Table S1. Reporters (amplicons representing genes and intergenic regions) whose expression was significantly decreased (activated by RpoS) in at least two of three biological replicates of the *G. sulfurreducens rpoS* mutant versus the wild type for cells grown with acetate as the electron donor and fumarate as electron acceptor. Results are sorted first by mainrole category, then in ascending order by Locus ID. Reporters in bold have been assigned more than one mainrole category.

Locus ID	**Common name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Changes**
GSU1835	Glutamine synthetase, type I	Amino acid biosynthesis	Glutamate family	-0.75	0.32	-1.68
GSU1088	Ubiquinone biosynthesis protein aarf, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	Menaquinone and ubiquinone	-0.69	0.31	-1.61
GSU0036	Capsule biosynthesis protein, putative	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	-0.68	0.30	-1.60
GSU0073	Outer membrane protein, putative	Cell envelope	Other	-0.80	0.19	-1.75
GSU1817	Outer membrane lipoprotein, Slp family, putative	Cell envelope	Other	-1.15	0.38	-2.22
GSU1961	Glycosyl transferase, group 2 family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-0.74	0.28	-1.67
GSU1970	Polysaccharide biosynthesis protein, putative	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-0.85	0.24	-1.81
GSU1975	**NAD-dependent epimerase/dehydratase family protein**	**Cell envelope**	**Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides**	-0.62	0.25	-1.54
GSU1983	Polysaccharide biosynthesis protein, putative	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-0.64	0.20	-1.56
GSU1984	Polysaccharide chain length determinant protein, putative	Cell envelope	Other	-0.72	0.21	-1.65
GSU3462	Lipoprotein, putative	Cell envelope	Other	-1.10	0.32	-2.14
GSU0583	Methyl-accepting chemotaxis protein	Cellular processes	Chemotaxis and motility	-0.73	0.30	-1.66
GSU1013	Chemotaxis motb protein, putative	Cellular processes	Chemotaxis and motility	-0.88	0.26	-1.84

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
GSU1118	Universal stress protein family	Cellular processes	Adaptations to atypical conditions	-1.07	0.34	-2.11
GSU2657	Spore coat protein A	Cellular processes	Sporulation and germination	-0.93	0.60	-1.91
GSU2794	Large conductance mechanosensitive channel protein	Cellular processes	Adaptations to atypical conditions	-0.63	0.23	-1.55
GSU0067	Carbonic anhydrase	Central intermediary metabolism	Other	-1.57	0.26	-2.98
GSU0918	S-adenosylmethionine synthetase family protein	Central intermediary metabolism	Other	-0.76	0.23	-1.70
GSU0997	Formamidopyrimidine-DNA glycosylase	DNA metabolism	DNA replication, recombination, and repair	-0.86	0.23	-1.82
GSU2829	Deoxyribodipyrimidine photolyase, putative	DNA metabolism	DNA replication, recombination, and repair	-0.96	0.46	-1.95
GSU0069	Oxidoreductase, iron-sulfur cluster-binding subunit	Energy metabolism	Electron transport	-0.95	0.39	-1.93
GSU0121	Nickel-iron hydrogenase, b-type cytochrome subunit	Energy metabolism	Electron transport	-0.91	0.27	-1.88
GSU0122	Nickel-dependent hydrogenase, large subunit	Energy metabolism	Electron transport	-1.23	0.43	-2.35
GSU0123	Nickel-dependent hydrogenase, small subunit	Energy metabolism	Electron transport	-0.99	0.30	-1.99
GSU0201	Isoquinoline 1-oxidoreductase, beta subunit	Energy metabolism	Fermentation	-1.38	0.25	-2.61
GSU0219	Cytochrome c oxidase, subunit I	Energy metabolism	Electron transport	-0.86	0.40	-1.81
GSU0222	Cytochrome c oxidase, subunit II	Energy metabolism	Electron transport	-0.80	0.23	-1.74
GSU0342	NADH dehydrogenase I, E subunit	Energy metabolism	Electron transport	-0.65	0.23	-1.56
GSU0350	NADH dehydrogenase I, M subunit	Energy metabolism	Electron transport	-0.79	0.17	-1.73
GSU0357	Cytochrome c family protein	Energy metabolism	Electron transport	-2.67	0.80	-6.35
GSU0377	Glycine cleavage system P protein, subunit 1	Energy metabolism	Amino acids and amines	-0.69	0.33	-1.62
GSU0466	Cytochrome c551 peroxidase, MacA	Energy metabolism	Electron transport	-2.30	0.39	-4.93
GSU0674	Prismane protein	Energy metabolism	Electron transport	-3.21	0.51	-9.27
GSU0804	Trp repressor binding protein wrba	Energy metabolism	Electron transport	-1.19	0.57	-2.28
GSU0911	Iron-sulfur cluster-binding protein	Energy metabolism	Electron transport	-0.72	0.38	-1.65
GSU1024	Cytochrome c3	Energy metabolism	Electron transport	-1.72	0.77	-3.28
GSU1058	Succinyl-coa synthase, beta subunit	Energy metabolism	TCA cycle	-0.64	0.29	-1.56
GSU1059	Succinyl-coa synthase, alpha subunit	Energy metabolism	TCA cycle	-1.02	0.30	-2.03
GSU1397	Cytochrome c family protein, putative	Energy metabolism	Electron transport	-2.13	0.41	-4.39
GSU1416	Iron-sulfur cluster-binding protein	Energy metabolism	Electron transport	-0.93	0.26	-1.90
GSU1465	Isocitrate dehydrogenase, NADP-	Energy metabolism	TCA cycle	-0.64	0.31	-1.56

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
	dependent					
GSU1469	Keto/oxoacid ferredoxin oxidoreductase, beta subunit	Energy metabolism	Fermentation	-0.71	0.29	-1.64
GSU1538	Methylamine utilization protein maug, putative	Energy metabolism	Amino acids and amines	-0.82	0.36	-1.76
GSU1606	Ribose 5-phosphate isomerase B, putative	Energy metabolism	Pentose phosphate pathway	-0.45	0.13	-1.36
GSU1640	Cytochrome d ubiquinol oxidase, subunit I	Energy metabolism	Electron transport	-0.92	0.44	-1.90
GSU1641	Cytochrome d ubiquinol oxidase, subunit II	Energy metabolism	Electron transport	-1.60	0.67	-3.04
GSU1648	Cytochrome c family protein	Energy metabolism	Electron transport	-1.48	0.48	-2.79
GSU1649	Cytochrome b/b6	Energy metabolism	Electron transport	-1.02	0.33	-2.03
GSU1650	Cytochrome b/b6 complex, iron-sulfur subunit	Energy metabolism	Electron transport	-1.02	0.49	-2.03
GSU1660	Aconitate hydratase 2	Energy metabolism	TCA cycle	-0.78	0.33	-1.71
GSU1975	**NAD-dependent epimerase/dehydratase family protein**	**Energy metabolism**	**Sugars**	-0.62	0.25	-1.54
GSU2076	Cytochrome c family protein	Energy metabolism	Electron transport	-1.19	0.58	-2.28
GSU2446	2-oxoglutarate dehydrogenase complex, E3 component, lipoamide dehydrogenase	Energy metabolism	TCA cycle	-0.63	0.21	-1.55
GSU2724	Cytochrome c family protein	Energy metabolism	Electron transport	-0.81	0.30	-1.75
GSU2725	Cytochrome c family protein	Energy metabolism	Electron transport	-1.16	0.42	-2.23
GSU2731	Polyheme membrane-associated cytochrome c, OmcC	Energy metabolism	Anaerobic/Electron Transport	-2.56	0.33	-5.90
GSU2732	Cytochrome c family protein, putative	Energy metabolism	Electron transport	-2.46	0.40	-5.49
GSU2737	Polyheme membrane-associated cytochrome c, OmcB	Energy metabolism	Anaerobic/Electron Transport	-1.25	0.43	-2.38
GSU2738	Cytochrome c family protein	Energy metabolism	Electron transport	-2.17	0.38	-4.49
GSU2743	Cytochrome c family protein	Energy metabolism	Electron transport	-1.55	0.42	-2.93
GSU2811	Cytochrome c Hsc	Energy metabolism	Electron transport	-0.96	0.42	-1.95
GSU2813	Cytochrome c551 peroxidase	Energy metabolism	Electron transport	-1.10	0.43	-2.15
GSU2882	Cytochrome c family protein	Energy metabolism	Electron transport	-0.69	0.46	-1.62
GSU3137	Cytochrome c family protein	Energy metabolism	Electron transport	-0.60	0.12	-1.52
GSU3187	Ferredoxin family protein	Energy metabolism	Electron transport	-1.04	0.40	-2.06
GSU3188	Rubredoxin	Energy metabolism	Electron transport	-0.94	0.49	-1.92
GSU3257	Glycogen synthase	Energy metabolism	Biosynthesis and degradation of polysaccharides	-0.64	0.19	-1.56
GSU3274	Cytochrome c family protein, putative	Energy metabolism	Electron transport	-1.20	0.56	-2.30

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
GSU3331	Pyruvate kinase	Energy metabolism	Glycolysis/gluconeogenesis	-0.73	0.22	-1.66
GSU3385	Phosphoenolpyruvate carboxykinase	Energy metabolism	Glycolysis/gluconeogenesis	-0.61	0.16	-1.53
GSU3430	NADH dehydrogenase I, M subunit	Energy metabolism	Electron transport	-0.58	0.21	-1.50
GSU0075	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.94	0.29	-1.92
GSU0186	Conserved hypothetical protein, authentic frameshift	Hypothetical proteins	Conserved	-0.73	0.22	-1.66
GSU0218	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.45	0.32	-2.73
GSU0544	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.77	0.26	-1.71
GSU0813	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.23	0.42	-2.35
GSU0817	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.80	0.33	-1.74
GSU0824	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.73	0.22	-1.66
GSU0849	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.75	0.60	-3.36
GSU1071	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.01	0.23	-2.01
GSU1087	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.76	0.29	-1.69
GSU1167	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.32	0.25	-2.49
GSU1209	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.71	0.21	-1.63
GSU1212	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.65	0.49	-3.14
GSU1213	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.54	0.50	-2.91
GSU1642	Conserved hypothetical protein	Hypothetical proteins	Conserved	-2.40	0.52	-5.29
GSU1726	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.78	0.44	-1.72
GSU2193	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.53	0.33	-2.89
GSU2347	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.25	0.34	-2.39
GSU2353	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.64	0.12	-1.56
GSU2441	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.66	0.21	-1.58
GSU2788	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.51	0.65	-2.85
GSU2792	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.14	0.42	-2.21
GSU3139	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.97	0.24	-1.95
GSU3251	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.06	0.59	-2.09

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
GSU3255	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.75	0.31	-1.68
GSU3289	Conserved hypothetical protein	Hypothetical proteins	Conserved	-2.91	0.35	-7.51
GSU3342	Conserved domain protein	Hypothetical proteins	Domain	-1.92	0.80	-3.78
GSU0071	Hypothetical protein	Hypothetical protein	Hypothetical	-0.98	0.32	-1.97
GSU0077	Hypothetical protein	Hypothetical protein	Hypothetical	-1.34	0.78	-2.53
GSU0078	Hypothetical protein	Hypothetical protein	Hypothetical	-1.28	0.55	-2.42
GSU0539	Hypothetical protein	Hypothetical protein	Hypothetical	-1.32	0.34	-2.49
GSU0715	Hypothetical protein	Hypothetical protein	Hypothetical	-1.57	0.51	-2.97
GSU0716	Hypothetical protein	Hypothetical protein	Hypothetical	-1.11	0.85	-2.16
GSU0719	Hypothetical protein	Hypothetical protein	Hypothetical	-1.15	0.47	-2.22
GSU0790	Hypothetical protein	Hypothetical protein	Hypothetical	-1.70	0.47	-3.24
GSU0915	Hypothetical protein	Hypothetical protein	Hypothetical	-0.76	0.34	-1.70
GSU0968	Hypothetical protein	Hypothetical protein	Hypothetical	-0.81	0.30	-1.75
GSU0996	Hypothetical protein	Hypothetical protein	Hypothetical	-1.67	0.86	-3.18
GSU1160	Hypothetical protein	Hypothetical protein	Hypothetical	-0.75	0.31	-1.68
GSU1395	Hypothetical protein	Hypothetical protein	Hypothetical	-1.33	0.35	-2.51
GSU1396	Hypothetical protein	Hypothetical protein	Hypothetical	-1.07	0.49	-2.10
GSU1558	Hypothetical protein	Hypothetical protein	Hypothetical	-1.17	0.40	-2.25
GSU1857	Hypothetical protein	Hypothetical protein	Hypothetical	-1.01	0.37	-2.02
GSU1949	Hypothetical protein	Hypothetical protein	Hypothetical	-0.92	0.35	-1.89
GSU1969	Hypothetical protein	Hypothetical protein	Hypothetical	-0.77	0.37	-1.71
GSU1994	Hypothetical protein	Hypothetical protein	Hypothetical	-0.77	0.28	-1.71
GSU1995	Hypothetical protein	Hypothetical protein	Hypothetical	-0.75	0.27	-1.68
GSU2036	Hypothetical protein	Hypothetical protein	Hypothetical	-0.73	0.23	-1.65
GSU2037	Hypothetical protein	Hypothetical protein	Hypothetical	-0.84	0.22	-1.79
GSU2412	Hypothetical protein	Hypothetical protein	Hypothetical	-0.86	0.41	-1.82
GSU2726	Hypothetical protein	Hypothetical protein	Hypothetical	-2.25	0.55	-4.76
GSU2733	Hypothetical protein	Hypothetical protein	Hypothetical	-2.10	0.38	-4.28
GSU2739	Hypothetical protein	Hypothetical protein	Hypothetical	-2.10	0.23	-4.30
GSU2742	Hypothetical protein	Hypothetical protein	Hypothetical	-1.79	0.47	-3.46
GSU2793	Hypothetical protein	Hypothetical protein	Hypothetical	-1.42	0.51	-2.68
GSU3189	Hypothetical protein	Hypothetical protein	Hypothetical	-0.98	0.35	-1.98
GSU3271	Hypothetical protein	Hypothetical protein	Hypothetical	-1.86	0.74	-3.64
GSU3273	Hypothetical protein	Hypothetical protein	Hypothetical	-1.02	0.52	-2.03
GSU3311	Hypothetical protein	Hypothetical protein	Hypothetical	-0.59	0.18	-1.51
GSU3336	Hypothetical protein	Hypothetical protein	Hypothetical	-0.60	0.22	-1.51
GSU3341	Hypothetical protein	Hypothetical protein	Hypothetical	-1.89	0.59	-3.72
GSU3344	Hypothetical protein	Hypothetical protein	Hypothetical	-1.37	0.43	-2.58
GSU3345	Hypothetical protein	Hypothetical protein	Hypothetical	-1.20	0.54	-2.29
GSU3351	Hypothetical protein	Hypothetical protein	Hypothetical	-1.38	0.51	-2.59
GSU0080	Protease deg q	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.69	0.23	-1.61

Locus ID	**Common name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Changes**
GSU0928	Peptidase, M16 family	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.61	0.14	-1.53
GSU1159	Intracellular protease, pfpi family	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.83	0.31	-1.78
GSU2060	Pmba protein, putative	Protein fate	Protein modification and repair	-0.61	0.16	-1.53
GSU2433	ATP-dependent protease, putative	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.80	0.28	-1.74
GSU3140	Peptidase, M1 family protein	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.89	0.46	-1.86
GSU3193	ATP-dependent protease La	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.83	0.22	-1.78
GSU0079	Transcriptional regulator, Cro/CI family	Regulatory functions	DNA interactions	-1.24	0.25	-2.36
GSU0700	Sensory box/response regulator	Regulatory functions	Small molecule interactions and Two-component systems	-1.14	0.56	-2.20
GSU0789	Response regulator	Regulatory functions	Protein interactions and Two-component systems	-1.21	0.43	-2.32
GSU1117	Response regulator	Regulatory functions	Protein interactions and Two-component systems	-0.94	0.36	-1.91
GSU1414	Sensory box histidine kinase/response regulator	Regulatory functions	Small molecule interactions and Two-component systems	-0.91	0.45	-1.87
GSU1654	Response regulator, putative	Regulatory functions	Protein interactions and Two-component systems	-1.18	0.31	-2.27
GSU1656	Sensory box/response regulator	Regulatory functions	Small molecule interactions and Two-component systems	-0.61	0.16	-1.52
GSU1992	Transcriptional regulator, Crp/Fnr family	Regulatory functions	DNA interactions	-0.59	0.16	-1.51
GSU2444	Sensor histidine kinase	Regulatory functions	Protein interactions	-0.73	0.21	-1.65
GSU2964	**Molybdenum transport regulatory protein mode**	**Regulatory functions**	**DNA interactions**	**-1.55**	**0.65**	**-2.93**
GSU3252	Sensor histidine kinase	Regulatory functions	Protein interactions and Two-component systems	-0.73	0.29	-1.65
GSU0718	Sensory box histidine kinase/response regulator	Signal transduction	Two-component systems	-1.22	0.36	-2.33

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
GSU1119	Sensor histidine kinase/response regulator	Signal transduction	Two-component systems	-0.83	0.37	-1.78
GSU1415	Response regulator	Signal transduction	Two-component systems	-1.34	0.57	-2.53
GSU1990	Sensor histidine kinase	Signal transduction	Two-component systems	-0.73	0.29	-1.66
GSU3138	Sensor histidine kinase/response regulator	Signal transduction	Two-component systems	-1.16	0.32	-2.24
GSU0720	Desulfoferrodoxin ferrous iron-binding domain	Transport and binding proteins	Cations and iron carrying compounds	-1.72	0.49	-3.30
GSU0814	Outer membrane efflux protein, putative	Transport and binding proteins	Unknown substrate	-1.21	0.32	-2.32
GSU0816	ABC transporter, ATP-binding protein	Transport and binding proteins	Unknown substrate	-1.17	0.33	-2.26
GSU1068	Sodium/solute symporter family protein	Transport and binding proteins	Unknown substrate	-0.83	0.20	-1.77
GSU1070	Sodium/solute symporter family protein	Transport and binding proteins	Unknown substrate	-0.87	0.20	-1.82
GSU1307	Ferritin	Transport and binding proteins	Cations and iron carrying compounds	-1.32	0.60	-2.49
GSU1557	Mechanosensitive ion channel family protein	Transport and binding proteins	Unknown substrate	-1.36	0.47	-2.56
GSU2005	Branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein, putative	Transport and binding proteins	Amino acids, peptides and amines	-1.63	0.37	-3.10
GSU2006	Branched-chain amino acid ABC transporter, permease protein	Transport and binding proteins	Amino acids, peptides and amines	-1.16	0.48	-2.23
GSU2007	Branched-chain amino acid ABC transporter, permease protein	Transport and binding proteins	Amino acids, peptides and amines	-1.25	0.40	-2.38
GSU2008	Branched-chain amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-0.83	0.42	-1.77
GSU2009	Branched-chain amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-0.89	0.23	-1.85
GSU2352	Sodium/solute symporter family protein	Transport and binding proteins	Unknown substrate	-0.93	0.23	-1.90
GSU2649	Amino acid ABC transporter, amino acid-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-2.55	1.04	-5.85

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Changes
GSU2964	**Molybdenum transport regulatory protein mode**	**Transport and binding proteins**	**Anions**	**-1.55**	**0.65**	**-2.93**
GSU3268	Ferrous iron transport protein B	Transport and binding proteins	Cations and iron carrying compounds	-1.33	0.44	-2.52
GSU3346	Potassium uptake protein, Kup system	Transport and binding proteins	Cations and iron carrying compounds	-0.82	0.33	-1.77
GSU0217	Nitroreductase family protein	Unknown function	Enzymes of unknown specificity	-1.36	0.31	-2.56
GSU0360	Ompa domain protein	Unknown function	General	-1.56	0.24	-2.94
GSU0480	Nifu-like domain protein	Unknown function	General	-0.70	0.16	-1.62
GSU0767	Tia invasion determinant-related protein	Unknown function	General	-0.98	0.44	-1.97
GSU0810	Ompa domain protein	Unknown function	General	-1.46	0.54	-2.75
GSU0815	Mce-related protein	Unknown function	General	-0.93	0.39	-1.91
GSU1014	Smr domain protein	Unknown function	General	-0.79	0.18	-1.73
GSU1394	Laccase family protein	Unknown function	General	-1.76	0.36	-3.39
GSU1398	SCO1/senc family protein	Unknown function	General	-1.86	0.52	-3.62
GSU1404	Radical SAM domain protein	Unknown function	Enzymes of unknown specificity	-1.07	0.37	-2.10
GSU1945	Fibronectin type III domain protein	Unknown function	General	-0.71	0.25	-1.63
GSU1982	General secretion pathway protein-related protein	Unknown function	General	-0.61	0.18	-1.52
GSU1986	Glycosyl transferase domain protein	Unknown function	General	-0.71	0.25	-1.63
GSU1991	CAAX amino terminal protease family protein	Unknown function	General	-0.62	0.09	-1.54
GSU2010	CBS domain protein	Unknown function	General	-1.12	0.34	-2.17
GSU2063	HD domain protein	Unknown function	General	-0.68	0.19	-1.60
GSU2443	Dehydrogenase complex, E1 component, alpha subunit	Unknown function	Enzymes of unknown specificity	-0.67	0.25	-1.59
GSU3330	NADH-dependent flavin oxidoreductase, Oye family	Unknown function	Enzymes of unknown specificity	-0.68	0.21	-1.61
GSU3343	Spovr-like family protein	Unknown function	General	-1.62	0.39	-3.06
[a]R00118	Null			-1.51	0.65	-1.60
[a]R04063	Null			-1.31	0.46	-2.49
[a]R05513	Null			-0.77	0.35	-1.71

[a] Intergenic region

Table S2. Reporters (amplicons representing genes and intergenic regions) whose expression was significantly increased (repressed by RpoS) in at least two of three biological replicates of the *G. sulfurreducens rpoS* mutant versus the wild type for cellsgrown with acetate as the electron donor and fumarate as electron acceptor. Results are sorted first by main role category, then in ascending order by Locus ID. Reporters in bold have been assigned more than one mainrole category.

Locus ID	**Common name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Change**
GSU1903	3-isopropylmalate dehydratase, large subunit, putative	Amino acid biosynthesis	Pyruvate family	0.61	0.14	1.52
GSU1917	Undecaprenyl diphosphate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers	Other	0.74	0.32	1.67
GSU0038	Lipoprotein, putative	Cell envelope	Other	0.85	0.31	1.81
GSU0116	Transglycosylase	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	0.65	0.19	1.57
GSU0757	Lipoprotein, putative	Cell envelope	Other	1.01	0.28	2.02
GSU1783	Type IV pilus biogenesis protein PilB, putative	Cell envelope	Surface structures	0.75	0.32	1.68
GSU1789	Glycosyl transferase, group 2 family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	0.78	0.19	1.72
GSU1851	Glycosyl transferase, group 1 family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	0.93	0.28	1.90

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU1854	UDP-glucose/GDP-mannose dehydrogenase family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	0.87	0.42	1.83
GSU2089	Rod shape-determining protein MreB	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	0.72	0.32	1.64
GSU2244	Glycosyl transferase, group 2 family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	0.70	0.23	1.63
GSU2497	Lipoprotein, putative	Cell envelope	Other	0.74	0.23	1.67
GSU2498	Lipoprotein, putative	Cell envelope	Other	0.72	0.18	1.65
GSU0207	Cold-shock domain family protein	Cellular processes	Adaptations to atypical conditions	0.98	0.56	1.97
GSU1330	**Metal ion efflux outer membrane protein family protein, putative**	**Cellular processes**	**Detoxification**	**1.42**	**0.94**	**2.67**
GSU1523	Stationary-phase survival protein sure	Cellular processes	Adaptations to atypical conditions	0.60	0.18	1.52
GSU2223	Chemotaxis protein chey	Cellular processes	Chemotaxis and motility	1.04	0.70	2.05
GSU3206	**dnaK suppressor protein, putative**	**Cellular processes**	**Cell division**	**0.70**	**0.26**	**1.62**
GSU0870	Mutator mutT protein	DNA metabolism	DNA replication, recombination, and repair	0.79	0.24	1.73
GSU1363	RNA-directed DNA polymerase	DNA metabolism	Other	0.92	0.28	1.90
GSU1521	**Integration host factor, alpha subunit**	**DNA metabolism**	**DNA replication, recombination, and repair**	**0.78**	**0.16**	**1.71**
GSU0364	Cytochrome c3	Energy metabolism	Electron transport	0.91	0.26	1.88
GSU0782	Nickel-dependent hydrogenase, small subunit	Energy metabolism	Electron transport	2.73	0.65	6.62
GSU0783	Nickel-dependent hydrogenase, iron-sulfur cluster-binding protein	Energy metabolism	Electron transport	2.01	0.58	4.03

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU0784	Nickel-dependent hydrogenase, membrane protein	Energy metabolism	Electron transport	2.53	0.51	5.79
GSU0785	Nickel-dependent hydrogenase, large subunit	Energy metabolism	Electron transport	1.92	0.47	3.78
GSU1786	Cytochrome c family protein	Energy metabolism	Electron transport	0.64	0.14	1.56
GSU1787	Cytochrome c family protein	Energy metabolism	Electron transport	0.97	0.27	1.96
GSU2501	Cytochrome c family protein	Energy metabolism	Electron transport	0.76	0.22	1.69
GSU2934	Cytochrome c family protein	Energy metabolism	Electron transport	0.74	0.23	1.67
GSU1916	Phosphatidate cytidylyltransferase	Fatty acid and phospholipid metabolism	Biosynthesis	0.63	0.18	1.54
GSU0561	Conserved domain protein	Hypothetical proteins	Domain	1.12	0.43	2.18
GSU0863	Conserved hypothetical protein	Hypothetical proteins	Conserved	0.68	0.30	1.61
GSU1598	Conserved hypothetical protein	Hypothetical proteins	Conserved	0.93	0.34	1.91
GSU1771	Conserved domain protein	Hypothetical proteins	Domain	0.62	0.36	1.54
GSU1889	Conserved hypothetical protein	Hypothetical proteins	Conserved	0.80	0.31	1.74
GSU0943	Hypothetical protein	Hypothetical protein	Hypothetical	0.68	0.20	1.60
GSU0965	Hypothetical protein	Hypothetical protein	Hypothetical	0.71	0.30	1.63
GSU1333	Hypothetical protein	Hypothetical protein	Hypothetical	1.51	1.08	2.84
GSU1339	Hypothetical protein	Hypothetical protein	Hypothetical	1.27	0.64	2.42
GSU2110	Hypothetical protein	Hypothetical protein	Hypothetical	0.66	0.23	1.58
GSU2374	Hypothetical protein	Hypothetical protein	Hypothetical	0.61	0.23	1.53
GSU2377	Hypothetical protein	Hypothetical protein	Hypothetical	0.73	0.24	1.65
GSU2499	Hypothetical protein	Hypothetical protein	Hypothetical	0.80	0.26	1.75
GSU2500	Hypothetical protein	Hypothetical protein	Hypothetical	1.06	0.25	2.09
GSU2780	Hypothetical protein	Hypothetical protein	Hypothetical	1.37	0.68	2.58
GSU2971	Hypothetical protein	Hypothetical protein	Hypothetical	0.71	0.28	1.64
GSU2972	Hypothetical protein	Hypothetical protein	Hypothetical	0.69	0.19	1.61

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU3402	Hypothetical protein	Hypothetical protein	Hypothetical	0.95	0.28	1.93
GSU3403	Hypothetical protein	Hypothetical protein	Hypothetical	2.33	0.64	5.04
GSU1710	Integrative genetic element Gsu5, integrase	Mobile and extrachromosomal element functions	Prophage functions	0.72	0.26	1.65
GSU2471	Group II intron, maturase	Mobile and extrachromosomal element functions	Transposon functions	0.67	0.18	1.59
GSU0538	Heat shock protein, Hsp20 family	Protein fate	Protein folding and stabilization	0.64	0.23	1.55
GSU0786	Hydrogenase maturation protease	Protein fate	Protein modification and repair	1.19	0.59	2.29
GSU1791	ATP-dependent Clp protease, ATP-binding subunit clpx	Protein fate	Degradation of proteins, peptides, and glycopeptides	0.64	0.29	1.56
GSU1792	ATP-dependent Clp protease, proteolytic subunit ClpP	Protein fate	Degradation of proteins, peptides, and glycopeptides	0.86	0.30	1.82
GSU1793	Trigger factor	Protein fate	Protein folding and stabilization and Protein and peptide secretion and trafficking	0.80	0.27	1.74
GSU2408	Heat shock protein, Hsp20 family	Protein fate	Protein folding and stabilization	1.04	0.41	2.06
GSU2410	Heat shock protein, Hsp20 family	Protein fate	Protein folding and stabilization	0.86	0.25	1.81
GSU2835	Methionine aminopeptidase, type I	Protein fate	Protein modification and repair	0.85	0.18	1.80
GSU0037	Seryl-tRNA synthetase	Protein synthesis	tRNA aminoacylation	0.58	0.27	1.50

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU0138	Peptide chain release factor 3	Protein synthesis	Translation factors	0.62	0.20	1.54
GSU0665	Ribosomal protein S6	Protein synthesis	Ribosomal proteins: synthesis and modification	0.89	0.26	1.85
GSU0906	Ribosomal protein S21	Protein synthesis	Ribosomal proteins: synthesis and modification	0.61	0.16	1.53
GSU1515	Threonyl-tRNA synthetase	Protein synthesis	tRNA aminoacylation	0.77	0.21	1.70
GSU1516	Translation initiation factor IF-3	Protein synthesis	Translation factors	0.90	0.42	1.87
GSU1517	Ribosomal protein L35	Protein synthesis	Ribosomal proteins: synthesis and modification	0.90	0.13	1.86
GSU1518	Ribosomal protein L20	Protein synthesis	Ribosomal proteins: synthesis and modification	0.79	0.28	1.73
GSU1810	tRNA(Ile)-lysidine synthetase	Protein synthesis	tRNA and rRNA base modification	1.04	0.49	2.06
GSU1886	Ribosomal subunit interface protein	Protein synthesis	Translation factors	0.78	0.25	1.71
GSU2234	Ribosomal protein L28	Protein synthesis	Ribosomal proteins: synthesis and modification	0.72	0.32	1.65
GSU2619	Queuine tRNA-ribosyltransferase	Protein synthesis	tRNA and rRNA base modification	0.61	0.19	1.53
GSU2847	Ribosomal protein L14	Protein synthesis	Ribosomal proteins: synthesis and modification	0.62	0.21	1.54
GSU2875	Ribosomal protein S9	Protein synthesis	Ribosomal proteins: synthesis and modification	0.61	0.13	1.53
GSU3093	Ribosomal protein S21	Protein synthesis	Ribosomal proteins: synthesis and modification	0.93	0.52	1.91

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU3235	Ribosomal protein L27	Protein synthesis	Ribosomal proteins: synthesis and modification	0.64	0.11	1.55
GSU1110	Nucleoside diphosphate kinase	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	0.77	0.28	1.70
GSU0031	Heat-inducible transcription repressor hrca	Regulatory functions	DNA interactions	0.84	0.16	1.79
GSU0475	Sensory box histidine kinase	Regulatory functions	Protein interactions and Two-component systems	0.95	0.34	1.93
GSU1521	**Integration host factor, alpha subunit**	**Regulatory functions**	**Other**	0.78	0.16	1.71
GSU1522	Transcriptional regulator, putative	Regulatory functions	Other	0.63	0.16	1.55
GSU2540	Transcriptional regulator, Cro/CI family	Regulatory functions	DNA interactions	0.73	0.21	1.65
GSU3206	**dnaK suppressor protein, putative**	**Regulatory functions**	**DNA interactions**	0.70	0.26	1.62
GSU1277	Transcription elongation factor grea	Transcription	Transcription factors	0.75	0.20	1.68
GSU1589	Ribosome-binding factor A	Transcription	RNA processing	0.64	0.26	1.56
GSU1330	**Metal ion efflux outer membrane protein family protein, putative**	**Transport and binding proteins**	**Cations and iron carrying compounds**	1.42	0.94	2.67
GSU1622	L-lactate permease	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	0.74	0.31	1.67
GSU2697	Multidrug resistance protein	Transport and binding proteins	Other	0.78	0.28	1.72
GSU3391	Branched-chain amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	0.62	0.14	1.54
GSU3392	Branched-chain amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	0.65	0.12	1.57

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU3401	Branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein, putative	Transport and binding proteins	Amino acids, peptides and amines	2.47	0.44	5.53
GSU3404	Amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	1.77	0.49	3.42
GSU0065	Cytidine/deoxycytidylate deaminase family protein	Unknown function	Enzymes of unknown specificity	0.57	0.12	1.50
GSU0455	Rare lipoprotein A domain protein	Unknown function	General	0.87	0.19	1.82
GSU1136	5-formyltetrahydrofolate cyclo-ligase family protein	Unknown function	General	0.73	0.16	1.66
GSU1580	ErfK/YbiS/YcfS/YnhG family protein	Unknown function	General	0.72	0.16	1.65
GSU1788	NHL repeat domain protein	Unknown function	General	1.24	0.39	2.36
GSU1794	HAM1 protein	Unknown function	General	1.83	0.28	3.56
GSU2493	NHL repeat domain protein	Unknown function	General	0.63	0.19	1.55
GSU2505	NHL repeat domain protein	Unknown function	General	1.06	0.37	2.09
GSU3078	mraZ protein, putative	Unknown function	General	0.80	0.20	1.74

Table S3. Significant GO terms and TIGR biological role categories from the EASE analysis of down-regulated reporters during growth with fumarate as electron acceptor

System	Gene Category	Probability
GO Biological Process	Electron transport	1.7 E-09
TIGR Role	Energy Metabolism, electron transport	2.5 E-09
GO Molecular Function	Electron transporter activity	3.5 E-06
GO Molecular Function	Transporter activity	5.7 E-05
GO Biological Process	Tricarboxylic acid (TCA) cycle	8.2 E-04
GO Biological Process	Main pathways of carbohydrate metabolism	8.3 E -04
TIGR Role	Energy Metabolism, TCA cycle	1.1 E-03
GO Molecular Function	Branched-chain aliphatic amino acid transporter activity	1.1 E-03
GO Biological Process	Branched-chain aliphatic amino acid transport	1.6 E-03
GO Molecular Function	Solute/sodium symporter activity	1.8 E-03
GO Biological Process	Carboxylic acid transport	1.9 E-03
GO Biological Process	Organic acid transport	1.9 E-03
GO Molecular Function	Pyruvate kinase activity	3.4 E-03
GO Molecular Function	Cytochrome c peroxidase activity	3.4 E-03
GO Molecular Function	Oxidoreductase activity/acting on diphenols and related substances as donors	3.4 E-03
GO Biological Process	Anaerobic electron transport	3.4 E-03
GO Molecular Function	Succinate-CoA ligase (ADP-forming) activity	3.4 E-03
GO Molecular Function	Succinate-CoA ligase activity	3.4 E-03
GO Molecular Function	Solute/cation symporter activity	3.4 E-03
GO Molecular Function	Symporter activity	3.4 E-03
GO Biological Process	Amino acid transport	3.8E-03
GO Biological Process	Amine/polyamine transport	4.6 E-03
GO Biological Process	Energy derivation by oxidation of organic compounds	4.8 E-03
GO Biological Process	Energy pathways	4.8 E-03
GO Molecular Function	Organic acid transporter activity	7.8 E-03
GO Molecular Function	Carboxylic acid transporter activity	7.8 E-03
TIGR Role	Transport and binding proteins, amino acids, peptides and amines	8.6 E-03
GO Molecular Function	CoA-ligase activity	9.7 E-03
GO Molecular Function	Acid-thiol ligase activity	9.7 E-03

Table S4. Significant GO terms and TIGR biological role categories from the EASE analysis of up-regulated reporters during growth with fumarate as electron acceptor

System	**Gene Category**	**Probability**
GO Biological Process	Protein metabolism	6.5 E-08
GO Biological Process	Protein biosynthesis	3.6 E-06
GO Biological Process	Macromolecule biosynthesis	3.6 E-06
GO Biological Process	Cell organization and biogenesis	6.6 E-06
GO Molecular Function	Structural constituent of ribosome	7.3 E-06
GO Biological Process	Ribosome biogenesis	8.8 E-06
TIGR Role	Protein synthesis, synthesis and modification	1.2 E-05
GO Biological Process	Ribosome biogenesis and assembly	1.5 E-05
GO Biological Process	Cytoplasm organization and biogenesis	1.7 E-05
GO Molecular Function	Heat shock proteins activity	1.4 E-04
GO Molecular Function	Structural molecule activity	1.7 E-04
GO Molecular Component	Ribosome	2.2 E-04
GO Molecular Component	Ribonucleoprotein complex	2.2 E-04
GO Molecular Function	Chaperone activity	2.4 E-04
GO Molecular Component	Intracellular	8.1 E-04
GO Molecular Component	Cytosolic ribosome (sensu Bacteria)	8.9 E-04
GO Molecular Component	Cytosol	8.9 E-04

Table S5. Reporters (amplicons representing genes and intergenic regions) whose expression was significantly decreased (activated by RpoS) in each biological replicate of the *G. sulfurreducens rpoS* mutant versus the wild type for cells grown with acetate as the electron donor and Fe(III) as electron acceptor. Results are sorted first by mainrole category, then in ascending order by Locus ID. Reporters in bold have been assigned more than one mainrole category.

Locus ID	**Common name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Change**
GSU3194	Thiamine monophosphate kinase	Biosynthesis of cofactors, prosthetic groups, and carriers	Thiamine	-1.33	0.36	-2.52
GSU0727	Lipoprotein, putative	Cell envelope	Other	-1.01	0.15	-2.01
GSU1817	Outer membrane lipoprotein, Slp family, putative	Cell envelope	Other	-1.03	0.28	-2.05
GSU1970	Polysaccharide biosynthesis protein, putative	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-1.35	0.31	-2.55
GSU1975	**NAD-dependent epimerase/dehydratase family protein**	**Cell envelope**	**Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides**	**-1.12**	**0.46**	**-2.17**
GSU1983	Polysaccharide biosynthesis protein, putative	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-0.95	0.42	-1.93
GSU2584	Lipoprotein, putative	Cell envelope	Other	-1.18	0.50	-2.27
GSU2633	Lipoprotein, putative	Cell envelope	Other	-1.74	0.46	-3.35
GSU0726	Chemotaxis protein ched, putative	Cellular processes	Chemotaxis and motility	-1.85	0.77	-3.60
GSU0067	Carbonic anhydrase	Central intermediary metabolism	Other	-1.97	0.60	-3.92

Locus ID	Common name	Mainrole	Subrole	Mean log$_2$ Ratio	SD	Fold Change
GSU0997	Formamidopyrimidine-DNA glycosylase	DNA metabolism	DNA replication, recombination, and repair	-1.43	0.37	-2.70
GSU2829	Deoxyribodipyrimidine photolyase, putative	DNA metabolism	DNA replication, recombination, and repair	-1.03	0.20	-2.04
GSU0201	Isoquinoline 1-oxidoreductase, beta subunit	Energy metabolism	Fermentation	-1.62	0.63	-3.08
GSU0219	Cytochrome c oxidase, subunit I	Energy metabolism	Electron transport	-1.35	0.35	-2.54
GSU0222	Cytochrome c oxidase, subunit II	Energy metabolism	Electron transport	-2.74	0.16	-6.67
GSU0357	Cytochrome c family protein	Energy metabolism	Electron transport	-1.67	0.77	-3.19
GSU0466	Cytochrome c551 peroxidase, MacA	Energy metabolism	Electron transport	-2.00	0.39	-4.01
GSU0674	Prismane protein	Energy metabolism	Electron transport	-1.82	1.46	-3.53
GSU0803	Phosphoenolpyruvate synthase	Energy metabolism	Glycolysis/gluconeogenesis	-1.45	0.43	-2.74
GSU0843	NADH oxidase, putative	Energy metabolism	Electron transport	-1.13	0.17	-2.19
GSU0845	Rieske 2Fe-2S family protein	Energy metabolism	Electron transport	-0.95	0.19	-1.93
GSU0846	Aconitate hydratase 1	Energy metabolism	TCA cycle	-1.32	0.21	-2.50
GSU0911	Iron-sulfur cluster-binding protein	Energy metabolism	Electron transport	-1.11	0.31	-2.15
GSU1024	Cytochrome c3	Energy metabolism	Electron transport	-1.66	0.47	-3.16
GSU1058	Succinyl-coa synthase, beta subunit	Energy metabolism	TCA cycle	-1.56	0.36	-2.94
GSU1059	Succinyl-coa synthase, alpha subunit	Energy metabolism	TCA cycle	-1.63	0.40	-3.10
GSU1397	Cytochrome c family protein, putative	Energy metabolism	Electron transport	-2.62	0.52	-6.15
GSU1538	Methylamine utilization protein maug, putative	Energy metabolism	Amino acids and amines	-3.09	0.75	-8.53
GSU1648	Cytochrome c family protein	Energy metabolism	Electron transport	-1.37	0.23	-2.58
GSU1649	Cytochrome b/b6	Energy metabolism	Electron transport	-1.57	0.52	-2.96
GSU1650	Cytochrome b/b6 complex, iron-sulfur subunit	Energy metabolism	Electron transport	-0.91	0.35	-1.87
GSU2737	Polyheme					
GSU1975	**NAD-dependent epimerase/dehydratase family protein**	**Energy metabolism**	**Sugars**	**-1.12**	**0.46**	**-2.17**
GSU2445	Aconitate hydratase, putative	Energy metabolism	TCA cycle	-1.56	0.38	-2.96
GSU2449	2-oxoglutarate dehydrogenase, E1 component	Energy metabolism	TCA cycle	-1.05	0.22	-2.06
GSU2725	Cytochrome c family protein	Energy metabolism	Electron transport	-1.69	0.32	-3.23

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU2731	polyheme membrane-associated cytochrome c, OmcC	Energy metabolism	Electron transport	-3.75	0.15	-13.5
GSU2732	Cytochrome c family protein	Energy metabolism	Electron transport	-2.23	0.34	-4.68
GSU2738	Cytochrome c family protein	Energy metabolism	Electron transport	-2.02	0.39	-4.05
GSU2743	Cytochrome c family protein	Energy metabolism	Electron transport	-1.79	0.61	-3.45
GSU2811	Cytochrome c Hsc	Energy metabolism	Electron transport	-1.51	0.34	-2.86
GSU2812	Glutaredoxin family protein	Energy metabolism	Electron transport	-1.11	0.31	-2.15
GSU2813	Cytochrome c551 peroxidase	Energy metabolism	Electron transport	-1.59	0.31	-3.02
GSU3137	Cytochrome c family protein	Energy metabolism	Electron transport	-0.69	0.15	-1.62
GSU3187	Ferredoxin family protein	Energy metabolism	Electron transport	-0.88	0.36	-1.85
GSU3254	Phosphoglucomutase/phosphomannomutase family protein	Energy metabolism	Sugars	-1.13	0.41	-2.19
GSU0202	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.45	0.57	-2.74
GSU0218	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.64	0.44	-3.11
GSU0478	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.87	0.18	-1.82
GSU0813	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.08	0.36	-2.12
GSU0817	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.77	0.19	-1.70
GSU0849	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.39	0.39	-2.62
GSU0982	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.68	0.17	-1.61
GSU1087	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.65	0.13	-1.57
GSU1167	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.03	0.60	-2.04
GSU1642	Conserved hypothetical protein	Hypothetical proteins	Conserved	-2.11	0.54	-4.31
GSU2193	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.24	0.41	-2.36
GSU2347	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.29	0.30	-2.44
GSU2437	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.01	0.24	-2.01
GSU2788	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.58	0.36	-2.98
GSU3139	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.29	0.14	-2.44

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU3151	Conserved hypothetical protein	Hypothetical proteins	Conserved	-1.11	0.34	-2.16
GSU3251	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.95	0.20	-1.93
GSU3255	Conserved hypothetical protein	Hypothetical proteins	Conserved	-0.83	0.27	-1.78
GSU3289	Conserved hypothetical protein	Hypothetical proteins	Conserved	-2.32	0.64	-5.01
GSU0077	Hypothetical protein	Hypothetical protein	Hypothetical	-1.13	0.23	-2.18
GSU0078	Hypothetical protein	Hypothetical protein	Hypothetical	-1.18	0.38	-2.26
GSU0712	Hypothetical protein	Hypothetical protein	Hypothetical	-1.64	0.60	-3.11
GSU0713	Hypothetical protein	Hypothetical protein	Hypothetical	-1.82	0.29	-3.54
GSU0714	Hypothetical protein	Hypothetical protein	Hypothetical	-2.72	0.72	-6.58
GSU0715	Hypothetical protein	Hypothetical protein	Hypothetical	-3.41	0.96	-10.60
GSU0716	Hypothetical protein	Hypothetical protein	Hypothetical	-2.95	0.67	-7.75
GSU0719	Hypothetical protein	Hypothetical protein	Hypothetical	-1.95	0.38	-3.87
GSU0790	Hypothetical protein	Hypothetical protein	Hypothetical	-1.76	0.62	-3.39
GSU0990	Hypothetical protein	Hypothetical protein	Hypothetical	-0.90	0.21	-1.87
GSU1395	Hypothetical protein	Hypothetical protein	Hypothetical	-1.61	0.75	-3.05
GSU1396	Hypothetical protein	Hypothetical protein	Hypothetical	-1.59	0.48	-3.01
GSU1558	Hypothetical protein	Hypothetical protein	Hypothetical	-1.40	0.50	-2.65
GSU1969	Hypothetical protein	Hypothetical protein	Hypothetical	-1.57	0.46	-2.98
GSU1994	Hypothetical protein	Hypothetical protein	Hypothetical	-1.64	0.77	-3.13
GSU2412	Hypothetical protein	Hypothetical protein	Hypothetical	-1.06	0.32	-2.08
GSU2726	Hypothetical protein	Hypothetical protein	Hypothetical	-2.68	0.62	-6.39
GSU2730	Hypothetical protein	Hypothetical protein	Hypothetical	-1.07	0.28	-2.09
GSU2733	Hypothetical protein	Hypothetical protein	Hypothetical	-2.02	0.42	-4.06
GSU2739	Hypothetical protein	Hypothetical protein	Hypothetical	-2.29	0.37	-4.90
GSU2742	Hypothetical protein	Hypothetical protein	Hypothetical	-2.10	0.44	-4.28
GSU3189	Hypothetical protein	Hypothetical protein	Hypothetical	-0.69	0.26	-1.61

Locus ID	**Common name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Change**
GSU3341	Hypothetical protein	Hypothetical protein	Hypothetical	-2.37	0.34	-5.18
GSU3344	Hypothetical protein	Hypothetical protein	Hypothetical	-1.56	0.34	-2.95
GSU3351	Hypothetical protein	Hypothetical protein	Hypothetical	-1.09	0.44	-2.13
GSU0538	Heat shock protein, Hsp20 family	Protein fate	Protein folding and stabilization	-0.77	0.21	-1.70
GSU0658	Clpb protein	Protein fate	Degradation of proteins, peptides, and glycopeptides	-0.93	0.17	-1.91
GSU3140	Peptidase, M1 family protein	Protein fate	Degradation of proteins, peptides, and glycopeptides	-1.43	0.28	-2.69
GSU3193	ATP-dependent protease La	Protein fate	Degradation of proteins, peptides, and glycopeptides	-1.50	0.22	-2.83
GSU0079	Transcriptional regulator, Cro/CI family	Regulatory functions	DNA interactions	-1.61	0.39	-3.04
GSU0700	Sensory box/response regulator	Regulatory functions	Small molecule interactions and Two-component systems	-2.42	1.68	-5.34
GSU0789	Response regulator	Regulatory functions	Protein interactions and Two-component systems	-0.84	0.42	-1.79
GSU0841	Sigma-54 dependent DNA-binding response regulator	Regulatory functions	Protein interactions and Two-component systems	-0.76	0.14	-1.70
GSU1414	Sensory box histidine kinase/response regulator	Regulatory functions	Small molecule interactions and Two-component systems	-0.97	0.27	-1.96
GSU2964	**Molybdenum transport regulatory protein mode**	**Regulatory functions**	**DNA interactions**	**-1.64**	**0.45**	**-3.11**
GSU2444	Sensor histidine kinase	Regulatory functions	Protein interactions	-1.10	0.26	-2.14
GSU0718	Sensory box histidine kinase/response regulator	Signal transduction	Two-component systems	-2.51	1.17	-5.69
GSU0842	Sensory box histidine kinase/response regulator	Signal transduction	Two-component systems	-2.00	0.16	-4.00
GSU1119	Sensor histidine kinase/response regulator	Signal transduction	Two-component systems	-0.94	0.16	-1.92
GSU1415	Response regulator	Signal transduction	Two-component systems	-1.33	0.45	-2.51
GSU3138	Sensor histidine kinase/response regulator	Signal transduction	Two-component systems	-1.36	0.42	-2.57

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU0496	Efflux transporter, RND family, MFP subunit	Transport and binding proteins	Unknown substrate	-0.84	0.14	-1.79
GSU072	Desulfoferrodoxin ferrous iron-binding domain	Transport and binding proteins	Cations and iron carrying compounds	-2.09	0.77	-4.27
GSU0816	ABC transporter, ATP-binding protein	Transport and binding proteins	Unknown substrate	-1.26	0.24	-2.39
GSU0844	Potassium uptake protein, Trk family	Transport and binding proteins	Cations and iron carrying compounds	-1.26	0.20	-2.40
GSU1016	Potassium uptake protein, Trk family	Transport and binding proteins	Cations and iron carrying compounds	-0.97	0.15	-1.96
GSU1307	Ferritin	Transport and binding proteins	Cations and iron carrying compounds	-1.65	0.36	-3.13
GSU2649	Amino acid ABC transporter, amino acid-binding protein	Transport and binding proteins	Amino acids, peptides and amines	-3.17	0.78	-8.99
GSU2650	Amino acid ABC transporter, permease protein, putative	Transport and binding proteins	Amino acids, peptides and amines	-2.22	0.76	-4.66
GSU2964	**Molybdenum transport regulatory protein mode**	**Transport and binding proteins**	**Anions**	**-1.64**	**0.45**	**-3.11**
GSU3346	Potassium uptake protein, Kup system	Transport and binding proteins	Cations and iron carrying compounds	-1.26	0.20	-2.39
GSU0066	Ahpc/Tsa family protein, selenocysteine-containing	Unknown function	General	-1.47	0.46	-2.77
GSU0217	Nitroreductase family protein	Unknown function	Enzymes of unknown specificity	-1.48	0.43	-2.79
GSU0360	Ompa domain protein	Unknown function	General	-2.33	1.41	-5.03
GSU0477	Hydrolase, haloacid dehalogenase-like family	Unknown function	Enzymes of unknown specificity	-1.69	1.04	-3.22

Locus ID	Common name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU0711	Endonuclease/exonuclease/phosphatase family protein	Unknown function	Enzymes of unknown specificity	-1.53	0.34	-2.89
GSU0767	Tia invasion determinant-related protein	Unknown function	General	-0.71	0.20	-1.64
GSU0810	Ompa domain protein	Unknown function	General	-1.61	0.42	-3.04
GSU0909	Pyridine nucleotide-disulphide oxidoreductase family protein	Unknown function	Enzymes of unknown specificity	-1.67	0.23	-3.19
GSU0972	Atpase, AAA family	Unknown function	General	-0.74	0.19	-1.67
GSU0989	NHL repeat domain protein	Unknown function	General	-0.73	0.17	-1.66
GSU1007	GAF domain/HD domain protein	Unknown function	General	-0.70	0.14	-1.62
GSU1014	Smr domain protein	Unknown function	General	-0.75	0.33	-1.68
GSU1394	Laccase family protein	Unknown function	General	-2.12	0.68	-4.34
GSU1950	Capk related-protein	Unknown function	General	-0.78	0.23	-1.71
GSU1968	Nucleotidyltransferase family protein	Unknown function	Enzymes of unknown specificity	-1.03	0.25	-2.04
GSU1974	Degt/dnrj/eryc1/strs family protein	Unknown function	General	-1.10	0.44	-2.14
GSU1982	General secretion pathway protein-related protein	Unknown function	General	-1.06	0.35	-2.09
GSU1986	Glycosyl transferase domain protein	Unknown function	General	-1.13	0.68	-2.19
GSU1991	CAAX amino terminal protease family protein	Unknown function	General	-0.57	0.11	-1.48
GSU2436	Dehydrogenase complex, E1 component, beta subunit	Unknown function	Enzymes of unknown specificity	-1.25	0.24	-2.37
GSU2443	Dehydrogenase complex, E1 component, alpha subunit	Unknown function	Enzymes of unknown specificity	-0.97	0.23	-1.97
GSU3343	Spovr-like family protein	Unknown function	General	-1.92	0.54	-3.79
[a]R00118	Null	Null	Null	-1.75	0.55	-3.35

[a] intergenic region

Table S6. Reporters (amplicons representing genes and intergenic regions) whose expression was significantly increased (repressed by RpoS) in each biological replicate of the *G. sulfurreducens rpoS* mutant versus the wild type for cells grown with acetate as the electron donor and Fe(III) as electron acceptor. Results are sorted first by mainrole category, then in ascending order by Locus ID.

Locus ID	**Common Name**	**Mainrole**	**Subrole**	**Mean $\log_2$ Ratio**	**SD**	**Fold Change**
GSU0268	Membrane protein, putative	Cell envelope	Other	0.64	0.15	1.56
GSU1489	Membrane protein, putative	Cell envelope	Other	0.70	0.06	1.63
GSU1499	Membrane protein, putative	Cell envelope	Other	0.98	0.17	1.98
GSU1783	Type IV pilus biogenesis protein pilb, putative	Cell envelope	Surface structures	0.62	0.09	1.54
GSU1789	Glycosyl transferase, group 2 family protein	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	0.99	0.27	1.98
GSU1996	Cytochrome c family protein	Energy metabolism	Electron transport	0.66	0.18	1.58
GSU0943	Hypothetical protein	Hypothetical proteins	Hypothetical	0.64	0.20	1.55
GSU1011	Hypothetical protein	Hypothetical proteins	Hypothetical	0.76	0.15	1.69
GSU1652	Hypothetical protein	Hypothetical proteins	Hypothetical	0.59	0.15	1.51
GSU2747	Hypothetical protein	Hypothetical proteins	Hypothetical	1.28	0.52	2.43
GSU3402	Hypothetical protein	Hypothetical proteins	Hypothetical	2.30	0.38	4.91
GSU3403	Hypothetical protein	Hypothetical proteins	Hypothetical	2.75	0.19	6.75
GSU1793	Trigger factor	Protein fate	Protein folding and stabilization and Protein and peptide secretion and trafficking	0.90	0.25	1.87
GSU2839	Ribosomal protein L30	Protein synthesis	Ribosomal proteins: synthesis and modification	0.62	0.16	1.54

Locus ID	Common Name	Mainrole	Subrole	Mean $\log_2$ Ratio	SD	Fold Change
GSU1630	Sensory box histidine kinase	Regulatory functions	Protein interactions	0.58	0.09	1.50
GSU1795	Ribonuclease PH	Transcription	RNA processing	0.96	0.22	1.94
GSU3401	Branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein, putative	Transport and binding proteins	Amino acids, peptides and amines	3.00	0.22	8.02
GSU3404	Amino acid ABC transporter, ATP-binding protein	Transport and binding proteins	Amino acids, peptides and amines	2.32	0.33	4.99
GSU3405	Amino acid ABC transporter, permease protein	Transport and binding proteins	Amino acids, peptides and amines	0.98	0.24	1.97
GSU1736	ACT domain protein	Unknown function	General	0.62	0.17	1.54
GSU1788	NHL repeat domain protein	Unknown function	General	0.97	0.15	1.96
GSU1794	HAM1 protein	Unknown function	General	0.87	0.16	1.83
GSU1796	DHH family protein	Unknown function	General	1.58	0.60	2.99
GSU2516	Rhodanese-like domain protein	Unknown function	General	1.03	0.18	2.04
[a]R02992	Null			0.76	0.18	1.69

[a] Intergenic region

Table S7. Significant GO terms and TIGR biological role categories from the EASE analysis of down-regulated reporters during growth with Fe(III) as electron acceptor

System	**Gene Category**	**Probability**
GO Biological Process	Electron transport	4.2 E-07
TIGR Role	Energy metabolism, electron transport	5.6 E-05
GO Biological Process	Tricarboxylic acid (TCA) cycle	1.3 E-04
TIGR Role	Energy metabolism, TCA cycle	1.9 E-04
GO Molecular Function	Electron transporter activity	3.4 E-04
GO Molecular Function	Succinate-CoA ligase activity	1.6 E-03
GO Molecular Function	Succinate-CoA ligase (ADP-forming) activity	1.6 E-03
GO Molecular Function	Cytochrome c peroxidase activity	1.6 E-03
GO Biological Process	Main pathways of carbohydrate metabolism	2.5 E-03
GO Molecular Function	Two-component response regulator activity	3.8 E-03
GO Molecular Function	Acid-thiol ligase activity	4.6 E-03
GO Molecular Function	CoA-ligase activity	4.6 E-03
GO Molecular Function	Aconitate hydratase activity	4.6 E-03
GO Molecular Function	Potassium ion transporter activity	5.9 E-03
GO Biological Process	Potassium ion transport	5.9 E-03
GO Molecular Function	Ligase activity/forming carbon-sulfur bonds	8.9 E-03

Table S8. Significant GO terms and TIGR biological role categories from the EASE analysis of up-regulated reporters during growth with Fe(III) as electron acceptor

System	**Gene Category**	**Probability**
GO Molecular Function	Amino acid transporter activity	4.7 E-04
GO Molecular Function	Amine/polyamine transporter activity	5.3 E-04
GO Biological Process	Amino acid transport	5.9 E-04
GO Biological Process	Amine/polyamine transport	6.6 E-04
GO Molecular Function	Organic Acid transporter activity	9.0 E-04
GO Molecular Function	Carboxylic acid transporter activity	9.0 E-04
TIGR Role	Transport and binding proteins, amino acids, peptides and amines	9.5 E-04
GO Biological Process	Carboxylic acid transport	9.9 E-04
GO Biological Process	Organic acid transport	9.9 E-04