## Supplemental Methods

### Generation of the *cycA* complementing plasmid, pMO738, and the CycA complemented strain.

A 763-bp fragment containing the *cycA* gene and 343 bp of upstream DNA assumed to contain the *cycA* promoter, was amplified by Herc II polymerase (Stratagene, La Jolla, CA) with primers Dde_3182F and Dde_3182R (Table S1) and cloned into pCR4Blunt-TOPO (Invitrogen, Carlsbad, CA). The recombinant plasmid was transformed into One Shot® TOP10 Competent Cells (Invitrogen) and plated on LC with 50 μg kanamycin/ml. Individual transformants were screened by colony PCR (2) to identify plasmids containing the proper sized amplicon and then the cloned gene verified by sequencing both strands. All sequencing was performed at the DNA Core Facility at the University of Missouri. One plasmid isolate was kept as the source of *cycA* gene and named pMO736.

The *cycA* gene, expressed from its native promoter, was removed from pMO736 by restriction enzyme digests and ligated into the EcoRV site of pMO719, a plasmid containing a G20 replicon allowing maintenance in SRB strains. After selection of the recombinant plasmid and verification of the insert sequence, one isolate was named pMO738.

To obtain a complemented *cycA* mutant, I2 cells were transformed with pMO738 by electroporation as previously described (2), with the following exceptions. Rich lactate/sulfate (60/30) medium was used (instead of rich lactate/sulfite (60/40) medium) throughout growth, electroporation, recovery and selective plating of I2 and the electroporation parameters were set at 1550 V, 250 Ω, and 25 μF. Electroporated I2 cells recovered overnight in the presence of 800 μg kanamycin/ml and the final selection for maintenance of pMO738 was accomplished by plating with 800 μg kanamycin/ml and 800 μg spectinomycin/ml. The plasmids were isolated from $Km^r/Sp^r$ transformants, transformed back into Alpha-Select™ Bronze Efficiency *E. coli* cells (Bioline), re-isolated and sequenced. Sequencing revealed all the plasmid sequences matched the original pMO738 and one isolate was chosen as the complemented strain, I2 (pMO738), for comparison of phenotypes.

## Generation of pMO9075, the complementation shuttle vector

In order to remove sequence repeats that resulted from the generation of pMO9072, sequential restriction digests and re-ligations were performed on pMO9072 to generate the complementation shuttle vector pMO9075 (Fig. S1). Initially, pMO9072 was digested with both EcoRV and BspEI (Fig. S1A), the linear fragment was purified, the ends from BspEI were made blunt, and then the remaining plasmid was re-ligated together. The newly constructed plasmid was captured in Alpha-Select™ Bronze Efficiency cells on LC plates containing 100 µg spectinomycin/ml. Plasmid was prepared from the cells, and primers pMO9075_F and pMO9075_R (Table S1) were used to verify the appropriate removal of the 125bp fragment by sequencing. The resulting intermediate plasmid was named pMO9072.5. A digestion with HpaI and XmnI was performed on pMO9072.5 (Figure S1B), the linear fragment was purified, then re-ligated and the newly constructed plasmid was captured in Alpha-Select™ Bronze Efficiency cells on LC plates containing 100 µg spectinomycin/ml. Plasmid was prepared from the cells, and primers pMO9073_F and pMO9073_R (Table S1) were used to verify the appropriate removal of the 307bp fragment by sequencing, and the resulting plasmid named pMO9073 (Fig. S1C). The last repeat sequence was removed by performing an EcoRI digest on pMO9073, the linear fragment was purified, then re-ligated and the newly constructed plasmid was captured in Alpha-Select™ Bronze Efficiency cells on LC plates containing 100 µg spectinomycin/ml. Plasmid was prepared from the cells, and primers pMO9075_F and pMO9075_R (Table S1) were used to verify the appropriate removal of the 289bp fragment by sequencing, and the resulting plasmid named pMO9075 (Fig. S1D).

## Generation of the *qrcA* complementing plasmid, pMO756

The *qrcA* gene (Dde_2932) was amplified by Herc II polymerase with the primers 2932_SLICF and 2932_SLICR (Table S1). To generate the complementation plasmid, the pMO9075 plasmid was amplified in two fragments by Herc II polymerase. Fragment 1 (2781bp) was amplified with the primers pMO9075_ SLIC_1F and pMO9075_ SLIC_2R; while fragment 2 (2080 bp) was amplified with the primers pMO9075_ SLIC_3F and pMO9075_ SLIC_4R, and both fragments were gel purified. The SLIC method (3) was used to join the three DNA fragments together by transformingequal molar ratios of the three. Briefly, the PCR products were cleaned using Wizard SV Gel and PCR clean-up system (Promega) and quantified. All three fragments were added in equal ratios (~400ng) and water added to make the final volume 15 µl. A T4 DNA polymerase prep mix was prepared freshly (6 µl BSA (1mg/ml), 6 µl NEB Buffer 2 (10x), 2.5 µl sterile deionized water, and 0.5 µl T4 DNA polymerase (3U/µl)) and then 5 µl of this "T4 prep mix" was added to the tube with the fragments. The mixture was allowed to incubate at room temperature for 30 minutes and the reaction stopped by the addition of 2 µl of dCTP (10 mM stock). To 50 µl of Alpha-Select™ Silver Efficiency *E. coli* cells, 5 µl of the reaction mixture was added and the cells transformed as described in the Bioline protocol. Following recovery, the cells were plated on LC plates containing 100 µg spectinomycin/ml. Individual Spectinomycin resistant transformants were screened by colony PCR (primers pMO9075_F and pMO9075_R) to identify those containing the appropriately sized insertion fragment and the cloned gene verified by sequencing both strands. The resulting plasmid was named pMO756.

To obtain a complemented *qrcA* mutant, cells were transformed with pMO756 by electroporation as previously described above for the I2 complementation with the following exceptions. The electroporation parameters were set at 1500 V, 250 Ω, and 25 µF. Electroporated QrcA mutant cells were recovered overnight in rich lactate/sulfate (60/30) medium and the final selection for maintenance of pMO756 was accomplished by plating with 800 µg kanamycin/ml and 800 µg spectinomycin/ml. The plasmids were isolated from Km$^r$/Sp$^r$ transformants, transformed back into Alpha-Select™ Bronze Efficiency *E. coli* cells, re-isolated and sequenced. Sequencing revealed all the plasmid sequences matched the original pMO756 and one isolate was chosen as the complemented strain, QrcA (pMO756), for comparison of phenotypes.

# Supplemental References

1. **Hauser, L. J., M. L. Land, S. D. Brown, F. Larimer, K. L. Keller, B. J. Rapp-Giles, M. N. Price, M. Lin, D. C. Bruce, J. C. Detter, R. Tapia, C. S. Han, L. A. Goodwin, J-F. Cheng, S. Pitluck, A. Copeland, S. Lucas, M. Nolan, A. L. Lapidus, A, V. Palumbo and J. D. Wall.** 2011. Complete genome sequence and updated annotation of *Desulfovibrio alaskensis* G20. J. Bacteriol. **193:**4268-4269.

2. **Keller, K. L., and J. D. Wall**. 2011. Genetics and molecular biology of the electron flow for sulfate respiration in *Desulfovibrio*. Front. Microbiol. **2:**135, 10.3389/fmicb.2011.00135.

3. **Li, M. Z., and S. J. Elledge.** 2007. Harnessing homologous recombination in vitro to generate recombinant DNA via SLIC. Nat. Methods **4:** 251–256.

4. **Yang, S., T. J. Tschaplinski, N. L. Engle, S. L. Carroll, S. L. Martin, B. H. Davison, A. V. Palumbo, M. J. Rodriguez, and S. D. Brown.** 2009. Transcriptomic and metabolomic profiling of *Zymomonas mobilis* during aerobic and anaerobic fermentation. BMC Genomics **10:**34.

**Supplemental Table 1. Primers used in this study**

| Target | Nucleotide Sequence (5’ – 3’) | Target/Use |
|---|---|---|
| Dde_3182F | AGGTGGACATGCTCTCCATTGTGA | Amplifying *cycA* gene |
| Dde_3182R | CTCGAACAAGCAAATCCGGACCAGT | Amplifying *cycA* gene |
| Dde_2932F | ATGGAGGACAGGCATTTAGACAGTTCA | Amplifying *qrcA* gene |
| Dde_2932R | CCTGCGACGAACTTCATGAATCCTCT | Amplifying *qrcA* gene |
| 2932_SLICF | GCCCTGCAA**TGCAGTCCCAGGAGGTACCAT**ATGGAGGACAGGCATTTAGACAGTTCA | Amplifying *qrcA* gene with overlaps required for SLIC |
| 2932_SLICR | GATCGTGATCCCCTGCGCCATCAGATCCTTGCCTGCGACGAACTTCATGAATCCTCT | Amplifying *qrcA* gene with overlaps required for SLIC |
| pMO9075_SLIC_1F | CAAGGATCTGATGGCGCAGGG | Amplifying the pBG1 backbone fragment for SLIC from pMO9075 |
| pMO9075_SLIC_2R | GGCCTTTTGCTGGCCTTTTGCTCACAT | Amplifying the pBG1 backbone fragment for SLIC from pMO9075 |
| pMO9075_SLIC_3F | ATGTGAGCAAAAGGCCAGCAAAAGGC | Amplifying the *spec* gene and pUC ori backbone fragment for SLIC from pMO9075 |
| pMO9075_SLIC_4R | **ATGGTACCTCCTGGGACTGCA**TTGCAGGGCTTCCCAACCT | Amplifying the *spec* gene and pUC ori backbone fragment for SLIC from pMO9075 |
| pCR4_F | GCTATGACCATGATTACGCCAAGCTCAG | Screening inserts in pCR4 |
| pCR4_R | ACGGCCAGTGAATTGTAATACGACTCAC | Screening inserts in pCR4 |
| pMO719_F | GCTTGAATTCGACCCAGCTTTCTTGT | Screening inserts into EcoRV site of pMO719 |
| pMO719_R | ATTTCTGTCCTGGCTGGTCTAGAGG | Screening inserts into EcoRV site of pMO719 |
| pMO9073_F | GCAGCTGGCACGACAGGTTT | Screening for deletions from pMO9702.5 in the generation of pMO9073 |
| pMO9073_R | CACCCAAAGGCTACACCACGTAC | Screening for deletions from pMO9702.5 in the generation of pMO9073 |

| | | |
|---|---|---|
| pMO9075_F | GCTGAAAGCGAGAAGAGCGCAC | Screening for deletions from pMO9702, pMO9073 and inserts into pMO9075 |
| pMO9075_R | TGGGTTCGTGCCTTCATCCG | Screening for deletions from pMO9702, pMO9073 and inserts into pMO9075 |
| Dde_0717F | TGCACAAGGAGCAGTTCAAG | Amplify Dde_0717 by qRT-PCR[a] |
| Dde_0717R | GACCAGCCAGTCCAGCTTAC | Amplify Dde_0717 by qRT-PCR |
| Dde_1074F | GCTGTCCGTCTTCATCATTCTC | Amplify Dde_1074 by qRT-PCR |
| Dde_1074R | ATACAAACGTGGCGCCTACTAC | Amplify Dde_1074 by qRT-PCR |
| Dde_1110F | AGCCCACCATCAAAGAACAC | Amplify Dde_1110 by qRT-PCR |
| Dde_1110R | AGCATATTTGTCAGCCCAGC | Amplify Dde_1110 by qRT-PCR |
| Dde_1253F | GTCATTCCCGTAAAACCGTG | Amplify Dde_1253 by qRT-PCR |
| Dde_1253R | TGGAAGGGTCTTCCTTGATG | Amplify Dde_1253 by qRT-PCR |
| Dde_2234F | TCCGCCGTGAAATATCTAGC | Amplify Dde_2234 by qRT-PCR |
| Dde_2234R | CTGACCTCTAGCAGGCAACC | Amplify Dde_2234 by qRT-PCR |
| Dde_2265F | CAACCTTCCGCCAGAACTAC | Amplify Dde_2265 by qRT-PCR |
| Dde_2265R | GGTCTGGGCTTCGAACATAC | Amplify Dde_2265 by qRT-PCR |
| Dde_2272F | AGCCGGTGTCCAACTGTAAC | Amplify Dde_2272 by qRT-PCR |
| Dde_2272R | CTTCGATGTCGTCACACAGG | Amplify Dde_2272by qRT-PCR |
| Dde_3103F | GATTCCGGGCTTTGAATACC | Amplify Dde_3103 by qRT-PCR |
| Dde_3103R | CAGTGTACATGAGCGGCTTG | Amplify Dde_3103 by qRT-PCR |
| Dde_3156F | TATGCCGACTACAGAGCACG | Amplify Dde_3156 by qRT-PCR |
| Dde_3156R | TTATTGGTGGAGGTGGATGC | Amplify Dde_3156 by qRT-PCR |

[a] Primer pairs for qRT-PCR were designed as described (4).

**Bold** print indicates the ribosomal binding site (TGCAGTCCCAGGAGGTACCAT) with the primer

**Supplemental Table 2. Change in gene annotations as per M. Price[a]**

| Locus | Original Annotation | | Reannotation | |
|---|---|---|---|---|
| Dde_0473 | FhcA | Formate dehydrogenase | FhcA | Putative cytoplasmic formate:hydrogen lyase, formate dehydrogenase subunit |
| Dde_0474 | FhcD | Formate dehydrogenase, chain A | FhcB | Putative cytoplasmic formate:hydrogen lyase, FeS subunit 1 |
| Dde_0475 | FhcB | Hydrogenase, FeS protein | FhcC | Putative cytoplasmic formate:hydrogen lyase, hydrogenase subunit |
| Dde_0476 | FhcC | [Fe] hydrogenase, large and small subunits | FhcD | Putative cytoplasmic formate:hydrogen lyase, FeS subunit 2 |
| Dde_1250 | GltA | Glutamate synthase (NADPH), homotetrameric | NfnA-2 | Electron-bifurcating transhydrogenase 2, subunit |
| Dde_1251 | COG-UbiB | Oxidoreductase, FAD-binding | NfnB-2 | Electron-bifurcating transhydrogenase 2, subunit |
| Dde_1252 | COG-CitT | Cation transporter | COG-CitT | Malate/fumarate uptake transporter, or antiporter with succinate |
| Dde_1253 | COG-SfcA | Malic enzyme | SfcA | Malate:NADPH oxidoreductase, decarboxylating |
| Dde_2136 | COG-HyaD | Hydrogenase expression/formation protein | COG-HyaD | Maturation protease for HysBA hydrogenase |
| Dde_2932 | QrcA | hexaheme cytochrome *c* | QrcA | Type I cytochrome $c_3$:menaquione oxidoreductase hexaheme cytochrome *c* |
| Dde_2933 | QrcB | molybdopterin-containing family protein | QrcB | Type I cytochrome $c_3$:menaquione oxidoreductase molybdopterin-containing subunit |
| Dde_2934 | QrcC | periplasmic FeS protein | QrcC | Type I cytochrome $c_3$:menaquione oxidoreductase molybdopterin-containing subunit |
| Dde_2935 | QrcD | integral membrane protein | QrcD | Type I cytochrome $c_3$:menaquione oxidoreductase integral membrane protein subunit |

[a] The genome of *D. alaskensis* G20 has been reannotated since the original transcriptomic and proteomic data were collected. Designations from recent reannotations are used in the manuscript text while the 2011 annotation of *D. alaskensis* G20 (1) appears in all supplemental material.

**Supplemental Table 3. Genes in *D. desulfuricans cycA*$^-$ mutant I2 identified as differentially expressed by comparison of transcripts with those from wild-type *D. desulfuricans* G20 by microarray analysis**

| Locus | Protein | Annotation[a] | $\log_2$ (I2/G20)[b] |
|---|---|---|---|
| **Lactate/sulfate (60/30) medium[c]** | | | |
| **Up-regulated** | | | |
| Dde_0899 | | Hypothetical protein | 1.80 |
| Dde_0900 | | Helix-turn-helix, Fis-type | 1.70 |
| Dde_0901 | | Hypothetical protein | 1.62 |
| Dde_0922 | | Adenine-specific DNA methylase-like | 1.52 |
| Dde_0923 | | Hypothetical protein | 1.37 |
| Dde_0924 | | Hypothetical protein | 1.37 |
| Dde_0929 | | Hypothetical protein | 1.34 |
| Dde_0930 | | Hypothetical protein | 1.30 |
| Dde_1154 | | Hypothetical protein | 1.24 |
| Dde_1155 | | Hypothetical protein | 1.11 |
| Dde_1156 | | Hypothetical protein | 1.04 |
| Dde_1157 | | Hypothetical protein | 1.04 |
| Dde_1981 | | Hypothetical protein | 1.03 |
| **Down-regulated** | | | |
| Dde_0645 | | Hypothetical protein | -1.19 |
| Dde_1250 | GltA | Glutamate synthase (NADPH), homotetrameric | -1.61 |
| Dde_1251 | COG-UbiB | Oxidoreductase, NAD-binding, putative | -1.79 |

|  |  |  |  |
|---|---|---|---|
| Dde_1253 | COG-SfcA | Malic enzyme | -2.74 |
| Dde_1254 | COG-FumA | Fumarate hydratase β subunit | -2.39 |
| Dde_1255 | COG-TtdA | Fumarate hydratase α subunit | -2.41 |
| Dde_1256 | FrdB | Fumarate reductase FeS protein | -0.90 |
| Dde_1257 | FrdA | Fumarate reductase flavoprotein subunit | -1.98 |
| Dde_1258 | FrdC | Fumarate reductase cytochrome b subunit | -2.47 |
| **Pyruvate (60) medium**[d] |  |  |  |
| **Up-regulated** |  |  |  |
| Dde_0001 | DnaA | Chromosomal replication initiator protein | 1.22 |
| Dde-0280 |  | Hypothetical protein | 1.06 |
| Dde_0282 |  | TPR repeat | 1.23 |
| Dde_0283 |  | Conserved hypothetical protein | 1.29 |
| Dde_0484 |  | Conserved hypothetical protein | 1.20 |
| Dde_0597 |  | Conserved hypothetical protein | 1.93 |
| Dde_0598 |  | Hypothetical protein | 1.34 |
| Dde_0599 |  | Hypothetical protein | 1.71 |
| Dde_0656 | COG-FdnI | Fe-S-cluster-binding protein | 1.14 |
| Dde_0657 | COG-HybA | Twin-arginine translocation pathway signal | 1.61 |
| Dde_0672 |  | Hypothetical protein | 1.26 |
| Dde_0678 | COG-PspE | Rhodanese-related sulfurtransferase | 0.99 |
| Dde_0681 | COG-HybA | FeS-cluster-containing hydrogenase components | 1.01 |
| Dde_0682 | COG-BisC | Twin-arginine translocation pathway signal | 1.03 |

| | | | |
|---|---|---|---|
| Dde_0707 | FdhD | Formate dehydrogenase accessory protein | 1.12 |
| Dde_0715 | | Hypothetical protein | 2.96 |
| Dde_0717 | FdhA-1 | Formate dehydrogenase, α subunit | 3.76 |
| Dde_0718 | FdhB-1 | Formate dehydrogenase β subunit | 3.33 |
| Dde_0719 | COG-MobB | Molybdopterin-guanine dinucleotide biosynthesis protein-like | 1.61 |
| Dde_0835 | | Polysaccharide deacetylase family protein | 1.30 |
| Dde_1076 | COG-BisC | Thiosulfate reductase, putative | 1.09 |
| Dde_1194 | COG-HisJ | ABC-type amino acid transport/signal transduction systems periplasmic component | 1.14 |
| Dde_1239 | | Hypothetical protein | 1.10 |
| Dde_1409 | DnaB | Replicative DNA helicase | 1.13 |
| Dde_1440 | ProC | Pyrroline-5-carboxylate reductase | 1.04 |
| Dde_1533 | TypA | Small GTP-binding protein | 1.33 |
| Dde_1546 | IclR | Regulatory protein | 1.14 |
| Dde_1581 | DprA | DNA processing protein | 1.00 |
| Dde_1597 | | Hypothetical protein | 1.35 |
| Dde_1939 | | Hypothetical protein | 1.44 |
| Dde_1980 | | Transcriptional regulator | 1.05 |
| Dde_2006 | | Hypothetical protein | 1.42 |
| Dde_2129 | COG-CarD | Transcriptional regulator | 1.27 |
| Dde_2153 | TolQ | Transport protein | 1.19 |
| Dde_2154 | COG-ExbB | Biopolymer transport protein | 1.57 |

|  |  |  |  |
|---|---|---|---|
| Dde_2155 | COG-ExbD2 | Biopolymer transport protein | 1.43 |
| Dde_2156 | COG- TonB | Periplasmic protein, links inner and outer membranes | 1.52 |
| Dde_2484 |  | Conserved hypothetical protein | 1.09 |
| Dde_2746 |  | Hypothetical protein | 1.13 |
| Dde_2883 |  | Sugar transferase | 1.08 |
| Dde_2926 |  | Hypothetical protein | 1.19 |
| Dde_3016 | NrdD | Ribonucleoside-triphosphate reductase | 1.16 |
| Dde_3028 | CooS | Carbon-monoxide dehydrogenase, catalytic subunit | 2.24 |
| Dde_3029 | CooC | Carbon monoxide dehydrogenase accessory protein | 2.03 |
| Dde_3103 | CPG-CbiK | Cobalamin biosynthesis protein | 1.27 |
| Dde_3160 |  | Conserved hypothetical protein | 1.11 |
| Dde_3161 | NusA | Transcription termination factor NusA | 1.04 |
| Dde_3513 | FdhA-3 | Formate dehydrogenase, α subunit | 1.46 |
| Dde_3648 |  | Hypothetical protein | 1.28 |
| **Down-regulated** |  |  |  |
| Dde_0132 | COG-701 | Permease | -0.99 |
| Dde_0197 |  | Conserved hypothetical protein | -1.35 |
| Dde_0198 |  | Hypothetical protein | -1.23 |
| Dde_0199 |  | Hypothetical protein | -1.45 |
| Dde_0221 | COG-CheY | Response regulator receiver | -1.52 |
| Dde_0222 |  | Conserved hypothetical protein | -2.53 |
| Dde_0223 | COG-HcaD | Flavoprotein oxidoreductase | -2.27 |

| | | | |
|---|---|---|---|
| Dde_0324 | COG-CheY | Response regulator receiver | -1.09 |
| Dde_0348 | | Conserved hypothetical protein | -1.33 |
| Dde_0398 | COG-IlvB | Acetolactate synthase, large catalytic subunit | -1.19 |
| Dde_0399 | COG-IlvH | Acetolactate synthase III, small subunit | -1.13 |
| Dde_0552 | | Conserved hypothetical protein | -1.46 |
| Dde_0645 | | Hypothetical protein | -1.84 |
| Dde_0646 | | Hypothetical protein | -1.08 |
| Dde_0692 | COG-CheY | Response regulator receiver | -1.63 |
| Dde_0693 | COG-CitT | putative transport protein | -1.81 |
| Dde_0694 | CheYI | Chemotaxis protein | -1.94 |
| Dde_0696 | CckA | Histidine kinase | -2.50 |
| Dde_0724 | | Hypothetical protein | -2.18 |
| Dde_0725 | | Fe-hydrogenase-like protein | -3.14 |
| Dde_0821 | | Hypothetical protein | -1.34 |
| Dde_0976 | | Hypothetical protein | -1.16 |
| Dde_1074 | COG-LdlP | L-lactate transport | -1.66 |
| Dde_1140 | | Uncharacterized membrane protein | -1.06 |
| Dde_1250 | GltA | Glutamate synthase (NADPH), homotetrameric | -3.16 |
| Dde_1251 | COG-UbiB | Oxidoreductase, NAD-binding, putative | -3.12 |
| Dde_1252 | COG-CitT | Cation transporter | -3.43 |
| Dde_1254 | COG-FumA | Fumarate hydratase β subunit | -3.30 |
| Dde_1255 | COG-TtdA | Fumarate hydratase α subunit | -3.25 |

|  |  |  |  |
|---|---|---|---|
| Dde_0324 | COG-CheY | Response regulator receiver | -1.09 |
| Dde_0348 |  | Conserved hypothetical protein | -1.33 |
| Dde_0398 | COG-IlvB | Acetolactate synthase, large catalytic subunit | -1.19 |
| Dde_0399 | COG-IlvH | Acetolactate synthase III, small subunit | -1.13 |
| Dde_0552 |  | Conserved hypothetical protein | -1.46 |
| Dde_0645 |  | Hypothetical protein | -1.84 |
| Dde_0646 |  | Hypothetical protein | -1.08 |
| Dde_0692 | COG-CheY | Response regulator receiver | -1.63 |
| Dde_0693 | COG-CitT | putative transport protein | -1.81 |
| Dde_0694 | CheYI | Chemotaxis protein | -1.94 |
| Dde_0696 | CckA | Histidine kinase | -2.50 |
| Dde_0724 |  | Hypothetical protein | -2.18 |
| Dde_0725 |  | Fe-hydrogenase-like protein | -3.14 |
| Dde_0821 |  | Hypothetical protein | -1.34 |
| Dde_0976 |  | Hypothetical protein | -1.16 |
| Dde_1074 | COG-LdlP | L-lactate transport | -1.66 |
| Dde_1140 |  | Uncharacterized membrane protein | -1.06 |
| Dde_1250 | GltA | Glutamate synthase (NADPH), homotetrameric | -3.16 |
| Dde_1251 | COG-UbiB | Oxidoreductase, NAD-binding, putative | -3.12 |
| Dde_1252 | COG-CitT | Cation transporter | -3.43 |
| Dde_1254 | COG-FumA | Fumarate hydratase β subunit | -3.30 |
| Dde_1255 | COG-TtdA | Fumarate hydratase α subunit | -3.25 |

|  |  |  |  |
|---|---|---|---|
| Dde_1256 | FrdB | Fumarate reductase FeS protein | -2.46 |
| Dde_1257 | FrdA | Fumarate reductase flavoprotein subunit | -2.84 |
| Dde_1258 | FrdC | Fumarate reductase cytochrome b subunit | -3.01 |
| Dde_1275 | DctP | TRAP dicarboxylate transporter | -1.20 |
| Dde_1343 | HspC | Heat shock protein, HSP20 family | -1.12 |
| Dde_1344 | COG-IbpS | Heat shock protein, HSP20 family | -1.08 |
| Dde_1347 |  | Conserved hypothetical protein | -1.40 |
| Dde_1605 | COG-GrsT | Oleoyl-[acyl-carrier protein] hydrolase | -1.05 |
| Dde_1614 | COG-GntR | Regulatory protein GntR, HTH | -1.17 |
| Dde_1615 |  | Membrane protein, putative | -1.40 |
| Dde_1616 |  | Metallo-beta-lactamase family protein | -1.20 |
| Dde_1709 | FlaB1 | Flagellin | -1.18 |
| Dde_1710 |  | Hypothetical protein | -1.03 |
| Dde_2169 |  | Conserved hypothetical protein | -1.24 |
| Dde_2170 |  | Conserved hypothetical protein | -1.21 |
| Dde_2365 |  | Conserved hypothetical protein | -2.02 |
| Dde_2382 |  | Hypothetical protein | -1.06 |
| Dde_2451 |  | Hypothetical protein | -1.28 |
| Dde_2509 |  | Conserved hypothetical protein | -1.26 |
| Dde_2551 |  | Conserved hypothetical protein | -1.00 |
| Dde_2643 | COG-UspA | Universal stress protein | -1.00 |
| Dde_2824 |  | Hypothetical protein | -3.12 |

| | | | |
|---|---|---|---|
| Dde_3018 | | Flagellin, putative | -1.38 |
| Dde_3211 | | Twin-arginine translocation pathway signal | -1.39 |
| Dde_3539 | COG-CoxL | Aldehyde oxidoreductase, putative | -1.02 |
| Dde_3600 | | Conserved hypothetical protein | -1.21 |
| Dde_3601 | | Hypothetical protein | -1.23 |
| Dde_3733 | GlpD | Glycerol-3-phosphate dehydrogenase | -1.06 |

[a] Gene annotation was obtained from http://www.microbesonline.org

[b] $\text{Log}_2$ R, R = I2/G20 ratio of transcripts measured by microarray analysis. Only ratios with at least an absolute two-fold differential expression in I2 compared with G20 are reported.

[c] Lactate/sulfate (60/30) is MO basal salts with 60 mM sodium lactate and 30 mM sodium sulfate providing a medium for sulfate respiration.

[d] MOPyr (60) is MO basal salts with 60 mM sodium pyruvate for growth by fermentation.

**Supplemental Table 4. List of genes encoding proteins altered in protein abundance from *D. desulfuricans cycA*$^-$ mutant I2 as compared to proteins from wild-type G20 as revealed by proteomic analysis**

| Locus | Protein | Annotation[a] | $\text{Log}_2$ (I2/G20)[b] |
|---|---|---|---|
| **Lactate/sulfate (60/30) medium[c]** | | | |
| **Up-regulated** | | | |
| Dde_0115 | FtsX | Cell division membrane protein | 1.17 |
| Dde_0139 | | ABC-type uncharacterized transport system, ATPase components. | 1.22 |
| Dde_0235 | | Predicted transcriptional regulator | 1.37 |
| Dde_0513 | | Aminotransferase, putative | 1.77 |
| Dde_0520 | COG-LeuA | 2-phosphinomethylmalic acid synthase, putative | 1.00 |
| Dde_0580 | DchA | Decaheme *c*-type cytochrome | 1.63 |
| Dde_0583 | RnfG | Electron transport subunit | 1.38 |
| Dde_0643 | | Signal transduction protein, putative | 1.36 |
| Dde_0651 | HmcC | Integral membrane protein | 1.01 |
| Dde_0706 | FdhE | Formate dehydrogenase formation protein | 1.58 |
| Dde_0717 | FdhA-1 | Formate dehydrogenase, α subunit, anaerobic | 4.53 |
| Dde_0718 | FdhB-1 | Formate dehydrogenase, β subunit | 4.51 |
| Dde_0719 | COG-MobB | Molybdopterin-guanine dinucleotide biosynthesis protein | 2.78 |
| Dde_1328 | COG-DppB | Dipeptide ABC transporter, nickel transport system permease protein | 1.10 |
| Dde_1334 | COG-FatA | Acyl-ACP thioesterase | 1.39 |

|  |  |  |  |
|---|---|---|---|
| Dde_1378 | ThiM | Hydroxyethylthiazole kinase | 1.12 |
| Dde_1390 | COG-MoaB | Molybdopterin binding domain | 1.48 |
| Dde_1556 | ThiH | Thiamin biosynthesis, thiazole moiety | 1.68 |
| Dde_1723 | COG-RsbU | Regulatory protein, putative | 1.22 |
| Dde_1748 | COG-HepA | ERCC4-like helicases | 3.54 |
| Dde_1814 | GltB-1 | Glutamate synthase, | 4.32 |
| Dde_2118 |  | Conserved hypothetical protein | 1.23 |
| Dde_2212 |  | Hypothetical protein | 1.01 |
| Dde_2218 | Ion | Peptidase S16, ATP-dependent protease | 1.37 |
| Dde_2328 | MetE | 5-methyltetrahydropteroyltriglutamate--homocysteine | 2.42 |
| Dde_2334 | SucCD | Succinyl-CoA ligase, alpha/beta subunit | 2.26 |
| Dde_2351 |  | Conserved hypothetical protein | 1.20 |
| Dde_2507 |  | Conserved hypothetical protein | 1.14 |
| Dde_2596 | RecN | DNA repair protein | 1.20 |
| Dde_2597 |  | Conserved hypothetical protein | 2.57 |
| Dde_2623 |  | Conserved hypothetical protein | 1.23 |
| Dde_2703 |  | Conserved hypothetical protein | 1.16 |
| Dde_2831 | COG-LivK | Substrate-binding protein, putative | 1.20 |
| Dde_2960 |  | TPR domain protein | 1.18 |
| Dde_3028 | CooS | Carbon-monoxide dehydrogenase, catalytic subunit | 2.02 |
| Dde_3029 | CooC | Carbon monoxide dehydrogenase accessory protein | 2.32 |
| Dde_3060 | COG-WcaG | NAD-dependent epimerase/dehydratase family protein | 1.18 |

|  |  |  |  |
|---|---|---|---|
| Dde_3393 |  | Tail fiber protein, putative | 1.11 |
| Dde_3523 | COG-EutG | Alcohol dehydrogenase, iron containing | 1.45 |
| Dde_3556 |  | Predicted acyltransferase | 1.91 |
| Dde_3620 | COG-HisJ | ABC-type amino acid transport, periplasmic protein | 6.24 |
| **Down-regulated** |  |  |  |
| Dde_0054 | PutA | Proline dehydrogenase | -1.14 |
| Dde_0194 |  | Conserved hypothetical protein | -1.45 |
| Dde_0360 |  | Predicted nucleoside-diphosphate sugar epimerase | -1.81 |
| Dde_0417 | GabT | 4-aminobutyrate aminotransferase | -1.44 |
| Dde_0479 | WbaZ-2 | Mannosyl transferase | -1.12 |
| Dde_0550 |  | Sensory box/GGDEF family protein | -1.28 |
| Dde_0564 |  | Conserved hypothetical protein | -1.03 |
| Dde_0801 | CobM | Precorrin-4 C11-methyltransferase | -1.30 |
| Dde_0822 |  | Conserved hypothetical protein | -1.46 |
| Dde_1051 | HtpX | Heat shock protein, integral membrane protein | -1.07 |
| Dde_1065 |  | Hypothetical protein | -1.03 |
| Dde_1071 |  | Multi-sensor signal transduction histidine kinase | -1.54 |
| Dde_1120 | FliD | Flagellar biosynthesis | -1.66 |
| Dde_1210 |  | Hydrogenase, iron-sulfur cluster-binding subunit, putative | -1.29 |
| Dde_1213 | COG-FrhD | Hydrogenase, Fe-S cluster binding subunit, putative | -1.47 |
| Dde_1251 | COG-UbiB | Oxidoreductase, NAD-binding, putative | -1.35 |
| Dde_1257 | FrdA | Fumarate reductase, flavoprotein subunit | -2.09 |

|  |  |  |  |
|---|---|---|---|
| Dde_1323 | COG-UbiD | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase family protein | -1.00 |
| Dde_1370 | COG-AmiC | N-acetylmuramoyl-L-alanine amidase | -1.81 |
| Dde_1380 |  | Conserved hypothetical protein | -1.22 |
| Dde_1405 | FlrC | Flagellar regulatory protein | -2.02 |
| Dde_1411 | RpsR | Ribosomal protein S18 | -1.04 |
| Dde_1415 | TolC | Type I secretion outer membrane protein, | -4.33 |
| Dde_1429 | COG-HisJ | Putative periplasmic binding protein | -1.02 |
| Dde_1534 |  | Conserved hypothetical protein | -2.39 |
| Dde_1570 | FlaD | Flagellin | -2.59 |
| Dde_1601 | COG-MdlB | ABD-type multidrug tansport system, ATPase and permease components | -1.21 |
| Dde_1709 | FlaB1 | Flagellin  and hook related proteins | -2.63 |
| Dde_1713 |  | Hypothetical protein | -1.34 |
| Dde_1726 |  | 4-diphosphocytidyl-2C-methyl-D-erythritol synthase: | -2.52 |
| Dde_1972 | COG-PcnB | TRNA nucleotidyl transferase-related protein | -1.35 |
| Dde_1987 | COG-WcaA | Glycosyltransferase involved in cell wall biosynthesis | -1.60 |
| Dde_2283 | PdxA | Pyridoxal phosphate biosynthetic protein | -1.46 |
| Dde_2396 | RnpA | Bacterial ribonuclease P protein | -2.14 |
| Dde_2470 |  | Hypothetical protein | -2.29 |
| Dde_2525 | MetF | 5,10-methylenetetrahydrofolate reductase | -1.01 |
| Dde_2581 | COG-Acd | 1-aminocyclopropane-1-carboxylate deaminase | -2.33 |
| Dde_2627 |  | Conserved hypothetical protein | -1.01 |
| Dde_2834 | COG-LysR | Transcriptional regulator, putative | -1.38 |

| | | | |
|---|---|---|---|
| Dde_2943 | Aor-2 | Aldehyde:ferredoxin oxidoreductase | -1.04 |
| Dde_3094 | | Phosphoesterase, putative | -1.62 |
| Dde_3126 | | Alcohol dehydrogenase, iron-containing | -2.12 |
| Dde_3182 | CycA | Cytochrome $c_3$, TpI-$c_3$ | -3.62 |
| Dde_3248 | COG-PspE | rhodanese-like domain protein | -1.03 |
| Dde_3424 | HsdR | Type I site-specific deoxyribonuclease | -1.27 |
| Dde_3530 | COG-UbiB | NIFe hydrogenase gamma subunit, putative | -1.25 |
| Dde_3637 | Tme | Malic enzyme | -1.04 |
| Dde_3647 | KdsB | 3-deoxy-D-manno-octulosonate cytidylyltransferase | -1.02 |
| Dde_3657 | COG-UpgB | ABC-type sugar transporter, periplasmic component | -1.57 |
| Dde_3698 | COG-WcaA | Glycosyl transferase | -1.21 |
| **Pyruvate (60) medium**[d] | | | |
| **Up-regulated** | | | |
| Dde_0002 | DnaN | DNA polymerase III, β subunit | 1.06 |
| Dde_0003 | GyrB | DNA gyrase, β subunit | 1.00 |
| Dde_0004 | GyrA | DNA gyrase, subunit A | 1.65 |
| Dde_0168 | GlnH | Periplasmic glutamine-binding protein | 1.91 |
| Dde_0217 | COG-PepP | Peptidase, putative | 1.06 |
| Dde_0410 | GlpK | Glycerol kinase | 2.60 |
| Dde_0428 | COG-RfaG | Glycosyltransferase | 1.13 |
| Dde_0518 | COG-GatA | 6-aminohexanoate-cyclic-dimer hydrolase | 4.48 |
| Dde_0546 | MurA | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 1.09 |

|  |  |  |  |
|---|---|---|---|
| Dde_0557 | COG-CaiC | Ligase/synthetase, putative | 3.14 |
| Dde_0598 |  | Hypothetical protein | 4.49 |
| Dde_0652 | HmcB | Transmembrane electron transfer protein | 1.14 |
| Dde_0679 | COG-PspE | Sulfurtransferase, rhodanese-like | 1.39 |
| Dde_0682 | COG-BisC | Oxidoreductase, putative | 2.77 |
| Dde_0706 | FdhE | Formate dehydrogenase formation protein | 2.08 |
| Dde_0717 | FdhA-1 | Formate dehydrogenase, α subunit | 8.57 |
| Dde_0719 | COG-MobB | Molybdopterin-guanine dinucleotide biosynthesis protein | 4.42 |
| Dde_0839 | COG-RfaG | Glycosyltransferase | 1.10 |
| Dde_0988 | AtpH | ATPase F1, δ subunit | 1.56 |
| Dde_0989 | AtpF | ATP synthase F0, βsubunit | 1.04 |
| Dde_1018 |  | Chemotaxis protein CheY1, putative | 1.27 |
| Dde_1047 | FtsZ | Cell division protein | 1.13 |
| Dde_1070 | TalC | Transaldolase C | 1.50 |
| Dde_1098 |  | Conserved hypothetical protein | 1.35 |
| Dde_1106 | COG-AroA | 5-enolpyruvylshikimate-3-phosphate synthase, putative | 1.30 |
| Dde_1129 | PyrH | uridylate kinase | 1.01 |
| Dde_1185 | DppA | Dipeptide transport protein | 1.67 |
| Dde_1198 | COG-CheR | MCP methyltransferase | 1.52 |
| Dde_1207 | COG-HrdC | Heterodisulfide reductase, C subunit | 1.09 |
| Dde_1214 |  | Conserved hypothetical protein | 1.05 |
| Dde_1323 | COG-UbiD | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase family protein | 1.14 |
| Dde_1328 | COG-DppB | ABC transporter dipeptide/oligopeptide/nickel transport system permease protein | 1.45 |
| Dde_1439 | Ndk | Nucleoside diphosphate kinase | 2.46 |
| Dde_1522 | COG-BaeS | Histidine kinase | 2.09 |

| | | | |
|---|---|---|---|
| Dde_1586 | FabK | Trans-2-enoyl-ACP reductase II | 1.11 |
| Dde_1594 | MetG | Methionine tRNA synthetase | 1.89 |
| Dde_1646 | COG-ThiJ | Peptidase | 1.47 |
| Dde_1672 | PurM | Phosphoribosylaminoimidazole synthetase | 1.78 |
| Dde_1757 | GpmA | phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | 1.56 |
| Dde_1759 | | Conserved hypothetical protein | 1.23 |
| Dde_1765 | PyrG | CTP synthase | 1.06 |
| Dde_1769 | | Conserved hypothetical protein | 1.48 |
| Dde_1810 | COG-ArgE | Peptidase | 1.02 |
| Dde_1814 | GltB-1 | Glutamate synthase, iron-sulfur cluster-binding subunit | 3.55 |
| Dde_2002 | COG-AcrR | transcriptional regulator, TetR family | 1.78 |
| Dde_2052 | RpoD | RNA polymerase sigma-70 factor | 1.12 |
| Dde_2056 | RpsU | Ribosomal protein S21 | 1.12 |
| Dde_2063 | FusA | Translation elongation factor G | 2.04 |
| Dde_2091 | COG-NadE | NAD+ synthase, putative | 1.94 |
| Dde_2117 | | TPR domain protein, putative | 2.20 |
| Dde_2130 | Rho | Transcription termination factor Rho | 1.48 |
| Dde_2134 | HysB | [NiFeSe] hydrogenase, small subunit | 2.62 |
| Dde_2135 | HysA | [NiFeSe] hydrogenase, large subunit, | 1.11 |
| Dde_2138 | HynA-1 | [NiFe] hydrogenase, large subunit | 1.77 |
| Dde_2140 | HypC | Hydrogenase assembly chaperone | 3.78 |
| Dde_2236 | Map | Methionine aminopeptidase | 2.82 |
| Dde_2238 | RspsK | Ribosomal subunit protein | 1.14 |
| Dde_2325 | | Hypothetical protein | 1.44 |
| Dde_2394 | YidC | Inner membrane protein, 60 kDa | 1.47 |
| Dde_2429 | FabC | 3-oxoacyl-(acyl-carrier-protein) reductase | 1.58 |
| Dde_2479 | | Conserved hypothetical protein | 1.56 |
| Dde_2498 | HsdM | Type I restriction-modification system | 1.46 |

|  |  |  |  |
|---|---|---|---|
| Dde_2578 | COG-Lrp | Heme biosynthesis protein, putative | 1.68 |
| Dde_2621 | HemC | Porphobilinogen deaminase | 1.73 |
| Dde_2688 | ThiD | Phosphomethylpyrimidine kinase | 2.24 |
| Dde_2727 | COG-UspA | Universal stress protein family | 1.15 |
| Dde_2764 | COG-HisJ | Amino acid binding protein, putative | 1.19 |
| Dde_2858 |  | Cytochrome c-554 precursor | 2.14 |
| Dde_2933 | MopB | Molydopterin-binding protein | 1.65 |
| Dde_2934 | MopC | Cytoplasmic FeS protein | 1.32 |
| Dde_2949 |  | Conserved hypothetical protein | 1.72 |
| Dde_2979 | COG-CynT | Carbonic anhydrase | 1.88 |
| Dde_2984 | PrfA | Peptide chain release factor 1 | 1.33 |
| Dde_3012 | PyrE | Orotate phosphoribosyl transferase | 1.96 |
| Dde_3028 | CooS | Carbon-monoxide dehydrogenase, catalytic subunit | 4.18 |
| Dde_3029 | CooC | Carbon monoxide dehydrogenase accessory protein | 3.62 |
| Dde_3125 |  | Conserved hypothetical protein | 1.06 |
| Dde_3243 |  | Conserved hypothetical protein | 1.43 |
| Dde_3459 | PurE | Phosphoribosylaminoimidazole carboxylase | 1.79 |
| Dde_3484 | TrpE | Anthranilate synthase, component I | 1.06 |
| Dde_3486 | AroA | 3-phosphoshikimate 1-carboxyvinyltransferase | 1.86 |
| Dde_3489 | COG-FbaB | Phospho-2-dehydro-3-deoxyheptonate aldolase, putative | 1.36 |
| Dde_3490 | COG-FbaB | Phospho-2-dehydro-3-deoxyheptonate aldolase, putative | 1.52 |
| Dde_3641 |  | Sulphate permease/anion transporter | 1.03 |
| Dde_3646 | CarA | Carbamoyl-phosphate synthase, glutamine subunit | 2.22 |
| Dde_3673 | PotD | Periplasmic polyamine transport protein | 1.52 |
| Dde_3712 | COG-UspA | Universal stress protein family | 1.44 |
| **Down-regulated** |  |  |  |
| Dde_0011 | HisS | Histidyl-tRNA synthetase | -2.56 |

| | | | |
|---|---|---|---|
| Dde_0060 | | Conserved hypothetical protein | -1.70 |
| Dde_0076 | MtnS | Methylthioribose salvage protein | -2.00 |
| Dde_0098 | COG-UspA | Universal stress protein family | -1.20 |
| Dde_0111 | | Zinc resistance-associated protein, putative | -2.40 |
| Dde_0184 | COG-GlnQ | ATP-binding protein | -1.30 |
| Dde_0204 | | Uncharacterized ACR protein | -1.27 |
| Dde_0303 | | Transcriptional regulator, putative | -1.32 |
| Dde_0312 | COG-GlcD | Oxidoreductase, FAD/iron-sulfur cluster-binding domain protein, putative | -1.45 |
| Dde_0325 | | Hypothetical protein | -2.26 |
| Dde_0327 | | Response regulator receiver, CheY-like | -1.38 |
| Dde_0377 | PurH | Phosphoribosylaminoimidazolecarboxamide formyltransferase | -1.72 |
| Dde_0408 | COG-GlpA | Glycerol-3-phosphate dehydrogenase, putative | -2.60 |
| Dde_0432 | Gmd | GDP-mannose 4,6-dehydratase | -2.18 |
| Dde_0532 | | Sensory box/GGDEF family protein | -1.89 |
| Dde_0692 | | Response regulator containing CheY-like receiver | -6.25 |
| Dde_0693 | COG-CitT | Transport protein, putative | -4.54 |
| Dde_0695 | | Response regulator containing CheY-like receiver | -5.33 |
| Dde_0765 | | CBS domain protein | -1.39 |
| Dde_0863 | | Conserved hypothetical protein | -2.32 |
| Dde_0970 | | Conserved hypothetical protein | -1.82 |
| Dde_1081 | ArgJ | Arginine biosynthesis protein | -1.75 |
| Dde_1145 | | Conserved hypothetical protein | -1.21 |
| Dde_1283 | UidR | Repressor for uid operon | -1.18 |
| Dde_1304 | b0965 | Coenzyme A binding protein, putative | -1.51 |
| Dde_1310 | | Conserved hypothetical protein | -3.13 |
| Dde_1425 | COG-Dut | DeoxyUTP pyrophosphatase subfamily 1 | -1.20 |
| Dde_1444 | | Conserved hypothetical protein | -1.13 |

|  |  |  |  |
|---|---|---|---|
| Dde_1600 | FepA | Receptor precursor-mostly Fe transport | -1.34 |
| Dde_1608 |  | Polyketide synthase modules and related proteins | -1.41 |
| Dde_1634 |  | Conserved hypothetical protein | -1.60 |
| Dde_1834 |  | Unknown function domain protein | -1.30 |
| Dde_1843 |  | Iron-sulfur cluster binding protein | -1.38 |
| Dde_1974 |  | Conserved hypothetical protein | -1.30 |
| Dde_1997 |  | Conserved hypothetical protein | -2.06 |
| Dde_2013 | DegQ | Serine endoprotease | -1.15 |
| Dde_2043 | PdxJ | Pyridoxal phosphate biosynthetic protein | -1.01 |
| Dde_2104 | CheB-1 | Response regulator receiver | -2.24 |
| Dde_2116 | RpoH | Sigma 70 family protein KO | -1.05 |
| Dde_2121 | CysS | Cysteinyl-tRNA synthetase | -1.12 |
| Dde_2142 | IleS | Isoleucyl-tRNA synthetase | -1.86 |
| Dde_2169 |  | Conserved hypothetical protein | -1.08 |
| Dde_2220 | ClpP | Peptidase S14 | -1.82 |
| Dde_2265 | Sat | ATP-sulfurylase | -1.44 |
| Dde_2317 | COG-Acd | Acetyl-CoA synthetase, putative | -1.70 |
| Dde_2334 | SucCD | Succinyl-CoA ligase, alpha/beta subunit | -1.35 |
| Dde_2462 |  | Conserved hypothetical protein | -1.91 |
| Dde_2592 |  | Conserved hypothetical protein | -1.34 |
| Dde_2819 |  | Hypothetical protein | -2.85 |
| Dde_3103 | COG- CbiK | Cobalamin biosynthesis protein | -1.21 |
| Dde_3200 |  | Fe-S cluster-binding/ATPase domain protein | -1.13 |
| Dde_3476 | IcdA | Isocitrate dehydrogenase | -1.26 |
| Dde_3635 | GltA | Glutamate synthase | -2.51 |
| Dde_3636 | COG-UbiB | Electron transfere protein, putative | -1.40 |
| Dde_3707 |  | Conserved hypothetical protein | -1.10 |

[a] Gene annotation was obtained from http://www.microbesonline.org

[b] $\text{Log}_2$ R, R = I2/G20 ratio of abundance values obtained from proteomic analysis of proteins with at least a two-fold up or down change in abundance in protein content in I2 versus G20.

[c] Lactate/sulfate (60/30) is MO basal salts with 60 mM sodium lactate and 30 mM sodium sulfate providing a medium for sulfate respiration.

[d] MOPyr (60) is MO basal salts with 60 mM sodium pyruvate for growth by fermentation.

**Supplemental Table 5. Validation of microarray data by quantitative reverse transcription PCR analysis[a].**

| Locus | Annotation | qRT-PCR | | Microarray | |
|---|---|---|---|---|---|
| | | Lactate/sulfate (60/30) | Pyruvate (60) | Lactate/sulfate (60/30) | Pyruvate (60) |
| Dde_0717 | Formate dehydrogenase α subunit | -1.15 | 8.28 | 0.72 | 3.76 |
| Dde_1074 | L-lactate transport | -0.49 | -2.88 | 0.12 | -1.66 |
| Dde_1110 | Adenylsulfate reductase α subunit | 0.46 | -1.55 | 0.50 | NR[b] |
| Dde_1253 | Malic enzyme | -4.54 | -5.90 | -2.74 | -3.71 |
| Dde_2234 | 30S ribosomal protein S13 | -1.01 | 1.39 | 0.03 | 0.51 |
| Dde_2265 | ATP-sulfurylase | -0.16 | -2.10 | 0.08 | NR |
| Dde_2272 | Iron-sulfur binding protein, putative | 0.01 | 0.01 | 0.30 | -0.29 |
| Dde_3103 | Cobalmin biosynthesis protein | -0.05 | 4.76 | 0.20 | 1.27 |
| Dde_3156 | Flagellar biosynthesis | -0.16 | -0.26 | 0.37 | -0.64 |

[a] Data presented are expressed as $\mathrm{Log}_2$ R, R=(I2/G20)

[b] NR: data do not meet criteria for reproducibility

**Supplemental Table 6. Protein Abundance Averages of G20 and I2 for Lactate/Sulfate (60mM/30mM) Medium (See Excel file)**

**Supplemental Table 7. Protein Abundance Averages of G20 and I2 for Pyruvate (60mM) Medium (See Excel file)**

**Supplemental Table 8. Protein Abundance Values for Each Technical Replicate for the Biological Replicates of G20 and I2 in Lactate/Sulfate (60mM/30mM) Medium (See Excel file)**

**Supplemental Table 9. Protein Abundance Values for Each Technical Replicate for the Biological Replicates of G20 and I2 in Pyruvate (60mM) Medium (See Excel file)**

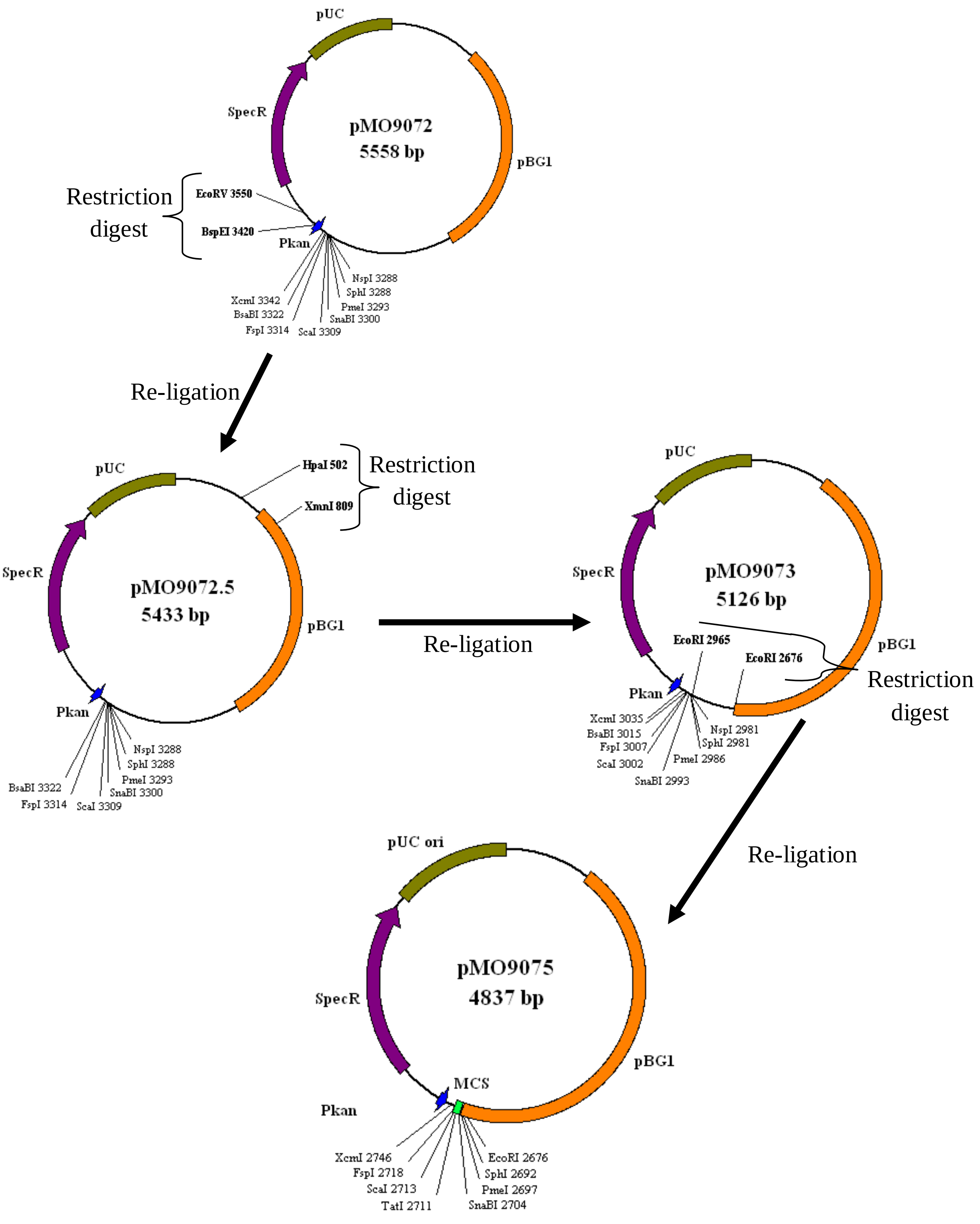
**Supplemental Table 10. Proteomics analysis summary for *D. alaskensis* G20 and CycA mutant, I2[a]**

| | **G20** | **I2** |
|---|---|---|
| **Lactate/sulfate medium[b]** | | |
| Total proteins identified | 1965 | 1926 |
| Proteins meeting confidence criteria [c] | 1666 | 1613 |
| Found only in wild type or mutant | 162 | 109 |
| Differentially expressed $\text{Log}_2\ R \geq \lvert 1 \rvert$[d] | 50 (R = I2/G20) | 42 (R = I2/G20) |
| HP/CHP[e] among differentially expressed | 9 | 8 |
| | | |
| **Pyruvate medium** [f] | | |
| Total proteins identified | 1579 | 1425 |
| Proteins meeting confidence criteria | 838 | 761 |
| Found only in wild type or mutant | 106 | 183 |
| Differentially expressed $\text{Log}_2\ R \geq \lvert 1 \rvert$ | 55 (R = I2/G20) | 87 (R = I2/G20) |
| HP/CHP among differentially expressed | 15 | 10 |

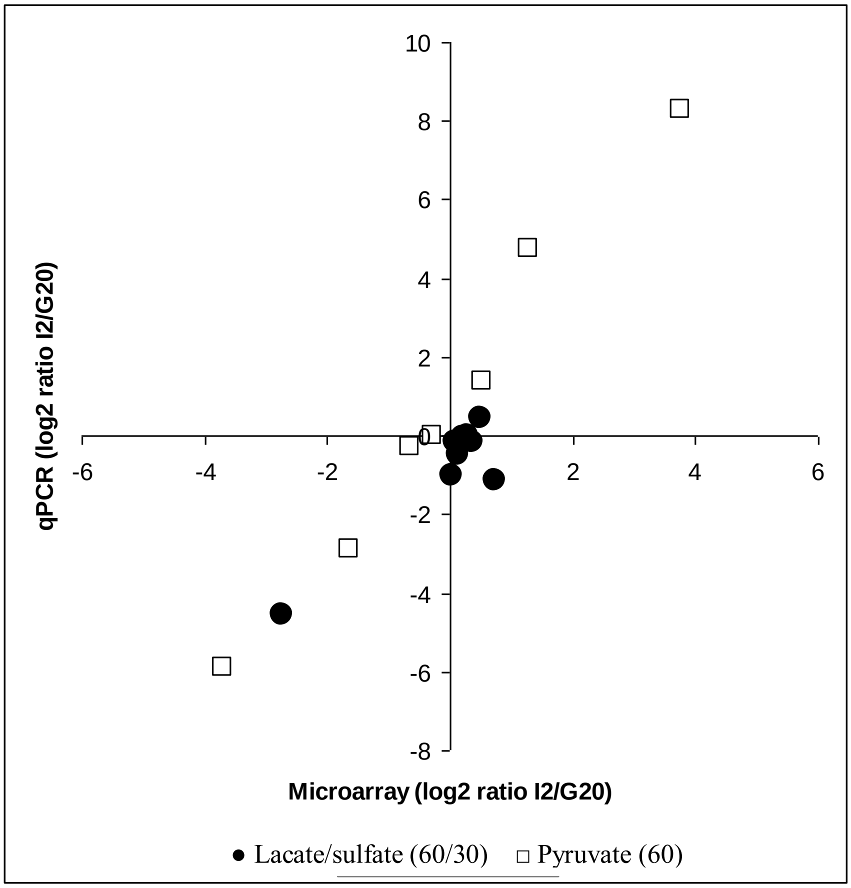
[a] Accurate mass tag and time proteomics analysis performed by Environmental Molecular Sciences Laboratory of the Pacific Northwest National Laboratory.

[b] Lactate/sulfate medium is MO basal salts plus 60 mM sodium lactate and 30 mM sodium sulfate.

[c] Criteria given in Methods and Materials.



**Supplemental Figure 1.** Generation of pMO9075, the complementation shuttle vector



**Supplemental Figure 2.** Comparison of selected microarray data with qRT-PCR data.

Microarray data were validated using for real-time quantitative reverse transcription-PCR (qRT-PCR) as described previously (4), except that the Bio-Rad MyiQ2 Two-Color Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA) and Roche FastStart SYBR Green Master reagent (Roche Applied Science, Indianapolis, IN) were used for this experiment.