

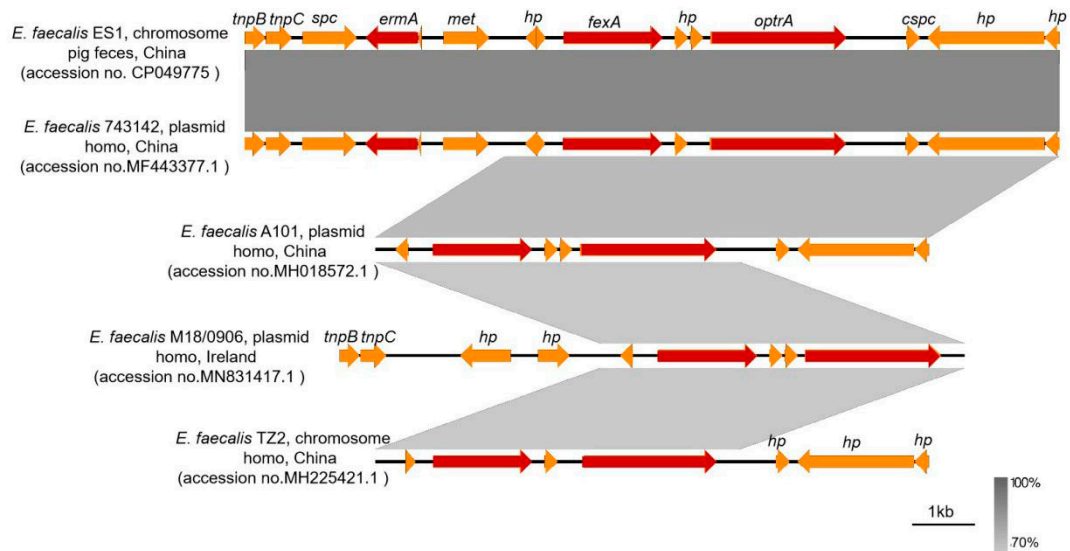
## Supplementary material

Table S1 primers used in this study.

Gene	Sequence	Amplicon size (bp)	reference
<i>fosA</i>	F: GCTGCACGCCCCGCTGGAATA	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: ATTTAGCCCCTTGTCGATAACG		

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 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.