Table S2

The expression levels of the differentially expressed genes (TPs vs. HVs) and their product description and subclassification.

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_00820 ^e	tagQ1	-1.70	TagQ1 / [Type VI secretion-associated lipoprotein TagQ]	Membrane proteins; Protein secretion/ export apparatus	
PA14_00830	tagR1	-1.70	TagR1 / [Type VI secretion posttranslational regulatory protein TagR]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_00875	ppkA	-1.84	PpkA / Serine/threonine protein kinase	Adapation, protection; Protein secretion/ export apparatus; Translation, post- translational modification, degradation	T6SS, HS1-T6SS
PA14_00890	рррА	-1.93	PppA / [serine/threonine phosphoprotein phosphatase]	Protein secretion/export apparatus; Putative enzymes	T6SS, HS1-T6SS
PA14_00900	tagF1	-1.74	TagF / [Type VI secretion-associated protein]	Protein secretion/export apparatus	T6SS, HS1-T6SS
PA14_00910	icmF1	-1.71	IcmF1 / [ImcF domain-containing protein, type VI secretion]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_00925	tssL1	-1.54	TssL1 / [Type IV / VI secretion system, DotU]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_00940	tssK1	-1.70	TssK1 / [Type VI secretion protein]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_00960	tssJ1		TssJ1 / [Type VI secretion lipoprotein]	Fatty acid and phospholipid metabolism	T6SS, HS1-T6SS
PA14_00970	PA14_0 0970		/ [Type VI secretion system, FHA domain- containing protein]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_00990	tssA1	-1.85	TssA1 / [Type VI secretion-associated protein, ImpA family]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_01010	hsiB1	-1.79	HsiB1 / [Type VI secretion protein TssB1 or ImpB]	Protein secretion/export apparatus	T6SS, HS1-T6SS
PA14_01020	hsiC1	-1.75	HsiC1 / [Type VI secretion protein TssB1, EvpB or ImpC]	Protein secretion/export apparatus	T6SS, HS1-T6SS
PA14_01030	hcp1	-1.57	Hcp1 / [Hcp1 family type VI secretion system effector]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_01040	tagJ1	-1.52	TagJ1 / [Type VI secretion virulence protein, SciE type]	Protein secretion/export apparatus	T6SS, HS1-T6SS
PA14_01060	tssE1	-1.64	TssE1 / [Type VI secretion system lysozyme- like protein TssE]	Protein secretion/export apparatus	T6SS, HS1-T6SS
PA14_01070	tssF1	-1.56	TssF1 / [Type VI secretion protine TssF or ImpG]	Protein secretion/export apparatus	T6SS, HS1-T6SS

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_01080	tssG1	-1.82	TssG1 / [Type VI secretion protein TssG]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_01100	clpV1	-1.77	ClpV1 / [Type VI secretion ATPase ClpV1]	Translation, post-translational modification, degradation	T6SS, HS1-T6SS
PA14_01110	vgrG1	-1.77	VgrG1 / [Type VI secretion system, Vgr family or ImpA family]	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_01150	eagT6	-2.00	EagT6 / Hypothetical protein	Hypothetical, unclassified, unknown	T6SS, HS1-T6SS
PA14_01160	PA14_0 1160	-1.77	/ [ImpA family type VI secretion-associated protein; Rhs element Vgr protein]	Hypothetical, unclassified, unknown	T6SS
PA14_01180	PA14_0 1180	-1.63	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_01200	PA14_0 1200	-1.64	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_01460	dctA	-1.54	DctA / C4-dicarboxylate transport protein	Transport of small molecules	
PA14_01580	gabP	-1.78	GabP / Gamma-aminobutyrate (GABA) permease	Transport of small molecules	
PA14_01610	PA14_0 1610	-1.51	/ Hypothetical protein [cupin 2 protein]	Carbon compound catabolism	
PA14_02230	cheW	-1.83	CheW / Purine-binding chemotaxis protein	Chemotaxis	
PA14_02260	PA14_0 2260	-1.73	/ Two-component response regulator [CheY]	Two-component regulatory systems	
PA14_02520	PA14_0	-2.34	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_02530	PA14_0 2530	1.50	 / Hypothetical protein [esterase or alpha/beta hydrolase fold protein] 	Hypothetical, unclassified, unknown	
PA14_02550	mdcA	5.86	MdcA / Malonate decarboxylase subunit alpha	Carbon compound catabolism	Malonate
PA14_02560	PA14_0 2560	4.20	/ Triphosphoribosyl-dephospho-CoA synthase	Biosynthesis of cofactors, prosthetic groups and carriers	Malonate
PA14_02570	mdcC	6.00	MdcC / Malonate decarboxylase subunit delta	Carbon compound catabolism	Malonate
PA14_02580	mdcD	3.00	MdcD / Malonate decarboxylase subunit beta	Carbon compound catabolism	Malonate
PA14_02590	mdcE	4.00	MdcE / Malonate decarboxylase subunit gamma	Carbon compound catabolism	Malonate
PA14_03190	tli3	-1.55	Tli3 / Hypothetical protein; probably T6SS related	Hypothetical, unclassified, unknown	T6SS
PA14_03210	PA14_0 3210	-1.65		Hypothetical, unclassified, unknown	T6SS

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_03220	vgrG2b	-1.65	VgrG2b / [ImpA family type VI secretion- associated protein; Rhs element Vgr protein]	Hypothetical, unclassified, unknown	T6SS
PA14_03610	PA14_0 3610	-1.71	/ Zn-dependent protease with chaperone function	Chaperones and heat shock proteins	
PA14_03700	sbp		Sbp / Sulfate-binding protein	Transport of small molecules	
PA14_03710	PA14_0 3710	2.04	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_03790	PA14_0 3790	-1.54	/ Sensory box GGDEF domain-containing protein	Two-component regulatory system	
PA14_04180	PA14_0 4180	3.04	/ Hypothetical protein [stress-induced protein YgiW]	Hypothetical, unclassified, unknown	Heavy metals
PA14_04290	PA14_0 4290	-1.87	/ [Arginine-specific autotransporter of <i>Pseudomonas aeruginosa</i> , AaaA]	Amino acid biosynthesis and metabolism; Membrane proteins	Amino acids
PA14_05110	PA14_0	-1.54	/ Hypothetical protein [GTPase (dynamin-	Hypothetical, unclassified, unknown	
PA14_05600	PA14_0 5600	-1.67	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_05620	sahH	-1.73	SahH / S-adenosyl-L-homocysteine hydrolase	Amino acid biosynthesis and metabolism; Central intermediary metabolism	Amino acids
PA14_06420	PA14_0 6420	-3.09	/ [LamB/YcsF family protein]	Antibiotic resistance and susceptibility	
PA14_06430	PA14_0 6430	-3.15	/ [acetyl-CoA carboxylase, bitoin carboxyl carrier protein AccB]	Putative enzymes	
PA14_06920	PA14_0 6920	-1.64	/ Class III pyridoxal phosphate-dependent aminotransferase	Putative enzymes; Transport of small molecules	
PA14_07090	metK	-1.80	MetK / S-adenosylmethionine synthetase	Amino acid biosynthesis and metabolism; Antibiotic resistance and susceptibility; Central intermediary metabolism	Amino acids
PA14_07330	PA14_0 7330	-1.55	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_07355	PA14_0 7355	1.93	/ [Alkylhydroperoxidase or carboxymucono- lactone decarboxylase family protein]	Hypothetical, unclassified, unknown	
PA14_07400	PA14_0 7400	-1.56	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_08450	PA14_0 8450	-1.53	/ Hypothetical protein	Membrane proteins	
PA14_09280	pchF	-1.56	PchF / Pyochelin synthetase	Transport of small molecules	Pyochelin

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_09300	PA14_0	-1.80	/ ABC transporter ATP-binding protein	Transport of small molecules	Pyochelin
	9300				
PA14_09320	PA14_0	-1.81	/ ABC transporter ATP-binding protein	Transport of small molecules	Pyochelin
	9320	1			
PA14_11370	PA14_1	-1.82	/ Lipoprotein	Fatty acid and phospholipid metabolism	
PA14_11410	1370 ribC	-1 75	RibC / Riboflavin synthase subunit alpha	Biosynthesis of cofactors, prosthetic groups	
1 414_11410	noc	-1.75		and carriers	
PA14_11470	pgpA	1.62	PgpA / Phosphatidylglycerophosphatase A	Fatty acid and phospholipid metabolism	
PA14_12570	PA14_1	-1.69	/ Transcriptional regulator, AsnC family	Transcriptional regulators	
	2570				
PA14_13010	PA14_1	3.08	/ [NLPA lipoprotein or methionine ABC	Hypothetical, unclassified, unknown	
	3010		transporter substrate-binding protein]		
PA14_13130	PA14_1	-1.59	/ Hypothetical protein [type V secretory	Hypothetical, unclassified, unknown	
	3130	1 0 2	pathway, adhesin AidA]	I hypothetical upple stilled upply surp	
PA14_13140	PA14_1		/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_13230	moaC		MoaC / Molybdenum cofactor biosynthesis protein	Biosynthesis of cofactors, prosthetic groups	
PA14_13300	PA14_1		/ Collagenase-like protease	and carriers Translation, post-translational modification,	
1714_10000	3300	1.74	7 Oblidgendse like protease	degradation	
PA14_13580	PA14_1	1.90	/ ABC transporter ATP-binding protein [Glycine	Transport of small molecules	
—	3580		betaine/L-proline transport ATP-binding protein]	•	
PA14_14210	PA14_1	-1.73	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	4210				
PA14_14290	PA14_1	-2.19	/ [Glutathione S-transferase family protein]	Hypothetical, unclassified, unknown	
	4290	1 50	ADC turns transport protein, paripleomia		
PA14_14390	PA14_1 4390	-1.50	/ ABC-type transport protein, periplasmic	Transport of small molecules	
PA14_15030	leuA	-2.12	LeuA / 2-isopropylmalate synthase	Amino acid biosynthesis and metabolism	Amino acids
PA14_15350	PA14_1	1.88	/ Integrase	Related to phage, transposon, or plasmid	
	5350				
PA14_16010	PA14_1	2.29	/ [Long-chain acyl-CoA thioester hydrolase]	Fatty acid and phospholipid metabolism	
	6010				
PA14_16180	PA14_1	-1.68	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	6180				

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_16190	PA14_1	-1.57	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	6190				
PA14_16200	PA14_1	-1.66	/ [Phosphatidylserine/phosphatidylglycero-	Hypothetical, unclassified, unknown	
	6200		phosphate/cardiolipin synthases,related		
			enzymes]		
PA14_16660	PA14_1	2.88	/ Metal-transporting P-type ATPase	Transport of small molecules	Heavy metals
	6660				
PA14_16840	PA14_1	-1.74	/ Lipoprotein	Fatty acid and phospholipid metabolism	
	6840				
PA14_17000	PA14_1	-3.18	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	7000				
PA14_17120	cdsA		CdsA / Phosphatidate cytidylyltransferase	Fatty acid and phospholipid metabolism	
PA14_17220	lpxB	1.55		Cell wall / LPS / capsule	
PA14_17340	ispD	1.52	IspD / 2-C-methyl-D-erythritol 4-phosphate	Biosynthesis of cofactors, prosthetic groups	
			cytidylyltransferase	and carriers	
PA14_17510	PA14_1	-1.95	/ [putative TolB-like translocation protein]	Protein secretion/export apparatus	
	7510				
PA14_17600	PA14_1	-1.54	/ Hypothetical protein	Protein secretion/export apparatus	
	7600		··· - · · · · · · · · · · · · · · · · ·		
PA14_17720	PA14_1	-1.67	/ LuxR family transcriptional regulator	Transcriptional regulators	
	7720	4.00			
PA14_17930	glpD	-1.60	GlpD / Glycerol-3-phosphate dehydrogenase	Central intermediary metabolism; Energy	
		4 74		metabolism	
PA14_17980	glpF		GlpF / Glycerol uptake facilitator protein	Transport of small molecules	T 000
PA14_19020	tse3	-1.52	Tse3 / Hypothetical protein T6SS secreted	Secreted factors (toxins, enzymes, alginate)	T6SS
DA44 40400		0.04	effector protein		
PA14_19100	rhlA	2.31	RhIA / Rhamnosyltransferase chain A	Secreted factors (toxins, enzymes, alginate)	
DA44 40400		1 50	(Malata debudragences	Control intermedian (motobolian	
PA14_19190	PA14_1	-1.59	/ Malate dehydrogenase	Central intermediary metabolism	
	9190 DA14_1	0.47	(I hypothetical protein		
PA14_19320	PA14_1 9320	-2.17	/ Hypothetical protein	Hypothetical, unclassified, unknown	
DA14 10400		2.27	LofA / 1 Ove pereviredevia LofA	Adaptation protoction	
PA14_19490	IsfA	2.37	LsfA / 1-Cys peroxiredoxin LsfA	Adaptation, protection	
		0.44	(NAD(D))), doe on don't ENAN, we should be		
PA14_19530	PA14_1	3.11	/ NAD(P)H-dependent FMN reductase	Central intermediary metabolism	
	9530				

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_19680	PA14_1 9680	2.67	/ [Murein hydrolase transporter LgrA]	Membrane proteins; Protein secretion/ export apparatus	
PA14_20010	hasR	-2.27	HasR / Heme uptake outer membrane receptor	Transport of small molecules	Heme
PA14_20390	phnJ	4.75	PhnJ / [Carbon-phosphorus lyase complex subunit]	Transport of small molecules	
PA14_20550	PA14_2 0550	-1.71	-	Hypothetical, unclassified, unknown	
PA14_21570	PA14_2 1570	2.99	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_21580	PA14_2 1580	2.78	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_21590	PA14_2	3.00	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_21600	PA14_2 1600	4.18	/ [DoxX family protein]	Membrane proteins	
PA14_21610	oprO	4.92	OprO / Pyrophosphate-specific outer membrane porin	Transport of small molecules	
PA14_22280	PA14_2	1.72	/ Pirin-related protein	Transcriptional regulators	
PA14_24050	хсрV	-1.68	XcpV / General secretion pathway protein I for T2SS	Protein secretion/export apparatus	T2SS
PA14_24300	PA14_2 4300	-1.56	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_24330	PA14_2 4330	-1.52	/ [RND efflux transporter]	Motility and attachment	
PA14_24850	PA14_2 4850	1.70	/ [Glutaredoxin or thiol-disulfide isomerase and thioredoxin]	Hypothetical, unclassified, unknown	
PA14_24950	PA14_2	-1.73	/ FAD-dependent glycerol-3-phosphate	Carbon compound catabolism; Energy	
PA14_24960	PA14_2 4960	-1.71	/ Carbohydrate kinase	Carbon compound catabolism	
PA14_25030	PA14_2	1.65	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_25410	PA14_2	-1.55	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_25540	ptpA	1.54	PtpA / Phosphotyrosine protein phosphatase	Amino acid biosynthesis and metabolism	Amino acids
PA14_25620	PA14_2 5620	1.72	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_25640	plsX	1.53	PIsX / Glycerol-3-phosphate acyltransferase	Fatty acid and phospholipid metabolism	

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_25650	fabD	-1.52	FabD / Malonyl CoA-acyl carrier protein transacylase	Fatty acid and phospholipid metabolism	
PA14_25980	aroF	-2.90	AroF / Phospho-2-dehydro-3-deoxyheptonate aldolase	Amino acid biosynthesis and metabolism	Amino acids
PA14_26020	PA14_2 6020	-1.63	/ Aminopeptidase	Secreted factors (toxins, enzymes, alginate)	
PA14_27100	lipA	-1.78	LipA / Lactonizing lipase precursor	Secreted factors (toxins, enzymes, alginate)	
PA14_27520	PA14_2 7520	-1.56	/ Glutathione peroxidase	Adaptation, protection	
PA14_27830	PA14_2 7830	5.81	/ [Two-component response repressor, PtrA]	Adaptation, protection; Transcriptional regulators	
PA14_28010	PA14_2 8010	-1.68	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_28390	PA14_2 8390	-2.00	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_29190	PA14_2 9190	-1.70	/ Tsi2-like immunity protein	Adaptation, protection	T6SS
PA14_29200	PA14_2 9200	-1.79	/ Tse2-like effector protein	Secreted factors (toxins, enzymes, alginate)	T6SS
PA14_29330	PA14_2 9330	-1.91	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_29400	PA14_2 9400	-1.86	/ Hypothetical protein	Cell wall / LPS / capsule	
PA14_29830	PA14_2	-1.80	/ Methyltransferase	Antibiotic resistance and susceptibility	
PA14_30700	PA14_3 0700	1.53	/ Sensor/response regulator hybrid [Hpt sensor hybrid histidine kinase]	Two-component regulatory systems	
PA14_30730	PA14_3 0730	-1.52	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_30800	PA14_3 0800	1.60	/ Hypothetical protein	Energy metabolism	
PA14_31040	PA14_3 1040	1.50	/ Cation efflux system protein	Protein secretion/export apparatus	
PA14_31050	PA14_3 1050	1.68	/ Hypothetical protein [Heat shock protein HtpX]	Hypothetical, unclassified, unknown	
PA14_31580	PA14_3 1580	1.83	/ Acyl-CoA dehydrogenase	Fatty acid and phospholipid metabolism; Putative enzymes	

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_31700	PA14_3	-1.71	/ CDP-alcohol phosphatidyltransferase	Fatty acid and phospholipid metabolism;	
PA14_31720	PA14_3	-2.38	/ [Lysophospholipase]	Fatty acid and phospholipid metabolism	
PA14_31750	PA14_3	-1.78	/ Acyltransferase	Fatty acid and phospholipid metabolism	
	1750				
PA14_31760	PA14_3 1760	-1.74	/ Phosphatidate cytidylyltransferase	Fatty acid and phospholipid metabolism	
PA14_31770	PA14_3	-1.82	/ Oxidoreductase	Energy metabolism	
	1770				
PA14_31820	PA14_3	-2.30	/ Aminotransferase	Amino acid biosynthesis and metabolism	Amino acids
	1820				
PA14_31960	PA14_3	6.80		Two-component regulatory systems	Heavy metals
	1960		[CzrR/CzcR]		
PA14_31990	czcB	4.50		Transport of small molecules	Heavy metals
PA14_32250	PA14_3	5.17		Hypothetical, unclassified, unknown	
PA14_32270	PA14_3	2.96		Transport of small molecules	
PA14_32905	PA14_3	-2.32		Hypothetical, unclassified, unknown	
PA14_32930	PA14_3	-1.55	· · ·	Hypothetical, unclassified, unknown	Amino opido
PA14_32985	gcvH2	-1.51		Amino acid biosynthesis and metabolism	Amino acids
PA14_33000	gcvP2		GcvP2 / Glycine dehydrogenase	Amino acid biosynthesis and metabolism	Amino acids
PA14_33010	glyA2		GlyA2 / Serine hydroxymethyltransferase	Amino acid biosynthesis and metabolism	Amino acids
PA14_33030	sdaA		SdaA / L-serine dehydratase	Amino acid biosynthesis and metabolism	Amino acids
PA14_33040	gcvT2	-1.55	GcvT2 / Glycine cleavage system protein T2	Amino acid biosynthesis and metabolism; Central intermediary metabolism	Amino acids
PA14_33500	pvdH	-2.35	PvdH / Diaminobutyrate-2-oxoglutarate	Adaptation, protection; Transport of small	Pyoverdine
			aminotransferase	molecules	-
PA14_33520	PA14_3	-1.55	/ Thioesterase	Adaptation, protection; Biosynthesis of	
	3520			cofactors, prosthetic groups and carriers;	
				Putative enzymes	
PA14_33550	PA14_3	-1.83	/ ABC transporter ATP-binding protein	Transport of small molecules	
	3550				
PA14_33680	fpvA		FpvA / Ferripyoverdine receptor	Transport of small molecules	Pyoverdine
PA14_33690	pvdE	-2.11	PvdE / Pyoverdine biosynthesis protein	Adapatation, protection; Membrane proteins;	Pyoverdine
DA44 00700	m dE	1.00	Dud (Duoverdine events stars	Transport of small molecules	Duovordina
PA14_33700	pvdF	-1.89	PvdF / Pyoverdine synthetase	Adaptation, protection; Secreted factors	Pyoverdine
DA14 22740	nudO	1 0 2	PudQ / [Chromophore moturation protain]	(toxins, enzymes, alginate)	Duovordino
PA14_33710	pvdO	-1.03	PvdO / [Chromophore maturation protein]	Adaptation, protection	Pyoverdine

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_33720	pvdN	-1.72	PvdN / [Chromophore maturation protein; class V aminotransferase	Adapatation, protection; Transport of small molecules	Pyoverdine
PA14_33750	PA14_3	-1.59	/ Outer membrane protein [pyoverdine efflux]	Transport of small molecules	Pyoverdine
PA14_33810	pvdA	-2.27	PvdA / L-ornithine 5-monooxygenase	Biosynthesis of cofactors, prosthetic groups and carriers	Pyoverdine
PA14_33820	pvdQ	-1.72	PvdQ / Penicillin acylase-related protein	Adaptation, protection; Antibiotic resistance and susceptibility	Pyoverdine
PA14_33860	lldA	1.85	LldA / L-lactate dehydrogenase	Energy metabolism	
PA14_33870	PA14_3 3870	1.80	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_34030	hcp3	-2.67	Hcp3 / [Hemolysin co-regulated T6SS effector]	Hypothetical, unclassified, unknown	T6SS, H3-T6SS
PA14_34050	hsiC3	-2.00	HsiC3 / [EvpB family T6SS protein]	Hypothetical, unclassified, unknown	T6SS, H3-T6SS
PA14_34370	PA14_3 4370	9.60	/ ABC maltose/mannitol transporter ATP- binding protein	Transport of small molecules	Mannitol
PA14_34390	PA14_3 4390	34.00	/ Binding-protein-dependent maltose/mannitol transport protein	Transport of small molecules	Mannitol
PA14_34600	PA14_3 4600	1.52	/ Glyceraldehyde-3-phosphate dehydrogenase	Carbon compound catabolism	
PA14_35780	PA14_3 5780	-1.59	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_35790	PA14_3 5790	-1.53	/ Homospermidine synthase	Putative enzymes; Secreted factors (toxins, enzymes, alginate)	
PA14_36290	PA14_3 6290	1.82	/ [Oxidoreductase]	Energy metabolism; Putative enzymes	
PA14_36300	PA14_3 6300	1.68	/ TetR family transcriptional regulator	Transcriptional regulators	
PA14_36330	hcnA	2.94	HcnA / Hydrogen cyanide synthase	Central intermediary metabolism	
PA14_37080	PA14_3 7080	-1.52	/ [Transcriptional regulator; cupA gene regulator C, CgrC]	Transcriptional regulators	
PA14_37250	PA14_3 7250	-1.86	/ Major facilitator transporter	Transport of small molecules	
PA14_37590	kynB	-1.69	KynB / Kynurenine formamidase	Amino acid biosynthesis and metabolism; Putative enzymes	Amino acids
PA14_38500	PA14_3 8500	1.65	/ IcIR family transcriptional regulator	Transcriptional regulators	

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_39350	rbsB	1.76	/ Ribose ABC transporter substrate-binding protein	Transport of small molecules	
PA14_39460	PA14_3 9460	-1.64	/ [Catalase]	Hypothetical, unclassified, unknown	
PA14_39590	metE	-1.98	MetE / 5-methyltetrahydropteroyltriglutamate/ homocysteine S-methyltransferase	Amino acid biosynthesis and metabolism	Amino acids
PA14_40650	PA14_4 0650	-1.83	/ Hypothetical protein [Tsi1-like T6SS immunity protein]	Hypothetical, unclassified, unknown	T6SS-related
PA14_40660	PA14_4 0660	-2.12	/ Hypothetical protein [Tse1-like T6SS effector protein]	Hypothetical, unclassified, unknown	T6SS-related
PA14_41420	PA14_4 1420	-1.57	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_41760	PA14_4 1760	-1.92	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_41790	PA14_4 1790	-1.63	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_42630	PA14_4 2630	1.66	/ Translocation protein in T3SS	Protein secretion/export apparatus	T3SS
PA14_42660	pscU	2.91	PscU / Translocation protein in T3SS	Protein secretion/export apparatus	T3SS
PA14_42700	, alkA		AlkA / DNA-3-methyladenine glycosylase II	DNA replication, recombination, modification and repair	
PA14_43610	PA14_4 3610	-1.78	/ AMP-binding protein	Fatty acid and phospholipid metabolism	
PA14_43780	PA14_4 3780	-1.60	/ Oxoreductase	Energy metabolism	
PA14_43790	PA14_4 3790	-1.63	/ Aldehyde dehydrogenase	Putative enzymes	
PA14_44710	xdhA	-1.56	XdhA / Xanthine dehydrogenase	Nucleotide biosynthesis and metabolism	
PA14_44800	PA14_4 4800	-1.75	/ Transporter [Xanthine/uracil/vitamin C permease]	Membrane proteins; Transport of small molecules	
PA14_44830	PA14_4 4830	-1.69	/ [Chitin or polysaccharide deacetylase family protein]	Carbon compound catabolism	
PA14_44840	PA14_4 4840	-1.73	/ [possible OHCU decarboxylase]	Hypothetical, unclassified, unknown	
PA14_44850	alc	-1.72	Alc / Allantoicase	Carbon compound catabolism	
PA14_44860	PA14_4 4860	-1.69	/ Ureidoglycolate hydrolase	Central intermediary metabolism	

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_44880	PA14_4	-2.43	/ Hypothetical protein	Membrane proteins	
	4880			—	
PA14_45350	ccmC		CcmC / Heme exporter protein	Transport of small molecules	Heme
PA14_46370	PA14_4	-1.78	/ Two-component sensor [Sensor histidine	Two-component regulatory systems	
	6370	2.00	kinase/response regulator]	Transport of small male sules	Iron utilization
PA14_46640	PA14_4 6640	-2.80	/ Siderophore receptor	Transport of small molecules	Iron utilization
PA14_46910	PA14_4	-1 97	/ ABC transporter substrate-binding protein	Transport of small molecules	Amino acids
PA14_46920	PA14_4		/ ABC transporter permease	Membrane proteins; Transport of small	Amino acids
17(11_10020	6920	1.01	[Glutamate/aspartate transporter GltJ]	molecules	
PA14_46930	PA14_4	-1.52	/ ABC transporter permease	Transport of small molecules	Amino acids
	6930		[Glutamate/aspartate transporter GltK]		
PA14_46950	PA14_4	-1.63	/ ABC transporter ATP-binding protein	Transport of small molecules	Amino acids
	6950		[Glutamate/aspartate transporter GtlL]		
PA14_46960	ggt	-1.94	Ggt / Gamma-glutamyltranspeptidase	Central intermediary metabolism	
PA14_46970	ansB	-2.29	AnsB / Glutaminase-asparaginase	Amino acid biosynthesis and metabolism	Amino acids
PA14_48060	aprA	1.67	AprA / Alkaline metalloproteinase	Secreted factors (toxins, enzymes, alginate)	
PA14_48140	aprX	1.86	/ Hypothetical protein [AprX in <i>P. aeruginosa</i>	Membrane proteins; Secreted factors (toxins,	
DA44 40000		4 74	PAO1]	enzymes, alginate)	
PA14_49320	PA14_4 9320	-1.71	/ [Alginate lyase 2]	Hypothetical, unclassified, unknown	
PA14_49560	toxA	-1 80	ToxA / Exotoxin A	Secreted factors (toxins, enzymes, alginate)	
1714_40000		-1.00			
PA14_49650	PA14_4	-2.15	/ Hypothetical protein	Hypothetical, unclassified, unknown	
—	9650				
PA14_49850	PA14_4	1.53	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	9850				
PA14_50610	PA14_5	-1.78	/ Short-chain dehydrogenase	Putative enzymes	
	0610				
PA14_50620		-1.63	/ Hypothetical protein [possible bacteriophage	Hypothetical, unclassified, unknown	
DA14 50770	0620 DA14 5	1 62	protein] / Transporter [putative alucenate transporter]	Transport of small molecules	
PA14_50770	PA14_5 0770	1.03	/ Transporter [putative gluconate transporter]	Transport of small molecules	
PA14_51680	PA14_5	2.36	/ Radical activating enzyme [SAM domain]	Putative enzymes	
.,	1680	2.00			

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_52080	PA14_5	1.71	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	2080				
PA14_52090	PA14_5	1.84	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_52120	2090 PA14_5	3.20	/ Hypothetical protein	Hypothetical, unclassified, unknown	
FA14_32120	2120	5.20		rippotrietical, unclassified, unknown	
PA14_53210	PA14_5	-1.55	/ Hypothetical protein	Hypothetical, unclassified, unknown	
_	3210				
PA14_53260	PA14_5	-1.67	/ Hypothetical protein [threonine dehydratase]	Hypothetical, unclassified, unknown	
	3260				
PA14_53400	PA14_5	1.72	/ Oxidoreductase	Putative enzymes	
DA14 52410	3400 PA14_5	1 02	/ Transprintional regulator [TatP family]	Transprintional regulators	
PA14_53410	7414_5 3410	1.83	/ Transcriptional regulator [TetR family]	Transcriptional regulators	
PA14_53820	PA14_5	1.79	/ [N-acetylmuramoyl-L-alanine amidase]	Antibiotic resistance and susceptibility	
	3820		. [· · · · · · · · · · · · · · · · · · ·	
PA14_54130	PA14_5	-1.54	/ Transcriptional regulator [LysR family]	Transcriptional regulators	
	4130				
PA14_54540	PA14_5	2.92	/ [Tricarboxylate transport protein TctC]	Hypothetical, unclassified, unknown	
DA14 54620	4540 DA14 5	1 02	/ Apul CoA dobudrogonogo	Putativa anzuman	
PA14_54630	PA14_5 4630	-1.95	/ Acyl-CoA dehydrogenase	Putative enzymes	
PA14_54640	PA14_5	-1.68	/ Enoyl-CoA hydratase	Putative enzymes	
_	4640				
PA14_54750	PA14_5	2.11	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	4750				
PA14_54850	PA14_5	2.50	/ [Bacteriophage-related integrase]	Hypothetical, unclassified, unknown	
PA14_54870	4850 PA14_5	1.79	/ [Transcriptional regulator, AraC family]	Hypothetical, unclassified, unknown	
FA14_04070	4870	1.79		rippotrietical, unclassified, unknown	
PA14_55810	PA14_5	-1.59	/ Two-component response regulator LuxR	Two-component regulatory systems	
	5810		family (PAO1 PrpB)		
PA14_56100	PA14_5	-1.52	/ Hypothetical protein [RDD domain-containing	Membrane proteins	
	6100		protein]		
PA14_56200	PA14_5	-1.60	/ Hypothetical protein [possible lipoprotein]	Fatty acid and phospholipid metabolism	
	6200				

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_56360	PA14_5 6360	1.65	 / Hypothetical protein [possible arylsulfate sulfotransferase] 	Hypothetical, unclassified, unknown	
PA14_58130	mreC	1.78	MreC / Rod shape-determining protein	Cell wall / LPS / capsule	
PA14_58240	PA14_5 8240		/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_58350	dppA1	-1.81	DppA1 / Dipeptide-binding ABC transporter substrate-binding protein	Transport of small molecules	
PA14_59390	PA14_5 9390	1.92	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_59780	rcsC	1.60	RcsC / Kinase sensor protein	Two-component regulatory systems	
PA14_59970	PA14_5 9970	1.61	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_60030	PA14_6 0030	1.54	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_60490	PA14_6 0490	-1.63	/ Cytochrome c family protein	Energy metabolism	
PA14_60530	PA14_6 0530	1.95	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_60730	PA14_6 0730	-1.67	/ Outer membrane protein	Membrane proteins; Transport of small molecules	
PA14_60750	pra	-1.81	Pra / protein activator	Carbon compound catabolism	
PA14_61270	PA14_6 1270	-1.97	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_61920	PA14_6 1920	-3.00	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_61940	PA14_6 1940	-1.89	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_62100	PA14_6 2100	2.92	/ Sulfite oxidase subunit YedZ	Membrane proteins	
PA14_62110	PA14_6 2110	2.77	/ Sulfite oxidase subunit YedY	Putative enzymes	
PA14_62130	ilvC	-1.54	IIvC / Ketol-acid reductoisomerase	Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers	Amino acids

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_62150	ilvH	-1.70	IIvH / Acetolactate synthase 3 regulatory subunit	Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers	Amino acids
PA14_62160	ilvl	-1.57	IIvI / Acetolactate synthase 3 catalytic subunit	Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers	Amino acids
PA14_64350	ureA	-1.86	UreA / Urease subunit gamma	Central intermediary metabolism	
PA14_64550	PA14_6 4550	2.25	/ [Thiosulfate reductase cytochrome B subunit]	Energy metabolism	
PA14_64840	PA14_6 4840	-1.70	/ Short-chain dehydrogenase	Putative enzymes	
PA14_64870	PA14_6 4870	-2.33	/ ABC transporter ATP-binding protein [for Branched-chain amino acid transport]	Transport of small molecules	Amino acids
PA14_64950	pncA	-2.69	PncA / [Nicotinamidase]	Central intermediary metabolism	
PA14_64960	pncB1	-2.09	PncB1 / Nicotinate phosphoribosyl-transferase	Biosynthesis of cofactors, prosthetic groups and carriers	
PA14_64980	nadE	-2.25	NadE / NAD synthetase	Amino acid biosynthesis and metabolism;	Amino acids
PA14_65030	PA14_6 5030	1.60	/ [Putative metalloendopeptidase-related membrane protein]	Membrane proteins	
PA14_65630	PA14_6 5630	1.50	/ [Putative aspartyl protease]	Putative enzymes	
PA14_66440	metY	-1.52	MetY / O-acetylhomoserine aminocarboxy- propyltransferase	Amino acid biosynthesis and metabolism	Amino acids
PA14_66540	PA14_6 6540	-2.89	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_67350	hutU	-1.87	HutU / Urocanate hydratase	Amino acid biosynthesis and metabolism	Amino acids
PA14_67510	estA	-1.58	EstA / Esterase	Fatty acid and phospholipid metabolism	
PA14_67620	PA14_6 7620	1.86	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_67640	PA14_6 7640	-1.77	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_67830	PA14_6 7830	-1.59	/ Hypothetical protein	Hypothetical, unclassified, unknown	
PA14_68260	PA14_6 8260	-1.61	/ C4-dicarboxylate-binding protein [DctP family]	Membrane proteins	
PA14_68280	PA14_6	-1.74	/ Dicarboxylate transporter [DctQ subunit]	Membrane proteins; Transport of small	

Locus	Gene	FC ^a	Product /Function ^b [function] ^c	Protein Class Assignment ^d	Subclass ^d
PA14_68290	PA14_6	-1.54	/ C4-dicarboxylate transporter [DctM subunit]	Membrane proteins	
	8290				
PA14_69380	PA14_6	-1.51	/ Peptidyl-prolyl cis-trans isomerase, FkbP-type	Chaperones and heat shock proteins;	
	9380			Translation, post-translational modification, degradation	
PA14_70600	PA14_7	-1.88	/ HU family DNA-binding protein	DNA replication, recombination, modification	
	0600			and repair	
PA14_71070	PA14_7	-1.82	/ AraC family transcriptional regulator	Transcriptional regulators	
	1070				
PA14_71460	glyA1	-2.38	GlyA1 / Serine hydroxymethyltransferase	Amino acid biosynthesis and metabolism	Amino acids
PA14_71900	PA14_7	1.60	/ Hypothetical protein	Hypothetical, unclassified, unknown	
	1900				
PA14_72410	PA14_7	-1.80	/ Multiple antibiotic resistance (MarC-like)	Antibiotic resistance and susceptibility	
	2410		protein		
PA14_72760	PA14_7	1.63	/ Beta-lactamase	Adaptation, protection; Antibiotic resistance	
PA14_73040	amiA	3.00	AmiA / N-acetylmuramoyl-L-alanine amidase	Cell wall / LPS / capsule	
PA14_73060	PA14_7	2.63	/ Carbonic anhydrase-like protein	Transport of small molecules	
	3060				

^aUpregulation (green) and downregulation (red) of gene expression in PA14 grown in blood from SBPs or TPs compared to HVs

^bProduct /Function from UCBPP-PA14 Genome database

^c[function from Pseudomonas Ortholog Database]

^dFrom the PseudoCap database

^eGenes highlighted in yellow were discussed in the text and/or figures

http://pseudomonas.com/ http://pseudoluge.pseudomonas.com/ http://pseudomonas.com/pseudocap