Table S3. Predicted binding sites of the global regulator ModE in the genome of *G. sulfurreducens*, which are mostly absent from the *G. metallireducens* genome.

ModE-binding site in *G. sulfurreducens*; alignment with *G. metallireducens*	**Genes predicted to be controlled**	**Parallel in *G. metallireducens***
TATTATAAAGGTAATAAGACATTGACA	5’ of GSU0759.2, GSU0759.1, GSU0759 (hypothetical proteins)	Homologous genes absent
AGGTATCCAATCATGAATACTTCGCCA || || | || | || || ||||||| AGATAACGAACCGGGAGTATTTCGCCA	Within GSU3378 (glutamate-ammonia ligase adenylyltransferase), 5’ of GSU3377 (endonuclease III-related)	Site not detected by ScanAce within Gmet_0071 (GSU3378 homolog), but 70% conserved
TTTTAAAATAAACATAATTTTATAACA || ||||||| || |||||||||||| TTGTAAAATATACTCAATTTTATAACA	5’ of GSU2490 (membrane protein), GSU2491 (major facilitator family transporter), GSU2492 (sensor histidine kinase)	Gmet_2465 (GSU2490 homolog) present, homologs of other genes absent; site detected by ScanAce, 85% conserved
CTGCGCTAAATACATACCTCTCTATCG | |||||| | | ||| ||| CATGGGCTAAAAAGTTGTACTCAATCA	5’ of GSUR045 (tRNA-Gly)	Site not detected by ScanAce 5’ of Gmet_R0040 (tRNA-Gly), 56% conserved
AAACGCTATAACCTTCATGACATAACG || || | | || | AATGACTTTTGGTATGCTGCGCAATGC	5’ of GSU2963, GSU2962, GSU2961, GSU2960 (*modDABC*); 3’ of GSU2964 (*modE*)	*modD* absent, *modABC* present; site not detected by ScanAce 3’ of truncated *modE* homolog (Gmet_0511)
TTTAAAAATATTAATTTATTTATAAAC	5’ of GSU3415, GSU3416, GSU3417 (oxidoreductase, conserved hypothetical protein, dioxygenase)	Genes present as Gmet_1705, Gmet_1704, Gmet_2446, but 5’ region is not syntenous
CAGAGATGGATTAATGAGTTTATATTG	Within GSU1363 (RNA-directed DNA polymerase), 5’ of GSU1364-GSU1365 (restriction system)	Homologous genes absent
CATTGAAAGATTAATGACTGCATGGCC	5’ of GSU1715 (hypothetical protein)	Homologous gene absent
TTTCACCATGAACTATCCTTCATATCG	5’ of GSU1383 (exonuclease, possibly CRISPR2-associated)	Homologous gene absent
CTTCAAAATGTTCAAAAATATCAAACC	5’ of GSU3407, GSU3408 (membrane	Homologous genes absent

<table>
<tr><td></td><td>protein, threonine aldolase), possibly also GSU3406, GSU3405, GSU3404 (amino acid transporter)</td><td></td></tr>
<tr><td>CGTTACACAAATACGCATATAGTGATA
| ||| | || ||| ||
CCTTAACAACCCCGTCAAGGGGTGGTA</td><td>5’ of GSU2429 (peptidyl-prolyl *cis-trans* isomerase)</td><td>Site not detected by ScanAce 5’ of Gmet_0815 (GSU2429 homolog), 44% conserved</td></tr>
<tr><td>TGTCAATGTCAAAATGTATTGCTAATA</td><td>5’ of GSU2150.1 (conserved hypothetical protein)</td><td>Homologous gene absent</td></tr>
<tr><td>CGTCGCTGTAAACAACAAAACAGAACG
  | ||||| || || ||| ||||
TTTGCTTGTAATCACCATCACAAAACG</td><td>5’ of GSU0490 (succinyl:acetate CoA-transferase)</td><td>Site not detected by ScanAce 5’ of Gmet_3044 (GSU0490 homolog), 63% conserved</td></tr>
<tr><td>ATTGGTTATATTCCAGGCTTTATAACC</td><td>Within GSU1945 (fibronectin type III domain protein)</td><td>Homologous gene absent</td></tr>
<tr><td>AAGCCTGGTATTGATATCTCCATAACC
 | | || || |||||| |||| |||
GAAACGGGGATCGATATCGCCATTACC</td><td>Within GSU0660 (4-diphosphocytidyl-2C-methyl-D-erythritol kinase)</td><td>Site not detected by ScanAce within Gmet_2849 (GSU0660 homolog), 70% conserved</td></tr>
<tr><td>AGGCGCAGTAAACATTATTGAATGTCA</td><td>5’ of GSU3406, GSU3405, GSU3404 (amino acid transporter), possibly also GSU3407, GSU3408 (membrane protein, threonine aldolase)</td><td>Homologous genes absent</td></tr>
<tr><td>ATACAAAATAATATTAAAGTGATAGTG</td><td>Within GSU2395 (conserved hypothetical protein)</td><td>Homologous gene absent</td></tr>
<tr><td>ATATATATACAAAATTATATATTGCGT
||||||||| | ||||| || |||
ATATATATAAATTCATATATTTTACGT</td><td>5’ of GSU0391, GSU0392, GSU0393, GSU0394, GSU0395 (efflux pump), maybe more</td><td>Genes present (except GSU0393) as Gmet_3129, Gmet_3128, Gmet_3127, Gmet_3126, maybe more; site not detected by ScanAce, 74% conserved</td></tr>
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