Supplementary Materials

TABLE S1. Oligonucleotides used in this work.

Oligo	Sequence 5'→3' ^{b)}	Genetic Modification/Use	Reference
SR	G*T*C*A*GACGCACA CGGCATACTTTACGC AGTGCCGAGTTAGGT TTTgTCGGCGTGGTG GTGTACACACGGGTG CACACGCCACGACGC TGC	Change of K43 (AAA) into T43 (ACA) in <i>rpsL</i> gene confers streptomycin resistance. Mismatch A-G (low MMR sensitivity).	This work
LM	C*T*T*G*AGGTCCAG	Change of E50 (GAA) into	Aparicio et al (2016)
	GAACACTTCGAAGCC CTTGTCACACAGGGTT TaGACAATGCCCGAA GCGCTGCTGGTGAAC AGCTCCT TGCCAA*C *C*T*T	a stop codon (TAA) in <i>pyrF</i> gene. Mismatch A-G (low MMR sensitivity)	
НМ	G*G*G*A*ATGTCGTG	Change of K55 (AAG) into	Aparicio et al (2016)
	GAACTTGAGGTCCAG GAACACTTCGAAGCC CTaGTCACACAGGGT TTCGACAATGCCCGA AGCGCTGCTGGTGA* A*C*A*G	a stop codon (TAG) in <i>pyrF</i> gene. Mismatch A-A (high MMR sensitivity)	
SI	C*T*T*G*AGGTCCAGG	Insertion of three stop	Aparicio et al (2016)
	AACACTTCGAAGCCC TTGTCACACAGGGTc tattatcaTTCGACAA TGCCCGAAGCGCTGC TGGTGAACAGCTCCTT GCCAA*C*C*T*T	codons (9 bp) in <i>pyrF</i> (short insertion)	
LD	A*C*A*G*GCATCGGTG	Complete deletion of pyrF	Aparicio et al (2016)
	GTTCGGCACAGGCCC TTGCTGGACAGCCGC AGGTTAAGGGCAGGG TCTCTTGGCAAGTCGA AAACGGCGCGCATTG TAAACGAAGTG	(long deletion)	

Rec3FW	TGGAGTCATGACCAT GCCTAGGCCGCGGC CGCGC <u>GAATTC</u> AGAA GGAGAATATACC ATG TCCTATCAGAAACGC CC	With Rec3REV, to amplify the <i>rec3</i> gene for Gibson assembly.	This work
Rec3REV	CCGCAAGCTTGCATG CCTGCAGGTCGACTC TAGA <u>GGATCC</u> TTA GA AGTCTTCTTCGTAAG TG	With Rec3REV, to amplify the <i>rec3</i> gene for Gibson assembly.	This work
RecβFW	TGGAGTCATGACCAT GCCTAGGCCGCGGC CGCGC <u>GAATTC</u> AGAA GGAGAATATACC ATG A GTACTGCACTCGCAAC	With Rec β REV, to amplify the <i>recβ</i> gene for Gibson assembly.	This work
RecβREV	CCGCAAGCTTGCATG CCTGCAGGTCGACTC TAGA <u>GGATCC</u> TCATG CTGCCACCTTCTG	With Rec β FW, to amplify the <i>recβ</i> gene for Gibson assembly.	This work
RecTFW	TGGAGTCATGACCAT GCCTAGGCCGCGGC CGCGC <u>GAATTC</u> AGAA GGAGAATATACC ATG T CCGCAAGAAACGTTG	With RecTREV, to amplify the $recT_{Psy}$ gene for Gibson assembly.	This work
RecTREV	CCGCAAGCTTGCATG CCTGCAGGTCGACTC TAGA <u>GGATCC</u> TCATG CGGTTTCTCCG	With RecTREV, to amplify the $recT_{Psy}$ gene for Gibson assembly.	This work
238F	GGTTTGATAGGGATA AGTCCAG	With PS2, to conduct diagnostic PCR and sequencing of <i>rec</i> insertions in pSEVA258	This work
PS2	GCGGCAACCGAGCG TTC	With PS2, to conduct	Aparicio et al (2016)
		diagnostic PCR and sequencing of <i>rec</i> insertions in pSEVA258	
rpsL-Fw	GACATGAAATGTTGC CGATG	With rpsL-Rv, to amplify <i>rpsL</i> gene of <i>P. putida</i>	This work

(0.8 Kb)

- rpsL-Rv CTGTTCTTGCGTGCT With rpsL-Fw, to amplify This work TTGAC *rpsL* gene of *P. putida* (0.8 Kb)
- b) Asterisks denote phosphorothioate linkages. Nucleotide changes mediated by oligos are shown in lower case. In the sequences of oligos used for Gibson assembly, EcoRI and BamHI sequences are underlined, positions of synthetic ribosomal binding sites appear in italics and start/stop codons are shown in bold face.

REFERENCES

Aparicio, T., Jensen, S.I., Nielsen, A.T., de Lorenzo, V. and Martínez-García, E. (2016) The Ssr protein (T1E_1405) from *Pseudomonas putida* DOT-T1E enables oligonucleotide-based recombineering in platform strain *P. putida* EM42. *Biotechnol J* **11**: 1309-1319.



To demonstrate the effects of a complete deletion of the *pyrF* gene on *P. putida* EM42 growth, curves were generated for wild-type *P. putida* EM42 and a $\Delta pyrF$ strain (1). Optical densities of shaken liquid strains were taken over a period of 24 hours using a Spectramax M2e Microplate reader (Molecular Devices, CA, USA). We prepared overnight LB-Ura cultures of *P. putida* EM42 wild-type and $\Delta pyrF$ strains at 30° C. Overnight strains were back-diluted in LB-Ura to an initial OD₆₀₀ = 0.03 before being loaded into a 96-well microtiter plate. Liquid growth rates were measured over a 24 h period (interval t = 15 min). Time elapsed (h) is shown on the x-axis, while optical density at 600nm (OD600) is shown on the y-axis. Strain type is indicated in the figure legend. Individual points represent mean values and horizontal brackets indicate SE calculated from two independent experimental replicates.