

Supplementary material

Table S1 primers used in this study.

Gene	Sequence	Amplicon size (bp)	reference
<i>fosA</i>	F: GCTGCACGCCCCTGGAATA	217	Zhang et al., 2020
	R: -CGACGCCCCCTCGCTTTTGT		
<i>fosB</i>	F: CAGAGATATTTAGGGGCTGACA	312	Zhang et al., 2020
	R: CTCAATCTATCTTCTAAACTTCCTG		
<i>fosC</i>	F: GGGTTACATGCCCTTGCTCA	354	Zhang et al., 2020
	R: AACCCGCACAACGACAGATG		
<i>fosX</i>	F: ATGATCAGTCATATGACATTTATCG	243	Zhang et al., 2020
	R: ATTAGCCCCTTGTCGATAACG		

Zhang, X., Bi, W., Chen, L., Zhang, Y., Fang, R., Cao, J., Zhou, T., 2020, Molecular mechanisms and epidemiology of fosfomycin resistance in enterococci isolated from patients at a teaching hospital in China, 2013-2016. *J Glob Antimicrob Resist* 20, 191-196.

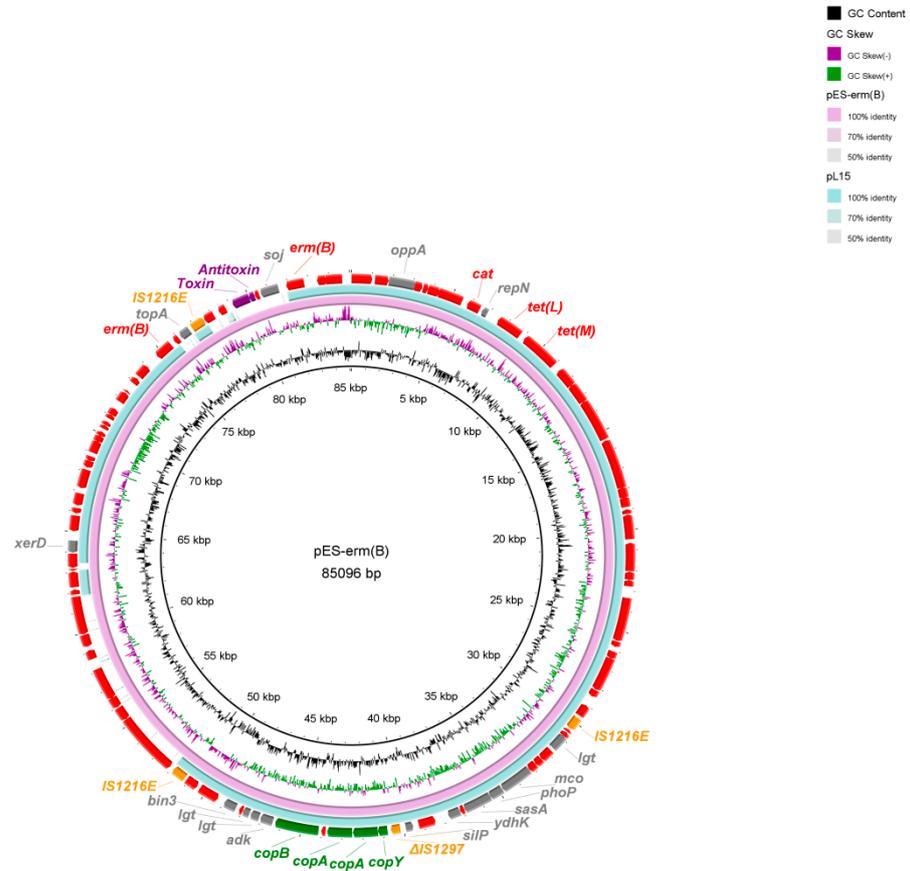


Fig S1. The genetic contents of plasmid pES-erm(B). Circular representation of alignments between reference *erm(B)* carrying plasmid pL15 (accession no. CP042214.1) and the homologous plasmid from *E. faecalis* ES1. The alignments were generated by Blastn and visualized by BLAST Ring Image Generator.

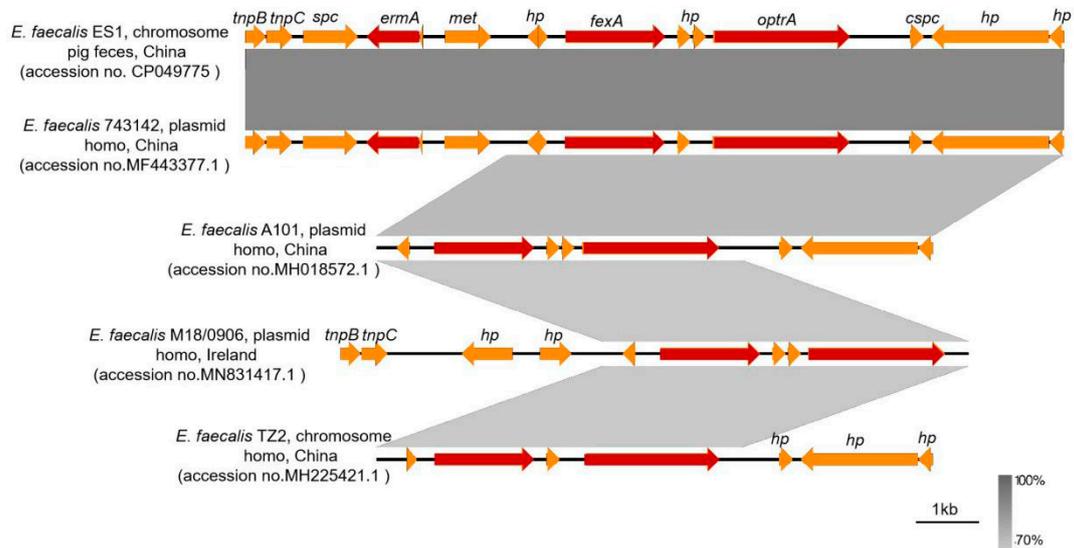


Fig S2. Genetic environment of *optrA*. Schematic representation and comparison of the genetic environment of the *optrA*-flanking region from this study and previous reported. Arrows indicate the direction of transcription of each of the genes, and different genes are shown in different colors. Regions of $\geq 70.0\%$ nucleotide sequence identity are shaded in grey.