Supporting Information

Chugani and Greenberg 10.1073/pnas.1005909107

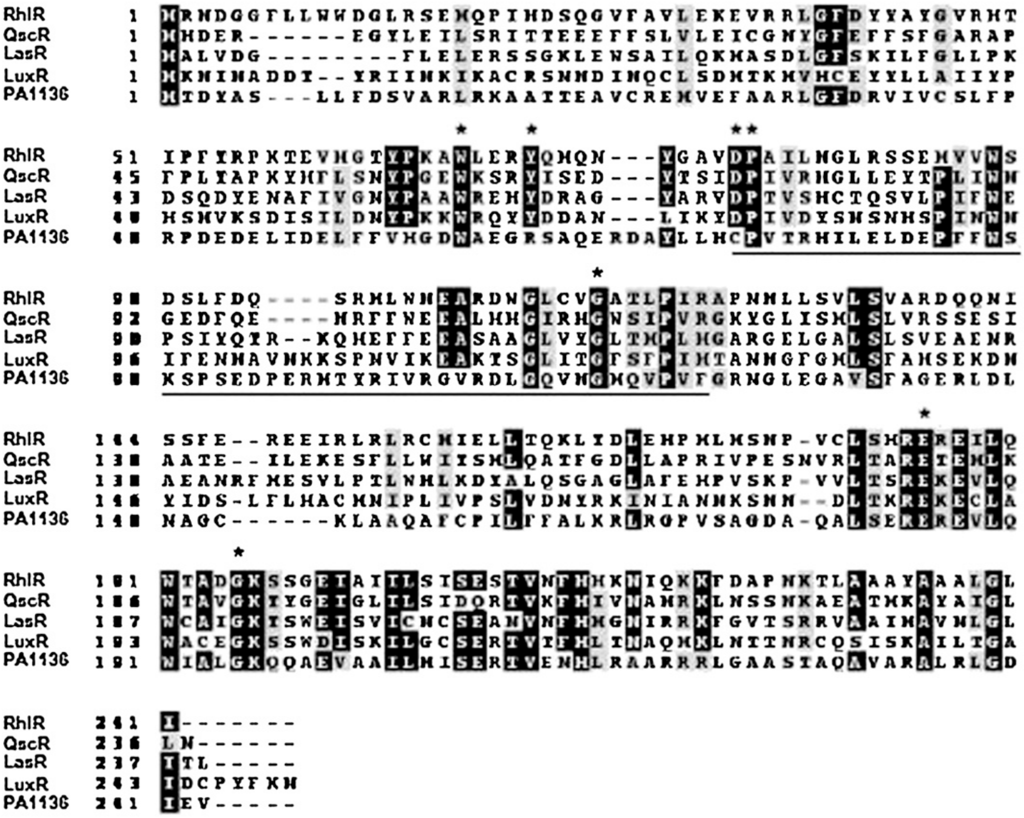

Fig. S1. Clustal W multiple alignment of LuxR (GenBank accession no. Y00509), LasR, RhlR, QscR, and PA1136. Conserved residues are shaded black, with the degree of shading determined using Boxshade (setting 0.8). The dark bar below the residues corresponding to LuxR amino acids 79–127 represents the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

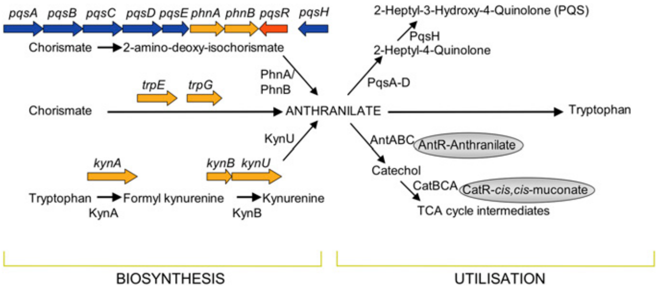

Fig. S2. Anthranilate synthesis and degradation pathways in *P. aeruginosa*. The branch-point intermediate anthranilate can be synthesized from chorismate or tryptophan via three distinct metabolic routes depending on environmental conditions. Using alternative pathways, anthranilate can be further metabolized 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.

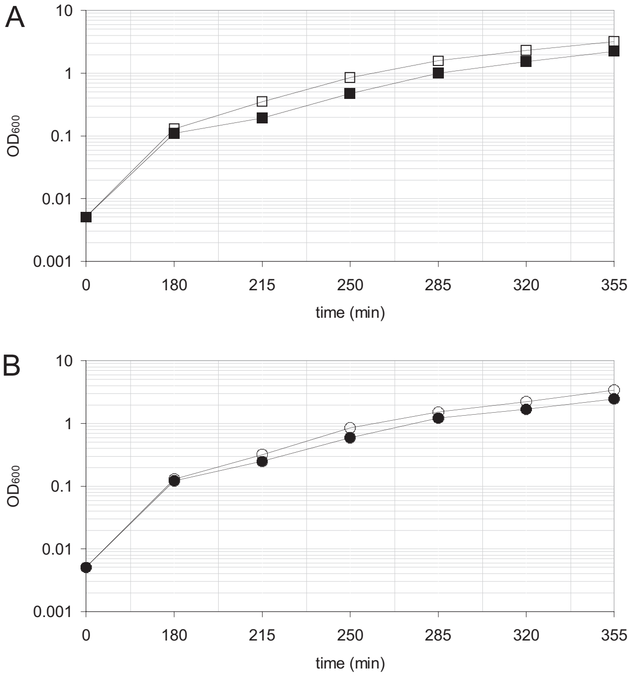

Fig. S3. Growth curve of the *P. aeruginosa* LasR-RhlR-QscR triple-mutant strain DA15 with a chromosomal *antR-lacZ* transcriptional fusion (*A*) or translational fusion (*B*). Open symbols indicate growth in the absence of added acyl-HSL, and closed symbols indicate growth in the presence of 2 μM C10-HSL.

Table S1. C10-HSL–regulated genes in a signal-receptor mutant

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			
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.