

Supplemental Table S1. Daptomycin (DAP) MICs, *mprF* single nucleotide polymorphisms (SNPs), surface charge, host defense peptide susceptibilities, and cell wall thickness profiles of the study strains.

| Strains | DAP MICs (μG/ML) | <i>mprF</i> SNPs [#] | Surface charge [§] | % survival against tPMPs [¶] | | % survival against hNP-1 [¶] | | Cell wall thickness (nm) [†] |
|---------|---------------------|-------------------------------|--------------------------------|--|---------|--|----------|--|
| | | | | 2 μg/ml | 1 μg/ml | 20 μg/ml | 10 μg/ml | |
| G1 | ≤0.5 | - | 87 ± 13 | 12 | 34 | 9 | 21 | 19 |
| G10 | ≤0.5 | - | 78 ± 10 | 33 | 41 | 8 | 27 | 23 |
| G12 | ≤0.5 | - | 132 ± 13 | 28 | 34 | 28 | 49 | 24 |
| G14 | ≤0.5 | - | 129 ± 17 | 42 | 60 | 47 | 68 | 27 |
| G16 | ≤0.5 | - | 174 ± 18 | 13 | 17 | 32 | 51 | 25 |
| G34 | ≤0.5 | - | 113 ± 26 | 10 | 14 | 13 | 30 | 25 |
| G40 | ≤0.5 | - | 148 ± 16 | 1 | 14 | 26 | 39 | 25 |
| G70 | ≤0.5 | - | 152 ± 26 | 1 | 0 | 1 | 11 | 24 |
| G71 | ≤0.5 | - | 116 ± 2.5 | 4 | 10 | 1 | 4 | 25 |
| G72 | ≤0.5 | - | 138 ± 22 | 3 | 8 | 8 | 16 | 27 |
| G89 | ≤0.5 | - | 194 ± 13 | 2 | 1 | 0 | 2 | 22 |
| G80 | ≤0.5 | I498N | 105 ± 8 | 2 | 16 | 1 | 11 | 25 |
| G86 | ≤0.5 | I498N | 93 ± 15 | 3 | 11 | 21 | 34 | 28 |
| G87 | ≤0.5 | I498N | 208 ± 15 | 1 | 11 | 58 | 79 | 26 |
| G88 | ≤0.5 | I498N | 141 ± 30 | 5 | 15 | 11 | 34 | 29 |
| G90 | ≤0.5 | I498N | 105 ± 18 | 2 | 19 | 11 | 31 | 26 |
| | | | | | | | | |
| G9 | 1 | - | 86 ± 18 | 29 | 41 | 23 | 51 | 25 |
| G35 | 1 | - | 89 ± 22 | 22 | 26 | 40 | 29 | 26 |
| G38 | 1 | - | 138 ± 28 | 36 | 40 | 50 | 67 | 26 |
| G69 | 1 | - | 127 ± 24 | 55 | 78 | 58 | 71 | 27 |
| G74 | 1 | - | 171 ± 18 | 8 | 21 | 14 | 16 | 23 |
| G94 | 1 | - | 180 ± 18 | 1 | 2 | 0 | 0 | 25 |
| G47 | 1 | Q692E | 190 ± 35 | 20 | 44 | 8 | 24 | 23 |
| G53 | 1 | Q692E | 190 ± 33 | 55 | 78 | 15 | 42 | 31 |
| G56 | 1 | Q692E | 115 ± 23 | 76 | 85 | 47 | 64 | 28 |
| G51 | 1 | > 30 SNPs | 180 ± 23 | 23 | 48 | 12 | 38 | 24 |
| G66 | 1 | > 30 SNPs | 87 ± 32 | 63 | 63 | 18 | 36 | 25 |

| 161 | 4 | L826F | 90 ± 14 | 24 | 52 | 71 | 73 | 22 |
|-----|---|-------|----------|----|----|-----|----|----|
| 165 | 4 | L341S | 103 ± 25 | 16 | 18 | 17 | 39 | 19 |
| 167 | 4 | L826F | 100 ± 10 | 83 | 99 | 100 | 86 | 22 |
| 169 | 4 | L826F | 105 ± 9 | 97 | 97 | 56 | 80 | 29 |
| 212 | 2 | L826F | 89 ± 24 | 20 | 45 | 41 | 64 | 28 |
| 234 | 2 | L826F | 90 ± 22 | 31 | 59 | 86 | 91 | 25 |
| 235 | 3 | L341S | 77 ± 7 | 41 | 63 | 38 | 48 | 29 |
| 333 | 2 | L826F | 64 ± 14 | 33 | 39 | 27 | 43 | 24 |

[#]*mprF* SNPs compared to the *mprF* sequences from *S. aureus* Mu50 (CC5).

^{\$}% cytochrome *c* bound vs *S. aureus* MU50. The higher the amounts of bound cytochrome *c*, the less relative positive surface charge exists.

[¥]Mean % survival of the strains after 2h exposure to host defense peptides (three experimental runs).

[†]Mean of 100 measurements for each strain.