Table A1: Strains and plasmids used in this study

Strain or plasmid	Genotype/characteristics	Source/reference
Strains		
TOP10	*Escherichia coli* cloning strain	Invitrogen
Mm900	*M. maripaludis* S2 *Δhpt*	J.A. Leigh
Δ*mmp0350*	*M. maripaludis* Mm900 Δ*mmp0350*	(28)
Δ*mmp0351*	*M. maripaludis* Mm900 Δ*mmp0351*	This study
Δ*mmp0352*	*M. maripaludis* Mm900 Δ*mmp0352*	This study
Δ*mmp0353*	*M. maripaludis* Mm900 Δ*mmp0353*	This study
Δ*mmp0354*	*M. maripaludis* Mm900 Δ*mmp0354*	(22)
Δ*mmp0355*	*M. maripaludis* Mm900 Δ*mmp0355*	This study
Δ*mmp0357*	*M. maripaludis* Mm900 Δ*mmp0357*	This study
Δ*mmp0358*	*M. maripaludis* Mm900 Δ*mmp0358*	This study
Δ*mmp0359*	*M. maripaludis* Mm900 Δ*mmp0359*	J. Wu
PAO1	Wild type *P. aeruginosa*, O5 serotype, CPA+, OSA+	K. Poole
Δ*wbpA*	*P. aeruginosa* PAO1 Δ*wbpA*::Gm, CPA+ OSA-	J. Lam
Δ*wbpI*	*P. aeruginosa* PAO1 Δ*wbpI*::Gm, CPA+, OSA-	J. Lam
Plasmids		
pCRPrtNeo	*hmv* promoter-*hpt* fusion with Neo^R cloned into pCR2.1TOPO; Amp^R	J.A. Leigh
pKJ1057	In-frame deletion of *mmp0351* in pCRPrtNeo with BamHI	This study
pKJ1059	In-frame deletion of *mmp0352* in pCRPrtNeo with BamHI	This study
pKJ980	In-frame deletion of *mmp0353* in pCRPrtNeo with BamHI	This study
pKJ600	In-frame deletion of *mmp0354* in pCRPrtNeo with BamHI	D.J. VanDyke
pKJ1148	In-frame deletion of *mmp0355* in pCRPrtNeo with XbaI	This study
pKJ703	In-frame deletion of *mmp0356* in pCRPrtNeo with BamHI	J. Wu
pKJ978	In-frame deletion of *mmp0357* in pCRPrtNeo with BamHI	This study
pKJ1182	In-frame deletion of *mmp0358* in pCRPrtNeo with BamHI	This study
pHW40	*nif* promoter-*lacZ* fusion with Neo^R cassette; Amp^R	J.A. Leigh
pKJ1099	*mmp0351* cloned into pHW40 with NsiI/MluI	This study
pKJ1101	*mmp0352** cloned into pHW40 with NsiI/MluI	This study
pKJ1161	*mmp0353* cloned into pHW40 with NsiI/MluI	This study
pKJ1021	*mmp0357** cloned into pHW40 with NsiI/MluI	This study
pWLG40	*hmv* promoter-*lacZ* fusion with Neo^R cassette; Amp^R	J.A. Leigh
pKJ1107	*epdE*-FLAG cloned into pWLG40 with NsiI/MluI	D.B. Nair
pCR2.1-TOPO	TA-cloning vector; Amp^R, Kan^R	Invitrogen
pUCP18	*E. coli – P. aeruginosa* shuttle vector, derived from pUC18, Amp^R	K. Poole
pKJ1170	*mmp0353*** with His-tag in pUCP18	This study
pKJ1195	*mmp0353*** in pUCP18	This study
pKJ1196	*mmp0357*** with His-tag in pUCP18	This study
pUCP19	*E. coli – P. aeruginosa* shuttle vector, derived from pUC18, Amp^R	K. Poole
pKJ1172	*mmp0353*** with His-tag in pUCP19	This study

pKJ1203	*mmp0353*** in pUCP19	This study
pKJ1198	*mmp0357*** with His-tag in pUCP19	This study
pUCP26	*E. coli – P. aeruginosa* shuttle vector, derived from pUC18, Tc^R	J. Lam
pKJ1221	*mmp0353*** in pUCP26	This study
pUCP27	*E. coli – P. aeruginosa* shuttle vector, derived from pUC18, Tc^R	J. Lam
pKJ1222	*mmp0353*** in pUCP27	This study

*gene after SDM to remove internal NsiI sites
** gene synthesized using *P. aeruginosa* codon preferences

Table A2: Primers used to construct in-frame deletions

Primer	Sequence (5' to 3')	Restriction site (underlined)
0351-P1	TCGGATCCGGATCGGTTGTTACCAAAGACG	BamHI
0351-P2	TCAGGCGCGCCGAGCTTGTGCAGCATCCTCGAT	AscI
0351-P3	TATGGCGCGCCCCAGTGCATCCTTCTGTATCTTTAG	AscI
0351-P4	CTAGGATCCTAACCCATCTAATCCAGTAACTAACG	BamHI
0352-P1	TCAGGATCCATAATTGCAGTTCACCTCTATGG	BamHI
0352-P2	ATCGGCGCGCCCAACAATACTGACTGCATC	AscI
0352-P3	GTAGGCGCGCCCAGCCGTTAGTTACTGGATTAG	AscI
0352-P4	TCAGGATCCTGCCATATAATCATTTAATTCCCTTGC	BamHI
0353-P1	ATGCGGATCCCGTGGAGGTGTTAATTAATG	BamHI
0353-P2	ATGGCGCGCCATTCGTTCATTTTTAACCTCCTG	AscI
0353-P3	ATGGCGCGCCAGGGTTATTAAAGTTGGAAATT	AscI
0353-P4	GCATGGATCCCGATTCAACAAATTCATTTCC	BamHI
0355-P1	GCTCTAGACCGATGTTATAATTAGGGTG	XbaI
0355-P2	ATGGCGCGCCACTGAGTATATATGTAGCC	AscI
0355-P3	TAGGCGCGCCAGATCAACTCACATATGGGTGG	AscI
0355-P4	GCTCTAGATATGGTCGTACTTACTTGG	XbaI
0357-P1	ATGCGGATCCCAGGATTTGGAGTTTACGATGC	BamHI
0357-P2	ATGGCGCGCCGCCTTGCACCAACGATAGTTAC	AscI
0357-P3	ATGGCGCGCCCCTGCATCTGAAACATACAATTA	AscI
0357-P4	GCATGGATCCATCAGCAACATTCATCCATAGTGG	BamHI
0358-P1	CGGGATCCTGCATATAATGAAGAATTAACTATCG	BamHI
0358-P2	TGGCGCGCCATGCATCGTAAACTCCAAATCC	AscI
0358-P3	AGGCGCGCCCAAACCATGACAACAGAAGCTGC	AscI
0358-P4	GCGGATCCGGAATCATACATTACATCTCCGAC	BamHI

Table A3: Primers used to construct gene complements

Primer	Sequence (5' to 3')	Restriction site (underlined)
351_comp-For	CCCATGCATGATACCTATTGCAAAACC	NsiI
351_comp-Rev	CCCACGCGTTAATTAACACCTCCACG	MluI
352_comp-For	CCCATGCATGTTAAAAGTGGCAGTTGTGG	NsiI
352_comp-Rev	GGGACGCGTTAATTACCGTTAGAGCTTTTCAAAGC	MluI
352_SDM-For*	GGATTAGATGGGTTAAATGC**G**TTAGAAACCGCAATTTATGC	-
352_SDM-Rev*	GCATAAATTGCGGTTTCTAA**C**GCATTTAACCCATCTAATCC	-
353_comp-For	CCCATGCATGAACGAATTAGGAAATTTAAAAATTGCAG	NsiI
353_comp-Rev	CCACGCGTTATTTCAAATTTCCAACTTTAATAACCCTAAATCC	MluI
357_comp-For	CCCATGCATGAAAATAGTAACTATCGTTGG	NsiI
357_comp-Rev	CCACGCGTTCACAAATTCCTCAAAACTTCAAC	MluI
357_SDM-For*	CTTAGAAAATATAATAAATGC**C**TTTATTGAAAGTAACG	-
357_SDM-Rev*	CGTTACTTTCAATAAA**G**GCATTTATTATATTTTCTAAG	-

*bolded nucleotides were used via SDM to remove internal NsiI restriction sites

Table A4: Primers used to screen and confirm *M. maripaludis* deletion mutants

Primer	Sequence (5' to 3')
0350_seq-For	TTTAAAACGTCACTTTCTTCG
0350_seq-Rev	CAATCATTCCGCTTTTTAAC
0351_seq-For	GGACAACGGCTTTAGACGTCGC
0351_seq-Rev	CGATCCTTATTCATATCTGAAAGCC
0352_seq-For	CCAGTGCATCCTTCTGTATCTTTAGATG
0352_seq-Rev	CCAATTACGTTAATTCCGTATTCAGC
0353_seq-For	CGATGACGACAAGAATCGCA
0353_seq-Rev	TATACGCCACAAATGCAGTG
0354_seq-For	ATTTAAACACTTGGACTTTG
0354_seq-Rev	TTTAGGACCGTTATTGAAC
0355_seq-For	CGATATTTAGTTGATATTCATGATTCC
0355_seq-Rev	GGTATTGTCCCAACCGGACAATGC
0356_seq-For	TCTCCTGTCGGATACCTAG
0356_seq-Rev	GGTTCCTGTTGTAGTTATGG
0357_seq-For	GAGCAACTTCATAGAGCTTG
0357_seq-Rev	GGCTTGAAGTATACTGTTGG
0358_seq-For	CCACAGTATATGCCAAACCATCTG
0358_seq-Rev	CCATACCATAAATGACGTACTATCG
0359_seq-For	CACTATTGCAATACTGAGTCC
0359_seq-Rev	CAATACATCTGAAGGTAGTG

Table A5: Primers used for RT-PCR

Primer	Sequence (5’ to 3’)
350-351_RT-For	GCAATGATCGGATCCGGATCGG
350-351_RT-Rev	CGACGTCTAAAGCCGTTGTCC
351-352_RT-For	CGGGTATTCATTATCCAATTCCGG
351-352_RT-Rev	CGTTGGAACAACAATACTGACTGC
352-353_RT-For	GGTACGAAAGGAATTGCTTATCTGG
352-353_RT-Rev	CCACCATTTGGTTGATATCCACG
353-354_RT-For	CCATTATGTGACGAATTAGATGC
353-354_RT-Rev	CCGCAATATACGCCACAAATGC
355-356_RT-For	CCACTATGGATGAATGTTGCTG
355-356_RT-Rev	GGTCATTAGACATTTGATATGC
356-357_RT-For	GGATGGGTGGAATATATTGGTTGG
356-357_RT-Rev	CCATCGGGCTTGAAGTATACTGTTGG
357-358_RT-For	CGATAGTACGTCATTTATGGTATGGTTC
357-358_RT-Rev	CCTGCAAGGGCTCCTGCAATCG
358-359_RT-For	GGAAGCTGATCTAGTAATTGGTTC
358-359_RT-Rev	GTAGCTCGCAATACATCTGAAGG
PA353_RT-For	CGAGCTGGTGAGCAAGAACGTGG
PA353_RT-Rev	GGCCCTTGATGGTCAGCTCCACG