**Table S4. NanoString analysis of genes differentially transcribed in a CsrS T284A mutant or during growth of wild type strain 854 in the presence of 15 mM MgCl2**

| Gene locus* | Gene Name | Gene Product | Log2-fold change T284A vs. WT | Log2-fold change Mg vs. unsupplemented |
|---|---|---|---|---|
| Spy_0140 | *ifs* | NADase inhibitor | -4.02 | -2.82 |
| Spy_0139 | *nga* | NAD glycohydrolase | -3.94 | -2.77 |
| Spy_0141 | *slo* | streptolysin O | -3.77 | -2.89 |
| Spy_1170 | - | hypothetical protein | -3.31 | -1.71 |
| Spy_0563 | *sagB* | Streptolysin S synthesis protein | -3.3 | -1.81 |
| Spy_1169 | *spd3* | DNase | -3.3 | -1.64 |
| Spy_1684 | *ska* | streptokinase | -3.28 | -1.84 |
| Spy_1714 | - | cell surface protein | -3.12 | -1.4 |
| Spy_1718 | *sic1.01* | inhibitor of complement protein | -3.02 | -1.54 |
| Spy_0562 | *sagA* | streptolysin S | -2.9 | -1.63 |
| Spy_1715 | *scpA* | C5A peptidase | -2.79 | -1.31 |
| Spy_1719 | *emm1.0* | M protein | -2.3 | -0.64 |
| Spy_1415 | *sdaD2* | phage-encoded DNase | -2.28 | -1.8 |
| Spy_1687 | *sclA* | hypothetical protein | -2.19 | -1.27 |
| Spy_0351 | *spyA* | C3 family ADP-ribosyltransferase | -2.1 | -1.37 |
| Spy_0561 | *epf* | extracellular matrix binding protein | -1.95 | -1.44 |
| Spy_1731 | - | hypothetical protein | -1.94 | -0.5 |
| Spy_1704 | *dppA* | dipeptide-binding protein | -1.82 | -0.75 |
| Spy_0571 | - | hypothetical protein | -1.62 | -0.93 |
| Spy_0635 | *rpmA* | 50S ribosomal protein L27 | -1.6 | -0.65 |
| Spy_0142 | - | hypothetical protein | -1.56 | -1.37 |
| Spy_0529 | - | (Fe-S)-binding protein | -1.55 | -0.6 |
| Spy_0622 | - | methyltransferase | -1.53 | -0.78 |
| Spy_0639 | *pyrR* | putative pyrimidine regulatory protein | -1.49 | -0.33 |
| Spy_0551 | *rplS* | 50S ribosomal protein L19 | -1.48 | -0.58 |
| Spy_1386 | - | hypothetical protein | -1.45 | -0.98 |
| Spy_1527 | - | putative ABC transporter (permease) | -1.33 | -0.77 |
| Spy_0545 | *agaS* | putative tagatose-6-phosphate aldose/ketose isomerase | -1.22 | -0.6 |
| Spy_0195 | - | MarR family transcription regulator | -1.21 | -0.18 |
| Spy_1556 | - | hypothetical protein | -1.2 | -0.44 |
| Spy_0598 | *mscL* | large-conductance mechanosensitive channel | -1.16 | -0.64 |
| Spy_0143 | - | hypothetical protein | -1.11 | -0.85 |
| Spy_1290 | - | hypothetical protein | -1.07 | -0.79 |
| Spy_0144 | - | hypothetical protein | -1.03 | -1.04 |

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|---|---|---|---|---|
| Spy_1782 | *pepO* | neutral endopeptidase | -1.02 | -0.64 |
| Spy_1557 | *mutY* | A/G-specific adenine glycosylase | -1.02 | -0.31 |
| Spy_1407 | - | esterase | -1.01 | -0.64 |
| Spy_1171 | - | conserved hypothetical protein, phage associated | -0.99 | -0.91 |
| Spy_1738 | *spd/speMF* | phage-associated deoxyribonuclease | -0.98 | -0.72 |
| Spy_1578 | - | Cro/CI family transcription regulator | -0.75 | -1 |
| Spy_1732 | *prsA* | foldase PrsA | -0.38 | -1.31 |
| Spy_0157 | *opuAA* | glycine betaine transport ATP-binding protein | 0.32 | 1.15 |
| Spy_0158 | *opuABC* | glycine betaine-binding protein/glycine betaine transporter permease | 0.38 | 1.04 |
| Spy_1139 | *nagB* | glucosamine-6-phosphate isomerase | 0.5 | 1.36 |
| Spy_1137 | - | putative transcription factor | 0.6 | 1.06 |
| Spy_1499 | *grpE* | putative Hsp-70 cofactor | 0.76 | 1.05 |
| Spy_1733 | - | hypothetical protein | 0.97 | -0.46 |
| Spy_0476 | *bglA* | beta-glucosidase | 0.99 | 0.52 |
| Spy_1711 | *lmb* | putative laminin adhesion | 1 | 0.93 |
| Spy_0981 | *cfa* | cAMP factor | 1.05 | 0.59 |
| Spy_0029 | *purD* | phosphoribosylamine-glycine ligase | 1.08 | 0.7 |
| Spy_1637 | *lacB.2* | putative galactose-6-phosphate isomerase (B subunit) | 1.15 | 1.28 |
| Spy_0475 | - | beta-glucoside permease IIABC component | 1.2 | 0.62 |
| Spy_1477 | - | guanine-hypoxanthine permease | 1.22 | 0.56 |
| Spy_1735 | *speB* | cysteine protease SpeB | 1.27 | -0.32 |
| Spy_1636 | *lacC.2* | putative galactose-6-phosphate isomerase (C subunit) | 1.29 | 1.09 |
| Spy_0858 | *xpt* | xanthine phosphoribosyltransferase | 1.3 | 0.94 |
| Spy_0146 | *metB* | cystathionine beta-lyase | 1.36 | 0.83 |
| Spy_1638 | *lacA* | galactose-6-phosphate isomerase subunit LacA | 1.42 | 1.09 |
| Spy_0859 | - | xanthine permease | 1.73 | 0.84 |
| Spy_1401 | - | putative PTS system, enzyme IIA component | 1.74 | 0.72 |
| Spy_1106 | *grab* | protein G-related alpha 2M-binding protein | 2.21 | 1.72 |

Genes are listed for which a change in expression of 1 log2-fold or more, up or down, was observed in mutant strain 854 CsrS T284A compared to wild type 854.

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| Green or red shading is proportional to the degree of down- or up-regulation, respectively, in the mutant compared to wild type or during wild type growth in supplemental magnesium compared to unsupplemented broth. |
| *Gene locus numbers refer to MGAS5005 genome. |