1044 **Supplementary Table 1**

1045

Designation	Genotype	Reference or Source
Salmonella enterica serovar Typhimurium		
IR715	ATCC 14028s wild-type, spontaneous Nal^R	Stojiljkovic et al, J. Bacteriol. 177(5):1357-1366 (1995)
JB10	IR715 Δ*pgtE*::*tetRA* (Nal^R, Tet^R)	This study
ML27	IR715 *pgtE*-FLAG (Nal^R)	This study
LAKglmS	*SL1344 glmS::Ptrc-mCherryST::FCF (Strep^R, Cm^R)*	Knodler et al, Cell Host Microbe. 16(2):249-256 (2014)
LAKML2	IR715 *glmS*::Ptrc-mCherrryST::FRT (Nal^R)	This study
D23580	D23580 wild-type	Kingsley et al, Genome Research. 19:2279–2287 (2009)
SPN1113	D23580 Δ*pgtE*::*tetRA*	This study
Escherichia coli		
CC118 λ*pir*	F- *araD139* Δ(*ara, leu*)7697 Δ*lacX74 phoA*D20 *galE galK thi rpsE rpoB argE*^{am} *recA1* λ$_{pir}$	Herrero et al, J Bacteriol. 172(11):6557-67 (1990)
S17-1 λ*pir*	F- *recA thi pro* rK- mK+ RP4:2-Tc::*Mu*Km Tn7 λ$_{pir}$	Herrero et al, J Bacteriol. 172(11):6557-67 (1990)
XL1-Blue	*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac* [F *proAB lacI^{q}Z*ΔM15 Tn10 (Tet^R)]	Agilent
DH5αMCR	F- *mcrA* Δ(*mrr-hsdRMS-mcrBC*) φ80d*lacZ*ΔM15 Δ(*lacZYA-argF*)U169 *deoR recA1 endA1 phoA supE44*λ- *thi-1 gyrA96 relA1*	Gibco BRL
One Shot TOP10	F- *mcrA* Δ(*mrr-hsdRMS-mcrBC*) φ80*lacZ*ΔM15 Δ*lacX74 recA1 araD139* Δ(*ara, leu*)7697 *galU galK rpsL*(Str^R) *endA1 nupG*	Invitrogen

1046
1047

1048 **Supplementary Table 2**

1049

Designation	Relevant characteristics	Reference or Source
pCP20	Ap^R, temperature-sensitive, FLP recombinase system	Datsenko et al, Proc. Natl. Acad. Sci. USA. 97, 6640-6645 (2000)
pWSK29	Ap^R, MCS, *lacZa*	Wang et al, Gene. 100, 195-199 (1991)
pWSK29::*pgtE*	Ap^R Tet^R, pWSK29::*pgtE* (*pgtE* complementation)	This study
pWSK29::*pgtE*-D206A	Ap^R Tet^R, pWSK29::*pgtE*(D206A) (PgtE inactive allele)	This study
pRDH10	Cm^R Tet^R, SacB (levansucrase: Sucrose sensitivity)	Kingsley et al, Applied and Environmental Microbiology, 1610-1618 (1999)
pRDH10::*pgtE*-FLAG	Cm^R Tet^S, SacB, pRDH10::*pgtE-FLAG* (pgtE-FLAG Tag)	This study
pCR-Blunt II-TOPO	Kan^R, MCS	Invitrogen
pGP704	Ap^R, MCS, *oriR6K*, *mobRP4*	Miller et al, J. Bacteriology. 170(6):2575-2583 (1988)
pSPN23	Ap^R Tet^R, pBluescriptII KS+::*tetRA* (*tetRA* cassette)	Raffatellu et al, Cell Host Microbe. 5(5):476-86 (2009)
pCRII::*pgtE*-LBRB	Kan^R, pCR-Blunt II-TOPO::*pgtE*-LBRB ($\Delta pgtE$ cassette)	This study
pGP704::*pgtE*-LBRB	Ap^R, pGP704::*pgtE*-LBRB ($\Delta pgtE$ cassette)	This study
pGP704::*pgtE*-LBRB::*tetRA*	Ap^R Tet^R, pGP704_pgtE_LBRB::*tetRA* ($\Delta pgtE$::*tetRA* cassette)	This study
pP*pgtE*-*gfp*	Ap^R, P*pgtE*-*gfpmut3.1* (*pgtE* transcriptional reporter plasmid)	This study
pMPM-A3ΔPlac	Ap^R, P15A ori	Ibarra et al., Microbiology Apr;156(Pt 4):1120-1133 (2010)

1050

1051

Supplementary Table 3

1052

Designation	Purpose	Primer sequence (5' to 3')	Reference or Source
pgtE_LB_for	Amplifying *pgtE* upstream region	ATCAGCAGAGATCATCATGG	This study
pgtE_RB_rev	Amplifying *pgtE* downstream region	AATTGAAGACGCGCTACG	This study
pgtE_LB_r_fus*	pCRII_*pgtE*_LBRB fusion	TGACAAGATGGCTTCTAGACCACATCGG	This study
pgtE_RB_f_fus *		GTCTAGAAGCCATCTTGTCAAATCGTCGG	This study
pgtE_LB_f_SalI*	pWSK29_*pgtE*_compl	GTCGACAATCTCGGCTATACCTTTGG	This study
pgtE_RB_r_EcoRO*		GATTCCCGTTATCTCCATCAACTGG	This study
pgtE_RB_r_seq	pCRII_pgtE_LBRB sequencing	CGTTGAAGAGTATGAGCGAC	This study
pgtE_pres_for	Colony PCR screening	CACCGCTGGTTTTATCTATG	This study
pgtE_pres_rev		ACGTCTCTCCTGATAGCGTC	This study
tetRA_pres_for	PCR confirmation of *tetRA* cassette presence	TTCGGAAGATATCGCTAACC	This study
tetRA_pres_rev		TAAAGCACCTTGCTGATGAC	This study
tetR_int_rev	*tetRA* cassette presence	CAGAGCCAGCCTTCTTATTC	This study
tetA_int_for		GATGACCTTCATGTTAACCC	This study
pgtE_for_compl	*pgtE* complementation	TTATGACCGATGACATCCC	This study
pgtE_rev_compl		AATGCGTCAAGTTCTCTGG	This study
PpgtE-XbaI-F*	*pgtE* transcriptional reporter plasmid	GCTCTAGAACGAATTAATGAAAGTGGC	This study
PpgtE-SmaI-R*		TCCCCCGGGATCATCATTACTGCAATAGCA	This study
FLAG_Upstream_Fwd**	Amplify upstream of *pgtE* stop codon	gggcgccatctccttgcatgACAAGGCGGGCGTAACAG	This study

FLAG_Upstream_Rev***	for FLAG tag Gibson assembly	<u>cttgtcatcgtcgtccttgtagtc</u>GAAGCGATACTGCAACCCC	This study
FLAG_Downstream_Fwd***	Amplify *pgtE* stop codon and downstream for FLAG tag Gibson assembly	<u>gactacaaggacgacgatgacaag</u>TAGACCACATCGGGATGTC	This study
FLAG_Downstream_Rev**		<u>ggccatccagcctcgcgtcg</u>CCTGGAGCGACTTTCTCTG	This study
FLAG_Verification_Fwd	Verify clean insertion of FLAG tag in *pgtE*	TTCCGGACGTCTCTCCTGAT	This study
FLAG_Verification_Rev		ACGCGATTATCTCTGGCTGG	This study

* = restriction sites are underlined

** = engineered sequence for pRDH10 homology are underlined

*** = engineered sequence for FLAG Tag are underlined

1053
1054