Supporting Information

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RhIR 1 QscR 1 LazR 1 LuxR 1 PA1136 1	MRNDGGFLLWWDGLRSENOPIHDSOGVFAVLEKEVRRLGTDYYAYGVRHT HHDER EGYLEILSRITTEEEFFSLVLEICGNYGTEFFSFGARAP YALVDG FLELERSSGKLENSAILOKHASDLGTSKILFGLLPK KKNINADDT YRIINKIKACRSNHDINOCLSDHTKHVHCEYYLLAIIYP HTDYAS LLFDSVARLRKAATTEAVCREHVEFAARLGFDRVIVCSLFP
RhiR 5 1 QscR 5 5 LasR 5 3 LuxR 6 0 PA1136 6 0	IPF IRF XTEVNGT TFK ANLER YQHQN YGAVDPA ILNGLRSSEN YVNS FPLIAP XXHFLSNYPGENKSRYISED YTSIDPIVRHGLLEYTPLINN DSQDYENAFIYGNYPA ANREHYDRAG YARVDPTVSHCTQSVLPIFNE HSHVKSDISILDNYPKKNRQYYDDAN LIKYDPIVDYSHSNHSPINNN RPDEDELIDELFFYHGDNAEGRSAQERDAYLLHCPVTRHILELDEPFFNS
RhIR 9 QscR 92 LasR 90 LuxR 96 PA1136 8	* D S L F D Q S R M L N N E A R D N G L C V G A T L P I R A P N N L L S V L S V A R D Q Q N I G E D F Q E N R F F N E E A L M H G I R H G N S I P V R G K Y G L I S K L S L V R S S E S I P S I Y Q T R - K Q H E F F E F A S A A G L V Y G L T M P L H G A R G E L G A L S L S V E A E N R I F E N M A V M K K S P N V I K E A K I S G L I T G F S F F I H T A N M G F G K L S F A H S E K D M K S P S E D P E R H T Y R I V R G V R D L G Q V M G H Q V P V F G R N G L E G A V S F A G E R L D L
RhiR 166 QscR 130 LasR 130 LuxR 196 PA1136 190	Y I D S - L F L HAC HN I P L I V P SL V D N Y R X I N I A N NK S N N DL TKREK ECLÂ
RhiR 191 QscR 196 LasR 197 LuxR 193 PA1136 191	* N TAD GX S SGETA I TL S I SE STVNTHHKNIQX KT DAP NK TL A A YAA A L GL N TAV GX I YG E I GL I L S I DORTYKTHI YNAHRKL NSSNKAEA TMKAYA I GL N CAI GX I SW E I SVIC N C SEANYNTHKGNI RRKT G VT SRVAA I NAYNL GL N AC E GX SSWDI SKIL G C SERTYITH I NA OMKL NTTNRC OS I SKAI L TGA N I AL GX Q Q A EYAAILH I SERTYENHL RAARR RL GAA STAQA YARAL RLGD
RhiR 2 6 1 QscR 2 3 6 LasR 2 3 7 LuxR 2 6 3 PA1136 2 6 1	I I N I T L I D C P YF X H E V

Fig. S1. Clustal W multiple alignment of LuxR (GenBank accession no. Y00509), LasR, RhIR, QscR, and PA1136. Conserved residues are shaded black, with the degree of shading determined using Boxshade (setting 0.8). The dark bar below the residues corresponding to LuxR amino acids 79–127 represents the fatty acyl-HSL-binding region. Asterisks over residues indicate complete conservation in all bonafide LuxR homologs.

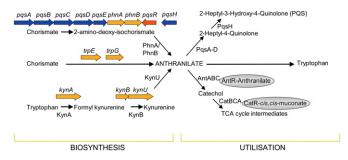


Fig. S2. Anthranilate synthesis and degradation pathways in *P. aeruginosa*. The branch-point intermediate anthranilate can be synthesized from chorismate or tryptophan via three distinct metabolic routes depending on environmental conditions. Using alternative pathways, anthranilate can be further metabolized for PQS or tryptophan biosynthesis. Anthranilate also can be directed to the TCA cycle for energy production via the enzyme products of the *antABC* and *catBCA* operons. The *antABC* operon is regulated by AntR and the inducer anthranilate, and the *catBCA* operon is regulated by CatR and the inducer *cis,cis*-muconate.

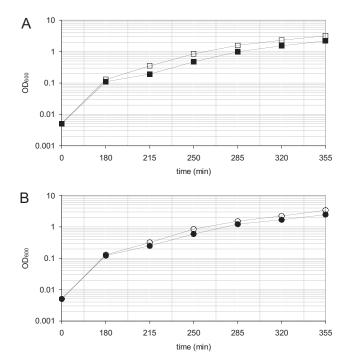


Fig. S3. Growth curve of the *P. aeruginosa* LasR-RhIR-QscR triple-mutant strain DA15 with a chromosomal *antR-lacZ* transcriptional fusion (*A*) or translational fusion (*B*). Open symbols indicate growth in the absence of added acyl-HSL, and closed symbols indicate growth in the presence of 2 μ M C10-HSL.

Table S1.	C10-HSL-regulated	genes in a	signal-receptor	r mutant
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ORF or operon*	Gene	Fold change	Description	
Induced				
PA0526-0527	dnr	2.6	Hypothetical protein (0526), transcriptional regulator Dnr (0527)	
PA0914-0915		2.6	Hypothetical (0914) and conserved hypothetical protein (0915)	
PA2119		2.7	Alcohol dehydrogenase (Zn-dependent)	
PA2507-2509	catBCA	16.4	Catechol 1,2-dioxygenase (2507), muconolactone delta- isomerase (2508), muconate cycloisomerase I (2509)	
PA2512-2514	antABC	27.8	Anthranilate dioxygenase large subunit (2512), anthranilate dioxygenase small subunit (2513), anthranilate dioxygenase reductase (2514)	
PA2515-2518	xylXYZL	3.7	Cis-1,2-dihydroxycyclohexa-3,4-diene carboxylate dehydrogenase (2515), toluate 1,2-dioxygenase electron transfer component (2516), toluate 1,2-dioxygenase beta subunit (2517), toluate 1,2-dioxygenase alpha subunit (2518)	
PA2682		3.1	Conserved hypothetical protein	
PA3911-3913		3.4	Conserved hypothetical proteins (3911, 3912), probable protease (3913)	
PA4577		2.8	Hypothetical protein	
Repressed		2.6		
PA0130-0132		-3.6	Probable aldehyde dehydrogenase (0130), hypothetical protein (0131), beta-alanine pyruvate transaminase (0132)	
PA0751-0755	opdH	-6.2	Conserved hypothetical proteins (0751, 0752), hypothetical proteins (0753, 0754), cis-aconitate porin OpdH (0755)	
PA0842-0844	plcR, plcH	-3	Probable glycosyl transferase (0842), phospholipase accessory protein PlcR precursor (0843), hemolytic phospholipase C precursor (0844)	
PA1255-1260		-2.6	Hypothetical proteins (1255, 1259), amino acid ABC transporter ATP- binding protein (1256), amino acid ABC transporter membrane protein (1257), probable permease of ABC transporter (1258), amino acid ABC transporter periplasmic- binding protein (1260)	
PA1390-1391		-2.7	Probable glycosyl transferases (1390)	
PA2323		-3	Probable glyceraldehyde-3-phosphate dehydrogenase	
PA2719		-3	Hypothetical protein	
PA3079-3080		-2.5	Hypothetical proteins (3080)	
PA3195	gapA	-2.5	Glyceraldehyde-3-phosphate dehydrogenase	
PA3498-3503		-3.1	Probable oxidoreductase (3498), hypothetical proteins (3499, 3501, 3502, 3503), conserved hypothetical protein (3500)	
PA3504-3514		-2.6	Probable aldehyde dehydrogenase (3504), hypothetical proteins (3505, 3510, 3513), probable decarboxylase (3506), probable short-chain dehydrogenases (3507, 3511), probable transcriptional regulator (3508), probable hydrolase (3509), probable permease of ABC transporter (3512), probable ATP-binding component of ABC transporter (3514)	
PA3709		-3.4	Probable major facilitator superfamily transporter	
PA3710		-3.6	Probable glucose-methanol-choline-type oxidoreductase	
PA3901	fecA	-4.6	Fe(III) dicitrate transport protein FecA	
PA5372-5373	betAB	-3.4	Choline dehydrogenase (5372), betaine aldehyde dehydrogenase (5373)	
PA5375	betT1	-2.7	Choline transporter BetT	
PA5468-5469		-2.5	Probable citrate transporter (PA5468), conserved hypothetical protein (PA5469)	

Genes predicted to be parts of an operon and showing significant fold changes as determined by Cyber-T analysis are in bold type. *Grouping of genes forming putative operons is according to the *Pseudomonas* Genome Project (http://www.pseudomonas.com); values shown are for the gene with the highest response.