

TABLE S1. Phenotypic data for *P. aeruginosa* PA14 mutants

Locus ^a (Mutated gene)	Mutant ID	Description	QS-dependent phenotypes ^b			
			Skim-milk proteolysis	Staphylolytic activity	Rhamnolipid production	Pyocyanin production
PA14 wild type			+++	+++	+++	+++
<i>QS core genes</i>						
PA14_19120 (<i>rhlR</i>)	37943	Transcriptional regulator	+++,,+,+ ^d	+	-	-
PA14_19130 (<i>rhlI</i>)	33961	Autoinducer synthesis protein RhlI	+++,,+,+ ^d	+	++	-
PA14_39980 (<i>qscR</i>)	42798	Transcriptional regulator	+++	+++	+++	++
PA14_45940 (<i>lasI</i>)	39292	Autoinducer synthesis protein LasI	+	-	++	-
PA14_45960 (<i>lasR</i>) ^c	N/A	Transcriptional regulator	-	-	++	-
<i>Known QS regulatory genes not rediscovered</i>						
PA14_17480 (<i>rpoS</i>)	32095	Sigma factor RpoS	+++	++	+++	++
PA14_45950 (<i>rsaL</i>)	46524	Regulatory protein RsaL	+++	+++	++	+++
PA14_51340 (<i>mvfR</i>)	47015	Transcriptional regulator MvfR	+++	+++	++	+++
PA14_52180 (<i>relA</i>)	55087	GTP pyrophosphokinase	+++	+++	++	+++
PA14_52570 (<i>rsmA</i>)	44507	RsmA, regulator of secondary metabolites	+++	+++	+++	+++
PA14_56070 (<i>mvaT</i>)	34492	Transcriptional regulator MvaT	+++	+++	++	+++
PA14_62530 (<i>cbrA</i>)	33836	Two component sensor CbrA	+++	+++	++	+++
<i>Known QS regulatory genes rediscovered</i>						
PA14_08370 (<i>vfr</i>)	52692	Cyclic AMP receptor-like protein	++	-, +, - ^d	++	+
PA14_30650 (<i>gacA</i>)	54630	Response regulator GacA	++	-, +, +, - ^d	+++	-
PA14_57940 (<i>rpoN</i>)	44482	RNA polymerase sigma-54 factor	++	+++	NG	+++
PA14_62490 (<i>dksA</i>)	41617	Suppressor protein DksA	++	+++	-	+++
<i>Novel genes</i>						
PA14_05260 (<i>pyrB</i>)	52690	Aspartate carbamoyltransferase	++	+++	NG	-
PA14_05380 (<i>pilK</i>)	52952	Methyltransferase PilK	++	+++	++	++
PA14_05620 (<i>sahH</i>)	56708	S-adenosyl-L-homocysteine hydrolase	+	++	NG	+
PA14_07700 (<i>apaH</i>)	36226	Bis(5'-nucleosyl)-tetraphosphatase	-	++	++	+++
PA14_09520 (<i>mexI</i>)	43615	Probable RND efflux transporter	++	++	+++	++
PA14_12080 (<i>sltB1</i>)	27636	Soluble lytic transglycosylase B	++	+++	++	++

PA14_52040 (<i>purM</i>)	47921	Phosphoribosylaminoimidazole synthetase	++	+++	NG	++
PA14_54370 (<i>lepA</i>)	38761	GTP-binding protein LepA	-	-	+++	++
PA14_56300	35583	Putative fumarase	++	+++	++	+++
PA14_58600	27307	Conserved hypothetical protein	++	+++	+++	+++
PA14_60280 (<i>fimU</i>)	44085	Type 4 fimbrial biogenesis protein FimU	++	+++, ++, - ^d	++	+++, ++, - ^d
PA14_62560 (<i>pcnB</i>)	41679	Poly(A) polymerase	++	++	++	++
PA14_62930 (<i>carA</i>)	39940	Carbamoyl-phosphate synthase small chain	-	+++	NG	+
PA14_64220 (<i>purD</i>)	29794	Phosphoribosylamine-glycine ligase	++	+++	NG	++
PA14_66110	56681	Putative glycosyl transferase	++	+++	++	+++
PA14_66600 (<i>aroB</i>)	38358	3-dehydroquinate synthase	++	++	NG	-
PA14_66940 (<i>hisI</i>)	40903	Phosphoribosyl-AMP cyclohydrolase	++	+++	++	++
PA14_67530	42570	Noncatalytic dihydroorotase-like protein	++	+++	++	++
PA14_67560 (<i>typA</i>)	37710	GTP-binding protein TypA/BipA	++	+++	+++	++, +++, + ^d
PA14_68370 (<i>cysQ</i>)	40356	3'(2'),5'-bisphosphate nucleotidase	++	+++	++	++
PA14_69670 (<i>lysA</i>)	27796	Diaminopimelate decarboxylase	++	+++	NG	++
PA14_70370 (<i>pyrE</i>)	46326	Orotate phosphoribosyltransferase	-	+++	NG	++
PA14_70370 (<i>pyrE</i>)	46326	Orotate phosphoribosyltransferase	-	+++	NG	+
PA14_72490 (<i>polA</i>)	31829	DNA polymerase I	+, ++, +++ ^d	++	+++	++
PA14_73370 (<i>gidA</i>)	44643	Glucose-inhibited division protein A	++	-	-	-

^a Unless labeled otherwise, all mutants have a MAR2xT7 transposon insertion in the respective ORF.

^b +++, ++, +, -, and NG indicate a phenotype resembling the wild type, slightly attenuated, substantially attenuated, absent, and no growth, respectively.

^c The *lasR* mutant contains a *TnphoA* insertion in codon 154. The PA14 library does not include a *lasR* mutant.

^d Due to inconsistent results, phenotypes from each replication are given.