

**Table S3.** The differentially expressed genes in  $\Delta prc$ -RS218 compared to those in WT-RS218 by RNA-seq.

contig	RS218 locus_tag	Gene name	Gene product / functional description	Fold change	P value
g100.t1	W817_00215	<i>C1129</i>	ligand-gated channel	0.46	0.042
g1000.t1	W817_02290	<i>prpR</i>	propionate catabolism operon regulatory protein PrpR	3.93	0.006
g1010.t1	W817_02335	<i>lacZ</i>	beta-galactosidase	0.48	0.011
g1013.t1	W817_02345	<i>yaiL</i>	nucleoprotein/polynucleotide-associated enzyme	1.42	0.047
g1015.t1	W817_02350	<i>yaiM</i>	S-formylglutathione hydrolase	0.28	0.012
g102.t1	W817_00230	<i>int</i>	recombinase	0.32	0.041
g1020.t1	W817_02375	<i>yaiP</i>	membrane protein	0.03	0.033
g103.t1	W817_00235	<i>P050</i>	RepFIB replication protein A	0.41	0.014
g1035.t1	W817_02440	<i>yaiZ</i>	hypothetical protein	2.88	0.007
g1037.t1	W817_02455	<i>iraP</i>	anti-RssB factor	2.79	0.011
g1046.t1	W817_02500	<i>yaiE</i>	hypothetical protein	2.46	0.012
g1066.t1	W817_02595	<i>yajD</i>	hypothetical protein	2.16	0.03
g1068.t1	W817_02605	<i>yajI</i>	hypothetical protein	2.4	0.013
g1069.t1	W817_02610	<i>ybaD</i>	NrdR family transcriptional regulator	2.13	0.027
g1075.t1	W817_02640	<i>yajO</i>	oxidoreductase	2.49	0.042
g1079.t1	W817_02660	<i>thiI</i>	tRNA s(4)U8 sulfurtransferase	0.43	0.008
g1080.t1	W817_02665	<i>thiJ</i>	oxidative-stress-resistance chaperone	1.49	0.009
g1092.t1	W817_02720	<i>bolA</i>	BolA family transcriptional regulator	3.85	0.04
g1095.t1	W817_02740	<i>clpX</i>	ATPase subunit of ClpXP protease	1.43	0.034
g1104.t1	W817_02775	<i>ybaE</i>	hypothetical protein	2.78	0.001
g1106.t1	W817_02785	<i>ybaO</i>	hypothetical protein	0.37	0.033
g1115.t1	W817_02830	<i>ylaB</i>	hypothetical protein	0.51	0.008
g1117.t1	W817_02840	<i>maa</i>	maltose O-acetyltransferase	0.13	0.017
g1131.t1	W817_02890	<i>apt</i>	adenine phosphoribosyltransferase	0.5	0.022
g115.t1	W817_00305	<i>P066</i>	hypothetical protein	0.37	0.049
g1151.t1	W817_02980	<i>copA</i>	copper exporting ATPase	0.46	0.039
g1152.t1	W817_02985	<i>ybaS</i>	glutaminase	0.44	0.007
g1156.t1	W817_03005	<i>C0520</i>	hypothetical protein	0.34	0.012
g1157.t1	W817_03010	<i>C0521</i>	adhesin	0.41	0.045
g1158.t1	W817_03015	<i>C0522</i>	hypothetical protein	0.47	0.035
g116.t1	W817_00310	<i>P067</i>	transposase	0.07	0.029
g117.t1	W817_00315	<i>yccB</i>	hypothetical protein	0.39	0.012
g1170.t1	W817_03070	<i>ybbS</i>	LysR family transcriptional regulator	0.48	0.006
g1174.t1	W817_03090	<i>hyi</i>	hydroxypyruvate isomerase	0.34	0.002
g118.t1	W817_00320	<i>istB</i>	ATPase AAA	2.37	0.035
g1190.t1	W817_03175	<i>ppiB</i>	peptidyl-prolyl cis-trans isomerase B	1.89	0.018
g1195.t1	W817_03210	<i>C0563</i>	integrase	0.31	0.012
g1196.t1	W817_03215	<i>tfaQ</i>	tail fiber assembly protein	0.26	0.013
g120.t1	W817_00330	<i>P073</i>	hypothetical protein	3.33	0.046
g1201.t1	W817_03245	<i>cusS</i>	sensor kinase CusS	0.49	0.01
g1205.t1	W817_03260	<i>cusF</i>	copper-binding protein	0.4	0.031
g1209.t1	W817_03280	<i>ybdG</i>	miniconductance mechanosensitive channel	1.14	0.038
g1215.t1	W817_03320	<i>fepA</i>	outer membrane receptor FepA	0.23	0.024
g1218.t1	W817_03335	<i>entF</i>	enterobactin synthase subunit F	0.43	0.043
g1221.t1	W817_03345	<i>fepC</i>	ferric enterobactin transport ATP-binding protein fepC	0.42	0.04
g1223.t1	W817_03350	<i>fepG</i>	iron-enterobactin transporter permease	0.59	0.038
g1227.t1	W817_03370	<i>entC</i>	isochorismate synthase EntC	0.51	0.016
g1228.t1	W817_03375	<i>entE</i>	enterobactin synthase subunit E	0.3	0.035
g1234.t1	W817_03400	<i>ybdD</i>	hypothetical protein	2.43	0.028
g1236.t1	W817_03410	<i>ybdL</i>	aminotransferase	0.2	0.004
g1237.t1	W817_03415	<i>ybdM</i>	hypothetical protein	0.18	0.012
g1238.t1	W817_03420	<i>ybdN</i>	hypothetical protein	0.15	0.017
g1245.t1	W817_03450	<i>uspG</i>	universal stress protein G	2.54	0.038
g1255.t1	W817_03505	<i>dpiB</i>	sensor histidine kinase DpiB	0.28	0.049
g1256.t1	W817_03510	<i>dpiA</i>	two-component response regulator DpiA	0.43	0.019
g1278.t1	W817_03615	<i>ybeL</i>	hypothetical protein	2.88	0.025
g1299.t1	W817_03745	<i>nagE</i>	N-acetylglucosamine PTS permease	1.82	0.044
g1305.t1	W817_03765	<i>terC</i>	tellurium resistance protein TerC	0.12	0.008
g1316.t1	W817_03820	<i>fldA</i>	flavodoxin	2.32	0.001
g1342.t1	W817_03945	<i>sdhC</i>	succinate dehydrogenase cytochrome b-556	2.04	0.006
g1352.t1	W817_03985	<i>C0725</i>	hypothetical protein	0.16	0.012
g1362.t1	W817_04035	<i>tolB</i>	the Tol-Pal cell envelope complex	1.44	0.025

g1369.t1	W817_04105	<i>aroG</i>	2-dehydro-3-deoxyphosphoheptonate aldolase	1.93	0.004
g1378.t1	W817_04150	<i>modA</i>	molybdenum ABC transporter substrate-binding protein	2.75	0.027
g1388.t1	W817_04185	<i>ybhI</i>	membrane protein	0.27	0.008
g1417.t1	W817_04310	<i>ybhG</i>	transporter	2.93	0.021
g1418.t1	W817_04315	<i>ybiH</i>	transcriptional regulator	2.87	0.032
g142.t1	W817_22780	<i>C5110</i>	DNA adenine methylase	0.42	0.034
g1432.t1	W817_04390	<i>glnP</i>	glutamine ABC transporter permease	2.38	0.003
g1433.t1	W817_04395	<i>glnH</i>	amino acid ABC transporter substrate-binding protein	3.57	0.03
g1437.t1	W817_04415	<i>ybiP</i>	phosphoethanolamine transferase	0.35	0.002
g1442.t1	W817_04440	<i>ybiT</i>	heme ABC transporter ATP-binding protein	0.45	0.036
g1448.t1	W817_04475	<i>moeA</i>	molybdopterin biosynthesis protein MoeA	2.35	0.007
g1449.t1	W817_04480	<i>iaaA</i>	isoaspartyl peptidase	2.4	0.001
g1457.t1	W817_04515	<i>rimO</i>	30S ribosomal protein S12 methylthiotransferase	0.39	0.003
g1458.t1	W817_04520	<i>yliH</i>	biofilm formation regulatory protein BssR	2.11	0.02
g1459.t1	W817_04525	<i>yliI</i>	aldose dehydrogenase	0.45	0.043
g1461.t1	W817_04535	<i>dacC</i>	penicillin-binding protein 6	1.33	0.015
g1472.t1	W817_04605		hypothetical protein	0	0.006
g1475.t1	W817_04620	<i>dam</i>	DNA adenine methylase	0.14	0.031
g1505.t1	W817_04775		tail sheath protein	0.3	0.014
g1512.t1	W817_04815	<i>ybjL</i>	transporter	0.51	0.026
g1525.t1	W817_04880	<i>artJ</i>	arginine ABC transporter substrate-binding protein	0.51	0.034
g1544.t1	W817_04980	<i>macA</i>	macrolide transporter subunit	1.43	0.002
g1546.t1	W817_04990	<i>cspD</i>	cold-shock protein	7.07	0.039
g1548.t1	W817_05000	<i>clpA</i>	ATP-dependent Clp protease ATP-binding protein	3.29	0.031
g1557.t1	W817_05045	<i>aat</i>	leucyl/phenylalanyl-tRNA--protein transferase	0.46	0.041
g1564.t1	W817_05080	<i>rarA</i>	recombinase RarA	1.39	0.006
g157.t1	W817_22865	<i>C5124</i>	tail protein	2.99	0.047
g158.t1	W817_22870	<i>C5125</i>	tail protein	2.59	0.02
g1580.t1	W817_05150	<i>ycaL</i>	metalloprotease	0.6	0.017
g1584.t1	W817_05165	<i>ihfB</i>	integration host factor subunit beta	1.98	0.017
g1610.t1	W817_05270	<i>pepN</i>	aminopeptidase N	2.13	0.006
g1611.t1	W817_05275	<i>ssuB</i>	aliphatic sulfonate ABC transporter ATP-binding protein	0.46	0.012
g1612.t1	W817_05280	<i>ssuC</i>	sulfonate ABC transporter	0.16	0.004
g1613.t1	W817_05285	<i>ycbN</i>	alkanesulfonate monooxygenase	0.06	0.005
g1634.t1	W817_05395	<i>mgsA</i>	methylglyoxal synthase	2.51	0.003
g1635.t1	W817_05400	<i>yccT</i>	hypothetical protein	0.39	0.003
g1636.t1	W817_05405	<i>C1031</i>	hypothetical protein	2.47	0.028
g1656.t1	W817_05480	<i>appA</i>	periplasmic AppA protein	0.44	0.046
g1660.t1	W817_05505	<i>yccM</i>	electron transporter YccM	0.38	0.017
g1670.t1	W817_05550	<i>agp</i>	glucose-1-phosphatase/inositol phosphatase	3.54	0.039
g1671.t1	W817_05555	<i>yccJ</i>	hypothetical protein	2.16	0.018
g1679.t1	W817_05590	<i>ycdK</i>	aminoacrylate peracid reductase	2.2	0.029
g1682.t1	W817_05605	<i>rutR</i>	TetR/AcrR family transcriptional regulator	1.41	0.029
g1686.t1	W817_05610	<i>putA</i>	proline dehydrogenase	3.45	0.013
g1687.t1	W817_05620	<i>putP</i>	proline:sodium symporter PutP	3.22	0.001
g1691.t1	W817_05630	<i>ycdO</i>	iron ABC transporter substrate-binding protein	0.42	0.002
g1692.t1	W817_05635	<i>ycdB</i>	peroxidase	0.41	0.017
g1696.t1	W817_05640	<i>phoH</i>	phoH-like family protein	2.29	0.013
g1698.t1	W817_05650	<i>ycdQ</i>	N-glycosyltransferase	0.26	0.042
g1700.t1	W817_05660	<i>pgaA</i>	poly-beta-1,6-N-acetyl-D-glucosamine export protein	0.36	0.024
g1701.t1	W817_05665	<i>ycdT</i>	hypothetical protein	0.29	0.038
g1715.t1	W817_05760	<i>sfaC</i>	putative S fimbrial switch regulatory protein	2.33	0.021
g1717.t1	W817_05780	<i>sfaE</i>	S fimbriae periplasmic chaperone SfaE	0.45	0.028
g1723.t1	W817_05810	<i>iroN</i>	outer membrane receptor IroN	0.16	0.012
g1724.t1	W817_05815	<i>iroE</i>	IroE protein	0.16	0.038
g1730.t1	W817_05830	<i>iroB</i>	glucosyltransferase	0.4	0.001
g1735.t1	W817_05880	<i>C1131</i>	cobalamin biosynthesis protein CobW	0.16	0.013
g1736.t1	W817_05885	<i>C1132</i>	transposase	0.09	0.042
g1738.t1	W817_05905	<i>C1137</i>	hypothetical protein	0.42	0.038
g1739.t1	W817_05910		hypothetical protein	0	0.009
g174.t1	W817_22955	<i>qor</i>	quinone oxidoreductase	2.22	0.027
g1768.t1	W817_06065	<i>mdoG</i>	periplasmic glucan biosynthesis	1.37	0.006
g178.t1	W817_22975	<i>C4623</i>	CoA-transferase	0.5	0.036
g1785.t1	W817_06155	<i>rimJ</i>	alanine acetyltransferase	2.72	0.035

g1786.t1	W817_06160	<i>yceH</i>	hypothetical protein	2.34	0.04
g1787.t1	W817_06165	<i>mviM</i>	putative virulence factor	2.09	0.016
g183.t1	W817_22995	<i>C4627</i>	nicotinamide mononucleotide transporter	0.41	0.017
g1836.t1	W817_06375	<i>ycfJ</i>	hypothetical protein V413_00470	3.15	0.022
g1849.t1	W817_06430	<i>ycfZ</i>	membrane protein	0.43	0.046
g1850.t1	W817_06435	<i>ymfA</i>	membrane protein	0.15	0.005
g1854.t1	W817_06455	<i>potA</i>	putrescine/spermidine ABC transporter ATPase	0.47	0.033
g1867.t1	W817_06520	<i>C1269</i>	hypothetical protein	0.05	0.043
g1868.t1	W817_06525	<i>C1271</i>	RNA-binding protein	0.18	0.025
g1869.t1	W817_06550	<i>C1275</i>	exonuclease	0.27	0.038
g1885.t1	W817_06705		Rz endopeptidase	0.33	0.024
g1888.t1	W817_06730	<i>ybcX</i>	terminase	0.5	0.028
g1893.t1	W817_06745	<i>C1315</i>	scaffold protein	1.76	0.038
g1917.t1	W817_06855	<i>sitA</i>	iron ABC transporter substrate-binding protein	0.47	0.018
g1920.t1	W817_06885	<i>ycgF</i>	blue light- and temperature-regulated antirepressor YcgF	0.28	0.042
g1922.t1	W817_06900	<i>ymgB</i>	two-component-system connector protein AriR	6.86	0.031
g1925.t1	W817_15550	<i>C1350</i>	transposase IS1	0.5	0.008
g1927.t1	W817_06925	<i>C1353</i>	hypothetical protein	0.07	0.011
g1928.t1	W817_06930	<i>ymgD</i>	hypothetical protein	0.22	0.041
g1929.t1	W817_06935	<i>ymgG</i>	hypothetical protein	0.51	0.03
g1930.t1	W817_06940	<i>C1357</i>	ATPase	0.42	0.016
g1935.t1	W817_06965	<i>ycgK</i>	protein YcgK	2.91	0.014
g1939.t1	W817_06985	<i>C1368</i>	hemolysin activation protein HecB	0.26	0.046
g1944.t1	W817_07010	<i>fadR</i>	fatty acid metabolism regulator	2.17	0.007
g1946.t1	W817_07020	<i>dadA</i>	D-amino acid dehydrogenase small subunit	2.67	0.017
g1950.t1	W817_07030	<i>cvrA</i>	cell volume regulation protein A	0.42	0.003
g1961.t1	W817_07085	<i>treA</i>	trehalase	0.32	0.004
g1969.t1	W817_07125	<i>yehH</i>	membrane protein	4.8	0.015
g1974.t1	W817_07145	<i>hemM</i>	outer membrane lipoprotein LolB	1.87	0.01
g1981.t1	W817_07175	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	1.43	0.045
g1983.t1	W817_07185	<i>chaA</i>	sodium:proton antiporter	0.44	0.019
g2025.t1	W817_07380	<i>ompW</i>	outer membrane protein W	2.78	0.03
g2044.t1	W817_07525	<i>C1490</i>	lysozyme	0.26	0.014
g2057.t1	W817_07585	<i>C1504</i>	tail attachment protein	2.71	0.036
g2065.t1	W817_07635	<i>C1512</i>	tail protein	0.35	0.035
g2079.t1	W817_07705	<i>trpA</i>	tryptophan synthase subunit alpha	6.33	0.015
g2080.t1	W817_07710	<i>trpB</i>	tryptophan synthase subunit beta	5.42	0.027
g2082.t1	W817_07715	<i>trpC</i>	phosphoribosylanthranilate isomerase	7.1	0.011
g2084.t1	W817_07720	<i>trpD</i>	anthranilate phosphoribosyltransferase	4.24	0.01
g2092.t1	W817_07755	<i>yciK</i>	oxoacyl-ACP reductase	2.35	0.003
g2093.t1	W817_07760	<i>sohB</i>	serine protease SohB	1.51	0.027
g2098.t1	W817_07785	<i>C1546</i>	hypothetical protein	0.34	0.017
g2100.t1	W817_07795	<i>acnA</i>	aconitate hydratase I	2.98	0.041
g2101.t1	W817_07800	<i>ribA</i>	GTP cyclohydrolase II	2.1	0.009
g2107.t1	W817_07830	<i>osmB</i>	osmotically inducible lipoprotein	1.9	0.048
g2111.t1	W817_07850	<i>rnb</i>	exoribonuclease II	0.66	0.021
g2112.t1	W817_07855	<i>yciW</i>	hypothetical protein	2.12	0.001
g2130.t1	W817_07945	<i>pspE</i>	thiosulfate:cyanide sulfurtransferase	3.11	0.026
g2133.t1	W817_07960	<i>ycjO</i>	sugar ABC transporter permease	0.36	0.02
g2142.t1	W817_08000	<i>ompG</i>	membrane protein	0.24	0.029
g2147.t1	W817_08025	<i>tpx</i>	lipid hydroperoxide peroxidase	2.1	0.037
g2156.t1	W817_08070	<i>uspE</i>	universal stress protein E	2.5	0.039
g2157.t1	W817_08075	<i>fnr</i>	fumarate/nitrate reduction regulatory protein	1.28	0.03
g2169.t1	W817_08145	<i>uspF</i>	universal stress protein F	4.68	0.024
g2177.t1	W817_08165	<i>hslJ</i>	heat shock protein	1.71	0.033
g2189.t1	W817_08200	<i>ynbA</i>	membrane protein	0.26	0.022
g2205.t1	W817_08275	<i>mdoD</i>	glucan biosynthesis protein D	1.52	0.03
g2206.t1	W817_08280	<i>ydchH</i>	hypothetical protein	4.24	0.028
g2208.t1	W817_08290	<i>ycdK</i>	acetyltransferase	0.38	0.029
g2214.t1	W817_08320	<i>ycdP</i>	predicted peptidase	0.7	0.017
g2255.t1	W817_08530	<i>rpsV</i>	30S ribosomal protein S22	2.58	0.018
g2257.t1	W817_08540	<i>osmC</i>	peroxiredoxin	2.32	0.035
g2258.t1	W817_08545	<i>dosP</i>	diguanylate phosphodiesterase	0.43	0.025
g2266.t1	W817_08590	<i>ydeM</i>	anaerobic sulfatase maturase	0.24	0.025

g2321.t1	W817_08880	<i>rspB</i>	starvation sensing protein RspB	0.15	0.035
g2322.t1	W817_08885	<i>rspA</i>	bifunctional D-altronate/D-mannonate dehydratase	0.36	0.007
g2333.t1	W817_08930	<i>ynfH</i>	dimethyl sulfoxide reductase subunit C	0.22	0.012
g2342.t1	W817_08975	<i>ydgD</i>	serine protease	0.6	0.01
g2349.t1	W817_09010	<i>ydgI</i>	arginine:ornithine antiporter	0.38	0.02
g2358.t1	W817_09045	<i>fumA</i>	fumarate hydratase	2.19	0.021
g237.t1	W817_23245	<i>yjcT</i>	D-allose kinase	0.5	0.035
g2374.t1	W817_09100	<i>add</i>	adenosine deaminase	2.25	0.019
g2379.t1	W817_09120	<i>rnfA</i>	electron transport complex RsxE subunit	0.49	0.048
g2383.t1	W817_09130	<i>rnfC</i>	electron transporter RnfC	0.31	0.013
g2385.t1	W817_09135	<i>rnfD</i>	electron transporter RnfG	0.54	0.047
g2387.t1	W817_09140	<i>RsxA</i>	electron transport complex protein RsxA	0.21	0.032
g2400.t1	W817_09195	<i>slyB</i>	outer membrane lipoprotein SlyB	1.81	0.012
g2404.t1	W817_09215	<i>ydhK</i>	fusaric acid resistance protein	0.37	0.036
g2405.t1	W817_09220	<i>sodC</i>	superoxide dismutase	2.22	0.011
g2415.t1	W817_09265	<i>sodB</i>	superoxide dismutase	3.37	0.034
g242.t1	W817_23265	<i>yjcX</i>	D-allose-binding periplasmic protein precursor	0.32	0.016
g2429.t1	W817_09350	<i>ydhW</i>	hypothetical protein	0.32	0.023
g2432.t1	W817_09355	<i>ydhV</i>	oxidoreductase	0.49	0.023
g2455.t1	W817_09450	<i>ydiB</i>	shikimate 5-dehydrogenase	0.33	0.007
g2474.t1	W817_09535	<i>nlpC</i>	lipoprotein NlpC	1.9	0.017
g2478.t1	W817_09555	<i>ihfA</i>	integration host factor subunit alpha	2.47	0.039
g2486.t1	W817_09605	<i>ydiY</i>	membrane protein	0.41	0.013
g2489.t1	W817_09620	<i>yniA</i>	hypothetical protein	2.66	0.047
g25.t1	W817_00435	<i>yijE</i>	lytic transglycosylase	0.42	0.011
g2507.t1	W817_09700	<i>ydjR</i>	hypothetical protein	0.24	0.015
g2532.t1	W817_09810	<i>seld</i>	selenophosphate synthetase	2.46	0.019
g2533.t1	W817_09815	<i>ydjA</i>	oxidoreductase	2.15	0.039
g2534.t1	W817_09820	<i>sppA</i>	protease IV	1.38	0.034
g2539.t1	W817_09835	<i>ydjE</i>	MFS transporter	0.09	0.029
g2542.t1	W817_09850	<i>ydjH</i>	sugar kinase	0.44	0.031
g2587.t1	W817_10075		hypothetical protein	2.9	0.006
g2594.t1	W817_10120	<i>mor</i>	DNA-binding protein	2.54	0.026
g2596.t1	W817_10135	<i>ydjK</i>	inner membrane metabolite transport protein ydjK	0.4	0.004
g2598.t1	W817_10140	<i>ydjL</i>	alcohol dehydrogenase	0.39	0.001
g2599.t1	W817_10145	<i>yeaC</i>	hypothetical protein	2.11	0.001
g2600.t1	W817_10150	<i>msrB</i>	methionine sulfoxide reductase B	2.45	0.034
g2609.t1	W817_10180	<i>yeaH</i>	hypothetical protein	0.31	0.03
g2610.t1	W817_10185	<i>yeaI</i>	membrane protein	0.12	0.035
g2611.t1	W817_10190	<i>YeaJ</i>	diguanylate cylase	0.21	0.045
g2618.t1	W817_10220	<i>yeaO</i>	hypothetical protein	2.3	0.017
g2627.t1	W817_10265	<i>fadD</i>	long-chain-fatty-acid-CoA ligase	2.77	0.004
g2627.t1	W817_10265	<i>fadD</i>	long-chain-fatty-acid--CoA ligase	2.77	0.004
g2628.t1	W817_10270	<i>yeaY</i>	predicted lipoprotein	2.02	0.029
g2650.t1	W817_10385	<i>yebQ</i>	multidrug MFS transporter	0.45	0.002
g2652.t1	W817_10390	<i>htpX</i>	heat shock protein HtpX	1.79	0.013
g2654.t1	W817_10395	<i>prc</i>	carboxy-terminal protease	0	0.013
g2667.t1	W817_10455	<i>yobA</i>	hypothetical protein	2.18	0.029
g2673.t1	W817_10490	<i>yebF</i>	protein yebF	0.36	0.033
g27.t1	W817_00455	<i>traA</i>	conjugal transfer protein TraA	0.46	0.004
g2704.t1	W817_10635	<i>yecM</i>	hypothetical protein	1.61	0.005
g2731.t1	W817_10770	<i>ftnA</i>	ferritin	2.1	0.014
g2739.t1	W817_10825	<i>sdiA</i>	transcriptional regulator	0.32	0.007
g2747.t1	W817_10870	<i>fliD</i>	flagellar capping protein	0.31	0.011
g2754.t1	W817_10900	<i>yedF</i>	hypothetical protein	4.23	0.034
g2759.t1	W817_10935	<i>fliE</i>	flagellar hook-basal body protein FliE	0.46	0.003
g2778.t1	W817_11025	<i>yedQ</i>	putative diguanylate cyclase YedQ	0.7	0.042
g2792.t1	W817_11100	<i>yedZ</i>	sulfite oxidase subunit YedZ	0.45	0.028
g2795.t1	W817_11125	<i>C2177</i>	truncated integrase B	0.4	0.008
g28.t1	W817_00460	<i>traL</i>	conjugal transfer protein TraL	0.21	0.011
g2800.t1	W817_11150	<i>ybtP</i>	lipoinner membrane ABC-transporter domain protein	2.17	0.02
g2825.t1	W817_11250	<i>C2204</i>	integrase	0.29	0.018
g2826.t1	W817_11255	<i>C2206</i>	hypothetical protein	2.51	0.034
g285.t1	W817_23485	<i>yjDL</i>	peptide permease	0.15	0.007

g2853.t1	W817_11360	<i>C2226</i>	transposase	0.3	0.038
g2859.t1	W817_11395	<i>C2234</i>	Colicin I receptor precursor	0.48	0.006
g2865.t1	W817_11425	<i>C2241</i>	acetyltransferase	0.17	0.013
g2866.t1	W817_11430	<i>yaiO</i>	membrane protein	0.34	0.029
g287.t1	W817_23495	<i>cadB</i>	arginine:agmatine antiporter	0.25	0.047
g2870.t1	W817_11455	<i>C2245</i>	hypothetical protein	0.29	0.04
g2871.t1	W817_11460	<i>ydcZ</i>	membrane protein	0.31	0.01
g288.t1	W817_23500	<i>cadC</i>	transcriptional regulator	0.31	0.047
g2888.t1	W817_11575	<i>C2269</i>	chemotaxis protein	1.8	0.022
g2897.t1	W817_11620	<i>yeeV1</i>	toxin	0.31	0.008
g29.t1	W817_00465	<i>traE</i>	conjugal transfer protein TraE	0.28	0.035
g290.t1	W817_23515	<i>dsbD</i>	thiol:disulfide interchange protein DsbD	1.28	0.012
g2901.t1	W817_11650	<i>sbmC</i>	DNA gyrase inhibitor	2.59	0.004
g2903.t1	W817_11660	<i>sbcB</i>	exonuclease I	2.1	0.01
g2926.t1	W817_11805	<i>wcaL</i>	colanic acid biosynthesis glycosyltransferase WcaL	2.35	0.036
g2927.t1	W817_11810	<i>wcaK</i>	colanic acid biosynthesis protein	2.51	0.007
g2928.t1	W817_11815	<i>wzxC</i>	colanic acid exporter	3.4	0.02
g2932.t1	W817_11840	<i>wcaI</i>	glycosyl transferase	3.7	0.045
g2933.t1	W817_11845	<i>wcaH</i>	GDP-mannose mannosyl hydrolase NudD	4.46	0.001
g2934.t1	W817_11850	<i>wcaG</i>	GDP-fucose synthetase	5.63	0.035
g2935.t1	W817_11855	<i>gmd</i>	GDP-mannose 4,6-dehydratase	7.8	0.041
g2936.t1	W817_11860	<i>wcaF</i>	acyl transferase	3.76	0.015
g2937.t1	W817_11865	<i>wcaE</i>	glycosyl transferase	4.12	0.012
g294.t1	W817_23535	<i>fxsA</i>	exclusion suppressor FxsA	1.46	0.005
g2941.t1	W817_11875	<i>wcaC</i>	colanic acid biosynthesis glycosyltransferase WcaC	5.48	0.002
g2943.t1	W817_11885	<i>wcaA</i>	glycosyl transferase	6.59	0.016
g2944.t1	W817_11890	<i>wzc</i>	tyrosine kinase	3.49	0.036
g2945.t1	W817_11895	<i>wzb</i>	protein-tyrosine phosphatase	12.24	0.024
g2946.t1	W817_11900	<i>wza</i>	polysaccharide export protein Wza	9.12	0.015
g2954.t1	W817_11935	<i>yegE</i>	predicted diguanylate cyclase yegE	1.43	0.009
g2965.t1	W817_11980	<i>mdtB</i>	MdtABC-TolC efflux pump	1.15	0.002
g2966.t1	W817_11985	<i>mdtC</i>	MdtABC-TolC efflux pump	1.52	0.026
g2976.t1	W817_12025	<i>C2359</i>	hypothetical protein	0.16	0.025
g298.t1	W817_23555	<i>yjeI</i>	membrane protein	2.13	0.009
g2995.t1	W817_12115	<i>thiM</i>	hydroxyethylthiazole kinase	0.38	0.046
g2997.t1	W817_12125	<i>yohM</i>	cobalt transporter	0.5	0.037
g3000.t1	W817_12135	<i>yehA</i>	fimbrial protein	0.21	0.002
g3001.t1	W817_12140	<i>yehB</i>	fimbrial outer membrane usher protein	0.09	0.025
g3002.t1	W817_12145	<i>yehC</i>	fimbrial assembly chaperone protein StcB	0.22	0.001
g3016.t1	W817_12205	<i>yehR</i>	hypothetical lipoprotein	0.42	0.009
g302.t1	W817_23575	<i>ecnA</i>	entericidin A	0.3	0.011
g3029.t1	W817_12270	<i>yohC</i>	membrane protein	2.38	0.019
g3051.t1	W817_12370	<i>cirA</i>	catecholate siderophore receptor CirA	0.28	0.019
g3066.t1	W817_12435	<i>C2444</i>	PTS fructose transporter subunit IIA	0.48	0.02
g3083.t1	W817_12510	<i>yejG</i>	hypothetical protein	0.38	0.025
g3093.t1	W817_12560	<i>narP</i>	nitrate/nitrite response regulator NarP	1.38	0.024
g3102.t1	W817_12595	<i>ccmB</i>	Heme exporter protein CcmB	2.72	0.005
g3103.t1	W817_12600	<i>ccmA</i>	cytochrome C biogenesis protein CcmA	2.12	0.023
g3113.t1	W817_12645	<i>mgo</i>	malate:quinone oxidoreductase	0.36	0.008
g3120.t1	W817_12670	<i>ompC</i>	outer membrane porin protein C	3.29	0.031
g3122.t1	W817_12675	<i>yojN</i>	RcsD phosphotransferase	0.09	0.027
g3127.t1	W817_12690	<i>atoS</i>	histidine kinase	2.18	0.036
g3137.t1	W817_12735	<i>yfaT</i>	hypothetical protein	0.35	0.028
g3150.t1	W817_12785	<i>glpT</i>	sugar phosphate permease	0.5	0.031
g3160.t1	W817_12820	<i>yfaU</i>	2-keto-3-deoxy-L-rhamnonate aldolase	0.45	0.03
g3222.t1	W817_13100	<i>folX</i>	dihydroneopterin triphosphate epimerase	2.5	0.017
g3229.t1	W817_13135	<i>argT</i>	Lysine-arginine-ornithine-binding periplasmic protein	2.58	0.019
g3243.t1	W817_13200	<i>fabB</i>	3-oxoacyl-ACP synthase	2.15	0.015
g3259.t1	W817_13275	<i>yfcV</i>	fimbrial yfcV	0.42	0.016
g3268.t1	W817_13325	<i>intC</i>	putative prophage CPS-53 integrase	0.31	0.042
g327.t1	W817_23705	<i>hfq</i>	RNA-binding protein Hfq	1.92	0.034
g3287.t1	W817_13440	<i>hkbM</i>	hypothetical protein	5.48	0.018
g3290.t1	W817_13460	<i>C2660</i>	lysozyme	0.48	0.048
g3301.t1	W817_13550	<i>C2677</i>	repressor	2.6	0.001

g3315.t1	W817_13665	<i>emrY</i>	multidrug resistance protein Y	0.21	0.043
g3317.t1	W817_13670	<i>emrK</i>	EmrKY-TolC multidrug resistance efflux pump	0.15	0.01
g3321.t1	W817_13690	<i>yfdV</i>	auxin efflux transporter type protein	0.21	0.012
g3323.t1	W817_13700	<i>yfdW</i>	formyl-CoA transferase	0.3	0.028
g3324.t1	W817_13705	<i>yfdX</i>	hypothetical protein	0.05	0.001
g3365.t1	W817_13895	<i>cysM</i>	cysteine synthase	2.59	0.004
g3378.t1	W817_13940	<i>cysU</i>	sulfate/thiosulfate transporter	4.33	0.039
g3389.t1	W817_13980	<i>ypeA</i>	acetyltransferase	2.22	0.025
g3390.t1	W817_13985	<i>amiA</i>	N-acetylmuramoyl-l-alanine amidase I	0.49	0.022
g340.t1	W817_23760	<i>yjfK</i>	hypothetical protein	0.35	0.039
g3407.t1	W817_14060	<i>eutT</i>	ethanolamine utilization cobalamin adenosyltransferase	2.27	0.042
g3408.t1	W817_14065	<i>eutQ</i>	ethanolamine utilization protein EutQ	2.4	0.024
g342.t1	W817_23770	<i>yjfM</i>	membrane protein	0.47	0.039
g3440.t1	W817_14200	<i>upp</i>	uracil phosphoribosyltransferase	0.46	0.021
g3447.t1	W817_14225	<i>yfgF</i>	cyclic di-GMP phosphodiesterase	0.35	0.014
g3449.t1	W817_14240	<i>yfgH</i>	membrane protein	0.2	0.028
g3459.t1	W817_14275	<i>C2830</i>	intimin	0.24	0.048
g346.t1	W817_23785	<i>yjfN</i>	hypothetical protein	2.68	0.006
g3472.t1	W817_14335	<i>sseA</i>	3-mercaptopyruvate sulfurtransferase	2.54	0.019
g3524.t1	W817_14565	<i>rseA</i>	anti-RNA polymerase sigma factor $\sigma E$	1.53	0.013
g3532.t1	W817_14610	<i>ung</i>	uracil-DNA glycosylase	2.19	0.023
g3537.t1	W817_14630	<i>yfiP</i>	hypothetical protein	0.29	0.004
g3541.t1	W817_14650	<i>kgtP</i>	alpha-ketoglutarate permease	2.13	0.009
g3545.t1	W817_14665	<i>insK</i>	IS150 conserved protein InsB	1.84	0.018
g3551.t1	W817_14725	<i>C2931</i>	translation inhibitor protein RaiA	2.75	0.033
g3557.t1	W817_14755	<i>yfiN</i>	predicted diguanylate cyclase yfiN	0.64	0.03
g3569.t1	W817_14810	<i>rceN</i>	DNA repair protein RecN	0.34	0.018
g3570.t1	W817_14815	<i>bamE</i>	outer membrane protein assembly factor	1.74	0.033
g3577.t1	W817_14885	<i>ycfK</i>	integrase	0.42	0.043
g3604.t1	W817_15000	<i>C2987</i>	endonuclease	0.06	0.036
g3623.t1	W817_15115	<i>C3009</i>	integrase	0.23	0.018
g363.t1	W817_23870	<i>C4805</i>	toxin HipA	0.48	0.024
g3638.t1	W817_15190	<i>stpA</i>	DNA-binding protein StpA	0.38	0.017
g364.t1	W817_23875	<i>exuT</i>	hexuronate transporter ExuT	0.2	0.03
g3648.t1	W817_15235	<i>nrdF</i>	ribonucleotide-diphosphate reductase subunit beta	0.41	0.039
g3652.t1	W817_15255	<i>ygaY</i>	transporter	0.18	0.012
g3668.t1	W817_15335	<i>csrA</i>	carbon storage regulator	1.72	0.035
g3669.t1	W817_15340	<i>alaS</i>	alanyl-tRNA synthetase	1.68	0.028
g3713.t1	W817_15555	<i>pphB</i>	serine/threonine protein phosphatase	0.46	0.047
g3722.t1	W817_15600	<i>rpoS</i>	RNA polymerase sigma factor RpoS	1.76	0.001
g3731.t1	W817_15640	<i>ygbE</i>		2.15	0.041
g3733.t1	W817_15650	<i>cysN</i>	sulfate adenylyltransferase subunit 1	2.48	0.016
g3736.t1	W817_15655	<i>cysD</i>	sulfate adenylyltransferase subunit 2	3.99	0.003
g3756.t1	W817_15750	<i>C3143</i>	membrane protein	0.38	0.003
g3768.t1	W817_15805	<i>gudD</i>	glucarate dehydratase	3.41	0.04
g3770.t1	W817_15810	<i>ygcY</i>	glucarate dehydratase	2.19	0.011
g3777.t1	W817_15850	<i>ygdH</i>	LOG family protein ygdH	2.27	0.007
g3782.t1	W817_15875	<i>fucA</i>	fucose phosphate aldolase	2.29	0.03
g3786.t1	W817_15890	<i>fucK</i>	L-fuculokinase	2.55	0.048
g3788.t1	W817_15900	<i>fucR</i>	L-fucose operon activator	2.1	0.04
g3798.t1	W817_15960	<i>C3190</i>	hypothetical protein	0.47	0.029
g3799.t1	W817_15965	<i>C3191</i>	EvpB/family type VI secretion protein	0.37	0.042
g3813.t1	W817_16015	<i>C3203</i>	type VI secretion protein VasK	0.46	0.013
g3814.t1	W817_16020	<i>C3204</i>	Uncharacterized protein ImpA	0.33	0.049
g3815.t1		<i>C3205</i>	type VI secretion system protein TssA	0.1	0.047
g3822.t1	W817_16075	<i>C3212</i>	phosphoglycerate dehydrogenase	0.44	0.043
g3824.t1	W817_16085	<i>C3214</i>	beta-cystathionase	0.29	0.041
g3836.t1	W817_16145	<i>ppdA</i>	prepilin peptidase dependent protein A	4.15	0.014
g3837.t1	W817_16150	<i>C3229</i>	thymidylate synthase	3.46	0.023
g384.t1	W817_23955	<i>ytfJ</i>	hypothetical protein	2.07	0.002
g3844.t1	W817_16180	<i>ygdR</i>	hypothetical protein	2.95	0.016
g385.t1	W817_23960	<i>ytfK</i>	hypothetical protein	4.05	0.029
g3850.t1	W817_16210	<i>lysR</i>	transcriptional regulator	0.41	0.016
g3854.t1	W817_16230	<i>kduI</i>	5-keto-4-deoxyuronate isomerase	0.49	0.004

g3857.t1	W817_16240	<i>C3248</i>	septum formation protein	0.15	0.026
g3862.t1	W817_16270	<i>ygeV</i>	Fis family transcriptional regulator	2.9	0.005
g387.t1	W817_23970	<i>msrA</i>	methionine sulfoxide reductase A	2.11	0.021
g3871.t1	W817_16310	<i>ygfJ</i>	Molybdenum cofactor cytidyltransferase	0.19	0.038
g3893.t1	W817_16425	<i>ygfZ</i>	global regulator	2.2	0.04
g3895.t1	W817_16435	<i>yqfB</i>	hypothetical protein	2.12	0.001
g3902.t1	W817_16470	<i>pepP</i>	Xaa-Pro aminopeptidase	2.23	0.003
g3905.t1	W817_16485	<i>ygfA</i>	5-formyltetrahydrofolate cyclo-ligase	0.21	0.013
g3912.t1	W817_16525	<i>yggE</i>	oxidative stress defense protein	1.44	0.016
g3928.t1	W817_16595	<i>C3319</i>	L-sorbose 1-phosphate reductase	0.3	0.001
g3934.t1	W817_16620	<i>yggG</i>	metallopeptidase	2.08	0.001
g3954.t1	W817_16715	<i>yggW</i>	HemN family oxidoreductase	0.46	0.04
g3996.t1	W817_16935	<i>glcG</i>	hypothetical protein	0.29	0.03
g3998.t1	W817_16940	<i>glcF</i>	glycolate oxidase	0.33	0.037
g3999.t1	W817_16945	<i>glcE</i>	FAD-binding protein	0.38	0.004
g4001.t1	W817_16955	<i>glcC</i>	GntR family transcriptional regulator	3.45	0.008
g4004.t1	W817_16965	<i>C3397</i>	acyl-CoA synthetase	0.37	0.011
g4005.t1	W817_16970	<i>C3398</i>	short-chain dehydrogenase	0.15	0.023
g401.t1	W817_24030	<i>pmbA</i>	peptidase PmbA	1.8	0.003
g4013.t1	W817_17010	<i>yghR</i>	hypothetical protein	0.42	0.042
g4014.t1	W817_17015	<i>yghS</i>	hypothetical protein	0.33	0.035
g4029.t1	W817_17090	<i>yghZ</i>	L-glyceraldehyde 3-phosphate reductase	2.4	0.014
g403.t1	W817_24035	<i>cybC</i>	cytochrome b562	2.52	0.017
g4039.t1	W817_17135	<i>yqhD</i>	alcohol dehydrogenase YqhD	2.95	0.02
g4042.t1	W817_17150	<i>yqhH</i>	lipoprotein YqhH	1.33	0.047
g4050.t1	W817_17190	<i>ygiK</i>	c4-dicarboxylate permease	0.51	0.021
g4058.t1	W817_17225"	<i>qseB</i>	quorum sensing two-component response regulator	1.5	0.018
g4061.t1	W817_17255	<i>ygiN</i>	quinol monooxygenase	2.67	0.022
g4075.t1	W817_17315	<i>tolC</i>	outer membrane channel protein	1.5	0.001
g4076.t1	W817_17320	<i>ygiB</i>	membrane protein	2.18	0.048
g4082.t1	W817_17340	<i>C3475</i>	disulfide oxidoreductase	2.2	0.025
g4086.t1	W817_17360	<i>ygiL</i>	putative Yqi fimbriae subunit YgiL precursor	0.35	0.004
g4092.t1	W817_17390	<i>glgS</i>	glycogen synthesis protein GlgS	4.18	0.021
g4093.t1	W817_17395	<i>yqiJ</i>	membrane protein	0.14	0.033
g4094.t1	W817_17400	<i>yqiK</i>	membrane protein	0.16	0.022
g4104.t1	W817_17450	<i>ygiP</i>	LysR family transcriptional regulator	0.49	0.012
g4121.t1	W817_17540	<i>ygiI</i>	amino acid permease	0.19	0.015
g4128.t1	W817_17575	<i>ygiR</i>	oxidoreductase	2.34	0.003
g4133.t1	W817_17595	<i>uxaA</i>	altronate hydrolase	2.68	0.042
g4135.t1		<i>exuT</i>	hexuronate transporter	1.8	0.013
g4154.t1	W817_17700	<i>tdcD</i>	propionate kinase	0.45	0.017
g4172.t1	W817_17795	<i>agaY</i>	tagatose-bisphosphate aldolase 2	0.23	0.033
g4175.t1	W817_17810	<i>agaD</i>	PTS N-acetylgalactosamine transporter subunit IID	2.68	0.025
g4185.t1	W817_17855	<i>yhbO</i>	general stress protein	0.49	0.039
g4197.t1	W817_17900	<i>deaD</i>	Cold-shock DEAD-box protein A	0.42	0.013
g421.t1	W817_24115	<i>yjgK</i>	Toxin-antitoxin biofilm protein TabA	2.18	0.031
g4239.t1	W817_18100	<i>rpoN</i>	RNA polymerase factor sigma-54	2.46	0.016
g4241.t1	W817_18105	<i>hpf</i>	ribosome hibernation promoting factor HPF	2.66	0.041
g4256.t1	W817_18175	<i>YhcJ</i>	N-acetylmannosamine-6-phosphate 2-epimerase	2.16	0.007
g4257.t1	W817_18180	<i>nanT</i>	sialic acid transporter	3.16	0.019
g4265.t1	W817_18220	<i>yhcB</i>	hypothetical protein	2.18	0.002
g4266.t1	W817_18225	<i>degQ</i>	serine endoprotease DegQ	1.55	0.029
g4272.t1	W817_18250	<i>yhcO</i>	hypothetical protein	0.25	0.028
g4273.t1	W817_18255	<i>C3671</i>	hydroxybenzoic acid transporter	0.3	0.037
g4277.t1	W817_18275	<i>tldD</i>	csrA activity inhibitor TldD	1.75	0.024
g4280.t1	W817_18290	<i>Maf</i>	maf-like protein YhdE	0.28	0.021
g4281.t1	W817_18295	<i>mreD</i>	rod shape-determining protein MreD	0.22	0.049
g4282.t1	W817_18300	<i>mreC</i>	rod shape-determining protein MreC	0.26	0.024
g4285.t1	W817_18315	<i>yhdH</i>	quinone oxidoreductase	2.37	0.048
g4293.t1	W817_18345	<i>rbsP</i>	D-ribose transporter ATP binding protein	0.21	0.038
g4297.t1	W817_18365	<i>C3698</i>	sugar kinase	2.22	0.012
g4308.t1	W817_18425	<i>yhdV</i>	hypothetical protein YhdV	2.45	0.003
g4313.t1	W817_18445	<i>artP</i>	arginine ABC transporter ATP-binding protein	2.41	0.012
g4325.t1	W817_18535	<i>trkA</i>	potassium transporter peripheral membrane protein	0.39	0.013

g4326.t1	W817_18540	<i>mscL</i>	large-conductance mechanosensitive channel	2.16	0.018
g436.t1	W817_24175	<i>idnT</i>	fructuronate transporter	0.68	0.021
g4371.t1	W817_18760	<i>pshM</i>	general secretion pathway protein M	0.37	0.019
g4385.t1	W817_18825	<i>fkpA</i>	periplasmic peptidylprolyl cis,trans isomerase	1.23	0.004
g4399.t1	W817_18880	<i>crp</i>	CRP transcriptional dual regulator	1.91	0.037
g4402.t1	W817_18890	<i>argD</i>	succinyldiaminopimelate aminotransferase	0.43	0.016
g4405.t1	W817_18910	<i>ppiA</i>	peptidylprolyl-cis-trans-isomerase A	1.16	0.012
g4412.t1	W817_18940	<i>yhfL</i>	membrane protein	0.51	0.001
g4421.t1	W817_18980	<i>yhfZ</i>	hypothetical protein	2.57	0.003
g443.t1	W817_24215	<i>yjgX</i>	sulfatase	0.26	0.013
g4434.t1	W817_19040	<i>mrcA</i>	penicillin-binding protein 1A	0.51	0.014
g4438.t1	W817_19055	<i>igaA</i>	intracellular growth attenuator protein igaA	0.75	0.007
g444.t1	W817_24220	<i>hek</i>	adhesin/virulence factor Hek	0.1	0.013
g4456.t1	W817_19120	<i>yhgA</i>	transposase	2.67	0.019
g4459.t1	W817_19140	<i>nfuA</i>	iron-sulfur cluster scaffold protein	1.85	0.033
g447.t1	W817_24240	<i>papG</i>	p pilus adhesin PapG protein	0.12	0.033
g4473.t1	W817_19205	<i>C3928</i>	hypothetical protein	0.03	0.04
g4475.t1	W817_19215	<i>sfmH</i>	hypothetical protein	0.13	0.045
g4477.t1	W817_19235	<i>aufC</i>	outer membrane usher protein	0.17	0.038
g448.t1	W817_24245	<i>papF</i>	fimbrial adapter papF	0.12	0.019
g4483.t1	W817_19255	<i>glgA</i>	glycogen synthase	2.64	0.034
g4485.t1	W817_19265	<i>glgX</i>	glycogen-debranching protein	2.86	0.04
g4494.t1	W817_19305	<i>yhhX</i>	oxidoreductase	2.11	0.011
g4498.t1	W817_19335	<i>yhhA</i>	membrane protein	2.58	0.049
g450.t1	W817_24255	<i>papK</i>	fimbrial adapter PapK	0.24	0.027
g4516.t1	W817_19415	<i>C3973</i>	PTS fructose transporter subunit IID	0.12	0.042
g4518.t1	W817_19425	<i>C3975</i>	dihydrodipicolinate synthase	0.15	0.014
g4542.t1	W817_19540	<i>mngR</i>	regulatory protein	2.2	0.014
g4551.t1	W817_19585	<i>yhiI</i>	membrane protein	2.14	0.018
g4556.t1	W817_19610	<i>uspA</i>	universal stress protein A	2.67	0.032
g4557.t1	W817_19615	<i>yhiP</i>	MFS transporter	1.78	0.048
g4567.t1	W817_19660	<i>yhiF</i>	LuxR family transcriptional regulator	0.29	0.014
g457.t1	W817_24335	<i>C4905</i>	F17 fimbrial usher	0.17	0.05
g4572.t1	W817_19680	<i>chuW</i>	coproporphyrinogen III oxidase	0.49	0.011
g4582.t1	W817_19730	<i>yhiU</i>	multidrug transporter	0.33	0.015
g4584.t1	W817_19735	<i>yhiV</i>	multidrug transporter	0.5	0.012
g4596.t1	W817_19795	<i>kdgK</i>	ketodeoxygluconokinase	2.24	0.003
g4656.t1	W817_20070	<i>yiaK</i>	2,3-diketo-L-gulonate reductase	2.66	0.03
g4668.t1	W817_20130	<i>yiaY</i>	alcohol dehydrogenase	0.38	0.02
g4692.t1	W817_20230	<i>secB</i>	preprotein translocase subunit SecB	1.69	0.001
g4699.t1	W817_20260	<i>yibD</i>	glycosyl transferase	0.42	0.046
g4701.t1	W817_20270	<i>kbl</i>	2-amino-3-ketobutyrate CoA ligase	2.14	0.041
g4702.t1	W817_20275	<i>rfaD</i>	ADP-L-glycero-D-mannoheptose-6-epimerase	1.33	0.003
g4707.t1	W817_20305	<i>rfaY</i>	lipopolysaccharide core heptose(II) kinase RfaY	1.52	0.046
g4720.t1	W817_20360	<i>radC</i>	DNA repair protein	2.86	0.001
g4723.t1	W817_20375	<i>slmA</i>	division inhibitor protein	0.48	0.004
g4735.t1	W817_20430	<i>recG</i>	ATP-dependent DNA helicase RecG	0.51	0.024
g4736.t1	W817_20435	<i>C4198</i>	sodium/glutamate symport carrier protein GltS	2.35	0.006
g4752.t1	W817_20505	<i>rhuM</i>	2-hydroxyacid dehydrogenase	0.52	0.007
g4764.t1	W817_20570	<i>uhpA</i>	DNA-binding transcriptional activator	0.5	0.001
g4768.t1	W817_20590	<i>yidF</i>	hypothetical protein	2.39	0.02
g477.t1	W817_24455	<i>C4929</i>	molybdopterin binding oxidoreductase	0.27	0.018
g4796.t1	W817_20740	<i>tnaA</i>	L-cysteine desulfhydrase	0.39	0.024
g4797.t1	W817_20745	<i>tnaB</i>	tryptophan permease	0.25	0.012
g4798.t1	W817_20750	<i>yidY</i>	multidrug transporter	0.49	0.026
g4803.t1	W817_20775	<i>yieH</i>	6-phosphogluconate phosphatase	0.38	0.011
g481.t1	W817_24470	<i>C4932</i>	sensor histidine kinase	0.33	0.049
g4812.t1	W817_20815	<i>phoU</i>	phosphate transport system protein PhoU	2.42	0.03
g4813.t1	W817_20820	<i>pstB</i>	phosphate ABC transporter ATP-binding protein	2.34	0.008
g4815.t1	W817_20830	<i>pstC</i>	phosphate transporter permease subunit PstC	2.4	0.032
g4830.t1	W817_20905	<i>gidA</i>	glucose-inhibited cell division protein A	0.47	0.036
g484.t1	W817_24500	<i>C4940</i>	hypothetical protein	0.06	0.044
g4841.t1	W817_20955	<i>rbsB</i>	D-ribose transporter subunit RbsB	2.25	0.005
g4846.t1	W817_21010	<i>hdfR</i>	HNS-dependent flhDC regulator	2.04	0.009



g4847.t1	W817_21015	<i>yifE</i>	hypothetical protein	2.64	0.002
g485.t1	W817_24505	<i>C4941</i>	hypothetical protein	0.07	0.049
g486.t1	W817_24510	<i>C4942</i>	hypothetical protein	0.22	0.026
g4869.t1	W817_21090	<i>rho</i>	transcription termination factor Rho	0.51	0.003
g49.t1	W817_00615	<i>traD</i>	conjugal transfer protein TraD	0.67	0.005
g4905.t1	W817_21255	<i>xerC</i>	tyrosine recombinase XerC	0.46	0.032
g4935.t1	W817_21425	<i>C4407</i>	FdrA	0.39	0.039
g494.t1	W817_24550	<i>C4952</i>	transcriptional regulator	0.06	0.037
g4942.t1	W817_21455	<i>C4412</i>	C4-dicarboxylate ABC transporter permease	2.53	0.031
g495.t1	W817_24555	<i>C4953</i>	hypothetical protein	0.17	0.012
g4994.t1	W817_21720	<i>yihX</i>	alpha-D-glucose-1-phosphatase	2.38	0.046
g5005.t1	W817_21785	<i>C4481</i>	sulfate ABC transporter substrate-binding protein	2.17	0.007
g5008.t1	W817_21795		hypothetical protein	0.28	0.031
g5032.t1	W817_21915	<i>yiiS</i>	DUF406 domain-containing protein YiiS	2.42	0.033
g5033.t1	W817_21920	<i>uspD</i>	universal stress protein D	2.5	0.025
g5040.t1	W817_21945	<i>yiiU</i>	septal ring assembly protein ZapB	2.09	0.006
g5041.t1	W817_21950	<i>menG</i>	ribonuclease activity regulator protein RraA	2.59	0.04
g5049.t1	W817_21990	<i>yiiX</i>	hypothetical protein	0.27	0.032
g5057.t1	W817_22020	<i>C4528</i>	5'-nucleotidase	0.44	0.025
g5060.t1	W817_22040	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	0.23	0.023
g5063.t1	W817_22055	<i>yijF</i>	hypothetical protein	0.35	0.013
g5064.t1	W817_22065	<i>gldA</i>	glycerol dehydrogenase	3.96	0.041
g5066.t1	W817_22070	<i>talC</i>	fructose-bisphosphate aldolase	3.07	0.035
g5072.t1	W817_22090	<i>pflD</i>	formate acetyltransferase	2.85	0.018
g5073.t1	W817_22095	<i>pflC</i>	pyruvate formate lyase II activase	3.08	0.005
g5076.t1	W817_22110	<i>yijP</i>	membrane protein	0.49	0.02
g5084.t1	W817_22145	<i>yjiZ</i>	L-galactonate transporter	0.25	0.021
g5089.t1	W817_22170	<i>fabR</i>	transcriptional regulator	1.92	0.044
g5090.t1	W817_22175	<i>yijD</i>	membrane protein	2.49	0.005
g5116.t1	W817_22325	<i>rsd</i>	anti-RNA polymerase sigma 70 factor	2.31	0.002
g5130.t1	W817_22405	<i>yjaA</i>	stress response protein	0.37	0.046
g5137.t1	W817_22430	<i>aceK</i>	isocitrate dehydrogenase	2.2	0.001
g5156.t1	W817_22525	<i>yjbE</i>	exopolysaccharide production protein	12.37	0.035
g5158.t1	W817_22535	<i>yjbG</i>	hypothetical protein	2.96	0.032
g5168.t1	W817_22595	<i>ubiC</i>	chorismate pyruvate lyase	2.41	0.004
g5170.t1	W817_22605	<i>plsB</i>	glycerol-3-phosphate O-acyltransferase	1.34	0.027
g518.t1	W817_24660	<i>C4973</i>	transcriptional regulator	0.46	0.004
g523.t1	W817_24685	<i>C4978</i>	sodium:proton antiporter	0.49	0.008
g524.t1	W817_24690	<i>C4979</i>	transposase IS2	0.48	0.024
g527.t1	W817_24720	<i>C4984</i>	GTPase	0.12	0.039
g538.t1	W817_24770	<i>yeeV2</i>	toxin	0.16	0.04
g544.t1	W817_24805	<i>C5006</i>	N-acetylneuraminic acid mutarotase	0.49	0.016
g548.t1	W817_24835	<i>fimI</i>	fimbrin fimI	0.39	0.008
g549.t1	W817_24840	<i>fimC</i>	molecular chaperone FimC	0.31	0.014
g55.t1	W817_00645	<i>P144</i>	endonuclease	0.42	0.004
g550.t1	W817_24845	<i>fimD</i>	fimbrial protein FimD	0.32	0.016
g556.t1	W817_24860	<i>fimH</i>	type 1 fimbrial adhesin FimH	0.53	0.004
g561.t1	W817_24890	<i>iraD</i>	DNA replication protein	0.43	0.034
g575.t1	W817_24955	<i>igbR</i>	transcriptional regulator DhaR	0.07	0.043
g576.t1	W817_24960	<i>ibeA</i>	invasion protein	0.35	0.032
g578.t1	W817_24970	<i>yjiE</i>	cell density-dependent motility repressor	0.26	0.004
g586.t1	W817_25020	<i>yjiL</i>	hypothetical protein	0.31	0.011
g596.t1	W817_25065	<i>hsdR</i>	endonuclease R	2.96	0.008
g601.t1	W817_25085	<i>yjiY</i>	carbon starvation protein CstA	2.19	0.027
g608.t1	W817_25120	<i>yjiN</i>	galactonate oxidoreductase	0.27	0.027
g616.t1	W817_25155	<i>yjiQ</i>	LuxR family transcriptional regulator	0.14	0.012
g620.t1	W817_25195	<i>rsmC</i>	16S rRNA methyltransferase	0.84	0.024
g627.t1	W817_25215	<i>prfC</i>	peptide chain release factor 3	0.43	0.028
g648.t1	W817_25320	<i>slt</i>	soluble lytic murein transglycosylase	1.49	0.02
g649.t1	W817_25325	<i>trpR</i>	Trp operon repressor	4.38	0.032
g65.t1	W817_00045	<i>P012</i>	membrane protein	0.36	0.009
g653.t1	W817_25345	<i>creA</i>	hypothetical protein	1.54	0.031
g67.t1	W817_00050	<i>P013</i>	ABC transporter permease	0.29	0.02
g673.t1	W817_00710	<i>C0019</i>	hypothetical protein	0.27	0.003

g686.t1	W817_00770	<i>rihA</i>	ribonucleoside hydrolase	2.17	0.019
g689.t1	W817_00785	<i>carA</i>	carbamoyl phosphate synthase small subunit	0.33	0.016
g693.t1	W817_00805	<i>caiE</i>	carnitine operon protein CaiE	0.41	0.002
g695.t1	W817_00815	<i>caiC</i>	crotonobetaine/carnitine-CoA ligase	0.48	0.044
g696.t1	W817_00820	<i>caiB</i>	crotonobetainyl-CoA:carnitine CoA-transferase	0.42	0.038
g698.t1	W817_00830	<i>caiT</i>	antiporter	0.32	0.007
g714.t1	W817_00910	<i>lptD</i>	LPS assembly outer membrane complex protein	1.35	0.041
g72.t1	W817_00075	<i>yihX</i>	glucose-1-phosphatase	3.12	0.003
g725.t1	W817_00970	<i>thiQ</i>	thiamine ABC transporter ATP-binding protein	0.37	0.008
g726.t1	W817_00975	<i>thiP</i>	thiamine transporter membrane protein	0.44	0.014
g737.t1	W817_01030	<i>fruR</i>	DNA-binding transcriptional dual regulator	1.61	0.006
g738.t1	W817_01035	<i>mraZ</i>	cell division protein MraZ	2.18	0.009
g742.t1	W817_01050	<i>ftsI</i>	cell division protein FtsI	2.56	0.028
g744.t1	W817_01055	<i>murE</i>	peptide ligase	2.83	0.002
g755.t1	W817_01110	<i>lpxC</i>	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.26	0.004
g764.t1	W817_01150	<i>hofC</i>	type IV pilin biogenesis protein	0.42	0.002
g771.t1	W817_01185	<i>usp</i>	HNH nuclease	0.38	0.002
g784.t1	W817_01245	<i>yacL</i>	hypothetical protein	2.24	0.043
g786.t1	W817_01255	<i>speE</i>	spermidine synthase	1.76	0.029
g79.t1	W817_00145	<i>P031</i>	transposase ISPsy3	0.31	0.02
g800.t1	W817_01320	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.22	0.03
g802.t1	W817_01330	<i>yadK</i>	fimbrial protein	0.22	0.033
g806.t1	W817_01350	<i>ecpD</i>	molecular chaperone EcpD	0.5	0.022
g81.t1	W817_00135	<i>cjrC</i>	colicin Js sensitive receptor protein	0.42	0.015
g812.t1	W817_01380	<i>sfsA</i>	sugar fermentation stimulation protein A	2.58	0.012
g818.t1	W817_01410	<i>fhuC</i>	ferrichrome transport ATP-binding protein FhuC	0.46	0.025
g821.t1	W817_01420	<i>fhuB</i>	ferrichrome transport system permease protein fhuB	0.31	0.04
g826.t1	W817_01435	<i>yadR</i>	iron-sulfur cluster insertion protein ErpA	2.13	0.012
g83.t1	W817_00125	<i>cjrA</i>	putative inner membrane lipoprotein	0.52	0.039
g833.t1	W817_01470	<i>yaeH</i>	hypothetical protein	2.21	0.01
g838.t1	W817_01485	<i>map</i>	methionine aminopeptidase	2.14	0.046
g852.t1	W817_01545	<i>fabZ</i>	3R-hydroxymyristoyl ACP dehydratase	1.79	0.008
g860.t1	W817_01575	<i>ldcC</i>	lysine decarboxylase CadA	1.36	0.023
g864.t1	W817_01595	<i>yaeP</i>	hypothetical protein	2.16	0.017
g869.t1	W817_01615	<i>yaeF</i>	hypothetical protein	0.41	0.041
g889.t1	W817_01740	<i>C0237</i>	Hcp	0.43	0.003
g912.t1	W817_01855	<i>C0258</i>	conjugative transfer protein	0.25	0.044
g914.t1	W817_01865	<i>ykfE</i>	C-lysozyme inhibitor	2.54	0.045
g919.t1	W817_01890	<i>yafL</i>	endopeptidase	0.49	0.046
g921.t1	W817_01900	<i>flhA</i>	flagellar biosynthesis protein FlhA	0.22	0.042
g927.t1	W817_01930	<i>C0275</i>	hypothetical protein	0.43	0.002
g933.t1	W817_01955	<i>crl</i>	transcriptional regulator	2.1	0.002
g939.t1	W817_01990	<i>hbp</i>	hemoglobin-binding protease hbp autotransporter	0.52	0.002
g946.t1	W817_02035	<i>yagX</i>	CFA/I fimbrial subunit C usher protein	0.36	0.005
g975.t1	W817_02185	<i>betB</i>	betaine-aldehyde dehydrogenase	2.05	0.008
g978.t1	W817_02200	<i>yahA</i>	cyclic di-GMP phosphodiesterase	0.53	0.045
g999.t1	W817_02290	<i>atoC</i>	acetoacetate metabolism regulatory protein AtoC	2.41	0.011