Supplementary Material

| | Romulus (NC_020877) | Stab21 (LR215719) | Sb-1 | Intesti13 | K (NC_005880) |
|------------------------|------------------------|----------------------|------|-----------|------------------|
| Romulus (NC_020877) | 100 | 42.5 | 43.4 | 43.3 | 43.1 |
| Stab21 (LR215719) | | 100 | 91.1 | 91.1 | 92.4 |
| Sb-1 | | | 100 | 99.7 | 96.7 |
| Intesti13 | | | | 100 | 96.8 |
| K (NC_005880) | | | | | 100 |

Figure S1. Percent genome similarity of the five phages (constructed in VIRIDIC using singlecopy genomes)

Supplementary Tables 1 through 3 show selected results of dilution spot assays conducted on the BIMs that were isolated in this study. Up to 8 BIMs per phage+host pairing was subcultured from their original isolation plate, re-grown in broth, and challenged in spot dilution assays. The red text "DNG on HIBA" means that no colonies could be recovered when this BIM was picked from the isolation plate and streaked on a fresh HIBA plate. Similarly, "DNG in HIB" indicates that this BIM could not be subsequently grown on broth, despite several attempts. These BIMs were therefore classified as being sensitive to the original challenge phage and are marked as S*. See the Figure 1 caption for explanation of color-coded cells.

| Isolated BIMs | S. gureus Strain | Phage Titer, log10(1+PFU/mL) | | | | | | |
|---------------|---------------------|------------------------------|------|-----------|--------|---------|--|--|
| against Phage | S. dureus Strain | К | Sb-1 | Intesti13 | Stab21 | Romulus | | |
| К | 19685 (parental) | 8.05 | 7.68 | 7.75 | 7.85 | 5.68 | | |
| ĸ | BIM#1 (DNG on HIBA) | S* | - | - | - | - | | |
| | D712 (parental) | 7.86 | 7.41 | 8.12 | 7.38 | 0.00 | | |
| | BIM#5 (DNG on HIBA) | S* | - | - | - | - | | |
| к | BIM#3 (DNG on HIBA) | S* | - | - | - | - | | |
| ĸ | BIM#2 | 0.00 | 7.92 | 7.95 | 7.00 | 0.00 | | |
| | BIM#4 | 0.00 | 6.60 | 6.78 | 0.00 | 0.00 | | |
| | BIM#1 | 0.00 | 4.56 | 4.82 | 0.00 | 0.00 | | |
| | 8015 (parental) | 7.95 | 7.16 | 7.99 | 7.58 | 0.00 | | |
| К | BIM#1 | 7.79 | 7.97 | 7.79 | 7.38 | 0.00 | | |
| | BIM#2 | 0.00 | 7.66 | 7.79 | 7.45 | 0.00 | | |
| | 306 (parental) | 8.11 | 7.38 | 7.92 | 7.89 | 7.58 | | |
| К | BIM#2 | 7.30 | 7.75 | 7.51 | 7.41 | 7.91 | | |
| | BIM#1 | 2.60 | 2.90 | 0.00 | 0.00 | 6.99 | | |

Table S1. Phage Sensitivity of BIMs that were isolated against phage K

| Isolated BIMs | S. gureus Strain | Phage Titer, log10(1+PFU/mL) | | | | | | |
|---------------|--------------------|------------------------------|------|-----------|--------|---------|--|--|
| against Phage | J. dureus Strain | К | Sb-1 | Intesti13 | Stab21 | Romulus | | |
| Intesti13 | 19685 (parental) | 8.05 | 7.68 | 7.75 | 7.85 | 5.68 | | |
| Intesti15 | BIM#1 | 0.00 | 0.00 | 0.00 | 0.00 | 5.73 | | |
| | D712 (parental) | 7.86 | 7.41 | 8.12 | 7.38 | 0.00 | | |
| Intesti13 | BIM#4 (DNG in HIB) | NA | NA | S* | NA | NA | | |
| | 8015 (parental) | 7.95 | 7.16 | 7.99 | 7.58 | 0.00 | | |
| Intesti13 | BIM#1 | 7.58 | 7.79 | 7.70 | 7.53 | 0.00 | | |
| | 306 (parental) | 8.11 | 7.38 | 7.92 | 7.89 | 7.58 | | |
| | BIM#8 | 7.90 | 7.30 | 7.30 | 7.38 | 7.90 | | |
| | BIM#2 | 7.00 | 4.41 | 3.34 | 7.30 | 7.79 | | |
| | BIM#3 | 6.60 | 4.48 | 3.15 | 7.08 | 7.81 | | |
| Intesti13 | BIM#6 | 7.90 | 4.73 | 3.51 | 6.60 | 7.99 | | |
| | BIM#7 | 7.30 | 4.90 | 3.78 | 7.30 | 7.86 | | |
| | BIM#4 | 3.15 | 4.34 | 0.00 | 0.00 | 7.87 | | |
| | BIM#5 | 2.90 | 3.90 | 3.00 | 2.60 | 8.01 | | |
| | BIM#1 | 3.00 | 4.30 | 2.90 | 2.78 | 8.00 | | |

 Table S2. Phage sensitivity of BIMS that were isolated against phage Intesti13

| Table S3. F | Phage | sensitivity | of | BIMs | that | were | isolated | against | Romulus |
|-------------|-------|-------------|----|------|------|------|----------|---------|---------|
| | | | | | | | | | |

| C gurgus Strain | Phage Titer, log10(1+PFU/mL) | | | | | | |
|---------------------|---|---|--|--|--|--|--|
| S. dureus Strain | К | Sb-1 | Intesti13 | Stab21 | Romulus | | |
| 19685 (parental) | 8.05 | 7.68 | 7.75 | 7.85 | 5.68 | | |
| BIM#5 (DNG on HIBA) | - | - | - | - | S* | | |
| BIM#2 | 7.88 | 8.26 | 8.19 | 7.96 | 0.00 | | |
| BIM#3 | 8.00 | 8.16 | 8.27 | 7.76 | 0.00 | | |
| BIM#4 | 7.89 | 8.11 | 8.15 | 7.60 | 0.00 | | |
| BIM#6 | 8.11 | 8.41 | 8.41 | 7.76 | 0.00 | | |
| BIM#7 | 8.05 | 8.11 | 8.22 | 7.70 | 0.00 | | |
| BIM#8 | 8.08 | 8.66 | 8.45 | 3.51 | 3.51 | | |
| BIM#1 | 7.94 | 8.51 | 8.64 | 0.00 | 0.00 | | |
| | BIM#5 (DNG on HIBA) BIM#2 BIM#3 BIM#4 BIM#6 BIM#7 BIM#8 | K 19685 (parental) 8.05 BIM#5 (DNG on HIBA) - BIM#2 7.88 BIM#3 8.00 BIM#4 7.89 BIM#6 8.11 BIM#7 8.05 BIM#8 8.08 | S. aureus Strain K Sb-1 19685 (parental) 8.05 7.68 BIM#5 (DNG on HIBA) - - BIM#2 7.88 8.26 BIM#3 8.00 8.16 BIM#4 7.89 8.11 BIM#6 8.11 8.41 BIM#7 8.05 8.11 BIM#8 8.08 8.66 | S. aureus Strain K Sb-1 Intesti13 19685 (parental) 8.05 7.68 7.75 BIM#5 (DNG on HIBA) - - - BIM#2 7.88 8.26 8.19 BIM#3 8.00 8.16 8.27 BIM#4 7.89 8.11 8.15 BIM#5 8.05 8.11 8.41 BIM#6 8.11 8.41 8.41 BIM#7 8.05 8.11 8.22 BIM#8 8.08 8.66 8.45 | S. aureus Strain K Sb-1 Intesti13 Stab21 19685 (parental) 8.05 7.68 7.75 7.85 BIM#5 (DNG on HIBA) - - - - BIM#2 7.88 8.26 8.19 7.96 BIM#3 8.00 8.16 8.27 7.76 BIM#4 7.89 8.11 8.15 7.60 BIM#6 8.11 8.41 7.76 BIM#7 8.05 8.11 8.22 7.70 BIM#8 8.08 8.66 8.45 3.51 | | |

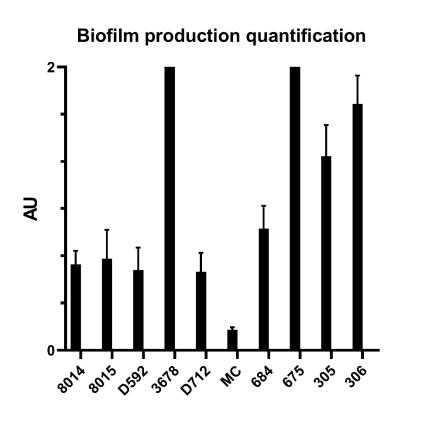




Figure S2. Biofilm formation by three strain pairs, relative to the *S. aureus* 3678 (reference biofilm forming strain ATCC 35556) positive control and media only (MC) negative control.

| Strain D712 | | | 8014 | | | |
|-------------|---------------|----------------|---------------|-------------|--|--|
| Antibiotic | MIC (mg/L) | MBIC (mg/L) | MIC (mg/L) | MBIC (mg/L) | | |
| DAP | 4 | 8 | 0.5 | 8 | | |
| VAN | 4 | 8 | 2 | 8 | | |
| СРТ | 0.5 | 4 | 1 | 1 | | |

Table.S4: List of MIC values in planktonic and biofilm state.

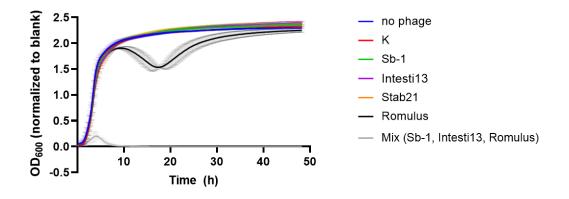


Figure S3. Planktonic growth of a Stab21-insensitive BIM of *S. aureus* 306 in the presence of single phages or a three-phage cocktail. Initial quantities of bacteria and phages were approximately 3×10^6 CFU and 1×10^5 PFU, respectively.