Supplemental Table S6: Functions enriched amongst gene sets analyzed with STRING databases. Sets of gene names corresponding to significant COGs, SNPs, and k-mers were created as described in the Materials and Methods section.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Term ID | term description | observed gene count | background gene count | false discovery rate |
| **p0045** |  |  |  |  |
| PFAM Protein Domains |  |  |
| PF10651 | Domain of unknown function (DUF2479) | 2 | 2 | 0.041 |
| **p0006** |  |  |  |  |
| none |  |  |  |  |
| **p0017** |  |  |  |  |
| SMART Protein Domains |  |  |
| SM00062 | Bacterial periplasmic substrate-binding proteins | 2 | 2 | 0.015 |
| SM00287 | Bacterial SH3 domain homologues | 2 | 4 | 0.0183 |
| Reference publications |  |  |
| PMID:29270158 | (2017) Commercial Biocides Induce Transfer of Prophage Phi13 from Human Strains of Staphylococcus aureus to Livestock CC398. | 4 | 6 | 0.007 |
| PMID:28515479 | (2017) Acquisition of virulence factors in livestock-associated MRSA: Lysogenic conversion of CC398 strains by virulence gene-containing phages. | 3 | 4 | 0.0397 |
| **p0017S** |  |  |  |  |
| PFAM Protein Domains |  |  |
| PF01420 | Type I restriction modification DNA specificity domain | 2 | 2 | 0.0149 |
| INTERPRO Protein Domains and Features |  |
| IPR000055 | Restriction endonuclease, type I, HsdS | 2 | 2 | 0.02 |
| **p002y** |  |  |  |  |
| Biological Process (GO) |  |  |
| GO:0008152 | metabolic process | 105 | 530 | 0.0464 |
| Molecular Function (GO) |  |  |
| GO:0046872 | metal ion binding | 36 | 135 | 0.0403 |
| GO:0005488 | binding | 81 | 393 | 0.0403 |
| GO:0003824 | catalytic activity | 91 | 451 | 0.0403 |
| GO:0043167 | ion binding | 58 | 270 | 0.0425 |
| UniProt Keywords |  |  |  |
| KW-0067 | ATP-binding | 56 | 244 | 0.0442 |
| **p003p** |  |  |  |  |
| none |  |  |  |  |
| **p0040** |  |  |  |  |
| KEGG Pathways |  |  |  |
| sauw00051 | Fructose and mannose metabolism | 3 | 15 | 0.0072 |
| PFAM Protein Domains |  |  |
| PF10651 | Domain of unknown function (DUF2479) | 2 | 2 | 0.0094 |
| PF05031 | Iron Transport-associated domain | 2 | 4 | 0.0116 |
| INTERPRO Protein Domains and Features |  |
| IPR018913 | BppU, N-terminal | 2 | 2 | 0.0208 |
| IPR037250 | NEAT domain superfamily | 2 | 4 | 0.0257 |
| IPR006635 | NEAT domain | 2 | 4 | 0.0257 |
| SMART Protein Domains |  |  |
| SM00725 | NEAr Transporter domain | 2 | 4 | 0.0107 |
| **pyo** |  |  |  |  |
| Keyword |  |  |  |  |
| KW-0479 | Metal-binding | 33 | 218 | 3.66E-05 |
| KW-0963 | Cytoplasm | 38 | 310 | 0.00025 |
| KW-0560 | Oxidoreductase | 20 | 133 | 0.004 |
| KW-0460 | Magnesium | 14 | 83 | 0.0131 |
| KW-0808 | Transferase | 29 | 279 | 0.0243 |
| KW-0143 | Chaperone | 6 | 19 | 0.0311 |
| KW-0456 | Lyase | 12 | 74 | 0.0311 |
| KEGG |  |  |  |  |
| sauw01100 | Metabolic pathways | 57 | 424 | 1.00E-08 |
| sauw01110 | Biosynthesis of secondary metabolites | 29 | 214 | 0.00041 |
| sauw00240 | Pyrimidine metabolism | 9 | 40 | 0.0174 |
| sauw01130 | Biosynthesis of antibiotics | 20 | 164 | 0.0185 |
| sauw00130 | Ubiquinone and other terpenoid-quinone biosynthesis | 4 | 8 | 0.0263 |
| sauw00260 | Glycine, serine and threonine metabolism | 7 | 29 | 0.0263 |
| sauw01120 | Microbial metabolism in diverse environments | 16 | 123 | 0.0263 |
| sauw03070 | Bacterial secretion system | 4 | 9 | 0.03 |
| Component |  |  |  |
| GO:0005737 | cytoplasm | 41 | 334 | 3.23E-05 |
| GO:0044424 | intracellular part | 43 | 351 | 3.23E-05 |
| GO:0044464 | cell part | 49 | 495 | 0.00034 |
| GO:0044444 | cytoplasmic part | 16 | 128 | 0.0216 |
| Function |  |  |  |  |
| GO:0043167 | ion binding | 39 | 270 | 1.05E-05 |
| GO:0046872 | metal ion binding | 26 | 135 | 1.05E-05 |
| GO:0003824 | catalytic activity | 51 | 451 | 2.17E-05 |
| GO:0005488 | binding | 45 | 393 | 7.96E-05 |
| GO:0036094 | small molecule binding | 25 | 191 | 0.0029 |
| GO:0097159 | organic cyclic compound binding | 33 | 305 | 0.0052 |
| GO:1901363 | heterocyclic compound binding | 33 | 305 | 0.0052 |
| GO:0046914 | transition metal ion binding | 8 | 26 | 0.0056 |
| GO:0016740 | transferase activity | 20 | 147 | 0.006 |
| GO:0048037 | cofactor binding | 11 | 52 | 0.006 |
| GO:0043168 | anion binding | 22 | 179 | 0.0089 |
| GO:0000287 | magnesium ion binding | 5 | 10 | 0.0107 |
| GO:0005515 | protein binding | 6 | 17 | 0.0123 |
| GO:0000166 | nucleotide binding | 21 | 177 | 0.0146 |
| GO:0008144 | drug binding | 17 | 147 | 0.0471 |
| GO:0097367 | carbohydrate derivative binding | 18 | 159 | 0.0471 |
| GO:0005524 | ATP binding | 16 | 136 | 0.0495 |
| Process |  |  |  |  |
| GO:0009987 | cellular process | 58 | 519 | 3.41E-05 |
| GO:0008152 | metabolic process | 58 | 530 | 3.45E-05 |
| GO:0044237 | cellular metabolic process | 53 | 469 | 3.45E-05 |
| GO:0044281 | small molecule metabolic process | 32 | 208 | 3.45E-05 |
| GO:0071704 | organic substance metabolic process | 55 | 492 | 3.45E-05 |
| GO:0006807 | nitrogen compound metabolic process | 48 | 423 | 8.62E-05 |
| GO:0044238 | primary metabolic process | 49 | 439 | 8.62E-05 |
| GO:1901564 | organonitrogen compound metabolic process | 36 | 306 | 0.0011 |
| GO:0034641 | cellular nitrogen compound metabolic process | 35 | 316 | 0.0041 |
| GO:0006082 | organic acid metabolic process | 20 | 135 | 0.0054 |
| GO:0046483 | heterocycle metabolic process | 29 | 248 | 0.006 |
| GO:1901576 | organic substance biosynthetic process | 35 | 326 | 0.006 |
| GO:0019752 | carboxylic acid metabolic process | 18 | 118 | 0.0063 |
| GO:1901565 | organonitrogen compound catabolic process | 8 | 25 | 0.0065 |
| GO:0006725 | cellular aromatic compound metabolic process | 28 | 243 | 0.0067 |
| GO:0044249 | cellular biosynthetic process | 34 | 322 | 0.0067 |
| GO:1901360 | organic cyclic compound metabolic process | 29 | 256 | 0.0067 |
| GO:0044282 | small molecule catabolic process | 9 | 34 | 0.0069 |
| GO:0009056 | catabolic process | 12 | 61 | 0.0072 |
| GO:0044248 | cellular catabolic process | 11 | 52 | 0.0072 |
| GO:0016054 | organic acid catabolic process | 7 | 22 | 0.0118 |
| GO:0008610 | lipid biosynthetic process | 8 | 30 | 0.0122 |
| GO:1901135 | carbohydrate derivative metabolic process | 16 | 109 | 0.0122 |
| GO:0006139 | nucleobase-containing compound metabolic process | 24 | 208 | 0.0131 |
| GO:0009063 | cellular amino acid catabolic process | 6 | 16 | 0.0131 |
| GO:1901606 | alpha-amino acid catabolic process | 6 | 16 | 0.0131 |
| GO:0055086 | nucleobase-containing small molecule metabolic process | 12 | 69 | 0.014 |
| GO:1901575 | organic substance catabolic process | 11 | 60 | 0.0153 |
| GO:0044255 | cellular lipid metabolic process | 8 | 33 | 0.0162 |
| GO:0006520 | cellular amino acid metabolic process | 13 | 83 | 0.0184 |
| GO:0006796 | phosphate-containing compound metabolic process | 15 | 110 | 0.0268 |
| GO:1901605 | alpha-amino acid metabolic process | 10 | 58 | 0.0319 |
| GO:0019637 | organophosphate metabolic process | 12 | 83 | 0.0438 |
| GO:0006457 | protein folding | 4 | 9 | 0.0454 |