

**Additional Table 2.** RNA-Seq results of *S. hominis* S34-1 wild-type versus S34-1Δ comparison

| Gene ID                         | S34-1 vs. ΔS34-1<br>Fold change | Annotation                                                                                   | P value     |
|---------------------------------|---------------------------------|----------------------------------------------------------------------------------------------|-------------|
| <i>Down-regulated in mutant</i> |                                 |                                                                                              |             |
| plasmid1_gene0006               | 0.1974148                       | MerR family transcriptional regulator [Lachnoclostridium]                                    | 1.97116E-84 |
| plasmid1_gene0013               | 0.4659825                       | hypothetical protein [Bacillus Hypothetical Cytosolic Protein<br>[Bacillus cereus BDRD-Cer4] | 5.98701E-18 |
| plasmid1_gene0017               | 0                               | thiocillin [Bacillus cereus]                                                                 | 6.8819E-62  |
| plasmid1_gene0022               | 0.3853318                       | replication protein [Staphylococcus warneri]                                                 | 9.90409E-26 |
| plasmid1_gene0023               | 0.2518031                       | glyoxalase [Staphylococcus glyoxalase family protein<br>[Staphylococcus hominis SK119]       | 2.06038E-13 |
| gene0016                        | 0.4995521                       | adenylosuccinate synthetase [Staphylococcus hominis]                                         | 1.90587E-10 |
| gene0174                        | 0.3635099                       | hypothetical protein [Salimicrobium sp. MJ3]                                                 | 0.044520716 |
| gene0283                        | 0.310019                        | hypothetical protein [Staphylococcus hominis]                                                | 0.00158768  |
| gene0315                        | 0.3165306                       | phosphoadenosine phosphosulfate reductase [Staphylococcus<br>hominis]                        | 5.537E-55   |
| gene0316                        | 0.4732922                       | sulfite reductase subunit alpha [Staphylococcus hominis]                                     | 5.63013E-28 |
| gene0317                        | 0.4340149                       | sulfite reductase [Staphylococcus hominis]                                                   | 9.20145E-35 |
| gene0318                        | 0.4745097                       | uroporphyrin-III C-methyltransferase [Staphylococcus<br>hominis]                             | 1.33711E-24 |
| gene0319                        | 0.3992826                       | precorrin-2 dehydrogenase [Staphylococcus hominis]                                           | 5.8159E-36  |
| gene0320                        | 0.3365521                       | membrane protein [Staphylococcus hominis]                                                    | 6.80074E-47 |
| gene0321                        | 0.3148598                       | sulfate adenylyltransferase [Staphylococcus sp. MDS7B]                                       | 1.97457E-51 |
| gene0322                        | 0.4232978                       | adenylylsulfate kinase [Staphylococcus hominis]                                              | 4.73001E-20 |
| gene0323                        | 0.3435355                       | Secretory antigen precursor SsaA [Staphylococcus<br>haemolyticus]                            | 5.42748E-38 |
| gene0362                        | 0.457624                        | transglycosylase [Staphylococcus hominis]                                                    | 2.36212E-16 |
| gene0459                        | 0.1974661                       | antiholin antiholin-like protein LrgB [Staphylococcus hominis<br>SK119]                      | 1.31418E-63 |
| gene0460                        | 0.2689859                       | murein hydrolase regulator LrgA [Staphylococcus hominis]                                     | 5.45027E-06 |
| gene0585                        | 0.4100433                       | hypothetical protein [Staphylococcus hominis]                                                | 3.60897E-14 |
| gene0798                        | 0.4052194                       | threonine dehydratase [Staphylococcus sp. MDS7B]                                             | 4.7018E-10  |
| gene0799                        | 0.2999272                       | isopropylmalate isomerase [Staphylococcus sp. MDS7B]                                         | 0.005190309 |
| gene0800                        | 0.3581454                       | 3-isopropylmalate dehydratase large subunit [Staphylococcus<br>sp. M0480]                    | 4.6616E-22  |
| gene0801                        | 0.3364761                       | 3-isopropylmalate dehydrogenase [Staphylococcus hominis]                                     | 2.1155E-09  |
| gene0803                        | 0.4749364                       | ketol-acid reductoisomerase [Staphylococcus]                                                 | 1.48717E-07 |
| gene0865                        | 0.4159535                       | hypothetical protein [Staphylococcus]                                                        | 0.001655029 |
| gene0880                        | 0.4293661                       | hypothetical protein [Staphylococcus]                                                        | 0.040796675 |
| gene1164                        | 0.4882841                       | DNA repair protein RecO [Staphylococcus hominis]                                             | 2.7669E-06  |
| gene1198                        | 0.3286667                       | hypothetical protein [Staphylococcus]                                                        | 0.003210093 |
| gene1388                        | 0.07568076                      | hypothetical protein [Staphylococcus hominis]                                                | 1.33371E-05 |
| gene1427                        | 0.4999374                       | 30S ribosomal protein S15 [Staphylococcus hominis]                                           | 1.52901E-10 |
| gene1498                        | 0.4836645                       | carbamoyl phosphate synthase small subunit [Staphylococcus]                                  | 4.0337E-26  |
| gene1641                        | 0.1983068                       | hypothetical protein [Staphylococcus hominis]                                                | 0.007495549 |
| gene1647                        | 0.3457724                       | hypothetical protein [Staphylococcus hominis]                                                | 1.10924E-05 |
| gene1670                        | 0.4924082                       | peptide ABC transporter substrate-binding protein<br>[Staphylococcus hominis]                | 9.4584E-11  |
| gene1925                        | 0.3462109                       | MerR family transcriptional regulator [Staphylococcus<br>hominis]                            | 7.0314E-17  |
| gene1970                        | 0.1643757                       | -                                                                                            | 0.001583033 |
| gene2097                        | 0.4948841                       | methionine ABC transporter substrate-binding protein<br>[Staphylococcus]                     | 5.24376E-09 |
| gene2098                        | 0.4699187                       | methionine ABC transporter permease [Staphylococcus<br>hominis]                              | 8.82595E-07 |
| gene2102                        | 0.4515412                       | cysteine synthase [Staphylococcus hominis]                                                   | 2.62215E-26 |
| <i>Up-regulated in mutant</i>   |                                 |                                                                                              |             |

|          |          |                                                                                    |             |
|----------|----------|------------------------------------------------------------------------------------|-------------|
| gene0163 | 3.323146 | hypothetical protein [Staphylococcus hominis]                                      | 2.80494E-68 |
| gene0215 | 2.249664 | diacetyl reductase [(S)-acetoin forming]                                           | 1.13075E-38 |
| gene0347 | 2.097634 | alpha-acetolactate decarboxylase [Staphylococcus hominis]                          | 9.5416E-06  |
| gene0369 | 2.134515 | short-chain dehydrogenase [Staphylococcus sp. MDS7B]                               | 1.80545E-32 |
| gene0412 | 2.040101 | acetyltransferase [Staphylococcus hominis]                                         | 1.54116E-10 |
| gene0419 | 2.030836 | MoeB [Staphylococcus sp. MDS7B]                                                    | 1.33826E-05 |
| gene0437 | 2.889369 | hypothetical protein [Staphylococcus]                                              | 4.85642E-21 |
| gene0455 | 2.365682 | glycine/betaine ABC transporter ATP-binding protein [Staphylococcus sp. MDS7B]     | 6.37696E-13 |
| gene0456 | 2.321234 | choline ABC transporter permease [Staphylococcus hominis]                          | 1.30728E-12 |
| gene0457 | 2.677133 | choline ABC transporter permease [Staphylococcus]                                  | 2.88621E-32 |
| gene0458 | 2.970472 | glycine/betaine ABC transporter substrate-binding protein [Staphylococcus hominis] | 4.36403E-50 |
| gene0474 | 2.029366 | cell wall biosynthesis protein ScdA [Staphylococcus hominis]                       | 2.61619E-06 |
| gene1592 | 2.339765 | cytochrome D ubiquinol oxidase subunit II [Staphylococcus]                         | 1.88039E-29 |
| gene1919 | 2.167976 | hypothetical protein [Staphylococcus hominis]                                      | 2.56687E-17 |
| gene2162 | 2.240674 | hypothetical protein [Staphylococcus sp. MDS7B]                                    | 1.48568E-13 |

---