#### Supplemental Table S5: Summary statistics for protein-protein interaction networks identified with STRING amongst genes corresponding to significant SNPs or k-mers (inside or adjacent to genes). PPI enrichment p-value corresponds to the likelihood nodes and edges would be selected from the *S. aureus* database by chance.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage | p0045 | p0006 | p0017 | p0017S | p002y | p003p | p0040 | pyo |
| number of nodes | 39 | 33 | 49 | 25 | 405 | 214 | 25 | 164 |
| number of edges | 18 | 6 | 26 | 6 | 1075 | 347 | 10 | 304 |
| average node degree | 0.92 | 0.36 | 1.06 | 0.48 | 5.31 | 3.24 | 0.8 | 3.71 |
| avg. local clustering coefficient | 0.36 | 0.30 | 0.33 | 0.21 | 0.38 | 0.38 | 0.52 | 0.38 |
| expected number of edges | 6 | 6 | 18 | 4 | 930 | 287 | 5 | 243 |
| PPI enrichment p-value | 0.00015 | 0.62 | 0.038 | 0.23 | 1.77E-06 | 3.24E-04 | 0.036 | 9.45E-05 |