i>asd</i>	62	0.59	0.287	Aspartate-semialdehyde dehydrogenase
WP_043693703.1	<i>tpiA</i>	62	0.59	0.272	Triosephosphate isomerase

WP_051169146.1	<i>ndh</i>	62	0.58	0.292	NADH dehydrogenase
WP_043695076.1	<i>map</i>	62	0.58	0.281	Methionine aminopeptidase 2
WP_043686644.1	<i>dus</i>	62	0.57	0.318	putative tRNA-dihydrouridine synthase
WP_043694623.1	<i>lexA</i>	62	0.56	0.331	LexA repressor
WP_043686743.1	<i>phoU2</i>	62	0.56	0.299	Phosphate-specific transport system accessory protein
WP_043699540.1	<i>fabH</i>	62	0.56	0.298	3-oxoacyl-[acyl-carrier-protein] synthase 3
WP_051168471.1	NA	64	0.79	0.29	Putative enoyl-CoA hydratase EchA13
WP_083899527.1	<i>gatB</i>	64	0.59	0.275	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
WP_043684862.1	<i>glf</i>	64	0.59	0.27	UDP-galactopyranose mutase
WP_043695803.1	<i>etfA</i>	64	0.59	0.257	Electron transfer flavoprotein subunit alpha
WP_043690371.1	<i>mutB</i>	64	0.59	0.246	putative methylmalonyl-CoA mutase large subunit
WP_043685147.1	NA	64	0.58	0.327	ABC transporter permease
WP_043686876.1	<i>citA</i>	64	0.58	0.306	Putative citrate synthase 2
WP_083899464.1	<i>ctaB</i>	64	0.58	0.297	Protoheme IX farnesyltransferase
WP_043689123.1	<i>lipA</i>	64	0.58	0.273	Lipoyl synthase
WP_043689651.1	<i>pheT</i>	64	0.58	0.238	Phenylalanine--tRNA ligase beta subunit
WP_043694554.1	<i>ideR</i>	64	0.57	0.311	Iron-dependent repressor
WP_043690337.1	<i>guaB1</i>	64	0.57	0.31	putative oxidoreductase
WP_043694157.1	NA	64	0.57	0.307	hypothetical protein
WP_043688534.1	<i>fadH</i>	64	0.57	0.306	2,4-dienoyl-CoA reductase
WP_043689521.1	<i>hisC</i>	64	0.57	0.302	Histidinol-phosphate aminotransferase
WP_043698178.1	<i>acdA</i>	64	0.57	0.266	Acyl-CoA dehydrogenase
WP_043688949.1	<i>ahpE</i>	64	0.57	0.25	Alkyl hydroperoxide reductase E
WP_043699071.1	<i>gpmA</i>	64	0.56	0.281	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
WP_043690208.1	NA	64	0.55	0.302	bifunctional nuclease family protein
WP_051168991.1	<i>fumA</i>	66	0.58	0.278	Fumarate hydratase class I, aerobic
WP_043697798.1	<i>prs</i>	66	0.58	0.275	Ribose-phosphate pyrophosphokinase
WP_039803160.1	NA	66	0.58	0.271	helix-turn-helix transcriptional regulator
WP_043694364.1	<i>pdxS</i>	66	0.58	0.268	Pyridoxal 5'-phosphate synthase subunit
WP_043684377.1	<i>gyrA</i>	66	0.58	0.265	DNA gyrase subunit A
WP_083899118.1	<i>gltA2</i>	66	0.58	0.242	Citrate synthase 1
WP_083899588.1	<i>kgd</i>	66	0.58	0.24	Multifunctional 2-oxoglutarate metabolism enzyme
WP_043686827.1	<i>serC</i>	66	0.57	0.293	Phosphoserine aminotransferase
WP_043689279.1	<i>aroG</i>	66	0.57	0.291	Phospho-2-dehydro-3-deoxyheptonate aldolase
WP_043689340.1	<i>qcrA</i>	66	0.57	0.283	Cytochrome bc1 complex Rieske iron-sulfur subunit
WP_043694071.1	<i>aspS</i>	66	0.57	0.269	Aspartate--tRNA ligase
WP_043694706.1	<i>recA</i>	66	0.57	0.261	recombinase RecA

WP_040864988.1	<i>icd</i>	66	0.57	0.237	Isocitrate dehydrogenase
WP_157229656.1	NA	66	0.55	0.336	putative 1,4-alpha-glucan branching enzyme
WP_043689789.1	<i>argC</i>	66	0.55	0.301	N-acetyl-gamma-glutamyl-phosphate reductase
WP_169334158.1	<i>dnaE2</i>	66	0.54	0.316	Error-prone DNA polymerase
WP_043693886.1	<i>ypdF</i>	66	0.54	0.302	Aminopeptidase
WP_043693056.1	<i>trml</i>	68	0.76	0.316	tRNA (adenine(58)-N(1))-methyltransferase
WP_043695779.1	<i>mnmA</i>	68	0.56	0.329	tRNA-specific 2-thiouridylase MnmA
WP_043697819.1	<i>prfC</i>	68	0.56	0.308	Peptide chain release factor 3
WP_043697729.1	<i>eno</i>	68	0.56	0.275	Enolase
WP_043696447.1	<i>prfB</i>	68	0.56	0.273	Peptide chain release factor 2
WP_043699520.1	<i>fba</i>	68	0.56	0.259	Fructose-bisphosphate aldolase
WP_083899705.1	<i>sugA</i>	68	0.55	0.299	Trehalose transport system permease protein
WP_043695032.1	<i>proS</i>	68	0.55	0.273	Proline--tRNA ligase
WP_043687229.1	<i>crtL</i>	68	0.54	0.33	Lycopene beta cyclase
WP_043686342.1	NA	68	0.54	0.326	thiolase domain-containing protein
WP_043695259.1	<i>ffh</i>	68	0.54	0.272	Signal recognition particle protein
WP_043689134.1	<i>dlaT</i>	68	0.53	0.249	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
WP_043699047.1	<i>hemA</i>	68	0.52	0.362	Glutamyl-tRNA reductase
WP_043689775.1	<i>wecE</i>	68	0.52	0.315	dTDP-4-amino-4,6-dideoxygalactose transaminase
WP_043685128.1	NA	68	0.52	0.29	glycosyltransferase
WP_043694150.1	NA	70	0.55	0.307	membrane protein
WP_043700371.1	NA	70	0.55	0.29	Putative monooxygenase
WP_043689499.1	<i>nadA</i>	70	0.55	0.279	Quinolinate synthase A
WP_043689484.1	<i>bioB</i>	70	0.55	0.266	Biotin synthase
WP_043686604.1	NA	70	0.55	0.233	Putative thiosulfate sulfurtransferase
WP_043695829.1	<i>COQ5</i>	70	0.52	0.307	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial
WP_043688733.1	<i>cysNC</i>	70	0.51	0.303	Bifunctional enzyme CysN/CysC
WP_043699605.1	<i>hemB</i>	70	0.5	0.289	Delta-aminolevulinic acid dehydratase
WP_043688721.1	<i>sbpA</i>	70	0.49	0.276	Sulfate-binding protein
WP_043688668.1	<i>clpX</i>	72	0.54	0.282	ATP-dependent Clp protease subunit
WP_043694271.1	NA	72	0.54	0.252	putative transcriptional regulatory protein
WP_043688958.1	<i>accD6</i>	72	0.53	0.3	putative propionyl-CoA carboxylase beta chain 6
WP_043694066.1	NA	72	0.53	0.295	kinase
WP_043693440.1	NA	72	0.53	0.282	SPFH/Band 7/PHB domain protein
WP_039796155.1	<i>rpoA</i>	72	0.53	0.251	RNA polymerase subunit alpha
WP_040780648.1	<i>pyrH</i>	72	0.52	0.279	Uridylate kinase
WP_043693844.1	<i>carA</i>	72	0.51	0.299	Carbamoyl-phosphate synthase small chain
WP_043689630.1	NA	72	0.51	0.293	Universal stress protein

WP_051169214.1	NA	72	0.49	0.315	sigma-70 family RNA polymerase sigma factor
WP_043688208.1	<i>rho</i>	74	0.53	0.277	Transcription termination factor Rho
WP_043694380.1	<i>thrS</i>	74	0.53	0.272	Threonine--tRNA ligase
WP_083899664.1	<i>nusG</i>	74	0.53	0.269	Transcription termination/antitermination protein
WP_043687244.1	<i>rplB</i>	74	0.53	0.264	50S ribosomal protein L2
WP_043700314.1	<i>ino1</i>	74	0.53	0.263	Inositol-3-phosphate synthase
WP_043688551.1	<i>ettA</i>	74	0.53	0.244	Energy-dependent translational throttle protein
WP_043695806.1	<i>etfB</i>	74	0.53	0.232	Electron transfer flavoprotein subunit beta
WP_157229882.1	<i>thiC</i>	74	0.52	0.287	Phosphomethylpyrimidine synthase
WP_051168563.1	<i>sdhA</i>	74	0.52	0.236	Succinate dehydrogenase flavoprotein subunit
WP_043685854.1	<i>hpt</i>	74	0.51	0.272	Hypoxanthine-guanine phosphoribosyltransferase
WP_043689518.1	<i>hisD</i>	74	0.5	0.289	Histidinol dehydrogenase
WP_043691079.1	<i>nuoA</i>	74	0.49	0.322	NADH-quinone oxidoreductase subunit A
WP_086006612.1	NA	74	0.49	0.289	Trans,polycis-polyprenyl diphosphate synthase ((2Z,6E)-farnesyl diphosphate specific)
WP_043697488.1	<i>ychF</i>	76	0.76	0.271	Ribosome-binding ATPase YchF
WP_043692960.1	<i>prcA1</i>	76	0.74	0.321	Proteasome subunit alpha 1
WP_043693560.1	NA	76	0.51	0.269	MoxR family ATPase
WP_043690233.1	<i>glcB</i>	76	0.51	0.243	Malate synthase G
WP_043688221.1	<i>atpA</i>	76	0.51	0.233	ATP synthase subunit alpha
WP_043687724.1	<i>guaA</i>	76	0.5	0.291	GMP synthase
WP_043695194.1	<i>tsf</i>	76	0.5	0.269	Elongation factor Ts
WP_043700023.1	<i>fadI</i>	76	0.5	0.248	3-ketoacyl-CoA thiolase FadI
WP_043695817.1	NA	76	0.49	0.309	Putative acetyltransferase
WP_043689748.1	<i>argB</i>	76	0.49	0.291	Acetylglutamate kinase
WP_043699440.1	<i>pccB</i>	78	0.51	0.283	Propionyl-CoA carboxylase beta chain
WP_174186519.1	<i>pafA</i>	78	0.5	0.278	Pup--protein ligase
WP_043688629.1	<i>valS</i>	78	0.49	0.285	Valine--tRNA ligase
WP_043697816.1	<i>rplY</i>	78	0.47	0.275	50S ribosomal protein L25
WP_040865481.1	<i>clpP2</i>	80	0.75	0.255	ATP-dependent Clp protease proteolytic subunit 2
WP_043694738.1	NA	80	0.74	0.274	35 kDa protein
WP_039799659.1	<i>ilvH</i>	80	0.73	0.32	Acetolactate synthase small subunit
WP_051168666.1	<i>sir</i>	80	0.49	0.262	Sulfite reductase
WP_043685903.1	<i>lsr2</i>	80	0.47	0.364	Nucleoid-associated protein Lsr2
WP_043695890.1	<i>nrdI</i>	80	0.47	0.28	Protein NrdI
WP_011206964.1	<i>carD</i>	82	0.47	0.263	RNA polymerase-binding transcription factor

WP_063709467.1	<i>infB</i>	82	0.47	0.257	Translation initiation factor IF-2
WP_051169014.1	<i>sufC</i>	82	0.47	0.245	Vegetative protein
WP_083887487.1	<i>infC</i>	82	0.46	0.323	Translation initiation factor IF-3
WP_043688864.1	NA	82	0.46	0.276	tRNA-Gly
WP_083899173.1	<i>atpB</i>	84	0.73	0.302	ATP synthase subunit a
WP_043688713.1	<i>lepA</i>	84	0.47	0.284	Elongation factor 4
WP_043698931.1	<i>rplJ</i>	84	0.47	0.28	50S ribosomal protein L10
WP_043689752.1	<i>argG</i>	84	0.46	0.24	Argininosuccinate synthase
WP_043693609.1	<i>iscU</i>	84	0.45	0.298	Iron-sulfur cluster assembly scaffold protein
WP_043689275.1	<i>ctaE</i>	84	0.45	0.282	putative cytochrome c oxidase subunit 3
WP_039798939.1	<i>efp</i>	84	0.45	0.258	Elongation factor P
WP_043688095.1	NA	84	0.45	0.252	putative acyl-CoA dehydrogenase fadE25
WP_043690281.1	<i>uvrA</i>	84	0.44	0.309	UvrABC system protein A
WP_174377723.1	<i>narK</i>	84	0.44	0.291	Nitrate/nitrite transporter NarK
WP_014981573.1	NA	84	0.42	0.299	DUF742 domain-containing protein
WP_043693618.1	NA	86	0.46	0.244	Fe-S cluster assembly protein SufB
WP_043697415.1	<i>typA</i>	86	0.44	0.269	GTP-binding protein TypA/BipA
WP_086006591.1	<i>rplD</i>	86	0.44	0.257	50S ribosomal protein L4
WP_019044571.1	<i>crp</i>	86	0.43	0.305	CRP-like cAMP-activated global transcriptional regulator
WP_043693613.1	<i>csd</i>	86	0.43	0.292	putative cysteine desulfurase
WP_043687868.1	NA	86	0.43	0.252	succinate dehydrogenase hydrophobic membrane anchor subunit
WP_174315456.1	<i>mtrA</i>	88	0.44	0.307	DNA-binding response regulator
WP_043693708.1	<i>gapA</i>	88	0.44	0.23	Glyceraldehyde-3-phosphate dehydrogenase
WP_043695197.1	<i>rpsB</i>	88	0.44	0.224	30S ribosomal protein S2
WP_043698933.1	<i>rplA</i>	88	0.44	0.22	50S ribosomal protein L1
WP_043691230.1	<i>rbpA</i>	88	0.41	0.275	RNA polymerase-binding protein
WP_011210678.1	NA	88	0.38	0.282	DUF2469 domain-containing protein
WP_043687710.1	<i>sigD</i>	90	0.72	0.279	ECF RNA polymerase sigma factor
WP_174377676.1	<i>clpP1</i>	90	0.7	0.254	ATP-dependent Clp protease proteolytic subunit 1
WP_043689602.1	<i>rpsA</i>	90	0.43	0.234	30S ribosomal protein S1
WP_040864934.1	<i>rplM</i>	90	0.42	0.266	50S ribosomal protein L13
WP_043687243.1	<i>rplC</i>	90	0.42	0.244	50S ribosomal protein L3
WP_043684967.1	<i>sodA</i>	90	0.42	0.238	Superoxide dismutase
WP_067803910.1	NA	92	0.41	0.254	30S ribosomal protein S9
WP_043698018.1	<i>sucC</i>	92	0.41	0.248	Succinate--CoA ligase subunit beta
WP_043687553.1	<i>rpsD</i>	92	0.41	0.245	30S ribosomal protein S4
WP_011210681.1	<i>rplS</i>	92	0.39	0.246	50S ribosomal protein L19
WP_043687255.1	<i>rplV</i>	94	0.68	0.261	50S ribosomal protein L22
WP_043688633.1	<i>rplU</i>	94	0.41	0.249	50S ribosomal protein L21
WP_043687383.1	NA	94	0.41	0.246	30S ribosomal protein S5
WP_043687358.1	<i>rplE</i>	94	0.41	0.244	50S ribosomal protein L5

WP_043699134.1	<i>aceA</i>	94	0.4	0.232	Isocitrate lyase
WP_043687258.1	<i>rpsC</i>	94	0.38	0.243	30S ribosomal protein S3
WP_043693545.1	<i>inhA</i>	94	0.37	0.286	Enoyl-[acyl-carrier-protein] reductase
WP_043687556.1	NA	96	0.38	0.229	50S ribosomal protein L17
WP_011211115.1	<i>whiB1</i>	96	0.36	0.285	Transcriptional regulator WhiB1
WP_043693920.1	<i>ybiT</i>	98	0.36	0.288	ABC transporter ATP-binding protein
WP_039798918.1	<i>rpoZ</i>	98	0.36	0.258	RNA polymerase subunit omega
WP_043695253.1	<i>rpsP</i>	98	0.36	0.226	30S ribosomal protein S16
WP_043693616.1	NA	100	0.68	0.281	Fe-S cluster assembly protein
WP_043686525.1	NA	100	0.68	0.256	DUF3073 domain-containing protein
WP_174377715.1	<i>ilvC</i>	100	0.36	0.229	Ketol-acid reductoisomerase (NADP(+))
WP_043687550.1	<i>rpsM</i>	100	0.35	0.265	30S ribosomal protein S13
WP_043689200.1	NA	102	0.67	0.28	iron-sulfur cluster assembly accessory protein
WP_039795549.1	<i>rpsH</i>	102	0.35	0.271	30S ribosomal protein S8
WP_040782761.1	<i>sucD</i>	102	0.34	0.217	Succinate--CoA ligase subunit alpha
WP_043687250.1	<i>rpsS</i>	102	0.33	0.221	30S ribosomal protein S19
WP_003418601.1	<i>infA</i>	102	0.27	0.254	Translation initiation factor IF-1
WP_043687380.1	<i>rplF</i>	104	0.34	0.254	50S ribosomal protein L6
WP_043695887.1	<i>nrde2</i>	104	0.34	0.244	Ribonucleoside-diphosphate reductase subunit alpha 2
WP_043694830.1	NA	104	0.32	0.242	Alkyl hydroperoxide reductase C
WP_043688224.1	<i>atpD</i>	106	0.33	0.225	ATP synthase subunit beta
WP_011211259.1	NA	106	0.31	0.289	DUF3117 domain-containing protein
WP_014981768.1	<i>rpsK</i>	106	0.31	0.23	30S ribosomal protein S11
WP_040864865.1	<i>rplX</i>	108	0.32	0.272	50S ribosomal protein L24
WP_011210730.1	<i>rpmB</i>	108	0.29	0.209	50S ribosomal protein L28
WP_039795505.1	<i>rplN</i>	110	0.29	0.271	50S ribosomal protein L14
WP_030525248.1	<i>rpsG</i>	110	0.29	0.218	30S ribosomal protein S7
WP_043698934.1	<i>rplK</i>	112	0.64	0.24	50S ribosomal protein L11
WP_003938093.1	<i>rpsJ</i>	112	0.28	0.227	30S ribosomal protein S10
WP_040870256.1	<i>rpsL</i>	114	0.27	0.175	30S ribosomal protein S12
WP_039797323.1	<i>rplT</i>	114	0.26	0.215	50S ribosomal protein L20
WP_040864842.1	<i>rplP</i>	118	0.24	0.218	50S ribosomal protein L16
WP_011207266.1	<i>rplW</i>	118	0.23	0.181	50S ribosomal protein L23
WP_028479292.1	<i>groS</i>	120	0.24	0.282	co-chaperone GroES
WP_011211653.1	NA	122	0.61	0.206	50S ribosomal protein L33
WP_169334227.1	NA	122	0.57	0.248	glycosyltransferase

RFD: Robinson-Fould Distance; π : Nucleotide diversity