

Table S1. List of strains, oligonucleotides and plasmids used in this study

Strain or plasmid	Description	Reference
<u>Strains</u>		
<i>E. coli</i>		
cc118λ-pir	Δ(ara-leu) <i>araD</i> Δ <i>lacX74 galE galK phoA20 thi1 rpsE rpoB argE(Am) recA</i> λ pir; Strep ^R	[63]
Top10	Δ <i>lacX74 ara</i> Δ139Δ(<i>ara-leu</i>)	Invitrogen
SY327 λpir	Δ <i>araD</i> , (lac pro) <i>argE(Am) recA56 rif^R nalA</i> λpir	[64]
<i>B. cenocepacia</i>		
wild-type	CF isolate from Germany, genomovar III	[65,58]
Δ <i>roxS</i>	Two-component family of histidine kinase Δ <i>roxS</i> (<i>I35_RS15825</i>)	This study
Δ <i>anr2</i>	Crp/Fnr family transcriptional regulator Δ <i>anr2</i> (<i>I35_RS16810</i>)	This study
Δ <i>anr1</i>	Crp/Fnr family transcriptional regulator Δ <i>anr1</i> (<i>I35_RS23120</i>)	This study
Δ <i>cyto</i>	Cytochrome BD oxidase subunit I Δ <i>cyto</i> (<i>I35_RS14435</i>)	This study
Δ <i>anr1-anr2</i>	Δ <i>anr1</i> (<i>I35_RS23120</i>) deletion and <i>anr2</i> (pSHAFT2:: <i>I35_RS16810</i>) double mutant, Km ^R , Cm ^R	This study
<i>fliA</i>	<i>fliA</i> (<i>I35_RS00760</i>) insertional mutant in pSHFAT2	This study
<i>fliA</i> ⁺	<i>fliA</i> complemented strain with pBBRMCS-5	This study
<i>P. aeruginosa</i>		
PA14	Wild type, UCBPP-PA14, human isolate	[66]
<u>Plasmids</u>		
pRK2013	Helper plasmid; Km ^R	[67]
pSHAFT2	Broad-host-range suicide plasmid, mobilisable for conjugation; Cm ^R	[68]
pBBR1MCS-5	Broad host-range cloning vector; Gm ^R	[69]
pDAI-SceI	Suicide plasmid with oriR6K, mob ⁺ , I-SceI restriction site, Tm ^R	[61]
pDONR221	Km ^R , Cm ^R , attP sites, ccdB, pUC origin	Invitrogen
pGPI-SceI	Suicide plasmid with oriR6K, mob ⁺ , I-SceI restriction site, Tm ^R	Steiner unpublished, [61]
pAUC40	Cm ^R , Strep ^R attR sites, R6K origin, sacB, ccdB	[70]
pBBR5::FLP	Gm ^R , sacB	[71]
pKD4	Km ^R	[72]
pGEM T easy vector	PCR cloning	Promega
pGPI-SceI_Δ <i>anr2</i> updw	pGPI-SceI containing the upstream (654 bp) and downstream (560 bp) regions of the <i>anr2</i> (<i>I35_RS16810</i>), Tm ^R	This study
pGPI-SceI_Δ <i>cydA</i> updw	pGPI-SceI containing the upstream (647 bp) and downstream (615 bp) regions of the <i>cydA</i> (<i>I35_RS14435</i>), Tm ^R	This study
pGPI-SceI_Δ <i>roxS</i> updw	pGPI-SceI containing the upstream (581 bp) and downstream (505 bp) regions of the <i>roxS</i> (<i>I35_RS15825</i>), Tm ^R	This study
pAUC40_Δ <i>anr1</i> updw	pAUC40 containing upstream (466 bp) and downstream (495 bp) regions of <i>anr1</i> (<i>I35_RS23120</i>), Cm ^R	This study

pSHAFT2_ <i>anr</i> ₂	pSHAFT2 containing a 259 bp region of <i>anr</i> ₂ (I35_RS16810), Cm ^R	This study
pSHAFT2_ <i>fliA</i>	pSHAFT2 containing a 238 bp region of <i>fliA</i> (I35_RS00760), Cm ^R	This study
pBBR1MSC-5_ <i>fliA</i>	pBBR1MSC-5 containing the entire <i>fliA</i> gene (I35_RS00760) (749 bp), Gm ^R	This study
<u>Oligonucleotides</u>		
roxSup_Fw_KpnI_	tccggtaccCCGAGCAGTTTACCCGTTTA	This study
roxSup_Rv_XbaI	tcctctagaAACAGGCCGAATTGTACAGG	This study
roxSdw_Fw_EcoRI	tccgaattcGTCGCCGAGATGTTGTTGTT	This study
roxSdw_Rv_KpnI	tccggtaccGGCCTCAACCAACACGTAGA	This study
<i>anr</i> ₂ up_Fw_KpnI	tccggtaccGATCGTATACTCCGGCGTTG	This study
<i>anr</i> ₂ up_Rv_XbaI	tcctctagaTACTCTGCCTCGCAGCATC	This study
<i>anr</i> ₂ dw_Rv_KpnI	tccggtaccTGCAACACCTCTGATACCGC	This study
<i>anr</i> ₂ dw_Fw_EcoRI	tccgaattcTCGACGATCAGGATTACACG	This study
<i>cydA</i> _Rv_up_NdeI	tcccatatgGCTACTTATCATGGTGGTCT	This study
<i>cydA</i> _Fw_up_XbaI	tcctctagaCGA ATA CGC GTA AAT CGC G	This study
<i>cydA</i> _Fw_dw_NdeI	tcccatatgTGAGTACGCCCTCGCAAC	This study
<i>cydA</i> _Rv_dw_EcoRI	tccgaattcACG CCG TCG GTC TTC ATC	This study
<i>fliA</i> _Fw_EcoRI	tccgaattcGACGAATACCAGGGGATGC	This study
<i>fliA</i> _Rv_XbaI	tcctctagaGCAGATTCAGACCCCGTTC	This study
<i>fliA</i> _comp_Rv_XbaI	tcctctagaTCGACAAGGGGTCAGGACT	This study
<i>fliA</i> _comp_Fw_EcoRI	tccgaattcGCCATGATGTACAACGCTCA	This study
pSHAFT_Fw	CTTCAGCTGATGTGTGATAACATACT	[73]
<i>anr</i> ₂ _IM_F	GCCTCGAGTCGGTCATCTG	This study
<i>anr</i> ₂ _IM_R	agatctCTGTACGGAATCACGCAGAC	This study
<i>anr</i> ₂ _Comp_F	tccaagcttGGTGGGACAATGATTTTCGTC	This study
<i>anr</i> ₂ _Comp_R	tcctctagaGTGCGGTATCAGAGGTGTTG	This study
<i>anr</i> ₁ _up_F	CAATTTTCGGCGGCGCAACAC	This study
<i>anr</i> ₁ _up_R	TGGCGGTGGACATGAGTCG	This study
<i>anr</i> ₁ _dw_F	ATCATCGACGCGCAAGCGCT	This study
<i>anr</i> ₁ _dw_R	AAACACGTGCCGCCTCCATC	This study
pKD4fwd-2	TAGGCTGGAGCTGCTTCGAAGTTC	This study
pKD4rev-2	CATATGAATATCCTCCTTAGTTCCTATTCCG	This study
GWattB1	GGGGACAAGTTTGTACAAAAAGCAGGCT	[74]
GWattB2	GGGGACCACTTTGTACAAGAAAGCTGGGT	[74]
PAIR_ADAPT_6BC##_HI	ACACTCTTCCCTACACGACGCTCTTCCGATCTBBB	[59]
PAIR_ADAPT_6BC##_LO_5PH	BBBT	[59]
T23_PAIR_COLLECT	BBBBBBAGATCGGAAGAGCGGTTCAGCAGGAATGC	[59]
T23_SLXA_PAIR_Amp	CGAG	[59]
SLXA_PAIR_REV_AMP	CTTCGGCGCGCCCTAGGGGGATCCTCGGCATTCC	[59]
T23_SEQ_G (Fw)	TGCTGAACCGCTCTTCCGATCT	[59]
T23_INDEX_1 (Index)	GGAACCTTCGGAATAGGAACTTCTTAGATGTGTATAA	[59]
PE_READ2_SEQ (Rv)	GA G	[59]
	CAAGCAGAAGACGGCATAACGAGATCGGTCTCGGC	[59]
	ATTC CTGCTGAACCGCTCTTCCGATCT	[59]
	ATTAGGAACTTCGGAATAGGAACTTCTTAGATGTGT	[59]
	ATAAGAGACAG	[21]
	CTAGAGAATAGGAACTTCGGAATAGGAACTTCTTA	[59]
	GATGTGTATAAG	[59]
	CGGTCTCGGCATTCTGCTGAACCGCTCTTCCGAT	[59]
	CT	[59]

Reference

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