Table S4. Genes found next to multicopy nucleotide sequences of unknown function in *G. metallireducens*.

Locus tag	**Nearby Genes**	**Annotations of nearby gene(s)**
49 RNA elements containing four GGGACCG repeats (Figure S2)		
Gmet_H401	within Gmet_0369	20 kDa subunit of NADH ubiquinone oxidoreductase or formate dehydrogenase
Gmet_H402	3’ of Gmet_0382 5’ of Gmet_0383	UDP-N-acetylglucosamine 1-carboxyvinyltransferase ATP phosphoribosyltransferase, short form
Gmet_H403	within Gmet_0415 (linker between fused proteins)	fusion protein: D-alanine--D-alanine ligase and cell division protein FtsQ
Gmet_H404	3’ of Gmet_0433 5’ of Gmet_0434	*flgH*; flagellar L-ring protein FlgH *flgI*; flagellar P-ring protein FlgI
Gmet_H405 Gmet_H406	3’ of Gmet_0434 5’ of Gmet_0435	*flgI*; flagellar P-ring protein FlgI flagellar protein FlgJ-like protein
Gmet_H407	3’ of Gmet_0467 5’ of Gmet_0468	*cobT*; nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase *cobS*; cobalamin 5'-phosphate synthase
Gmet_H408	within Gmet_0468	*cobS*; cobalamin 5'-phosphate synthase
Gmet_H409 Gmet_H410	within Gmet_0478	*cbiD*; precorrin-5 C1-methyltransferase
Gmet_H411 Gmet_H412 Gmet_H413	within Gmet_0485	*cobQ*; precorrin-3B C17-methyltransferase/adenosylcobyric acid synthase
Gmet_H414 Gmet_H415	3’ of Gmet_0544 5’ of Gmet_0543	(R)-2-hydroxyglutaryl-CoA dehydratase activator, putative cytochrome *c*, 2 heme-binding sites
Gmet_H416	3’ of Gmet_0698 5’ of Gmet_0699	*metC-1*; cystathionine beta-lyase *metC-2*; cystathionine beta-lyase
Gmet_H417	within Gmet_0714 5’ of Gmet_0715	NUDIX hydrolase membrane protein, putative
Gmet_H418	3’ of Gmet_0721 5’ of Gmet_0722	conserved hypothetical protein SEC-C motif domain protein
Gmet_H419 Gmet_H420	3’ of Gmet_0905 5’ of Gmet_0906	ATPase, AAA family conserved hypothetical protein
Gmet_H421	3’ of Gmet_1753 5’ of Gmet_1752	glutamine amidotransferase, class-II archaeal-type glutamate synthase subunit, putative
Gmet_H422	3’ of Gmet_2328 5’ of Gmet_2327	YicC family stress-induced protein TIGR00255 *gmk*; guanylate kinase
Gmet_H423	3’ of Gmet_2349 5’ of Gmet_2348	lipid A export ATP-binding/membrane protein, MsbA family *kdtA*; 3-deoxy-D-manno-octulosonic-acid transferase
Gmet_H424	within Gmet_2545	ABC transporter, ATP-binding protein

Gmet_H425 Gmet_H426	3' of Gmet_2562 5' of Gmet_2563	sensor histidine kinase (PAS, HATPase_c) sigma-54-dependent transcriptional response regulator (REC, sigma-54 interaction, HTH8)
Gmet_H427 Gmet_H428	3' of Gmet_2563 5' of Gmet_2564	sigma-54-dependent transcriptional response regulator (REC, sigma-54 interaction, HTH8) YcaC-related hydrolase, putative
Gmet_H429	within Gmet_2764	*lpdA-1*; 2-oxoglutarate dehydrogenase complex, E3 protein, dihydrolipoamide dehydrogenase
Gmet_H430 Gmet_H431 Gmet_H432	within Gmet_2766	*sucB*; 2-oxoglutarate dehydrogenase, E2 protein, dihydrolipoamide succinyltransferase
Gmet_H433	3' of Gmet_2776 3' of Gmet_2777	UDP-2,3-diacylglucosamine hydrolase, putative conserved hypothetical protein
Gmet_H434 Gmet_H435	5' of Gmet_2819 5' of Gmet_2820	putative rRNA methylase *shc-1*; squalene cyclase domain protein
Gmet_H436	3' of Gmet_2891 within Gmet_2890	conserved hypothetical protein glycosyl transferase, group 1
Gmet_H437	within Gmet_2892	glycosyl transferase, family 2
Gmet_H438	3' of Gmet_2898 5' of Gmet_2897	cytochrome *c*, 8 heme-binding sites conserved hypothetical protein
Gmet_H439	within Gmet_2906	conserved hypothetical protein
Gmet_H440	3' of Gmet_2909 5' of Gmet_2910	*thiE*/*thiD*; 4-amino-5-hydroxymethyl-2-methyl-pyrimidine phosphate kinase and thiamin monophosphate synthase *thiC-1*; 4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase
Gmet_H441	3' of Gmet_2986 3' of Gmet_2987	heat shock protein, Hsp20 family ATP alpha-hydrolase TIGR00268
Gmet_H442	3' of Gmet_3096 5' of Gmet_3095	*fliQ*; flagellar biogenesis protein FliQ *fliR*; flagellar biogenesis protein FliR
Gmet_H443	3' of Gmet_3097 5' of Gmet_3096	*fliP*; flagellar biogenesis protein FliP *fliQ*; flagellar biogenesis protein FliQ
Gmet_H444	3' of Gmet_3157 5' of Gmet_3158	sensor histidine kinase (HAMP, HisKA, HATPase_c) sigma-54-dependent transcriptional response regulator (REC, sigma-54 interaction, HTH8)
Gmet_H445	3' of Gmet_3158 5' of Gmet_3159	sigma-54-dependent transcriptional response regulator (REC, sigma-54 interaction, HTH8) alpha-glucan phosphorylase
Gmet_H446	3' of Gmet_3392 5' of Gmet_3391	3-polyprenyl-4-hydroxybenzoate decarboxylase, putative thiamin biosynthesis enzyme ThiH-related radical SAM domain protein
Gmet_H447 Gmet_H448	3' of Gmet_3430 5' of Gmet_3431	heterodisulfide reductase, iron-sulfur binding subunit, putative

		heterodisulfide reductase, cytochrome reductase subunit
Gmet_H449	3’ of Gmet_3549 3’ of Gmet_3550	PPIC-type PPIASE domain protein, SurA family DnaJ-related molecular chaperone
24 pairs of predicted global regulator binding sites, class 1 (Figure S3)		
Gmet_I101A Gmet_I101B	3’ of Gmet_0006 3’ of Gmet_0007	conserved hypothetical protein transposase of IS*Gme9*, IS481 family
Gmet_I102A Gmet_I102B	5’ of Gmet_0045 3’ of Gmet_0046	transposase of IS*Gme8*, IS110 family transposase of IS*Gme8*, IS110 family
Gmet_I103A Gmet_I103B	5’ of Gmet_0093 5’ of Gmet_0094	transposase of IS*Gme9*, IS481 family transposase of IS*Gme8*, IS110 family
Gmet_I104A Gmet_I104B	3’ of Gmet_0131 5’ of Gmet_0132	conserved hypothetical protein transposase of IS*Gme8*, IS110 family
Gmet_I105A Gmet_I105B	3’ of Gmet_0179 5’ of Gmet_0180	DTW domain protein putative dehydratase, NodN/MaoC domain
Gmet_I106A Gmet_I106B	5’ of Gmet_0488 3’ of Gmet_0489	transposase of IS*Gme8*, IS110 family conserved hypothetical protein
Gmet_I107A Gmet_I107B	3’ of Gmet_0663 5’ of Gmet_0664	nitrogenase molybdenum-iron protein, alpha chain nitrogenase molybdenum-iron protein, beta subunit
Gmet_I108A Gmet_I108B	3’ of Gmet_0669 5’ of Gmet_0670	nitrogenase molybdenum-iron cofactor biosynthesis protein NifEN transposase of IS*Gme8*, IS110 family
Gmet_I109A Gmet_I109B	3’ of Gmet_0722 5’ of Gmet_0723	SEC-C motif domain protein transposase of IS*Gme8*, IS110 family
Gmet_I110A Gmet_I110B	3’ of Gmet_0811 3’ of Gmet_0812	efflux pump outer membrane protein sigma-54-dependent transcriptional response regulator (REC, sigma-54 interaction)
Gmet_I111A Gmet_I111B	3’ of Gmet_0891 5’ of Gmet_0892	DNA topoisomerase I conserved hypothetical protein
Gmet_I112A Gmet_I112B	5’ of Gmet_0958 5’ of Gmet_0959	transposase of IS*Gme8*, IS110 family type IV prepilin-like proteins leader peptide processing enzyme
Gmet_I113A Gmet_I113B	3’ of Gmet_1142 5’ of Gmet_1143	conserved hypothetical protein transposase of IS*Gme8*, IS110 family
Gmet_I114A Gmet_I114B	5’ of Gmet_1717 5’ of Gmet_1718	3-hydroxyacyl-CoA dehydrogenase transposase of IS*Gme8*, IS110 family
Gmet_I115A Gmet_I115B	5’ of Gmet_2067 3’ of Gmet_2068	electron transfer flavoprotein, beta subunit succinyl-CoA synthetase, alpha subunit
Gmet_I116A Gmet_I116B	5’ of Gmet_2072 5’ of Gmet_2073	3-hydroxyacyl-CoA dehydrogenase transposase of IS*Gme8*, IS110 family
Gmet_I117A Gmet_I117B	5’ of Gmet_2493 3’ of Gmet_2494	tryptophan synthase, alternate beta subunit, putative indole-3-glycerol phosphate synthase
Gmet_I118A Gmet_I118B	5’ of Gmet_2517 3’ of Gmet_2518	efflux pump outer membrane protein efflux pump inner membrane protein

Gmet_I119A Gmet_I119B	3’ of Gmet_2784 3’ of Gmet_2785	cobyrinic acid a,c-diamide synthase family protein conserved hypothetical protein
Gmet_I120A Gmet_I120B	3’ of Gmet_2809 5’ of Gmet_2810	protein of unknown function DUF490 transposase of IS*Gme8*, IS110 family
Gmet_I121A Gmet_I121B	5’ of Gmet_2975 3’ of Gmet_2976	transposase of IS*Gme8*, IS110 family peptidyl-tRNA hydrolase-related protein
Gmet_I122A Gmet_I122B	3’ of Gmet_3244 5’ of Gmet_3245	conserved hypothetical protein FAD-dependent dehydrogenase with ferredoxin-like domain
Gmet_I123A Gmet_I123B	5’ of Gmet_3328 3’ of Gmet_3329	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein periplasmically oriented, membrane bound [NiFe]-hydrogenase maturation protease
Gmet_I124A Gmet_I124B	3’ of Gmet_3428 5’ of Gmet_3429	heterodisulfide reductase subunit transposase of IS*Gme8*, IS110 family
21 pairs of predicted global regulator binding sites, class 2 (Figure S4)		
Gmet_I201A Gmet_I201B	3’ of Gmet_0052 3’ of Gmet_0053	peptidase, M16 family transglutaminase domain protein
Gmet_I202A Gmet_I202B	5’ of Gmet_0188 3’ of Gmet_0189	metal-dependent hydrolase, beta-lactamase superfamily III delta-aminolevulinic acid dehydratase
Gmet_I203A Gmet_I203B	3’ of Gmet_0471 5’ of Gmet_0472	4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase cobalt ABC transporter membrane protein CbiM, N-terminal domain
Gmet_I204A Gmet_I204B	3’ of Gmet_0564 5’ of Gmet_0565	conserved hypothetical protein conserved hypothetical protein
Gmet_I205A Gmet_I205B	3’ of Gmet_0568 5’ of Gmet_0569	ABC transporter, periplasmic protein conserved hypothetical protein
Gmet_I206A Gmet_I206B	3’ of Gmet_0696 5’ of Gmet_0697	sensor histidine kinase (HisKA, HATPase_c) inositol-1-monophosphatase
Gmet_I207A Gmet_I207B	5’ of Gmet_0776 3’ of Gmet_0777	sigma-54-dependent nitrogen response regulator NtrX (REC, sigma-54 interaction, HTH8) nitrogen regulation sensor histidine kinase NtrY (HAMP, PAS, HisKA, HATPase_c)
Gmet_I208A Gmet_I208B	3’ of Gmet_0990 5’ of Gmet_0991	phosphoglucomutase/phosphomannomutase family protein nitrogen fixation iron-sulfur cluster assembly protein NifU
Gmet_I209A Gmet_I209B	3’ of Gmet_2509 5’ of Gmet_2510	pyruvate dehydrogenase complex E1 protein, alpha subunit pyruvate dehydrogenase complex E1 protein, beta subunit
Gmet_I210A Gmet_I210B	3’ of Gmet_2572 3’ of Gmet_2573	DUF343-containing conserved hypothetical protein ATP-dependent RNA helicase RhlE

Gmet_I211A Gmet_I211B	5’ of Gmet_2674 3’ of Gmet_2675	predicted zinc-dependent hydrolase metal-dependent phosphohydrolase, HD superfamily
Gmet_I212A Gmet_I212B	3’ of Gmet_2723 3’ of Gmet_2724	peroxiredoxin ATP-dependent helicase, UvrD superfamily
Gmet_I213A Gmet_I213B	3’ of Gmet_2737 5’ of Gmet_2738	sensor histidine kinase (HAMP, HisKA, HATPase_c) molybdopterin-binding iron-sulfur oxidoreductase MopB-3
Gmet_I214A Gmet_I214B	3’ of Gmet_2979 3’ of Gmet_2980	hypothetical protein ErfK/YbiS/YcfS/YnhG family protein
Gmet_I215A Gmet_I215B	3’ of Gmet_2993 5’ of Gmet_2994	histidine triad (HIT) family hydrolase endonuclease IV
Gmet_I216A Gmet_I216B	3’ of Gmet_3236 5’ of Gmet_3237	magnesium-dependent DNase TatD YgdL family protein
Gmet_I217A Gmet_I217B	3’ of Gmet_3245 5’ of Gmet_3246	FAD-dependent dehydrogenase with ferredoxin-like domain iron-sulfur oxidoreductase, putative
Gmet_I218A Gmet_I218B	3’ of Gmet_3248 5’ of Gmet_3249	biotin-dependent acyl-CoA carboxyltransferase conserved hypothetical protein
Gmet_I219A Gmet_I219B	3’ of Gmet_3252 5’ of Gmet_3253	conserved hypothetical protein glyoxalase/bleomycin resistance protein/dioxygenase family protein
Gmet_I220A	5’ of Gmet_3273 5’ of Gmet_3274	conserved hypothetical protein conserved hypothetical protein
Gmet_I221A Gmet_I221B	3’ of Gmet_3402 3’ of Gmet_3403	thiamine biosynthesis protein ThiI-related adenine nucleotide alpha hydrolase superfamily protein transglycosylase-related protein
Gmet_I222A Gmet_I222B	3’ of Gmet_3425 5’ of Gmet_3426	heterodisulfide reductase, subunit B heterodisulfide reductase, subunit A
8 pairs of predicted global regulator binding sites, class 3 (Figure S5)		
Gmet_I301A Gmet_I301B	3’ of Gmet_0301 5’ of Gmet_0302	*moaA-1*; molybdopterin precursor Z synthesis protein MoaA *mosC-1*; molybdenum cofactor sulfurase C-terminal domain protein
Gmet_I302A Gmet_I302B	3’ of Gmet_0484 5’ of Gmet_0485	*cbiG*; precorrin-3B C17-methyltransferase *cobQ*; precorrin-3B C17-methyltransferase/adenosylcobyric acid synthase
Gmet_I303A Gmet_I303B	3’ of Gmet_1103 5’ of Gmet_1104	*greB*; transcription elongation factor GreB mannose-1-phosphate guanylyltransferase
Gmet_I304A Gmet_I304B	3’ of Gmet_2672 3’ of Gmet_2673	conserved hypothetical protein *coaBC*; phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase
Gmet_I305A Gmet_I305B	5’ of Gmet_3074 3’ of Gmet_3075	conserved hypothetical protein TIGR00294 adenosine nucleotide-binding predicted transcriptional regulator ExsB

Gmet_I306A Gmet_I306B	5’ of Gmet_3115 3’ of Gmet_3116	*flgB*; flagellar basal-body rod protein FlgB conserved hypothetical protein
Gmet_I307A Gmet_I307B	3’ of Gmet_3198 5’ of Gmet_3199	*proB*; glutamate 5-kinase *proA*; glutamyl-5-phosphate reductase
Gmet_I308A Gmet_I308B	3’ of Gmet_3432 3’ of Gmet_3433	sensor histidine kinase (HisKA, HATPase_c) aspartate/tyrosine/aromatic aminotransferase
19 predicted global regulator binding sites, class 4 (Figure S6)		
Gmet_I401	3’ of Gmet_0306 5’ of Gmet_0307	conserved hypothetical protein (CoA-binding, CoA ligase, unique) conserved hypothetical protein
Gmet_I402 Gmet_I403	5’ of Gmet_0770 3’ of Gmet_0771	*ppsA*; phosphoenolpyruvate synthase *wrbA*; tryptophan repressor TrpR-binding flavodoxin
Gmet_I404 Gmet_I405	5’ of Gmet_2021 3’ of Gmet_2022	hypothetical protein hypothetical protein
Gmet_I406	5’ of Gmet_2160 5’ of Gmet_2161	transposase, IS*Gme6* UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase/peptidyl-prolyl *cis-trans* isomerase
Gmet_I407 Gmet_I408 Gmet_I409	5’ of Gmet_2580 3’ of Gmet_2581	excinuclease ABC family protein mechanosensitive ion channel family protein
Gmet_I410	5’ of Gmet_2715 3’ of Gmet_2716	hypoxanthine/guanine transport membrane protein hypoxanthine/guanine phosphoribosyltransferase, putative
Gmet_I411	3’ of Gmet_2721 3’ of Gmet_2722	GAF domain/GGDEF domain protein peptidyl-prolyl *cis-trans* isomerase, cyclophilin-type
Gmet_I412	5’ of Gmet_2734 5’ of Gmet_2735	radical SAM domain iron-sulfur oxidoreductase, putative ligand-gated TonB-dependent porin
Gmet_I413 Gmet_I414	5’ of Gmet_3080 3’ of Gmet_3081	thioredoxin/NifU-like domain protein integrase core domain protein, IS*Gme9*
Gmet_I415	5’ of Gmet_R0051 5’ of Gmet_3391	proline tRNA hypothetical protein
Gmet_I416	5’ of Gmet_3416 3’ of Gmet_3417	ABC transporter, ATP-binding/membrane protein predicted GTPase MglA
Gmet_I417 Gmet_I418	5’ of Gmet_3499 3’ of Gmet_3500	OmpA domain protein conserved hypothetical protein
Gmet_I419 Gmet_I420	3’ of Gmet_3508 5’ of Gmet_3509	efflux pump membrane fusion protein efflux pump inner membrane protein
24 predicted regulatory short RNAs, group 1 (Figure S1)		
Gmet_R1001	5’ of Gmet_0016	*hemE*; uroporphyrinogen decarboxylase
Gmet_R1002	5’ of Gmet_0031	conserved hypothetical protein
Gmet_R1003	3’ of Gmet_0088	sigma-54-dependent transcriptional regulator
	3’ of Gmet_0089	ATP-dependent DNA helicase UvrD/REP

Gmet_R1004	5’ of Gmet_0153	NADH dehydrogenase I, B/C/D subunits
Gmet_R1005	5’ of Gmet_0213	L,L-diaminopimelate aminotransferase
Gmet_R1006	5’ of Gmet_0251	cytochrome *c* oxidase, subunit IV
Gmet_R1007	5’ of Gmet_0552	transketolase, C-terminal domain
Gmet_R1008	5’ of Gmet_0663	nitrogenase molybdenum-iron protein, alpha chain
Gmet_R1009	5’ of Gmet_0882	polysaccharide deacetylase-related
Gmet_R1010	5’ of Gmet_0902	saccharopine dehydrogenase
Gmet_R1011	5’ of Gmet_0903	*nspC*; carboxynorspermidine decarboxylase
Gmet_R1012, Gmet_R1013	5’ of Gmet_0904	*speA*; biosynthetic arginine decarboxylase
Gmet_R1014	5’ of Gmet_1045	aldehyde ferredoxin oxidoreductase, tungsten-containing
Gmet_R1015	5’ of Gmet_1054	sensor histidine kinase (FhlA, HisKA, HATPase_c)
Gmet_R1016	5’ of Gmet_1139	phage baseplate outer wedge protein
Gmet_R1017	5’ of Gmet_1713	electron transfer flavoprotein, beta subunit
Gmet_R1018	5’ of Gmet_1721	thioesterase superfamily protein
Gmet_R1019	5’ of Gmet_1905	*cysT*; sulfate ABC transporter, membrane protein CysT
Gmet_R1020	5’ of Gmet_2257	electron transfer flavoprotein, alpha subunit
Gmet_R1021	3’ of Gmet_3093	conserved hypothetical protein
	3’ of Gmet_3094	*flhB*; flagellar biosynthesis protein FlhB
Gmet_R1022	5’ of Gmet_3106	*fliK*; flagellar hook-length control protein FliK
Gmet_R1023	3’ of Gmet_3145	ferritin-like domain protein
	3’ of Gmet_3146	peptidyl-prolyl *cis-trans* isomerase, FKBP-type
Gmet_R1024	5’ of Gmet_3291	enoyl-CoA hydratase/isomerase
4 predicted short RNAs of unknown function, group 2 (Figure S8a)		
Gmet_R2001	5’ of Gmet_0082 3’ of Gmet_0083	hypothetical protein hypothetical protein
Gmet_R2002	5’ of Gmet_1003	hypothetical protein
Gmet_R2003	5’ of Gmet_2755	hypothetical protein
Gmet_R2004	5’ of Gmet_2967 3’ of Gmet_2968	conserved hypothetical protein conserved hypothetical protein
16 predicted regulatory short RNAs, group 3 (Figure S7)		
Gmet_R3001	5’ of Gmet_0131	conserved hypothetical protein
Gmet_R3002	5’ of Gmet_0232	conserved hypothetical protein
Gmet_R3003	5’ of Gmet_0241, Gmet_0240	conserved hypothetical protein, helix-turn-helix and Zn ribbon transcriptional regulator
Gmet_R3004	5’ of Gmet_0292	cytochrome *c*, 2 heme-binding sites
Gmet_R3005	5’ of Gmet_0970-Gmet_0975	transcriptional regulator, XRE family five type IV pilus biogenesis proteins (Figure 8)
Gmet_R3006, Gmet_R3007	5’ of Gmet_1087	cytochrome *c*, 1 heme-binding site
Gmet_R3008, Gmet_R3009	5’ of Gmet_1191, Gmet_1190	cytochrome *c*, 1 heme-binding site efflux pump outer membrane protein
Gmet_R3010	5’ of Gmet_1195	serine protease, subtilase family

Gmet_R3011	5’ of Gmet_1703	cytochrome *c*, 7 heme-binding sites
Gmet_R3012	5’ of Gmet_1763	conserved hypothetical protein related to Gmet_0131
Gmet_R3013	5’ of Gmet_2037	*N*-acylhomoserine lactone synthetase-related protein
Gmet_R3014	5’ of Gmet_2168	cytochrome *c*, 2 heme-binding sites
Gmet_R3015, Gmet_R3016	5’ of Gmet_3485-Gmet_3487	peptidoglycan-binding ErfK/YbiS/YcfS/YnhG family protein lipoprotein, putative ErfK/YbiS/YcfS/YnhG-related protein
6 predicted short RNAs, group 4 (Figure S8b)		
Gmet_R4001	3’ of Gmet_0173 5’ of Gmet_0174	putative lipoprotein conserved hypothetical protein
Gmet_R4002	3’ of Gmet_0325 5’ of Gmet_0326	cytochrome *c*, 4 heme-binding sites oxidoreductase, iron-sulfur cluster-binding subunit
Gmet_R4003	3’ of Gmet_2082 5’ of Gmet_2081	*bamF*; predicted benzoyl-CoA reductase electron transfer protein, selenocysteine-containing *bamG*; predicted benzoyl-CoA reductase electron transfer protein, NADH dehydrogenase 24 kDa subunit-like
Gmet_R4004 (fragment)	3’ of Gmet_2836 5’ of Gmet_2835	conserved hypothetical protein nitroreductase 3 family protein
Gmet_R4005	3’ of Gmet_3388 3’ of Gmet_3389	conserved hypothetical protein ribonuclease D, putative
Gmet_R4006	3’ of Gmet_3420 5’ of Gmet_3419	*recR*; recombination protein RecR pyruvate:ferredoxin/flavodoxin oxidoreductase
8 copies of a palindromic nucleotide sequence, group 5 (Figure S8c)		
Gmet_R5001	within Gmet_0309	succinate dehydrogenase/fumarate reductase iron-sulfur protein
Gmet_R5002	3’ of Gmet_0745 5’ of Gmet_0746	*ruvA*; Holliday junction resolution DNA helicase RuvA *ruvB*; Holliday junction resolution DNA helicase RuvB
Gmet_R5003	3’ of Gmet_1067 5’ of Gmet_1068	CRISPR-associated TM1801 family protein transposase, IS*Gme16*
Gmet_R5004	within Gmet_1068	CRISPR-associated integrase, IS*Gme16*
Gmet_R5005	5’ of Gmet_1069 5’ of Gmet_1070	transposase, IS*Gme2* RecB family exonuclease Cas4
Gmet_R5006	3’ of Gmet_1154 3’ of Gmet_1155	membrane protein membrane protein, TerC family
Gmet_R5007	3’ of Gmet_2410 5’ of Gmet_2409	superoxide dismutase, iron/manganese-containing intracellular protease, PfpI family, putative
Gmet_R5008	3’ of Gmet_3127 5’ of Gmet_3126	efflux pump inner membrane protein conserved hypothetical protein
4 RNA elements with complementary ends, group 6 (Figure S8d)		
Gmet_R6001	3’ of Gmet_0475 5’ of Gmet_0476	*cbiO-1*; cobalt ABC transporter, ATP-binding protein

		cbiX; sirohydrochlorin cobaltochelatase
Gmet_R6002	3’ of Gmet_0743 5’ of Gmet_0744	conserved hypothetical protein TIGR01033 *ruvC*; crossover junction endodeoxyribonuclease RuvC
Gmet_R6003	3’ of Gmet_1717 5’ of Gmet_1716	3-hydroxyacyl-CoA dehydrogenase enoyl-CoA hydratase/isomerase
Gmet_R6004	3’ of Gmet_3426 5’ of Gmet_3427	*hdrA*; heterodisulfide reductase, subunit A heterodisulfide reductase subunit
7 predicted short RNAs, group 7 (Figure S8e)		
Gmet_R7001	3’ of Gmet_0870 5’ of Gmet_0871	*cysE*; serine *O*-acetyltransferase Rrf2 family transcriptional regulator
Gmet_R7002	3’ of Gmet_1210 5’ of Gmet_1211	*mauG*; methylamine utilization cytochrome *c* peroxidase MauG, 2 heme-binding sites *gap-2*; glyceraldehyde-3-phosphate dehydrogenase, type I
Gmet_R7003	3’ of Gmet_2110 3’ of Gmet_2112	protein of unknown function UPF0261 predicted phosphohydrolase
Gmet_R7004	3’ of Gmet_2154 5’ of Gmet_2153	multicopper oxidase, type 2 *bamO*; electron transfer flavoprotein, beta subunit
Gmet_R7005	3’ of Gmet_2166 5’ of Gmet_R3014	transposase, IS*Gme5* conserved nucleotide sequence
Gmet_R7006	3’ of Gmet_2442 5’ of Gmet_2441	iron/manganese-dependent transcriptional regulator *cbiM-2*; cobalt ABC transporter membrane protein CbiM
Gmet_R7007	5’ of Gmet_2718 5’ of Gmet_2719	protein of unknown function DUF323 conserved hypothetical protein
4 predicted short RNAs, group 8 (Figure S8f)		
Gmet_R8001 Gmet_R8002	3’ of Gmet_1317 5’ of Gmet_1320	protein of unknown function DUF86 nucleotidyltransferase-related protein
Gmet_R8003	3’ of Gmet_1320 5’ of Gmet_1321	nucleotidyltransferase-related protein conserved hypothetical protein
Gmet_R8004	3’ of Gmet_1322 5’ of Gmet_1324	periplasmic or secreted lipoprotein conserved hypothetical protein (LbetaH repeats_WxcM)
4 predicted short RNAs, group 9 (Figure S8g)		
Gmet_R9001	3’ of Gmet_2486 5’ of Gmet_2485	hypothetical protein conserved hypothetical protein
Gmet_R9002	3’ of Gmet_2490 5’ of Gmet_R0119	conserved hypothetical protein conserved nucleotide sequence
Gmet_R9003	3’ of Gmet_2491 5’ of Gmet_2490	transcriptional regulator, frameshifted conserved hypothetical protein
Gmet_R9004	3’ of Gmet_2534 3’ of Gmet_2535	transcriptional regulator, putative hypothetical protein
2 predicted short RNAs (Figure S8h)		
Gmet_R0064	3’ of Gmet_0141	conserved hypothetical protein related to cytochrome

	5’ of Gmet_0140	*c* assembly proteins conserved hypothetical protein
Gmet_R0066	3’ of Gmet_0257 3’ of Gmet_0258	membrane protein, putative tRNA dihydrouridine synthase-like flavin mononucleotide-binding domain protein
2 predicted short RNAs (Figure S8i)		
Gmet_R0068	near Gmet_R0067 3’ of Gmet_0312	conserved nucleotide sequence hypothetical protein
Gmet_R0094	3’ of Gmet_1608 5’ of Gmet_1609	*hup-2*; histone-like protein LexA-ImpB/MucB/SamB protein pseudogene fusion
2 predicted short RNAs (Figure S8j)		
Gmet_R0074	3’ of Gmet_0717 5’ of Gmet_0718	hypothetical protein hypothetical protein
Gmet_R0075	3’ of Gmet_0719 5’ of Gmet_0720	conserved hypothetical protein conserved hypothetical protein
2 conserved palindromic sequences (Figure S8k)		
Gmet_R0091	3’ of Gmet_1352 5’ of Gmet_1353	*glnA*; glutamine synthetase, type I *ispG*; 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
Gmet_R0114	3’ of Gmet_2372 5’ of Gmet_2373	*eno*; enolase nicotinate phosphoribosyltransferase
2 predicted short RNAs (Figure S8l)		
Gmet_R0097	5’ of Gmet_1702 near Gmet_R3011	hypothetical protein conserved nucleotide sequence
Gmet_R0099	3’ of Gmet_1703 3’ of Gmet_1704	cytochrome *c*, 7 heme-binding sites conserved hypothetical protein
3 predicted short RNAs (Figure S8m)		
Gmet_R0105	3’ of Gmet_2004 5’ of Gmet_2003	glycosyl transferase membrane protein, putative
Gmet_R0106	3’ of Gmet_2006 5’ of Gmet_2005	*sufS*; selenocysteine lyase polysaccharide deacetylase domain protein
Gmet_R0107	3’ of Gmet_2008 5’ of Gmet_2007	glycosyl transferase coenzyme F390 synthetase superfamily protein
2 predicted short RNAs (Figure S8n)		
Gmet_R0110	3’ of Gmet_2163 5’ of Gmet_3609	laccase family protein conserved hypothetical protein
Gmet_R0111	3’ of Gmet_2170 5’ of Gmet_2169	methyltransferase, putative glycosyl transferase, putative
2 predicted short RNAs (Figure S8o)		
Gmet_R0126	3’ of Gmet_2725 5’ of Gmet_2724	hypothetical protein ATP-dependent helicase, UvrD superfamily
Gmet_R0127	3’ of Gmet_2726 5’ of Gmet_3623	neutral zinc metallopeptidase, putative hypothetical protein
2 predicted short RNAs (Figure S8p)		
Gmet_R0146	3’ of Gmet_3471	pirin family protein, C-terminal fragment,

	3’ of Gmet_3472	frameshifted response regulator (REC)
Gmet_R0147	5’ of Gmet_3483 5’ of Gmet_R0055	type I restriction-modification enzyme S subunit, fragment Asn tRNA