Supplementary Information

RNA-Sequencing Reveals Multitude Effects of Silver Nanoparticles on *Pseudomonas aeruginosa* Biofilms

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Silver nanoparticles preparation and characterization.

Colloidal biostabilized silver nanoparticles (SNP) prepared in our laboratory using a proprietary process (USA Patent No.: 75146000, Eurasia Patent no.: 010338, China Patent no.: 200580014830.9, South Africa Patent no.: 2006/08551; PCT/IN05/00153: Europe, Australia, Singapore, Israel, Egypt, Bangladesh, Indonesia and Srilanka). The size range of nanoparticles was 7-20 nm measured by high resolution transmission electron microscopy (HR-TEM) (Philips, Holland CM 200) and ~40 nm from nanoparticles tracking analysis NTA (NanoSight LM10); characteristic surface plasmon resonance at ~436 nm (UV-2450 spectrophotometer Shimadzu, Japan). Zeta potential of SNP was +18.6 mV (Zetasizer nano,Malvern).

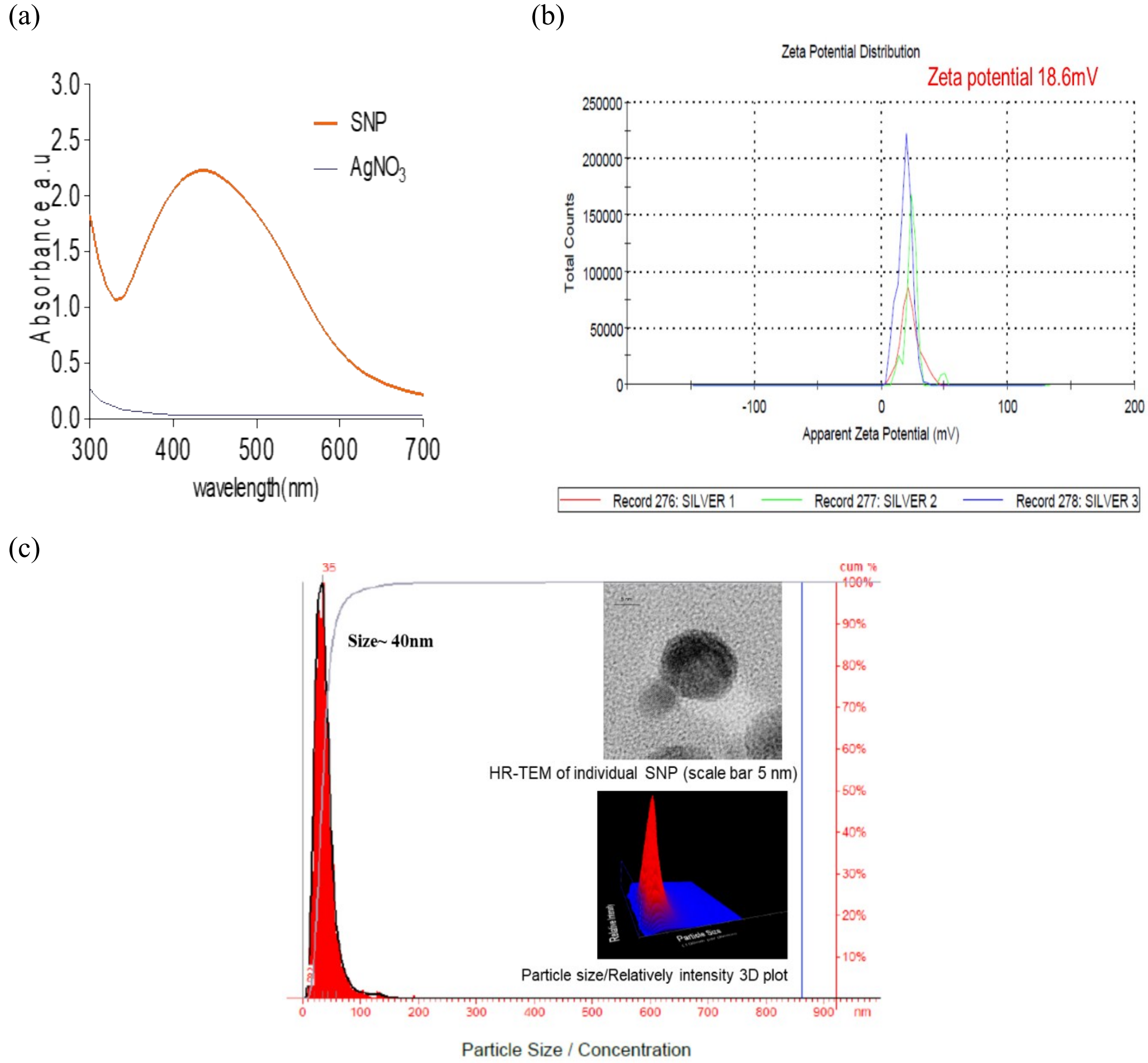


Figure S1. (a) Characteristic plasmon peak obtained for SNP at ~ 436nm. (b) Zeta potential of SNP. (c) The size distribution of SNP 40nm (NTA) and 7-20 nm from HR-TEM.

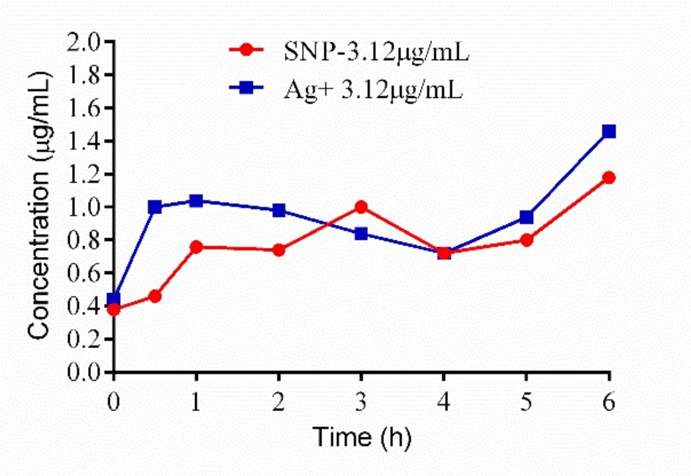


Figure S2. Assessment of silver content in biofilm by atomic absorption spectroscopy.

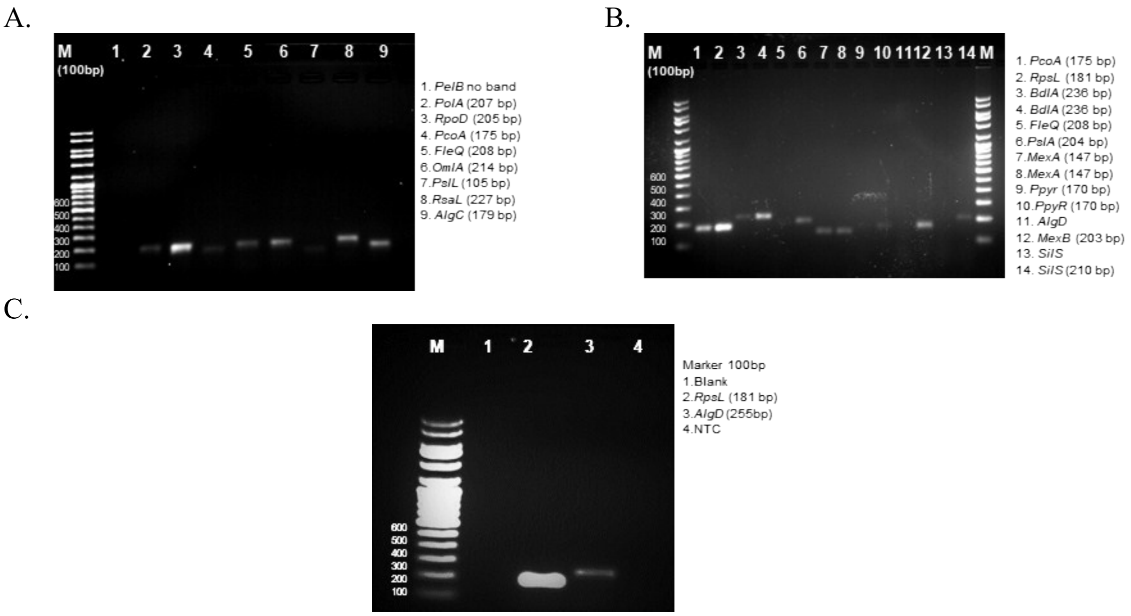
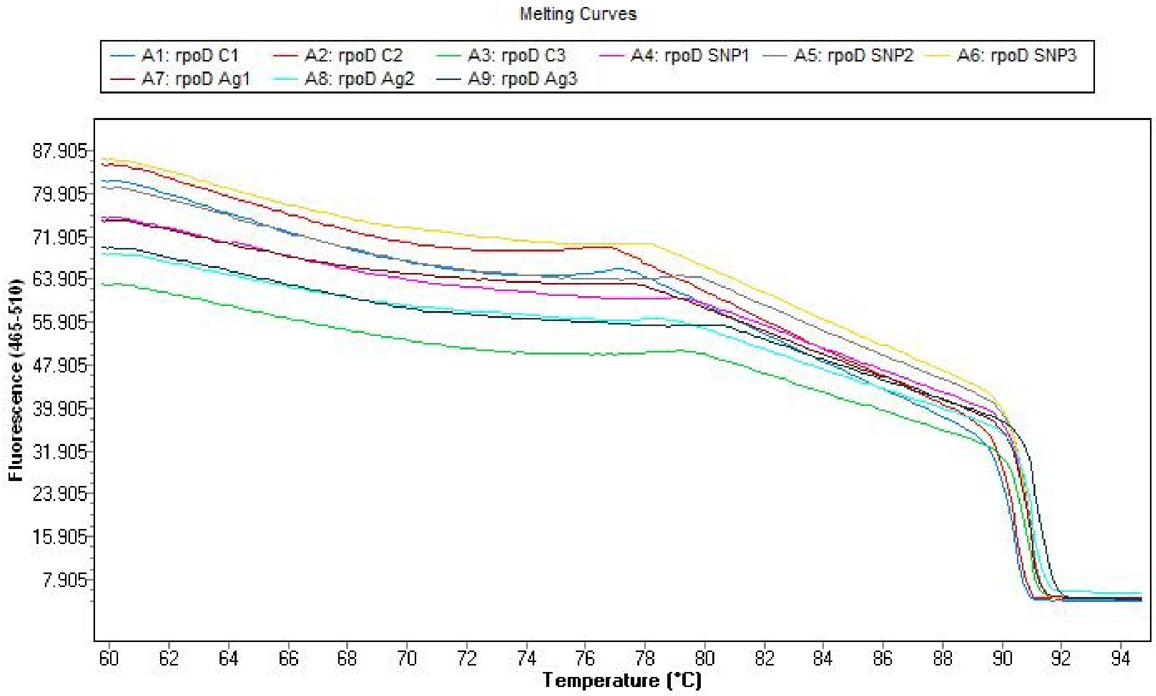
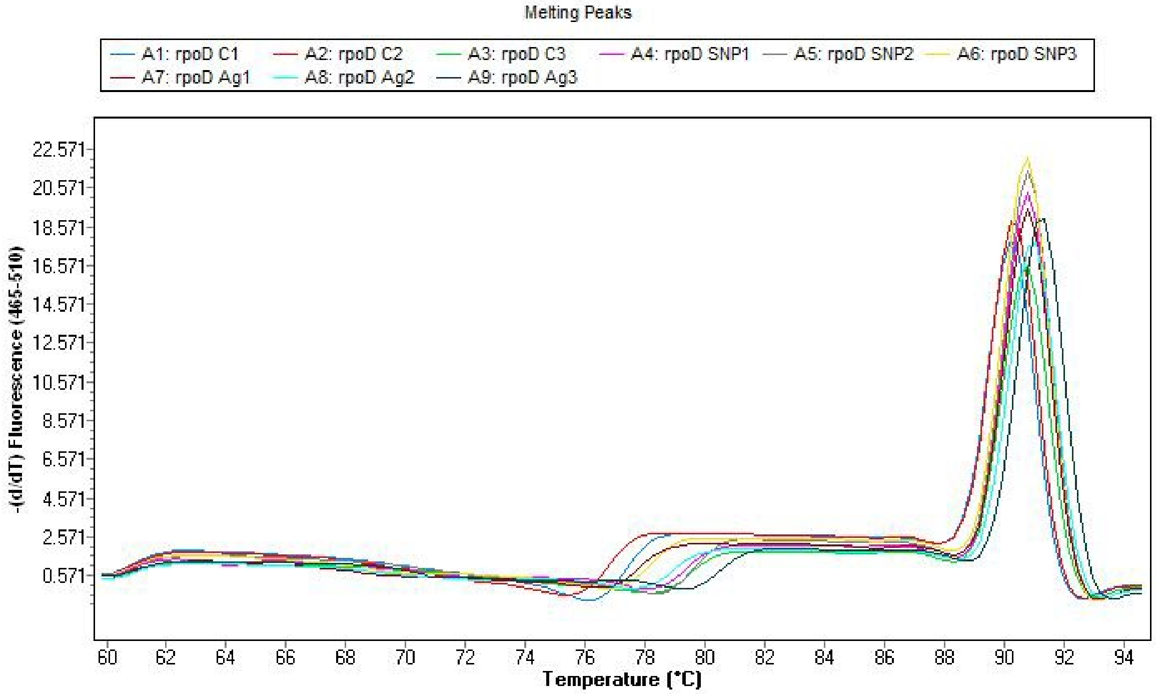


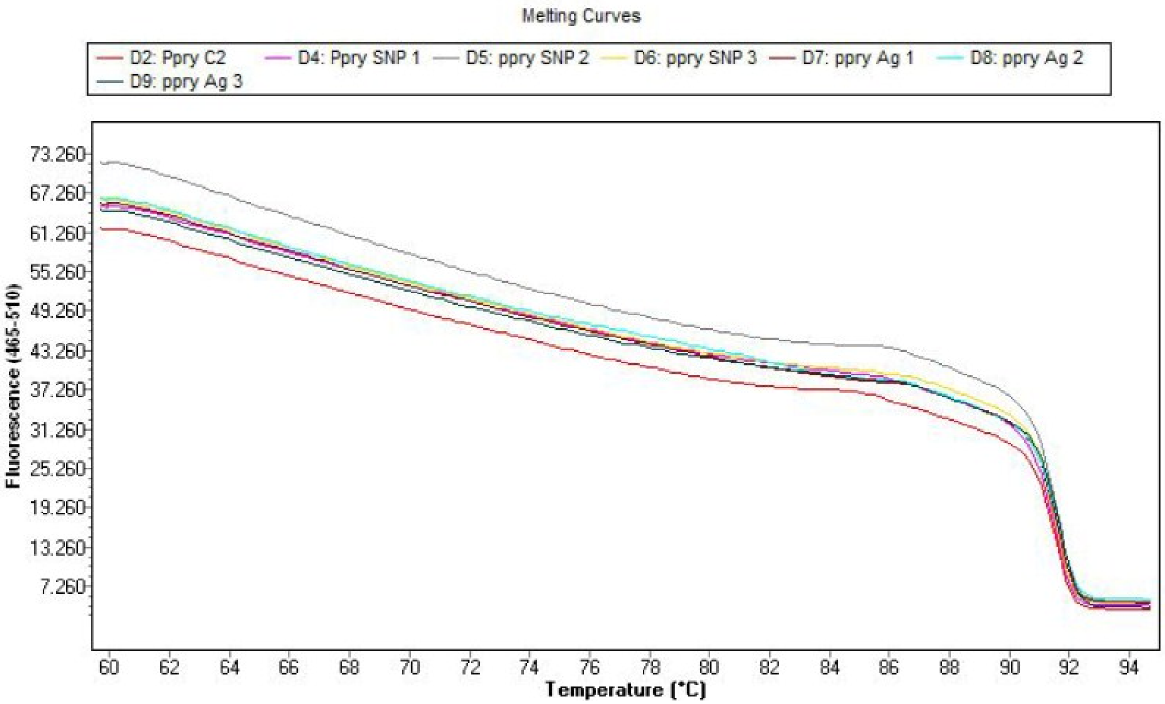
Figure S3. Confirmation on the gene product after PCR amplification using the designed primers.

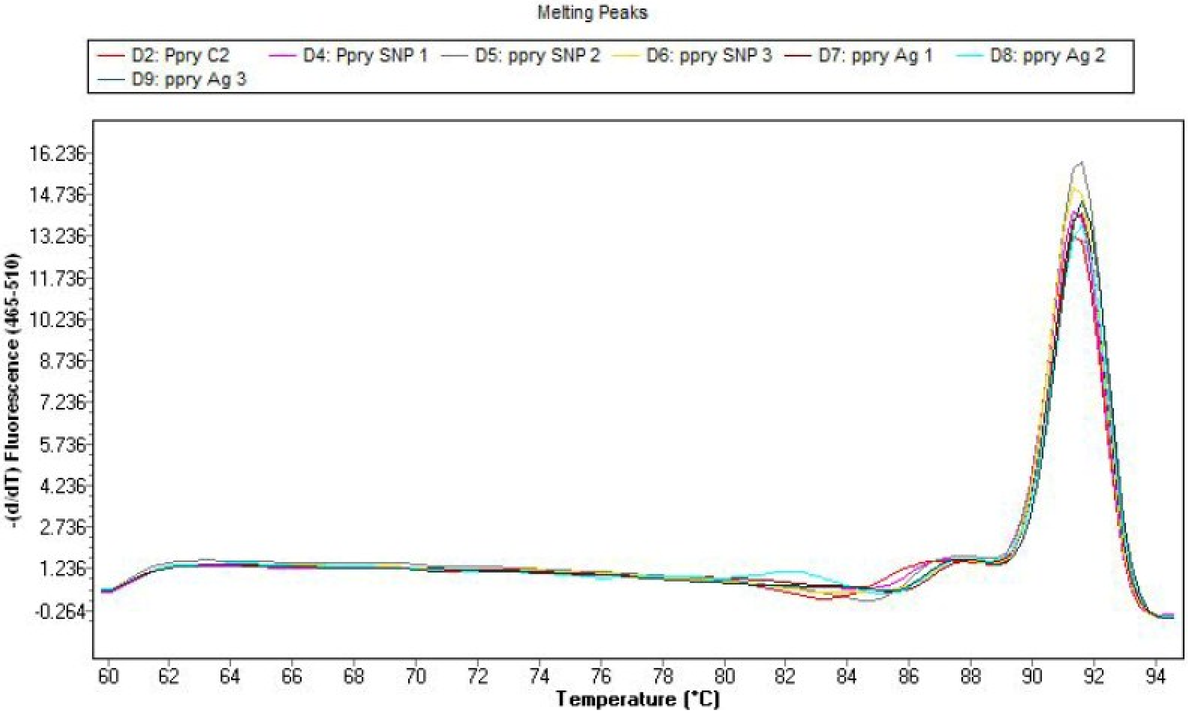
A.

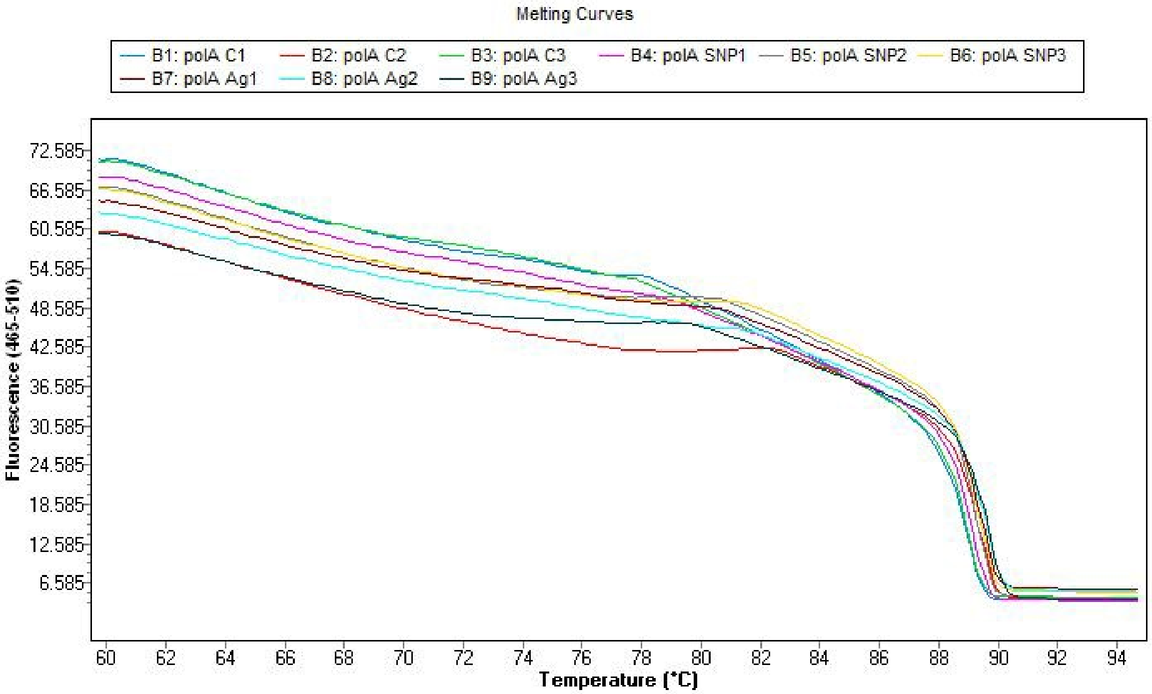

Melting Curves
A1: rpoD C1
A2: rpoD C2
A3: rpoD C3
A4: rpoD SNP1
A5: rpoD SNP2
A6: rpoD SNP3
A7: rpoD Ag1
A8: rpoD Ag2
A9: rpoD Ag3
Fluorescence (465-510)
87.905
79.905
71.905
63.905
55.905
47.905
39.905
31.905
23.905
15.905
7.905
60
62
64
66
68
70
72
74
76
78
80
82
84
86
88
90
92
94
Temperature (°C)

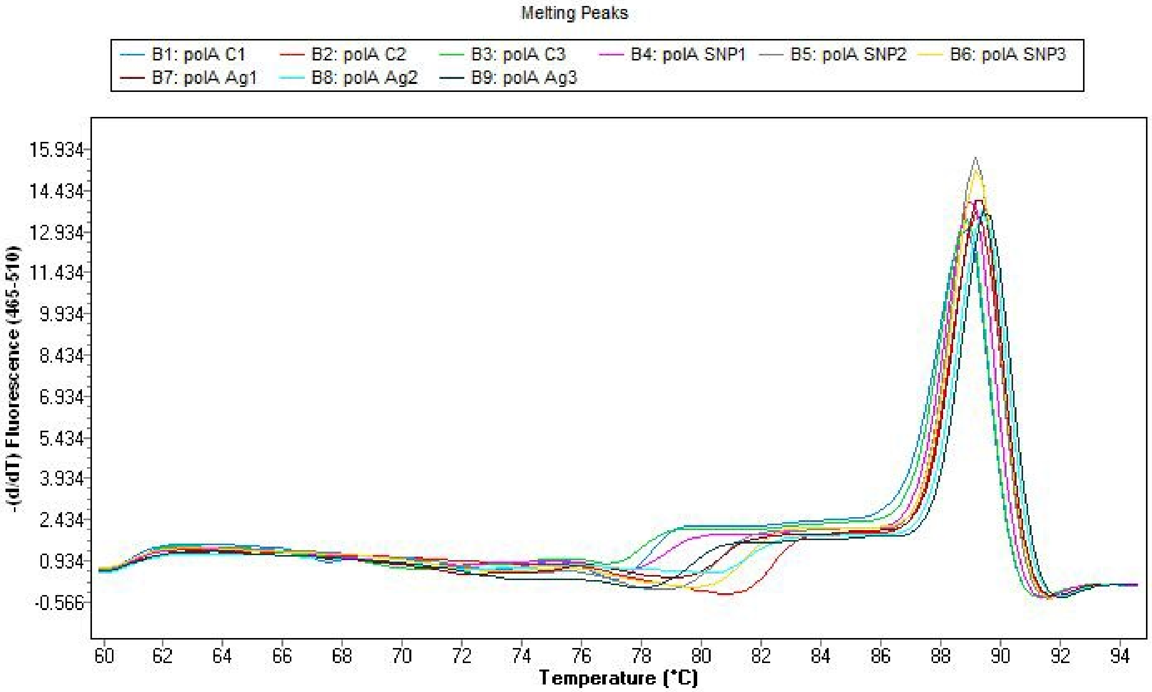
B.


Melting Peaks
A1: rpoD C1
A2: rpoD C2
A3: rpoD C3
A4: rpoD SNP1
A5: rpoD SNP2
A6: rpoD SNP3
A7: rpoD Ag1
A8: rpoD Ag2
A9: rpoD Ag3
-(d/dT) Fluorescence (465-510)
22.571
20.571
18.571
16.571
14.571
12.571
10.571
8.571
6.571
4.571
2.571
0.571
60
62
64
66
68
70
72
74
76
78
80
82
84
86
88
90
92
94
Temperature (°C)


Melting Curves
D2: Ppry C2
D4: Ppry SNP 1
D5: ppry SNP 2
D6: ppry SNP 3
D7: ppry Ag 1
D8: ppry Ag 2
D9: ppry Ag 3
Fluorescence (465-510)
73.260
67.260
61.260
55.260
49.260
43.260
37.260
31.260
25.260
19.260
13.260
7.260
60
62
64
66
68
70
72
74
76
78
80
82
84
86
88
90
92
94
Temperature (°C)


Melting Peaks
D2: Ppry C2
D4: Ppry SNP 1
D5: ppry SNP 2
D6: ppry SNP 3
D7: ppry Ag 1
D8: ppry Ag 2
D9: ppry Ag 3
-(d/dT) Fluorescence (465-510)
16.236
14.736
13.236
11.736
10.236
8.736
7.236
5.736
4.236
2.736
1.236
-0.264
60
62
64
66
68
70
72
74
76
78
80
82
84
86
88
90
92
94
Temperature (°C)


Melting Curves


Melting Peaks

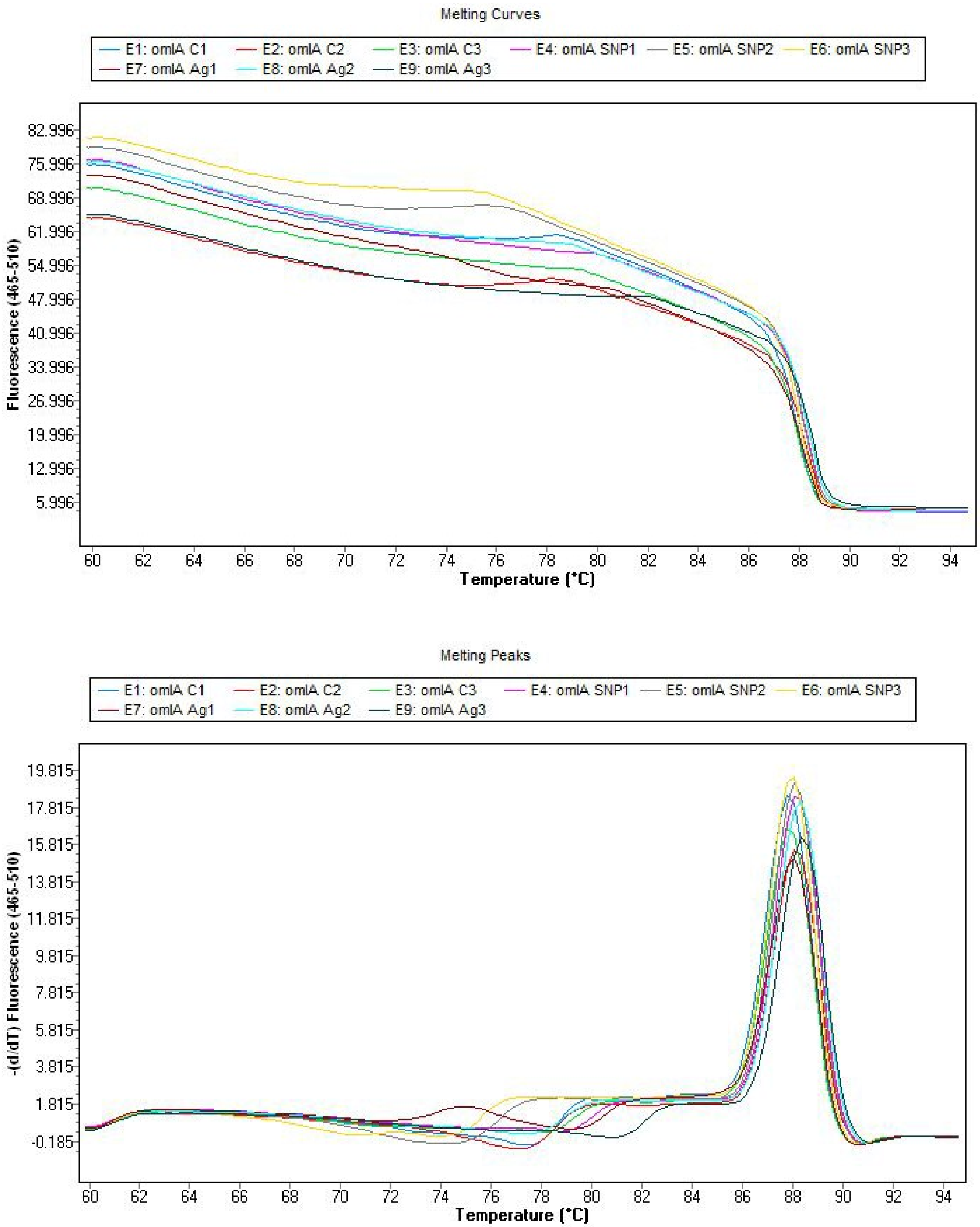


Figure S4. qRT-PCR analysis of few representative genes and their melting curves and peaks.

Table S1 List of primers used in this study

Gene target	**Size(bp)**	**Sequence 5’-3’**	**Annealing temperature (°C)**
*rpsL*_F *rpsL*_R	181	CGACCCTGCTTACGGTCTTT GTGTACGTCTGACCAACGGT	60
*rpoD*_F *rpoD*_R	205	CGAGGAAGAAGAAAGCGACG CAGCTTGATCGGCATGAACA	60
Exopolysaccharide related genes			
*pslA*_F *pslA*_R	204	GATGAAACGCGGCATGTACC CGGATCAGCTTCTCCAGGTC	60
*pslL*_F *pslL*_R	105	CATCAGCACCTTCAACATGG AGGTAGTCGCTGACCCGATA	58
*algD*_F *algD*_R	255	AGTACACCTGCAACGTCTGG GCATCAACGAACCGAGCATC	60
*ppyr*_F *ppyr*_R	170	CAAGCACTTGCACAGCAGAC GTGATCGCCGCCTATTTCCT	60
*algC*_F *algC*_R	179	CCTACCCCGGTGCTGTACTA GATGCCAGGTCGTTTTTCTC	58
Motility associated genes			
*bdlA*_F *bdlA*_R	236	ATCTGTTGCGAGTGCTGTGA GGCAAGCTCTACAAGGTGGT	60
*fleQ*_F *fleQ*_R	208	GGTCTACCGCGAGATGTACG GGAATGGTAATGCAGGTTGC	60
Efflux and outer membrane related genes			
*mexA*_F *mexA*_R	147	CGGTGACCCTGAATACCGAG GGTCGATCTGGTAGAGCTGC	60
*mexB*_F *mexB*_R	203	AAGGTCAATCCCGACGGTTC TCGTACGGGTAGACCACCTT	61
*pcoA*_F *pcoA*_R	175	GCCGAGATGAAGATGAGTCC GAATGCGGACGTCGAAATAG	60
*omlA*_F *omlA*_R	214	AAAATCGACATCCAGCAAGG GGTCGCTGTCGTTGAAGAAC	60
Quorum Sensing			
*rsaL*_F *rsaL*_R	227	GAGAGAACACAGCCCCAAAA TCTCTGATCTTGCCTCTCAGG	58
DNA replication gene			
*polA*_F *polA*_R	207	GGAGGATCCGAAGAAGCTCA ATGTCCTCGAAACGGATGGT	60

Table S2 Biomass quantification of *P. aeruginosa* biofilms.

Biofilm incubation (h)	Biomass optical density (590 nm)

24	2.18 ± 0.63
48	3.67 ± 0.21
72	3.46 ± 0.37

± Standard deviation

Table S3 Total number of differentially expressed genes of *P. aeruginosa* biofilms after 6 h in response to SNP and Ag^+.

Samples	Number of up-regulated genes	Number of down-regulated genes	Total (up + down)	Percentage of differential population (%)
SNP	777	822	1599	28.12
Ag^+	881	1577	2458	43.22

Table S4 Genes involved in biofilm formation, c-di-GMP, quorum sensing, and denitrification that are differentially regulated in *P. aeruginosa* in response to treatment with SNP and Ag^+.

Exopolysaccharides genes		**SNP**		**Ag^+**	
Gene Id	**Description**	**FC**	**log FC**	**FC**	**log FC**
pslA	biofilm formation protein	-3.2	-1.7		
pslD	biofilm formation protein			-34.8	-5.1
pslC	biofilm formation protein	243.9	7.9	243.9	7.9
pslE	biofilm formation protein	111.8	6.8	2.2	1.1
pslL	hypothetical protein	159.6	7.3	159.6	7.3
pelB	pellicle/biofilm biosynthesis protein	-25.3	-4.7	-4.7	-2.2
pelG	pellicle/biofilm biosynthesis Wzx-like polysaccharide			-12.3	-3.6
pelF	pellicle/biofilm biosynthesis glycosyltransferase			-11.1	-3.5
algZ	alginate biosynthesis protein AlgZ/FimS	-252.2	-8.0	-15.7	-4.0
algD	GDP-mannose 6-dehydrogenase AlgD			-25.8	-4.7
alg8	glycosyltransferase alg8			-22.8	-4.5
algI	alginate o-acetylase AlgI			-21.7	-4.4
algJ	alginate o-acetylase AlgJ			-28.8	-4.8
algF	alginate o-acetyltransferase AlgF			-7.3	-2.9
algW	AlgW protein			-28.9	-4.9
amrZ	alginate and motility regulator Z	680.2	9.4		
algQ	anti-RNA polymerase sigma 70 factor	3.1	1.6		
mucC	positive regulator for alginate biosynthesis MucC	312.9	8.3	2.3	1.2
algU	RNA polymerase sigma factor AlgU			2.2	1.1
algC	phosphomannomutase	-138.9	-7.1	-103.9	-6.7
lecA	PA-I galactophilic lectin	-2.2	-1.1	301.4	8.2
lecB	fucose-binding lectin PA-IIL	-2.3	-1.2	4.7	2.2
PA4625	cyclic diguanylate-regulated TPS partner A, CdrA	-2.2	-1.1		
cupC2	chaperone CupC2	623.1	9.3	623.1	9.3
cupC3	usher CupC3	176.5	7.5	176.5	7.5
cupA1	fimbrial subunit CupA1	215.1	7.7	215.1	7.7
cupB6	fimbrial subunit CupB6	194.1	7.6	194.1	7.6
cupB3	usher CupB3			43.9	5.5
cupC1	fimbrial subunit CupC1	-293.0	-8.2		
pilB	type 4 fimbrial biogenesis protein PilB	2.1	1.0	2.3	1.2
pilF	type 4 fimbrial biogenesis protein PilF	37.8	5.2		
pilG	pilus biosynthesis/twitching motility protein PilG	2.2	1.1	7.8	3.0
pilM	type 4 fimbrial biogenesis protein PilM	2.7	1.5	12.1	3.6
pilT	twitching motility protein PilT	2.3	1.2		
pilW	type 4 fimbrial biogenesis protein	548.7	9.1	548.7	9.1
pilX	type 4 fimbrial biogenesis protein			756.6	9.6
pilY1	type 4 fimbrial biogenesis protein			19.7	4.3
pilO	type 4 fimbrial biogenesis protein	-4.0	-2.0	2.1	1.1

fimU	type 4 fimbrial biogenesis protein			21.2	4.4
flp	type IVb pilin Flp	-762.2	-9.6	-153.3	-7.3
pilQ	type 4 fimbrial biogenesis outer membrane protein PilQ	-4.1	-2.0	-2.5	-1.3
pilP	type 4 fimbrial biogenesis protein PilP	-105.8	-6.7	-30.3	-4.9
fimT	type 4 fimbrial biogenesis protein FimT	-256.1	-8.0	-66.4	-6.1
pilV	type 4 fimbrial biogenesis protein PilV	-23.2	-4.5	-4.5	-2.2
pilY2	type 4 fimbrial biogenesis protein PilY2	-536.4	-9.1		
pilE	type 4 fimbrial biogenesis protein PilE	-5.7	-2.5		
pilD	type 4 prepilin peptidase PilD			-38.8	-5.3
pilZ	type 4 fimbrial biogenesis protein PilZ			-142.2	-7.2
pilR	two-component response regulator PilR			-25.3	-4.7
pilN	type 4 fimbrial biogenesis protein PilN			-145.8	-7.2
pilU	twitching motility protein PilU			-21.0	-4.4
pilH	twitching motility protein PilH			-523.3	-9.0
pilK	methyltransferase PilK			-172.8	-7.4

Cyclic di-GMP (c-di-GMP) signaling and chemotactic responses

		SNP		**Ag+**	
Gene Id	**Description**	**FC**	**log FC**	**FC**	**log FC**
PA0169	diguanylate cyclases SiaD	-127.9	-7.0	-47.8	-5.6
flgI	flagellar basal body P-ring protein	-163.1	-7.4	-61.0	-5.9
fliJ	flagellar biosynthesis chaperone	-407.9	-8.7		
flgG	flagellar basal body rod protein FlgG			-129.2	-7.0
flgJ	peptidoglycan hydrolase FlgJ			-28.1	-4.8
flgK	flagellar hook-associated protein FlgK			-49.5	-5.6
fliD	B-type flagellar hook-associated flagellar capping protein			-4.1	-2.0
fleS	two-component sensor			-28.0	-4.8
fliE	flagellar hook-basal body complex protein			-265.4	-8.1
fliF	flagellar MS-ring protein			-37.7	-5.2
fliI	flagellum-specific ATP synthase			-25.0	-4.6
fliM	flagellar motor switch protein FliM	-186.3	-7.5	-209.0	-7.7
flhA	flagellar biosynthesis protein FlhA	-255.8	-8.0	-31.9	-5.0
flhF	flagellar biosynthesis regulator FlhF			-26.2	-4.7
fleN	flagellar synthesis regulator FleN	-63.6	-6.0	-30.1	-4.9
fliA	flagellar biosynthesis sigma factor FliA	-174.9	-7.5	-51.6	-5.7
cheZ	protein phosphatase CheZ	-1022.4	-10.0	-488.4	-8.9
motC	flagellar motor protein	-244.4	-7.9	-58.8	-5.9
motD	flagellar motor protein MotD	-203.2	-7.7	-76.0	-6.2
PA1442	flagellar basal body protein FliL			-313.4	-8.3
bifA	protein BifA	215.5	7.8	4.8	2.3
bdlA	biofilm dispersion protein	85.7	6.4	4.0	2.0
rpoS	RNA polymerase sigma factor RpoS			5.8	2.5
flgC	flagellar basal body rod protein FlgC	504.4	9.0		
flgD	flagellar basal body rod modification protein	2.5	1.3	3.3	1.7
fleQ	transcriptional regulator FleQ	4.9	2.3		
fliG	flagellar motor switch protein FliG	3.7	1.9	3.9	2.0
PA1103	flagellar assembly protein FliH	2.5	1.3	2.2	1.1
flgF	flagellar basal body rod protein FlgF			6.6	2.7
flgM	protein FlgM			2.0	1.0
PA3356	hypothetical protein			3.1	1.6
PA1930	chemotaxis transducer	171.6	7.4	3.6	1.9
PA2780	bacterial swarming regulator BswR	599.8	9.2		
PA2788	chemotaxis transducer	69.7	6.1	69.7	6.1
PA2573	chemotaxis transducer			138.3	7.1
PA2867	chemotaxis transducer			5.4	2.4
wspE	chemotaxis sensor/effector fusion protein	48.1	5.6	48.1	5.6

wspD	hypothetical protein	161.2	7.3	161.2	7.3
PA4633	chemotaxis transducer	104.0	6.7	6.6	2.7
PA4290	chemotaxis transducer			137.6	7.1
pctA	chemotactic transducer PctA			3.3	1.7
aer2	aerotaxis transducer Aer2	109.0	6.8	13.1	3.7
PA0179	two-component response regulator			5.5	2.4
pilG	pilus biosynthesis/twitching motility protein	2.2	1.1	7.8	3.0
fliP	flagellar biosynthesis protein FliP	289.6	8.2	289.6	8.2
PA1458	two-component sensor cheA	2.5	1.3	2.6	1.4
PA1459	chemotaxis-specific methylesterase cheB	165.0	7.4		
fimV	motility protein FimV	5.0	2.3	2.3	1.2
motB	flagellar motor protein MotB	213.1	7.7	4.4	2.1

Quorum sensing related genes

Quorum Sensing genes		**SNP**		**Ag$^+$**	
Gene Id	**Description**	**FC**	**log FC**	**FC**	**log FC**
lasR	transcriptional regulator LasR	-2.2	-1.2		
lasI	acyl-homoserine-lactone synthase			3.3	1.7
lasA	protease Xcp type II secretion system			7.4	2.9
rhlC	rhamnosyltransferase			-17.3	-4.1
rhlI	acyl-homoserine-lactone synthase	507.8	9.0	3.3	1.7
rhlR	transcriptional regulator RhlR			5.6	2.5
rhlB	rhamnosyltransferase subunit B			4.1	2.0
rhlA	rhamnosyltransferase subunit A			2.1	1.1
wapR	alpha-1,3-rhamnosyltransferase WapR	8.4	3.1	8.9	3.2
aprF	alkaline protease secretion protein AprF	-250.5	-8.0	-23.4	-4.5
aprD	alkaline protease ATP-binding protein			-16.7	-4.1
aprE	alkaline protease secretion protein AprE	342.5	8.4		
qteE	quorum threshold expression protein QteE	-316.0	-8.3		
pvdQ	acyl-homoserine lactone acylase PvdQ			48.6	5.6
Negative transcriptional regulator					
rsaL	regulatory protein RsaL	13.4	3.7	11.9	3.6
rpoS	RNA polymerase sigma factor RpoS			5.8	2.5
mvaT	transcriptional regulator MvaT	4.9	2.3		
Positive transcriptional regulator					
mvfR	transcriptional regulator MvfR			-16.9	-4.1
PA1196	transcriptional regulator	-129.3	-7.0	-24.2	-4.6
quiP	acyl-homoserine lactone acylase QuiP	-56.6	-5.8	-12.6	-3.7
gacA	response regulator GacA			4.5	2.2
vfr	cAMP-regulatory protein			-2.4	-1.3
vqsM	HTH-type transcriptional regulator VqsM	-277.8	-8.1	-152.2	-7.2
PA2591	transcriptional regulator vqsR			3.7	1.9
dksA	suppressor protein DksA			-2.3	-1.2
		SNP		**Ag$^+$**	
	Siderophores synthesis genes	**FC**	**log FC**	**FC**	**log FC**
pvdA	L-ornithine N5-oxygenase	-2.4	-1.3		
pvdR	pyoverdine biosynthesis protein PvdR	-154.0	-7.3		
pvdT	pyoverdine biosynthesis protein PvdT	-90.9	-6.5		
pvdP	pyoverdine biosynthesis protein PvdP	-55.4	-5.8	-51.8	-5.7
pvdN	pyoverdine biosynthesis protein PvdN	-141.0	-7.1		
pvdO	pyoverdine biosynthesis protein PvdO	-595.9	-9.2		
pvdH	diaminobutyrate--2-oxoglutarate aminotransferase	-321.1	-8.3		
pvdL	peptide synthase	-142.4	-7.2		
pvdG	pyoverdine biosynthesis protein PvdG	-236.7	-7.9		
pvdS	extracytoplasmic-function sigma-70 factor	-321.1	-8.3		

fptA	Fe(III)-pyochelin outer membrane receptor	-41.9	-5.4	-23.5	-4.6
pchA	salicylate biosynthesis isochorismate synthase			-47.3	-5.6
fpvR	protein FpvR	-2.5	-1.3	146.3	7.2
pvdE	pyoverdine biosynthesis protein PvdE			6.6	2.7
fpvA	ferripyoverdine receptor			7.3	2.9
pvdD	pyoverdine synthetase D	-2.4	-1.2	2.2	1.2
pvdJ	pyoverdine biosynthesis protein PvdJ	-3.5	-1.8	3.8	1.9
pchD	pyochelin biosynthesis protein PchD	135.3	7.1	135.3	7.1
pchF	pyochelin synthetase			61.4	5.9
pchP	phosphorylcholine phosphatase			13.1	3.7
		SNP		**Ag+**	
	PQS signalling	FC	log FC	FC	log FC
pqsA	anthranilate--CoA ligase	-4.9	-2.3	-24.1	-4.6
pqsB	hypothetical protein	-9.0	-3.2	-124.3	-7.0
pqsC	hypothetical protein	-345.9	-8.4	-518.0	-9.0
phnB	anthranilate synthase component II	-600.6	-9.2	-112.3	-6.8
pqsD	2-heptyl-4(1H)-quinolone synthase PqsD			-200.3	-7.6
pqsE	thioesterase PqsE			-148.8	-7.2
pqsH	2-heptyl-3-hydroxy-4(1H)-quinolone synthase	-2.1	-1.1	2.6	1.4
	Phenazine synthesis	**SNP**		**Ag+**	
phzA2	phenazine biosynthesis protein PhzA			-247.7	-8.0
phzB2	phenazine biosynthesis protein PhzB	-2.7	-1.4		
phzC2	phenazine biosynthesis protein PhzC	-99.1	-6.6	-16.8	-4.1
phzE2	phenazine biosynthesis protein PhzE	-192.2	-7.6	-36.1	-5.2
phzF2	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	-192.3	-7.6	-26.1	-4.7
phzG2	pyridoxamine 5'-phosphate oxidase	-113.9	-6.8		
phzM	phenazine-specific methyltransferase	-67.6	-6.1	-87.1	-6.4
phzA1	phenazine biosynthesis protein	-344.9	-8.4		
phzS	hypothetical protein	-299.6	-8.2	-276.1	-8.1
phzB1	phenazine biosynthesis protein			-2.0	-1.0
phzH	phenazine-modifying protein	454.9	8.8	-55.4	-5.8
phzD2	phenazine biosynthesis protein			4.3	2.1

Expression of genes involved in oxidative stress

Genes	**Function**	**SNP**	**Ag$^+$**
katN	non-heme catalase	-204.6	-
katE	catalase HPII	-	-15.8
katB	catalase	+144	-
sodM	superoxide dismutase	-	-82.9
soxR	redox-sensitive transcriptional activator	-	-35.9
gor	glutathione reductase	-667.7	-271.5
cyoA	cytochrome o ubiquinol oxidase subunit II	-	-67.9
cyoB	cytochrome o ubiquinol oxidase subunit I	+112.5	+112.5
cyoE	Protoheme IX farnesyltransferase	+249.6	+249.6
mutY	A/G specific adenine glycosylase	+2.0	+2.6
msrA	Peptide methionine sulfoxide reductase	-	-52.2
PA2826	glutathione peroxidase	-	-34.8
trxB1	thioredoxin reductase	+2.4	+3.2
trxB2	thioredoxin reductase	-380.8	-278.6
oxyR	transcriptional regulator	-194.0	-72.5
ahpF	alkyl hydroperoxide reductase	-115.6	-226.6
tpx	thiol peroxidase	+223.3	-

PA0848	alkyl hydroperoxide reductase	+67.0	-
ccpR	cytochrome C551 peroxidase	+3.7	+2.8

Gene involved in denitrification process

Denitrification		**SNP**		**Ag$^+$**	
		FC	**log FC**	**FC**	**log FC**
nirS	nitrite reductase			3.3	1.7
nirQ	denitrification regulatory protein	260.6	8.0	260.6	8.0
nirJ	heme d1 biosynthesis protein	-77.8	-6.3	-29.1	-4.9
nirS	nitrite reductase	-2.1	-1.1		
norC	nitric oxide reductase subunit C	-821.3	-9.7	-77.1	-6.3
nirB	assimilatory nitrite reductase large subunit			-6.9	-2.8
dnr	transcriptional regulator	-264.8	-8.0		
norB	nitric oxide reductase subunit B			158.8	7.3
anr	transcriptional regulator	605.3	9.2		
narH	respiratory nitrate reductase subunit beta	-469.8	-8.9		
narG	respiratory nitrate reductase subunit alpha	-47.8	-5.6		
narX	two-component sensor			-18.1	-4.2
narL	transcriptional regulator			-51.3	-5.7
nosR	regulatory protein	-84.3	-6.4		
nosZ	nitrous-oxide reductase	-94.8	-6.6		
	Alkane degradation	**FC**	**log FC**	**FC**	**log FC**
alkB1	alkane-1 monooxygenase	-157.6	-7.3	-14.7	-3.9
alkB2	alkane-1 monooxygenase			-14.9	-3.9
PA1245	hypothetical protein (Apr type I secretion system)			51.0	5.7
PA5349	rubredoxin reductase	-138.2	-7.1	-73.3	-6.2
rubA2	rubredoxin			-184.3	-7.5
rubA1	rubredoxin			2.1	1.1

Table S5 Gene involved in two component system (TCS) in response to SNP**.**

Two component system			**FC**	**logFC**
phoP	response regulator	positive regulation of phospholipid biosynthetic process, Cationic antimicrobial peptide resistance	-267.1	-8.1
PA1181	sensor protein	phosphorelay sensor kinase activity	-53.8	-5.8
PA1335	response regulator	regulation of transcription, (aauR)	-141.7	-7.1
PA1437	response regulator	regulation of transcription, DNA-templated	-206.8	-7.7
PA4112	sensor/response	signal transducer activity	-63.9	-6.0
retS		Regulator of Exopolysaccharide and Type III Secretion	-64.0	-6.0
PA5364	response regulator		-116.9	-6.9
PA0178	sensor	Bacterial chemotaxis	-47.2	-5.6
PA0601		response regulator	-3.0	-1.6
PA1336	sensor (aauS)		-344.8	-8.4
parR	response regulator	beta-Lactam resistance	-127.9	-7.0
PA3346	response regulator	hsbR	-201.1	-7.7
nosR	regulatory protein	generation of precursor metabolites and energy	-84.3	-6.4
rocS1	sensor		-24.9	-4.6
PA0600	sensor (agtS)	peptidoglycan and controlling virulence	92.9	6.5
PA0601	response regulator	peptidoglycan and controlling virulence (agtR)	-3.0	-1.6
PA0930	sensor(pirS)	Iron acquistion	166.6	7.4

PA1458	sensor	chemotaxis	2.5	1.3
PA1459	response regulator	chemotaxis-specific methylesterase cheB	165.0	7.4
PA1611	sensor/response regulator hybrid	HptB-HsbR phosphorelay.acute/chronic infection cycle in conjunction with the GacS network	113.7	6.8
PA2523	response regulator	cztR_silR_copR: heavy metal response regulator	309.6	8.3
pfeR	response regulator	Iron acquistion	242.3	7.9
PA3078	sensor (cprS)	Triggers LPS modification and adaptive antimicrobials peptide resistance	514.9	9.0
gltR	response regulator	cellular catabolic process,Glycolysis / Gluconeogenesis	305.1	8.3
PA3271	sensor		255.7	8.0
PA4381	response regulator	Polymyxin resistance (colR)	162.6	7.3
PA4396	response regulator	Diguanylate cyclase GGDEF DOMAIN	202.0	7.7
cbrA	sensor		75.3	6.2
pmrB	system signal sensor kinase	induced by low Mg2+ and catonic antimicrobial peptides.polymyxinB, colistin resistance	155.1	7.3
irlR	response regulator	cztR_silR_copR: heavy metal response regulator	277.3	8.1
PA5165	sensor	positive regulation of organic acid transport	208.8	7.7
phoB	regulator	Quorum sensing and swarming motility	852.0	9.7
gacS	sensor/response	biofilm formation,antibiotic resistance,swarming motility	40.0	5.3
rocR	response regulator	biofilm maturation,fimbrial genes	188.7	7.6
Swarming and biofilm formation			**FC**	**logFC**
PA2824	sensor/response	sensor/response regulator hybrid protein sagS	94.2	6.6
bfiS	protein BfiS		74.3	6.2
bfmR	protein BfmR		300.2	8.2
Quorum sensing			**FC**	**log FC**
pmrB	regulator	signal sensor kinase	155.1	7.3
Redox response			**FC**	**log FC**
PA4494	sensor	sensor histidine kinase RoxS	165.2	7.4
Copper tolerance			**FC**	**log FC**
PA4885	response regulator	irlR	277.3	8.1

Table S6 Genes involved in two component system (TCS) in response to Ag^+.

	Two component system	**Downregulated genes**	**FC**	**log FC**
fleS	sensor		-28.0	-4.8
phoP	response regulator PhoP	positive regulation of phospholipid biosynthetic process,Cationic antimicrobial peptide resistance	-972.4	-9.9
PA1181	sensor protein	phosphorelay sensor kinase activity	-10.1	-3.3
PA1335	response regulator (aauR)	regulation of transcription, DNA-templated	-13.2	-3.7
PA1437	response regulator	regulation of transcription, DNA-templated	-49.1	-5.6
PA1438	two-component sensor	Heavy metal sensor kinase	-23.4	-4.5
kdpE	response regulator	phosphorelay signal transduction system	-36.1	-5.2
parS	sensor	Cationic antimicrobial peptide resistance	-26.3	-4.7
PA2571	two-component sensor	transferring phosphorus-containing groups and motility	-24.0	-4.6
PA3204	response regulator cpxR	regulation of transcription, DNA-templated	-49.9	-5.6
PA3206	two-component sensor	phosphorylation	-4.1	-2.1
wspR	response regulator	diguanylate cyclase activity	-111.6	-6.8
narX	two-component sensor	generation of precursor metabolites and energy	-18.1	-4.2
PA3900	transmembrane sensor	sigma factor antagonist activity	-28.2	-4.8
rocA1	response regulator	positive regulation of transcription	-118.2	-6.9
PA4032	response regulator	regulation of transcription, DNA-templated	-68.3	-6.1
PA4112	sensor/response hybrid	signal transducer activity	-4.0	-2.0
pprA	sensor		-18.3	-4.2
pilR	response regulator	Pilin biosynthesis	-25.3	-4.7

retS	Regulator of Exopolysaccharide and Type III Secretion		-23.0	-4.5
ntrC	response regulator	regulation of nitrogen utilization	-23.7	-4.6
PA5364	response regulator		-142.3	-7.2
algB	response regulator	positive regulation of secondary metabolite biosynthetic process	-50.2	-5.6
PA5484	two-component sensor	phosphatase activity	-37.9	-5.2
PA3346	response regulator hsbR		-19.7	-4.3
ladS	lost adherence sensor		-7.1	-2.8
roxR	response regulator		-617.3	-9.3
rocA1	response regulator		-118.2	-6.9
	Two component system	**Upregulated genes**	**FC**	**log FC**
PA0179	response regulator	Bacterial chemotaxis	5.5	2.4
PA0600	sensor (agtS)	peptidoglycan and controlling virulence	92.9	6.5
PA0601	response regulator (agtR)	peptidoglycan and controlling virulence	3.7	1.9
PA0930	sensor(pirS)	Iron acquistion	166.6	7.4
PA1458	two-component sensor	chemotaxis	2.6	1.4
PA1611	sensor/response regulator hybrid protein	HptB-HsbR phosphorelay.acute/chronic infection cycle in conjunction with the GacS network	2.9	1.5
PA2523	response regulator czcR	cztR_silR_copR: heavy metal response regulator	6.2	2.6
PA2572	response regulator	Affects motility,virulence and antibiotic resistance works with PA2573	3.3	1.7
PA2573	chemotaxis transducer	Bacterial chemotaxis	138.3	7.1
pfeR	response regulator	Iron acquistion	242.3	7.9
PA3078	sensor (cprS)	Triggers LPS modification and adaptive antimicrobials peptide resistance	514.9	9.0
gltR	response regulator	cellular catabolic process,Glycolysis / Gluconeogenesis	305.1	8.3
PA3271	two-component sensor		255.7	8.0
pprB	response regulator		268.6	8.1
PA4381	response regulator colR	Polymyxin resistance	5.0	2.3
PA4396	response regulator	Diguanylate cyclase GGDEF DOMAIN	202.0	7.7
roxS	sensor histidine kinase	necessary for the aerobic growth	6.8	2.8
cbrA	two-component sensor		2.2	1.1
cbrB	response regulator		4.6	2.2
pmrB	regulator system signal sensor kinase	induced by low Mg2+ and catonic antimicrobial peptides.polymyxinB, colistin resistance	6.6	2.7
PA4843	response regulator GcbA	diguanylate cyclase activity	5.1	2.4
irlR	response regulator	cztR_silR_copR: heavy metal response regulator	277.3	8.1
PA5165	two-component sensor	positive regulation of organic acid transport	11.2	3.5
phoB	response regulator	Quorum sensing and swarming motility	852.0	9.7
gacS	sensor/response regulator	biofilm formation,antibiotic resistance,swarming motility	2.1	1.1
rocR	response regulator	biofilm maturation,fimbrial genes	188.7	7.6
Swarming and biofilm formation			**FC**	**log FC**
bfiS	protein BfiS		5.0	2.3
bfmR	protein BfmR		6.6	2.7
Quorum sensing			**FC**	**log FC**
pmrA	response regulator		-161.9	-7.3
Redox response			**FC**	**log FC**
PA4494	sensor histidine kinase	sensor histidine kinase RoxS	6.8	2.8
PA4493	response regulator	response regulator RoxR	-617.3	-9.3
Copper tolerance			**FC**	**log FC**
copS	two-component sensor		-25.4	-4.7
PA4885	response regulator	irlR	277.3	8.1
cueR	protein CueR		6.6	2.7

Table S7 Differentially expression of Resistance-nodulation-cell division (RND) efflux pumps.

	Resistance-nodulation-cell division (RND)	**SNP**		**Ag^+**	
	RND efflux pumps	**FC**	**log FC**	**FC**	**log FC**
mexA	multidrug resistance protein MexA	-295.3	-8.2	-216.5	-7.8
oprM	outer membrane protein OprM	-124.2	-7.0	-69.7	-6.1
mexD	(RND) multidrug efflux transporter	-57.8	-5.9	-16.2	-4.0
mexE	(RND) multidrug efflux membrane fusion protein			-81.6	-6.3
mexG	hypothetical protein	-628.4	-9.3	-102.6	-6.7
mexI	(RND) efflux transporter (Quorum sensing)	-2.4	-1.3	72.0	6.2
mexH	(RND) efflux membrane fusion protein(QS)	199.8	7.6	3.3	1.7
mexR	multidrug resistance operon repressor MexR	-203.9	-7.7	-266.9	-8.1
PA2526	(RND) efflux transporter muxC			-10.9	-3.4
PA1875	hypothetical protein novel efflux pump biofilm			-26.6	-4.7
	RND multidrug efflux membrane fusion protein	**SNP**		**Ag^+**	
		FC	**log FC**	**FC**	**log FC**
PA3523	(RND) efflux membrane fusion protein			-73.1	-6.2
PA3677	(RND) efflux membrane fusion protein			-15.3	-3.9
PA4374	(RND) efflux membrane fusion protein	-160.1	-7.3	-29.9	-4.9
PA0157	(RND) efflux membrane fusion protein			-31.6	-5.0
PA0156	(RND) efflux membrane fusion protein	193.1	7.6	2.8	1.5
PA2018	multidrug efflux protein (beta-Lactam resistance)	70.9	6.1	70.9	6.1
		SNP		**Ag^+**	
	RND multidrug efflux membrane transporter	**FC**	**log FC**	**FC**	**log FC**
PA3522	(RND) efflux transporter	-57.3	-5.8	-16.1	-4.0
PA0158	(RND) efflux transporter	-3.3	-1.7		
PA3676	(RND) efflux transporter	36.1	5.2		
		SNP		**Ag^+**	
	Porins	**FC**	**log FC**	**FC**	**log FC**
oprB	porin B	-265.3	-8.1	-57.9	-5.9
oprO	pyrophosphate-specific outer membrane porin			-12.9	-3.7
opdC	histidine porin OpdC			-25.4	-4.7
PA3038	porin	-123.4	-6.9	-80.2	-6.3
PA4179	porin	-139.7	-7.1		
PA2291	glucose-sensitive porin	54.6	5.8	-2.1	-1.0
opdP	glycine-glutamate dipeptide porin OpdP	-124.5	-7.0		
oprC	copper transport outer membrane porin OprC	140.5	7.1		
oprP	phosphate-specific outer membrane porin OprP	168.1	7.4	6.6	2.7
lptF	outer membrane porin F			2.8	1.5
opdK	vanillate porin OpdK	2.5	1.3	177.4	7.5
PA1025	porin	145.2	7.2	145.2	7.2
opdT	tyrosine porin OpdT			8.2	3.0
PA3920	metal transporting P-type ATPase	-157.6	-7.3	-140.8	-7.1

Table S8 Downregulated transporter genes after SNP treatment.

	Downregulated transporter genes in response to SNP		
Amino acid transporter		**FC**	**log FC**

aroP1	aromatic amino acid transporter AroP	-64.2	-6.0
PA5154	ABC transporter permease	-8.1	-3.0
PA2041	amino acid permease	-150.1	-7.2
aroP2	aromatic amino acid transporter AroP	-493.3	-8.9
PA4023	transporter	-14.5	-3.9
rplL	50S ribosomal protein L7/L12	-2.7	-1.4
Carbohydrate transmembrane transporter activity (GO:0015144)		**FC**	**log FC**
PA2068	major facilitator superfamily transporter	-233.4	-7.9
Cation transporter		**FC**	**log FC**
kdpB	potassium-transporting ATPase subunit B	-87.4	-6.4
glpT	glycerol-3-phosphate transporter	-268.9	-8.1
PA5468	citrate transporter	-138.8	-7.1
PA3920	metal transporting P-type ATPase	-157.6	-7.3
PA1054	monovalent cation/H+ antiporter subunit A	-64.6	-6.0
PA1059	monovalent cation/H+ antiporter subunit G	-59.8	-5.9
Transmembrane transporter activity		**FC**	**log FC**
aroP1	aromatic amino acid transporter AroP	-64.2	-6.0
flhA	flagellar biosynthesis protein FlhA	-255.8	-8.0
fhp	flavohemoprotein	-153.2	-7.3
PA3532	hypothetical protein	-157.2	-7.3
PA4897	hypothetical protein	-61.0	-5.9
PA5207	phosphate transporter	-76.1	-6.3
PA2777	hypothetical protein	-283.8	-8.1
PA2041	amino acid permease	-150.1	-7.2
wzt	ABC transporter	-71.5	-6.2
kdpB	potassium-transporting ATPase subunit B	-87.4	-6.4
PA1339	amino acid ABC transporter ATP binding protein	-2.3	-1.2
xcpQ	type II secretion system protein D	-91.6	-6.5
PA5568	inner membrane protein translocase subunit YidC	-7.9	-3.0
PA4467	hypothetical protein	-97.0	-6.6
PA5121	hypothetical protein	-41.0	-5.4
aroP2	aromatic amino acid transporter AroP	-493.3	-8.9
PA4142	secretion protein	-130.6	-7.0
rbsB	ribose ABC transporter substrate-binding protein	-155.1	-7.3
phoU	phosphate uptake regulatory protein PhoU	-124.2	-7.0
PA3304	hypothetical protein	-105.5	-6.7
PA1386	ABC transporter ATP-binding protein	-142.7	-7.2
glpT	sn-glycerol-3-phosphate transporter	-268.9	-8.1
PA1236	major facilitator superfamily transporter	-119.8	-6.9
PA5376	ABC transporter ATP-binding protein	-123.3	-6.9
PA4023	transporter	-14.5	-3.9
PA0352	transporter	-97.4	-6.6
ccmA	cytochrome c biogenesis ATP-binding export protein CcmA	-258.0	-8.0
PA5518	potassium efflux transporter	-106.3	-6.7
PA0688	alkaline phosphatase L	-163.6	-7.4
braF	branched-chain amino acid ABC transporter ATP-binding protein	-235.8	-7.9
coxB	cytochrome C oxidase subunit II	-16.0	-4.0
PA4706	hemin importer ATP-binding subunit	-235.8	-7.9
PA4292	phosphate transporter	-246.4	-7.9
PA3920	metal transporting P-type ATPase	-157.6	-7.3
ccmB	heme exporter protein CcmB	-269.5	-8.1
PA3187	ABC transporter ATP-binding protein	-234.0	-7.9
PA2408	ABC transporter ATP-binding protein	-2.3	-1.2
pstB	phosphate ABC transporter ATP-binding protein	-217.1	-7.8
PA3401	hypothetical protein	-154.4	-7.3
fptA	Fe(III)-pyochelin outer membrane receptor	-41.9	-5.4
ccoN1	cbb3-type cytochrome C oxidase subunit I	-2.6	-1.4
	Lipid transporters	**FC**	**log FC**

PA3211	ABC transporter permease	-158.0	-7.3
PA4459	Lipopolysaccharide export system protein LptC	-11.2	-3.5
PA0860	ABC transporter ATP-binding protein/permease	-101.1	-6.7
PA4460	Lipopolysaccharide export system protein LptA	-16.7	-4.1
	ABC transporters	**FC**	**log FC**
PA0314	L-cysteine ABC transporter protein FliY	-117.4	-6.9
PA0860	ABC transporter ATP-binding protein/permease	-101.1	-6.7
braF	branched-chain amino acid ABC transporter ATP-binding protein	-235.8	-7.9
PA1386	ABC transporter ATP-binding protein	-142.7	-7.2
ccmA	cytochrome c biogenesis ATP-binding export protein CcmA	-258.0	-8.0
rbsB	ribose ABC transporter substrate-binding protein	-155.1	-7.3
PA2408	ABC transporter ATP-binding protein	-2.3	-1.2
PA2409	ABC transporter permease	-199.9	-7.6
PA3187	ABC transporter ATP-binding protein	-234.0	-7.9
PA3188	sugar ABC transporter permease	-300.0	-8.2
PA3190	sugar ABC transporter substrate-binding protein	-2.4	-1.3
PA3211	ABC transporter permease	-158.0	-7.3
potA	polyamine transporter ATP-binding protein PotA	-300.1	-8.2
PA4222	ABC transporter ATP-binding protein	-52.5	-5.7
PA5076	ABC transporter	-113.0	-6.8
PA5154	ABC transporter permease	-8.1	-3.0
PA5155	amino acid ABC transporter permease	-8.2	-3.0
PA5317	dipeptide ABC transporter substrate-binding protein	-114.5	-6.8
pstB	phosphate ABC transporter ATP-binding protein	-217.1	-7.8
PA5376	ABC transporter ATP-binding protein	-123.3	-6.9
	Ion channel (PC00133)		
kdpB	potassium-transporting ATPase subunit B	-87.4	-6.4
PA3920	metal transporting P-type ATPase	-157.6	-7.3

Table S9 Upregulated transporter genes in response to SNP.

	Amino acid transporter	**FC**	**log FC**
PA1340	amino acid ABC transporter permease	166.2	7.4
gabP	gamma-aminobutyrate permease	155.8	7.3
aotQ	arginine/ornithine ABC transporter permease AotQ	322.4	8.3
PA3597	amino acid permease	168.1	7.4
braB	branched-chain amino acid transporter	142.1	7.2
	Cation transporter	FC	log FC
PA3234	acetate permease	69.7	6.1
gltP	glutamate/aspartate:proton symporter	2.5	1.3
rho	transcription termination factor Rho	176.5	7.5
PA0119	C4-dicarboxylate transporter DctA	164.8	7.4
cmaX	transporter	222.7	7.8
	Carbohydrate transporter	**FC**	**log FC**
PA3234	acetate permease	69.7	6.1
	Transmembrane transporter activity	**FC**	**log FC**
fecA	Fe(III) dicitrate transporter FecA	94.5	6.6
PA5548	major facilitator superfamily transporter	184.4	7.5
PA1340	amino acid ABC transporter permease	166.2	7.4
PA3234	acetate permease	69.7	6.1
ambA	protein Amb	341.7	8.4
betT1	choline transporter BetT	143.4	7.2
gltP	glutamate/aspartate:proton symporter	2.5	1.3
dipZ	thiol:disulfide interchange protein	125.2	7.0

PA0716	hypothetical protein	804.2	9.7
PA5160	drug efflux transporter	145.4	7.2
ftsE	cell division protein FtsE	4.7	2.2
PA2938	transporter	2.5	1.3
secA	preprotein translocase subunit SecA	5.5	2.5
PA0119	C4-dicarboxylate transporter DctA	164.8	7.4
braB	branched-chain amino acid transporter	142.1	7.2
modC	molybdenum ABC transporter ATP-binding protein ModC	204.8	7.7
uraA	uracil permease	173.2	7.4
PA5529	sodium/proton antiporter	5.5	2.5
PA0689	hypothetical protein	3.9	2.0
aprE	alkaline protease secretion protein AprE	342.5	8.4
gabP	gamma-aminobutyrate permease	155.8	7.3
PA5230	ABC transporter permease	98.9	6.6
pslL	hypothetical protein	159.6	7.3
PA1382	type II secretion system protein	3.1	1.6
PA4595	ABC transporter ATP-binding protein	4.9	2.3
pstS	phosphate ABC transporter substrate-binding protein	228.8	7.8
PA3597	amino acid permease	168.1	7.4
PA0485	hypothetical protein	233.9	7.9
cupC3	usher CupC3	176.5	7.5
PA0603	Polyamine-transporting ATPase ABC transporter ATP-binding protein	6.5	2.7
	ABC transporters	**FC**	**log FC**
PA0204	ABC transporter permease	274.6	8.1
PA0603	ABC transporter ATP-binding protein	6.5	2.7
PA1810	ABC transporter	60.2	5.9
modC	molybdenum ABC transporter ATP-binding protein ModC	204.8	7.7
PA1964	ABC transporter ATP-binding protein	213.1	7.7
PA2307	ABC transporter permease	164.9	7.4
PA2811	ABC transporter permease	159.0	7.3
PA4496	ABC transporter	137.8	7.1
PA4595	ABC transporter ATP-binding protein	4.9	2.3
PA4913	ABC transporter	2.7	1.4
PA5082	ABC transporter	247.1	7.9
PA5153	amino acid ABC transporter substrate-binding protein	5.9	2.6
PA5217	iron ABC transporter substrate-binding protein	111.3	6.8
PA5230	ABC transporter permease	98.9	6.6

Table S10 Downregulated transporter genes in response to Ag^+.

	Cation transmembrane transporter activity (GO:0008324)	**FC**	**log FC**
cyoA	cytochrome o ubiquinol oxidase subunit II	-68.0	-6.1
fptA	Fe(III)-pyochelin outer membrane receptor	-23.5	-4.6
mgtA	Mg(2+) transport ATPase	-14.4	-3.8
PA4218	transporter	-13.6	-3.8
foxA	ferrioxamine receptor FoxA	-20.6	-4.4
coxA	cytochrome C oxidase subunit I	-21.3	-4.4
rplL	50S ribosomal protein L7/L12	-7.0	-2.8
PA4431	iron-sulfur protein	-370.9	-8.5
PA2042	serine/threonine transporter SstT	-47.8	-5.6
PA2435	cation-transporting P-type ATPase	-17.0	-4.1
atpA	ATP synthase subunit alpha	-3.2	-1.7
kdpB	potassium-transporting ATPase subunit B	-32.7	-5.0
kdpC	potassium-transporting ATPase subunit C	-61.3	-5.9

PA0846	sulfate transporter CysZ	-22.8	-4.5
fliI	flagellum-specific ATP synthase	-25.0	-4.6
PA1360	hypothetical protein	-37.9	-5.2
phoU	phosphate uptake regulatory protein PhoU	-200.1	-7.6
PA3920	metal transporting P-type ATPase	-140.8	-7.1
atpD	ATP synthase subunit beta	-2.6	-1.4
PA1429	cation-transporting P-type ATPase	-12.5	-3.6
ccoN1	cbb3-type cytochrome C oxidase subunit I	-2.1	-1.1
PA2911	TonB-dependent receptor	-15.7	-4.0
PA4358	ferrous iron transporter B	-25.2	-4.7
PA2435	cation-transporting P-type ATPase	-17.0	-4.1
PA2068	major facilitator superfamily transporter	-14.5	-3.9
	Transmembrane transporters	**FC**	**log FC**
PA2322	gluconate permease	-50.0	-5.6
aroP2	aromatic amino acid transporter AroP	-47.7	-5.6
PA5249	hypothetical protein	-35.9	-5.2
PA3304	hypothetical protein	-39.5	-5.3
PA2987	lipoprotein-releasing system ABC transporter ATP-binding protein	-123.7	-7.0
PA0352	transporter	-12.2	-3.6
PA2777	hypothetical protein	-35.4	-5.1
PA4143	toxin transporter	-15.7	-4.0
xcpQ	type II secretion system protein D	-51.4	-5.7
flhA	flagellar biosynthesis protein FlhA	-31.9	-5.0
PA4292	phosphate transporter	-46.1	-5.5
PA1875	hypothetical protein novel efflux pump biofilm	-26.6	-4.7
PA5518	potassium efflux transporter	-9.9	-3.3
PA3468	hypothetical protein	-25.5	-4.7
PA1882	transporter	-104.5	-6.7
PA5207	phosphate transporter	-40.0	-5.3
PA5099	transporter	-23.5	-4.6
PA4706	hemin importer ATP-binding subunit	-22.0	-4.5
PA2042	serine/threonine transporter SstT	-47.8	-5.6
pstA	phosphate ABC transporter permease	-10.1	-3.3
PA3521	Probable outer membrane protein	-22.9	-4.5
aprF	alkaline protease secretion protein AprF	-23.4	-4.5
PA3336	major facilitator superfamily transporter	-87.0	-6.4
PA0688	alkaline phosphatase L	-30.6	-4.9
PA0450	phosphate transporter	-10.4	-3.4
pstB	phosphate ABC transporter ATP-binding protein	-40.6	-5.3
PA1360	hypothetical protein	-37.9	-5.2
aroP1	aromatic amino acid transporter AroP	-60.0	-5.9
PA1144	major facilitator superfamily transporter	-12.7	-3.7
PA4757	leucine export protein LeuE	-153.6	-7.3
PA4136	major facilitator superfamily transporter	-14.0	-3.8
recN	DNA repair protein RecN	-40.4	-5.3
PA2837	hypothetical protein	-23.5	-4.6
ftsE	cell division protein FtsE	-10.8	-3.4
PA2026	hypothetical protein	-33.8	-5.1
PA5568	inner membrane protein translocase subunit YidC	-174.6	-7.4
	Amino acid transporters	**FC**	**Log FC**
aroP2	aromatic amino acid transporter AroP	-47.7	-5.6
PA5249	hypothetical protein	-35.9	-5.2
rplL	50S ribosomal protein L7/L12	-7.0	-2.8
braF	branched-chain amino acid ABC transporter ATP-binding protein BraF	-132.2	-7.0
braD	branched-chain amino acid ABC transporter permease BraD	-36.6	-5.2
PA2042	serine/threonine transporter SstT	-47.8	-5.6
PA5075	ABC transporter permease	-24.8	-4.6
PA1360	hypothetical protein	-37.9	-5.2
aroP1	aromatic amino acid transporter AroP	-60.0	-5.9

PA4757	leucine export protein LeuE	-153.6	-7.3
	Carbohydrate transmembrane transporter activity (GO:0015144)	**FC**	**Log FC**
PA2322	gluconate permease	-50.0	-5.6
PA2068	major facilitator superfamily transporter	-14.5	-3.9
	Lipid transporter activity (GO:0005319)	**FC**	**Log FC**
PA3211	ABC transporter permease	-59.1	-5.9
PA4143	toxin transporter	-15.7	-4.0
PA4455	ABC transporter permease	-127.3	-7.0
PA4459	Lipopolysaccharide export system protein LptC	-5.4	-2.4
PA4460	Lipopolysaccharide export system protein LptA	-6.4	-2.7
PA0860	ABC transporter ATP-binding protein/permease	-18.9	-4.2
	ATP-binding cassette (ABC) transporter (PC00003)	**FC**	**Log FC**
cysA	sulfate.thiosulfate ABC transporter ATP-binding protein	-34.2	-5.1
spuE	spermidine ABC transporter substrate-binding protein	-154.2	-7.3
PA0313	L-cysteine ABC transporter protein YecS	-87.2	-6.4
PA0314	L-cysteine ABC transporter protein FliY	-43.9	-5.5
PA0602	ABC transporter	-124.1	-7.0
PA0605	ABC transporter permease	-54.3	-5.8
PA0606	ABC transporter permease	-40.7	-5.3
PA0860	ABC transporter ATP-binding protein/permease	-18.9	-4.2
aotM	arginine/ornithine ABC transporter permease	-96.9	-6.6
aotP	arginine/ornithine ABC transporter ATP-binding protein	-88.5	-6.5
braF	branched-chain amino acid ABC transporter ATP-binding protein	-132.2	-7.0
braD	branched-chain amino acid ABC transporter permease	-36.6	-5.2
PA1257	amino acid ABC transporter permease	-26.2	-4.7
PA1386	ABC transporter ATP-binding protein	-53.4	-5.7
PA1807	ABC transporter ATP-binding protein	-21.0	-4.4
PA2678	ABC transporter permease	-48.3	-5.6
PA3187	ABC transporter ATP-binding protein	-54.3	-5.8
PA3189	sugar ABC transporter permease	-54.0	-5.8
PA3211	ABC transporter permease	-59.1	-5.9
PA3228	ABC transporter ATP-binding protein/permease	-92.3	-6.5
potC	polyamine ABC transporter permease	-43.9	-5.5
PA3888	ABC transporter permease	-46.8	-5.5
PA3889	ABC transporter	-36.2	-5.2
PA3891	ABC transporter ATP-binding protein	-29.1	-4.9
PA4455	ABC transporter permease	-127.3	-7.0
PA4456	ABC transporter ATP-binding protein	-337.2	-8.4
PA4497	ABC transporter	-15.2	-3.9
PA4500	ABC transporter	-42.3	-5.4
PA4506	peptide ABC transporter ATP-binding protein	-104.5	-6.7
PA4594	ABC transporter ATP-binding protein	-24.6	-4.6
PA5231	ABC transporter ATP-binding protein/permease	-49.2	-5.6
	Ion channel (PC00133)		
mgtA	Mg(2+) transport ATPase	-14.4	-3.8
atpA	ATP synthase subunit alpha	-3.2	-1.7
kdpB	potassium-transporting ATPase subunit B	-32.7	-5.0
fliI	flagellum-specific ATP synthase	-25.0	-4.6
PA3920	metal transporting P-type ATPase	-140.8	-7.1
atpD	ATP synthase subunit beta	-2.6	-1.4
PA1429	cation-transporting P-type ATPase	-12.5	-3.6
PA2435	cation-transporting P-type ATPase	-17.0	-4.1

Table S11 Upregulated transporter genes in response to Ag^+.

	Cation transmembrane transporter activity (GO:0008324)	**FC**	**log FC**

kdpF	potassium-transporting ATPase subunit F	1195.9	10.2
kdpA	potassium-transporting ATPase subunit A	13.1	3.7
cyoB	cytochrome o ubiquinol oxidase subunit I	112.5	6.8
amtB	ammonium transporter	8.1	3.0
PA0119	C4-dicarboxylate transporter DctA	3.3	1.7
ccoN2	cbb3-type cytochrome C oxidase subunit I	2.6	1.4
	Transmembrane transporters	**FC**	**log FC**
PA4837	hypothetical protein	104.6	6.7
fpvA	ferripyoverdine receptor	7.3	2.9
PA1856	cbb3-type cytochrome C oxidase subunit I	231.2	7.9
trkA	potassium transporter inner membrane associated protein	4.4	2.1
fecA	Fe(III) dicitrate transporter FecA	94.5	6.6
PA0521	cytochrome C oxidase subunit	327.3	8.4
PA4514	iron transport outer membrane receptor	3.1	1.6
kefB	glutathione-regulated potassium-efflux system protein	3.3	1.7
kdpA	potassium-transporting ATPase subunit A	13.1	3.7
PA4038	hypothetical protein	302.6	8.2
cyoB	cytochrome o ubiquinol oxidase subunit I	112.5	6.8
pslL	hypothetical protein	159.6	7.3
PA2114	major facilitator superfamily transporter	3.2	1.7
PA5094	ABC transporter ATP-binding protein	133.8	7.1
PA4837	hypothetical protein	104.6	6.7
gabP	gamma-aminobutyrate permease	155.8	7.3
PA0485	hypothetical protein	233.9	7.9
PA0603	ABC transporter ATP-binding protein	10.5	3.4
PA1964	ABC transporter ATP-binding protein	213.1	7.7
pvdE	pyoverdine biosynthesis protein PvdE	6.6	2.7
PA5529	sodium/proton antiporter	6.4	2.7
PA3019	ABC transporter ATP-binding protein	3.3	1.7
PA0689	hypothetical protein	9.1	3.2
tatC	transporter TatC	276.7	8.1
PA5160	drug efflux transporter	145.4	7.2
ambA	protein AmbA	341.7	8.4
cupC3	usher CupC3	176.5	7.5
PA3781	transporter	173.6	7.4
PA1419	transporter	147.1	7.2
uraA	uracil permease	3.3	1.7
PA3597	amino acid permease	168.1	7.4
PA5548	major facilitator superfamily transporter	184.4	7.5
cupB3	usher CupB3	43.9	5.5
PA5230	ABC transporter permease	2.2	1.1
opmD	Probable outer membrane protein	6.6	2.7
PA2938	transporter	31.8	5.0
PA4974	probable outer membrane protein precursor(beta-lactam resistance)	3.3	1.7
	Amino acid transporter (PC00046)	**FC**	**log FC**
gabP	gamma-aminobutyrate permease	155.8	7.3
aotQ	arginine/ornithine ABC transporter permease	4.3	2.1
PA3597	amino acid permease	168.1	7.4
	Carbohydrate transporter (PC00067)	**FC**	**log FC**
PA3234	acetate permease	6.8	2.8
	ATP-binding cassette (ABC) transporter (PC00003)	**FC**	**log FC**
PA0204	ABC transporter permease gene	274.6	8.1
PA0603	ABC transporter ATP-binding protein	10.5	3.4
aotQ	arginine/ornithine ABC transporter permease	4.3	2.1
PA1810	ABC transporter	3.3	1.7
modC	molybdenum ABC transporter ATP-binding protein ModC	13.1	3.7
PA1964	ABC transporter ATP-binding protein	213.1	7.7
PA2307	ABC transporter permease	164.9	7.4
pvdE	pyoverdine biosynthesis protein PvdE	6.6	2.7

PA2811	ABC transporter permease	3.7	1.9
PA3019	ABC transporter ATP-binding protein	3.3	1.7
PA4496	ABC transporter(Bacterial chemotaxis)	6.6	2.7
PA4502	ABC transporter(Bacterial chemotaxis)	6.6	2.7
PA4913	ABC transporter	12.4	3.6
PA5082	ABC transporter	247.1	7.9
PA5094	ABC transporter ATP-binding protein	133.8	7.1
PA5096	ABC transporter	2.2	1.1

Table S12 Differential expression of the metabolic genes in response to SNP.

	Response to stimulus (downregulated genes)	**FC**	**log FC**
PA4142	secretion protein	-130.6	-7.0
htpG	chaperone protein HtpG	-2.0	-1.0
PA1068	heat shock protein	-94.8	-6.6
fliM	flagellar motor switch protein FliM	-186.3	-7.5
recQ	ATP-dependent DNA helicase RecQ	-84.7	-6.4
PA0431	hypothetical protein	-326.3	-8.4
PA5121	hypothetical protein	-41.0	-5.4
pvdR	pyoverdine biosynthesis protein PvdR	-154.0	-7.3
rnhB	ribonuclease HII	-298.8	-8.2
mexA	multidrug resistance protein MexA	-295.3	-8.2
snr1	cytochrome C Snr1	-64.5	-6.0
recC	exodeoxyribonuclease V subunit gamma	-25.8	-4.7
PA2409	ABC transporter permease	-199.9	-7.6
PA3304	hypothetical protein	-105.5	-6.7
PA0253	transcriptional regulator	-379.7	-8.6
	Response to stimulus (upregulated genes)	**FC**	**log FC**
katB	catalase	144.2	7.2
crc	catabolite repression control protein	2.4	1.3
pstS	phosphate ABC transporter substrate-binding protein	228.8	7.8
PA4371	hypothetical protein	156.4	7.3
PA4562	hypothetical protein (Putative lipid II flippase MurJ)	82.4	6.4
PA0397	cation efflux system protein	494.3	8.9
mutL	DNA mismatch repair protein	3.1	1.6
PA4061	thioredoxin	255.7	8.0
PA3818	type III secretion system regulator SuhB	523.8	9.0
ccpR	cytochrome C551 peroxidase	3.7	1.9
PA4701	hypothetical protein	142.3	7.2
PA2827	methionine sulfoxide reductase B	1481.3	10.5
PA3458	transcriptional regulator	469.3	8.9
aprE	alkaline protease secretion protein AprE	342.5	8.4
pslL	hypothetical protein	159.6	7.3
PA0485	hypothetical protein	233.9	7.9
	RNA metabolic process (downregulated genes)	**FC**	**log FC**
RNA catabolic process			
rnhB	ribonuclease HII	-298.8	-8.2
mRNA processing process			
PA3614	hypothetical protein	-114.7	-6.8
rRNA metabolic process			
rne	ribonuclease E	-2.7	-1.4
PA4936	rRNA methylase	-2.8	-1.5
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-197.9	-7.6
hemK	methyl transferase	-109.0	-6.8
PA3179	ribosomal large subunit pseudouridine synthase B	-156.0	-7.3

PA5019	hypothetical protein	-108.2	-6.8
tRNA metabolic process			
miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	-2.2	-1.2
metG	methionine--tRNA ligase	-3.3	-1.7
ileS	isoleucine--tRNA ligase	-5.7	-2.5
PA0976	7-cyano-7-deazaguanine synthase	-268.3	-8.1
hisS	histidine--tRNA ligase	-421.1	-8.7
PA5492	ribosome biogenesis GTP-binding protein YsxC	-2.4	-1.3
pheS	phenylalanine--tRNA ligase subunit alpha	-178.1	-7.5
gltX	glutamate--tRNA ligase	-2.4	-1.3
PA3129	tRNA-dihydrouridine synthase C	-94.3	-6.6
trmD	tRNA (guanine-N(1)-)-methyltransferase	-2.2	-1.2
Transcription DNA dependent		**FC**	**Log FC**
mexR	multidrug resistance operon repressor MexR	-203.9	-7.7
PA1210	quercetin 2,3-dioxygenase	-136.8	-7.1
PA0048	transcriptional regulator	-232.5	-7.9
PA2267	transcriptional regulator	-152.5	-7.3
wbpI	UDP-2,3-diacetamido-2,3-dideoxy-D-glucuronate 2-epimeras	-3.9	-2.0
gbdR	protein GbdR	-164.0	-7.4
PA1866	hypothetical protein	-79.5	-6.3
PA0243	transcriptional regulator	-270.7	-8.1
PA1045	ATP-dependent DNA helicase DinG	-84.4	-6.4
PA2917	transcriptional regulator	-306.9	-8.3
PA5048	nuclease	-48.2	-5.6
PA0253	transcriptional regulator	-379.7	-8.6
PA4341	transcriptional regulator	-270.2	-8.1
	RNA metabolic process (upregulated genes)		
RNA catabolic process		**FC**	**Log FC**
pnp	polynucleotide phosphorylase	2.9	1.5
mRNA processing process			
glnD	bifunctional uridylyltransferase/uridylyl-removing protein	82.3	6.4
rRNA metabolic process			
rluC	ribosomal large subunit pseudouridine synthase C	6.0	2.6
PA3806	dual-specificity RNA methyltransferase RlmN	3.1	1.6
cafA	cytoplasmic axial filament protein	259.8	8.0
rpsI	30S ribosomal protein S9	2.2	1.1
tRNA metabolic process			
alaS	alanine--tRNA ligase	4.9	2.3
PA4852	hypothetical protein(tRNA-dihydrouridine synthase B)	222.7	7.8
leuS	leucine--tRNA ligase	84.8	6.4
truB	tRNA pseudouridine synthase B	2.0	1.0
PA3806	dual-specificity RNA methyltransferase RlmN	3.1	1.6
PA5567	tRNA modification GTPase TrmE	162.6	7.3
glnS	glutamine--tRNA ligase	133.1	7.1
tgt	queuine tRNA-ribosyltransferase	289.8	8.2
Transcription DNA dependent		**FC**	**Log FC**
cspD	cold-shock protein CspD	2.5	1.3
PA1380	transcriptional regulator	230.3	7.8
PA0535	transcriptional regulator	400.8	8.6
nusG	transcription antitermination protein NusG	2.5	1.3
PA1879	hypothetical protein	200.4	7.6
PA5157	transcriptional regulator	472.3	8.9
PA0218	transcriptional regulator	121.7	6.9
PA1283	transcriptional regulator	6.1	2.6
PA1826	transcriptional regulator	122.8	6.9
PA2780	bacterial swarming regulator BswR	599.8	9.2
PA3678	transcriptional regulator	235.2	7.9
PA0961	cold-shock protein	313.0	8.3
PA1630	transcriptional regulator	769.7	9.6

PA0436	transcriptional regulator	1052.2	10.0
PA1135	molecular chaperone Hsp31/glyoxalase	253.9	8.0
PA2846	transcriptional regulator	260.2	8.0
PA1836	transcriptional regulator	361.5	8.5
PA3174	transcriptional regulator	305.1	8.3
glmR	GlmR transcriptional regulator	143.7	7.2
PA5301	transcriptional regulator	3.6	1.8
rpoH	RNA polymerase sigma factor RpoH	2.7	1.4
PA2121	transcriptional regulator	122.8	6.9
PA3458	transcriptional regulator	469.3	8.9
	DNA metabolic process (downregulated genes)		
DNA recombination		**FC**	**log FC**
PA0793	hypothetical protein	-152.4	-7.3
PA0728	bacteriophage integrase	-184.0	-7.5
recQ	ATP-dependent DNA helicase RecQ	-84.7	-6.4
recC	exodeoxyribonuclease V subunit gamma	-25.8	-4.7
PA5201	hypothetical protein	-77.4	-6.3
ruvB	Holliday junction ATP-dependent DNA helicase RuvB	-3.2	-1.7
	DNA repair	**FC**	**Log FC**
recQ	ATP-dependent DNA helicase RecQ	-84.7	-6.4
PA1866	hypothetical protein	-79.5	-6.3
PA1045	ATP-dependent DNA helicase DinG	-84.4	-6.4
rnhB	ribonuclease HII	-298.8	-8.2
recC	exodeoxyribonuclease V subunit gamma	-25.8	-4.7
PA5201	hypothetical protein	-77.4	-6.3
ruvB	Holliday junction ATP-dependent DNA helicase RuvB	-3.2	-1.7
DNA replication		**FC**	**Log FC**
parC	DNA topoisomerase IV subunit A	-145.5	-7.2
parE	DNA topoisomerase IV subunit B	-191.6	-7.6
dnaX	DNA polymerase III subunits gamma/tau	-88.5	-6.5
ssb	single-stranded DNA-binding protein	-2.4	-1.3
polA	DNA polymerase I	-66.0	-6.0
rnhB	ribonuclease HII	-298.8	-8.2
dnaN	DNA polymerase III subunit beta	-3.3	-1.7
PA3200	hypothetical protein	-102.0	-6.7
	DNA metabolic process (upregulated genes)	**FC**	**log FC**
DNA catabolic process			
PA2959	hypothetical protein	2.8	1.5
DNA recombination			
PA3867	DNA invertase	290.8	8.2
PA2823	hypothetical protein	2.5	1.3
	DNA repair	**FC**	**log FC**
crc	catabolite repression control protein	2.4	1.3
mutL	DNA mismatch repair protein	3.1	1.6
mfd	transcription-repair coupling factor	16.8	4.1
PA1865	Fanconi-associated nuclease	59.4	5.9
PA4701	hypothetical protein	142.3	7.2
mutY	A/G specific adenine glycosylase	2.1	1.1
rnt	ribonuclease T	659.1	9.4
DNA replication		**FC**	**log FC**
dnaB	replicative DNA helicase	3.5	1.8
PA0947	DNA replication initiation factor	315.5	8.3
topA	DNA topoisomerase I	2.9	1.6
PA1527	hypothetical protein	2.0	1.0
	Protein metabolic process (downregulated genes)		
	Cellular protein modification process	**FC**	**log FC**
pqsB	hypothetical protein	-9.0	-3.2
ggt	gamma-glutamyltranspeptidase	-54.1	-5.8
PA5002	hypothetical protein	-63.8	-6.0

map	methionine aminopeptidase	-230.4	-7.8
lpxO2	lipopolysaccharide biosynthetic protein LpxO	-95.7	-6.6
atoB	acetyl-CoA acetyltransferase	-306.4	-8.3
lipB	lipoate-protein ligase B	-65.1	-6.0
PA5445	coenzyme A transferase	-242.4	-7.9
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-197.9	-7.6
hemK	methyl transferase	-109.0	-6.8
PA4558	FkbP-type peptidyl-prolyl cis-trans isomerase	-410.6	-8.7
PA2618	arginyl-tRNA--protein transferase	-255.8	-8.0
pepP	aminopeptidase	-67.8	-6.1
PA3368	acetyltransferase	-2.0	-1.0
Ferredoxin metabolic process		**FC**	**Log FC**
gor	glutathione reductase	-667.8	-9.4
ahpF	alkyl hydroperoxide reductase	-115.6	-6.9
ndh	NADH dehydrogenase	-276.9	-8.1
sth	soluble pyridine nucleotide transhydrogenase	-358.8	-8.5
lpdV	branched-chain alpha-keto acid dehydrogenase complex dihydrolipoyl dehydrogenase	-561.4	-9.1
PA5349	rubredoxin reductase	-138.2	-7.1
trxB2	thioredoxin reductase	-380.8	-8.6
Protein complex assembly		**FC**	**Log FC**
argH	argininosuccinate lyase	-129.8	-7.0
fumC1	fumarate hydratase	-3.0	-1.6
	Protein folding	**FC**	**Log FC**
htpG	chaperone protein HtpG	-2.0	-1.0
PA1068	heat shock protein	-94.8	-6.6
surA	chaperone SurA	-2.2	-1.1
mucD	serine protease MucD	-3.3	-1.7
PA4558	FkbP-type peptidyl-prolyl cis-trans isomerase	-410.6	-8.7
	Proteolysis	**FC**	**Log FC**
PA5551	hypothetical protein	-177.5	-7.5
PA2831	hypothetical protein	-160.5	-7.3
ggt	gamma-glutamyltranspeptidase	-54.1	-5.8
PA3787	hypothetical protein	-159.0	-7.3
map	methionine aminopeptidase	-230.4	-7.8
ftsH	cell division protein FtsH	-2.9	-1.5
mucD	serine protease MucD	-3.3	-1.7
PA2618	arginyl-tRNA--protein transferase	-255.8	-8.0
pepP	aminopeptidase	-67.8	-6.1
	Translation	**FC**	**Log FC**
PA1737	3-hydroxyacyl-CoA dehydrogenase	-337.7	-8.4
PA2106	hypothetical protein	-246.4	-7.9
PA0868	peptidyl-tRNA hydrolase	-437.4	-8.8
metG	methionine--tRNA ligase	-3.3	-1.7
ileS	isoleucine--tRNA ligase	-5.7	-2.5
rplK	50S ribosomal protein L11	-3.4	-1.8
PA0202	amidase	-62.1	-6.0
aspS	aspartate--tRNA ligase	-577.6	-9.2
rplI	50S ribosomal protein L9	-1052.1	-10.0
hisS	histidine--tRNA ligase	-421.1	-8.7
frr	ribosome recycling factor	-324.5	-8.3
map	methionine aminopeptidase	-230.4	-7.8
PA5492	ribosome biogenesis GTP-binding protein YsxC	-2.4	-1.3
pheS	phenylalanine--tRNA ligase subunit alpha	-178.1	-7.5
gltX	glutamate--tRNA ligase	-2.4	-1.3
rpsR	30S ribosomal protein S18	-2300.7	-11.2
pepP	aminopeptidase	-67.8	-6.1
rpsP	30S ribosomal protein S16	-1077.9	-10.1
ffh	signal recognition particle protein Ffh	-131.8	-7.0

Protein metabolic process (upregulated genes)			
Cellular protein modification process		**FC**	**Log FC**
PA3945	hypothetical protein	3.7	1.9
PA2578	acetyltransferase	396.5	8.6
PA4667	hypothetical protein	125.5	7.0
PA4344	hydrolase	182.2	7.5
cat	chloramphenicol acetyltransferase	134.7	7.1
PA2827	methionine sulfoxide reductase B	1481.3	10.5
PA0164	gamma-glutamyltranspeptidase	137.6	7.1
cysE	O-acetylserine synthase	230.0	7.8
murG	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	103.6	6.7
Ferredoxin metabolic process		**FC**	**Log FC**
PA2691	hypothetical protein	118.9	6.9
trxB1	thioredoxin reductase	2.5	1.3
Protein complex assembly		**FC**	**Log FC**
dipZ	thiol:disulfide interchange protein	125.2	7.0
fumC2	fumarate hydratase	84.4	6.4
	Protein folding		
ppiD	peptidyl-prolyl cis-trans isomerase D	3.1	1.6
ppiC2	peptidyl-prolyl cis-trans isomerase C2	1059.9	10.0
PA4061	thioredoxin	255.7	8.0
	Proteolysis		
PA3020	lytic transglycosylase	115.3	6.8
PA4344	hydrolase	182.2	7.5
PA1304	oligopeptidase	54.2	5.8
htpX	protease HtpX	2.8	1.5
PA3047	D-alanyl-D-alanine carboxypeptidase	214.7	7.7
PA0667	hypothetical protein	3.7	1.9
PA3623	hypothetical protein	2.9	1.5
PA0164	gamma-glutamyltranspeptidase	137.6	7.1
	Translation	**FC**	**LogFC**
alaS	alanine--tRNA ligase	4.9	2.3
leuS	leucine--tRNA ligase	84.8	6.4
gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	152.9	7.3
PA4005	hypothetical protein	396.5	8.6
PA5567	tRNA modification GTPase TrmE	162.6	7.3
rpsG	30S ribosomal protein S7	5.2	2.4
lepA	elongation factor 4	247.1	7.9
lepB	signal peptidase I	3.4	1.8
ftsY	signal recognition particle receptor FtsY	2.3	1.2
glnS	glutamine--tRNA ligase	133.1	7.1
rpsI	30S ribosomal protein S9	2.2	1.1
rpsB	30S ribosomal protein S2	1094.0	10.1
cysN	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase	116.9	6.9
Cellular amino acid metabolic process (downregulated genes)			
	Cellular amino acid biosynthetic metabolic process	**FC**	**Log FC**
pvdL	peptide synthase	-142.4	-7.2
carB	carbamoyl phosphate synthase large subunit	-2.2	-1.1
carA	carbamoyl phosphate synthase small subunit	-159.3	-7.3
pvdJ	pyoverdine biosynthesis protein PvdJ	-3.5	-1.8
trpG	anthranilate synthase component II	-298.8	-8.2
trpD	anthranilate phosphoribosyltransferase	-344.9	-8.4
aroB	3-dehydroquinate synthase	-327.2	-8.4
aroK	shikimate kinase	-174.5	-7.4
PA5522	glutamine synthetase	-214.6	-7.7
mmsB	3-hydroxyisobutyrate dehydrogenase	-142.9	-7.2
hisF1	imidazole glycerol phosphate synthase subunit HisF	-234.9	-7.9
pvdN	pyoverdine biosynthesis protein PvdN	-141.0	-7.1

selD	selenide, water dikinase	-349.9	-8.5
PA2557	AMP-binding protein	-148.6	-7.2
PA3169	methylthioribose-1-phosphate isomerase	-168.1	-7.4
argH	argininosuccinate lyase	-129.8	-7.0
PA1217	2-isopropylmalate synthase	-132.4	-7.0
spuI	glutamine synthetase	-2.1	-1.0
spuB	glutamine synthetase	-3.2	-1.7
phhC	aromatic amino acid aminotransferase	-2.8	-1.5
dapA	4-hydroxy-tetrahydrodipicolinate synthase	-206.0	-7.7
prpC	methylcitrate synthase	-204.1	-7.7
hisF1	imidazole glycerol phosphate synthase subunit HisF	-234.9	-7.9
hisB	imidazoleglycerol-phosphate dehydratase	-280.1	-8.1
metH	B12-dependent methionine synthase	-122.2	-6.9
aroB	3-dehydroquinate synthase	-327.2	-8.4
dapB	dihydrodipicolinate reductase	-129.1	-7.0
pheA	bifunctional chorismate mutase/prephenate dehydratase	-82.5	-6.4
cysM	cysteine synthase B	-180.3	-7.5
pqsA	anthranilate--CoA ligase	-4.9	-2.3
PA2402	peptide synthase	-6.0	-2.6
ilvI	acetolactate synthase 3 catalytic subunit	-4.9	-2.3
PA3568	propionyl-CoA synthetase	-2.0	-1.0
pvdD	pyoverdine synthetase D	-2.4	-1.2
argB	acetylglutamate kinase	-199.9	-7.6
trpA	tryptophan synthase subunit alpha	-112.2	-6.8
PA1742	amidotransferase	-250.5	-8.0
phnB	anthranilate synthase component II	-600.6	-9.2
PA2555	AMP-binding protein	-217.1	-7.8
lysC	aspartokinase	-4.9	-2.3
pyrH	uridylate kinase	-122.7	-6.9
Cellular amino acid catabolic process		**FC**	**log FC**
gdhA	glutamate dehydrogenase	-67.7	-6.1
mmsB	3-hydroxyisobutyrate dehydrogenase	-142.9	-7.2
hmgA	homogentisate 1,2-dioxygenase	-2.4	-1.3
bkdA2	2-oxoisovalerate dehydrogenase subunit beta	-3.3	-1.7
accD	acetyl-CoA carboxylase carboxyl transferase subunit beta	-414.9	-8.7
gdhB	NAD-specific glutamate dehydrogenase	-4.1	-2.0
prpC	methylcitrate synthase	-204.1	-7.7
ldh	leucine dehydrogenase	-88.3	-6.5
PA3471	NAD-dependent malic enzyme	-71.4	-6.2
gcvP1	glycine dehydrogenase	-4.1	-2.0
aruB	N-succinylarginine dihydrolase	-2.4	-1.3
aruG	arginine N-succinyltransferase subunit beta	-531.1	-9.1
sdhD	succinate dehydrogenase subunit D	-981.5	-9.9
Cellular amino acid biosynthetic metabolic process (upregulated genes)		**FC**	**log FC**
PA2040	glutamine synthetase	2.5	1.3
hisG	ATP phosphoribosyltransferase	2.4	1.3
PA1750	phospho-2-dehydro-3-deoxyheptonate aldolase	103.3	6.7
PA1729	hypothetical protein	686.5	9.4
aroC	chorismate synthase	2.5	1.3
PA4344	hydrolase	182.2	7.5
PA0006	D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase	207.1	7.7
acsB	acetyl-CoA synthetase	2.5	1.3
mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	205.4	7.7
hisE	phosphoribosyl-ATP pyrophosphatase	1324.0	10.4
pchD	pyochelin biosynthesis protein PchD	135.3	7.1
hisF2	imidazole glycerol phosphate synthase subunit HisF	2.3	1.2
spuA	glutamine amidotransferase	636.2	9.3
spuH	polyamine transporter PotI	255.7	8.0
ilvE	branched-chain amino acid aminotransferase	4.9	2.3

PA4960	phosphoserine phosphatase	86.2	6.4
ilvD	dihydroxy-acid dehydratase	3.7	1.9
glnA	glutamine synthetase	7.0	2.8
wbpL	glycosyltransferase WbpL	2.4	1.3
PA3356	hypothetical protein	89.5	6.5
gltB	glutamate synthase subunit alpha	3.7	1.9
PA4078	nonribosomal peptide synthetase	3.7	1.9
Cellular amino acid catabolic process		**FC**	**log FC**
PA5046	malic enzyme	2.7	1.4
kynA	tryptophan 2,3-dioxygenase	256.6	8.0
PA4150	dehydrogenase E1 component	228.1	7.8
hcnC	hydrogen cyanide synthase subunit HcnC	177.4	7.5
PA0534	hypothetical protein	344.9	8.4
aruF	arginine N-succinyltransferase subunit alpha	218.7	7.8
accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	233.9	7.9
fahA	fumarylacetoacetase	171.2	7.4
mqoB	malate:quinone oxidoreductase	146.0	7.2
gcvP2	glycine dehydrogenase	231.7	7.9
Fatty acid metabolic process (downregulated genes)		**FC**	**Log FC**
pvdL	peptide synthase	-142.4	-7.2
PA1737	3-hydroxyacyl-CoA dehydrogenase	-337.7	-8.4
pvdJ	pyoverdine biosynthesis protein PvdJ	-3.5	-1.8
PA2557	AMP-binding protein	-148.6	-7.2
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-74.0	-6.2
pqsC	hypothetical protein	-345.9	-8.4
PA1869	acyl carrier protein	-95.2	-6.6
PA5436	acetyl-CoA carboxylase subunit A	-511.6	-9.0
PA2815	acyl-CoA dehydrogenase	-148.0	-7.2
kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	-107.0	-6.7
fadD1	long-chain-fatty-acid--CoA ligase	-4.1	-2.0
PA2475	cytochrome P450	-135.7	-7.1
accD	acetyl-CoA carboxylase carboxyl transferase subunit beta	-414.9	-8.7
PA2550	acyl-CoA dehydrogenase	-147.2	-7.2
PA2552	acyl-CoA dehydrogenase	-115.8	-6.9
fabB	3-oxoacyl-ACP synthase	-184.2	-7.5
fabA	3-hydroxydecanoyl-ACP dehydratase	-351.0	-8.5
PA1535	acyl-CoA dehydrogenase	-157.6	-7.3
PA3286	beta-ketodecanoyl-[acyl-carrier-protein] synthase	-258.0	-8.0
PA4435	acyl-CoA dehydrogenase	-79.0	-6.3
PA2552	acyl-CoA dehydrogenase	-115.8	-6.9
PA5445	coenzyme A transferase	-242.4	-7.9
pqsA	anthranilate--CoA ligase	-4.9	-2.3
PA2402	peptide synthase	-6.0	-2.6
PA3568	propionyl-CoA synthetase	-2.0	-1.0
PA1821	enoyl-CoA hydratase	-445.5	-8.8
pvdD	pyoverdine synthetase D	-2.4	-1.2
PA4615	oxidoreductase	-466.1	-8.9
PA0508	acyl-CoA dehydrogenase	-101.8	-6.7
PA2555	AMP-binding protein	-217.1	-7.8
Phospholipid metabolic process		**FC**	**Log FC**
glmU	bifunctional glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	-66.3	-6.1
Steriod metabolic process			
PA3957	short-chain dehydrogenase	-230.9	-7.9
PA2099	short-chain dehydrogenase	-239.5	-7.9
PA1470	short-chain dehydrogenase	-245.4	-7.9
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-74.0	-6.2
PA4361	oxidoreductase	-2.1	-1.1
PA3330	short-chain dehydrogenase	-197.9	-7.6

gmd	GDP-mannose 4,6-dehydratase	-186.3	-7.5
rmd	oxidoreductase Rmd GDP-6-deoxy-D-mannose reductase	-99.0	-6.6
arnA	bifunctional UDP-glucuronic acid decarboxylase/UDP-4-amino-4-deoxy-L-arabinose formyltransferase	-91.0	-6.5
PA4786	3-ketoacyl-ACP reductase	-133.6	-7.1
PA4615	oxidoreductase	-466.1	-8.9
rmlB	dTDP-D-glucose 4,6-dehydratase	-61.3	-5.9
PA4079	short-chain dehydrogenase	-189.6	-7.6
betC	choline sulfatase	-59.9	-5.9
PA3727	hypothetical protein	-130.7	-7.0
	Fatty acid metabolic process (upregulated genes)	**FC**	**Log FC**
PA1022	acyl-CoA dehydrogenase	388.2	8.6
PA5020	acyl-CoA dehydrogenase	123.4	6.9
acsB	acetyl-CoA synthetase	2.5	1.3
gbcA	protein GbcA	172.4	7.4
pchD	pyochelin biosynthesis protein PchD	135.3	7.1
atuD	citronellyl-CoA dehydrogenase	191.6	7.6
etfA	electron transfer flavoprotein subunit alpha	3.1	1.6
fadD2	long-chain-fatty-acid--CoA ligase	287.6	8.2
fabF1	3-oxoacyl-ACP synthase	178.7	7.5
PA3972	acyl-CoA dehydrogenase	67.4	6.1
accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	233.9	7.9
PA5174	beta-ketoacyl synthase	467.0	8.9
PA1829	hypothetical protein	30.2	4.9
PA4330	enoyl-CoA hydratase	519.2	9.0
accC	acetyl-CoA carboxylase biotin carboxylase subunit	164.8	7.4
PA4078	nonribosomal peptide synthetase	3.7	1.9
Phospholipid metabolic process		**FC**	**Log FC**
pssA	phosphatidylserine synthase	136.3	7.1
lpxB	lipid-A-disaccharide synthase	97.8	6.6
lpxD	UDP-3-O-acylglucosamine N-acyltransferase	2.1	1.0
PA1689	hypothetical protein	211.5	7.7
rmlA	glucose-1-phosphate thymidylyltransferase	26.3	4.7
PA0597	nucleotidyl transferase	329.5	8.4
Steriod metabolic process			
PA1897	hypothetical protein	9.8	3.3
PA5521	short-chain dehydrogenase	847.2	9.7
gbcB	protein GbcB; class 1	202.0	7.7
rfaD	ADP-L-glycero-D-manno-heptose-6-epimerase	222.7	7.8
PA4907	short-chain dehydrogenase	291.9	8.2
fabI	NADH-dependent enoyl-ACP reductase	139.4	7.1
PA2918	short-chain dehydrogenase	287.4	8.2
fabG	3-oxoacyl-[acyl-carrier-protein] reductase FabG	8.0	3.0
Generation of precursor metabolites and energy (downregulated genes)			
Tricarboxylic acid cycle		**FC**	**Log FC**
fumC1	fumarate hydratase	-3.0	-1.6
prpC	methylcitrate synthase	-204.1	-7.7
PA3471	NAD-dependent malic enzyme	-71.4	-6.2
Glycolysis		**FC**	**Log FC**
PA3001	glyceraldehyde-3-phosphate dehydrogenase	-194.7	-7.6
tpiA	triosephosphate isomerase	-3.3	-1.7
glk	glucokinase	-105.5	-6.7
Oxidative phosphorylation		**FC**	**Log FC**
PA1054	monovalent cation/H+ antiporter subunit A	-64.6	-6.0
nuoL	NADH-quinone oxidoreductase subunit L	-199.1	-7.6
ccoP1	cytochrome C oxidase cbb3-type subunit CcoP	-10.0	-3.3
ccoQ1	cytochrome C oxidase cbb3-type subunit CcoQ	-19.9	-4.3
ccoO1	cbb3-type cytochrome C oxidase subunit II	-4.8	-2.3
ccoN1	cbb3-type cytochrome C oxidase subunit I	-2.6	-1.4

nuoN	NADH-quinone oxidoreductase subunit N	-124.0	-7.0
coxB	cytochrome C oxidase subunit II	-16.0	-4.0
coxA	cytochrome C oxidase subunit I	-113.7	-6.8
Respiratory electron transport chain		**FC**	**Log FC**
PA1054	monovalent cation/H+ antiporter subunit A	-64.6	-6.0
nuoL	NADH-quinone oxidoreductase subunit L	-199.1	-7.6
etfB	electron transfer flavoprotein subunit beta	-4.4	-2.1
nuoE	NADH-quinone oxidoreductase subunit E	-2.7	-1.4
PA5568	inner membrane protein translocase subunit YidC	-7.9	-3.0
PA2575	hypothetical protein	-600.6	-9.2
gor	glutathione reductase	-667.8	-9.4
PA4140	hypothetical protein	-100.9	-6.7
ccoN1	cbb3-type cytochrome C oxidase subunit I	-2.6	-1.4
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-74.0	-6.2
spdH	spermidine dehydrogenase SpdH	-85.9	-6.4
ahpF	alkyl hydroperoxide reductase	-115.6	-6.9
ndh	NADH dehydrogenase	-276.9	-8.1
nosZ	nitrous-oxide reductase	-94.8	-6.6
PA1416	hypothetical protein	-109.0	-6.8
sth	soluble pyridine nucleotide transhydrogenase	-358.8	-8.5
ccoO1	cbb3-type cytochrome C oxidase subunit II	-4.8	-2.3
PA4615	oxidoreductase	-466.1	-8.9
coxB	cytochrome C oxidase subunit II	-16.0	-4.0
nuoN	NADH-quinone oxidoreductase subunit N	-124.0	-7.0
lpdV	branched-chain alpha-keto acid dehydrogenase complex dihydrolipoyl dehydrogenase	-561.4	-9.1
PA5349	rubredoxin reductase	-138.2	-7.1
coxA	cytochrome C oxidase subunit I	-113.7	-6.8
trxB2	thioredoxin reductase	-380.8	-8.6
	Generation of precursor metabolites and energy (upregulated genes)		
Tricarboxylic acid cycle		**FC**	**Log FC**
PA5046	malic enzyme	2.7	1.4
fumC2	fumarate hydratase	84.4	6.4
Glycolysis		**FC**	**Log FC**
epd	D-erythrose 4-phosphate dehydrogenase	418.9	8.7
PA5438	transcriptional regulator	2.0	1.0
pgk	phosphoglycerate kinase	191.1	7.6
PA3184	HTH-type transcriptional regulator	259.2	8.0
Oxidative phosphorylation		**FC**	**Log FC**
PA4133	cbb3-type cytochrome C oxidase subunit I	4.3	2.1
nadB	L-aspartate oxidase	345.1	8.4
cyoB	cytochrome o ubiquinol oxidase subunit I	112.5	6.8
nuoI	NADH-quinone oxidoreductase subunit I	405.2	8.7
PA0521	cytochrome C oxidase subunit	327.3	8.4
nuoH	NADH-quinone oxidoreductase subunit H	223.3	7.8
ccoO2	cbb3-type cytochrome C oxidase subunit II	730.5	9.5
Respiratory electron transport chain		**FC**	**Log FC**
wbpA	UDP-N-acetyl-d-glucosamine 6-dehydrogenase	3.6	1.9
PA0421	hypothetical protein	129.4	7.0
rho	transcription termination factor Rho	176.5	7.5
PA4133	cbb3-type cytochrome C oxidase subunit I	4.3	2.1
nadB	L-aspartate oxidase	345.1	8.4
cioB	cyanide insensitive terminal oxidase	2.5	1.3
cyoB	cytochrome o ubiquinol oxidase subunit I	112.5	6.8
PA4100	dehydrogenase	132.4	7.0
nuoI	NADH-quinone oxidoreductase subunit I	405.2	8.7
gbcB	protein GbcB	202.0	7.7
hcnC	hydrogen cyanide synthase subunit HcnC	177.4	7.5
PA0534	hypothetical protein	344.9	8.4

PA2691	hypothetical protein	118.9	6.9
PA0317	hypothetical protein	159.4	7.3
PA0918	cytochrome b561	130.2	7.0
PA0521	cytochrome C oxidase subunit	327.3	8.4
nuoH	NADH-quinone oxidoreductase subunit H	223.3	7.8
trxB1	thioredoxin reductase	2.5	1.3
betA	choline dehydrogenase	131.9	7.0
mqoB	malate:quinone oxidoreductase	146.0	7.2
PA0364	oxidoreductase	69.7	6.1
ccoO2	cbb3-type cytochrome C oxidase subunit II	730.5	9.5
Antioxidant activity		**FC**	**Log FC**
KatB	catalase	144.2	7.2
PA0848	alkyl hydroperoxide reductase	67.0	6.1
PA4371	hypothetical protein	156.4	7.3
tpx	thiol peroxidase	223.3	7.8
ccpR	cytochrome C551 peroxidase	3.7	1.9

Table S13 Differential expression of the metabolic genes in response to Ag^+.

Response to stimulus (downregulated genes)		**FC**	**log FC**
PA4142	secretion protein	-26.9	-4.8
PA4135	transcriptional regulator	-80.0	-6.3
htpG	chaperone protein HtpG	-2.4	-1.2
PA1068	heat shock protein	-17.7	-4.1
lrp	leucine-responsive regulatory protein	-66.5	-6.1
mutS	DNA mismatch repair protein MutS	-79.1	-6.3
ospR	transcriptional regulator	-34.4	-5.1
PA2548	hypothetical protein	-24.3	-4.6
recC	exodeoxyribonuclease V subunit gamma	-14.4	-3.9
PA1285	transcriptional regulator	-75.2	-6.2
katE	catalase HPII	-15.9	-4.0
PA3468	hypothetical protein	-25.5	-4.7
PA4010	3-methyladenine DNA glycosylase	-47.0	-5.6
recQ	ATP-dependent DNA helicase	-63.3	-6.0
msrA	peptide methionine sulfoxide reductase	-52.2	-5.7
PA5022	potassium efflux protein KefA	-10.1	-3.3
PA3523	(RND) efflux membrane fusion protein	-73.1	-6.2
mexE	(RND) multidrug efflux membrane fusion protein	-81.6	-6.3
snr1	cytochrome C Snr1	-12.1	-3.6
PA3304	hypothetical protein	-39.5	-5.3
rhdA	thiosulfate:cyanide sulfurtransferase	-41.5	-5.4
PA3489	electron transport complex subunit A	-57.9	-5.9
PA1882	transporter	-104.5	-6.7
sdsA1	SDS hydrolase SdsA1	-17.1	-4.1
fliM	flagellar motor switch protein FliM	-209.0	-7.7
soxR	redox-sensitive transcriptional activator	-35.9	-5.2
cyaB	protein CyaB	-97.3	-6.6
mexA	multidrug resistance protein MexA	-216.5	-7.8
PA2915	hypothetical protein	-39.0	-5.3
Response to stimulus (upregulated genes)		**FC**	**log FC**
amtB	ammonium transporter	8.1	3.0
mutL	DNA mismatch repair protein	32.6	5.0
PA0942	transcriptional regulator	10.4	3.4
PA3341	transcriptional regulator	259.3	8.0
PA4061	thioredoxin	3.3	1.7
PA4701	hypothetical protein	2.2	1.1
PA2827	methionine sulfoxide reductase B	6.8	2.8
ruvC	crossover junction endodeoxyribonuclease RuvC	6.6	2.7
PA3458	transcriptional regulator	469.3	8.9
PA4606	hypothetical protein	5.5	2.4
PA4371	hypothetical protein	156.4	7.3
PA4562	hypothetical protein (Putative lipid II flippase MurJ)	7.5	2.9
PA0397	cation efflux system protein	494.3	8.9
PA3818	type III secretion system regulator SuhB	3.4	1.8
ccpR	cytochrome C551 peroxidase	2.8	1.5
PA4701	hypothetical protein	2.2	1.1

aprE	alkaline protease secretion protein AprE	342.5	8.4
pslL	hypothetical protein	159.6	7.3
PA0485	hypothetical protein	233.9	7.9
PA2024	ring-cleaving dioxygenase	314.6	8.3
RNA metabolic process (downregulated genes)		**FC**	**log FC**
gatC	aspartyl/glutamyl-tRNA amidotransferase subunit C	-177.9	-7.5
gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	-187.3	-7.5
PA4135	transcriptional regulator	-80.0	-6.3
rpsK	30S ribosomal protein S11	-4.4	-2.1
tyrZ	tyrosine--tRNA ligase	-3.0	-1.6
leuS	leucine--tRNA ligase	-4.2	-2.1
capB	major cold shock protein CspA	-2.5	-1.3
micA	tRNA (guanine-N(7)-)-methyltransferase	-151.1	-7.2
lrp	leucine-responsive regulatory protein	-66.5	-6.1
gbdR	protein GbdR	-30.7	-4.9
ospR	transcriptional regulator	-34.4	-5.1
PA1866	hypothetical protein	-14.9	-3.9
argS	arginine--tRNA ligase	-32.7	-5.0
PA4936	rRNA methylase	-45.6	-5.5
gcp	tRNA N6-adenosine threonylcarbamoyltransferase	-49.0	-5.6
PA2270	transcriptional regulator	-57.3	-5.8
PA1285	transcriptional regulator	-75.2	-6.2
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-37.0	-5.2
PA3179	ribosomal large subunit pseudouridine synthase B	-14.6	-3.9
glnS	glutamine--tRNA ligase	-2.1	-1.1
cca	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase	-27.5	-4.8
rpsI	30S ribosomal protein S9	-3.1	-1.6
PA3727	hypothetical protein	-154.1	-7.3
PA3614	hypothetical protein	-322.4	-8.3
PA1839	RNA methyltransferase	-32.5	-5.0
PA1264	transcriptional regulator	-19.5	-4.3
ptxS	transcriptional regulator PtxS	-33.1	-5.0
rph	ribonuclease PH	-47.0	-5.6
PA5019	Ribosomal RNA large subunit methyltransferase J rlmJ	-40.4	-5.3
mvfR	transcriptional regulator MvfR	-16.9	-4.1
PA3626	tRNA pseudouridine synthase D	-16.7	-4.1
PA3466	ATP-dependent RNA helicase	-12.6	-3.7
PA4939	ATP phosphoribosyltransferase	-207.2	-7.7
trmU	tRNA-specific 2-thiouridylase MnmA	-60.0	-5.9
PA3272	ATP-dependent DNA helicase	-3.9	-2.0
PA0167	transcriptional regulator	-50.8	-5.7
pcnB	poly(A) polymerase	-121.2	-6.9
PA4341	transcriptional regulator	-43.9	-5.5
ksgA	ribosomal RNA small subunit methyltransferase A rsmA	-41.9	-5.4
PA4358	ferrous iron transporter B	-25.2	-4.7
fmt	methionyl-tRNA formyltransferase	-17.9	-4.2
ileS	isoleucine--tRNA ligase	-8.7	-3.1
PA2834	transcriptional regulator	-11.2	-3.5
PA1015	transcriptional regulator	-63.4	-6.0
PA0976	7-cyano-7-deazaguanine synthase	-50.2	-5.6
hisS	histidine--tRNA ligase	-245.0	-7.9
PA3297	ATP-dependent helicase	-29.8	-4.9
PA0243	transcriptional regulator	-101.2	-6.7
soxR	redox-sensitive transcriptional activator SoxR	-35.9	-5.2
proS	proline--tRNA ligase	-59.2	-5.9
PA1045	ATP-dependent DNA helicase DinG	-15.8	-4.0
pheS	phenylalanine--tRNA ligase subunit alpha	-235.3	-7.9
PA0225	transcriptional regulator	-114.0	-6.8
rbsR	ribose operon repressor RbsR	-33.4	-5.1
PA1197	NAD-dependent protein deacylase	-65.8	-6.0
PA1467	hypothetical protein	-34.8	-5.1
PA0370	hypothetical protein	-56.7	-5.8
PA5079	D-tyrosyl-tRNA(Tyr) deacylase	-96.3	-6.6
PA4580	hypothetical protein	-43.8	-5.5
PA3961	ATP-dependent helicase	-6.7	-2.7
PA0048	transcriptional regulator	-36.7	-5.2
glpR	glycerol-3-phosphate regulon repressor	-44.8	-5.5
PA3817	methyltransferase	-22.6	-4.5
wbpI	UDP-2,3-diacetamido-2,3-dideoxy-D-glucuronate 2-epimeras	-9.0	-3.2
RNA metabolic process (upregulated genes)		**FC**	**log FC**
cspD	cold-shock protein CspD	6.2	2.6
PA1290	transcriptional regulator	7.0	2.8
PA1380	transcriptional regulator	230.3	7.8
rnhA	ribonuclease HI	2.2	1.1
PA0535	transcriptional regulator	3.5	1.8

glnD	bifunctional uridylyltransferase/uridylyl-removing protein	5.3	2.4
pheT	phenylalanine--tRNA ligase subunit beta	3.0	1.6
PA1879	hypothetical protein	200.4	7.6
cdhR	CdhR family transcriptional regulator	220.0	7.8
PA5157	transcriptional regulator	472.3	8.9
PA0218	transcriptional regulator	121.7	6.9
recG	ATP-dependent DNA helicase RecG	4.1	2.0
metG	methionine--tRNA ligase	2.2	1.1
PA1826	transcriptional regulator	122.8	6.9
rpoS	RNA polymerase sigma factor RpoS	5.8	2.5
PA0942	transcriptional regulator	10.4	3.4
PA3341	transcriptional regulator	259.3	8.0
argR	transcriptional regulator ArgR	2.2	1.1
PA3678	transcriptional regulator	235.2	7.9
rluC	ribosomal large subunit pseudouridine synthase C	4.6	2.2
PA1630	transcriptional regulator	19.7	4.3
PA0436	transcriptional regulator	9.7	3.3
PA5492	ribosome biogenesis GTP-binding protein YsxC	3.2	1.7
PA1135	molecular chaperone Hsp31/glyoxalase	253.9	8.0
PA2846	transcriptional regulator	3.3	1.7
PA1836	transcriptional regulator	6.2	2.6
PA3174	transcriptional regulator	305.1	8.3
glmR	GlmR transcriptional regulator	6.6	2.7
PA5301	transcriptional regulator	4.8	2.3
rpoH	RNA polymerase sigma factor RpoH	2.4	1.3
PA5567	tRNA modification GTPase TrmE	162.6	7.3
rnc	ribonuclease III	6.2	2.6
PA2121	transcriptional regulator	122.8	6.9
PA3458	transcriptional regulator	469.3	8.9
rluD	pseudouridine synthase	115.5	6.9
valS	valine--tRNA ligase	2.2	1.1
PA5048	nuclease	2.4	1.3
tgt	queuine tRNA-ribosyltransferase	2.7	1.5
era	GTPase Era	2.2	1.1
PA0456	cold-shock protein	2.1	1.1
DNA metabolic process (downregulated genes)		**FC**	**log FC**
holB	DNA polymerase III subunit delta	-19.7	-4.3
PA3198	hypothetical protein	-22.5	-4.5
PA0728	bacteriophage integrase	-34.4	-5.1
xseA	exodeoxyribonuclease VII large subunit	-24.5	-4.6
parE	DNA topoisomerase IV subunit B	-35.8	-5.2
parC	DNA topoisomerase IV subunit A	-62.0	-6.0
polA	DNA polymerase I	-49.4	-5.6
mutS	DNA mismatch repair protein MutS	-79.1	-6.3
PA1866	hypothetical protein	-14.9	-3.9
PA2959	hypothetical protein	-54.6	-5.8
uvrC	excinuclease ABC subunit C	-37.1	-5.2
recD	exodeoxyribonuclease V subunit alpha	-15.6	-4.0
recB	exodeoxyribonuclease V subunit beta	-27.2	-4.8
recC	exodeoxyribonuclease V subunit gamma	-14.4	-3.9
PA5201	hypothetical protein	-43.4	-5.4
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-37.0	-5.2
recN	DNA repair protein RecN	-40.4	-5.3
PA0242	hypothetical protein	-17.8	-4.2
PA4010	3-methyladenine DNA glycosylase	-47.0	-5.6
recQ	ATP-dependent DNA helicase RecQ	-63.3	-6.0
dnaN	DNA polymerase III subunit beta	-2.9	-1.5
PA1045	ATP-dependent DNA helicase DinG	-15.8	-4.0
PA0370	hypothetical protein	-56.7	-5.8
dnaX	DNA polymerase III subunits gamma/tau	-33.1	-5.0
ssb	single-stranded DNA-binding protein	-2.1	-1.1
DNA metabolic process (upregulated genes)		**FC**	**log FC**
dnaB	replicative DNA helicase	2.6	1.4
rnhA	ribonuclease HI	2.2	1.1
PA3867	DNA invertase	290.8	8.2
PA0947	DNA replication initiation factor	2.2	1.1
PA2823	hypothetical protein	4.4	2.1
PA1527	hypothetical protein Chromosome partition protein Smc	3.5	1.8
DNA repair		**FC**	**log FC**
PA4701	hypothetical protein	2.2	1.1
mutY	A/G specific adenine glycosylase;	2.7	1.4
ruvC	crossover junction endodeoxyribonuclease RuvC	6.6	2.7
ruvB	Holliday junction ATP-dependent DNA helicase RuvB	2.2	1.1
rnt	ribonuclease T	4.8	2.3
PA1865	Fanconi-associated nuclease	59.4	5.9
PA3172	phosphoglycolate phosphatase	5.7	2.5

mutL	DNA mismatch repair protein	32.6	5.0
Protein metabolic process (downregulated genes)			
	Cellular protein modification process	**FC**	**log FC**
PA1377	hypothetical protein	-176.7	-7.5
stp1	serine/threonine phosphoprotein phosphatase Stp1	-46.6	-5.5
pqsB	hypothetical protein	-124.3	-7.0
ptpA	phosphotyrosine protein phosphatase	-3.6	-1.8
PA4498	metallopeptidase	-27.8	-4.8
ggt	gamma-glutamyltranspeptidase	-50.6	-5.7
PA3853	transferase	-24.5	-4.6
lpxO1	lipopolysaccharide biosynthetic protein LpxO	-75.2	-6.2
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-37.0	-5.2
PA3717	FkbP-type peptidyl-prolyl cis-trans isomerase	-65.4	-6.0
PA4558	FkbP-type peptidyl-prolyl cis-trans isomerase	-260.9	-8.0
pepP	aminopeptidase	-139.5	-7.1
PA1062	hypothetical protein	-64.9	-6.0
uppS	ditrans,polycis-undecaprenyl-diphosphate synthase	-129.9	-7.0
algI	alginate o-acetylase AlgI	-21.7	-4.4
glmS	glucosamine--fructose-6-phosphate aminotransferase	-110.6	-6.8
fmt	methionyl-tRNA formyltransferase	-17.9	-4.2
PA3944	hypothetical protein	-56.0	-5.8
map	methionine aminopeptidase	-1069.8	-10.1
argE	acetylornithine deacetylase	-14.7	-3.9
lipB	lipoate-protein ligase B	-24.9	-4.6
PA5445	coenzyme A transferase	-61.5	-5.9
pqsD	2-heptyl-4(1H)-quinolone synthase PqsD	-200.3	-7.6
msrA	peptide methionine sulfoxide reductase	-52.2	-5.7
PA4785	acetyl-CoA acetyltransferase	-26.5	-4.7
PA1472	hypothetical protein	-82.6	-6.4
slyD	peptidyl-prolyl cis-trans isomerase SlyD	-3.4	-1.8
pcm	protein-L-isoaspartate O-methyltransferase	-133.1	-7.1
PA1428	hypothetical protein	-78.4	-6.3
PA4114	spermidine acetyltransferase	-98.2	-6.6
atoB	acetyl-CoA acetyltransferase	-32.3	-5.0
PA3262	FkbP-type peptidyl-prolyl cis-trans isomerase	-718.5	-9.5
PA3925	acyl-CoA thiolase	-28.8	-4.8
Ferredoxin metabolic process			
sth	soluble pyridine nucleotide transhydrogenase	-218.4	-7.8
lpdV	branched-chain alpha-keto acid dehydrogenase complex dihydrolipoyl dehydrogenase	-80.3	-6.3
PA5349	rubredoxin reductase;	-73.3	-6.2
trxB2	thioredoxin reductase	-278.7	-8.1
lpd3	dihydrolipoamide dehydrogenase	-24.1	-4.6
ahpF	alkyl hydroperoxide reductase	-226.7	-7.8
gor	glutathione reductase	-271.6	-8.1
nirB	assimilatory nitrite reductase large subunit	-6.9	-2.8
Protein complex assembly		**FC**	**logFC**
purB	adenylosuccinate lyase	-24.7	-4.6
PA3516	adenylosuccinate lyase	-11.7	-3.5
argH	argininosuccinate lyase	-24.3	-4.6
Protein folding		**FC**	**logFC**
htpG	chaperone protein HtpG	-2.4	-1.2
surA	chaperone SurA	-2.2	-1.1
PA3717	FkbP-type peptidyl-prolyl cis-trans isomerase	-65.4	-6.0
PA4558	FkbP-type peptidyl-prolyl cis-trans isomerase	-260.9	-8.0
slyD	peptidyl-prolyl cis-trans isomerase SlyD	-3.4	-1.8
PA1068	heat shock protein	-17.7	-4.1
mucD	serine protease MucD	-6.8	-2.8
PA3262	FkbP-type peptidyl-prolyl cis-trans isomerase	-718.5	-9.5
Proteolysis		**FC**	**log FC**
PA2286	hypothetical protein	-43.8	-5.5
PA4498	metallopeptidase	-27.8	-4.8
PA0277	hypothetical protein	-66.9	-6.1
ggt	gamma-glutamyltranspeptidase	-50.6	-5.7
pilD	type 4 prepilin peptidase PilD	-38.8	-5.3
pepP	aminopeptidase	-139.5	-7.1
PA5047	hypothetical protein	-54.1	-5.8
PA3764	membrane-bound lytic murein transglycosylase F	-49.8	-5.6
PA5133	hypothetical protein	-26.3	-4.7
prlC	oligopeptidase A	-49.6	-5.6
map	methionine aminopeptidase	-1069.8	-10.1
argE	acetylornithine deacetylase	-14.7	-3.9
PA2393	dipeptidase	-75.4	-6.2
PA4404	hypothetical protein	-13.6	-3.8
mucD	serine protease MucD	-6.8	-2.8

Translation		**FC**	**log FC**
infB	translation initiation factor IF-2	-6.4	-2.7
gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	-187.3	-7.5
PA1737	3-hydroxyacyl-CoA dehydrogenase	-63.1	-6.0
rpsM	30S ribosomal protein S13	-3.4	-1.7
rpsN	30S ribosomal protein S14	-3.5	-1.8
rpsK	30S ribosomal protein S11	-4.4	-2.1
rpsO	30S ribosomal protein S15	-2.0	-1.0
rpsD	30S ribosomal protein S4	-3.9	-2.0
leuS	leucine--tRNA ligase	-4.2	-2.1
PA4498	metallopeptidase	-27.8	-4.8
rpsQ	30S ribosomal protein S17	-2.8	-1.5
flhF	flagellar biosynthesis regulator FlhF	-26.2	-4.7
rplE	50S ribosomal protein L5	-3.0	-1.6
frr	ribosome recycling factor	-242.7	-7.9
rplD	50S ribosomal protein L4	-7.0	-2.8
rpsL	30S ribosomal protein S12	-2.8	-1.5
rplF	50S ribosomal protein L6	-4.7	-2.2
ftsY	signal recognition particle receptor FtsY	-20.9	-4.4
glnS	glutamine--tRNA ligase	-2.1	-1.1
rpsI	30S ribosomal protein S9	-3.1	-1.6
rimK	ribosomal protein S6 modification protein	-37.4	-5.2
typA	regulatory protein TypA	-162.2	-7.3
pepP	aminopeptidase	-139.5	-7.1
rpsB	30S ribosomal protein S2	-2.4	-1.2
PA4939	ATP phosphoribosyltransferase	-207.2	-7.7
rpsP	30S ribosomal protein S16	-1481.4	-10.5
uppS	ditrans,polycis-undecaprenyl-diphosphate synthase	-129.9	-7.0
ffh	signal recognition particle protein Ffh	-221.2	-7.8
algI	alginate o-acetylase AlgI	-21.7	-4.4
PA4358	ferrous iron transporter B	-25.2	-4.7
rplW	50S ribosomal protein L23	-9.8	-3.3
fmt	methionyl-tRNA formyltransferase	-17.9	-4.2
ileS	isoleucine--tRNA ligase	-8.7	-3.1
rplK	50S ribosomal protein L11	-2.9	-1.5
aspS	aspartate--tRNA ligase	-597.2	-9.2
rplM	50S ribosomal protein L13	-4.3	-2.1
hisS	histidine--tRNA ligase	-245.0	-7.9
map	methionine aminopeptidase	-1069.8	-10.1
proS	proline--tRNA ligase	-59.2	-5.9
pheS	phenylalanine--tRNA ligase subunit alpha	-235.3	-7.9
rpsG	30S ribosomal protein S7	-2.4	-1.2
PA5079	D-tyrosyl-tRNA(Tyr) deacylase	-96.3	-6.6
lysS	lysine--tRNA ligase	-78.7	-6.3
PA2106	hypothetical protein	-93.6	-6.5
rplX	50S ribosomal protein L24	-5.0	-2.3
argS	arginine--tRNA ligase	-32.7	-5.0
rplB	50S ribosomal protein L2	-7.0	-2.8
PA4163	amidase	-17.8	-4.2
Protein metabolic process (upregulated genes)			
Cellular protein modification process		**FC**	**log FC**
PA3945	hypothetical protein	8.3	3.1
PA2578	acetyltransferase	396.5	8.6
PA4344	hydrolase	182.2	7.5
PA0483	acetyltransferase	501.0	9.0
PA2827	methionine sulfoxide reductase B msrB	6.8	2.8
pppA	serine/threonine phosphatase	305.1	8.3
PA0164	gamma-glutamyltranspeptidase	137.6	7.1
PA2103	molybdopterin biosynthesis protein MoeB	3.3	1.7
PA0916	ribosomal protein S12 methylthiotransferase RimO	4.9	2.3
cysE	O-acetylserine synthase	5.2	2.4
PA3368	acetyltransferase	105.5	6.7
murG	undecaprenyldiphospho-muramoylpentapeptidebeta-N-acetylglucosaminyltransferase	2.1	1.1
cat	chloramphenicol acetyltransferase	12.4	3.6
Ferredoxin metabolic process		**FC**	**log FC**
PA2691	hypothetical protein	8.2	3.0
trxB1	thioredoxin reductase	3.3	1.7
hcnB	hydrogen cyanide synthase subunit HcnB	3.3	1.7
Protein complex assembly		**FC**	**log FC**
dipZ	thiol:disulfide interchange protein	125.2	7.0
fumC2	fumarate hydratase	84.4	6.4
Protein folding		**FC**	**log FC**
ppiC2	peptidyl-prolyl cis-trans isomerase C2	1059.9	10.0
PA4061	thioredoxin	3.3	1.7
Proteolysis		**FC**	**log FC**

PA3020	lytic transglycosylase	2.2	1.1
PA4344	hydrolase	182.2	7.5
htpX	protease HtpX	2.8	1.5
lasA	protease LasA	7.4	2.9
PA3047	D-alanyl-D-alanine carboxypeptidase	3.0	1.6
PA5396	hypothetical protein	3.3	1.7
PA3623	hypothetical protein	5.5	2.5
PA0164	gamma-glutamyltranspeptidase	137.6	7.1
PA1304	oligopeptidase	54.2	5.8
Translation		**FC**	**log FC**
pheT	phenylalanine--tRNA ligase subunit beta	3.0	1.6
gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	6.6	2.7
metG	methionine--tRNA ligase	2.2	1.1
PA4005	hypothetical protein	2.1	1.1
PA5492	ribosome biogenesis GTP-binding protein YsxC	3.2	1.7
PA5567	tRNA modification GTPase TrmE	162.6	7.3
valS	valine--tRNA ligase	2.2	1.1
gshB	glutathione synthetase	2.6	1.4
era	GTPase Era	2.2	1.1
Cellular amino acid metabolic process (downregulated genes)			
Cellular amino acid biosynthetic process		**FC**	**log FC**
leuB	3-isopropylmalate dehydrogenase	-260.3	-8.0
leuD	isopropylmalate isomerase small subunit	-26.5	-4.7
leuC	isopropylmalate isomerase large subunit	-151.4	-7.2
dsdA	D-serine dehydratase	-25.1	-4.7
thrC	threonine synthase	-36.0	-5.2
aroK	shikimate kinase	-32.6	-5.0
argG	argininosuccinate synthase	-384.2	-8.6
hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino] imidazole-4-carboxamide isomerase	-43.3	-5.4
speA	arginine decarboxylase	-44.3	-5.5
phzH	phenazine-modifying protein	-55.4	-5.8
pyrH	uridylate kinase	-41.1	-5.4
hisB	imidazoleglycerol-phosphate dehydratase	-49.4	-5.6
PA1750	phospho-2-dehydro-3-deoxyheptonate aldolase	-3.7	-1.9
prpC	methylcitrate synthase	-16.9	-4.1
prpB	2-methylisocitrate lyase	-18.9	-4.2
PA5313	omega amino acid--pyruvate transaminase	-25.4	-4.7
PA1576	3-hydroxyisobutyrate dehydrogenase	-78.1	-6.3
PA2557	AMP-binding protein	-10.0	-3.3
phnB	anthranilate synthase component II	-112.3	-6.8
dauB	NAD(P)H-dependent anabolic L-arginine dehydrogenase DauB	-35.7	-5.2
pheA	bifunctional chorismate mutase/prephenate dehydratase	-165.7	-7.4
pqsA	anthranilate--CoA ligase	-24.1	-4.6
PA3255	hypothetical protein	-52.5	-5.7
PA0743	NAD-dependent L-serine dehydrogenase	-18.9	-4.2
hom	homoserine dehydrogenase	-51.9	-5.7
proA	gamma-glutamyl phosphate reductase	-26.9	-4.7
carA	carbamoyl phosphate synthase small subunit	-125.5	-7.0
ilvH	acetolactate synthase 3 regulatory subunit	-299.2	-8.2
trpC	indole-3-glycerol phosphate synthase	-2.4	-1.3
serC	phosphoserine aminotransferase	-109.1	-6.8
guaA	GMP synthase	-21.5	-4.4
argH	argininosuccinate lyase	-24.3	-4.6
argF	ornithine carbamoyltransferase	-36.9	-5.2
dapA	4-hydroxy-tetrahydrodipicolinate synthase	-181.4	-7.5
PA0266	5-aminovalerate aminotransferase DavT	-57.7	-5.9
dapB	dihydrodipicolinate reductase	-54.5	-5.8
argE	acetylornithine deacetylase	-14.7	-3.9
hisH1	imidazole glycerol phosphate synthase subunit HisH	-45.1	-5.5
trpD	anthranilate phosphoribosyltransferase	-225.7	-7.8
pvdL	peptide synthase	-5.2	-2.4
bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	-24.1	-4.6
PA1217	2-isopropylmalate synthase	-74.2	-6.2
hisF2	imidazole glycerol phosphate synthase subunit HisF	-231.8	-7.9
cysM	cysteine synthase B	-371.9	-8.5
argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	-48.0	-5.6
trpG	anthranilate synthase component II	-34.9	-5.1
PA2555	AMP-binding protein	-10.7	-3.4
lysC	aspartokinase	-5.1	-2.4
PA4180	acetolactate synthase	-20.6	-4.4
PA1997	acetoacetyl-CoA synthetase	-8.7	-3.1
ilvI	acetolactate synthase 3 catalytic subunit	-4.1	-2.0
PA3169	methylthioribose-1-phosphate isomerase	-119.4	-6.9
PA1089	hypothetical protein	-72.1	-6.2

metH	B12-dependent methionine synthase	-105.1	-6.7
selD	selenide, water dikinase	-65.4	-6.0
aruC	bifunctional succinylornithine transaminase/acetylornithine aminotransferase	-55.4	-5.8
trpF	N-(5'-phosphoribosyl)anthranilate isomerase	-61.9	-6.0
trpB	tryptophan synthase subunit beta	-26.4	-4.7
edd	phosphogluconate dehydratase	-55.6	-5.8
hisI	phosphoribosyl-AMP cyclohydrolase	-588.1	-9.2
hisF1	imidazole glycerol phosphate synthase subunit HisF	-22.0	-4.5
acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	-2.5	-1.3
PA5508	glutamine synthetase	-25.4	-4.7
aroB	3-dehydroquinate synthase	-91.7	-6.5
Cellular amino acid catabolic process		**FC**	**log FC**
mqoA	malate:quinone oxidoreductase	-48.0	-5.6
accD	acetyl-CoA carboxylase carboxyl transferase subunit beta	-283.9	-8.1
dxs	1-deoxy-D-xylulose-5-phosphate synthase	-71.9	-6.2
prpC	methylcitrate synthase	-16.9	-4.1
PA1576	3-hydroxyisobutyrate dehydrogenase	-78.1	-6.3
PA0743	NAD-dependent L-serine dehydrogenase	-18.9	-4.2
PA2317	oxidoreductase	-26.1	-4.7
gcvT1	glycine cleavage system aminomethyltransferase T	-140.7	-7.1
dadA1	D-amino acid dehydrogenase small subunit	-105.8	-6.7
gdhB	NAD-specific glutamate dehydrogenase	-4.3	-2.1
PA3471	NAD-dependent malic enzyme	-39.9	-5.3
PA5309	oxidoreductase	-51.3	-5.7
tktA	transketolase	-203.4	-7.7
gcvT2	glycine cleavage system protein T2	-15.1	-3.9
PA4548	D-amino acid oxidase	-61.8	-6.0
liuB	methylcrotonyl-CoA carboxylase subunit beta	-73.7	-6.2
pta	phosphate acetyltransferase	-96.0	-6.6
hutI	imidazolonepropionase	-28.0	-4.8
Cellular amino acid metabolic process (upregulated genes)			
Cellular amino acid biosynthetic metabolic process		**FC**	**log FC**
PA3356	hypothetical protein	3.1	1.6
mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	205.4	7.7
PA1296	2-hydroxyacid dehydrogenase	5.9	2.6
PA3568	propionyl-CoA synthetase	117.9	6.9
wbpL	glycosyltransferase WbpL	3.9	2.0
aroC	chorismate synthase	407.4	8.7
proB	gamma-glutamyl kinase	2.8	1.5
hemL	glutamate-1-semialdehyde aminotransferase	3.1	1.6
PA5523	aminotransferase	246.6	7.9
hisE	phosphoribosyl-ATP pyrophosphatase	4.3	2.1
PA3327	non-ribosomal peptide synthetase	3.1	1.6
leuA	2-isopropylmalate synthase	3.9	2.0
PA4078	nonribosomal peptide synthetase	224.2	7.8
serA	D-3-phosphoglycerate dehydrogenase	2.1	1.0
PA2040	glutamine synthetase	17.4	4.1
pvdJ	pyoverdine biosynthesis protein PvdJ	3.8	1.9
pvdD	pyoverdine synthetase D	2.2	1.2
spuA	glutamine amidotransferase	5.5	2.5
liuE	3-hydroxy-3-isohexenylglutaryl-CoA/hydroxy- methylglutaryl-CoA lyase	7.4	2.9
liuA	isovaleryl-CoA dehydrogenase	3.0	1.6
liuR	liu genes regulator	3.4	1.8
PA2402	peptide synthase	2.0	1.0
PA4344	hydrolase	182.2	7.5
speC	ornithine decarboxylase	2.2	1.1
PA2104	cysteine synthase	2.3	1.2
pchD	pyochelin biosynthesis protein PchD	135.3	7.1
lysA	diaminopimelate decarboxylase	13.1	3.7
ilvD	dihydroxy-acid dehydratase	362.9	8.5
PA1729	hypothetical protein	686.5	9.4
PA0006	D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase	3.3	1.7
Cellular amino acid catabolic process		**FC**	**log FC**
gcvP1	glycine dehydrogenase	6.6	2.7
glyA2	serine hydroxymethyltransferase	88.5	6.5
gcvP2	glycine dehydrogenase	13.1	3.7
ltaA	low specificity l-threonine aldolase	3.5	1.8
hmgA	homogentisate 1,2-dioxygenase	6.6	2.7
fahA	fumarylacetoacetase	6.6	2.7
PA2776	hypothetical protein	3.3	1.7
hcnB	hydrogen cyanide synthase subunit HcnB	3.3	1.7
hcnC	hydrogen cyanide synthase subunit HcnC	3.3	1.7
accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	5.3	2.4
PA4150	dehydrogenase E1 component	228.1	7.8

PA0318	hypothetical protein	2.2	1.1
kynA	tryptophan 2,3-dioxygenase	256.6	8.0
aruF	arginine N-succinyltransferase subunit alpha	3.3	1.7
bkdA1	2-oxoisovalerate dehydrogenase subunit alpha	6.5	2.7
bkdB	branched-chain alpha-keto acid dehydrogenase complex lipoamide acyltransferase	4.4	2.1
bfmR	protein BfmR	6.6	2.7
	Fatty acid metabolic process (downregulated genes)	**FC**	**log FC**
PA3860	AMP-binding protein	-17.8	-4.2
PA3426	enoyl-CoA hydratase	-43.9	-5.5
PA2552	acyl-CoA dehydrogenase	-22.6	-4.5
fabB	3-oxoacyl-ACP synthase	-55.6	-5.8
fabA	3-hydroxydecanoyl-ACP dehydratase	-376.5	-8.6
PA5436	acetyl-CoA carboxylase subunit A	-116.8	-6.9
rplB	50S ribosomal protein L2	-7.0	-2.8
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-29.3	-4.9
PA0506	acyl-CoA dehydrogenase	-5.1	-2.3
accD	acetyl-CoA carboxylase carboxyl transferase subunit beta	-283.9	-8.1
PA1869	acyl carrier protein	-303.2	-8.2
PA5236	CDP-6-deoxy-delta-3,4-glucoseen reductase	-34.9	-5.1
PA2557	AMP-binding protein	-10.0	-3.3
PA1535	acyl-CoA dehydrogenase	-29.5	-4.9
PA1284	acyl-CoA dehydrogenase	-18.6	-4.2
pqsA	anthranilate--CoA ligase	-24.1	-4.6
fabF1	3-oxoacyl-ACP synthase	-2.1	-1.0
PA1631	acyl-CoA dehydrogenase	-29.3	-4.9
kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	-120.0	-6.9
liuD	methylcrotonyl-CoA carboxylase subunit alpha	-15.6	-4.0
pvdL	peptide synthase	-5.2	-2.4
PA1217	2-isopropylmalate synthase	-74.2	-6.2
PA0494	acetyl-CoA carboxylase biotin carboxylase subunit	-24.6	-4.6
PA2330	hypothetical protein	-31.7	-5.0
PA1737	3-hydroxyacyl-CoA dehydrogenase	-63.1	-6.0
PA2815	acyl-CoA dehydrogenase	-55.3	-5.8
PA2555	AMP-binding protein	-10.7	-3.4
PA1821	enoyl-CoA hydratase	-503.5	-9.0
PA0508	acyl-CoA dehydrogenase	-190.3	-7.6
PA0507	acyl-CoA dehydrogenase	-31.9	-5.0
ambB	protein AmbB	-7.8	-3.0
PA1997	acetoacetyl-CoA synthetase	-8.7	-3.1
faoA	fatty acid oxidation complex subunit alpha	-4.5	-2.2
PA1617	AMP-binding protein	-61.6	-5.9
PA1748	enoyl-CoA hydratase	-96.8	-6.6
PA4615	oxidoreductase	-65.4	-6.0
PA4435	acyl-CoA dehydrogenase	-206.8	-7.7
PA4995	acyl-CoA dehydrogenase	-12.2	-3.6
liuB	methylcrotonyl-CoA carboxylase subunit beta	-73.7	-6.2
PA0746	acyl-CoA dehydrogenase	-14.5	-3.9
PA3924	long-chain-fatty-acid--CoA ligase	-20.1	-4.3
fpr	ferredoxin-NADP reductase	-577.0	-9.2
fadD1	long-chain-fatty-acid--CoA ligase	-5.6	-2.5
	Phospholipid metabolic process	**FC**	**log FC**
pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	-58	-5.8
glmU	bifunctional glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	-24.8	-4.6
cdsA	phosphatidate cytidylyltransferase	-41.4	-5.3
betC	choline sulfatase	-11.1	-3.4
PA3727	hypothetical protein	-154.1	-7.2
PA5310	hypothetical protein	-21.2	-4.4
PA2536	phosphatidate cytidylyltransferase	-18.0	-4.1
cls	cardiolipin synthetase	-22.9	-4.5
galU	UTP-glucose-1-phosphate uridylyltransferase	-4.9	-2.3
PA1115	hypothetical protein	-7.2	-2.8
	Fatty acid metabolic process (upregulated genes)	**FC**	**log FC**
PA4979	acyl-CoA dehydrogenase	191.6	7.6
fadD2	long-chain-fatty-acid--CoA ligase	287.6	8.2
PA1022	acyl-CoA dehydrogenase	388.2	8.6
PA1221	hypothetical protein	119.8	6.9
PA4330	enoyl-CoA hydratase	16.3	4.0
PA3568	propionyl-CoA synthetase	117.9	6.9
PA5020	acyl-CoA dehydrogenase	123.4	6.9
ambE	protein AmbE	4.9	2.3
PA3327	non-ribosomal peptide synthetase	3.1	1.6
leuA	2-isopropylmalate synthase	3.9	2.0
PA5174	beta-ketoacyl synthase	3.8	1.9
PA0744	enoyl-CoA hydratase	3.3	1.7

PA4078	nonribosomal peptide synthetase	224.2	7.8
PA1829	hypothetical protein	30.2	4.9
atuD	citronellyl-CoA dehydrogenase	191.6	7.6
pvdD	pyoverdine synthetase D	2.2	1.2
pvdJ	pyoverdine biosynthesis protein PvdJ	3.8	1.9
PA2402	peptide synthase	2.0	1.0
pchF	pyochelin synthetase	61.4	5.9
gbcB	protein GbcB	202.0	7.7
pchD	pyochelin biosynthesis protein PchD	135.3	7.1
PA3972	acyl-CoA dehydrogenase	67.4	6.1
Generation of precursor metabolites and energy (downregulated genes)			
Respiratory electron transport chain		**FC**	**log FC**
PA2552	acyl-CoA dehydrogenase	-22.6	-4.5
PA1054	monovalent cation/H+ antiporter subunit A	-24.2	-4.6
PA2575	hypothetical protein	-19.9	-4.3
coxA	cytochrome C oxidase subunit I	-21.3	-4.4
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-29.3	-4.9
nqrD	Na(+)-translocating NADH-quinone reductase subunit D	-51.9	-5.7
nqrB	Na(+)-translocating NADH-quinone reductase subunit B	-83.8	-6.4
nqrA	Na(+)-translocating NADH-quinone reductase subunit A	-25.3	-4.7
PA0506	acyl-CoA dehydrogenase	-5.1	-2.3
PA5236	CDP-6-deoxy-delta-3,4-glucoseen reductase	-34.9	-5.1
PA5149	hypothetical protein	-4.9	-2.3
PA3559	nucleotide sugar dehydrogenase	-24.6	-4.6
ahpF	alkyl hydroperoxide reductase	-226.7	-7.8
nuoA	NADH-quinone oxidoreductase subunit A	-2.3	-1.2
nuoE	NADH-quinone oxidoreductase subunit E	-202.7	-7.7
nuoL	NADH-quinone oxidoreductase subunit L	-55.0	-5.8
nuoM	NADH-quinone oxidoreductase subunit M	-22.1	-4.5
PA1535	acyl-CoA dehydrogenase	-29.5	-4.9
PA1284	acyl-CoA dehydrogenase	-18.6	-4.2
PA1208	hypothetical protein	-22.6	-4.5
algD	GDP-mannose 6-dehydrogenase AlgD	-25.8	-4.7
sth	soluble pyridine nucleotide transhydrogenase	-218.4	-7.8
PA1631	acyl-CoA dehydrogenase	-29.3	-4.9
PA2317	oxidoreductase	-26.1	-4.7
ccoP1	cytochrome C oxidase cbb3-type subunit CcoP	-11.2	-3.5
ccoN1	cbb3-type cytochrome C oxidase subunit I	-2.1	-1.1
etfB	electron transfer flavoprotein subunit beta	-11.4	-3.5
PA2330	hypothetical protein	-31.7	-5.0
atpD	ATP synthase subunit beta	-2.6	-1.4
atpG	ATP synthase subunit gamma	-2.2	-1.1
atpA	ATP synthase subunit alpha	-3.2	-1.7
atpH	ATP synthase subunit delta	-8.0	-3.0
atpF	ATP synthase subunit B	-2.5	-1.3
atpB	ATP synthase subunit A	-3.5	-1.8
atpI	ATP synthase subunit I	-203.5	-7.7
PA5309	oxidoreductase	-51.3	-5.7
glcD	glycolate oxidase subunit GlcD	-11.3	-3.5
PA2815	acyl-CoA dehydrogenase	-55.3	-5.8
PA0508	acyl-CoA dehydrogenase	-190.3	-7.6
PA0507	acyl-CoA dehydrogenase	-31.9	-5.0
PA1538	flavin-containing monooxygenase	-10.7	-3.4
PA4140	hypothetical protein	-18.9	-4.2
PA5568	inner membrane protein translocase subunit YidC	-174.6	-7.4
PA0559	hypothetical protein	-14.4	-3.8
rho	transcription termination factor Rho	-3.0	-1.6
pntAA	NAD(P) transhydrogenase subunit alpha	-50.9	-5.7
katE	catalase HPII	-15.9	-4.0
PA5349	rubredoxin reductase;	-73.3	-6.2
PA2298	oxidoreductase	-19.6	-4.3
fliI	flagellum-specific ATP synthase	-25.0	-4.6
PA4615	oxidoreductase	-65.4	-6.0
PA4548	D-amino acid oxidase	-61.8	-6.0
PA4435	acyl-CoA dehydrogenase	-206.8	-7.7
gor	glutathione reductase	-271.6	-8.1
PA4995	acyl-CoA dehydrogenase	-12.2	-3.6
PA0746	acyl-CoA dehydrogenase	-14.5	-3.9
PA4692	sulfite oxidase subunit YedY	-66.8	-6.1
cyoA	cytochrome o ubiquinol oxidase subunit II	-68.0	-6.1
lpdV	branched-chain alpha-keto acid dehydrogenase complex dihydrolipoyl dehydrogenase	-80.3	-6.3
trxB2	thioredoxin reductase	-278.7	-8.1
lpd3	dihydrolipoamide dehydrogenase	-24.1	-4.6
fpr	ferredoxin-NADP reductase	-577.0	-9.2
nirB	assimilatory nitrite reductase large subunit	-6.9	-2.8

Generation of precursor metabolites and energy (upregulated genes)		FC	log FC
PA4979	acyl-CoA dehydrogenase	191.6	7.6
nuoB	NADH-quinone oxidoreductase subunit B	4.4	2.1
nuoF	NADH dehydrogenase I subunit F	2.2	1.1
nuoG	NADH-quinone oxidoreductase subunit G	19.0	4.2
nuoH	NADH-quinone oxidoreductase subunit H	223.3	7.8
nuoI	NADH-quinone oxidoreductase subunit I	6.6	2.7
ccoN2	cbb3-type cytochrome C oxidase subunit I	2.6	1.4
PA1022	acyl-CoA dehydrogenase	388.2	8.6
hcnB	hydrogen cyanide synthase subunit HcnB	3.3	1.7
hcnC	hydrogen cyanide synthase subunit HcnC	3.3	1.7
PA5020	acyl-CoA dehydrogenase	123.4	6.9
ccoP2	cytochrome C oxidase cbb3-type subunit CcoP	44.3	5.5
ccoQ2	cytochrome C oxidase cbb3-type subunit CcoQ	1195.9	10.2
ccoO2	cbb3-type cytochrome C oxidase subunit II	8.8	3.1
ccoN2	cbb3-type cytochrome C oxidase subunit I	2.6	1.4
PA1856	cbb3-type cytochrome C oxidase subunit I	231.2	7.9
PA2776	hypothetical protein	3.3	1.7
mqoB	malate:quinone oxidoreductase	3.3	1.7
PA1829	hypothetical protein	30.2	4.9
nadB	L-aspartate oxidase	8.2	3.0
PA4100	dehydrogenase	132.4	7.0
trxB1	thioredoxin reductase	3.3	1.7
cyoB	cytochrome o ubiquinol oxidase subunit I	112.5	6.8
norB	nitric oxide reductase subunit B	158.8	7.3
hcnB	hydrogen cyanide synthase subunit HcnB	3.3	1.7
hcnC	hydrogen cyanide synthase subunit HcnC	3.3	1.7
atuD	citronellyl-CoA dehydrogenase	191.6	7.6
betA	choline dehydrogenase	131.9	7.0
PA0521	cytochrome C oxidase subunit	327.3	8.4
PA1940	hypothetical protein	7.0	2.8
gbcB	protein GbcB	202.0	7.7
PA3972	acyl-CoA dehydrogenase	67.4	6.1
PA0364	oxidoreductase	69.7	6.1
PA3710	GMC-type oxidoreductase	66.4	6.1

Table S14 Genes involved in ribosomal protein synthesis in response to SNP.

Gene Id	Description	Fold change	Log FC
rpsP	30S ribosomal protein S16	-1077.9	-10.1
rplQ	50S ribosomal protein L17	-2532.8	-11.3
rpmJ	50S ribosomal protein L36	-1941.1	-10.9
rplR	50S ribosomal protein L18	-515.9	-9.0
rpsH	30S ribosomal protein S8	-7.2	-2.9
rpoC	DNA-directed RNA polymerase subunit beta	-2.5	-1.3
rplL	50S ribosomal protein L7/L12	-2.7	-1.4
rplA	50S ribosomal protein L1	-2.4	-1.2
rplK	50S ribosomal protein L11	-3.4	-1.8
rpsT	30S ribosomal protein S20	-537.9	-9.1
rplI	50S ribosomal protein L9	-1052.1	-10.0
rpsR	30S ribosomal protein S18	-2300.7	-11.2
rpsF	30S ribosomal protein S6	-2277.6	-11.2
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-197.9	-7.6
rpmF	50S ribosomal protein L32	-989.6	-10.0
rplS	50S ribosomal protein L19	-2.6	-1.4
PA4671	50S ribosomal protein L25	4.8	2.2
rpsB	30S ribosomal protein S2	1094.0	10.1
rpmD	50S ribosomal protein L30	628.3	9.3
rpsG	30S ribosomal protein S7	5.2	2.4
rpsI	30S ribosomal protein S9	2.2	1.1

Table S15 Genes involved in ribosomal protein synthesis in response to Ag^+.

Gene Id	Description	Fold change	Log FC

rplS	50S ribosomal protein L19	-6.6	-2.7
rimM	ribosome maturation factor	-799.0	-9.6
rpsP	30S ribosomal protein S16	-1481.4	-10.5
rpoA	DNA-directed RNA polymerase subunit alpha	-2.3	-1.2
rpsD	30S ribosomal protein S4	-3.9	-2.0
rpsK	30S ribosomal protein S11	-4.4	-2.1
rpsM	30S ribosomal protein S13	-3.4	-1.7
rpmJ	50S ribosomal protein L36	-385.0	-8.6
secY	preprotein translocase subunit	-2.6	-1.4
rplO	50S ribosomal protein L15	-6.4	-2.7
rpmD	50S ribosomal protein L30	-2.7	-1.4
rpsE	30S ribosomal protein S5	-6.6	-2.7
rplR	50S ribosomal protein L18	-1567.1	-10.6
rplF	50S ribosomal protein L6	-4.7	-2.2
rpsH	30S ribosomal protein S8	-21.2	-4.4
rpsN	30S ribosomal protein S14	-3.5	-1.8
rplE	50S ribosomal protein L5	-3.0	-1.6
rplX	50S ribosomal protein L24	-5.0	-2.3
rplN	50S ribosomal protein L14	-2.9	-1.5
rpsQ	30S ribosomal protein S17	-2.8	-1.5
rplP	50S ribosomal protein L16	-3.5	-1.8
rpsC	30S ribosomal protein S3	-3.5	-1.8
rplV	50S ribosomal protein L22	-7.5	-2.9
rpsS	30S ribosomal protein S19	-5.0	-2.3
rplB	50S ribosomal protein L2	-7.0	-2.8
rplW	50S ribosomal protein L23	-9.8	-3.3
rplD	50S ribosomal protein L4	-7.0	-2.8
rplC	50S ribosomal protein L3	-5.5	-2.5
rpsJ	30S ribosomal protein S10	-5.4	-2.4
fusA1	elongation factor G	-2.8	-1.5
rpsG	30S ribosomal protein S7	-2.4	-1.2
rpsL	30S ribosomal protein S12	-2.8	-1.5
rplL	50S ribosomal protein L7/L12	-7.0	-2.8
rplJ	50S ribosomal protein L10	-4.3	-2.1
rplA	50S ribosomal protein L1	-2.5	-1.3
rplK	50S ribosomal protein L11	-2.9	-1.5
tufB	elongation factor Tu	-3.2	-1.7
rpsI	30S ribosomal protein S9	-3.1	-1.6
rplM	50S ribosomal protein L13	-4.3	-2.1
rpsT	30S ribosomal protein S20	-954.5	-9.9
rpmA	50S ribosomal protein L27	-2.1	-1.1
rplU	50S ribosomal protein L21	-2.6	-1.4
rpmH	50S ribosomal protein L34	-1376.5	-10.4