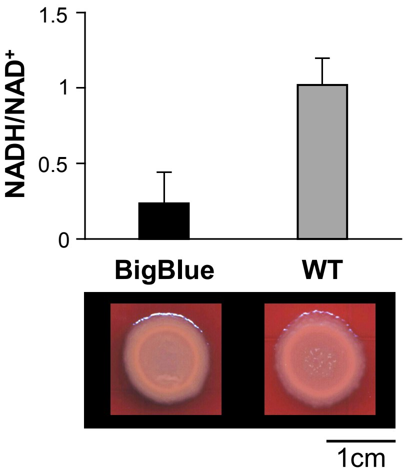

FIG S1. NADH/NAD$^+$ ratio of WT and BigBlue colonies sampled after 36 hours of growth in the colony morphology assay. Error bars represent the standard deviation of biological triplicates.

Table S1. KEGG pathway analysis of cluster 1 and cluster 2 proteins in Figure 1A.

Cluster 1

Locus Tag	Gene	Product	KEGG Pathway Name	Xref
Metabolism				
PA14_01600		putative aldehyde dehydrogenase	Valine, leucine and isoleucine degradation; beta-Alanine metabolism; Inositol phosphate metabolism; Propanoate metabolism; Carbon metabolism	pau00280 pau00410 pau00562 pau00640 pau01200
PA14_01620	aptA	beta alanine--pyruvate transaminase	Valine, leucine and isoleucine degradation; beta-Alanine metabolism; Propanoate metabolism	pau00280 pau00410 pau00640
PA14_03330		hypothetical protein	Histidine metabolism; Biosynthesis of secondary metabolites; Biosynthesis of amino acids	pau00340 pau01110 pau01230
PA14_03450	gabT		Alanine, aspartate and glutamate metabolism	pau00250
PA14_03450	gabT		Alanine, aspartate and glutamate metabolism; Lysine degradation; Butanoate metabolism	pau00250
PA14_04760	coaD		Pantothenate and CoA biosynthesis	pau00770
PA14_09470	phzB1	phenazine biosynthesis		
PA14_10040		amidase	Arginine and proline metabolism; Phenylalanine metabolism; Tryptophan metabolism; Aminobenzoate degradation; Styrene degradation	pau00330 pau00360 pau00380 pau00627 pau00643
PA14_11000	hpaA	4-hydroxyphenylacetate 3-monooxygenase large chain	Tyrosine metabolism; Degradation of aromatic compounds	pau00350
PA14_13330		hypothetical protein	Aminobenzoate degradation; Folate biosynthesis; Two-component system	pau00627
PA14_14700	cysE	serine O-acetyltransferase	Cysteine and methionine metabolism; Sulfur metabolism; Biosynthesis of amino acids	pau00270
PA14_17190	fabZ	(3R)-hydroxymyristoyl-ACP dehydratase	Fatty acid biosynthesis; Fatty acid metabolism; Biotin metabolism	pau00061 pau01212 pau00780
PA14_18890		electron transport complex RsxE subunit		
PA14_20890	rfaD		Lipopolysaccharide biosynthesis	pau00540
PA14_23280	pheA	chorismate mutase	Phenylalanine, tyrosine and tryptophan biosynthesis; Biosynthesis of secondary metabolites; Biosynthesis of antibiotics; Biosynthesis of amino acids	pau00400 pau01100 pau01110 pau01130 pau01230
PA14_24640	pyrD		Pyrimidine metabolism	pau00240
PA14_25210		5'-methylthioadenosine phosphorylase	Cysteine and methionine metabolism	pau00270

Table S1 - cluster 1 (continued)

PA14_25250			Glycolysis / Gluconeogenesis; Biosynthesis of secondary metabolites; Biosynthesis of antibiotics; Biosynthesis of amino acids	pau00010 pau01110 pau01130 pau01230
PA14_27500		aminotransferase AlaT	Alanine, aspartate and glutamate metabolism; Valine, leucine and isoleucine biosynthesis; Biosynthesis of secondary metabolites; Biosynthesis of antibiotics; 2-Oxocarboxylic acid metabolism; Biosynthesis of amino acids	pau00250 pau00290 pau01110 pau01130 pau01210 pau01230
PA14_28650	thrS	threonyl-tRNA synthetase	Aminoacyl-tRNA biosynthesis	pau00970
PA14_42730		putative oxidase	Cysteine and methionine metabolism	pau00270
PA14_43680	fabA	3-hydroxydecanoyl-(acyl carrier protein) dehydratase	Fatty acid biosynthesis; Fatty acid metabolism	pau00061
PA14_43950	sucC	succinyl-CoA synthetase subunit beta	TCA cycle; Propanoate metabolism; C5-Branched dibasic acid metabolism; Biosynthesis of secondary metabolites; Biosynthesis of antibiotics	pau00020 pau00640 pau00660 pau01110 pau01130
PA14_44070	gltA		Citrate cycle (TCA cycle)	pau00020
PA14_44070	gltA		Glyoxylate and dicarboxylate metabolism; Biosynthesis of secondary metabolites; Biosynthesis of antibiotics; 2-Oxocarboxylic acid metabolism; Biosynthesis of amino acids	pau00630 pau01110 pau01130 pau01210 pau01230
PA14_44350		putative cytochrome c oxidase subunit	Oxidative phosphorylation	pau00190
PA14_47210	cyoA	cytochrome o ubiquinol oxidase subunit II	Oxidative phosphorylation	pau00190
PA14_52040	purM	phosphoribosylaminoimidazole synthetase	Purine metabolism; Biosynthesis of secondary metabolites, antibiotics	pau0023; pau01110 pau01130
PA14_52800	acsA		Glycolysis / Gluconeogenesis; Pyruvate, Propanoate, Methane metabolism; Biosynthesis of secondary metabolites, antibiotics	pau00010 pau00620 pau00640 pau00680 pau01110 pau01130
PA14_52850		acyl-CoA lyase beta chain	C5-Branched dibasic acid metabolism	pau00660
PA14_52990	phhA		Phenylalanine metabolism; Phenylalanine, tyrosine and tryptophan biosynthesis	pau00360 pau00400
PA14_57710	cysN	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	Purine metabolism; Selenocompound metabolism; Sulfur metabolism	pau00230 pau00450 pau00920
PA14_65710	aspP	adenosine diphosphate sugar pyrophosphatase	Purine metabolism	pau00230
PA14_66900	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	Ubiquinone and other terpenoid-quinone biosynthesis; Biosynthesis of secondary metabolites	pau00130 pau01110
PA14_70040	dadA	D-amino acid dehydrogenase small subunit	Phenylalanine metabolism	pau00360

Table S1 - cluster 1 (continued)

PA14_71650	aspA		Alanine, aspartate and glutamate metabolism	pau00250
PA14_71720		pyruvate carboxylase subunit B	TCA cycle; Pyruvate metabolism; Biosynthesis of amino acids	pau00020
PA14_73300	atpE	F0F1 ATP synthase subunit C	Oxidative phosphorylation	pau00190
PA14_13090			Fatty acid degradation; Synthesis and degradation of ketone bodies; Valine, leucine and isoleucine, Lysine, Benzoate degradation; Tryptophan, Pyruvate, Glyoxylate and dicarboxylate, Propanoate, Butanoate metabolism; Terpenoid backbone biosynthesis; Biosynthesis of secondary metabolites, antibiotics; Fatty acid metabolism; Two-component system	pau00071 pau00072 pau00280 pau00310 pau00362 pau00380 pau00620 pau00630 pau00640 pau00650 pau00900 pau01110 pau01130 pau01212 pau02020
PA14_08760	rpoB	DNA-directed RNA polymerase subunit beta	Purine metabolism; Pyrimidine metabolism; RNA polymerase	pau00230 pau00240 pau03020
PA14_69230	ppk	polyphosphate kinase	Oxidative phosphorylation; RNA degradation	pau00190 pau03018
Motility				
PA14_58650			Two-component system; Bacterial chemotaxis	pau0202; pau02030
PA14_60280	fimU			
PA14_60310	pilY1	type 4 fimbrial biogenesis protein PilY1		
PA14_60870	morA	motility regulator		
PA14_66630	pilP	type 4 fimbrial biogenesis protein PilP		
Recombination/Replication				
PA14_09200	ssb	single-stranded DNA-binding protein	DNA replication; Mismatch repair; Homologous recombination	pau03030 pau03430 pau03440
PA14_09200	ssb	single-stranded DNA-binding protein	Homologous recombination	pau03440
PA14_17500	mutS	DNA mismatch repair protein MutS	Mismatch repair	pau03430
PA14_17530	recA	recombinase A	Homologous recombination	pau03440
PA14_54590	ung		Base excision repair	pau03410
PA14_00010	dnaA	chromosomal replication initiation protein		
Signaling				
PA14_06070	creC	sensory histidine kinase CreC	Two-component system	pau02020

Table S1 - cluster 1 (continued)

PA14_13090			Fatty acid degradation; Synthesis and degradation of ketone bodies; Valine, leucine and isoleucine, Lysine, Benzoate degradation; Tryptophan, Pyruvate, Glyoxylate and dicarboxylate, Propanoate, Butanoate metabolism; Terpenoid backbone biosynthesis; Biosynthesis of secondary metabolites, antibiotics; Fatty acid metabolism; Two-component system	pau00071 pau00072 pau00280 pau00310 pau00362 pau00380 pau00620 pau00630 pau00640 pau00650 pau00900 pau01110 pau01130 pau01212 pau02020
PA14_30630	pqsH	quinolone biosynthesis		
PA14_45500		putative purine-binding chemotaxis protein	Two-component system	pau02020
PA14_45500		putative purine-binding chemotaxis protein	Bacterial chemotaxis	pau02030
PA14_68260		c4-dicarboxylate-binding protein	Two-component system	pau02020
PA14_72390		putative two-component sensor	Two-component system	pau02020
PA14_72720		putative two-component response regulator	Two-component system	pau02020
PA14_58650			Two-component system; Bacterial chemotaxis	pau0202; pau02030
Transcriptiont/Translation				
PA14_05560			RNA degradation	pau03018
PA14_14040	rhl		RNA degradation	pau03018
PA14_27370			RNA degradation	pau03018
PA14_62560	pcnB	poly(A) polymerase	RNA degradation	pau03018
PA14_08760	rpoB	DNA-directed RNA polymerase subunit beta	Purine metabolism; Pyrimidine metabolism; RNA polymerase	pau00230 pau00240 pau03020
PA14_69230	ppk	polyphosphate kinase	Oxidative phosphorylation; RNA degradation	pau00190 pau03018
PA14_08720	rplK	50S ribosomal protein L11	Ribosome	pau03010
PA14_08740	rplJ		Ribosome	pau03010
PA14_08750	rplL		Ribosome	pau03010
PA14_08790	rpsL		Ribosome	pau03010
PA14_08810	rpsG	30S ribosomal protein S7	Ribosome	pau03010
PA14_08840	rpsJ	30S ribosomal protein S10	Ribosome	pau03010
PA14_08850	rplC	50S ribosomal protein L3	Ribosome	pau03010
PA14_08870	rplW	50S ribosomal protein L23	Ribosome	pau03010
PA14_08880	rplB	50S ribosomal protein L2	Ribosome	pau03010

Table S1 - cluster 1 (continued)

PA14_08900	rplV	50S ribosomal protein L22	Ribosome	pau03010
PA14_08930	rpmC	50S ribosomal protein L29	Ribosome	pau03010
PA14_08950	rplN	50S ribosomal protein L14	Ribosome	pau03010
PA14_08970	rplE	50S ribosomal protein L5	Ribosome	pau03010
PA14_09000	rplF	50S ribosomal protein L6	Ribosome	pau03010
PA14_09040	rplO	50S ribosomal protein L15	Ribosome	pau03010
PA14_09080	rpsM	30S ribosomal protein S13	Ribosome	pau03010
PA14_09100	rpsD	30S ribosomal protein S4	Ribosome	pau03010
PA14_16000	rplS	50S ribosomal protein L19	Ribosome	pau03010
PA14_17060	rpsB		Ribosome	pau03010
PA14_25630	rpmF	50S ribosomal protein L32	Ribosome	pau03010
PA14_28660	infC	translation initiation factor IF-3		
PA14_28680	rplT	50S ribosomal protein L20	Ribosome	pau03010
PA14_57580	rpsI	30S ribosomal protein S9	Ribosome	pau03010
PA14_60400	rpsT		Ribosome	pau03010
PA14_60450	rpmA	50S ribosomal protein L27	Ribosome	pau03010
PA14_60460	rplU	50S ribosomal protein L21	Ribosome	pau03010
PA14_62720	rpsO		Ribosome	pau03010
PA14_62760	infB	translation initiation factor IF-2		
PA14_70180	rpmG	50S ribosomal protein L33	Ribosome	pau03010
PA14_70190	rpmB	50S ribosomal protein L28	Ribosome	pau03010
Transport				
PA14_01040		putative secretion protein		
PA14_03950	spuG	polyamine transport protein PotH	ABC transporters	pau02010
PA14_04910	ftsE	cell division ATP-binding protein FtsE	ABC transporters	pau02010
PA14_09050	secY	preprotein translocase subunit SecY	Protein export	pau03060
PA14_11270	oprG			
PA14_14630	secD	preprotein translocase subunit SecD	Protein export	pau03060
PA14_15960	ffh		Protein export	pau03060
PA14_17640	potA	polyamine transport protein PotA	ABC transporters	pau02010
PA14_21450		hypothetical protein	Bacterial secretion system	pau03070
PA14_41110		putative solute-binding protein	ABC transporters	pau02010

Table S1 - cluster 1 (continued)

PA14_46920		putative permease of ABC transporter	ABC transporters	pau02010
PA14_46950		putative ATP-binding component of ABC transporter	ABC transporters	pau02010
PA14_01970		putative RND efflux transporter		
PA14_69340		putative ATP-binding component of ABC transporter		
Others				
CON__ENSEMBL:ENSBTAP00000001528				
CON__ENSEMBL:ENSBTAP00000025008				
CON__P01966				
CON__Q1A7A4				
PA14_01540				
PA14_01730				
PA14_01930	pcaR			
PA14_03320		hypothetical protein		
PA14_03610				
PA14_04300				
PA14_04640		hypothetical protein		
PA14_04790				
PA14_05440		hypothetical protein		
PA14_05660				
PA14_05820				
PA14_06240				
PA14_06340		putative molybdenum transport regulator		
PA14_07780		hypothetical protein		
PA14_12280	lnt			
PA14_12570				
PA14_12670				
PA14_14140		hypothetical protein		
PA14_14690		putative methyltransferase		
PA14_15070	oprC	outer membrane copper receptor OprC		
PA14_16840				
PA14_17170		hypothetical protein		
PA14_18590				

Table S1 - cluster 1 (continued)

PA14_18700	rnt	ribonuclease T		
PA14_18860		hypothetical protein		
PA14_18870				
PA14_19730				
PA14_23260	gyrA			
PA14_23390	orfE	putative polysaccharide biosynthesis protein		
PA14_24500	pelC	putative lipoprotein		
PA14_24910	moeA2	molybdenum cofactor biosynthesis protein A2		
PA14_24990		hypothetical protein		
PA14_25100				
PA14_25140				
PA14_26540		hypothetical protein		
PA14_27180				
PA14_27990				
PA14_29400		hypothetical protein		
PA14_29830				
PA14_30160		hypothetical protein		
PA14_30240	infA			
PA14_34230				
PA14_35600	pslL			
PA14_35670	pslG	putative glycosyl hydrolase		
PA14_35900				
PA14_36280		putative antibiotic biosynthesis monooxygenase		
PA14_37580				
PA14_37650				
PA14_37745		carbamoyl transferase		
PA14_39130				
PA14_40650				
PA14_40890		short chain dehydrogenase		
PA14_41930				
PA14_42790				
PA14_42860				

Table S1 - cluster 1 (continued)

PA14_42990		hypothetical protein		
PA14_45260		hypothetical protein		
PA14_45920		hypothetical protein		
PA14_46260		hypothetical protein		
PA14_47440				
PA14_49410				
PA14_49640				
PA14_49920				
PA14_49930				
PA14_50300				
PA14_50590		HSP90 family protein		
PA14_51100		acyl-CoA dehydrogenase		
PA14_51740	tolR	TolR protein		
PA14_51840				
PA14_52140				
PA14_52460	mgtE			
PA14_53120		hypothetical protein		
PA14_53400		oxidoreductase		
PA14_53510				
PA14_56870		hypothetical protein		
PA14_57020	groES	co-chaperonin GroES		
PA14_57275	ftsZ	cell division protein FtsZ		
PA14_57760	algW			
PA14_57920		hypothetical protein		
PA14_58580		putative hydroxylase		
PA14_59200		hypothetical protein		
PA14_59220				
PA14_60120	dcd2	putative deoxycytidine deaminase		
PA14_60445	obgE	GTPase ObgE		
PA14_61050	mscL			
PA14_61360				
PA14_61990		hypothetical protein		

Table S1 - cluster 1 (continued)

PA14_62260				
PA14_65010				
PA14_65270	hflC	protease subunit HflC		
PA14_66120				
PA14_66270	glnE	glutamate-ammonia-ligase adenylyltransferase		
PA14_66760		hypothetical protein		
PA14_66790	hslU	ATP-dependent protease ATP-binding subunit HslU		
PA14_67090	mdoG	glucan biosynthesis protein G		
PA14_67940				
PA14_68660	rimK			
PA14_69110				
PA14_69820		hypothetical protein		
PA14_70400		hypothetical protein		
PA14_71430				

Table S1 - (continued) **Cluster 2**

Locus Tag	Gene	Product	KEGG Pathway Name	Xref
Metabolism				
PA14_00120			Lipopolysaccharide biosynthesis	pau00540
PA14_00280	hemF	coproporphyrinogen III oxidase	Porphyrin and chlorophyll metabolism; Biosynthesis of secondary metabolites	pau00860 pau01110
PA14_01240			Nitrogen metabolism	pau00910
PA14_01760	nuh		Purine metabolism; Nicotinate and nicotinamide metabolism	pau00230 pau00760
PA14_02590	mdcE	malonate decarboxylase gamma subunit		
PA14_03900	spuC	putative aminotransferase	Arginine and proline metabolism	pau00330
PA14_04410	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	Phosphotransferase system (PTS)	pau02060
PA14_05220		cystathionine beta-synthase	Glycine, serine and threonine metabolism; Cysteine and methionine metabolism; Biosynthesis of antibiotics, amino acids	pau00260 pau00270 pau01130 pau01230
PA14_05230		cystathionine gamma-lyase	Glycine, serine and threonine metabolism; Cysteine and methionine metabolism; Selenocompound metabolism; Biosynthesis of antibiotics, amino acids	pau00260 pau00270 pau00450 pau01130 pau01230
PA14_05270	pyrR	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	Pyrimidine metabolism	pau00240
PA14_06720	nirF	heme d1 biosynthesis protein NirF		
PA14_06750	nirS	nitrite reductase precursor	Nitrogen metabolism	pau00910
PA14_06770	nirQ	regulatory protein NirQ		
PA14_06810	norC	nitric-oxide reductase subunit C	Nitrogen metabolism	pau00910
PA14_06830	norB	nitric-oxide reductase subunit B	Nitrogen metabolism	pau00910
PA14_07170	epd	D-erythrose 4-phosphate dehydrogenase	Vitamin B6 metabolism	pau00750
PA14_08460		hypothetical protein	Nitrogen metabolism	pau00910
PA14_09160	bfrA		Porphyrin and chlorophyll metabolism	pau00860
PA14_09210	pchA	salicylate biosynthesis isochorismate synthase	Ubiquinone and other terpenoid-quinone biosynthesis; Biosynthesis of siderophore group nonribosomal peptides, secondary metabolites, antibiotics	pau00130 pau01053 pau01110 pau01130
PA14_09220	pchB	isochorismate-pyruvate lyase	Biosynthesis of siderophore group nonribosomal peptides, secondary metabolites, antibiotics	pau01053 pau01110 pau01130
PA14_09230	pchC	pyochelin biosynthetic protein PchC		
PA14_09280	pchF	pyochelin synthetase	Biosynthesis of siderophore group nonribosomal peptides	pau01053
PA14_09400	phzS	phenazine biosynthesis		
PA14_11760		ethanolamine ammonia-lyase small subunit	Glycerophospholipid metabolism	pau00564

Table S1 - cluster 2 (continued)

PA14_11770	eutB	ethanolamine ammonia-lyase large subunit	Glycerophospholipid metabolism	pau00564
PA14_12490		AMP nucleosidase	Purine metabolism	pau00230
PA14_13230	moaC	molybdenum cofactor biosynthesis protein C	Folate biosynthesis; Sulfur relay system	pau00790 pau04122
PA14_14470	pepA	leucyl aminopeptidase	Glutathione metabolism	pau00480
PA14_16090	thrC	threonine synthase	Glycine, serine and threonine metabolism; Vitamin B6 metabolism; Biosynthesis of amino acids	pau00260 pau00750 pau01230
PA14_16390			Glycine, serine and threonine metabolism	pau00260
PA14_18120	mmsA	methylmalonate-semialdehyde dehydrogenase	Valine, leucine and isoleucine degradation; beta-Alanine, Inositol phosphate, Propanoate metabolism	pau00280 pau00410 pau00562 pau00640
PA14_18140	mmsB	3-hydroxyisobutyrate dehydrogenase	Valine, leucine and isoleucine degradation	pau00280
PA14_18710	pyrC	dihydroorotase	Pyrimidine metabolism	pau00240
PA14_19470	mqoA		TCA cycle; Pyruvate metabolism; Biosynthesis of secondary metabolites, antibiotics	pau00020 pau00620 pau01110 pau01130
PA14_20200	nosZ	nitrous-oxide reductase	Nitrogen metabolism	pau00910
PA14_20560	amiE	acylamide amidohydrolase	Arginine and proline, Phenylalanine, Tryptophan metabolism; Aminobenzoate, Styrene degradation	pau00330 pau00360 pau00380 pau00627 pau00643
PA14_22910	edd		Pentose phosphate pathway	pau00030
PA14_23250	mtnA		Cysteine and methionine metabolism	pau00270
PA14_23880	folC	folylpolyglutamate synthetase	Folate biosynthesis	pau00790
PA14_24270	pepN	aminopeptidase N	Glutathione metabolism	pau00480
PA14_25080	fadB	multifunctional fatty acid oxidation complex subunit alpha	Fatty acid, Valine, leucine and isoleucine; Geraniol; Lysine, Limonene and pinene, Caprolactam degradation; Tryptophan, beta-Alanine, Propanoate, Butanoate metabolism; Biosynthesis of unsaturated fatty acids, secondary metabolites, antibiotics; Fatty acid metabolism	pau00071 pau00280 pau00281 pau00310 pau00903 pau00930 pau00380 pau00410 pau00640 pau00650 pau01040 pau01110 pau01130 pau01212
PA14_25320	nqrC	Na(+)-translocating NADH-quinone reductase subunit C		
PA14_27730	fadE	acyl-CoA dehydrogenase	Fatty acid degradation	pau00071
PA14_27730	fadE	acyl-CoA dehydrogenase	Fatty acid metabolism	pau01212
PA14_28710	pheT	phenylalanyl-tRNA synthetase subunit beta	Aminoacyl-tRNA biosynthesis	pau00970
PA14_30330	serS	seryl-tRNA synthetase	Aminoacyl-tRNA biosynthesis	pau00970

Table S1 - cluster 2 (continued)

PA14_30340	cysG	siroheme synthase	Porphyrin and chlorophyll metabolism; Biosynthesis of secondary metabolites	pau00860 pau01110
PA14_31820			Histidine, Tyrosine, Phenylalanine metabolism; Phenylalanine, tyrosine and tryptophan, Novobiocin biosynthesis Biosynthesis of secondary metabolites, antibiotics, amino acids	pau00340 pau00350 pau00360 pau00400 pau00401 pau01110 pau01130 pau01230
PA14_33500	pvdH	diaminobutyrate--2-oxoglutarate aminotransferase		
PA14_33630	pvdJ	PvdJ		
PA14_33650	pvdD	pyoverdine synthetase D		
PA14_33710	pvdO	PvdO		
PA14_33740	pvdP			
PA14_33810	pvdA			
PA14_34330			Sulfur metabolism	pau00920
PA14_36570	glgA	glycogen synthase	Starch and sucrose metabolism; Biosynthesis of secondary metabolites	pau00500 pau01110
PA14_36630		putative glycosyl hydrolase	Starch and sucrose metabolism; Biosynthesis of secondary metabolites	pau00500 pau01110
PA14_36710	glgB	glycogen branching enzyme	Starch and sucrose metabolism; Biosynthesis of secondary metabolites	pau00500 pau01110
PA14_36740		hypothetical protein	Starch and sucrose metabolism	pau00500
PA14_38590	bdhA		Synthesis and degradation of ketone bodies; Butanoate metabolism	pau00072 pau00650
PA14_39640	cobN	cobaltochelatase subunit CobN	Porphyrin and chlorophyll metabolism	pau00860
PA14_41670	ppsA		Pyruvate, Methane metabolism	pau00620 pau00680
PA14_41950			Fatty acid, Valine, leucine and isoleucine, Geraniol, Lysine, Benzoate, Aminobenzoate, Limonene and pinene, Caprolactam degradation; Phenylalanine, Tryptophan, beta-Alanine, Propanoate, Butanoate metabolism; Biosynthesis of secondary metabolites, antibiotics; Fatty acid metabolism	pau00071 pau00280 pau00281 pau00310 pau00362 pau00627 pau00903 pau00930 pau00360 pau00380 pau00410 pau00640 pau00650 pau01110 pau01130 pau01212
PA14_42850	folE	GTP cyclohydrolase I	Folate biosynthesis	pau00790
PA14_43790		putative aldehyde dehydrogenase		
PA14_44390		putative cytochrome c oxidase subunit	Oxidative phosphorylation	pau00190
PA14_47550			Glutathione metabolism	pau00480
PA14_47550			Arachidonic acid metabolism	pau00590

Table S1 - cluster 2 (continued)

PA14_49710			Pyruvate metabolism	pau00620
PA14_50660		hypothetical protein	Cysteine and methionine, Sulfur metabolism; Biosynthesis of antibiotics, amino acids	pau00270 pau00920 pau01130 pau01230
PA14_52690	aruG	arginine/ornithine succinyltransferase AII subunit	Arginine and proline metabolism	pau00330
PA14_53480	pta	phosphate acetyltransferase	Taurine and hypotaurine, Pyruvate, Propanoate, Methane metabolism	pau00430 pau00620 pau00640 pau00680
PA14_54000	prpD		Propanoate metabolism	pau00640
PA14_56240	pykA		Glycolysis / Gluconeogenesis; Purine, Pyruvate metabolism; Biosynthesis of secondary metabolites, antibiotics, amino acids	pau00010 pau00230 pau00620 pau01110 pau01130 pau01230
PA14_57370	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	D-Glutamine and D-glutamate metabolism	pau00471
PA14_57370	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	Peptidoglycan biosynthesis	pau00550
PA14_57530	sspA	stringent starvation protein A		
PA14_57810	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Amino sugar and nucleotide sugar metabolism	pau00520
PA14_57810	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Peptidoglycan biosynthesis	pau00550
PA14_58030	fumC	fumarate hydratase	TCA cycle; Pyruvate metabolism; Biosynthesis of secondary metabolites, antibiotics	pau00020 pau00620 pau01110 pau01130
PA14_58190	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	Aminoacyl-tRNA biosynthesis	pau00970
PA14_60330	ispH	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Terpenoid backbone biosynthesis; Biosynthesis of secondary metabolites, antibiotics	pau00900 pau01110p au01130
PA14_62200	mrcB	penicillin-binding protein 1B	Peptidoglycan biosynthesis	pau00550
PA14_62850	folP	dihydropteroate synthase	Folate biosynthesis	pau00790
PA14_63020	fur			
PA14_65480	rhdA	thiosulfate sulfurtransferase	Cysteine and methionine metabolism; Sulfur metabolism; Sulfur relay system	pau00270 pau00920 pau04122
PA14_66440	metY		Cysteine and methionine metabolism	pau00270
PA14_67240	hutG	N-formylglutamate amidohydrolase	Histidine metabolism	pau00340
PA14_67260		putative histidine/phenylalanine ammonia-lyase	Histidine metabolism	pau00340
PA14_67350	hutU		Histidine metabolism	pau00340
PA14_67890	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	Histidine metabolism; Biosynthesis of secondary metabolites, amino acids	pau00340 pau01110 pau01230
PA14_68190	rmlD	dTDP-4-dehydrorhamnose reductase	Streptomycin, Polyketide sugar unit biosynthesis; Biosynthesis of secondary metabolites	pau00521 pau00523 pau01110

Table S1 - cluster 2 (continued)

PA14_68340	arcB	ornithine carbamoyltransferase	Arginine and proline metabolism; Biosynthesis of secondary metabolites, antibiotics, amino acids	pau00330 pau01110 pau01130 pau01230
PA14_68350	arcC	carbamate kinase	Purine, Arginine and proline, Nitrogen metabolism	pau00230 pau00330 pau00910
PA14_70160		omega amino acid--pyruvate transaminase	Valine, leucine and isoleucine degradation; beta-Alanine, Propanoate metabolism	pau00280 pau00410 pau00640
PA14_71260		putative FMN oxidoreductase		
PA14_71630	adhA		Glycolysis / Gluconeogenesis; Fatty acid degradation; Tyrosine metabolism; Chloroalkane and chloroalkene, Naphthalene degradation; Biosynthesis of secondary metabolites, antibiotics; Degradation of aromatic compounds	pau00010 pau00071 pau00350 pau00625 pau00626 pau01110 pau01220
PA14_63250			Fatty acid degradation; Synthesis and degradation of ketone bodies; Valine, leucine and isoleucine, Lysine, Benzoate degradation; Tryptophan, Pyruvate, Glyoxylate and dicarboxylate, Propanoate, Butanoate metabolism; Terpenoid backbone biosynthesis; Biosynthesis of secondary metabolites, antibiotics; Fatty acid metabolism; Two-component system	pau00071 pau00072 pau00280 pau00310 pau00362 pau00380 pau00620 pau00630 pau00640 pau00650 pau00900 pau01110 pau01130 pau01212 pau02020
PA14_03700	sbp		Sulfur metabolism ABC transporters	pau00920 pau02010
PA14_12920		taurine ABC transporter periplasmic protein	Sulfur metabolism	pau00920 pau02010
Motility				
PA14_45800	fliM	flagellar motor switch protein FliM	Flagellar assembly	pau02040
PA14_66640	pilO	type 4 fimbrial biogenesis protein PilO		
PA14_66650	pilN	type 4 fimbrial biogenesis protein PilN		
Recombination/Replication				
PA14_70390	crc		Base excision repair	pau03410
PA14_66720	priA		Homologous recombination	pau03440
Signaling				
PA14_02270			Two-component system; Bacterial chemotaxis	pau02020 pau02030
PA14_05390	chpA	ChpA	Two-component system	pau02020
PA14_08370	vfr		Two-component system	pau02020
PA14_30820			Two-component system Bacterial chemotaxis	pau02020 pau02030
PA14_45800	fliM	flagellar motor switch protein FliM	Bacterial chemotaxis	pau02030

Table S1 - cluster 2 (continued)

PA14_48030			Two-component system	pau02020
PA14_48030			Bacterial chemotaxis	pau02030
PA14_49180	phoP	two-component response regulator PhoP	Two-component system	pau02020
PA14_49440			Two-component system	pau02020
PA14_51380	pqsE	quinolone signal response protein		
PA14_52350		hypothetical protein	Two-component system	pau02020
PA14_63250			Fatty acid degradation; Synthesis and degradation of ketone bodies; Valine, leucine and isoleucine, Lysine, Benzoate degradation; Tryptophan, Pyruvate, Glyoxylate and dicarboxylate, Propanoate, Butanoate metabolism; Terpenoid backbone biosynthesis; Biosynthesis of secondary metabolites, antibiotics; Fatty acid metabolism; Two-component system	pau00071 pau00072 pau00280 pau00310 pau00362 pau00380 pau00620 pau00630 pau00640 pau00650 pau00900 pau01110 pau01130 pau01212 pau02020
PA14_68230		two-component sensor	Two-component system	pau02020
PA14_69470	algR	alginate biosynthesis regulatory protein AlgR	Two-component system	pau02020
PA14_72380	algB	two-component response regulator AlgB	Two-component system	pau02020
Transcription/Translation				
PA14_61780			Ribosome	pau03010
Transport				
PA14_03700	sbp		Sulfur metabolism ABC transporters	pau00920 pau02010
PA14_03920	spuD		ABC transporters	pau02010
PA14_04090		putative binding protein component of ABC transporter	ABC transporters	pau02010
PA14_07860		putative ATP-binding component of ABC transporter		
PA14_09300		putative ATP-binding component of ABC transporter		
PA14_09320		putative ATP-binding component of ABC transporter		
PA14_09340	fptA	Fe(III)-pyochelin outer membrane receptor precursor		
PA14_12920		taurine ABC transporter periplasmic protein	Sulfur metabolism	pau00920 pau02010
PA14_13010			ABC transporters	pau02010
PA14_13600		putative binding protein component of ABC transporter	ABC transporters	pau02010
PA14_20580	amiC	aliphatic amidase expression-regulating protein	ABC transporters	pau02010
PA14_22440		putative ATP-binding/permease fusion ABC transporter		

Table S1 - cluster 2 (continued)

PA14_22980		putative binding protein component of ABC sugar transporter	ABC transporters	pau02010
PA14_25430		hypothetical protein	ABC transporters	pau02010
PA14_27770		ABC transporter ATP-binding protein		
PA14_33540		putative permease of ABC transporter	ABC transporters	pau02010
PA14_52790	aotJ		ABC transporters	pau02010
PA14_55040		putative ATP-binding component of ferric enterobactin transport		
PA14_64900			ABC transporters	pau02010
PA14_68900		putative binding protein component of ABC iron transporter	ABC transporters	pau02010
PA14_73410		putative inner membrane protein translocase component YidC	Protein export	pau03060
PA14_58350		putative binding protein component of ABC transpor	ABC transporters; Bacterial chemotaxis	pau02010 pau02030
Others				
CON__P50448				
PA14_00480				
PA14_00710	osmC			
PA14_00790	prlC	oligopeptidase A		
PA14_01350		hypothetical protein		
PA14_01780		putative nucleoside 2-deoxyribosyltransferase		
PA14_04100				
PA14_04890		putative zinc protease		
PA14_05060		hypothetical protein		
PA14_05510		hypothetical protein		
PA14_05960				
PA14_06000				
PA14_06040				
PA14_07020		hypothetical protein		
PA14_10820				
PA14_11140		putative nonribosomal peptide synthetase		
PA14_11320				
PA14_12090		RlpA family lipoprotein		
PA14_12110		hypothetical protein		
PA14_12260				
PA14_13000				

Table S1 - cluster 2 (continued)

PA14_13140		hypothetical protein		
PA14_13150				
PA14_13170				
PA14_13260	moaB1	MoaB1		
PA14_14290				
PA14_15200				
PA14_16250	lasB			
PA14_16260				
PA14_16370				
PA14_16560		putative lipoprotein		
PA14_16620		hypothetical protein		
PA14_16640				
PA14_16750		hypothetical protein		
PA14_17050	map			
PA14_17250				
PA14_17670				
PA14_17720				
PA14_18800				
PA14_19065				
PA14_19100	rhlA	rhamnosyltransferase chain A		
PA14_19360		GNAT family acetyltransferase		
PA14_19410				
PA14_19490				
PA14_19590		putative molybdopterin-binding protein		
PA14_20290				
PA14_20520		hypothetical protein		
PA14_20770		hypothetical protein		
PA14_21120				
PA14_21960		hypothetical protein		
PA14_23110				
PA14_23200		short chain dehydrogenase		
PA14_23470	wbpM			

Table S1 - cluster 2 (continued)

PA14_23680	ibpA			
PA14_23700				
PA14_23730				
PA14_24675		hypothetical protein		
PA14_24900	moaB2	molybdopterin biosynthetic protein B2		
PA14_24970				
PA14_25420		hypothetical protein		
PA14_25500		hypothetical protein		
PA14_25600		putative peptidase		
PA14_26190				
PA14_27000				
PA14_27070				
PA14_27950		hypothetical protein		
PA14_28450	eco			
PA14_28490				
PA14_29020	cpo			
PA14_29470				
PA14_29710		hypothetical protein		
PA14_30210	clpS	ATP-dependent Clp protease adaptor protein ClpS		
PA14_30620				
PA14_30840				
PA14_31290	pa1L			
PA14_32890		hypothetical protein		
PA14_32950				
PA14_33050		hypothetical protein		
PA14_33160				
PA14_33280	pvdL	peptide synthase		
PA14_33290				
PA14_33600		hypothetical protein		
PA14_33610		peptide synthase		
PA14_33680	fpvA			
PA14_33730		putative dipeptidase precursor		

Table S1 - cluster 2 (continued)

PA14_33750		putative outer membrane protein precursor		
PA14_33830		hypothetical protein		
PA14_34510		hypothetical protein		
PA14_36200				
PA14_36530				
PA14_37780		hypothetical protein		
PA14_38220		hypothetical protein		
PA14_38710		hypothetical protein		
PA14_39410				
PA14_40250		putative outer membrane protein precursor		
PA14_40880		hypothetical protein		
PA14_40960		pilin biosynthetic protein		
PA14_41640				
PA14_42130				
PA14_45840		hypothetical protein		
PA14_45930		hypothetical protein		
PA14_45950	rsaL			
PA14_46300		hypothetical protein		
PA14_47120		hypothetical protein		
PA14_47130		hypothetical protein		
PA14_47490				
PA14_47930		hypothetical protein		
PA14_48810		NAD-dependent deacetylase		
PA14_49030				
PA14_49510	pyoS3I	immunity protein S3I structureal gene		
PA14_49520	pyoS3A	pyocin killing protein		
PA14_49870				
PA14_51170	pauA	pimeloyl-CoA synthetase		
PA14_51830				
PA14_53230		oxidoreductase		
PA14_53500				
PA14_54410	mucB	negative regulator for alginate biosynthesis MucB		

Table S1 - cluster 2 (continued)

PA14_55080				
PA14_55580	nemO			
PA14_55980				
PA14_56550				
PA14_56730				
PA14_58000	sodM	superoxide dismutase		
PA14_58010		hypothetical protein		
PA14_58330				
PA14_59845				
PA14_61060				
PA14_61080				
PA14_61720		hypothetical protein		
PA14_62240				
PA14_62350				
PA14_62650		hypothetical protein		
PA14_62690		hypothetical protein		
PA14_63830				
PA14_64170				
PA14_64480	osmE			
PA14_65000	azu			
PA14_65470				
PA14_66090		hypothetical protein		
PA14_66200		hypothetical protein		
PA14_66340				
PA14_68040				
PA14_68400				
PA14_69010		hypothetical protein		
PA14_69050				
PA14_69260		isoprenoid biosynthesis protein with amidotransferase-like domain		
PA14_70490				
PA14_70740				
PA14_71450				

Table S2. Mass-spectrometry signal intensities for denitrification enzymes detected in WT and Δ*phz* samples taken over the course of colony development. Missing values indicate levels below detection limit.

		time (h)						
		24	30	33	36	39	42	54
WT	*napA*					43838		59708
	napD	30165	15583			17786		14066
	napF							14693
	nirF		17021	77596		27452	18684	
	nirM		27990	32545	23530	28399	52547	41801
	nirS		247200	308800	307650	134230	278970	342820
	norC							
	nosZ							34733
Δ*phz*	*napA*					41763		55884
	napD				14914		11584	12022
	napF			67381		9453.9		
	nirF		135650	26688	37463	32975	73904	69905
	nirM				16481		61337	33303
	nirS	367520	150880	659770	766800	954980	984730	1009300
	norC						40956	
	nosZ			85967		139610	127000	173970

Table S3. Strains and plasmids used in this study.

Strains/plasmids	Number	Used in figures	Characteristics	Source or reference
Pseudomonas aeruginosa				
PA14		1	Clinical isolate UCBPP-PA14	(1)
PA14 Δ*phz*	LD24	1	PA14 with deletions of operons *phzA1-G1* and *phzA2-G2*	This study
BigBlue	LD64	1	PA14 containing two copies of *phzM*	(2)
PA14 Δ*anr*	LD915		PA14 with deletions of *anr*	This study
PA14 Δ*phz* Δ*anr*	LD916		PA14 with deletions of *phzA1-G1*, *phzA2-G2* and *anr*	This study
PA14 WT *attB*::MCS-*gfp*	LD876	3, 4	PA14 with MCS-*gfp* inserted at the *attB* site using pLD844 (pSEK101)	This study
PA14 Δ*phz attB*::MCS-*gfp*	LD880	3, 4	PA14 Δ*phz* with MCS-*gfp* inserted at the *attB* site using pLD844 (pSEK101)	This study
PA14 WT *attB*::*napEp-gfp*	LD877	3	PA14 with *napEp-gfp* inserted at the *attB* site using pLD852 (pSEK101-*napEp*)	This study
PA14 Δ*phz attB*::*napEp-gfp*	LD881	3	PA14 Δ*phz* with *napEp-gfp* inserted at the *attB* site using pLD852 (pSEK101-*napEp*)	This study
PA14 WT *attB*::*narK1p-gfp*	LD921	3, 4	PA14 with *narK1p-gfp* inserted at the *attB* site using pLD902 (pSEK101-*narK1p*)	This study
PA14 Δ*phz attB*::*narK1p-gfp*	LD922	3, 4	PA14 Δ*phz* with *narK1p-gfp* inserted at the *attB* site using pLD902 (pSEK101-*narK1p*)	This study
PA14 WT *attB*::*nirSp-gfp*	LD927	3	PA14 with *nirSp-gfp* inserted at the *attB* site using pLD903 (pSEK101-*nirSp*)	This study
PA14 Δ*phz attB*::*nirSp-gfp*	LD928	3	PA14 Δ*phz* with *nirSp-gfp* inserted at the *attB* site using pLD903 (pSEK101-*nirSp*)	This study
PA14 WT *attB*::*norCp-gfp*	LD1149	3	PA14 with *norCp-gfp* inserted at the *attB* site using pSEK101-*norCp*	This study
PA14 Δ*phz attB*::*norCp-gfp*	LD1150	3	PA14 Δ*phz* with *norCp-gfp* inserted at the *attB* site using pSEK101-*norCp*	This study
PA14 WT *attB*::*nosRp-gfp*	LD933	3	PA14 with *nosRp-gfp* inserted at the *attB* site using pLD904 (pSEK101-*nosRp*)	This study
PA14 Δ*phz attB*::*nosRp-gfp*	LD934	3	PA14 Δ*phz* with *nosRp-gfp* inserted at the *attB* site using pLD904 (pSEK101-*nosRp*)	This study
PA14 WT *attB*::MCS-*gfp*	LD2478	5, 6	PA14 with MCS-*gfp* inserted at the *attB* site using pLD2477 (pMQ37)	This study
PA14 Δ*phz attB*::MCS-*gfp*	LD2479	5, 6	PA14 Δ*phz* with MCS-*gfp* inserted at the *attB* site using pLD2477 (pMQ37)	This study
PA14 WT *attB*::*napEp*$_{200bp}$-*gfp*	LD2522	5, 6	PA14 with P*napE*$_{200bp}$-*gfp* inserted at the *attB* site using pLD2521 (pMQ37-*napEp*$_{200bp}$)	This study
PA14 Δ*phz attB*::*napEp*$_{200bp}$-*gfp*	LD2523	5, 6	PA14 Δ*phz* with P*napE*$_{200bp}$-*gfp* inserted at the *attB* site using pLD2521 (pMQ37-*napEp*$_{200bp}$)	This study
PA14 Δ*phzHM attB*::*napEp*$_{200bp}$-*gfp*	LD2706	5	PA14 Δ*phzHM* with P*napE*$_{200bp}$-*gfp* inserted at the *attB* site using pLD2521 (pMQ37-*napEp*$_{200bp}$)	This study
PA14 Δ*phzHS attB*::*napEp*$_{200bp}$-*gfp*	LD2707	5	PA14 Δ*phzHS* with P*napE*$_{200bp}$-*gfp* inserted at the *attB* site using pLD2521 (pMQ37-*napEp*$_{200bp}$)	This study

Table S3 (continued)

PA14 WT *attB*::*napEp*$_{\text{100bp}}$-*gfp*	LD2528	6	PA14 with P*napE*$_{\text{100bp}}$-*gfp* inserted at the *attB* site using pLD2527 (pMQ37-*napEp*$_{\text{100bp}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{100bp}}$-*gfp*	LD2529	6	PA14 Δ*phz* with P*napE*$_{\text{100bp}}$-*gfp* inserted at the *attB* site using pLD2527 (pMQ37-*napEp*$_{\text{100bp}}$)	This study
PA14 WT *attB*::*napEp*$_{\text{70bp}}$-*gfp*	LD2665	6	PA14 with P*napE*$_{\text{70bp}}$-*gfp* inserted at the *attB* site using pLD2664 (pMQ37-*napEp*$_{\text{70bp}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{70bp}}$-*gfp*	LD2666	6	PA14 Δ*phz* with P*napE*$_{\text{70bp}}$-*gfp* inserted at the *attB* site using pLD2664 (pMQ37-*napEp*$_{\text{70bp}}$)	This study
PA14 WT *attB*::*napEp*$_{\text{70bp-shuffle-3}}$-*gfp*	LD2668	6	PA14 with P*napE*$_{\text{70bp-shuffle-3}}$-*gfp* inserted at the *attB* site using pLD2667 (pMQ37-*napEp*$_{\text{70bp-shuffle-3}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{70bp-shuffle-3}}$-*gfp*	LD2669	6	PA14 Δ*phz* with P*napE*$_{\text{70bp-shuffle-3}}$-*gfp* inserted at the *attB* site using pLD2667 (pMQ37-*napEp*$_{\text{70bp-shuffle-3}}$)	This study
PA14 WT *attB*::*napEp*$_{\text{70bp-shuffle-1\&2}}$-*gfp*	LD2762	6	PA14 with P*napE*$_{\text{70bp-shuffle-1\&2}}$-*gfp* inserted at the *attB* site using pLD2761 (pMQ37-*napEp*$_{\text{70bp-shuffle-1\&2}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{70bp-shuffle-1\&2}}$-*gfp*	LD2763	6	PA14 Δ*phz* with P*napE*$_{\text{70bp-shuffle-B}}$-*gfp* inserted at the *attB* site using pLD2761 (pMQ37-*napEp*$_{\text{70bp-shuffle-1\&2}}$)	This study
PA14 WT *attB*::*napEp*$_{\text{70bp-shuffle-1}}$-*gfp*	LD2856	6	PA14 with P*napE*$_{\text{70bp-shuffle-1}}$-*gfp* inserted at the *attB* site using pLD2855 (pMQ37-*napEp*$_{\text{70bp-shuffle-1}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{70bp-shuffle-1}}$-*gfp*	LD2857	6	PA14 Δ*phz* with P*napE*$_{\text{70bp-shuffle-1}}$-*gfp* inserted at the *attB* site using pLD2855 (pMQ37-*napEp*$_{\text{70bp-shuffle-1}}$)	This study
PA14 WT *attB*::*napEp*$_{\text{70bp-shuffle-2}}$-*gfp*	LD2859	6	PA14 with P*napE*$_{\text{70bp-shuffle-2}}$-*gfp* inserted at the *attB* site using pLD2858 (pMQ37-*napEp*$_{\text{70bp-shuffle-D}}$)	This study
PA14 Δ*phz attB*::*napEp*$_{\text{70bp-shuffle-2}}$-*gfp*	LD2860	6	PA14 Δ*phz* with P*napE*$_{\text{70bp-shuffle-2}}$-*gfp* inserted at the *attB* site using pLD2858 (pMQ37-*napEp*$_{\text{70bp-shuffle-D}}$)	This study
PA14 WT *attB*::*mexGp-gfp*	LD2525	5	PA14 with *mexGp-gfp* inserted at the *attB* site using pLD2524 (pMQ37-*mexGp*)	This study
PA14 Δ*phz attB*::*mexGp-gfp*	LD2526	5	PA14 Δ*phz* with *mexGp-gfp* inserted at the *attB* site using pLD2524 (pMQ37-*mexGp*)	This study
PA14 Δ*phzHM attB*::*mexGp-gfp*	-	5	PA14 Δ*phzHM* with *mexGp-gfp* inserted at the *attB* site using pLD2524 (pMQ37-*mexGp*)	This study
PA14 Δ*phzHS attB*::*mexGp-gfp*	-	5	PA14 Δ*phzHS* with *mexGp-gfp* inserted at the *attB* site using pLD2524 (pMQ37-*mexGp*)	This study
PA14 WT *attB*::MCS-*gfp*	LD2820	4, 7, 8	PA14 with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 Δ*phz attB*::MCS-*gfp*	LD2821	4, 7, 8	PA14 Δ*phz* with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 Δ*anr attB::MCS-gfp*	LD2944	7	PA14 Δ*anr* with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 Δ*phz* Δ*anr attB::MCS-gfp*	LD2945	7	PA14 Δ*phz Δanr* with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 Δ*dnr attB*::MCS-*gfp*	LD2994	7	PA14 Δ*dnr* with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 Δ*phz* Δ*dnr attB*::MCS-*gfp*	LD2995	7	PA14 Δ*phz Δdnr* with MCS-*gfp* inserted at the *attB* site using pLD2722 (pSEK103)	This study
PA14 WT *attB*::*napEp-gfp*	LD2818	4, 8	PA14 with *napEp-gfp* inserted at the *attB* site using pLD2817 (pSEK103-*napEp*)	This study
PA14 Δ*phz attB*::*napEp-gfp*	LD2819	4, 8	PA14 Δ*phz* with *napEp-gfp* inserted at the *attB* site using pLD2817 (pSEK103-*napEp*)	This study

Table S3 (continued)

PA14 WT *attB*::*nirSp-gfp*	LD2932	4, 8	PA14 with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 Δ*phz attB*::*nirSp-gfp*	LD2933	4, 8	PA14 Δ*phz* with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 Δ*anr attB*::*nirSp-gfp*	LD2948	7	PA14 Δ*anr* with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 Δ*phz* Δ*anr attB*::*nirSp-gfp*	LD2949	7	PA14 Δ*phz Δanr* with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 Δ*dnr attB*::*nirSp-gfp*	LD2996	7	PA14 Δ*dnr* with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 Δ*phz* Δ*dnr attB*::*nirSp-gfp*	LD2997	7	PA14 Δ*phz Δdnr* with *nirSp-gfp* inserted at the *attB* site using pLD2929 (pSEK103-*nirSp*)	This study
PA14 WT *attB*::*nirSp*$_{\text{shuffle-A}}$-*gfp*	LD2977	7	PA14 with *nirSp*$_{\text{shuffle-A}}$-*gfp* inserted at the *attB* site using pLD2976 (pSEK103-*nirSp*$_{\text{shuffle-A}}$)	This study
PA14 Δ*phz attB*::*nirSp*$_{\text{shuffle-A}}$-*gfp*	LD2978	7	PA14 Δ*phz* with *nirSp*$_{\text{shuffle-A}}$-*gfp* inserted at the *attB* site using pLD2976 (pSEK103-*nirSp*$_{\text{shuffle-A}}$)	This study
PA14 WT *attB*::*nirSp*$_{\text{shuffle-B}}$-*gfp*	LD2980	7	PA14 with *nirSp*$_{\text{shuffle-B}}$-*gfp* inserted at the *attB* site using pLD2979 (pSEK103-*nirSp*$_{\text{shuffle-B}}$)	This study
PA14 Δ*phz attB*::*nirSp*$_{\text{shuffle-B}}$-*gfp*	LD2981	7	PA14 Δ*phz*with *nirSp*$_{\text{shuffle-B}}$-*gfp* inserted at the *attB* site using pLD2979 (pSEK103-*nirSp*$_{\text{shuffle-B}}$)	This study
Escherichia coli				
UQ950	LD44		*E. coli* DH5α λ(*pir*) strain for cloning; F^{-}Δ(*argF-lac*) 169φ80d*lacZ58*(ΔM15) *glnV44*(AS) *rfbD1 gyrA96*(Nal^{R}) *recA1 endA1 spoT thi-1 hsdR17 deoR* λpir^{+}	D. Lies
BW29427	LD661		Donor strain for biparental conjugation; *thrB1004 pro thi rpsL hsdS lacZ* ΔM15RP4–1360 Δ(*araBAD*)*567* Δ*dapA1341*::[*erm pir*(wt)]	B. Wanner
S17-1	LD2901		Str^{R} , Tp^{R} , F^{-} RP4-2-Tc::Mu *aphA*::Tn7 *recA* λpir lysogen	(3)
Saccharomyces cerevisiae				
InvSc1	LD622		*MATa/MATα leu2/leu2 trp1-289/trp1-289 ura3-52/ura3-52 his3-*Δ*1/his3-*Δ*1*	Invitrogen
Plasmids				
pLD905 (pMQ30-Δ*anr*)	LD905		Δ*anr* flanking fragments introduced into pMQ30 by gap repair cloning in yeast strain InvSc1	This study
pLD868 (pMQ30-Δ*dnr*)	LD868		Δ*dnr* flanking fragments introduced into pMQ30 by gap repair cloning in yeast strain InvSc1	This study
pYL122	LD742		Amp^{R} *rhlA-gfp* transcription fusion in mini-CTX-*lacZ*	(3)
pUC18-mini-Tn7			Amp^{R} ColE1 replicon mini-Tn7 base vector	(4)
pLD844 (pSEK101)	LD844		*rhlA* promoter of pYL122 was removed (XhoI and EcoRI) and replaced with a multiple cloning site (MCS) from pUC18-mini-Tn7	This study
pLD852 (pSEK101-*napEp*)	LD852		475 bp *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD844	This study
pLD902 (pSEK101-*narK1p*)	LD902		837 bp *narK1* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD844	This study
pLD903 (pSEK101-*nirSp*)	LD903		758 bp *nirS* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD844	This study

Table S3 (continued)

pSEK101-*norCp*			550 bp *norC* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD844	This study
pLD904 (pSEK101-*nosRp*)	LD904		497 bp *nosR* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD844	This study
pMQ30	LD621		Yeast-based allelic-exchange vector; *sacB*$^{+}$, CEN/ ARSH, URA3^{+}, Gm^{R}	(5)
pLD2477 (pMQ37)	LD2477		MCS-*gfp* flanked by upstream and downstream 1 kb genomic sequences at *attB* site was inserted in pMQ30 through gap repair cloning	This study
pLD2521 (pMQ37-*napEp*$_{\text{200bp}}$)	LD2521		204 bp of *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2527 (pMQ37-*napEp*$_{\text{100bp}}$)	LD2527		105 bp of *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2664 (pMQ37-*napEp*$_{\text{70bp}}$)	LD2664		67 bp of *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2667 (pMQ37-*napEp*$_{\text{70bp-shuffle-3}}$)	LD2667		67 bp of shuffle-3 *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2761 (pMQ37-*napEp*$_{\text{70bp-shuffle-1\&2}}$)	LD2761		67 bp of shuffle-1&2 *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2855 (pMQ37-*napEp*$_{\text{70bp-shuffle-1}}$)	LD2855		67 bp of shuffle-1 *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2858 (pMQ37-*napEp*$_{\text{70bp-shuffle-2}}$)	LD2858		67 bp of shuffle-2 *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2524 (pMQ37-*mexGp*)	LD2524		448 bp of *mexG* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2477	This study
pLD2722 (pSEK103)	LD2722		*aacC1* (gentamicin resistance cassette) from pMQ30 was inserted at the BspDI site of pLD844	This study
pLD2817 (pSEK103-*napEp*)	LD2817		204 bp of *napE* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2722	This study
pLD2929 (pSEK103-*nirSp*)	LD2929		224 bp of *nirS* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2722	This study
pLD2976 (pSEK103-*nirSp*$_{\text{shuffle-A}}$)	LD2976		224 bp of shuffle-A *nirS* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2722	This study
pLD2979 (pSEK103-*nirSp*$_{\text{shuffle-B}}$)	LD2979		224 bp of shuffle-B *nirS* promoter sequence inserted at the MCS (SpeI and XhoI) of pLD2722	This study
pFLP2	LD743		Site-specific excision vector with cI857-controlled FLP recombinase; *sacB*$^{+}$, Amp^{R}	(6)

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Table S4. Primers used in this study.

Number	Name	Sequence	Characteristics
335	PnarK1 for SpeI	taccactagtCTCGCCGCTGTAGGTGAC	To make pLD902 (pSEK101-narK1p) by restriction-ligation
336	PnarK1 rev XhoI	aagcctcgagCTAAACTCTCTGCACGGACAGC	To make pLD902 (pSEK101-narK1p) by restriction-ligation
337	PnirS for SpeI	taccactagtCTCTCGCCGACCAGGATG	To make pLD903 (pSEK101-nirSp) by restriction-ligation
338	PnirS rev XhoI	aagcctcgagTCTATCTCCTCAGGAGCCCTG	To make pLD903 (pSEK101-nirSp) by restriction-ligation
339	PnosR for SpeI	taccactagtGTATCTCACCTGCGGCAAC	To make pLD904 (pSEK101-nosRp) by restriction-ligation
340	PnosR rev XhoI	aagcctcgagGTTCCATCTACTACTGGCTACCG	To make pLD904 (pSEK101-nosRp) by restriction-ligation
297	napEprom(transcr.)-1	TACCactagtGCTGCTGGTGTCGGAGAT	To make pLD852 (pSEK101-napEp) by restriction-ligation
298	napEprom(transcr.)-2	AAGCctcgagTCTATGCAGGCGACTGTAGAAAG	To make pLD852 (pSEK101-napEp) by restriction-ligation
384	PnorC for SpeI	taccactagtACCCTCTACTGGTGCCTGAC	To make pSEK101-norCp by restriction-ligation
385	PnorC rev XhoI	aagcctcgagCTCCTGGAATGGGTGGTG	To make pSEK101-norCp by restriction-ligation
1962	addGentR-1	tgtctaactcatcgatCGAATTGACATAAGCCTGTTCG	To make pLD2722 (pSEK103) from pLD844 (pSEK101) by restriction-ligation
1963	addGentR-2	CTTGGTCTGACAATCGATGC	To make pLD2722 (pSEK103) from pLD844 (pSEK101) by restriction-ligation
1081	attB::gfp-yeast1	ggaattgtgagcggataacaatttcacacaggaaacagctTGGGGAGGGTCGAATAGG	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1082	attB::gfp-yeast2	cttaagcttctagagctctcgagtcgacggatccactagtTTTTCAGTACGCGGATATGG	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1083	attB::gfp-yeast3	actagtggatccgtcgactcgagagctctagaagcttAAGGAGGAAAAACATATGAGTA	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1084	attB::gfp-yeast4	ggcttttcagtacgcggatatgcatgcCACCGACAAACAACAGATAA	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1085	attB::gfp-yeast5	tatctgttgtttgtcggtggcatgcATATCCGCGTACTGAAAAGCC	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1086	attB::gfp-yeast6	aggcaaattctgttttatcagaccgcttctgcgttctgatCGGTCAGCAACTGGAACAC	To make pLD2477 (pMQ37) from pMQ30 by gap repair cloning in yeast strain InvSc1
1190	PmexG-F	acgtacactagtACCGCAAGCGGTTATTAGC	To make pLD2524 (pMQ37-mexGp) by restriction-ligation
1191	PmexG-R	acgtacctcgaGGTCGTTCCTTGTGCTGGTC	To make pLD2524 (pMQ37-mexGp) by restriction-ligation
943	PnapE-primerF2	acgtacactagtGCGAGAGTCGTGTCGTTCAC	To make pLD2521 (pMQ37-napEp200bp) and pLD2817 (pSEK103-napEp) by restriction-ligation

Table S4 (continued)

1332	PnapE-primerF100bp	acgtacactagtCGAACGCTCTGTTTCCAG	To make pLD2527 (pMQ37-napEp100bp) by restriction-ligation
1605	PnapE-primerF70bp	acgtacactagtCGAGGTTTTGCCCGTACT	To make pLD2664 (pMQ37-napEp70bp) by restriction-ligation
944	PnapE-primerR	acgtacctcgaGGCCCAGCCTCTATGCAG	To make pLD2521, pLD2527, pLD2664 and pLD2817 by restriction-ligation
1872	shuffle-F	taggct ttcggatccgtggtctggtgcaaacgcacc TCGAGAGCTCTAGAAGCTTAAGGA	To make pLD2667 (pMQ37-napEp70bp-shuffle-A) by restriction-ligation
1871	shuffle-R	tctcga ggtgcgtttgcaccagaccacggatccgaa AGCCTAGACCCTACTTGCAGTACG	To make pLD2667 (pMQ37-napEp70bp-shuffle-A) by restriction-ligation
2117	shuffle-B-F	TTACTAGTAGTCGGTTTTGCCCGTCGAATGATCGA GGTCTAGGCTTTCTACAGTCGC	To make pLD2761 (pMQ37-napEp70bp-shuffle-B) by restriction-ligation
2116	shuffle-B-R	CCTAGACCTCGATCATTCGACGGGCAAAACCGACT ACTAGTAAGCATATCCGCGTACTGA	To make pLD2761 (pMQ37-napEp70bp-shuffle-B) by restriction-ligation
2181	PnapE-shuffle-C-F	acgtacactagtAGTCGGTTTTGCCCGTACTGCAAGTAG	To make pLD2855 (pMQ37-napEp70bp-shuffle-C) by restriction-ligation
2182	PnapE-shuffle-D-F	acgtacactagtCGAGGTTTTGCCCGTCGAATGATCGAGGTCTAGGCTTTCTACAGTCG	To make pLD2858 (pMQ37-napEp70bp-shuffle-D) by restriction-ligation
2237	PnarK1-primerF	acgtacgtacgtactagtAGAATCTGTCCCGCTGGT	To make pLD2928 (pSEK103-narK1p) by restriction-ligation
2238	PnarK1-primerR	acgtacgtacgtctcgagGGCTAAACTCTCTGCACGGA	To make pLD2928 (pSEK103-narK1p) by restriction-ligation
2239	PnirS-primerF	acgtacgtacgtactagtGTCCCGCATGTCCTACTCCT	To make pLD2929 (pSEK103-nirSp) by restriction-ligation
2240	PnirS-primerF	acgtacgtacgtctcgagGGTCTATCTCCTCAGGAGCCC	To make pLD2929 (pSEK103-nirSp) by restriction-ligation
138	anr del-1 yeast	ggaattgtgagcggataacaatttcacacaggaaacagctGCCACTTTGAACTGGCCTTC	To make pLD905 (pMQ30-Δanr) by gap repair cloning in yeast strain InvSc1
139	anr del-2 yeast	GGAGTCGAGGATGTGCACTTcaaTCCTTGCAGTGTGCTTG	To make pLD905 (pMQ30-Δanr) by gap repair cloning in yeast strain InvSc1
140	anr del-3 yeast	CAAGCACACTGCAAGGATTGaagTGCACATCCTCGACTCC	To make pLD905 (pMQ30-Δanr) by gap repair cloning in yeast strain InvSc1
141	anr del-4 yeast	ggaattgtgagcggataacaatttcacacaggaaacagctGCCACTTTGAACTGGCCTTCGCCACTTTGAACTGGCCTTC	To make pLD905 (pMQ30-Δanr) by gap repair cloning in yeast strain InvSc1
144	dnr del-1 yeast	ggaattgtgagcggataacaatttcacacaggaaacagcGATGCCTGGCTCGACTTC	To make pLD868 (pMQ30-Δdnr) by gap repair cloning in yeast strain InvSc1
145	dnr del-2 yeast	GCTTTCTCCCGTCCAGCTaaaCCTTCTCGCGGATCAT	To make pLD868 (pMQ30-Δdnr) by gap repair cloning in yeast strain InvSc1
146	dnr del-3 yeast	ATGATCCGCGAGAAGGTTTagcTGGACGGGAGAAAGC	To make pLD868 (pMQ30-Δdnr) by gap repair cloning in yeast strain InvSc1
147	dnr del-4 yeast	ccaggcaaattctgttttatcagaccgcttctgcgttctgatGTGCTGCAGACGGTCAAC	To make pLD868 (pMQ30-Δdnr) by gap repair cloning in yeast strain InvSc1

Table S4 (continued)

1087	attB::gfp-inCheck1	AGGGCCAATCGATAGAGTTT	To verify the genotype of gfp reporter strains
1088	attB::gfp-inCheck2	TCTTCGTGATCTGAAGCCATT	To verify the genotype of gfp reporter strains
1089	attB::gfp-outCheck1	TAGAAGAACAGGCGGACGAT	To verify the genotype of gfp reporter strains
1090	attB::gfp-outCheck2	AGCATCATCGGTACCCAGTC	To verify the genotype of gfp reporter strains
400	pDawn-B-2	acatAAGCTTaaggagctgactgggttgaa	To verify the genotype of gfp reporter strains
1805	GFPseq-R	GTTGTATTCCAACTTGTGTCCAA	To verify the genotype of gfp reporter strains
142	anr check-1	AACTCGCGGATCATCTTCAC	To verify the genotype of Δanr deletion strains
143	anr check-2	CGAAGATCAGTACGCTGTCG	To verify the genotype of Δanr deletion strains
148	dnr check-1	GCTACGGCATCGAGGACAC	To verify the genotype of Δdnr deletion strains
149	dnr check-2	GCAGATGCACTCGAACCAG	To verify the genotype of Δdnr deletion strains

Table S5. The *napEp* and *nirSp* sequences

Name	Promoter sequence (5' to 3')
napEp-200bp	GCGAGAGTCGTGTCGTTCACGGCTTGCAGAGTACGGACAGGGTACTGAACCGCCCCTGAACGCTTGCTGAACCCGGGCTGAACGACTCGCGTTTGCCGGCGAACGCTCTGTTTCCAGGCTGCCGCGCGCCGGCTCGGCGAGGTTTTTGCCCGTACTGCAAGTAGGGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-100bp	CGAACGCTCTGTTTCCAGGCTGCCGCGCGCCGGCTCGGCGAGGTTTTTGCCCGTACTGCAAGTAGGGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-70bp	CGAGGTTTTTGCCCGTACTGCAAGTAGGGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-70bp-shuffle-1	**AGTCGG**TTTTGCCCGTACTGCAAGTAGGGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-70bp-shuffle-1&2	**AGTCGG**TTTTGCCCGT**CGAATGATCGA**GGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-70bp-shuffle-2	CGAGGTTTTTGCCCGT**CGAATGATCGA**GGTCTAGGCTTTCTACAGTCGCCTGCATAGAGGCTGGGCC
napEp-70bp-shuffle-3	CGAGGTTTTTGCCCGTACTGCAAGTAGGGTCTAGGCTTTC**GGATCCGTGGTCTGGTGCAAACGCA**CC
nirSp	GTCCCGCATGTCCTACTCCTGCGCTAGGGATTAGGACCGCACGCTATTCACAGTTGGAAGGTGCCACAAGCGCAAAGCAACGCAATCTTGATTCCGGTCAAGCAAGGGTAAAGACCCTGCTTTCTATGATCCTTTCGCGCCATGAATTCCCGGGAGTTCCCGACGCAGCCACCCCCAAAACACTGCTAAGGGAGCGCCTCGCAGGGCTCCTGAGGAGATAGACC
nirSp-shuffle-A	GTCCCGCATGTCCTACTCCTGCGCTAGGGATTAGGACCGCACGCTATTCACAGTTGGAAGGTGCCACAAGCGCAAAGCAACGCAATC**GTTCTAT**CGGTCAAGCAAGGGTAAAGACCCTGCTTTCTATGATCCTTTCGCGCCATGAATTCCCGGGAGTTCCCGACGCAGCCACCCCCAAAACACTGCTAAGGGAGCGCCTCGCAGGGCTCCTGAGGAGATAGACC
nirSp-shuffle-B	**GCTTGCCCAGCACATCCTGACCAGCTGGGGGGCCAGCTCGCCGCAACTTAATCTAGTCAAGACCACATAGAGGGCAAAGTGCATTT**CTTGATTCCGGTCAAGC**GACAAGAAGGCCTCGTA**TTTCTATGATC**AGCCAGAGATATATTCAGTCCATCTACCAGGCGGCCTGGTCGGCGCCAGCTCGCGCCGGGACCTCACTACCTGAGGAACGGAACTCCCACCAG**

Shaded sequences indicate shuffled regions
Underlined sequences indicate -10 and -35 elements
Red font indicates the position of Anr/Dnr binding site