TABLE S1. *P. aeruginosa* genes expressed two-fold or greater when grown to mid-log phase in LB supplemented with oleate ($C_{18:1}{}^{\Delta 9}$) versus LB as identified using microarray.

Accession Number	Gene	Fold Change[1]	Description
PA0002	*dnaN*	2.1	DNA polymerase III, beta chain
PA0014		2.5	hypothetical protein
PA0015		2.4	hypothetical protein (COG predictions: putative Zn-dependent protease)
PA0016	*trkA*	2.6	potassium uptake protein TrkA
PA0069	*splB*	2.5	SplB (COG predictions: DNA repair photolyase)
PA0105	*coxB*	3.5	cytochrome c oxidase, subunit II
PA0141		2.7	conserved hypothetical protein
PA0169		4.1	hypothetical protein
PA0170		2.6	hypothetical protein
PA0172	*rsbU*	2.4	RsbU (COG prediction: serine phosphatase RsbU, regulator of sigma subunit)
PA0195	*pntA*	8.0	still frameshift pyridine nucleotide transhydrogenase alpha subunit
PA0196	*pntB*	8.8	pyridine nucleotide transhydrogenase, beta subunit
PA0257	*tra5*	2.3	Tra5 (COG prediction: transposase and inactivated derivatives)
PA0276		2.4	hypothetical protein
PA0277	*htpX*	2.1	HtpX (COG prediction: Zn-dependent protease with chaperone function)
PA0329		2.0	conserved hypothetical protein
PA0383		4.8	conserved hypothetical protein
PA0384		2.4	hypothetical protein
PA0389	*ubiE*	2.2	UbiE (COG prediction: methylase involved in ubiquinone/menaquinone biosynthesis)
PA0427	*oprM*	2.1	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor
PA0430	*metF*	2.1	5,10-methylenetetrahydrofolate reductase
PA0431	*spoT*	2.1	SpoT (COG prediction: guanosine polyphosphate pyrophosphohydrolases/synthetases)
PA0471	*fiuR*	2.8	probable transmembrane sensor
PA0506	*fadE*	15.9	probable acyl-CoA dehydrogenase
PA0508	*fadE*	15.6	probable acyl-CoA dehydrogenase
PA0513	*nirG*	2.5	probable transcriptional regulator
PA0514	*nirL*	2.9	heme d1 biosynthesis protein NirL
PA0515	*nirD*	2.7	probable transcriptional regulator
PA0517	*nirC*	4.8	probable c-type cytochrome precursor
PA0518	*nirM*	5.6	cytochrome c-551 precursor
PA0519	*nirS*	5.8	nitrite reductase precursor
PA0524	*norB*	4.3	nitric-oxide reductase subunit B
PA0525	*norD*	2.1	probable dinitrification protein NorD
PA0527	*dnr*	2.5	transcriptional regulator Dnr
PA0546	*metK*	2.1	methionine adenosyltransferase

PA0557		3.0	hypothetical protein
PA0586	*ycgB*	2.4	conserved hypothetical protein
PA0612	*ptrB*	2.3	repressor, PtrB
PA0613		2.3	hypothetical protein
PA0629		2.0	conserved hypothetical protein
PA0632		2.0	hypothetical protein
PA0637		2.8	conserved hypothetical protein
PA0638		2.1	probable bacteriophage protein
PA0643		2.0	hypothetical protein
PA0645		3.2	hypothetical protein
PA0654	*speD*	2.1	S-adenosylmethionine decarboxylase proenzyme
PA0672	*hemO*	3.4	heme oxygenase
PA0705	*migA*	2.0	alpha-1,6-rhamnosyltransferase MigA
PA0772	*recO*	2.0	DNA repair protein RecO
PA0910		2.1	hypothetical protein
PA0914		2.1	hypothetical protein
PA0915		2.0	conserved hypothetical protein
PA0916	*miaB*	2.1	MiaB (COG prediction: 2-methylthioadenine synthetase)
PA0924		2.7	hypothetical protein
PA0925	*hslJ*	2.1	HslJ (COG predction: heat shock protein)
PA0927	*ldhA*	2.0	D-lactate dehydrogenase (fermentative)
PA0929	*pirR*	2.3	two-component response regulator
PA0931	*pirA*	2.8	ferric enterobactin receptor PirA
PA0975		2.8	probable radical activating enzyme
PA0976		2.9	conserved hypothetical protein ; tRNA-Lys
PA0977		4.9	hypothetical protein
PA0978		2.0	conserved hypothetical protein
PA0983		2.2	conserved hypothetical protein
PA0997	*pqsB*	4.5	Homologous to beta-keto-acyl-acyl-carrier protein synthase
PA0998	*pqsC*	3.2	Homologous to beta-keto-acyl-acyl-carrier protein synthase
PA0999	*pqsD*	2.2	3-oxoacyl-[acyl-carrier-protein] synthase III
PA1002	*phnB*	2.4	anthranilate synthase component II
PA1012	*yycJ*	2.4	PhnP (COG prediction: metal-dependent hydrolases of the beta-lactamase superfamily)
PA1103	*fliH*	2.1	probable flagellar assembly protein
PA1117		2.2	hypothetical protein
PA1161	*rrmA*	2.1	rRNA methyltransferase
PA1180	*phoQ*	2.4	two-component sensor PhoQ
PA1242	*aprE*	2.1	AprE (COG prediction: subtilisin-like serine proteases)
PA1273	*cobB*	2.1	cobyrinic acid a,c-diamide synthase
PA1301		2.0	probable transmembrane sensor
PA1302	*hxuC*	2.7	probable heme utilization protein precursor

PA1317	*cyoA*	2.1	cytochrome o ubiquinol oxidase subunit II
PA1318	*cyoB*	2.5	cytochrome o ubiquinol oxidase subunit I
PA1319	*cyoC*	2.0	cytochrome o ubiquinol oxidase subunit III
PA1320	*cyoD*	3.3	cytochrome o ubiquinol oxidase subunit IV
PA1370		2.2	hypothetical protein
PA1414		2.3	hypothetical protein
PA1421	*speB2*	2.4	guanidinobutyrase
PA1479	*ccmE*	2.3	cytochrome C-type biogenesis protein CcmE
PA1546	*hemN*	3.4	oxygen-independent coproporphyrinogen III oxidase
PA1549	*fixI*	2.1	probable cation-transporting P-type ATPase
PA1550		2.1	hypothetical protein
PA1552		2.3	probable cytochrome c
PA1556	*fixO*	2.0	probable cytochrome c oxidase subunit
PA1557	*fixN*	3.4	probable cytochrome oxidase subunit (cbb3-type)
PA1560		2.2	hypothetical protein
PA1614	*gpsA*	2.1	glycerol-3-phosphate dehydrogenase, biosynthetic
PA1673		2.6	hypothetical protein
PA1747		3.4	hypothetical protein
PA1748		4.0	probable enoyl-CoA hydratase/isomerase
PA1766		2.2	hypothetical protein
PA1816	*dnaQ*	2.1	DNA polymerase III, epsilon chain
PA1830		3.0	hypothetical protein
PA1882		2.7	probable transporter
PA1926		2.2	conserved hypothetical protein
PA1970		3.1	hypothetical protein
PA1971	*braZ*	3.7	branched chain amino acid transporter BraZ
PA2018	*mexY*	2.6	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter
PA2022		2.9	probable nucleotide sugar dehydrogenase
PA2077		73.0	hypothetical protein
PA2078		146.2	hypothetical protein
PA2119	*adh*	3.0	alcohol dehydrogenase (Zn-dependent)
PA2231	*pslA*	2.9	probable glycosyl transferase
PA2232	*pslB*	2.4	probable phosphomannose isomerase/GDP-mannose pyrophosphorylase
PA2233	*pslC*	3.1	probable glycosyl transferase
PA2234	*pslD*	3.0	probable exopolysaccharide transporter
PA2235	*pslE*	2.7	hypothetical protein
PA2236	*pslF*	3.7	hypothetical protein
PA2237	*pslG*	2.6	probable glycosyl hydrolase
PA2238	*pslH*	2.5	hypothetical protein
PA2239	*pslI*	2.8	probable transferase
PA2240	*pslJ*	2.5	hypothetical protein

PA2242	*pslL*	2.3	hypothetical protein
PA2287		2.5	hypothetical protein
PA2385	*pvdQ*	2.7	3-oxo-C12-homoserine lactone acylase PvdQ
PA2386	*pvdA*	3.0	L-ornithine N5-oxygenase
PA2389	*acrA*	2.6	AcrA (COG prediction: membrane-fusion protein)
PA2393		3.7	probable dipeptidase precursor
PA2394	*pvdN*	3.2	PvdN
PA2395	*pvdO*	2.7	PvdO
PA2397	*pvdE*	3.5	pyoverdine biosynthesis protein PvdE
PA2411		2.1	probable thioesterase
PA2424	*pvdL*	3.1	PvdL
PA2426	*pvdS*	3.8	sigma factor PvdS
PA2441		2.9	hypothetical protein
PA2452		2.7	hypothetical protein
PA2458	*rhsA*	5.6	RhsA (COG prediction: Rhs family protein)
PA2567		2.0	hypothetical protein
PA2609	*trpD*	2.1	TrpD (COG prediction: anthranilate phosphoribosyltransferase)
PA2618		2.1	hypothetical protein
PA2619	*infA*	3.2	initiation factor
PA2630	*ycfD*	2.2	conserved hypothetical protein
PA2631	*yjcF*	2.0	probable acetyl transferase
PA2633	*pulD*	2.0	PulD (COG prediction: type II secretory pathway, component PulD)
PA2634	*aceA*	6.2	probable isocitrate lyase
PA2662		2.1	conserved hypothetical protein
PA2663		3.0	hypothetical protein
PA2688	*pfeA*	2.6	Ferric enterobactin receptor, outer membrane protein PfeA precursor
PA2693	*vdlD*	2.0	conserved hypothetical protein
PA2706		2.8	hypothetical protein
PA2707		2.8	hypothetical protein
PA2730		2.2	hypothetical protein
PA2732		2.7	hypothetical protein
PA2733		2.4	conserved hypothetical protein
PA2734	*hsdS*	2.9	HsdS (COG prediction: destriction endonuclease S subunits)
PA2735		2.5	probable restriction-modification system protein
PA2737		2.1	conserved hypothetical protein
PA2791		2.3	hypothetical protein
PA2808	*ptrA*	2.7	two-component response repressor, PtrA
PA2814		7.8	hypothetical protein
PA2821		2.0	probable glutathione S-transferase
PA2840	*deaD*	3.2	probable ATP-dependent RNA helicase
PA2882		2.1	probable two-component sensor

PA2899		3.0	probable transcriptional regulator
PA2951	*etfA*	2.0	electron transfer flavoprotein alpha-subunit
PA2953	*fixC*	3.8	electron transfer flavoprotein-ubiquinone oxidoreductase
PA2960	*pilZ*	2.0	type 4 fimbrial biogenesis protein PilZ
PA2963	*yceG*	2.0	conserved hypothetical protein
PA3001		2.5	probable glyceraldehyde-3-phosphate dehydrogenase
PA3006	*psrA*	2.9	transcriptional regulator PsrA
PA3009		2.3	hypothetical protein
PA3012		5.9	hypothetical protein
PA3013	*fadA5*	9.4	fatty-acid oxidation complex beta-subunit
PA3014	*fadB5*	7.5	fatty-acid oxidation complex alpha-subunit
PA3049	*rmf*	3.3	ribosome modulation factor
PA3059	*pelF*	3.3	PelF
PA3061	*pelD*	3.3	PelD
PA3064	*pelA*	4.3	PelA
PA3070		2.1	conserved hypothetical protein
PA3092	*fadH1*	4.2	2,4-dienoyl-CoA reductase FadH1
PA3136		4.7	probable secretion protein
PA3137		5.6	probable major facilitator superfamily (MFS) transporter
PA3143		2.3	hypothetical protein
PA3165	*hisC2*	2.0	histidinol-phosphate aminotransferase
PA3172		2.3	probable hydrolase
PA3173	*yciK*	2.0	probable short-chain dehydrogenase
PA3179	*yciL*	2.4	conserved hypothetical protein
PA3268		3.3	probable TonB-dependent receptor
PA3289		2.0	hypothetical protein
PA3309	*uspK*	2.4	UspK, Usp-type stress protein essential for survival during pyruvate fermentation
PA3328		2.2	probable FAD-dependent monooxygenase
PA3337	*rfaD*	2.1	ADP-L-glycero-D-mannoheptose 6-epimerase
PA3340	*fimV*	2.0	FimV (COG prediction: Tfp pilus assembly protein)
PA3392	*nosZ*	4.5	nitrous-oxide reductase precursor
PA3393	*nosD*	2.5	NosD protein
PA3395	*nosY*	2.3	NosY protein
PA3411		2.5	hypothetical protein
PA3436		2.7	hypothetical protein
PA3439	*folX*	2.5	d-erythro-7,8-dihydroneopterin triphosphate epimerase
PA3452	*mqoA*	2.4	malate:quinone oxidoreductase
PA3483		2.2	hypothetical protein
PA3547	*algL*	2.4	poly(beta-d-mannuronate) lyase precursor AlgL
PA3553	*arnC*	2.4	probable glycosyl transferase
PA3555	*arnD*	2.5	conserved hypothetical protein

PA3556	*arnT*	2.3	inner membrane L-Ara4N transferase ArnT
PA3559		2.8	probable nucleotide sugar dehydrogenase
PA3564	*tatD*	2.2	TatD (COG prediction: Mg-dependent DNase)
PA3579		2.4	probable carbohydrate kinase
PA3600		2.2	conserved hypothetical protein
PA3607	*potA*	2.2	polyamine transport protein PotA
PA3608	*potB*	4.2	polyamine transport protein PotB
PA3609	*potC*	3.9	polyamine transport protein PotC
PA3610	*potD*	6.0	polyamine transport protein PotD
PA3613		2.8	hypothetical protein
PA3636	*kdsA*	2.2	2-dehydro-3-deoxyphosphooctonate aldolase
PA3640	*dnaE*	2.2	DNA polymerase III, alpha chain
PA3720		2.2	hypothetical protein
PA3741		3.8	hypothetical protein
PA3767	*cumB*	2.4	CumB (COG prediction: cytosine/adenosine deaminases)
PA3784		2.3	hypothetical protein
PA3799		2.1	conserved hypothetical protein
PA3835		3.3	hypothetical protein
PA3839		2.2	probable sodium:sulfate symporter
PA3874	*narH*	2.4	respiratory nitrate reductase beta chain
PA3877	*narK1*	3.1	nitrite extrusion protein 1
PA3901	*fecA*	2.8	Fe(III) dicitrate transport protein FecA
PA3930	*cioA*	2.8	cyanide insensitive terminal oxidase
PA3957		2.1	probable short-chain dehydrogenase
PA3964		2.7	hypothetical protein
PA3990		2.6	conserved hypothetical protein
PA4011		2.2	hypothetical protein
PA4033		2.2	hypothetical protein
PA4052	*nusB*	2.0	NusB protein
PA4054	*ribB*	2.1	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase
PA4112		2.0	probable sensor/response regulator hybrid
PA4113	*ydeA*	2.4	probable major facilitator superfamily (MFS) transporter
PA4114	*bltD*	2.4	spermidine acetyltransferase
PA4137	*opdL*	2.3	probable porin
PA4139		2.2	hypothetical protein
PA4155		2.1	hypothetical protein
PA4161	*fepG*	2.5	ferric enterobactin transport protein FepG
PA4167	*yafB*	7.7	probable oxidoreductase
PA4328	*uspA*	3.2	UspA (COG prediction: universal stress protein UspA and related nucleotide-binding proteins)
PA4358		2.0	probable ferrous iron transport protein

PA4359		2.4	conserved hypothetical protein
PA4405		2.4	hypothetical protein
PA4454	*ttg2C*	2.2	Ttg2C (COG prediction: ABC-type transport system involved in resistance to organic solvents, periplasmic component)
PA4459		2.2	conserved hypothetical protein
PA4461	*yhbG*	2.1	probable ATP-binding component of ABC transporter
PA4467		2.7	hypothetical protein
PA4468	*sodM*	2.1	superoxide dismutase
PA4469		3.0	hypothetical protein
PA4470	*fumC1*	3.2	fumarate hydratase
PA4471		3.1	hypothetical protein
PA4514	*piuA*	5.9	probable outer membrane receptor for iron transport
PA4515	*piuC*	2.7	conserved hypothetical protein
PA4544	*rluD*	2.3	pseudouridine synthase
PA4571		2.0	probable cytochrome c
PA4586		2.8	hypothetical protein
PA4587	*ccpR*	3.1	cytochrome c551 peroxidase precursor
PA4588	*gdhA*	2.6	glutamate dehydrogenase
PA4625		4.0	hypothetical protein
PA4641		3.0	still frameshift hypothetical protein
PA4644		2.8	hypothetical protein
PA4648		3.0	hypothetical protein
PA4689		2.2	hypothetical protein
PA4709	*phuS*	2.1	probable hemin degrading factor
PA4710	*phuR*	10.4	Haem/Haemoglobin uptake outer membrane receptor PhuR precursor
PA4711		2.2	hypothetical protein
PA4728	*folK*	2.1	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
PA4757	*rhtB*	2.0	RhtB (COG prediction: putative threonine efflux protein)
PA4770	*lldP*	5.7	L-lactate permease
PA4771	*lldD*	11.2	L-lactate dehydrogenase
PA4772		7.1	probable ferredoxin
PA4777	*pmrB*	2.0	PmrB: two-component regulator system signal sensor kinase PmrB
PA4839	*speA*	2.4	biosynthetic arginine decarboxylase
PA4843		2.1	probable two-component response regulator
PA4853	*fis*	2.6	DNA-binding protein Fis
PA4854	*purH*	2.2	phosphoribosylaminoimidazolecarboxamide formyltransferase
PA4855	*purD*	2.6	phosphoribosylamine--glycine ligase
PA4895		2.8	probable transmembrane sensor
PA4962		2.5	conserved hypothetical protein
PA4995		2.9	probable acyl-CoA dehydrogenase
PA5012	*waaF*	2.0	heptosyltransferase II

PA5019	*comJ*	2.1	ComJ (COG prediction: protein involved in catabolism of external DNA)
PA5027	*uspA*	2.6	UspA (COG prediction: universal stress protein UspA and related nucleotide-binding proteins)
PA5030		2.9	probable major facilitator superfamily (MFS) transporter
PA5035	*gltD*	3.5	glutamate synthase small chain
PA5036	*gltB*	3.5	glutamate synthase large chain precursor
PA5072		2.4	probable chemotaxis transducer
PA5117	*typA*	2.2	regulatory protein TypA
PA5124	*ntrB*	2.3	two-component sensor NtrB
PA5158	*opmG*	2.9	probable outer membrane protein precursor
PA5159	*pmrA*	3.7	multidrug resistance protein
PA5160	*pmrB*	2.8	drug efflux transporter ; tRNA-Thr
PA5165		2.4	probable two-component sensor
PA5170	*arcD*	4.1	arginine/ornithine antiporter
PA5171	*arcA*	2.9	arginine deiminase
PA5172	*arcB*	2.1	ornithine carbamoyltransferase, catabolic
PA5199	*envZ*	2.0	two-component sensor EnvZ
PA5202		2.4	hypothetical protein
PA5208		2.1	conserved hypothetical protein
PA5232	*emrA*	2.4	EmrA (COG prediction: multidrug resistance efflux pump)
PA5296	*rep*	2.7	ATP-dependent DNA helicase Rep
PA5298	*xpt*	2.1	xanthine phosphoribosyltransferase
PA5359		2.3	hypothetical protein
PA5407		2.2	hypothetical protein
PA5424		2.1	conserved hypothetical protein
PA5427	*adhA*	2.8	alcohol dehydrogenase
PA5435	*oadA*	2.6	probable transcarboxylase subunit
PA5436		2.4	probable biotin carboxylase subunit of a transcarboxylase
PA5440	*yegQ*	2.6	probable peptidase
PA5475		2.4	hypothetical protein
PA5497	*nrdJa*	2.7	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, NrdJa
PA5548		2.5	probable major facilitator superfamily (MFS) transporter
PA5553	*atpC*	2.2	ATP synthase epsilon chain
PA5554	*atpD*	2.0	ATP synthase beta chain

[1] Fold change values were averaged over three different GeneChips® for each condition (LB and LB+0.2% oleate) with P-values ≤ 0.05.

TABLE S2. *P. aeruginosa* genes expressed two-fold or greater when grown to mid-log phase in LB versus LB supplemented with oleate ($C_{18:1}^{\Delta 9}$) as identified using microarray.

Accession Number	**Gene**	**Fold Change[1]**	**Description**
PA0031	*betC*	5.7	choline sulfatase
PA0048		2.5	probable transcriptional regulator
PA0049		8.0	hypothetical protein
PA0129	*gabP*	6.2	gamma-aminobutyrate permease
PA0130	*putA*	4.3	PutA (COG prediction: NAD-dependent aldehyde dehydrogenase)
PA0131		4.0	hypothetical protein
PA0132	*oapT*	5.4	beta-alanine-pyruvate transaminase
PA0186	*atsR*	4.1	probable binding protein component of ABC transporter
PA0191		16.2	probable transcriptional regulator
PA0197	*tonB*	7.9	TonB (COG prediction: periplasmic protein, links inner and outer membranes)
PA0198	*exbB1*	10.8	transport protein ExbB
PA0201		15.2	hypothetical protein
PA0241		2.0	probable major facilitator superfamily (MFS) transporter
PA0280	*cysA*	27.1	sulfate transport protein CysA
PA0281	*cysW*	32.8	sulfate transport protein CysW
PA0282	*cysT*	19.5	sulfate transport protein CysT
PA0283	*sbp*	14.4	sulfate-binding protein precursor
PA0284		17.9	hypothetical protein
PA0291	*oprE*	2.2	Anaerobically-induced outer membrane porin OprE precursor
PA0298	*spuB*	2.0	probable glutamine synthetase
PA0299	*spuC*	3.4	putrescine aminotransferase
PA0304	*potI*	2.1	polyamine transport protein PotI
PA0364		6.1	probable oxidoreductase
PA0365		7.1	hypothetical protein
PA0366		4.6	probable aldehyde dehydrogenase
PA0399		2.7	cystathionine beta-synthase
PA0400	*metC*	2.1	probable cystathionine gamma-lyase
PA0473	*psfA*	3.5	probable glutathione S-transferase
PA0492	*yscF*	2.1	conserved hypothetical protein
PA0493		5.8	probable biotin-requiring enzyme
PA0494		5.2	probable acyl-CoA carboxylase subunit
PA0495		5.4	hypothetical protein
PA0496	*ybgK*	7.3	conserved hypothetical protein
PA0602		3.0	probable binding protein component of ABC transporter
PA0730		2.6	probable transferase
PA0741	*ywnB*	2.2	conserved hypothetical protein

PA0742		4.1	hypothetical protein
PA0744		4.5	probable enoyl-CoA hydratase/isomerase
PA0745		3.1	probable enoyl-CoA hydratase/isomerase
PA0746		5.9	probable acyl-CoA dehydrogenase
PA0752		2.1	conserved hypothetical protein
PA0753		2.4	hypothetical protein
PA0754		2.1	hypothetical protein
PA0755	*opdH*	2.6	cis-aconitate porin OpdH
PA0783	*putP*	2.3	sodium/proline symporter PutP
PA0789		9.5	probable amino acid permease
PA0792	*prpD*	2.9	propionate catabolic protein PrpD
PA0793		3.9	hypothetical protein
PA0794		4.2	probable aconitate hydratase
PA0795	*prpC*	4.5	citrate synthase 2
PA0796	*prpB*	4.9	carboxyphosphonoenolpyruvate phosphonomutase
PA0797		4.3	probable transcriptional regulator
PA0830		10.7	hypothetical protein
PA0831	*oruR*	2.5	transcriptional regulator OruR
PA0839		2.5	probable transcriptional regulator
PA0840		3.5	probable oxidoreductase
PA0841		3.7	hypothetical protein
PA0850		2.9	hypothetical protein
PA0852	*cpbD*	2.4	chitin-binding protein CbpD precursor
PA0865	*hpd*	27.5	4-hydroxyphenylpyruvate dioxygenase
PA0866	*aroP2*	90.6	aromatic amino acid transport protein AroP2
PA0867	*mliC*	6.1	membrane-bound lysozyme inhibitor of c-type lysozyme MliC
PA0870	*phhC*	5.9	aromatic amino acid aminotransferase
PA0871	*phhB*	3.4	pterin-4-alpha-carbinolamine dehydratase
PA0872	*phhA*	7.9	phenylalanine-4-hydroxylase
PA0887	*acsA*	31.7	acetyl-coenzyme A synthetase
PA1070	*braG*	3.9	branched-chain amino acid transport protein BraG
PA1071	*braF*	4.3	branched-chain amino acid transport protein BraF
PA1073	*braD*	3.7	branched-chain amino acid transport protein BraD
PA1074	*braC*	4.2	branched-chain amino acid transport protein BraC
PA1245	*aprX*	3.3	hypothetical protein
PA1293		3.0	hypothetical protein
PA1337	*ansB*	4.7	glutaminase-asparaginase
PA1338	*ggt*	5.8	gamma-glutamyltranspeptidase precursor
PA1339		2.3	probable ATP-binding component of ABC transporter
PA1340		2.9	probable permease of ABC transporter
PA1341		2.9	probable permease of ABC transporter

PA1342		2.8	probable binding protein component of ABC transporter
PA1409	*aphA*	9.5	acetylpolyamine aminohydrolase
PA1410	*potF1*	5.7	probable periplasmic spermidine/putrescine-binding protein
PA1493	*cysP*	3.2	sulfate-binding protein of ABC transporter
PA1524	*xdhA*	2.8	xanthine dehydrogenase
PA1537		4.2	probable short-chain dehydrogenase
PA1538		3.1	probable flavin-containing monooxygenase
PA1542		5.0	hypothetical protein
PA1632	*kdpF*	6.2	KdpF protein
PA1634	*kdpB*	4.3	potassium-transporting ATPase, B chain
PA1635	*kdpC*	3.9	potassium-transporting ATPase, C chain
PA1649		3.5	probable short-chain dehydrogenase
PA1694	*pscQ*	2.0	translocation protein in type III secretion
PA1699	*pcr1*	2.5	conserved hypothetical protein in type III secretion
PA1702	*pcr4*	2.1	conserved hypothetical protein in type III secretion
PA1707	*pcrH*	2.9	regulatory protein PcrH
PA1708	*popB*	2.4	translocator protein PopB
PA1709	*popD*	2.4	Translocator outer membrane protein PopD precursor
PA1710	*exsC*	3.3	exoenzyme S synthesis protein C precursor
PA1711	*exsE*	2.7	ExsC interacting protein
PA1712	*exsB*	2.7	exoenzyme S synthesis protein B
PA1718	*pscE*	2.1	type III export protein PscE
PA1722	*pscI*	2.1	type III export protein PscI
PA1742		2.7	probable amidotransferase
PA1756	*cysH*	3.5	3'-phosphoadenosine-5'-phosphosulfate reductase
PA1759		2.9	probable transcriptional regulator
PA1760		5.1	probable transcriptional regulator
PA1761		3.1	hypothetical protein
PA1818	*speC*	6.9	probable Orn/Arg/Lys decarboxylase
PA1819	*yjdE*	4.5	probable amino acid permease
PA1837		5.1	hypothetical protein
PA1838	*cysI*	4.5	sulfite reductase
PA1947	*rbsA*	2.2	ribose transport protein RbsA
PA1948	*rbsC*	2.4	membrane protein component of ABC ribose transporter
PA1949	*rbsR*	2.2	ribose operon repressor RbsR
PA1978	*agmR*	6.5	probable transcriptional regulator
PA1984	*exaC1*	118.7	probable aldehyde dehydrogenase
PA1985	*pqqA*	4.0	pyrroloquinoline quinone biosynthesis protein A
PA1986	*pqqB*	5.1	pyrroloquinoline quinone biosynthesis protein B
PA1987	*pqqC*	4.5	pyrroloquinoline quinone biosynthesis protein C
PA1988	*pqqD*	4.4	pyrroloquinoline quinone biosynthesis protein D

PA1989	*pqqE*	3.7	pyrroloquinoline quinone biosynthesis protein E
PA1990		4.2	probable peptidase
PA1991		3.8	probable iron-containing alcohol dehydrogenase
PA1992		3.2	probable two-component sensor
PA1999	*atoD*	73.8	probable CoA transferase, subunit A
PA2000	*atoA*	116.9	probable CoA transferase, subunit B
PA2001	*atoB*	48.1	acetyl-CoA acetyltransferase
PA2002	*atoE*	34.5	AtoE (COG prediction: Short chain fatty acids transporter)
PA2003	*bdhA*	6.2	3-hydroxybutyrate dehydrogenase
PA2004	*gntT*	7.4	GntT (COG prediction: H+/gluconate symporter and related permeases)
PA2006		34.9	probable major facilitator superfamily (MFS) transporter
PA2007	*maiA*	35.7	maleylacetoacetate isomerase
PA2008	*fahA*	59.4	fumarylacetoacetase
PA2009	*hmgA*	85.7	homogentisate 1,2-dioxygenase
PA2012	*liuD*	14.2	alpha subunit of geranoyl-CoA carboxylase, GnyA
PA2013	*liuC*	12.0	gamma-carboxygeranoyl-CoA hydratase, GnyH
PA2014	*liuB*	11.4	beta subunit of geranoyl-CoA carboxylase, GnyB
PA2015	*liuA*	11.0	Citronelloyl-CoA dehydrogenase, GnyD
PA2016	*liuR*	6.1	Regulatory gene of gnyRDBHAL cluster, GnyR
PA2041		4.4	probable amino acid permease
PA2062		5.5	probable pyridoxal-phosphate dependent enzyme
PA2073		4.9	probable transporter (membrane subunit)
PA2079		3.5	probable amino acid permease
PA2080	*kynU*	2.0	kynureninase KynU
PA2081	*kynB*	2.7	kynurenine formamidase, KynB
PA2083		3.9	probable ring-hydroxylating dioxygenase subunit
PA2109		13.6	hypothetical protein
PA2110		11.4	hypothetical protein
PA2111		13.3	hypothetical protein
PA2112		11.0	conserved hypothetical protein
PA2113	*opdO*	20.1	pyroglutamate porin OpdO
PA2114		26.3	probable major facilitator superfamily (MFS) transporter
PA2116		5.4	conserved hypothetical protein
PA2123		5.0	probable transcriptional regulator
PA2202		20.7	probable amino acid permease
PA2203		20.2	probable amino acid permease
PA2204		16.0	probable binding protein component of ABC transporter
PA2247	*bkdA1*	31.0	2-oxoisovalerate dehydrogenase (alpha subunit)
PA2248	*bkdA2*	19.1	2-oxoisovalerate dehydrogenase (beta subunit)
PA2249	*bkdB*	15.2	branched-chain alpha-keto acid dehydrogenase (lipoamide component)
PA2250	*lpdV*	29.5	lipoamide dehydrogenase-Val

PA2252		3.1	probable AGCS sodium/alanine/glycine symporter
PA2258	*ptxR*	2.9	transcriptional regulator PtxR
PA2310	*tauD*	4.9	TauD (COG prediction: probable taurine catabolism dioxygenase)
PA2311		3.2	hypothetical protein
PA2312		9.5	probable transcriptional regulator
PA2321	*gntV*	2.6	gluconokinase
PA2322	*gntU*	7.0	gluconate permease
PA2323	*gapN*	2.3	probable glyceraldehyde-3-phosphate dehydrogenase
PA2327		2.8	probable permease of ABC transporter
PA2329		3.1	probable ATP-binding component of ABC transporter
PA2330	*caiA*	4.0	CaiA (COG prediction: acyl-CoA dehydrogenases)
PA2331		5.8	hypothetical protein
PA2333		3.7	probable sulfatase
PA2334		13.8	probable transcriptional regulator
PA2358		3.5	hypothetical protein
PA2359		23.4	probable transcriptional regulator
PA2532	*tpx*	2.9	thiol peroxidase
PA2533		4.1	probable sodium:alanine symporter
PA2552	*acdB*	6.7	probable acyl-CoA dehydrogenase
PA2553		17.3	probable acyl-CoA thiolase
PA2554		7.1	probable short-chain dehydrogenase
PA2555		5.9	probable AMP-binding enzyme
PA2557		16.6	probable AMP-binding enzyme
PA2575		2.3	FMR2 (COG prediction: oxidoreductase related to nitroreductase)
PA2594	*tauA*	7.2	TauA (COG prediction: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components)
PA2597	*caiA*	3.0	CaiA (COG prediction: acyl-CoA dehydrogenases)
PA2598		6.5	hypothetical protein
PA2599	*tauA*	10.6	TauA (COG prediction: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components)
PA2600		5.7	hypothetical protein
PA2602		2.4	hypothetical protein
PA2679	*ubiE*	3.1	UbiE (COG prediction: methylase involved in ubiquinone/menaquinone biosynthesis)
PA2776	*dadA*	3.1	DadA (COG prediction: glycine/D-amino acid oxidases)
PA2779		2.2	hypothetical protein
PA2862	*lipA*	6.9	lactonizing lipase precursor
PA3025	*glpD2*	2.4	probable FAD-dependent glycerol-3-phosphate dehydrogenase
PA3026	*glcD*	2.4	GlcD (COG prediction: FAD/FMN-containing dehydrogenases)
PA3038	*opdQ*	18.0	probable porin
PA3067		2.3	probable transcriptional regulator
PA3068	*gdhB*	4.3	NAD-dependent glutamate dehydrogenase

PA3181	*edaA*	3.7	2-keto-3-deoxy-6-phosphogluconate aldolase
PA3182	*pgl*	3.1	6-phosphogluconolactonase
PA3183	*zwf*	3.3	glucose-6-phosphate 1-dehydrogenase
PA3186	*oprB*	4.9	probable glucose-sensitive porin ; Glucose/carbohydrate outer membrane porin OprB precursor
PA3187	*gltK*	37.2	probable ATP-binding component of ABC transporter
PA3188	*gltG*	171.2	probable permease of ABC sugar transporter
PA3189	*gltF*	48.9	probable permease of ABC sugar transporter
PA3190	*gltB*	107.3	probable binding protein component of ABC sugar transporter
PA3191		3.0	probable two-component sensor
PA3192	*gltR*	2.9	two-component response regulator GltR
PA3193	*glk*	2.9	glucokinase
PA3194	*edd*	2.4	phosphogluconate dehydratase
PA3195	*gapA*	17.7	glyceraldehyde 3-phosphate dehydrogenase
PA3232		6.2	probable nuclease
PA3233		29.1	hypothetical protein
PA3234	*yjcG*	62.0	probable sodium:solute symporter
PA3235	*yjcH*	157.2	conserved hypothetical protein
PA3271		2.1	probable two-component sensor
PA3300	*fadD2*	3.7	long-chain-fatty-acid-CoA ligase
PA3355	*araJ*	2.5	AraJ (COG prediction: arabinose efflux permease)
PA3356	*glnA*	4.7	GlnA (COG prediction: glutamine synthetase)
PA3364	*amiC*	3.6	aliphatic amidase expression-regulating protein
PA3365	*amiB*	5.7	probable chaperone
PA3366	*amiE*	3.7	aliphatic amidase
PA3442	*ycbE*	4.0	probable ATP-binding component of ABC transporter
PA3443	*ycbM*	8.6	probable permease of ABC transporter
PA3444	*ssuD*	13.1	conserved hypothetical protein
PA3445	*tauA*	12.1	TauA (COG prediction: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components)
PA3446	*ssuE*	48.6	conserved hypothetical protein
PA3450	*lsfA*	14.8	probable antioxidant protein
PA3454		2.2	probable acyl-CoA thiolase
PA3464		2.4	hypothetical protein
PA3471	*sfcA*	2.5	probable malic enzyme
PA3501		2.2	hypothetical protein
PA3502		2.3	hypothetical protein
PA3505		2.1	hypothetical protein
PA3507		2.1	probable short-chain dehydrogenase
PA3509		2.1	probable hydrolase
PA3510		4.6	hypothetical protein

PA3513	*tauA*	6.1	TauA (COG prediction: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components)
PA3535	*eprS*	2.7	probable serine protease
PA3779	*dctP*	4.3	DctP (COG prediction: TRAP-type C4-dicarboxylate transport system, periplasmic component)
PA3780	*dctM*	9.8	DctM (COG prediction: TRAP-type C4-dicarboxylate transport system, small permease component)
PA3781	*dctQ*	6.4	DctM (COG prediction: TRAP-type C4-dicarboxylate transport system, large permease component)
PA3836		3.2	hypothetical protein
PA3837		3.4	probable permease of ABC transporter
PA3838		3.1	probable ATP-binding component of ABC transporter
PA3841	*exoS*	2.4	exoenzyme S
PA3922		10.5	conserved hypothetical protein
PA3923		6.9	hypothetical protein
PA3931	*nlpA*	37.1	NlpA (COG prediction: ABC-type metal ion transport system, periplasmic component/surface antigen)
PA3932		32.4	probable transcriptional regulator
PA3934		3.3	conserved hypothetical protein
PA3935	*tauD*	6.1	taurine dioxygenase
PA3936		10.2	probable permease of ABC taurine transporter
PA3937	*tauB*	10.5	probable ATP-binding component of ABC taurine transporter
PA3938	*tauA*	11.6	probable periplasmic taurine-binding protein precursor
PA3939		3.8	hypothetical protein
PA3959		2.5	hypothetical protein
PA3960		2.6	hypothetical protein
PA4014		2.5	hypothetical protein
PA4015	*maoC*	2.2	MaoC (COG prediction: acyl dehydratase)
PA4021	*acoR*	5.9	AcoR (COG prediction: transcriptional activator of acetoin/glycerol metabolism)
PA4023	*eutP*	117.5	probable transport protein
PA4024	*eutB*	40.3	ethanolamine ammonia-lyase large subunit
PA4025	*eutC*	10.7	probable ethanolamine ammonia-lyase light chain
PA4191		15.3	probable iron/ascorbate oxidoreductase
PA4192		33.4	probable ATP-binding component of ABC transporter
PA4193		41.6	probable permease of ABC transporter
PA4194		34.1	probable permease of ABC transporter
PA4195		33.8	probable binding protein component of ABC transporter
PA4198		10.4	probable AMP-binding enzyme
PA4199		3.5	probable acyl-CoA dehydrogenase
PA4200	*gloB*	2.3	GloB (COG prediction: Zn-dependent hydrolases, including glyoxylases)
PA4290		9.1	probable chemotaxis transducer

PA4442	*cysN*	5.1	ATP sulfurylase GTP-binding subunit/APS kinase
PA4443	*cysD*	8.4	ATP sulfurylase small subunit
PA4496		13.6	probable binding protein component of ABC transporter
PA4497		5.2	probable binding protein component of ABC transporter
PA4498		7.5	probable metallopeptidase
PA4500		13.0	probable binding protein component of ABC transporter
PA4501	*opdD*	19.1	Glycine-glutamate dipeptide porin OpdP
PA4502		20.3	probable binding protein component of ABC transporter
PA4503	*dppB*	22.3	probable permease of ABC transporter
PA4504	*dppC*	14.8	probable permease of ABC transporter
PA4505	*dppD*	9.6	probable ATP-binding component of ABC transporter
PA4506	*dppF*	10.6	probable ATP-binding component of ABC dipeptide transporter
PA4548	*yfiT*	2.0	probable D-amino acid oxidase
PA4590	*pra*	2.5	protein activator
PA4603		2.3	hypothetical protein
PA4604		2.8	conserved hypothetical protein
PA4605		5.5	conserved hypothetical protein
PA4606	*cstA*	7.4	CstA (COG prediction: carbon starvation protein, predicted membrane protein)
PA4613	*katB*	2.3	catalase
PA4661	*pagL*	3.2	Lipid A 3-O-deacylase
PA4733	*acsB*	4.7	acetyl-coenzyme A synthetase
PA4787		3.5	probable transcriptional regulator
PA4847	*accB*	2.1	biotin carboxyl carrier protein (BCCP)
PA4872	*prpB*	2.3	PrpB (COG prediction: PEP phosphonomutase and related enzymes)
PA4888	*desB*	22.8	acyl-CoA delta-9-desaturase, DesB
PA4890	*desT*	2.2	DesT, transcriptional regulators
PA4899		2.4	probable aldehyde dehydrogenase
PA4976	*aspC*	2.7	aspartate transaminase
PA4978		3.5	hypothetical protein
PA4979		5.3	probable acyl-CoA dehydrogenase
PA4986		2.3	probable oxidoreductase
PA5015	*aceE*	2.4	pyruvate dehydrogenase
PA5024	*ytnM*	16.9	(COG prediction: permeases)
PA5082		2.2	probable binding protein component of ABC transporter
PA5100	*hutU*	2.5	urocanase
PA5101	*phnD*	3.9	PhnD (COG prediction: ABC-type phosphate/phosphonate transport system, periplasmic component)
PA5102	*desA*	8.6	DesA (COG prediction: fatty acid desaturase)
PA5103	*proX*	17.9	ProX (COG prediction: ABC-type proline/glycine betaine transport systems, periplasmic components)
PA5112	*estA*	3.0	esterase EstA

PA5152		4.2	probable ATP-binding component of ABC transporter
PA5153		4.9	probable periplasmic binding protein
PA5154		8.9	probable permease of ABC transporter
PA5155		6.7	probable permease of ABC transporter
PA5167		3.4	probable c4-dicarboxylate-binding protein
PA5168		4.3	probable dicarboxylate transporter
PA5169		4.2	probable C4-dicarboxylate transporter
PA5174		6.6	probable beta-ketoacyl synthase
PA5188		2.1	probable 3-hydroxyacyl-CoA dehydrogenase
PA5212		5.7	hypothetical protein
PA5302	*dadX*	9.5	catabolic alanine racemase
PA5303	*tdcF*	7.9	TdcF (COG prediction: Putative translation initiation inhibitor, yjgF family)
PA5304	*dadA*	8.0	D-amino acid dehydrogenase, small subunit
PA5312	*kauB*	3.7	probable aldehyde dehydrogenase
PA5348		3.4	probable DNA-binding protein
PA5375	*betT1*	4.5	choline transporter BetT
PA5377		2.4	probable permease of ABC transporter
PA5379	*sdaB*	2.6	L-serine dehydratase
PA5380	*gbdR*	14.2	probable transcriptional regulator
PA5396		6.6	hypothetical protein
PA5397		12.8	hypothetical protein
PA5398	*dgcA*	8.0	DgcA (COG prediction: dimethylglycine catabolism)
PA5400		5.8	probable electron transfer flavoprotein alpha subunit
PA5410	*gbcA*	13.5	glycine betaine catabolism protein
PA5411	*gbcB*	3.8	glycine betaine catabolism protein
PA5416	*soxB*	13.1	sarcosine oxidase beta subunit
PA5417	*soxD*	8.5	sarcosine oxidase delta subunit
PA5419	*soxG*	8.3	sarcosine oxidase gamma subunit
PA5420	*purU2*	7.6	formyltetrahydrofolate deformylase
PA5421	*fdhA*	4.0	glutathione-independent formaldehyde dehydrogenase
PA5429	*aspA*	3.7	aspartate ammonia-lyase
PA5442		3.7	conserved hypothetical protein
PA5445		4.4	probable coenzyme A transferase
PA5452	*wbpW*	2.3	phosphomannose isomerase/GDP-mannose WbpW
PA5506	*rpiR*	3.0	RpiR (COG prediction: transcriptional regulators)
PA5507	*pncA*	4.0	PncA (COG prediction: amidases related to nicotinamidase)
PA5508		4.2	probable glutamine synthetase
PA5509		2.9	hypothetical protein
PA5510		3.6	probable transporter
PA5542	*ampC*	3.0	AmpC (COG prediction: beta-lactamase class C and other penicillin binding proteins)
PA5543		4.8	hypothetical protein

PA5544		2.5	conserved hypothetical protein
PA5545	*imp*	3.9	Imp (COG prediction: TRAP-type uncharacterized transport system, periplasmic component)

[1] Fold change values were averaged over three different GeneChips® for each condition (LB and LB+0.2% oleate) with P-values ≤ 0.05.