Table S3. The functional categories in which the representation of differentially-expressed genes was greater than their representation among all of the B728a genes^a.

			Δg	acS						alA						retS			T		Δ	rp	oS					Δh	rpL	,				Δa	lgU				Δι	pol	V	٦
Functional category	A	В	CΙ	ÞΕ	F	G	A	В	СГ) E	F	G	Α	В	C	D E	EF	C	ì A	В	C	Ď	Е	F	G	A I	В	$C \mid I$	ĴΕ	F	G	Α	В	CI	ΣE	F	G	A B	C	D E	E F C	į
Amino acid metabolism & transport																																										
AA metabolism & transport (GABA)																																										
Carbohydrate metabolism & transport																																										
Cell division																																										
Chaperones/Heat shock proteins																																										
Chemosensing & chemotaxis																																										
Cofactor metabolism																																										
Cold shock proteins																																										
Compatible solute synthesis																																										
Cyclic di-GMP cyclase proteins																																										
Degradation of xenobiotics																																										
Energy generation																																										
Fatty acid metabolism																																										
Flagellar synthesis & motility																																										
Glutathione metabolism																																										
Hypothetical																																										
Iron metabolism and transport																																										
Iron-sulfur proteins																																										
Light and oxygen sensing																																										
LPS synthesis & transport																																										
Mechanosensitive ion channel																																										
Nitrogen metabolism																																										
Nucleotide metabolism & transport																																										
Organic acid metabolism and transport																																										
Osmosensing & regulation																																										
Outer membrane proteins																																										
Oxidative stress tolerance																																										

Table S3 (continued).

		Δ	Δgc	ıcS				Δs	alA				Δ	ret	S				Δ	rpc	oS.			1	Δhr	рL				Δα	algU	T			Δr_l	υοN	r
Functional category	Α	ВС	D	E	F C	jΑ	В	CI	DΕ	F	G	ΑВ	С	D	E F	F (j A	A B				G	A				F C	ìΑ	В	C	DΈ	F	G	АВ	CΓ) E	F G
Oxidative stress tolerance																																					
(Antioxidant enzyme)				Ш				Ш					\perp	Ш	_	_	1						Ш		\perp								Ш				$\perp \perp$
Peptidoglycan/cell wall polymers																																					
Phage & IS elements																																					
Phosphate metabolism & transport																																					
Phospholipid metabolism																																					
Phytotoxin synthesis & transport				Ш																																	
Pili synthesis and regulation																																					
Plant-associated proteins																																					
Polyamine metabolism & transport																																					
Polysaccharide synthesis & regulation																																					
Post-translational modification																																					
Proteases																																					
QAC metabolism & transport																																					
Quorum regulation																																					
Replication & DNA repair																																					
RNA degradation																																					
Secondary metabolism																																					
Secretion/Efflux/Export																																					
Siderophore synthesis & transport																																					
Signal transduction mechanisms																																					
Special																																					
Stress resistance																																					
Sulfur metabolism & transport																																					
TAT secretion system																																					
Terpenoid backbone synthesis																																					
Toxin-Antitoxin system																																					
Transcription																																					
Transcription - Sigma factor																																					
Transcriptional regulation																																					

Table S3 (continued).

				gac						Δsa							Δr		_						rpc						Δh							alg						Δr_l			
Functional category	A	В	C I	D E	EF	7	j A	A B	3 ($^{\circ}$ $^{\circ}$	E	F	Ċ	3 A	A I	3 (CI) I	3 I	F (G.	A l	В	C	D	Е	F	G.	A I	3 ($C \mid C$) E	F	G	A	В	C	D	ΕI	F	G.	A l	В	$C \mid I$) E	EF	G
Translation																																															
Transport																																															
Transport (inorganic ions)																																															
Transport (organic compounds)																																															
Transport (peptides)																																															
Type III secretion system																																															
Type VI secretion system																																															

^a The data are shown for analyses performed for each regulatory mutant under each of the seven treatments, indicated by letters A-G: A, basal medium; B, osmotic stress, C, oxidative stress; D, iron starvation; E, nitrogen starvation; F, epiphytic sites; and G, apoplastic sites. Data are not shown for the $\triangle ahlR$ or $\triangle aefR$ mutants. Red and pink boxes indicate repression by the regulator; that is, the genes with transcripts that were increased in the mutant were significantly over-represented in that functional category (red, q-value < 0.05; pink, q-value < 0.1). Green and light green boxes indicate activation by the regulator; that is, the genes with transcripts that were decreased in the mutant were significantly over-represented in that functional category (green, q-value < 0.05; light green q-value < 0.1). The functional categories and over-representation test were performed as described previously (2).