

Table S1:

Species (indicator strain)	Group	Zone of inhibition diameter (mm)	
		GS-5	Δ smbAB
<i>S. uberis</i> (UT387)	Pyogenic	26.0 ± 2.0	12.0 ± 1.0
<i>S. agalactiae</i> (NEM306)	Pyogenic	18.0 ± 0.5	4.0 ± 1.0
<i>S. agalactiae</i> (A909)	Pyogenic	19.0 ± 1.0	4.0 ± 1.0
<i>S. dysgalactiae</i> (CI)	Pyogenic	26.0 ± 1.0	0.0 ± 0.0
<i>S. iniae</i> (K388)	Pyogenic	31.0 ± 1.0	7.0 ± 1.0
<i>S. pyogenes</i> (JRS4)*	Pyogenic	26.0 ± 1.0	9.5 ± 1.5
<i>S. pyogenes</i> (AM3)	Pyogenic	24.0 ± 1.0	10.5 ± 1.5
<i>S. pyogenes</i> (K32)	Pyogenic	28.0 ± 1.0	10.5 ± 1.5
<i>S. anginosus</i> (CI)	Anginosus	16.0 ± 1.0	4.5 ± 0.5
<i>S. constellatus</i> (CI)	Anginosus	10.0 ± 1.0	4.5 ± 0.5
<i>S. gordonii</i> (DL-1)*	Mitis	9.5 ± 0.5	4.0 ± 0.5
<i>S. gordonii</i> (M5)	Mitis	11.5 ± 1.5	6.5 ± 0.5
<i>S. gordonii</i> (ATCC10558)	Mitis	12.5 ± 3.5	6.0 ± 1.0
<i>S. pneumoniae</i> (ATCC 6303)	Mitis	10.0 ± 1.0	1.0 ± 0.5
<i>S. pneumoniae</i> (ATCC49619)	Mitis	11.5 ± 1.5	0.0 ± 0.0
<i>S. pneumoniae</i> (ATCC43079)	Mitis	13.5 ± 0.5	1.5 ± 1.0
<i>S. sanguinis</i> (SK36)*	Mitis	23.0 ± 1.0	0.0 ± 0.0
<i>S. oralis</i> (NCTC7864)	Mitis	7.0 ± 1.0	0.0 ± 0.0
<i>S. mitis</i> (CI)	Mitis	4.5 ± 0.5	3.5 ± 0.5
<i>S. salivarius</i> (ATCC25975)	Salivarius	15.0 ± 1.0	6.0 ± 1.0
<i>S. salivarius</i> (BAA491)	Salivarius	24.0 ± 1.0	0.0 ± 0.0
<i>S. gallolyticus</i> (TX20005)	Bovis	12.0 ± 1.0	1.5 ± 0.5
<i>S. gallolyticus</i> (BAA2069)	Bovis	22.0 ± 2.0	3.0 ± 0.5
<i>S. gallolyticus</i> (43143)	Bovis	25.0 ± 1.0	1.0 ± 0.5
<i>S. equinus</i> (ATCC700410)	Bovis	20.0 ± 1.0	0.0 ± 0.0
<i>S. downei</i> (ATCC 33798)	Mutans	14.0 ± 1.0	0.0 ± 0.0
<i>S. sobrinus</i> (6715)	Mutans	7.0 ± 1.0	0.0 ± 0.0
<i>S. sobrinus</i> ATCC 27352	Mutans	7.0 ± 0.5	0.0 ± 0.0
<i>S. sobrinus</i> ATCC33478	Mutans	5.5 ± 0.5	0.0 ± 0.0
<i>S. criceti</i> AHT	Mutans	7.0 ± 0.5	0.0 ± 0.0
<i>S. ratti</i> FA-1	Mutans	6.0 ± 0.5	0.0 ± 0.0
<i>S. ratti</i> BHT	Mutans	9.0 ± 0.5	0.0 ± 0.0
<i>L. lactis</i> MG1363	Other	20.0 ± 6.0	2.0 ± 2.0
<i>E. faecalis</i> OG1X	Other	7.5 ± 0.5	3.5 ± 0.5
<i>L. rhamnosus</i> (CI)	Other	22.0 ± 1.0	7.0 ± 1.0
<i>Staph. epidermidis</i> 1457	Other	0.0 ± 0.0	0.0 ± 0.0
<i>B. subtilis</i> JH642	Other	0.0 ± 0.0	0.0 ± 0.0

CI, Clinical isolate. *, Strains used for heterologous expression of SmbFT

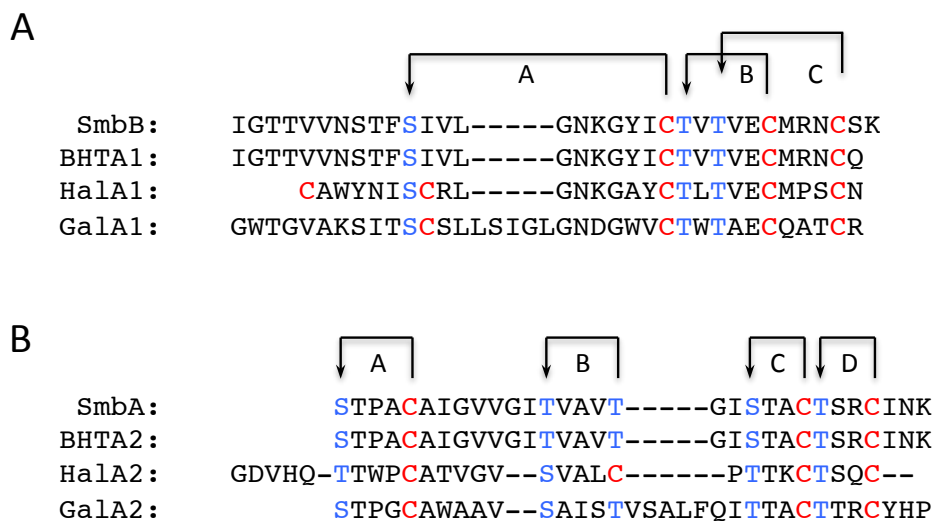


Figure S1: Sequence alignment of two-component lantibiotics closely related to Smb. The α peptide (A1) is encoded by SmbB while the β -peptide (A2) by SmbA. Other sequences were retrieved from GenBank and they are: *S. ratti* BHT strain BHTA1 (AAZ76603) and BHTA2 (AAZ76602); *Bacillus halodurans* C-125 HalA1 (NP_241320) and HalA2 (NP_241319); and *S. galloyticus* BAA 2069 SGALA1 (YP_004287012). The GALA2 peptide was not annotated in the BAA 2069 genome and was identified by analyzing the untranslated sequence near the GALA1 coding region. Curved arrows indicate residues involved in putative and/or established ring structure formation and the letters inside the arrows indicate the ring designation in the structure