

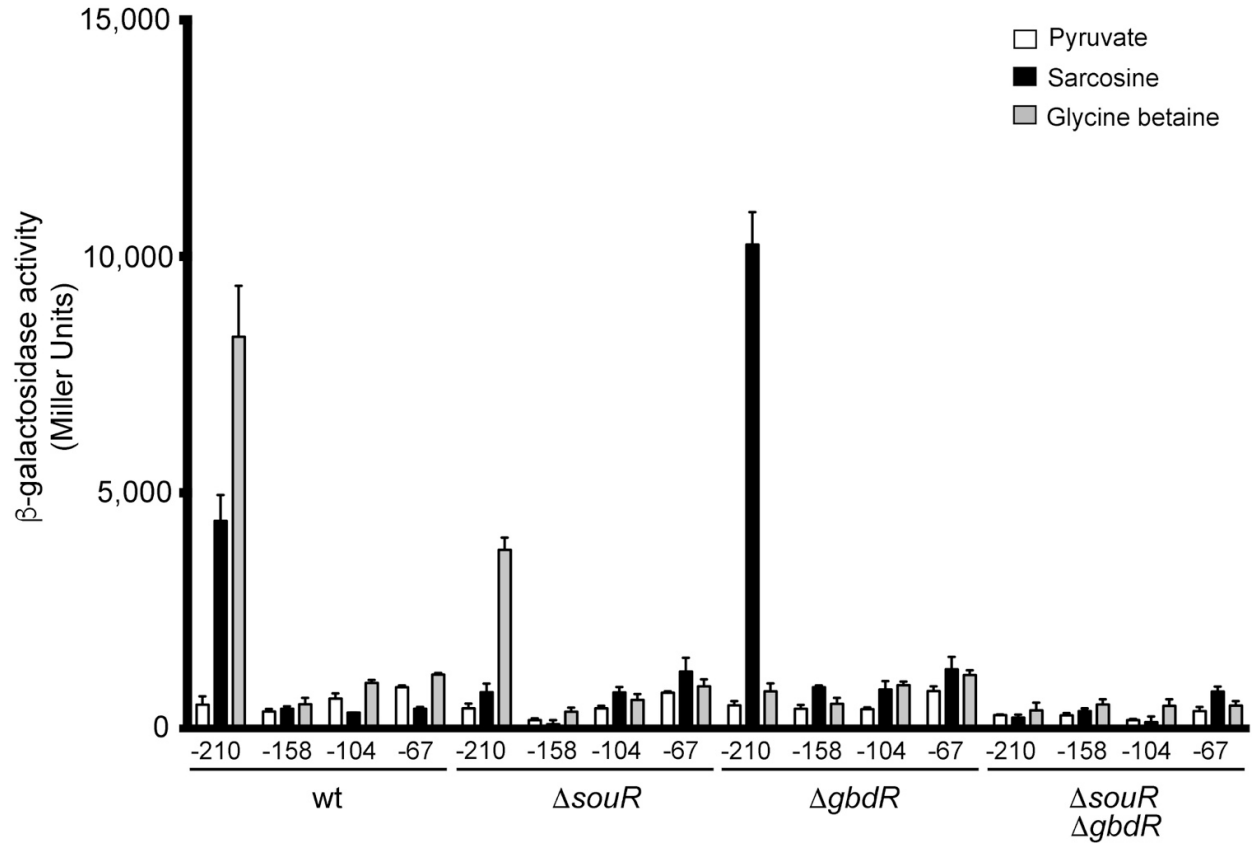
Supplemental Table 1: Bacterial strains and plasmids used in this study.

Designation	Genotype or description	Reference or Source
<i>P. aeruginosa</i> strains		
MJ101	PA14 wild type	(50)
MJ285	$\Delta gbdR$ in MJ285	(7)
GGW039	<i>soxB</i> '-lacZYA-'soxG in MJ285	This study
GGW034	$\Delta souR$ in MJ101	This study
GGW036	$\Delta souR$ in MJ285	This study
GGW076	$\Delta gfnR$ in MJ101	This study
GGW078	$\Delta gfnR$ in MJ285	This study
<i>E. coli</i> strains		
NEB5 α	<i>fhuA2</i> Δ (<i>argF-lacZ</i>)U169 <i>phoA</i> <i>glnV44</i> Φ 80 Δ (<i>lacZ</i>)M15 <i>gyrA96</i> <i>recA1</i> <i>relA1</i> <i>endA1</i> <i>thi-1</i> <i>hsdR17</i>	NEB
S17-1 λ pir	<i>thi pro hsdR</i> - <i>hsdM</i> ⁺ Δ <i>recA</i> RP4-2::TcMu-Km::Tn7	(51)
T7 Express	See manufacturer	NEB
GGW040	pGW005 in S17-1 λ pir	This study
GGW031	pGW008 in S17-1 λ pir	This study
GGW064	pGW024 in S17-1 λ pir	This study
MJ500	pBT20 in SM10 λ pir	(13, 30)
GGW047	pGW015 in T7 Express	This study
Plasmids		
pMQ30	suicide vector, Gm ^R , <i>sacB</i>	(26)
pMQ80	High copy <i>Pseudomonas</i> vector, Gm ^R	(26)
pUC18-mini-Tn7T-Gm	<i>attTn7</i> integration vector, Gm ^R	(28)
pTNS2	carrying the <i>attTn7</i> transposase	(29)
pMW5	<i>lacZYA</i> reporter plasmid Gm ^R	(7)
pMALc2X	MBP-fusion vector, Ap ^R	NEB
pKH10	MBP-GbdR expression vector	(22)
pGW005	<i>soxB</i> '-lacZYA-'soxG in pMQ30	This study
pGW007	<i>souR</i> complementation in pMQ80	This study
pGW008	<i>souR</i> (PA14_9770) in pMQ30	This study
pGW023	<i>gfnR</i> (PA14_17380) in pMQ30	This study
pGW024	<i>gfnR</i> (PA14_17380) in pUC18-mini-Tn7T-Gm	This study
pGW011	P _{glyA1} -210 to +1 in pMW5	This study
pGW012	P _{glyA1} -158 to +1 in pMW5	This study
pGW013	P _{glyA1} -104 to +1 in pMW5	This study
pGW014	P _{glyA1} -67 to +1 in pMW5	This study
pGW015	<i>souR</i> (PA14_17380) in pMALc2X	This study

Supplementary Table 2. Primer sequences.

SoxKO-F1	aagcttCTACCGGGCTGATCGACTAC
SoxKO-R1	AAGTACGAAGGCGACTCGACCATGGTGGTGGATGCTCCTGAACTGTTG
SoxKO-F2	CCATGGTCGAGTCGCCTTCGTACTTACTTCTGGCTCTGGTTGCAG
SoxKO-R2	ggtaccTTGCACTGGAAAGTCGTCTG
PA14_9770 KO F1	CCG GGA GGT GGG TTA CTT TC
PA14_9770 KO R1	CTT CAG ACT CCG ACT GCC GCG CGC TGA AAC GCC TTC TTT CCA T
PA14_9770 KO F2	CGC GGC AGT CGG AGT CTG AAG GCA ACG TCC GCT CGA CGA AAT G
PA14_9770 KO R2	CCG CCG ACA GCG TAT AAG GA
PA14_9770 Rescue F	GCT CGG TAC CCA TGG AAA GAA GGC GTT TCA GCG CCG
PA14_9770 Rescue R	GCC AAG CTT TCA TTT CGT CGA GCG GAC GTT GCC
PglyA1_F1	TGT ATT AAG CTT GGT GTT CTC GCA AGA CGA AGA GC
PglyA1_50bp_del_F2	TGT ATT AAG CTT CCG CAT CGG TTG CCG AAT CCC AC
PglyA1_100bp_del_F3	TGA TAT TAA GCT TGC ATA GGC ATC TGG GCC GGC AGG
PglyA1_150bp_del_F4	TCG CTA TTA AGC TTC GCT GGC AAA GGG ACC GCG TGT
PglyA1_R1	ATA TCA AGG TAC CAT TCC GGC GCG GTT CCG GCG C
souR_MPB_F (Ecor1)	TTT CAG AAT TCG AAA GAA GGC GTT TCA GCG CCG C
souR_MPB_R (BamHI)	CTA GAG GAT CCT CAT TTC GTC GAG CGG ACG TTG CCG
PA3630KO_F1	CAT TCG GGC CCA TCC AGA AGA T
PA3630KO_R1	CGC GCG GCC TTC GCA GGC CTG CAA CTG GTG GAC TAT CTC AAG GAA
PA3630KO_F2	AGG CCT GCG AAG GCC GCG CGG AGG AAA CGC CCA TGC GTT CG
PA3630KO_R2	TTG TCG TAG TCC TTC GGA TTG ATG
PA3630 RescueF KpnI	CATGGTACCGCGAAGGCGACGGCGGCACGGG
PA3630 Rescue R HindIII	CATAAGCTT G CGA CCA GAA CCT CAC CAG GTA G
PA3630 KO screen F	GGA CAG ACC TTC CTG CAA CA
PA3630 KO screen R	CAG AGG TAC ATG ACG CGT GG
PA2762_F1	GGCAAGTGGGAGGTGAACTA
PA2762_R1	AAGTACTTGCGCACCGTCTC
rplU_F1	GCAGCACAAAGTCACCGAAGG
rplU_R1	CCGTGGGAAACCACTTCAGC
sdaB_F1	CATGGAATGGGTCAACCTGT
sdaB_R1	AGATCGAGGCGTTCTTCTTG
soxA_F1	GTTCTCAACCGGGTCTACA
soxA_R1	ATTCGGTCTGGTGGTACAGC
PA3630_F1	GTG CGG CAA GTG CAA ATT CT
PA3630_R1	GGG GCA TCC TTG GGA ATC TT
PA3629-prom-5'-biotin	5'biotin-CGC TCT TCC AGG CGG GCG ACC TGG C
PA3629-prom-3'	ATA GGT ACC GAT GGA AGC CGG CGG GCC G
PA2762-prom-5'-biotin	5'biotin-CAGGAAGGCAGTGGATGAAT
PA2762-prom-3'	CCTTTGCCTGTGGTGGAC
glyA1-prom-5'-biotin	5'biotin-GTGTTCTCGCAGGACGAAG
glyA1-prom-3'	CTTTGCCAGCGATGGTATG
cbcX-prom-5'-biotin	5'biotin-GAACTCCTCTGCAGGGTAAGG
cbcX-prom-3'	CCGGCAAAGACCACTATGAT
PA1999_prom_R1_KpnI	GGATggtaccCTCTTCCGGCTCTTGTGATT
PA1999_F_biot	GAGGCTTTTCTCCAGGCTCT
TnM5 amp F	TAC AGT TTA CGA ACC GAA CAG GC
SouR tnm R	GAA GAA CAG GCG AAC GCA TC
PA4183 TnM R	TTC TTG GTG CGC TTT GGT TG
GbdR TnM R	TGG CAT AGC CCC CAA TTT GT
sdaB TnM R	AGG CCT GCA GAT GAT GTT GG
PA2762 TnM R	CTC CCA GCG TTC GTA GTT CA
OpdP TnM R	TTG GGA ATG CGG AAG GTG AA
soxA TnM R	GTG GTG GTT CAT CCA GTC GT

GfnR TnM R	GGA CAG ACC TTC CTG CAA CA
adhC TnM R	TCT CGA CAT AGC TCG GCA AC
dhcA Tnm R	GGA CTC GAC AAG CGA GTA GG
Rnd1 TnM20	TATAATGTGTGGAATTGTGAGCGG
Rnd1 PA Arb primer 2	GGCCACGCGTCGACTAGTACNNNNNNNNNNNACGCC
Rnd2 TnM20	ACAGGAAACAGGACTCTAGAGG
Rnd2 Arb primer	GGCCACGCGTCGACTAGTAC
BT20TnMSeq	CACCCAGCTTTCTTGACAC



Supplementary Figure 1. P_{glyA1} promoter mapping of sarcosine or glycine betaine induced SouR and GbdR-dependent induction. Results from β -galactosidase assay of the four promoter truncation constructs (noted as bases upstream of the translational start site) in each of the four strains listed below the x-axis. The data shown are representative of three biological experiments and error bars represent standard deviation.