

SI Appendix

SUPPLEMENTAL MATERIAL for:

Evolution of the *Pseudomonas aeruginosa* quorum sensing hierarchy

Maxim Kostylev, Daniel Y. Kim, Nicole E. Smalley,

Indraneel Salukhe, E. Peter Greenberg, and Ajai A. Dandekar

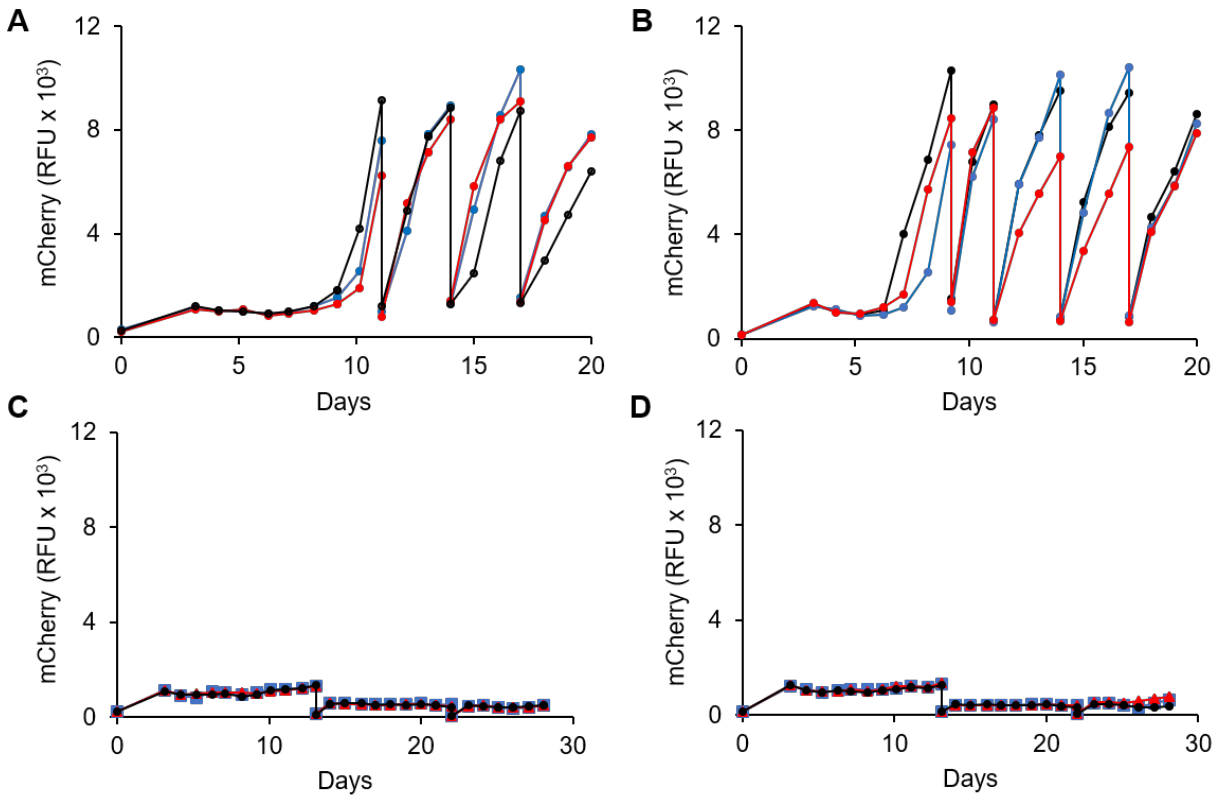


Fig. S1. Emergence of LasR and LasI mutant variants that grow in casein broth with added C4-HSL. The bacteria were marked by inserting *mCherry* in the chromosomal *att* site and growth was monitored as an increase in mCherry fluorescence (RFU). C4-HSL (30 μ M) was added at the beginning of experiments and at day-4 in A (the LasR mutant) and B (the LasI mutant). The periodic step drops in fluorescence correspond to transfers into fresh casein broth. LasR (C) or LasI (D) mutant variants did not emerge without added C4-HSL. In C and D transfers were made at day 13 and day 22. The different colors indicate independent lineages.

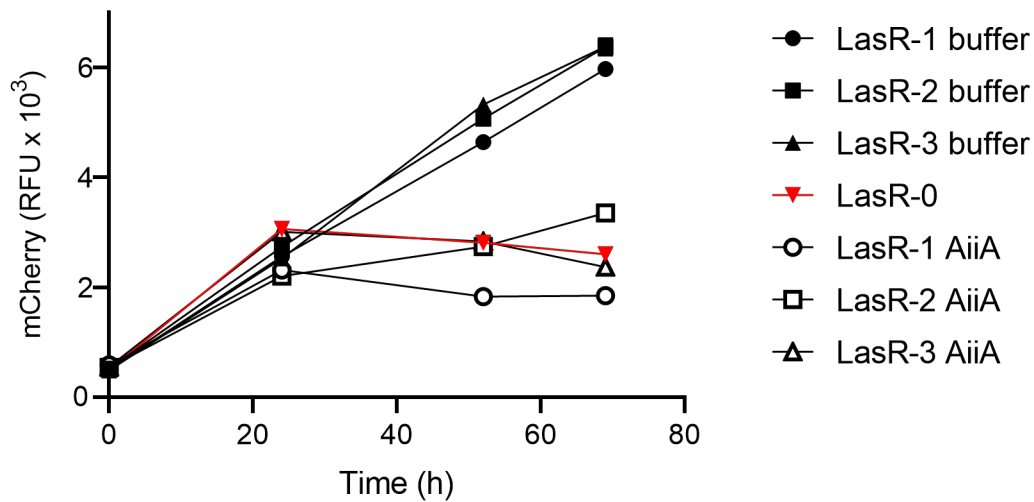


Fig. S2. Quorum sensing-dependent growth of three LasR variants isolated from cultures shown in Fig. S1. The variants (black lines) and the parent LasR mutant (red line) in casein broth (closed symbols) and casein broth plus AiiA lactonase (open symbols); variants LasR-1 (circles), LasR-2 (squares) and LasR-3 (triangles). All variants were marked with *mCherry*, and *mCherry* fluorescence (RFU) was a proxy for growth. Results are means of duplicate experiments; SEM values are smaller than the symbol size.

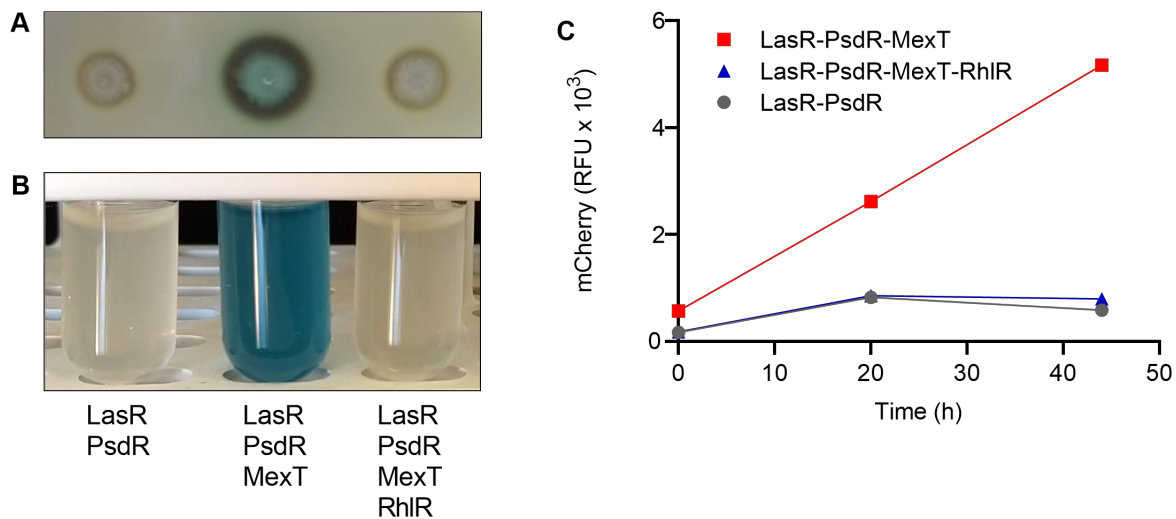


Fig. S3. The involvement of RhIR in protease production, pyocyanin synthesis, and growth on casein in a LasR mutant background. (A) A milk agar plate was inoculated by spotting it with 1 μ L of overnight LB-MOPS cultures. Image was taken after incubation at 37°C for 22 h. From left to right: LasR-PsdR deletion mutant, LasR-PsdR-MexT mutant, and LasR-PsdR-MexT-RhIR mutant. Only LasR-PsdR-MexT has a large halo of cleared milk, indicating secreted protease activity. (B) Image of the mutant cultures grown overnight in *Pseudomonas* P broth, a phosphate-limited medium that enhances the production of pyocyanin (blue-green color). (C) The three mutants were marked with *mCherry* and growth in casein broth was followed by monitoring *mCherry* fluorescence (RFU). Three mL of casein broth in 18 mm tubes was inoculated with 60 μ L of overnight LB-MOPS broth cultures. Data are means of duplicate experiments and error bars representing the SEM are smaller than the symbols.

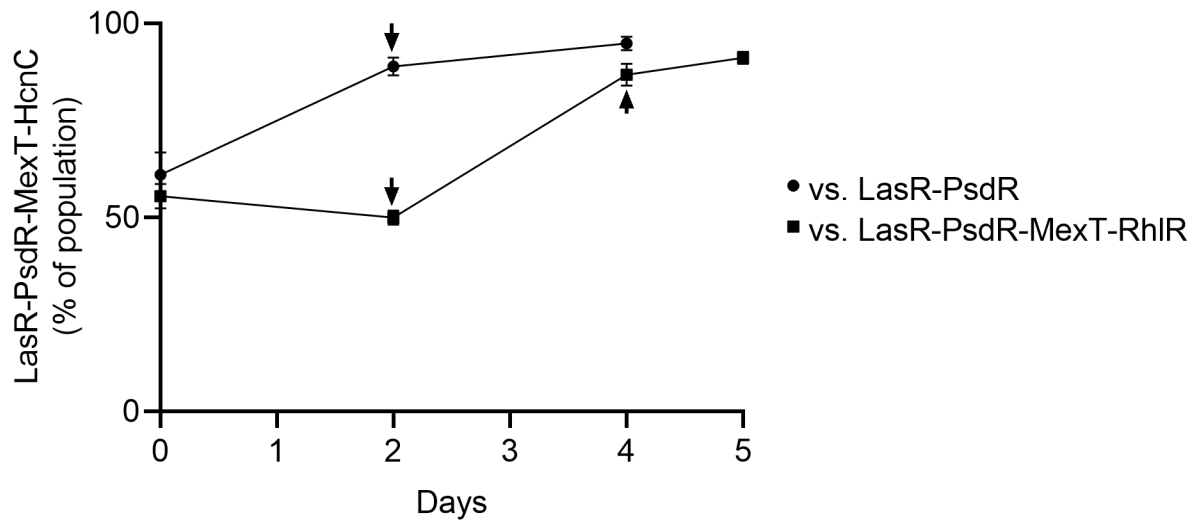


Fig. S4. Competition between the LasR-PsdR-MexT-HcnC mutant and QS mutants that cannot grow in casein broth by themselves. Arrows indicate a transfer to fresh casein broth (inoculum 2% v/v). Data are the means of duplicate experiments and error bars represent the SEM.

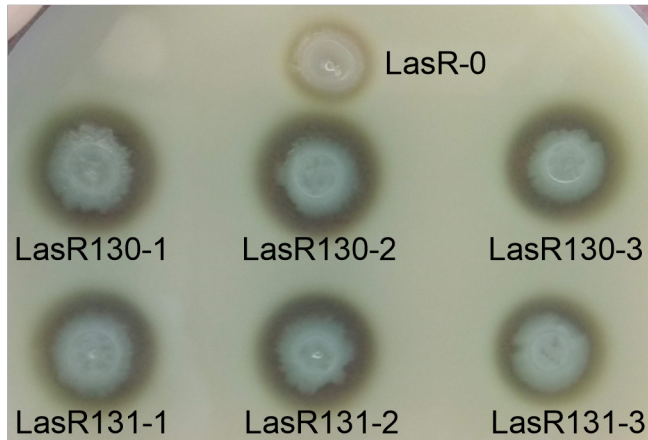


Fig. S5. LasR mutant protease-producing variants isolated from co-cultures of the PAO1 LasR mutant (LasR-0) with the clinical *P. aeruginosa* isolates E131 or E132. A milk agar plate spotted with 1 μ L of overnight LB-MOPS cultures. Image was taken after incubation at 37°C for 22 h. The parent non-protease producer is at the top. See Table S1 for details about the variants.

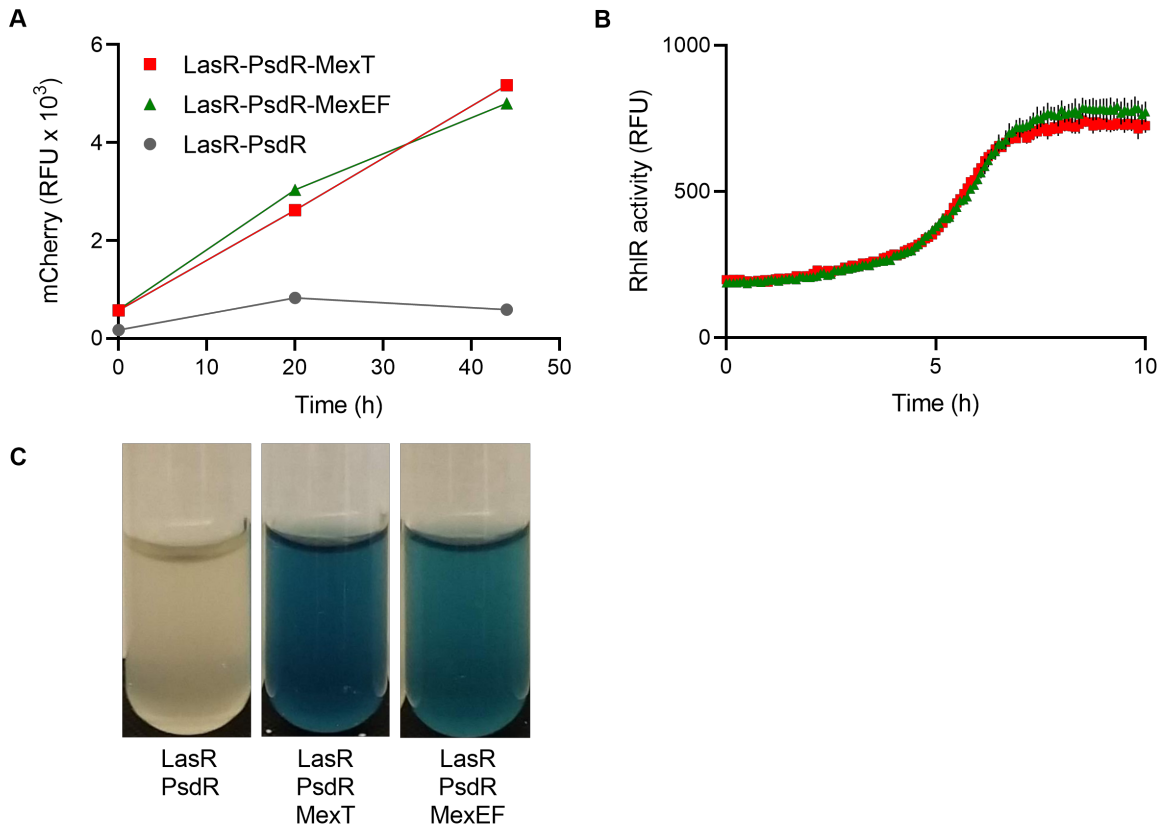


Fig. S6. Deletion of either *mexEF* or *mexT* in a LasR-PsdR mutant results in similar phenotypes. (A) Mutants were grown in casein broth and their growth was measured by monitoring mCherry fluorescence (RFU). Three mL of casein broth in 18 mm tubes was inoculated with 60 μ L of overnight LB-MOPS broth cultures. (B) RhIR activity of both mutants, measured as GFP fluorescence and reported as relative fluorescence units (RFU). Both strains contained the P_{rhIA} -*gfp* fusion plasmid pProbe-GT- P_{rhIA} -*gfp*. (C) Images of the mutant cultures grown for 20 h in *Pseudomonas* P broth, a phosphate-limited medium that enhances the production of pyocyanin (blue-green color). In panels A and B, data are means of duplicate and triplicate experiments, respectively. Error bars represent the SEM. In panel A, the error bars are smaller than the symbol size.

Table S1. Bacterial strains, and plasmids

Bacterial strain or plasmid	Description	Reference or source
<u>P. aeruginosa</u>		
PAO1	Wildtype	(1)
E92	Cystic fibrosis lung clinical isolate	(2)
E130	Cystic fibrosis lung clinical isolate	(2)
E131	Cystic fibrosis lung clinical isolate	(2)
LasR	PAO1 containing an unmarked, in-frame <i>lasR</i> deletion (3), marked with <i>mCherry</i> at the <i>att</i> site	This study
LasI	PAO1 containing an unmarked, in-frame <i>lasI</i> deletion (4) and marked with <i>mCherry</i> at the <i>att</i> site	This study
LasR-PsdR	Derived from LasR; contains an in-frame <i>psdR</i> deletion	This study
LasR-PsdR-MexT	Derived from LasR-PsdR; contains an in-frame <i>mexT</i> deletion	This study
LasR-PsdR-MexEF	Derived from LasR-PsdR; contains a deletion, $\Delta(2808249-2810363)$, which spans all <i>mexE</i> and part of <i>mexF</i>	This study
LasR-PsdR-MexT-RhIR	Derived from LasR-PsdR-MexT; contains an in-frame deletion in <i>rhIR</i>	This study
LasR-PsdR-MexT-PqsA	Derived from LasR-PsdR-MexT; contains a deletion in <i>pqsA</i> $\Delta(1078495-1079995)$	This study
LasR-PsdR-MexT-PqsE	Derived from LasR-PsdR-MexT; contains an in-frame deletion in <i>pqsE</i>	This study
LasR-PsdR-MexT-PqsA/E	Derived from LasR-PsdR-MexT-PqsA; contains an in-frame deletion of <i>pqsE</i>	This study
LasR-PsdR-MexT-HcnC	Derived from LasR-PsdR-MexT; contains a deletion in <i>hcnC</i>	This study
<u>LasR mutant variants</u>		
LasR-1	Isolated after 7 transfers in 1% casein	This study
LasR-2	Isolated after 10 transfers in 1% casein	This study
LasR-3	Isolated after 8 transfers in 1% casein	This study
LasR130-1	Isolated after 2 transfers in 1% casein	This study
LasR130-2	Isolated after 2 transfers in 1% casein	This study
LasR130-3	Isolated after 2 transfers in 1% casein	This study
LasR131-1	Isolated after 2 transfers in 1% casein	This study
LasR131-2	Isolated after 2 transfers in 1% casein	This study
LasR131-3	Isolated after 2 transfers in 1% casein	This study
<u>LasI mutant variants</u>		
LasI-1	Isolated after 8 transfers in 1% casein	This study
LasI-2	Isolated after 8 transfers in 1% casein	This study
LasI-3	Isolated after 8 transfers in 1% casein	This study
<u>E. coli</u>		
NEB5alpha	<i>fhuA2</i> $\Delta(\text{argF-lacZ})$ U169 <i>phoA</i> <i>glnV44</i> $\Phi 80$ $\Delta(\text{lacZ})$ M15 <i>gyrA96</i> <i>recA1</i> <i>relA1</i> <i>endA1</i> <i>thi-1</i> <i>hsdR17</i>	New England Biolabs
S17-1	<i>recA</i> pro <i>hsdR</i> RP4-2Tc::Mu-Km::Tn7	(5)
<u>Plasmids</u>		
pProbe-GT-P _{rhIA} <i>gfp</i>	pVS1/p15a vector with <i>gfp</i> under the control of P _{rhIA}	(2, 6)
pEXG2	Allelic exchange vector with pBR origin, gentamicin resistance, <i>sacB</i>	(7)
pEXG2-psdR-KO	pEXG2 containing sequences for <i>psdR</i> knockout	(8)
pEXG2-mexT-KO	pEXG2 containing sequences for <i>mexT</i> knockout	This study
pEXG2-mexEF-KO	pEXG2 containing sequences for <i>mexEF</i> knockout	This study
pEXG2-rhIR-KO	pEXG2 containing sequences for <i>rhIR</i> knockout	This study
pEXG2-pqsA-KO	pEXG2 containing sequences for <i>pqsA</i> knockout	This study
pEXG2-pqsE-KO	pEXG2 containing sequences for <i>pqsE</i> knockout	This study
pEXG2-hcnC-KO	pEXG2 containing sequences for <i>hcnC</i> knockout	(3)
pUC18-mini-Tn7T-Gm- <i>mCherry</i>	Derived from pUC18-mini-Tn7T-Gm (9); used for the integration of <i>mCherry</i> at the <i>att</i> site	(10)
pFLP2	Used to express the <i>flp</i> recombinase gene for excising a resistance marker from the <i>mCherry</i> cassette delivered in the pUC18-mini-Tn7T-Gm- <i>mCherry</i>	(11)
pECP61_5_ <i>mCherry</i> -PrhIA	Contains <i>mCherry</i> under the control of promoter from <i>rhIA</i> ; used in the C4-HSL bioassay	(12)

Table S2. Primers used for knockout plasmid construction^a

Construct	Fragment	Direction	Primer sequence
pEXG2-mexT-KO	vector	fwd	GTGGCCTTCATGAAGGCGCACTGGTGAAGAAAGGCGACCTCGAGCTCGAATTC GGTACC
		rev	CTACTACACCGGCCTGCTGGTGGCCTACCCGGGGATCCTCTAGAGTCGAC
	upstream sequence	fwd	TGCAGGTCGACTCTAGAGGATCCCCGGGTAGGCCACCAGCAGGCCGGTG
		rev	GACGCCTCGTGCGGGTAGCTGCCGGAGGGCTCACATAGCCATTATCAATAACGA CGGGTG
	downstream sequence	fwd	TGCCTGACAAAACCACCCGTCGTTATTGATAATGGCTATGTGAGCCCTCCGGCAG CTACC
		rev	GGTACCGAATTCGAGCTCGAGGTCGCCTTTCTCACCAGTGC
pexG2-mexEF-KO	vector	fwd	AACCAGTACGCCCTGCGTTGCTGTGAACTCGAGCTCGAATTCGGTACC
		rev	CACCGCCAGGACCACCTTGCCTTGCGCCGGGGATCCTCTAGAGTCGAC
	upstream sequence	fwd	TGCAGGTCGACTCTAGAGGATCCCCGGGCGCAAGCGCAAGGTGGTCTCTG
		rev	AGCCGGGTCACTTCTTCCGGGAGCTTTTCCATGCTTGACTCCGCCAGT
	downstream sequence	fwd	AACCGACTGGCGGAGTCAAGCATGGAAGCTCCCGGAAGAAGTGACC
		rev	GGTACCGAATTCGAGCTCGAGTTCCAGCAGCGAACGCAGGGCGTAC
pEXG2-pqsE-KO	vector	fwd	GACGCCTGCATGGCCTGTCCAGCCTCTCGAGCTCGAATTCGGTACC
		rev	CGTCTTCGAGACTCTCGCCGGCGCTCCCGGGGATCCTCTAGAGTCGAC
	upstream sequence	fwd	AGTTCGACTCTAGAGGATCCCCGGGAGCGCCGGCGAGAGTCTC
		rev	CCGCAATGGATGTCCCGTCTCACCTCAACATGGCCGTTACCTCCTC
	downstream sequence	fwd	AACCTGAGGAGGTGAACCGCCATGTTGAGGTGAGACGGGACATCCATTGC
		rev	TTAAGGTACCGAATTCGAGCTCGAGAGGCTGGACAGGCCATGCAG
pEXG2-rhIR-KO	upstream sequence	fwd	TTTTTGAGCTCACGAAGTCAACGCTTTCT
		rev	TCATGGCAACCCTATCTGTTAT
	downstream sequence	fwd	CTCATGTGTGTGCTGGTATGT
		rev	TTTTTTAAGCTTGTGCAACTGGTTCGAATTCCT
pEXG2-pqsA-KO	upstream sequence	fwd	gaccggaagctTCGAGCAAGGGTTGTAACGGTT
		rev	TCAACATGCCCGTTCTCCGGAACAGAACCTCGGTGAG
	downstream sequence	fwd	CTGACCGAGGTTCTGTTCCGGAGGAACGGGCATGTTGA
		rev	gccaccggaattcCGGTTCTCGATCAGATGGTC

^a pEXG2-mexT-KO, pEXG2-mexEF-KO, and pEXG2-pqsE-KO constructs were made by using *E. coli*-mediated DNA assembly, as described previously (13); pEXG-rhIR-KO and pEXG-pqsA-KO constructs were made using restriction enzyme-based methods, following a protocol described in ref. 14.

SI References

1. Stover CK, et al. (2000) Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen. *Nature* 406:959–964.
2. Feltner JB, et al. (2016) LasR variant cystic fibrosis isolates reveal an adaptable quorum-sensing hierarchy in *Pseudomonas aeruginosa*. *mBio* 7:e01513-16.
3. Wang M, Schaefer AL, Dandekar AA, Greenberg EP (2015) Quorum sensing and policing of *Pseudomonas aeruginosa* social cheaters. *Proc Natl Acad Sci* 112:2187–2191.
4. Toussaint JP, et al. (2017) Gene duplication in *Pseudomonas aeruginosa* improves growth on adenosine. *J Bacteriol* 199:e00261-17.
5. Simon R, Priefer U, Pühler A (1983) A broad host range mobilization system for in vivo genetic engineering: transposon mutagenesis in gram negative bacteria. *Bio/Technology* 1:784–791.
6. Miller WG, Leveau JH, Lindow SE (2000) Improved *gfp* and *inaZ* broad-host-range promoter-probe vectors. *Mol Plant Microbe Interact* 13:1243–1250.
7. Rietsch A, Vallet-Gely I, Dove SL, Mekalanos JJ (2005) ExsE, a secreted regulator of type III secretion genes in *Pseudomonas aeruginosa*. *Proc Natl Acad Sci* 102:8006–8011.
8. Zhou H, et al. (2019) Modulation of *Pseudomonas aeruginosa* quorum sensing by glutathione. *J Bacteriol* 201:e00685-18
9. Choi KH, Schweizer HP (2006) mini-Tn7 insertion in bacteria with single *attTn7* sites: example *Pseudomonas aeruginosa*. *Nat Protoc* 1:153–161.
10. Zhao K, et al. (2013) Psl trails guide exploration and microcolony formation in *Pseudomonas aeruginosa* biofilms. *Nature* 497:388–391.
11. Hoang TT, Karkhoff-Schweizer RR, Kutchma AJ, Schweizer HP (1998) A broad-host-range F1p-FRT recombination system for site-specific excision of chromosomally-located DNA sequences: application for isolation of unmarked *Pseudomonas aeruginosa* mutants. *Gene* 212:77–86.
12. Ding F, et al. (2018) The *Pseudomonas aeruginosa* orphan quorum sensing signal receptor *qscR* regulates global quorum sensing gene expression by activating a single linked operon. *mBio* 9:e01274-18.
13. Kostylev M, Otwell AE, Richardson RE, Suzuki Y (2015) Cloning should be simple: *Escherichia coli* DH5 α -mediated assembly of multiple DNA fragments with short end homologies. *PLoS One* 10:e0137466.
14. Hmelo LR, et al. (2015) Precision-engineering the *Pseudomonas aeruginosa* genome with two-step allelic exchange. *Nat Protoc* 10:1820–1841.