| Gene Locus | Gene Name | Gene Product | Log2-fold change ΔcsrR vs. WT | Log2-fold change ΔropB vs. WT |
|------------|-----------|--------------|-------------------------------|-------------------------------|
| Spy_0017   | -         | putative secreted protein | -1.6                          | 1.04                          |
| Spy_0034   | -         | transcription regulator   | 2.45                          | -0.08                         |
| Spy_0113   | -         | transposase              | 3.75                          | -1.1                          |
| Spy_0115   | -         | hypothetical protein      | 7.2                           | -0.88                         |
| Spy_0139   | nga       | NAD glycohydrolase       | 5.03                          | -0.67                         |
| Spy_0140   | ifs       | NADase inhibitor         | 4.64                          | -0.58                         |
| Spy_0141   | slo       | streptolysin O           | 4.8                           | -0.46                         |
| Spy_0142   | -         | hypothetical protein      | 2.22                          | -1.56                         |
| Spy_0143   | -         | hypothetical protein      | 9.19                          | -1.37                         |
| Spy_0144   | -         | hypothetical protein      | 8.87                          | -1.38                         |
| Spy_0157   | opuAA     | glycine betaine transport ATP-binding protein | -2.27 | -0.04 |
| Spy_0158   | opuABC    | glycine betaine-binding protein/glycine betaine transporter permease | -2.84 | -0.49 |
| Spy_0186   | -         | transcription regulator   | 2.5                           | -0.05                         |
| Spy_0275   | -         | serine/threonine transporter SstT | -1.06 | 0.06 |
| Spy_0281   | -         | hypothetical protein      | 2.81                          | 0.81                          |
| Spy_0282   | csrR      | response regulator       | -7.21                         | 0.81                          |
| Spy_0351   | spyA      | C3 family ADP-ribosyltransferase | 4.73  | -0.03 |
| Spy_0352   | -         | hypothetical protein      | 6.11                          | -0.42                         |
| Spy_0355   | -         | hypothetical protein      | 1.54                          | -2.12                         |
| Spy_0356   | speJ      | exotoxin type J          | 1.22                          | -0.14                         |
| Spy_0402   | -         | hypothetical protein      | 1.29                          | -0.43                         |
| Spy_0500   | -         | N-acetylmuramoyl-L-alanine amidase | 1.62  | 0.21 |
| Spy_0501   | -         | hypothetical protein      | 1.14                          | -0.16                         |
| Spy_0561   | epf       | extracellular matrix binding protein | 3.47  | -1.12 |
| Spy_0562   | sagA      | streptolysin S           | 2.64                          | -1.06                         |
| Spy_0563   | sagB      | Streptolysin S synthesis protein | 2.93  | -0.55 |
| Spy_0571   | -         | hypothetical protein      | 1.93                          | 0.05                          |
| Spy_0598   | mscL      | large-conductance mechanosensitive channel | -1.77 | -0.64 |
| Spy_0639   | pyrR      | putative pyrimidine regulatory protein | -1.35 | 0.87 |
| Spy_0640   | pyrP      | putative uracil permease | -1.46 | 2.07 |
| Spy_0652   | -         | hypothetical protein      | -1.19                         | -0.12                         |
| Spy_0668   | mac       | IgG-degrading protease    | 3.83                          | -1.95                         |
| Spy_0673   | papS      | tRNA CCA-pyrophosphorylase | 1.29  | -0.03 |
| Spy_0713   | bcaT      | branched-chain amino acid aminotransferase | -1.14 | -0.54 |
| Spy_0777   | -         | hypothetical protein      | 2.68                          | 0.21                          |
| Spy_0784 | yesN  | putative two-component sensor histidine kinase | 1.02 | 0.12 |
|--------|-------|-----------------------------------------------|------|------|
| Spy_0809 | srtE  | conserved hypothetical protein - lantibiotic | 1.1  | -0.5 |
| Spy_0913 | -     | putative integrase/recombinase                 | -1.03| 0.4  |
| Spy_0947 | ciaH  | sensor protein                                 | 1.25 | -0.69|
| Spy_0966 | speA2 | enterotoxin                                    | 3.95 | -0.08|
| Spy_1139 | nagB  | glucosamine-6-phosphate isomerase             | -1.31| -0.93|
| Spy_1169 | spd3  | DNase                                         | 2.5  | -0.92|
| Spy_1170 | -     | hypothetical protein                           | 2.37 | -0.87|
| Spy_1171 | -     | conserved hypothetical protein, phage associated | 1.11 | -1.18|
| Spy_1284 | ccdA  | putative cytochrome C-type biogenesis protein | 1.08 | -1.26|
| Spy_1290 | -     | hypothetical protein                           | 3.41 | -0.81|
| Spy_1291 | -     | ATP-dependent RNA helicase                    | 3.57 | -0.59|
| Spy_1329 | -     | putative O-acetylserine lyase                  | -1.17| -0.32|
| Spy_1407 | -     | esterase                                       | 2.16 | 0.61 |
| Spy_1415 | sdaD2 | phage-encoded DNase                           | 1.49 | -0.84|
| Spy_1472 | hit   | bis(5’-nucleosyl)-tetraphosphatase (asymmetrical) | 0.98 | -0.05|
| Spy_1477 | -     | guanine-hypoxanthine permease                 | -1   | -0.05|
| Spy_1479 | manL  | PTS system mannose-specific transporter subunit IIAB | -2.13| -0.35|
| Spy_1499 | grpE  | putative Hsp-70 cofactor                      | -2.13| -0.02|
| Spy_1504 | -     | hypothetical protein                           | -1.36| -0.71|
| Spy_1531 | isp2  | hypothetical protein                           | 1.91 | 0.29 |
| Spy_1540 | endoS | endo-beta-N-acetylglucosaminidase F2           | 1.09 | 0.75 |
| Spy_1556 | -     | hypothetical protein                           | 3.75 | 0.54 |
| Spy_1557 | mutY  | A/G-specific adenine glycosylase               | 1.28 | 0.05 |
| Spy_1601 | -     | membrane protease                             | 1.92 | 0.59 |
| Spy_1635 | lacD.2| putative tagatose 1,6-diphosphate aldolase     | -2.11| 0.07 |
| Spy_1636 | lacC.2| putative galactose-6-phosphate isomerase (C subunit) | -1.77| 0.17|
| Spy_1637 | lacB.2| putative galactose-6-phosphate isomerase (B subunit) | -1.38| 0.42|
| Spy_1638 | lacA  | galactose-6-phosphate isomerase subunit LacA  | -1.92| 0.4  |
| Spy_1684 | -     | streptokinase                                 | 4.65 | -0.32|
| Spy_1687 | sclA  | hypothetical protein                           | 1.27 | -2.39|
| Spy_1702 | smeZ  | mitogenic exotoxin Z                          | 1.26 | -0.39|
| Spy_1704 | dppA  | dipeptide-binding protein                     | -1.21| -0.1 |
| Spy_1714 | -     | cell surface protein                          | 2.98 | -0.03|
| Gene locus | Description                          | Value1 | Value2 |
|------------|--------------------------------------|--------|--------|
| Spy_1715   | scpA  | C5A peptidase                     | 3.84   | -0.18  |
| Spy_1718   | sic1.01 | inhibitor of complement protein  | 6.14   | -0.04  |
| Spy_1719   | emm1.0 | M protein                         | 1.94   | 0.63   |
| Spy_1731   | -     | hypothetical protein              | 1.6    | 0.96   |
| Spy_1737   | ropB  | transcription regulator           | -1.49  | -7.46  |
| Spy_1738   | spd/speMF | phage-associated deoxyribonuclease | 1.7    | -0.95  |
| Spy_1825   | -     | PadR family transcription regulator | -2.75  | -0.88  |
| Spy_1851   | hasA  | hyaluronan synthase               | 3.13   | -2.06  |
| Spy_1857   | guaB  | inosine monophosphate dehydrogenase | -1.76  | -0.51  |

*Gene locus numbers refer to MGAS5005 genome.