

Supplementary tables

Table S1. Genes that were up-regulated at least two-fold with growth on Fe(III) oxide compared with Fe(III) citrate as the electron acceptor (P-value cutoff ≤ 0.05)

Gene	Annotation	Fold change	P value	T value
Gmet_0442	flagellin fliC	94.509 up	0.000527	-11.408
Gmet_1044	molybdopterin biosynthesis sulfur carrier protein moaD	90.156 up	0.0473	-3.442
Gmet_0719	conserved hypothetical protein	77.044 up	0.0000544	-21.877
Gmet_1045	aldehyde ferredoxin oxidoreductase tungsten containing	76.354 up	0.024	-4.247
Gmet_1043	molybdopterin biosynthesis sulfur carrier protein sulfurylase; moeB	76.339 up	0.0328	-3.858
Gmet_1046	ethanol dehydrogenase, putative	75.546 up	0.0334	-3.841
Gmet_0438	flagellar hook-associated protein FlgK	56.927 up	4.68x10 ⁻⁷	-89.469
Gmet_0430	flagellar basal body rod protein FlgF	55.842 up	0.0000413	-25.231
Gmet_0439	flagellar hook-filament junction protein FlgL	52.739 up	4.07x10 ⁻⁷	-81.59
Gmet_0432	flagellar basal body P-ring formation protein FlgA	49.008 up	0.0000315	-32.008
Gmet_0431	flagellar basal body rod protein FlgG	43.844 up	0.000107	-17.966
Gmet_3115	flagellar basal-body rod protein FlgB	43.056 up	0.000238	-14.225
Gmet_3112	flagellar M-ring mounting plate protein FliF	42.517 up	0.0000408	-24.285
Gmet_0908	hypothetical protein	42.056 up	0.0027	-7.732
Gmet_3104	flagellar operon protein of unknown function DUF3766	39.524 up	0.0104	-5.415
Gmet_3098	flagellar biogenesis protein FliO	39.065 up	0.000232	-14.31
Gmet_0440	carbon storage regulator, CsrA/carbon storage regulator, CsrA	38.440 up	0.000198	-15.016
Gmet_0909	cytochrome c, 9 heme-binding sites	37.794 up	0.00226	-8.078
Gmet_0427	flagellar biogenesis protein FlhF	37.620 up	0.0000946	-18.375
Gmet_2043	repeat-containing protein	37.508 up	0.0000161	-39.331
Gmet_0910	lipoprotein cytochrome c, 10 heme-binding sites	32.723 up	0.00243	-7.926
Gmet_0444	flagellar filament cap protein FliD	32.146 up	0.00159	-8.84
Gmet_3101	flagellar basal body-associated protein FliL	31.002 up	0.000244	-13.945
Gmet_0433	flagellar L-ring lipoprotein FlgH	29.494 up	0.0000417	-23.53
Gmet_3589	lipoprotein, putative	29.302 up	0.000157	-15.917
Gmet_0441	flagellar assembly protein FliW	29.175 up	0.0000958	-18.385
Gmet_0434	flagellar P-ring protein FlgI	29.036 up	0.000742	-10.45
Gmet_0428	flagellar biogenesis protein FlhG (ATPase)	28.361 up	0.0002	-15.017
Gmet_3105	flagellar hook capping protein FlgD	27.424 up	0.00868	-5.662
Gmet_0437	flagellar biogenesis protein FlgN, putative	27.292 up	0.000326	-12.822

Gmet_3099	flagellar motor switch protein FliN	26.197 up	0.0000533	-21.859
Gmet_0429	RNA polymerase sigma-28 factor for flagellar operon fliA	25.445 up	0.00037	-12.479
Gmet_3266	chemotaxis sensor histidine kinase CheA-4	24.699 up	0.0003	-13.166
Gmet_3118	chemotaxis protein phosphatase CheX-1	23.733 up	6.77x10 ⁻⁷	-70.028
Gmet_1042	phosphate-selective porin O and P	23.706 up	0.000288	-13.427
Gmet_3106	flagellar hook-length control protein FliK	23.315 up	0.00586	-6.304
Gmet_3100	flagellar motor switch protein FliM	21.723 up	0.000205	-14.78
Gmet_2042	conserved hypothetical protein	21.680 up	0.000247	-14.029
Gmet_2030	periplasmic polysaccharide biosynthesis/export protein	20.876 up	0.00014	-16.389
Gmet_0749	serine protease, subtilase family	20.766 up	0.000631	-10.841
Gmet_0445	flagellin export facilitator protein FliS	20.467 up	0.00253	-7.859
Gmet_0446	hypothetical protein	19.882 up	0.00206	-8.288
Gmet_3103	flagellar hook protein FlgE	18.710 up	0.00663	-6.099
Gmet_0557	cytochrome c, 4 heme-binding sites; omcP	18.539 up	0.00243	-7.935
Gmet_0531	rhodanese homology domain pair protein	18.433 up	0.000684	-10.644
Gmet_3113	flagellar hook-basal body complex protein FliE	18.384 up	0.0000306	-29.381
Gmet_2423	methyl-accepting chemotaxis sensory transducer; mcp018	18.368 up	0.0000311	-27.122
Gmet_0679	cytochrome c, 5 heme-binding sites; omcX	17.969 up	0.00373	-7.06
Gmet_0532	phosphate-selective porin O and P	17.862 up	0.000382	-12.357
Gmet_3092	hypothetical protein	17.526 up	0.00418	-6.882
Gmet_1041	tungstate ABC transporter, periplasmic tungstate-binding protein; tupA	17.518 up	0.000213	-14.541
Gmet_2428	chemotaxis protein CheY-3	17.494 up	0.000179	-15.475
Gmet_3267	chemotaxis protein-glutamate methyltransferase CheR-1	17.323 up	0.000056	-21.498
Gmet_0426	flagellar biogenesis protein FlhA	17.141 up	0.0000832	-19.461
Gmet_0558	cytochrome c, 23-27 heme-binding sites; omcO	17.057 up	0.00225	-8.107
Gmet_3586	conserved hypothetical protein	16.971 up	0.000559	-11.209
Gmet_3096	flagellar biosynthesis protein FliQ	16.693 up	0.000279	-13.552
Gmet_0571	cytochrome c, 26 heme-binding sites	16.506 up	0.00988	-5.472
Gmet_3109	flagellum-specific ATPase FliI	16.218 up	0.000473	-11.736
Gmet_2584	hypothetical protein	15.943 up	0.0152	-4.84
Gmet_1606	BioD and DRTGG domain protein	15.867 up	0.00038	-12.355
Gmet_3476	response regulator receiver modulated metal dependent phosphohydrolase	15.725 up	0.0000904	-18.62
Gmet_0461	chemotaxis MotA protein	15.705 up	0.000531	-11.38
Gmet_2424	methyl-accepting chemotaxis sensory transducer mcp005	15.425 up	0.0000556	-21.615
Gmet_2015	rhodanese homology domain	15.355 up	0.000384	-12.293

	superfamily selenoprotein, putative			
Gmet_0556	NHL repeat domain protein	15.191 up	0.00786	-5.823
Gmet_1039	tungstate ABC transporter, ATP-binding protein; tupC	15.109 up	0.000146	-16.166
Gmet_3323	methyl viologen-reducing hydrogenase maturation protease; mvhP	14.574 up	0.000319	-12.963
Gmet_0748	hypothetical protein	14.418 up	0.000321	-12.903
Gmet_2029	polysaccharide chain length determinant protein, putative	14.281 up	0.0000316	-31.271
Gmet_3091	cytochrome c, 2 heme-binding sites macA	13.924 up	0.0499	-3.383
Gmet_0435	flagellar rod-binding protein FlgJ, putative	13.668 up	0.00294	-7.569
Gmet_3111	flagellar motor switch protein FliG	13.537 up	0.000247	-13.89
Gmet_3119	chemotaxis protein CheY-1	13.501 up	0.0000403	-24.975
Gmet_0716	hypothetical protein	12.919 up	0.000203	-15.088
Gmet_2825	methyl-accepting chemotaxis sensory transducer mcp001	12.457 up	0.0000387	-25.922
Gmet_2032	TPR domain lipoprotein	12.254 up	0.000112	-17.584
Gmet_2429	STAS domain protein	11.949 up	0.0000846	-19.538
Gmet_2028	protein tyrosine kinase, putative	11.823 up	0.0000324	-27.734
Gmet_3268	metal dependent phosphohydrolase	11.401 up	0.000245	-13.949
Gmet_3085	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	11.265 up	0.000513	-11.539
Gmet_2653	hypothetical protein	11.224 up	0.000108	-17.743
Gmet_3477	sensor histidine kinase response regulator (HAMP, PAS, PAS, PAS, PAS, HATPase_c, REC, PAS)	11.213 up	0.0000423	-23.6
Gmet_1088	lipoprotein cytochrome c, 1 heme-binding site	11.119 up	0.000541	-11.322
Gmet_2723	peroxiredoxin, typical 2-Cys subfamily; prx-1	11.058 up	0.00136	-9.157
Gmet_1090	trehalose-phosphatase; otsB	10.534 up	0.000571	-11.135
Gmet_1040	tungstate ABC transporter, membrane protein; tupB	10.534 up	0.00313	-7.462
Gmet_1707	sensor histidine kinase response regulator (PAS, PAS, PAC, HisKA, HATPase_c, REC)	10.412 up	0.00047	-11.762
Gmet_0463	flagellar protein FlaG protein	10.240 up	0.000041	-25.074
Gmet_3472	response regulator receiver domain-containing protein	10.144 up	0.0000804	-19.778
Gmet_3097	fliP flagellar biosynthesis protein FliP	10.037 up	0.000839	-10.171
Gmet_3110	flagellar assembly protein fliH	9.854 up	0.000515	-11.518
Gmet_1089	Na ⁺ /H ⁺ antiporter NhaA	9.843 up	0.000247	-14.055
Gmet_3095	flagellar biosynthesis protein FliR	9.741 up	0.0000332	-27.912
Gmet_3319	methyl viologen-reducing hydrogenase, small subunit, mvhS	9.737 up	0.00708	-5.99
Gmet_2655	hypothetical protein	9.617 up	0.0000535	-22.036
Gmet_2016	aminotransferase, AHBA_syn family	9.415 up	0.0000733	-20.306

Gmet_3114	flagellar basal-body rod protein FlgC	9.232 up	0.00115	-9.527
Gmet_0460	chemotaxis MotB protein	9.221 up	0.0000314	-27.323
Gmet_2027	hypothetical protein	9.172 up	0.000247	-14.114
Gmet_2665	serine protease inhibitor, Kunitz family	8.945 up	0.000378	-12.352
Gmet_2701	phosphate ABC transporter, periplasmic phosphate-binding protein; pstS	8.796 up	0.000105	-17.931
Gmet_0534	cytochrome c, 5 heme-binding sites	8.710 up	0.0013	-9.268
Gmet_1037	pyranopterin monophosphate cyclase moaC	8.591 up	0.00221	-8.139
Gmet_2654	thioredoxin group II protein	8.558 up	0.000918	-9.981
Gmet_2021	acyl carrier protein; acpP-3	8.473 up	0.0000451	-22.884
Gmet_1095	conserved hypothetical protein	8.472 up	0.0172	-4.673
Gmet_0155	cytochrome c, 1 heme-binding site	8.443 up	0.0000727	-20.26
Gmet_2895	hypothetical protein	8.438 up	0.00128	-9.307
Gmet_1038	molybdopterin--molybdenum ligase; moeA-1	8.265 up	0.0086	-5.674
Gmet_0574	lipoprotein, putative	8.162 up	0.000428	-12.013
Gmet_3265	chemotaxis protein CheW-1	8.135 up	0.000378	-12.391
Gmet_2447	hypothetical protein	7.977 up	0.000133	-16.675
Gmet_2734	radical SAM family protein	7.930 up	0.031	-3.933
Gmet_3473	response receiver ATPase (REC, PulE)	7.905 up	0.0000428	-23.807
Gmet_2422	methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor mcp036	7.893 up	0.000207	-14.725
Gmet_2031	glycosyltransferase domain protein	7.893 up	0.0000826	-19.239
Gmet_2425	diguanilate cyclase	7.849 up	0.000615	-10.909
Gmet_0529	methyl-accepting chemotaxis sensory transducer mcp032	7.833 up	0.0000291	-31.099
Gmet_3116	lipoprotein, putative	7.717 up	0.000193	-15.25
Gmet_2985	conserved hypothetical protein	7.680 up	0.00654	-6.128
Gmet_2512	hypothetical protein	7.661 up	0.00061	-10.94
Gmet_1908	cytochrome b1 (bacterioferritin)	7.653 up	0.0106	-5.374
Gmet_3321	methyl viologen-reducing hydrogenase-associated ferredoxin mvhF	7.645 up	0.00369	-7.099
Gmet_2656	hypothetical protein	7.587 up	0.000301	-13.127
Gmet_0573	ResC/HemX-like cytochrome c biogenesis membrane protein	7.578 up	0.0000915	-18.739
Gmet_1036	molybdopterin adenylyltransferase MoaB, putative	7.558 up	0.000626	-10.863
Gmet_1607	chemotaxis protein CheY-4	7.552 up	0.00467	-6.678
Gmet_2834	ron-sulfur-oxygen hybrid cluster protein (prismane); hcp	7.513 up	0.00336	-7.295
Gmet_2020	AMP-forming acyl-CoA synthetase	7.435 up	0.0000848	-19.465
Gmet_0169	nodulin 21-like transmembrane protein	7.303 up	0.000642	-10.79
Gmet_0462	flagellar protein FlbD	7.236 up	0.00961	-5.516
Gmet_2420	chemotaxis protein-glutamate	7.152 up	0.0247	-4.213

	methyltransferase CheR-2			
Gmet_3320	methyl viologen-reducing hydrogenase, large subunit; mvhL	7.132 up	0.00161	-8.814
Gmet_0775	OmpA domain porin (beta-barrel, OmpA, OmpA)	7.076 up	0.0193	-4.531
Gmet_0158	hypothetical protein	7.052 up	0.000208	-14.646
Gmet_0705	membrane protein, putative	7.021 up	0.0125	-5.123
Gmet_0436	negative regulator of flagellin synthesis FlgM	6.968 up	0.0144	-4.925
Gmet_1618	protein of unknown function DUF327	6.964 up	0.00326	-7.364
Gmet_0704	conserved hypothetical protein	6.957 up	0.0465	-3.466
Gmet_0572	ResB-like family cytochrome c biogenesis protein	6.895 up	0.000111	-17.548
Gmet_2658	PDZ/DHR/GLGF:ankyrin	6.894 up	0.000298	-13.208
Gmet_3120	hypothetical protein	6.885 up	0.000117	-17.132
Gmet_2652	PDZ domain thioredoxin group II protein	6.832 up	0.0000584	-21.262
Gmet_0156	protein of unknown function DUF488	6.822 up	0.000199	-15.08
Gmet_2427	chemotaxis sensor histidine kinase CheA-1	6.790 up	0.00666	-6.092
Gmet_2470	cytochrome c, 27 heme-binding sites	6.767 up	0.000572	-11.104
Gmet_3646	conserved hypothetical protein	6.720 up	0.0000315	-28.844
Gmet_0244	hypothetical protein	6.660 up	0.0328	-3.864
Gmet_2024	asparagine synthetase;asnB-2	6.655 up	0.000469	-11.774
Gmet_2017	FemAB superfamily protein	6.631 up	0.00103	-9.745
Gmet_0241	lipoprotein, putative	6.571 up	0.0193	-4.533
Gmet_0168	NADH dehydrogenase I, L subunit; nuoL-2	6.539 up	0.00176	-8.61
Gmet_2409	intracellular protease, PfpI family, putative	6.449 up	0.00143	-9.072
Gmet_2659	hypothetical protein	6.340 up	0.0000907	-18.715
Gmet_3475	GTPase, putative	6.275 up	0.000488	-11.647
Gmet_1092	polyphosphate-dependent ADP kinase	6.271 up	0.0139	-4.967
Gmet_2583	multicopper oxidase, putative	6.257 up	0.000638	-10.809
Gmet_0849	sensor cyclic diguanylate phosphodiesterase (HAMP, GAF, HD-GYP), putative heme-binding site	6.255 up	0.000316	-13.002
Gmet_1015	hypothetical protein	6.215 up	0.0468	-3.457
Gmet_2014	glycosyltransferase, family 2	6.127 up	0.000167	-15.707
Gmet_0565	hypothetical protein	6.063 up	0.000202	-14.858
Gmet_2025	Formyl transferase-like	6.029 up	0.0000415	-24.678
Gmet_2660	hypothetical protein	6.018 up	0.00044	-11.929
Gmet_1811	4Fe-4S ferredoxin, iron-sulfur binding protein	5.900 up	0.00369	-7.101
Gmet_3117	response regulator receiver domain-containing protein	5.878 up	0.00939	-5.559
Gmet_0153	NADH dehydrogenase I, B/C/D subunits; nuoBCD	5.827 up	0.000115	-17.222
Gmet_3621	hypothetical protein	5.789 up	0.000329	-12.789

Gmet_2469	fibronectin type III-like repeat protein	5.783 up	0.00313	-7.458
Gmet_1812	polysulphide reductase, NrfD	5.709 up	0.000572	-11.122
Gmet_3546	pentapeptide repeat-containing protein	5.662 up	0.00106	-9.673
Gmet_3618	hypothetical protein	5.656 up	0.0036	-7.147
Gmet_0167	NADH dehydrogenase I, K subunit lipoprotein; nuok-2	5.648 up	0.00739	-5.91
Gmet_1833	integration host factor, beta subunit; ihfB-1	5.609 up	0.000208	-14.668
Gmet_1868	cytochrome c, 4 heme-binding sites	5.566 up	0.00159	-8.847
Gmet_2018	FemAB superfamily protein	5.556 up	0.000285	-13.411
Gmet_1813	hypothetical protein	5.529 up	0.000585	-11.029
Gmet_2448	major royal jelly-related protein	5.437 up	0.0165	-4.734
Gmet_3318	hypothetical protein; mvhR	5.435 up	0.00219	-8.162
Gmet_2622	conserved hypothetical protein	5.427 up	0.0323	-3.887
Gmet_0171	NADH dehydrogenase I, M subunit; nuoM-2	5.392 up	0.0000337	-29.812
Gmet_0717	hypothetical protein	5.370 up	0.0123	-5.155
Gmet_2033	conserved hypothetical protein	5.297 up	0.0144	-4.916
Gmet_3094	flagellar biogenesis protein FlhB	5.289 up	0.000825	-10.217
Gmet_3495	serine phosphatase, SpoIIE domain-containing	5.182 up	0.0367	-3.729
Gmet_1083	sensor histidine kinase (PAS, PAS, PAC, HisKA, HATPase_c)	5.173 up	0.000945	-9.908
Gmet_2026	type II secretion system ATPase ExeA	5.165 up	0.000289	-13.348
Gmet_0456	hypothetical protein	5.104 up	0.0242	-4.236
Gmet_2465	major facilitator transporter	5.099 up	0.000123	-16.963
Gmet_1706	response regulator receiver modulated diguanylate cyclase	5.096 up	0.0373	-3.709
Gmet_1022	respiratory nitrate reductase, gamma subunit; narI-2	5.080 up	0.00346	-7.241
Gmet_1851	pentapeptide repeat-containing protein	5.054 up	0.0007	-10.592
Gmet_1866	cytochrome c, 3-4 heme-binding sites	5.037 up	0.00795	-5.801
Gmet_2594	fatty acyltransferase-like lipase, putative	5.028 up	0.0115	-5.247
Gmet_3388	hypothetical protein	5.004 up	0.0000834	-19.267
Gmet_2498	heat shock protein Hsp90; htpG	4.994 up	0.00032	-12.895
Gmet_2446	dioxygenase, putative	4.988 up	0.00628	-6.19
Gmet_0170	cytochrome c, 8 heme-binding sites	4.950 up	0.0000406	-24.163
Gmet_3514	lipoprotein, putative	4.945 up	0.00174	-8.634
Gmet_0455	sialic acid synthase; neuB	4.930 up	0.00601	-6.264
Gmet_2661	ankyrin repeat protein	4.887 up	0.00128	-9.304
Gmet_0160	pyridoxamine 5'-phosphate oxidase-related FMN-binding protein	4.869 up	0.000371	-12.457
Gmet_3322	conserved hypothetical protein; mvhU	4.848 up	0.0236	-4.272
Gmet_3324	HAMP domain-containing methyl-	4.848 up	0.0326	-3.876

	accepting chemotaxis sensory transducer; mvhV			
Gmet_1928	ferritin-like domain protein	4.822 up	0.00367	-7.114
Gmet_1245	TonB-dependent receptor, putative	4.813 up	0.000031	-27.659
Gmet_2945	TPR domain protein	4.808 up	0.0336	-3.833
Gmet_2003	exopolysaccharide synthesis multitransmembrane protein H (exosortase), epsH	4.776 up	0.00649	-6.145
Gmet_0566	radical SAM domain iron-sulfur cluster-binding oxidoreductase	4.770 up	0.000926	-9.959
Gmet_1967	membrane protein, putative	4.768 up	0.00833	-5.721
Gmet_0568	ABC transporter, periplasmic substrate-binding lipoprotein	4.761 up	0.0023	-8.038
Gmet_0154	NADH dehydrogenase I, E subunit; nuoE-2	4.743 up	0.00832	-5.721
Gmet_2748	sensor histidine kinase (GAF, HisKA, HATPase_c)	4.738 up	0.00009	-18.685
Gmet_1966	lipoprotein, putative	4.719 up	0.00328	-7.347
Gmet_2023	polysaccharide deacetylase domain protein	4.704 up	0.000149	-16.083
Gmet_0907	conserved hypothetical protein	4.704 up	0.0217	-4.384
Gmet_1680	conserved hypothetical protein	4.694 up	0.00299	-7.543
Gmet_2666	hypothetical protein	4.681 up	0.00321	-7.411
Gmet_0157	NADH dehydrogenase I, F subunit, nuoF-2	4.670 up	0.00895	-5.625
Gmet_1831	conserved hypothetical protein	4.663 up	0.014	-4.974
Gmet_0967	type IV pilus tip-associated adhesin, pilY1-2	4.637 up	0.0000394	-25.638
Gmet_3121	hemerythrin family protein	4.607 up	0.000358	-12.576
Gmet_3187	DNA polymerase II, putative	4.592 up	0.00294	-7.572
Gmet_0789	aldehyde dehydrogenase family 11 protein	4.577 up	0.00797	-5.792
Gmet_1469	AMP-forming acyl-CoA synthetase	4.563 up	0.00327	-7.369
Gmet_0564	conserved hypothetical protein	4.519 up	0.00363	-7.13
Gmet_1702	deoxyguanosine triphosphate triphosphohydrolase, putative	4.461 up	0.0228	-4.313
Gmet_3269	chemotaxis protein-glutamate methyltransferase CheB	4.439 up	0.000526	-11.421
Gmet_0561	lipoprotein, putative	4.425 up	0.00014	-16.343
Gmet_0793	conserved hypothetical protein	4.397 up	0.000113	-17.39
Gmet_3108	flagellar export protein FliJ	4.391 up	0.00485	-6.612
Gmet_2896	cytochrome c, 4 heme-binding sites	4.361 up	0.00963	-5.512
Gmet_2664	radical SAM domain iron-sulfur cluster-binding oxidoreductase, putative	4.306 up	0.00211	-8.237
Gmet_0152	NADH dehydrogenase I, A subunit; nuoA-2	4.254 up	0.0109	-5.333
Gmet_2618	6-phosphogluconolactonase; pgl	4.251 up	0.0225	-4.333
Gmet_0033	ATPase, AAA family	4.249 up	0.000245	-13.876
Gmet_0580	lipoprotein cytochrome c, 14 heme-binding sites	4.248 up	0.0071	-5.985
Gmet_1968	conserved hypothetical protein	4.231 up	0.0449	-3.503

Gmet_2703	phosphate ABC transporter, membrane protein PstA	4.213 up	0.000398	-12.2
Gmet_1470	conserved hypothetical protein	4.207 up	0.0000326	-29.493
Gmet_0029	chaperonin GroEL	4.204 up	0.00199	-8.353
Gmet_1082	sigma-54-dependent transcriptional response regulator (REC, sigma54 interaction, HTH8)	4.193 up	0.0037	-7.078
Gmet_0030	serine protein kinase, putative; prkA	4.121 up	0.00564	-6.359
Gmet_0560	conserved hypothetical protein	4.110 up	0.00534	-6.46
Gmet_1091	conserved hypothetical protein	4.071 up	0.036	-3.754
Gmet_2608	conserved hypothetical protein	4.062 up	0.00249	-7.881
Gmet_1867	cytochrome c, 7-8 heme-binding sites	4.053 up	0.0177	-4.63
Gmet_1468	alpha/beta hydrolase superfamily protein	4.052 up	0.000746	-10.432
Gmet_0889	LysM domain protein	4.050 up	0.000321	-12.915
Gmet_1923	cytochrome b/b6 complex, cytochrome b subunit	3.969 up	0.00214	-8.214
Gmet_1395	type IV pilus biogenesis protein PilC	3.962 up	0.0245	-4.224
Gmet_2702	phosphate ABC transporter, membrane protein PstC	3.946 up	0.0121	-5.18
Gmet_0457	aminotransferase, AHBA_syn family	3.928 up	0.00708	-5.993
Gmet_0821	methyl-accepting chemotaxis sensory transducer, mcp013	3.900 up	0.0125	-5.114
Gmet_0145	protein of unknown function DUF167	3.897 up	0.00417	-6.886
Gmet_2720	zinc protease TldD, putative modulator of DNA gyrase	3.895 up	0.00451	-6.741
Gmet_0166	lipoprotein, putative	3.888 up	0.00735	-5.919
Gmet_2006	selenocysteine lyase; sufS	3.883 up	0.00236	-7.987
Gmet_2002	conserved hypothetical protein	3.882 up	0.00498	-6.574
Gmet_3474	sensor histidine kinase (HATPase_c)	3.881 up	0.00604	-6.253
Gmet_2426	sensor histidine kinase response regulator (HAMP, HisKA, HATPase_c, REC), putative heme-binding site	3.853 up	0.00353	-7.194
Gmet_0299	HPP family protein	3.815 up	0.0249	-4.204
Gmet_2013	polysaccharide deacetylase, putative	3.812 up	0.000204	-14.862
Gmet_1552	ABC transporter, ATP-binding protein	3.812 up	0.00255	-7.833
Gmet_2419	chemotaxis protein-glutamine deamidase and protein-glutamate methyltransferase CheD	3.776 up	0.00707	-5.985
Gmet_3210	chemotaxis protein phosphatase CheC	3.772 up	0.00724	-5.944
Gmet_1832	OmpA family outer membrane protein	3.728 up	0.0000503	-22.364
Gmet_1734	conserved hypothetical protein	3.722 up	0.0162	-4.754
Gmet_2044	hypothetical protein	3.680 up	0.0126	-5.104

Gmet_1998	porin lipoprotein, putative	3.671 up	0.000112	-17.55
Gmet_0159	NADH dehydrogenase I, G subunit,nuoG-2	3.656 up	0.00373	-7.063
Gmet_0454	sugar cytidyltransferase and glycosyltransferase domain protein	3.644 up	0.0418	-3.592
Gmet_2019	ornithine/diaminopimelate/arginine decarboxylase 2	3.630 up	0.0165	-4.731
Gmet_0974	type IV pilus assembly lipoprotein PilP, putative; pilP	3.613 up	0.0173	-4.664
Gmet_0172	NADH dehydrogenase I, N subunit lipoprotein; nuoN-2	3.607 up	0.00161	-8.778
Gmet_3362	periplasmic trypsin-like serine protease lipoprotein	3.607 up	0.0294	-3.991
Gmet_0142	cytochrome c, 8 heme-binding sites	3.603 up	0.00515	-6.524
Gmet_2827	chemotaxis protein CheY-8	3.600 up	0.0016	-8.813
Gmet_0559	conserved hypothetical protein	3.599 up	0.0109	-5.328
Gmet_2431	chemotaxis protein CheY-2	3.569 up	0.00347	-7.231
Gmet_0563	membrane protein	3.568 up	0.00218	-8.183
Gmet_2022	hypothetical protein	3.561 up	0.0000471	-22.936
Gmet_3149	conserved hypothetical protein	3.549 up	0.000898	-10.036
Gmet_3147	protein of unknown function DUF1458	3.548 up	0.00801	-5.773
Gmet_2505	peptidoglycan L,D-transpeptidase, YkuD family	3.530 up	0.00287	-7.617
Gmet_0032	SpoVR-like family protein	3.522 up	0.00605	-6.245
Gmet_0031	conserved hypothetical protein	3.501 up	0.0179	-4.616
Gmet_0834	hemerythrin family protein	3.462 up	0.000517	-11.467
Gmet_1997	hypothetical protein	3.455 up	0.000428	-11.998
Gmet_2721	sensor diguanylate cyclase (GAF, GGDEF)	3.452 up	0.00302	-7.526
Gmet_1617	lipoprotein, putative	3.446 up	0.0144	-4.922
Gmet_1924	cytochrome c, 5 heme-binding sites	3.441 up	0.0000727	-20.413
Gmet_2004	glycosyltransferase	3.435 up	0.00144	-9.035
Gmet_2617	barnase inhibitor barstar	3.412 up	0.0228	-4.314
Gmet_2639	response receiver sensor histidine kinase (REC, HisKA, HATPase_c)	3.394 up	0.00371	-7.081
Gmet_3107	conserved hypothetical protein	3.386 up	0.0218	-4.381
Gmet_2435	potassium-transporting ATPase, C subunit;kdpC	3.386 up	0.0143	-4.934
Gmet_3400	twitching motility pilus retraction protein; pilT-3	3.368 up	0.0148	-4.875
Gmet_1970	membrane protein, putative	3.358 up	0.00725	-5.945
Gmet_0146	conserved hypothetical protein	3.352 up	0.000546	-11.272
Gmet_0695	ammonium transporter; amtB	3.339 up	0.00935	-5.57
Gmet_0183	peroxiredoxin, atypical 2-Cys subfamily	3.301 up	0.0000857	-19.061
Gmet_2811	sensor histidine kinase (Cache, HAMP, PAS, PAC, HisKA, HATPase_c)	3.299 up	0.000247	-14.013
Gmet_0356	conserved hypothetical protein	3.294 up	0.000248	-14.062
Gmet_1189	magnesium transport protein CorA-1	3.272 up	0.0016	-8.813

Gmet_1999	lipoprotein, putative	3.267 up	0.000548	-11.286
Gmet_1996	lipoprotein, putative	3.266 up	0.00452	-6.742
Gmet_0911	conserved hypothetical protein	3.249 up	0.0237	-4.265
Gmet_0987	sensor diguanylate cyclase/phosphodiesterase (PAS, GGDEF, EAL)	3.245 up	0.0000295	-28.801
Gmet_2768	glucose-1-phosphate adenylyltransferase	3.238 up	0.0036	-7.153
Gmet_2894	conserved hypothetical protein	3.229 up	0.00333	-7.32
Gmet_0975	type IV pilus secretin lipoprotein PilQ	3.212 up	0.0213	-4.407
Gmet_0712	methyl-accepting chemotaxis sensory transducer, mcp011	3.206 up	0.0000459	-22.931
Gmet_3617	conserved hypothetical protein	3.189 up	0.000348	-12.65
Gmet_2410	superoxide dismutase, iron/manganese-containing, sodA	3.186 up	0.0108	-5.349
Gmet_0968	hypothetical protein	3.185 up	0.00057	-11.12
Gmet_3317	chemotaxis protein CheW-8 (MvhQ)	3.158 up	0.0354	-3.773
Gmet_0272	lipoprotein, putative	3.153 up	0.0467	-3.461
Gmet_2642	sensor histidine kinase response receiver domain protein (GAF, HATPase_c, REC, REC, REC)	3.134 up	0.00226	-8.071
Gmet_2418	response receiver chemotaxis protein-glutamate methyltransferase CheB-2	3.129 up	0.00876	-5.65
Gmet_0913	cytochrome c, 9 heme-binding sites	3.120 up	0.00341	-7.261
Gmet_0355	histone-like protein; hup-1	3.115 up	0.00685	-6.048
Gmet_0452	hypothetical protein	3.106 up	0.0443	-3.523
Gmet_2007	coenzyme F390 synthetase superfamily protein	3.033 up	0.000722	-10.518
Gmet_1558	cysteine synthase A; cysK-2	3.032 up	0.0426	-3.569
Gmet_2468	conserved hypothetical protein	3.019 up	0.0128	-5.082
Gmet_2704	phosphate ABC transporter ATP-binding protein	2.992 up	0.011	-5.306
Gmet_2008	glycosyl transferase family protein	2.985 up	0.0276	-4.068
Gmet_2430	methyl-accepting chemotaxis sensory transducer	2.971 up	0.00134	-9.203
Gmet_2719	hypothetical protein	2.955 up	0.0257	-4.161
Gmet_0581	high-molecular-weight cytochrome c	2.940 up	0.000282	-13.487
Gmet_1005	multi-sensor signal transduction histidine kinase	2.918 up	0.0438	-3.535
Gmet_1384	cytochrome c biogenesis protein, transmembrane region	2.913 up	0.012	-5.189
Gmet_0912	cytochrome c family protein	2.908 up	0.0136	-5.007
Gmet_1733	O-methyltransferase family protein	2.889 up	0.0125	-5.134
Gmet_2061	Na ⁺ /solute symporter	2.888 up	0.027	-4.102
Gmet_1965	fibronectin, type III	2.887 up	0.0278	-4.06
Gmet_0725	hypothetical protein	2.864 up	0.00361	-7.142
Gmet_1922	Rieske (2Fe-2S) region	2.853 up	0.00794	-5.808
Gmet_1553	hypothetical protein	2.850 up	0.00938	-5.558
Gmet_1919	response regulator receiver	2.844 up	0.00966	-5.502

	(CheY-like) modulated metal dependent phosphohydrolase			
Gmet_0425	hypothetical protein	2.843 up	0.000247	-13.956
Gmet_0035	metal dependent phosphohydrolase	2.820 up	0.000201	-15.082
Gmet_1963	signal peptide protein	2.793 up	0.00439	-6.785
Gmet_1079	CheW protein	2.775 up	0.0206	-4.449
Gmet_0034	metallophosphoesterase	2.767 up	0.000166	-15.699
Gmet_1559	peptidase M23B	2.737 up	0.0138	-4.992
Gmet_0833	Alpha amylase, catalytic region	2.733 up	0.00602	-6.265
Gmet_1918	PAS/PAC sensor hybrid histidine kinase	2.710 up	0.0444	-3.513
Gmet_3275	metal dependent phosphohydrolase	2.709 up	0.0169	-4.698
Gmet_1188	peptidoglycan binding domain-containing protein	2.694 up	0.0199	-4.495
Gmet_2641	MCP methyltransferase, CheR-type	2.690 up	0.000299	-13.183
Gmet_1371	hypothetical protein	2.666 up	0.00468	-6.68
Gmet_2826	CheB methylesterase	2.633 up	0.0187	-4.567
Gmet_3478	PAS/PAC sensor signal transduction histidine kinase	2.606 up	0.000041	-24.406
Gmet_1155	integral membrane protein TerC	2.604 up	0.0104	-5.417
Gmet_1551	response regulator receiver domain-containing protein	2.589 up	0.0428	-3.562
Gmet_2158	two component LuxR family transcriptional regulator	2.570 up	0.0157	-4.795
Gmet_1220	response regulator receiver domain-containing protein	2.569 up	0.00336	-7.297
Gmet_2938	methyl-accepting chemotaxis sensory transducer	2.560 up	0.000301	-13.141
Gmet_1373	hypothetical protein	2.555 up	0.00199	-8.357
Gmet_2440	cobalt ABC transporter CbiQ, permease subunit	2.548 up	0.00192	-8.462
Gmet_0298	PAS/PAC sensor protein	2.541 up	0.0216	-4.392
Gmet_1190	Outer membrane efflux protein	2.539 up	0.0272	-4.086
Gmet_0458	polysaccharide biosynthesis protein CapD	2.536 up	0.00312	-7.469
Gmet_3122	rhodanese-like protein	2.519 up	0.0107	-5.362
Gmet_2939	diguanylate cyclase/phosphodiesterase	2.507 up	0.0166	-4.723
Gmet_2157	two component AraC family transcriptional regulator	2.504 up	0.0327	-3.872
Gmet_1946	glyceraldehyde-3-phosphate dehydrogenase	2.497 up	0.00512	-6.533
Gmet_0583	spermine synthase	2.495 up	0.0311	-3.928
Gmet_1969	glycosyl transferase, group 1	2.483 up	0.0263	-4.137
Gmet_2011	hypothetical protein	2.483 up	0.00547	-6.412
Gmet_0598	PKD	2.482 up	0.0467	-3.46
Gmet_0825	cytochrome c family protein	2.482 up	0.00965	-5.507
Gmet_0835	hypothetical protein	2.473 up	0.049	-3.404
Gmet_1078	methyl-accepting chemotaxis sensory transducer	2.467 up	0.0113	-5.275
Gmet_0736	hypothetical protein	2.452 up	0.0175	-4.644
Gmet_0930	cytochrome c family protein	2.450 up	0.00389	-6.994
Gmet_3455	PAS/PAC sensor signal	2.433 up	0.00272	-7.72

	transduction histidine kinase			
Gmet_3152	glycine dehydrogenase subunit 2	2.430 up	0.0295	-3.985
Gmet_1230	serine phosphatase	2.430 up	0.00241	-7.956
Gmet_1153	hypothetical protein	2.427 up	0.00709	-5.985
Gmet_1429	Outer membrane lipoprotein Slp	2.422 up	0.0394	-3.654
Gmet_0533	hypothetical protein	2.417 up	0.0392	-3.661
Gmet_0342	thrombospondin type 3 repeat-containing OmpA/MotB protein	2.404 up	0.0328	-3.863
Gmet_0666	PAS/PAC sensor signal transduction histidine kinase	2.355 up	0.00535	-6.452
Gmet_0966	hypothetical protein	2.348 up	0.00349	-7.213
Gmet_0567	hypothetical protein	2.333 up	0.0295	-3.987
Gmet_1655	CoA-binding protein	2.325 up	0.0104	-5.413
Gmet_2506	rhomboid-like protein	2.320 up	0.000823	-10.215
Gmet_3504	cobalamin B12-binding/radical SAM family protein	2.314 up	0.00695	-6.026
Gmet_2010	glycosyl transferase family protein	2.312 up	0.0374	-3.708
Gmet_3310	lipoprotein	2.307 up	0.0121	-5.175
Gmet_2437	two component transcriptional regulato	2.305 up	0.014	-4.957
Gmet_1025	hypothetical protein	2.304 up	0.0319	-3.901
Gmet_0960	histidine kinase	2.295 up	0.00193	-8.43
Gmet_2009	O-antigen polymerase	2.295 up	0.0196	-4.514
Gmet_1218	PAS/PAC sensor signal transduction histidine kinas	2.283 up	0.000043	-23.664
Gmet_1909	pyridoxamine 5'-phosphate oxidase-related, FMN-binding	2.270 up	0.0418	-3.594
Gmet_0451	glucuronate isomerase	2.251 up	0.0406	-3.626
Gmet_0162	ankyrin	2.249 up	0.0196	-4.51
Gmet_1243	histidine kinase	2.241 up	0.00691	-6.034
Gmet_2001	glycosyl transferase, group 1	2.234 up	0.00562	-6.372
Gmet_1654	HhH-GPD	2.221 up	0.0037	-7.081
Gmet_0028	groES co-chaperonin GroES	2.210 up	0.00329	-7.348
Gmet_2760	dehydrogenase, E1 component	2.191 up	0.000984	-9.831
Gmet_2078	hypothetical protein	2.184 up	0.0427	-3.565
Gmet_2436	smosensitive K ⁺ channel	2.182 up	0.0208	-4.435
Gmet_2156	hypothetical protein	2.178 up	0.00207	-8.274
Gmet_2897	NHL repeat-containing protein	2.173 up	0.0125	-5.118
Gmet_0972	fimbrial assembly	2.170 up	0.0266	-4.115
Gmet_3483	pseudo	2.167 up	0.0275	-4.074
Gmet_0815	PpiC-type peptidyl-prolyl cis-trans isomerase	2.166 up	0.0477	-3.432
Gmet_1023	pseudo	2.158 up	0.00329	-7.341
Gmet_1544	hypothetical protein	2.155 up	0.00796	-5.798
Gmet_1447	chromosome partitioning ATPase	2.155 up	0.000478	-11.701
Gmet_0173	hypothetical protein	2.153 up	0.0128	-5.082
Gmet_2305	MCP methyltransferase, CheR-typ	2.148 up	0.0257	-4.165
Gmet_2824	multi-sensor hybrid histidine kinase	2.132 up	0.00673	-6.071
Gmet_0151	pseudo	2.122 up	0.00604	-6.256
Gmet_0969	hypothetical protein	2.118 up	0.000615	-10.917
Gmet_0424	hypothetical protein	2.106 up	0.00156	-8.897
Gmet_1404	hypothetical protein	2.097 up	0.0239	-4.255
Gmet_2582	excinuclease ATPase subunit-like	2.093 up	0.0059	-6.293

Gmet_2663	hypothetical protein	2.090 up	0.0457	-3.485
Gmet_1543	YHS	2.077 up	0.0228	-4.31
Gmet_0138	hypothetical protein	2.073 up	0.0433	-3.549
Gmet_1614	cation transporter E1-E2 family ATPase	2.073 up	0.000134	-16.69
Gmet_2390	O-acetylhomoserine/O- acetylserine sulfhydrylase	2.068 up	0.0139	-4.978
Gmet_1545	hypothetical protein	2.064 up	0.00653	-6.128
Gmet_3213	thiamine-monophosphate kinase	2.057 up	0.002	-8.357
Gmet_3170	4Fe-4S ferredoxin, iron-sulfur binding protein	2.057 up	0.0437	-3.536
Gmet_2651	metallophosphoesterase	2.040 up	0.0201	-4.475
Gmet_1608	histone-like DNA-binding protein	2.017 up	0.00904	-5.612
Gmet_3031	Na ⁺ /solute symporter	2.012 up	0.0281	-4.048
Gmet_0959	type 4 prepilin peptidas	2.011 up	0.0273	-4.081

Table S2. Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant characteristic(s)	Source or reference
Strains		
<i>E. coli</i>		
TOP10	<i>recA1 endA1 gyrA96 thi-1 hsdR17</i> ($r_K^- m_K^+$) <i>supE44 relA1 ΔlacU169</i>	Invitrogen, Carlsbad, CA
<i>G. metallireducens</i>		
GS-15 (ATCC 53774)	Wild type	(1)
2896	<i>ΔGmet 2896::Sp^r</i>	This work
0558	<i>ΔGmet 0558::Sp^r</i>	This work
0557	<i>ΔGmet 0557::Sp^r</i>	This work
1868	<i>ΔGmet 1868::Sp^r</i>	This work
1867	<i>ΔGmet 1867::Sp^r</i>	This work
0930	<i>ΔGmet 0930::Sp^r</i>	This work
0679	<i>ΔGmet 0679::Sp^r</i>	This work
0825	<i>ΔGmet 0825::Sp^r</i>	This work
2839	<i>ΔGmet 2839::Sp^r</i>	This work
0912	<i>ΔGmet 0912::Sp^r</i>	This work
0913	<i>ΔGmet 0913::Sp^r</i>	This work
0910	<i>ΔGmet 0910::Sp^r</i>	This work
0571	<i>ΔGmet 0571::Sp^r</i>	This work
0580	<i>ΔGmet 0580::Sp^r</i>	This work
2470	<i>ΔGmet 2470::Sp^r</i>	This work
0534	<i>ΔGmet 0534::Sp^r</i>	This work
0581	<i>ΔGmet 0581::Sp^r</i>	This work
1866	<i>ΔGmet 1866::Sp^r</i>	This work
0907	<i>ΔGmet 0907::Sp^r</i>	This work
0911	<i>ΔGmet 0911::Sp^r</i>	This work
0908	<i>ΔGmet 0908::Sp^r</i>	This work
0556	<i>ΔGmet 0556::Sp^r</i>	This work
Plasmids		
pCR2.1-TOPO	PCR cloning vector; Ap ^r , Km ^r	Invitrogen, Carlsbad, CA
pUC19- <i>Sp^rloxP</i>	pUC19 carrying <i>Sp^rloxP</i> ; Ap ^r , Sp ^r	(3)
pCM66	Broad-host-range expression vector; Km ^r	(2)
pJS1	pCM66 carrying Gmet 2896	This work
pJS2	pCM66 carrying Gmet 0558	This work
pJS3	pCM66 carrying Gmet 0557	This work
pJS4	pCM66 carrying Gmet 1867	This work
pJS5	pCM66 carrying Gmet 1868	This work
pJS6	pCM66 carrying Gmet 0930	This work
pJS7	pCM66 carrying Gmet 0556	This work

TABLE S3. Primers used for mutant construction, complementation, and qRT-PCR

Primer name	Purpose	Sequence (5' to 3')	Source or reference
JsSpF	<i>Sp^r</i> cassette		This work
JsSpR	<i>Sp^r</i> cassette		This work
Gm2896comF	2896 into pJS1	CAGGGATCCAACGAGGAGGAAGGAA CAATG ^b	This work
Gm2896comR	2896 into pJS1	TGCGGTACCCCATCGGCTCGTCACAA CCTAC ^c	This work
Gmet2896up	$\Delta 2896::Sp^r$	CGGCCCTCCACCACGTTACTCTGG	This work
Gmet2896AvrIIup	$\Delta 2896::Sp^r$	CAGCCTAGGCATTGTTCCCTCCTCCTC GTTA ^a	This work
Gmet2896AvrII dn	$\Delta 2896::Sp^r$	GTACCTAGGTCCACCATGGCGGGGAG CGC ^a	This work
Gmet2896dn	$\Delta 2896::Sp^r$	GGATCTTGCCGGCGCTCGTCG	This work
Gm0558comF	0558 into pJS2	TATTCTAGATTGCTCAGGAGCTCGCCA TGT ^d	This work
Gm0558comR	0558 into pJS2	GCAGGATCCCCCTCCCCTCTTGATCGC T ^b	This work
Gmet0558up	$\Delta 0558::Sp^r$	GCCGGAATTGATGCTGGCGGTG	This work
Gmet0558AvrIIup	$\Delta 0558::Sp^r$	CAGCCTAGGCATGGCGAGCTCCTGAG CAAG ^a	This work
Gmet0558AvrII dn	$\Delta 0558::Sp^r$	GTACCTAGGCTGCCACTTCCAGCCGA CACCAC ^a	This work
Gmet0558dn	$\Delta 0558::Sp^r$	TCAGGGTGCCTCGCACGGTTA	This work
Gm0557comF	0557 into pJS3	TATGCATGCACACGCAACGAGGTTTT CAAGATG ^c	This work
Gm0557comR	0557 into pJS3	GCATCTAGAGCAAGGCAGACACGTCC TA ^d	This work
Gmet0557up	$\Delta 0557::Sp^r$	CGGCCCTTACGCTTGACCCGG	This work
Gmet0557AvrIIup	$\Delta 0557::Sp^r$	CAGCCTAGGCATCTTGAAAACCTCGT TGCGTG ^a	This work
Gmet0557AvrII dn	$\Delta 0557::Sp^r$	GTACCTAGGTAATACCGGCAGCGCCA TGTG ^a	This work
Gmet0557dn	$\Delta 0557::Sp^r$	CCAGGGTATGGTCAGTGGTGCTG	This work
Gm1867comF	1867 into pJS4	GCGGCATGCAATAATCCATGAGTAAG CAACAATG ^c	This work
Gm1867comR	1867 into pJS4	TATTCTAGAGGCACCTCTGTGGGTCTA d	This work
Gmet1867up	$\Delta 1867::Sp^r$	ACGATACCACCCAGACCTTCG	This work
Gmet1867AvrIIup	$\Delta 1867::Sp^r$	CAGCCTAGGCATTGTTGCTTACTCATG GAT ^a	This work
Gmet1867AvrII dn	$\Delta 1867::Sp^r$	GTACCTAGGCTTTCCTGTCATGGTGTC G ^a	This work
Gmet1867dn	$\Delta 1867::Sp^r$	ACATTCCGTGGCATCAACTATTGCA	This work
Gm1868comF	1868 into pJS5	TATGCATGCCCTGAGGCAAGGCACGC CATG ^c	This work
Gm1868comR	1868 into pJS5	GCGTCTAGAATCGCCATTGTTGCTTAC TCATG ^d	This work
Gmet1868up	$\Delta 1868::Sp^r$	GGTGATGTTTATGTGGTTGATGTG	This work
Gmet1868AvrIIup	$\Delta 1868::Sp^r$	CAGCCTAGGAAAAGGTTGTCTGTTTT AACC ^a	This work
Gmet1868AvrII dn	$\Delta 1868::Sp^r$	GTACCTAGGACTCGGTGTGCACTAA CTGTCA ^a	This work
Gmet1868dn	$\Delta 1868::Sp^r$	GTTTCATATTCCTTGTTTACGGACG	This work
Gmet0930comF	0930 into pJS6	TATTCTAGACGAAAGGAGCAGAAAGG	This work

Gmet0930comR	0930 into pJS6	GATG ^d GCAGGATCCCCTATCCC GGAACATCA AAAATTA ^b	This work
Gmet0930up	$\Delta 0930::Sp^r$	GGTGGCTTAACGAGTGTGCGTGG	This work
Gmet0930AvrIIup	$\Delta 0930::Sp^r$	CAGCCTAGGCATCCCTTTCTGCTCCTT TC ^a	This work
Gmet0930AvrIIIdn	$\Delta 0930::Sp^r$	GTACCTAGGTCGTTACCGGCGCAGGC A ^a	This work
Gmet0930dn	$\Delta 0930::Sp^r$	GGGAGGCGGCAACATTGGAGCCG	This work
Gm0556comF	0556 into pJS7	TATGCATGCGAATGCGGAGGCATTAC CATG ^e	This work
Gm0556comR	0556 into pJS7	GCATCTAGATCCACCCCGAGGGGTTTC TA ^d	This work
Gmet0556up	$\Delta 0556::Sp^r$	CGTGGGGCTCACCACCTTCAAGC	This work
Gmet0556AvrIIup	$\Delta 0556::Sp^r$	CAGCCTAGGCATGGTAATGCCTCCGC ATTC ^a	This work
Gmet0556AvrIIIdn	$\Delta 0556::Sp^r$	GTACCTAGGGGACGCAATACTGATCA TGAG ^a	This work
Gmet0556dn	$\Delta 0556::Sp^r$	GTATATGATGATCCCACGGCC	This work
Gmet0679up	$\Delta 0679::Sp^r$	ACGATGACCTCCTGCAGCGCTGCG	This work
Gmet0679AvrIIup	$\Delta 0679::Sp^r$	CAGCCTAGGCATGATTGGTTCTCCTT GACCAA ^a	This work
Gmet0679AvrIIIdn	$\Delta 0679::Sp^r$	GTACCTAGGGTTGATATGGCGGTGAA GCAGGTGA ^a	This work
Gmet0679dn	$\Delta 0679::Sp^r$	TGCGGCGTTGACGACAGGGTGGCGG	This work
Gmet0825up	$\Delta 0825::Sp^r$	GCGGATAACCTCCCGAACCGACAGCA	This work
Gmet0825AvrIIup	$\Delta 0825::Sp^r$	CAGCCTAGGCATCGGATACAGTCCCT TTCCG ^a	This work
Gmet0825AvrIIIdn	$\Delta 0825::Sp^r$	GTACCTAGGCCTCACCTGCCACCAGG ATGCGC ^a	This work
Gmet0825dn	$\Delta 0825::Sp^r$	GCACCAGGTCCGTTGACGTAGA	This work
Gmet2839up	$\Delta 2839::Sp^r$	CTGCCTCCACGCCTTTCTTGTT	This work
Gmet2839AvrIIup	$\Delta 2839::Sp^r$	CAGCCTAGGCATCGTTCCTCCTCTGTG a	This work
Gmet2839AvrIIIdn	$\Delta 2839::Sp^r$	GTACCTAGGGCCAAAGCCGCTCCTGC GAAG ^a	This work
Gmet2839dn	$\Delta 2839::Sp^r$	ACCGCCTGAAGGAAGACAAGAAG	This work
Gmet0912up	$\Delta 0912::Sp^r$	GCGAGTGGTATCAGAGCTATCCGA	This work
Gmet0912AvrIIup	$\Delta 0912::Sp^r$	CAGCCTAGGCACGGATTCTCCCCCTTT CTAGAAG ^a	This work
Gmet0912AvrIIIdn	$\Delta 0912::Sp^r$	GTACCTAGGTGGCAACATCATCGATC GTA ^a	This work
Gmet0912dn	$\Delta 0912::Sp^r$	CATGGCCTGACTCAGCCCAGTC	This work
Gmet0913up	$\Delta 0913::Sp^r$	GGAGAGGGGGTTGCCCCGAAC	This work
Gmet0913AvrIIup	$\Delta 0913::Sp^r$	CAGCCTAGGCATGTGGCATACTCCTT GTTG ^a	This work
Gmet0913AvrIIIdn	$\Delta 0913::Sp^r$	GTACCTAGGTTAGGGCCGACGCAACA ACAG ^a	This work
Gmet0913dn	$\Delta 0913::Sp^r$	TGCCGTAGTCATCCCTTTGCTC	This work
Gmet0910up	$\Delta 0910::Sp^r$	CGTCCAACCAGACCTTCCGGCGCG	This work
Gmet0910AvrIIup	$\Delta 0910::Sp^r$	CAGCCTAGGCATAACGCTACTCTCCTTT C ^a	This work
Gmet0910AvrIIIdn	$\Delta 0910::Sp^r$	GTACCTAGGACTGCTTGTGGGGCCGG ACT ^a	This work
Gmet0910dn	$\Delta 0910::Sp^r$	CGGTGTTCCGCCCTTGAATCGA	This work

Gmet0571up	$\Delta 0571::Sp^r$	CCATCTGGAGCACCTCTGGAG	This work
Gmet0571AvrIIup	$\Delta 0571::Sp^r$	CAGCCTAGGCATATCATGCCTCCAGC AC ^a	This work
Gmet0571AvrIIIdn	$\Delta 0571::Sp^r$	GAACCTAGGGGTATGCGGCAACCAGC AT ^a	This work
Gmet0571dn	$\Delta 0571::Sp^r$	CAAGATTGAGAAGCCCACGATGC	This work
Gmet0580up	$\Delta 0580::Sp^r$	CCTGGCTCACCATTGCGGCACTTC	This work
Gmet0580AvrIIup	$\Delta 0580::Sp^r$	CAGCCTAGGCATGACTTCCCCACGT CAA ^a	This work
Gmet0580AvrIIIdn	$\Delta 0580::Sp^r$	GTACCTAGGCGCGACAACGTGTGTCA ATTG ^a	This work
Gmet0580dn	$\Delta 0580::Sp^r$	AATCTCGGTTATTGGCGGCACCG	This work
Gmet2470up	$\Delta 2470::Sp^r$	GCTGGAGAACCCCGGCAAGATCC	This work
Gmet2470AvrIIup	$\Delta 2470::Sp^r$	CAGCCTAGGCACGCCACCCCTCCCC ATT ^a	This work
Gmet2470AvrIIIdn	$\Delta 2470::Sp^r$	GTACCTAGGACCCGACTGGCGTGTGG CCC ^a	This work
Gmet2470dn	$\Delta 2470::Sp^r$	GTGGCCGATGTCGTTGCCGCCGG	This work
Gmet0534up	$\Delta 0534::Sp^r$	GGTGGCGAGCGGCATCCAGGGA	This work
Gmet0534AvrIIup	$\Delta 0534::Sp^r$	CAGCCTAGGCATTACCTCTCCTTTAC C ^a	This work
Gmet0534AvrIIIdn	$\Delta 0534::Sp^r$	GTACCTAGGGGTGGAGATGGTGAACC GTGC ^a	This work
Gmet0534dn	$\Delta 0534::Sp^r$	GAAAGCAGCAGGGCGAGCGGAAGCA GC	This work
Gmet0581up	$\Delta 0581::Sp^r$	GCACCGGCAATGACAGCAGCCA	This work
Gmet0581AvrIIup	$\Delta 0581::Sp^r$	CAGCCTAGGCATACCTTACCGTTAC ATGGC ^a	This work
Gmet0581AvrIIIdn	$\Delta 0581::Sp^r$	GTACCTAGGCACCAACTACACGACGC AGCAC ^a	This work
Gmet0581dn	$\Delta 0581::Sp^r$	CGATGGTCACTTTTTCGTGCCGCC	This work
Gmet1866up	$\Delta 1866::Sp^r$	GGGAGGCAAGTAAACAAACGGATG	This work
Gmet1866AvrIIup	$\Delta 1866::Sp^r$	CAGCCTAGGCATCGCCTGGCACCTCT GT ^a	This work
Gmet1866AvrIIIdn	$\Delta 1866::Sp^r$	GTACCTAGGTTCCCCTGTCGAAAATCT GT ^a	This work
Gmet1866dn	$\Delta 1866::Sp^r$	CGATGGATAGACGAGGGCTGAG	This work
Gmet0907up	$\Delta 0907::Sp^r$	GCCGGCGAACTGGGTGTCACC	This work
Gmet0907AvrIIup	$\Delta 0907::Sp^r$	CAGCCTAGGCATTGAAAATCCCTTCC GTTT ^a	This work
Gmet0907AvrIIIdn	$\Delta 0907::Sp^r$	GTACCTAGGTACGCGGATGAGCCTTC TACGG ^a	This work
Gmet0907dn	$\Delta 0907::Sp^r$	CCGTAACCGTAGAGGGAGAACT	This work
Gmet0911up	$\Delta 0911::Sp^r$	AGCCTCATATCTCCCCTCGCA	This work
Gmet0911AvrIIup	$\Delta 0911::Sp^r$	CAGCCTAGGCATTAGTGGACCTCCTT TCTC ^a	This work
Gmet0911AvrIIIdn	$\Delta 0911::Sp^r$	GTACCTAGGCGACACGCAAGGACGCT TCG ^a	This work
Gmet0911dn	$\Delta 0911::Sp^r$	CGGTGGCATGCTCGCTGTTCCAGA	This work
Gmet0908up	$\Delta 0908::Sp^r$	GGAAAAGGTTGTCCACCGGG	This work
Gmet0908AvrIIup	$\Delta 0908::Sp^r$	CAGCCTAGGCATTAGTGGACCTCCTT TCTCA ^a	This work
Gmet0908AvrIIIdn	$\Delta 0908::Sp^r$	GTACCTAGGATCAACGGCCGCTTCGT TCTG ^a	This work

Gmet0908dn	<u>Δ0908::Sp^r</u>	GCTCTGGCACTGGGTCGCCGAGA	This work
0557QF	qRT-PCR	CCATTAATCCGATTGCCACT	This work
0557QR	qRT-PCR	AAATCCATGCCGTAATCCAC	This work
2896QF	qRT-PCR	GCATCCGGTCAACTTCGTAT	This work
2896QR	qRT-PCR	ACTCCAGGTTATTGGCAACG	This work
0909QF	qRT-PCR	ATTGCAACGACTGTCACGAT	This work
0909QR	qRT-PCR	GGGATTATCCATTGCCTTGA	This work
0930QF	qRT-PCR	GTCGCTCCACAACATTGAGA	This work
0930QR	qRT-PCR	GACGGATCGGTTGCATACTT	This work
1868QF	qRT-PCR	ATCCAACACTCTTGCCATCC	This work
1868QR	qRT-PCR	ACCATTGGGCTCAGACTTGT	This work
2029QF	qRT-PCR	GAGTATCATCGCATCGCTCA	This work
2029QR	qRT-PCR	CCGTGCTGAATTCCTCTTTC	This work

^a *AvrII* restriction site is underlined

^b *BamHI* restriction site is underlined

^c *Kpn I* restriction site is underlined

^d *XbaI* restriction site underlined

^e *Sph I* restriction site is underlined

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