Supplementary materials

https://doi.org/10.1631/jzus.B2000606

Development of a *pyrF*-based counterselectable system for targeted gene deletion in *Streptomyces rimosus*

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Table S1 Similarity and identity values of orotidine-5′-phosphate decarboxylase amino acid sequences among *Streptomyces* stains

Source	Amino acid residues	GenBank accession No.	Similarity	Identity
S. rimosus	286	ELQ81494.1	--	--
S. avermitilis	280	KUN53591.1	81.2%	77.7%
S. coelicolor	281	TYP05411.1	86.1%	90.4%
S. venezuelae	278	WP_150188059.1	81.8%	76.9%
S. aureofaciens	277	WP_030290267.1	82.1%	74.3%

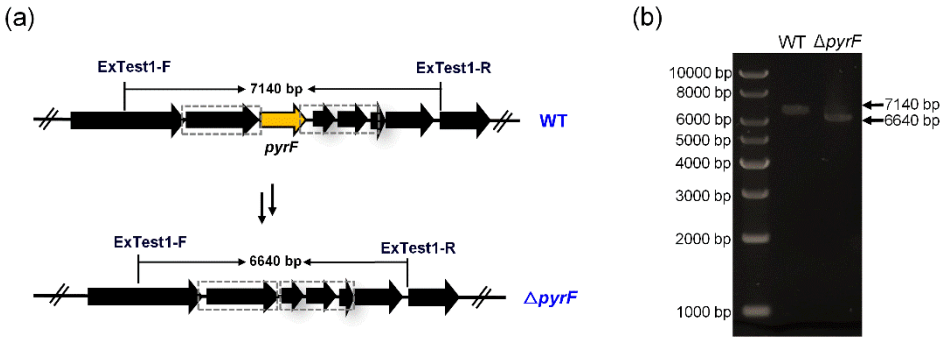

Fig. S1 The Δ*pyrF* strain was identified by PCR amplification using external primers ExTest1-F/ExTest1-R (primers found only in the genome), the expected amplicon for WT strain is 7140 bp and that 6640 bp for the Δ*pyrF* strain.

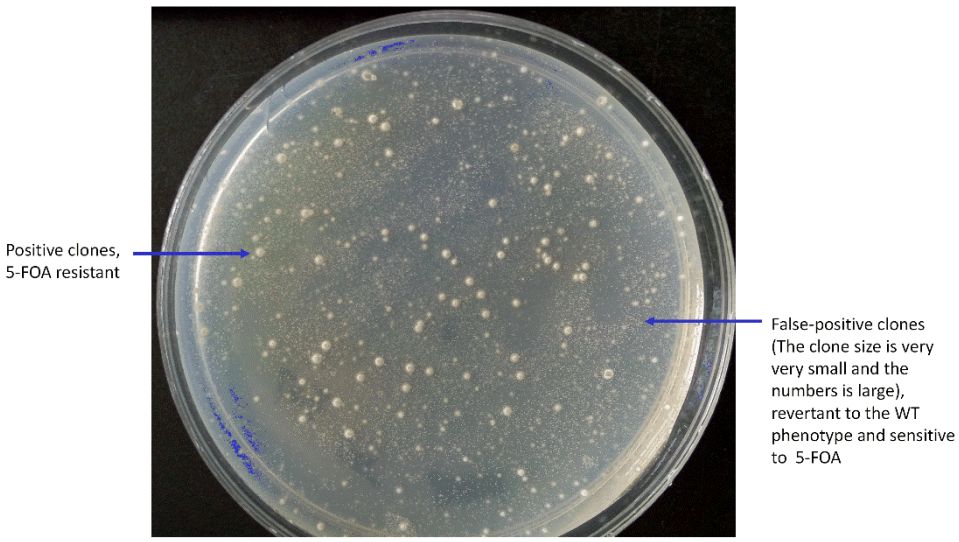

Fig. S2 Characteristics and phenotype of the Δ*pyrF* Δ*otcR* strain screened on solid MM medium with 5-FOA (100 μM) and uracil (300 μM).