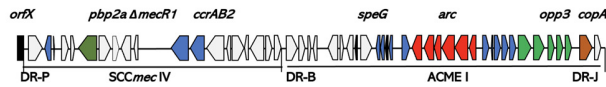
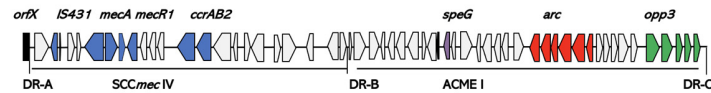


Supplementary file1

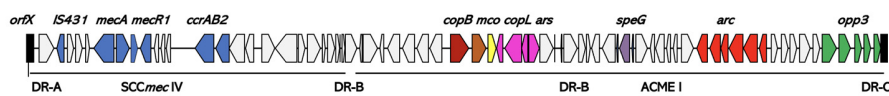
(A) Reference ACME type I: *S. aureus* FPR3757 (USA300)



(B) 4561, ACME I (51871 bp)



(C) 57114, ACME I (74673 bp)



(D) 292, ACME I (82634 bp)



(E) 5034, ACME I (77434 bp)

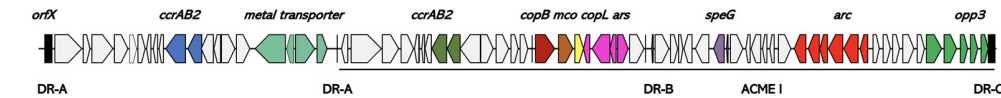


Figure S1. Schematic representation of ACME-I in *S. epidermidis*. comparative maps of ACME-I composite island in 4 ST-200, ST-new, ST-598 and ST-2 *S. epidermidis* isolates. The size of each ACME composite island is indicated after the strain names. Four distinct ACME-I composite island were defined according to the additional modules in these elements (B-E). Each gene or group of genes of interest is shaded in color; *arc* (red) and *opp3* operon (light green), *speG* (light purple), *copB* (Maroon), *mco* (orange), *copL* (orange), *ars* operon (pink), *mecA*, *mecR1*, *IS431*, *IS1272*, and *ccrAB2* (dark blue). The direct repeat (DR) sequences DRA, DR-B, DR-C are indicated.