

Supplemental Table 8: Genes originating from lateral gene transfer in Rokubacteria Amazon FNV 2010 15_13 as identified by CompareM. The complete output is available upon request.

Gene Id	Length (bp)	Annotation of deviants	Deviations from mean
fig 6666666.168244.peg.3060	4971	General secretion pathway protein N	2.85
fig 6666666.168244.peg.884	1536	Basic proline rich protein precursor	5.42
fig 6666666.168244.peg.3138	2232	Hypothetical protein	3.70
fig 6666666.168244.peg.1411	1866	Basic proline rich protein precursor	3.56
fig 6666666.168244.peg.266	147	Dipeptide transport system permease DppC	0.76
fig 6666666.168244.peg.3100	1290	Basic proline rich protein precursor	5.16
fig 6666666.168244.peg.1595	1305	Hypothetical protein	1.69
fig 6666666.168244.peg.1306	2901	PE-PGRS	1.64
fig 6666666.168244.peg.1991	1395	Hypothetical protein	2.18
fig 6666666.168244.peg.1367	153	Hypothetical protein	1.23
fig 6666666.168244.peg.2626	1383	Hypothetical protein	2.79
fig 6666666.168244.peg.2780	2865	Putative autotransporter	1.42
fig 6666666.168244.peg.769	1056	Hypothetical protein	3.57
fig 6666666.168244.peg.2126	645	Hypothetical protein	3.23
fig 6666666.168244.peg.3182	2739	Regulatory protein LuxR	0.18
fig 6666666.168244.peg.2499	126	Hypothetical protein	2.06
fig 6666666.168244.peg.2217	1998	Beta-hexosaminidase	0.82
fig 6666666.168244.peg.1616	5028	Conserved repeat domain	1.14
fig 6666666.168244.peg.801	123	Hypothetical protein	3.12
fig 6666666.168244.peg.744	327	LSU L24p	1.50
fig 6666666.168244.peg.2054	636	Basic proline rich protein precursor	3.89
fig 6666666.168244.peg.34	171	Hypothetical protein	2.79
fig 6666666.168244.peg.2705	750	Hypothetical protein	3.15
fig 6666666.168244.peg.2912	1416	Probable poly(beta-D-mannuronate) O-acetylase	0.36
fig 6666666.168244.peg.1280	1788	Choline dehydrogenase	1.52
fig 6666666.168244.peg.2305	1452	Hypothetical protein	2.38
fig 6666666.168244.peg.939	123	N-methylhydantoinase A	2.59
fig 6666666.168244.peg.2840	3111	RND multidrug efflux transporter; acriflavine resistance	-0.04

fig 6666666.168244.peg.667	927	Collagen triple helix repeat domain	0.57
fig 6666666.168244.peg.1446	114	Hypothetical protein	2.89
fig 6666666.168244.peg.1222	171	Hypothetical protein	1.89
fig 6666666.168244.peg.1548	2139	Hypothetical protein	1.33
fig 6666666.168244.peg.2979	1098	TolA precursor	1.28
fig 6666666.168244.peg.2221	630	Hypothetical protein	1.89
fig 6666666.168244.peg.2586	960	Enoyl-[acyl-carrier-protein] reductase [FMN]	1.23
fig 6666666.168244.peg.2232	201	Hypothetical protein	2.85
fig 6666666.168244.peg.480	135	Hypothetical protein	2.94
fig 6666666.168244.peg.2583	588	Possible transmembrane protein	0.91
fig 6666666.168244.peg.2673	2070	Hypothetical protein	0.45
fig 6666666.168244.peg.1824	1473	Malonate transporter	1.26
fig 6666666.168244.peg.1773	114	Hypothetical protein	2.72
fig 6666666.168244.peg.2192	1077	Cell surface protein	1.38
fig 6666666.168244.peg.427	2034	DNA ligase	-0.47
fig 6666666.168244.peg.1281	267	Hypothetical protein	2.91
fig 6666666.168244.peg.2523	195	Hypothetical protein	2.01
fig 6666666.168244.peg.2723	126	Hypothetical protein	3.36
fig 6666666.168244.peg.2173	825	Inner membrane protein translocase YidC long form	1.50
fig 6666666.168244.peg.2125	252	Hypothetical protein	1.58
fig 6666666.168244.peg.1854	177	Hypothetical protein	3.56
fig 6666666.168244.peg.1637	1704	Hypothetical protein	1.99
fig 6666666.168244.peg.1675	378	Hypothetical protein	0.34
fig 6666666.168244.peg.1497	2091	Hypothetical protein	1.16
fig 6666666.168244.peg.1452	1602	LipT	1.77
fig 6666666.168244.peg.1805	432	Chemotaxis protein methyltransferase CheR	0.28
fig 6666666.168244.peg.1775	1215	COG0477:permeases of major facilitator superfamily	0.94
fig 6666666.168244.peg.1486	213	Hypothetical protein	3.77
fig 6666666.168244.peg.2763	153	Hypothetical protein	3.52
fig 6666666.168244.peg.1609	2826	Putative transcriptional regulator	-0.39
fig 6666666.168244.peg.469	390	Hypothetical protein	3.28

fig 6666666.168244.peg.452	2715	Macrolide-specific ABC-type efflux carrier	-0.29
fig 6666666.168244.peg.224	1062	Epoxide hydrolase	1.16
fig 6666666.168244.peg.1179	114	Hypothetical protein	3.58
fig 6666666.168244.peg.2907	1434	Gamma-glutamyltranspeptidase	0.17
fig 6666666.168244.peg.891	177	Hypothetical protein	3.45
fig 6666666.168244.peg.626	996	Ribose ABC transport system permease RbsC	1.15
fig 6666666.168244.peg.2677	1005	Similarity with known prokaryotic or eukaryotic proteins	0.99
fig 6666666.168244.peg.570	159	Hypothetical protein	1.65
fig 6666666.168244.peg.1019	732	Peptidase M23B	-0.13
fig 6666666.168244.peg.2313	165	Hypothetical protein	2.48
fig 6666666.168244.peg.650	2046	N-methylhydantoinase A	-0.02
fig 6666666.168244.peg.1699	606	Transcriptional regulator TetR family	0.01
fig 6666666.168244.peg.2784	1446	Alpha-galactosidase	1.01
fig 6666666.168244.peg.6	1509	Alanyl-dipeptidyl peptidase	2.11
fig 6666666.168244.peg.1770	222	Hypothetical protein	2.41
fig 6666666.168244.peg.821	1329	Membrane protein Sypl involved in exopolysaccharide production	0.08
fig 6666666.168244.peg.1622	2505	Mannose-1-phosphate guanylyltransferase/phosphomannomutase	-0.71
fig 6666666.168244.peg.2948	819	RNA binding methyltransferase FtsJ-like	-0.03
fig 6666666.168244.peg.2774	261	Protein ycel precursor	1.88
fig 6666666.168244.peg.497	129	Hypothetical protein	3.26
fig 6666666.168244.peg.2304	117	Hypothetical protein	3.71
fig 6666666.168244.peg.625	918	Ribose ABC transport system permease protein RbsC	0.58
fig 6666666.168244.peg.810	186	Hypothetical protein	3.51
fig 6666666.168244.peg.557	756	3-oxoacyl-[acyl-carrier-protein] reductase	0.68
fig 6666666.168244.peg.1524	693	Hypothetical protein	1.12
fig 6666666.168244.peg.2831	123	Hypothetical protein	1.76
fig 6666666.168244.peg.3085	783	3-oxoacyl-[acyl-carrier-protein] reductase	0.65
fig 6666666.168244.peg.1388	381	Arsenate reductase	0.65
fig 6666666.168244.peg.3094	249	Hypothetical protein	1.52

fig 6666666.168244.peg.483	213	Hypothetical protein	1.79
fig 6666666.168244.peg.947	1686	Hypothetical protein	0.89
fig 6666666.168244.peg.410	2961	Adenylate cyclase/guanylate cyclase	0.08
fig 6666666.168244.peg.871	3066	Hypothetical protein	0.48
fig 6666666.168244.peg.1253	1830	Hypothetical protein	0.77
fig 6666666.168244.peg.271	1416	Aspartyl-tRNA(Asn) amidotransferase subunit A @ glutamyl-tRNA(Gln) amidotransferase subunit A	0.70
fig 6666666.168244.peg.1338	174	Hypothetical protein	3.57
fig 6666666.168244.peg.2290	864	Carbon monoxide dehydrogenase medium chain	0.19
fig 6666666.168244.peg.1952	420	Hypothetical protein	1.61
fig 6666666.168244.peg.2414	126	Hypothetical protein	2.40
fig 6666666.168244.peg.2738	936	Quinolinate synthetase	-0.14
fig 6666666.168244.peg.2022	1134	Hypothetical protein	0.38
fig 6666666.168244.peg.168	714	Glycosyl transferase family 2	0.07
fig 6666666.168244.peg.2001	618	Cysteinyl-tRNA synthetase	4.08