

Table S1. Antimicrobial susceptibility of *S. aureus* and *E. coli* strains to erythromycin, determined using broth microdilution

Strain	Antibiotic resistance gene ^a	MIC of erythromycin (μg/ml)	Reference
<i>S. aureus</i> /vector			
RN4220/pBUS1	<i>tet(L)</i>	≤0.5	(1)
RN4220/pBUS1-P _{cap}	<i>tet(L)</i>	≤0.5	This study
RN4220/pBUS1-P _{cap} -HC	<i>tet(L)</i>	≤0.5	This study
RN4220/pTSSC-P _{cap}	<i>tet(L)</i>	≤0.5	This study
RN4220/pTSSCm-P _{cap}	<i>tet(L)</i>	≤0.5	This study
RN4220/pJW13	<i>tet(L), erm(44)</i>	>256	(2)
RN4220/pJW13-HC	<i>tet(L), erm(44)</i>	>256	This study
RN4220/pTJW13	<i>tet(L), erm(44)</i>	>256	This study
RN4220/pJW13-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	>256	This study
RN4220/pJW13-HC-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	>256	This study
RN4220/pTJW13-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	>256	This study
<i>E. coli</i> /vector			
AG100A/pBUS1	<i>tet(L)</i>	4	(1); this study
AG100A/pBUS1-P _{cap}	<i>tet(L)</i>	4	This study
AG100A/pBUS1-P _{cap} -HC	<i>tet(L)</i>	4	This study
AG100A/pJW13	<i>tet(L), erm(44)</i>	64	This study
AG100A/pJW13-HC	<i>tet(L), erm(44)</i>	64	This study
AG100A/pJW13-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	64	This study
AG100A/pJW13-HC-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	64	This study
AG100/pTSSC-P _{cap}	<i>tet(L)</i>	64	This study
AG100/pTSSCm-P _{cap}	<i>tet(L)</i>	64	This study
AG100/pTJW13	<i>tet(L), erm(44)</i>	>256	This study
AG100/pTJW13-RGS-His	<i>tet(L), erm(44)-rgs-his₆</i>	>256	This study

^a Antibiotic resistance genes: *erm(44)*, macrolide-lincosamide-streptogramin B rRNA methylase gene; *erm(44)-rgs-his₆*, *erm(44)* with CSRGSHHHHH codons fused to the 3' end of the gene; *tet(L)* tetracycline efflux gene.

REFERENCES

1. Rossi J, Bischoff M, Wada A, Berger-Bächi B. 2003. MsrR, a putative cell envelope-associated element involved in *Staphylococcus aureus* *sarA* attenuation. *Antimicrob. Agents Chemother.* **47**:2558-2564.
2. Wipf JRK, Schwendener S, Perreten V. 2014. The novel macrolide-lincosamide-streptogramin B resistance gene *erm(44)* is associated with a prophage in *Staphylococcus xylosus*. *Antimicrob. Agents Chemother.* **58**:6133-6138.

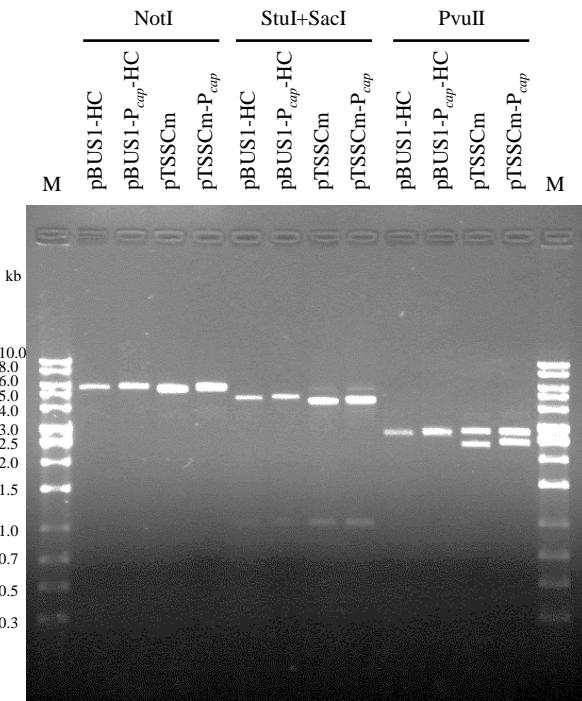


FIG. S1. Restriction digestion pattern of the shuttle vectors isolated from *S. aureus* RN4220. Fifty nanograms (pBUS1-HC, pBUS1- P_{cap} -HC) or 100 ng (pTSSCm and pTSSCm- P_{cap}) of the double-stranded DNA was used for restriction digest. The vectors were linearized using NotI. The presence of the 1-kb fragment containing *rrnB*(T1)₅ was confirmed after StuI and SacI digestion. The PvuII-cleavage products were 0.2 kb, 2.7 kb and 2.7 kb for pBUS1-HC; 0.2 kb, 2.7 kb and 2.8 kb for pBUS1- P_{cap} -HC; 0.2 kb, 2.3 kb and 2.8 kb for pTSSCm; and 0.2, 2.4 and 2.8 kb for pTSSCm- P_{cap} . M: 1 kb DNA ladder (Solis BioDyne).