

Transcriptomic and phenotypic analysis reveals new functions for the Tat pathway in *Yersinia pseudotuberculosis*

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Supplemental Information

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Table S1. Oligonucleotides that were used in qRT-PCR.

LocusTag/Gene Name	Oligonucleotide Sequence
YPTB3770	5'-GATCAGTGGTCTCTCTTTTCG-3' 5'-CGTTCGGCGATAATCACATA-3'
YPTB3700/ <i>bfr</i>	5'-TTGAATATCGGAGAAGATGTTGAA-3' 5'-CGGTCGATCAAGCTAAGTTC-3'
YPTB2299/ <i>sodB</i>	5'-GGAACCATACTTCTACTG-3' 5'-TACTGACAATCGCCAATG-3'
pYV0013/ <i>yadA</i>	5'-GCAACAGGCGTTAATTCT-3' 5'-CGTGACTAGAGTGTCCAAT-3'
YPTB0576/ <i>osmY</i>	5'-AGAAATCACAGTCGGTCAGT-3' 5'-CGCCGTTTACCGCTTTAG-3'
YPTB1352/ <i>sdaC</i>	5'-TGGATGACAATGTGGCTAAT-3' 5'-CAGGAGACAGGCTCAGTA-3'
YPTB1728/ <i>wrbA</i>	5'-ACACCATCACTTCAACCT-3' 5'-ATGTTACCTTGAAACG-3'
YPTB3812/ <i>uspA</i>	5'-TGCCAAAGTTTCCCTGAT-3' 5'-ATCCTGATGATGACCACAC-3'
YPTB2410/ <i>mgfB</i>	5'-GGAAGAGGATGCCAGAGA-3' 5'-GAATCGCAATAAGCCACTGA-3'
YPTB2772	5'-TACGGCTCTACTTACGAACC-3' 5'-TCAGACCACCTTTAGCGATAT-3'
YPTB2215	5'-ACGCTGGGTGTGTTCAAG-3' 5'-CGGTGTCTTCTTCACATACTCAA-3'
YPTB1389	5'-GGCAGTCCGATATTCAGTGAT-3' 5'-GAAGGTGTGGCTCAGATAGG-3'
YPTB2903/ <i>gcrA</i>	5'-GCGAAATCTGGCTATGCT-3' 5'-GGATCGTCAGTTGAGGATAC-3'
YPTB3963/ <i>pstC-2</i>	5'-CTTATGGCATTGGCTGTA-3' 5'-GCTAACGCAGAGGTAATAC-3'
YPTB2434/ <i>phoP</i>	5'-CCGACGATTATGTGACCAA-3' 5'-GGATAAGGGTTTCAATGATAGTG-3'

Table S2. Differentially expressed genes in *ΔtatC* at 26°C, 37°C exponential and stationary phase

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
Virulence Genes							
Down Regulated Loci							
pYV0013	<i>yadA</i>	-3	-9	-2.1		adhesin <i>yadA</i>	virulence factor,pYV
pYV0024	<i>sycE</i>		-1.8			putative <i>yopE</i> chaperone	virulence factor,pYV
pYV0025	<i>yopE</i>	-2	-2.8			effector protein	virulence factor,pYV
pYV0040	<i>yopK</i>		-2.4			<i>yop</i> targeting protein <i>yopK</i> , <i>yopQ</i>	virulence factor,pYV
pYV0047	<i>yopM</i>		-1.9			targeted effector protein	virulence factor,pYV
pYV0054	<i>yopD</i>	-2	-2.4			effector protein, translocator protein	virulence factor,pYV
pYV0057	<i>lcrV</i>		-2			V antigen, antihost protein/regulator	virulence factor,pYV
pYV0058	<i>lcrG</i>		-2.3			Yop regulator	virulence factor,pYV
pYV0063	<i>sycN</i>		-1.8			type III secretion protein	virulence factor,pYV
pYV0067	<i>yscN</i>		-2.1			type III secretion ATP synthase	virulence factor,pYV
pYV0068	<i>yscO</i>		-2			type III secretion protein	virulence factor,pYV
pYV0077	<i>yscA</i>		-1.9			type III secretion protein SctA	virulence factor,pYV
pYV0078	<i>yscB</i>		-2.3			type III secretion protein SctB	virulence factor,pYV
YPTB1064	<i>yhhZ-4</i>	-1.8	-1.9			type VI secretion system effector, Hcp1 family	virulence factor
YPTB1483	<i>impB-2</i>		-1.8			type VI secretion protein	virulence factor
YPTB1484	<i>impC</i>		-1.9			type VI secretion protein	virulence factor
YPTB1488	<i>hcp-1</i>		-3			hypothetical protein, putative type VI secretion protein	virulence factor
YPTB2113	<i>ailB</i>	-2.4	-3.4			attachment invasion locus protein	virulence factor
YPTB2695	<i>csgG</i>		-2			curli production assembly/transport component	virulence factor
YPTB3251	<i>impC-2</i>		-2			type VI secretion system effector, Hcp1 family	virulence factor
YPTB3701	<i>bfd</i>	-1.8				bacterioferritin-associated ferredoxin	virulence factor
Upregulated loci							
YPTB0640	<i>impA-2</i>		2.2			ImpA domain protein	virulence factor
YPTB0641	<i>impB-5</i>	1.8	2.7			type VI secretion protein	virulence factor
YPTB0642	<i>impC-4</i>	2	2.5			EvpB family type VI secretion protein,	virulence factor
YPTB0643	<i>hcp-5</i>	2.6	2.8			type VI secretion system secreted protein	virulence factor
YPTB0644	<i>impF-2</i>		2			type VI secretion system lysozyme-related protein	virulence factor
YPTB0645	<i>impG-4, vasa-4</i>		1.8			type VI secretion protein	virulence factor
YPTB0647	<i>clpV-4, vasG-4</i>		2			type VI secretion ATPase, <i>cpIB</i> homolog	virulence factor
YPTB0648	<i>vgrG-4</i>		2.1			type VI secretion system Vgr family protein	virulence factor
YPTB0653	<i>vasD-4, lip-4</i>		1.8			putative lipoprotein	virulence factor
YPTB0654			1.8			type VI secretion system protein	virulence factor
YPTB0655	<i>impJ-4, vasE-4</i>		1.8			type VI secretion protein	virulence factor
YPTB0657		2	2.6			hypothetical protein, putative type VI secretion protein	virulence factor
YPTB0830	<i>luxS</i>		2			quorum-sensing autoinducer 2 (AI-2), LuxS	virulence factor
YPTB1668	<i>invA</i>		2.1			invasin, host cell invasion factor	virulence factor
YPTB2394	<i>yadE</i>		2.7			YadA domain protein	virulence factor
YPTB2542	<i>ompX, ailD</i>	3.6	3.5			virulence-related outer membrane protein	virulence factor
YPTB2867	<i>ailA</i>		1.8			virulence-related outer membrane protein	virulence factor
YPTB3584	<i>pcp-1</i>		2.5			17 kDa surface antigen	virulence factor

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB3639	<i>hcp-1</i>		2			type VI secretion system effector, Hcp1 family	
YPTB3700	<i>bfr</i>	2.2	9.8	2.5	2	bacterioferritin	
Flagella/Motility/Chemotaxis							
Upregulated loci							
YPTB2408	<i>flhC</i>				2	flagellar transcriptional activator (pseudogene)	flagellar assembly
YPTB2409	<i>flhD</i>				1.8	flagellar transcriptional activator	flagellar assembly
Stress Adaptation							
Downregulated loci							
YPTB0071	<i>cpxP</i>	-2.6	-2.6	-1.8		periplasmic stress adaptor protein CpxP	stress response
YPTB1624	<i>cspC-2</i>		-2			cold-shock DNA-binding domain protein	transcription
YPTB2156	<i>cstA-1</i>		-3.3			carbon starvation protein	transcription
YPTB2414	<i>cspC-1</i>		-2.6			cold-shock DNA-binding domain protein	transcription
YPTB0352	<i>terZ</i>		-2			stress protein	stress response, tellirium
YPTB0353	<i>terA</i>		-1.8			stress protein	stress response, tellirium
Upregulated loci							
YPTB0224	<i>rpoH</i>		1.9			RNA polymerase, sigma 32 subunit	transcription
YPTB0576	<i>osmY</i>	1.8	5.9	1.9		hyperosmotically inducible periplasmic protein	stress response, osmotic
YPTB0756	<i>sodC</i>	1.9	2.8			Cu/Zn superoxide dismutase	stress response
YPTB0776	<i>rpoS</i>		4.1	2		RNA polymerase, sigma 70 subunit, RpoD family	transcription
YPTB0811	<i>katY</i>			2.1	1.9	catalase/peroxidase HPI	transcription
YPTB0844	<i>yfiA, raiA</i>	3.4	1.8			sigma 54 modulation protein	transcription
YPTB1088	<i>cspE</i>		2.8			cold-shock protein	transcription
YPTB1246	<i>katA</i>		2.8			catalase	stress response, metabolic
YPTB1955	<i>phoH</i>		3.9			PhoH family protein	stress response
YPTB2151	<i>osmB</i>		1.9			osmotically inducible lipoprotein B	stress response, osmotic
YPTB2223	<i>uspE</i>		2.8			universal stress protein E	stress response
YPTB2299	<i>sodB</i>	2	2.8			superoxide dismutase	transcription
YPTB2375	<i>htpX</i>		2.1			heat shock protein	stress response, heat shock
YPTB2437	<i>pepT-2</i>	1.9				peptidase T	stress response, oxidative
YPTB2546	<i>dps</i>	1.8	4.5			DNA starvation/stationary phase protection	replication, repair
YPTB2743	<i>yfeX</i>		1.9			putative iron dependent peroxidase	stress response, oxidative
YPTB2865	<i>csiE</i>		2.1			stationary phase inducible protein	stress response
YPTB2935	<i>hdeB</i>		2.1			acid-resistance protein	stress response, acid
YPTB3026	<i>ptrA</i>		1.8			peptidase M16 domain protein	folding, sorting, degradation
YPTB3462	<i>terY</i>		1.9			von Willebrand factor type A	stress response, tellirium
YPTB3468	<i>hdeD</i>	2.2	2.7			acid-resistance membrane protein	stress response, acid
YPTB3527	<i>yhbH</i>		1.9			sigma 54 modulation protein/ribosomal protein S30E	transcription
YPTB3764	<i>ompR</i>	2				two component transcriptional regulator	transcription
YPTB3811	<i>uspB</i>		5.9		1.8	universal stress protein B	stress response
YPTB3812	<i>uspA</i>	2	2.6			universal stress protein A	stress response
YPTB3904	<i>ibpA</i>				2.5	heat shock protein Hsp20	stress response, heat shock
Genetic information processing							
Downregulated loci							
YPTB0041	<i>rph</i>		-2			ribonuclease PH	
YPTB0047	<i>rpmB</i>				-1.8	ribosomal protein L28	translation
YPTB0048	<i>rpmG</i>				-1.8	ribosomal protein L33	translation
YPTB0102	<i>rpmE</i>		-2.2			ribosomal protein L31	translation
YPTB0279	<i>rplK</i>		-2.6			ribosomal protein L11	translation

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB0280	<i>rplA</i>		-2.3			ribosomal protein L1	translation
YPTB0281	<i>rplJ</i>		-2.3			ribosomal protein L10	translation
YPTB0282	<i>rplL</i>		-2			ribosomal protein L7/L12	translation
YPTB0408	<i>efp-2,</i> <i>yeiP</i>				-1.8	translation elongation factor B	translation
YPTB0438	<i>rpsF</i>		-2.5			ribosomal protein S6	translation
YPTB0439	<i>priB</i>		-2.4			primosomal replication protein N	replication and repair
YPTB0440	<i>rpsR</i>		-2.3			ribosomal protein S18	translation
YPTB0441	<i>rplI</i>		-2.3			ribosomal protein L9	translation
YPTB0464	<i>rplU</i>	-1.8	-2.7		-1.8	ribosomal protein L21	translation
YPTB0465	<i>rpmA</i>	-1.8	-2.6		-1.9	ribosomal protein L27	translation
YPTB0486	<i>deaD</i>		-2			DEAD/DEAH box helicase domain protein	folding, sorting, degradation, RNA degradation
YPTB0614	<i>nhaR</i>		-2			transcriptional regulator/LysR family	
YPTB0615	<i>rpsT</i>		-2			ribosomal protein S20	translation
YPTB0834	<i>rpsP</i>		-1.9			ribosomal protein S16	translation
YPTB0835	<i>rimM</i>		-2			16S rRNA processing protein	
YPTB0913	<i>rdgC</i>		-2.2			recombination associated protein	
YPTB0994	<i>recR</i>		-1.9			recombination protein	replication and repair
YPTB1121	<i>glnS</i>		-2.3			glutaminyl-tRNA synthetase	translation
YPTB1214	<i>rhIE</i>		-2.4			DEAD/DEAH box helicase domain	folding, sorting, degradation, RNA degradation
YPTB1299	<i>rplY</i>		-1.8			ribosomal protein L25	translation
YPTB1395	<i>infA</i>	-2	-2.5			translation initiation factor IF-1	translation
YPTB1404	<i>serS</i>		-1.8			seryl-tRNA synthetase	translation
YPTB1417	<i>rpsA</i>				-1.9	ribosomal protein S1	translation
YPTB1436	<i>asnC</i>		-1.9			asparaginyl-tRNA synthase	translation
YPTB1463	<i>rmL,</i> <i>yccW</i>		-1.8			23S rRNA methyltransferase	ribosome biogenesis
YPTB2005	<i>prfA</i>		-1.8			peptide chain release factor 1	translation
YPTB2006	<i>hemK,</i> <i>prmC</i>		-1.8			protein-(glutamine-NS) methyltransferase	translation
YPTB2033			-2.1			methyltransferase	
YPTB2036	<i>aspS</i>		-1.8			aspartyl-tRNA synthetase	translation
YPTB2039	<i>ruvC</i>		-1.8			crossover junction endodeoxyribonuclease	replication and repair
YPTB3003	<i>rpsB</i>		-1.8			ribosomal protein S2	translation
YPTB3416	<i>rpsU</i>		-2.1			ribosomal protein S21	translation
YPTB3507	<i>rpsI</i>		-2.1			ribosomal protein S9	translation
YPTB3508	<i>rplM</i>		-2.1			ribosomal protein L13	translation
YPTB3577	<i>fis</i>		-2.6			transcriptional regulator, Fis family	
YPTB3695	<i>rplB</i>		-1.9			ribosomal protein L2	translation
YPTB3696	<i>rplW</i>		-2.3			ribosomal protein L25/L23	translation
YPTB3697	<i>rplD</i>		-2.4			ribosomal protein L4/L1e	translation
YPTB3698	<i>rplC</i>		-2.6			ribosomal protein L3	translation
YPTB3699	<i>rpsJ</i>		-2.9			ribosomal protein S10	translation
YPTB3704	<i>rpsG</i>		-2			ribosomal protein S7	translation
YPTB3946	<i>rnpA</i>		-2.8			ribonuclease P component	RNA processing
Upregulated loci							
YPTB2983	<i>rof</i>		2.2			Rho-binding antiterminator, Rof	
YPTB0291	<i>rsd</i>		2.2			regulator of RpoD, Rsd/AlgQ	
YPTB3544			1.8			ribonuclease	

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
Metabolism							
Downregulated loci							
YPTB0042	<i>pyrE</i>		-2.3			orotate phosphoribosyltransferase	Nucleotide metabolism
YPTB0267	<i>fadB</i>		-1.9			fatty oxidation complex, alpha subunit FadB	lipid, C metabolism
YPTB0402	<i>aspA</i>		-2			aspartate ammonia-lyase	aa metabolism
YPTB0719	<i>speD</i>		-1.8			S-adenosylmethionine decarboxylase proenzyme	aa metabolism
YPTB0720	<i>speE</i>		-2.1			spermidine synthase	aa metabolism
YPTB0754	<i>pyrG</i>		-1.8			CTP synthase	Nucleotide metabolism
YPTB0783			-1.8			dihydroxyacetone kinase, L subunit	lipid metabolism
YPTB0901	<i>gpt</i>		-2.2			Xanthine phosphoribosyltransferase	Nucleotide metabolism
YPTB0935	<i>ribH</i>		-2.1			6,7-dimethyl-8-ribityllumazine synthase	vitamin and cofactor metabolism
YPTB0952	<i>cyoA</i>		-1.8			ubiquinol oxidase, subunit II	energy metabolism
YPTB0991	<i>apt-2</i>		-2.1			adenine phosphoribosyltransferase	Nucleotide metabolism
YPTB0996	<i>adk</i>		-2.3		-1.8	nucleoside-triphosphate—adenylate kinase	Nucleotide metabolism
YPTB1032	<i>purE</i>	-1.9	-1.8			phosphoribosylaminoimidazole carboxylase, catalytic subunit	Nucleotide metabolism
YPTB1143	<i>sdhC</i>		-2.9			succinate dehydrogenase, cytochrome b556 subunit	C metabolism
YPTB1144	<i>sdhD</i>		-2.4			succinate dehydrogenase, hydrophobic membrane anchor protein	C metabolism
YPTB1145	<i>sdhA</i>		-2.4			succinate dehydrogenase, flavoprotein subunit	C metabolism
YPTB1146	<i>sdhB</i>		-2.3			succinate dehydrogenase and fumarate reductase iron-sulfur protein	C metabolism
YPTB1147	<i>kgd,suc A</i>		-2			2-oxoglutarate dehydrogenase, E1 subunit	C,aa metabolism
YPTB1148	<i>sucB</i>		-2			2-oxoglutarate dehydrogenase, E2 subunit, dihydrolipoamide succinyltransferase	C, aa metabolism
YPTB1149	<i>sucC</i>		-2			succinyl-CoA synthetase, beta subunit	C metabolism
YPTB1647	<i>sdaA</i>		-2.4			L-serine dehydratase 1	aa metabolism
YPTB2001	<i>prsA</i>		-2.7			ribose-phosphate pyrophosphokinase	C metabolism
YPTB2046	<i>msbB</i>		-1.8			lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase	LPS
YPTB2047	<i>pykA</i>		-2.2			pyruvate kinase	C metabolism
YPTB2074	<i>dadA</i>		-2.9			D-amino-acid dehydrogenase	aa metabolism
YPTB2100			-1.8			nucleotide sugar dehydrogenase	C metabolism
YPTB2197	<i>aldB</i>				-1.9	aldehyde dehydrogenase	C, aa, xenobiotics
YPTB2469	<i>fabF</i>		-1.8			3-oxoacyl-(acyl-carrier-protein) synthase 2	lipid metabolism
YPTB2794	<i>upp</i>		-1.9			uracil phosphoribosyltransferase	Nucleotide metabolism
YPTB2845	<i>ndk</i>		-1.9			nucleoside-diphosphate kinase	Nucleotide metabolism
YPTB2862	<i>suhB</i>		-2.6			inositol-phosphate phosphatase	C metabolism
YPTB3001	<i>pyrH</i>		-1.9			uridylate kinase	Nucleotide metabolism
YPTB3404	<i>ribB</i>		-2.3			3,4-dihydroxy-2-butanone 4-phosphate synthase	Vitamin/cofactor synthesis
YPTB3774	<i>malQ</i>				-1.9	4-alpha-glucanotransferase	C metabolism
YPTB3775					-2.4	maltodextrin phosphorylase	C metabolism
YPTB3853			-1.9			pyridoxal-phosphate dependent protein	Nucleotide metabolism
YPTB3970	<i>atpH</i>		-1.8			ATP synthase F1, delta subunit	energy metabolism
YPTB3973	<i>atpB</i>		-2.8			ATP synthase F0, A subunit	energy metabolism
YPTB3974	<i>atpI</i>		-2.5			ATP synthase I chain	energy metabolism
Upregulated loci							
YPTB0074	<i>pfkA</i>		1.8			6-phosphofructokinase	C metabolism
YPTB0135	<i>ilvM</i>				2	acetolactate synthase isozyme small subunit II	C, aa, vitamin and cofactor metabolism
YPTB0136	<i>ilvE</i>				2	branched chain amino acid transferase	aa metabolism
YPTB0110	<i>argC</i>		2			N-acetyl-gamma-glutamyl-phosphate reductase	aa metabolism

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YPTB0111	<i>argB</i>		2.4			acetylglutamate kinase	aa metabolism
YPTB0112	<i>argH</i>		2.4			argininosuccinate lyase	aa metabolism
YPTB0145	<i>ilvC</i>	1.9				ketol-acid reductoisomerase	aa, vitamin and cofactor metabolism
YPTB0249	<i>ysgA</i>		3.6			carboxymethylenebutenolidase	Xenobiotics degradation
YPTB0250	<i>udp</i>		1.8			uridine phosphorylase	nucleotide metabolism
YPTB0266	<i>fadA</i>			1.8		acetyl-CoA C-acyltransferase FadA	lipid, aa metabolism
YPTB0345	<i>metF-1</i>		2.5			methylenetetrahydrofolate reductase	energy metabolism
YPTB0410	<i>frdD</i>		2			fumarate reductase D subunit	C metabolism
YPTB0411	<i>frdC</i>		2			fumarate reductase subunit C	C metabolism
YPTB0412	<i>frdB</i>		2			succinate dehydrogenase and fumarate reductase iron-sulfur protein	C metabolism
YPTB0413	<i>frdA</i>		1.9			fumarate reductase, flavoprotein subunit	C metabolism
YPTB0519	<i>nrdD</i>	2			1.9	anaerobic ribonucleoside-triphosphate reductase	Nucleotide metabolism
YPTB0583	<i>deoB</i>		1.8			phosphopentomutase	C metabolism
YPTB0755	<i>eno</i>		1.8			phosphopyruvate hydratase	C metabolism
YPTB0767	<i>cysQ</i>		2			3'(2'),5'-bisphosphate nucleotidase	Nucleotide metabolism
YPTB0809	<i>cybB</i>			2.1	1.8	cytochrome B561	Energy metabolism
YPTB0810	<i>cybC-2</i>			2.1	1.9	cytochrome b562	Energy metabolism
YPTB1166	<i>gpmA</i>		2.1			phosphoglycerate mutase	C, N, aa metabolism
YPTB1218	<i>dld</i>		2.1			D-lactate dehydrogenase	C metabolism
YPTB1241	<i>adiA</i>		7.4			arginine decarboxylase	aa metabolism
YPTB1408	<i>pflB</i>		1.9			formate acetyltransferase	C metabolism
YPTB1578	<i>lldD</i>		2.2			FMN-dependent alpha-hydroxy acid dehydrogenase	C metabolism
YPTB1659	<i>ftnA</i>	2	2.3			Ferroxidase	vitamin and cofactor metabolism
YPTB2103	<i>adhE</i>		3.7			iron containing alcohol dehydrogenase	C metabolism
YPTB2143	<i>acnA</i>		2			aconitate hydratase 1	C metabolism
YPTB2191	<i>bioD</i>	1.9				dethiobiotin synthase	vitamin and cofactor metabolism
YPTB2306	<i>pykF</i>		2.9			pyruvate kinase	C metabolism
YPTB2421	<i>appA</i>		1.8			histidine acid phosphatase	C metabolism
YPTB2454	<i>aroE-2</i>		1.9			Shikimate dehydrogenase substrate binding domain protein	aa metabolism
YPTB2558	<i>menB</i>		2			naphthoate synthase	vitamin and cofactor metabolism
YPTB2559	<i>menH, yfbB</i>		1.8			alpha/beta hydrolase fold	vitamin and cofactor metabolism
YPTB2593		1.9	2.2			HAD-superfamily hydrolase, subfamily IA, variant 3	nucleotide metabolism
YPTB2938	<i>ureD</i>		2.1			urease accessory protein UreD	Nucleotide,aa metabolism
YPTB2939	<i>ureG</i>		2			urease accessory protein UreG	Nucleotide,aa metabolism
YPTB2941	<i>ureE</i>		2.4			UreE urease accessory domain protein	Nucleotide,aa metabolism
YPTB2942	<i>ureC</i>		2.4			urease, alpha subunit	Nucleotide,aa metabolism
YPTB2943	<i>ureB</i>		2.1			urease, beta subunit	Nucleotide,aa metabolism
YPTB2944	<i>ureA</i>		2.3			urease, gamma subunit	Nucleotide,aa metabolism
YPTB3023	<i>argA</i>		1.9			amino-acid N-acetyltransferase	aa metabolism
YPTB3068	<i>cynT</i>	2.1	3	2.2		carbonic anhydrase	N metabolism
YPTB3196	<i>pgk</i>		2.2			phosphoglycerate kinase	C metabolism Glycolysis
YPTB3197	<i>epd</i>		1.9			D-erythrose-4-phosphate dehydrogenase	Vitamin/cofactor synthesis
YPTB3210	<i>aguB</i>		1.8			N-carbamoylputrescine amidase	aa metabolism
YPTB3539	<i>cbuC-1</i>		3			cytochrome b562	Energy metabolism
YPTB3545	<i>gabD-1</i>		2.5			succinic semialdehyde dehydrogenase	C, aa metabolism
YPTB3567	<i>yhdH</i>		3.5			quinone oxidoreductase, YhdH/YhfP family	Energy metabolism
YPTB3568	<i>yedY</i>		2.1			oxidoreductase molybdopterin binding	Energy metabolism

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB3569	<i>yedZ</i>		1.9			ferric reductase domain protein /putative sulfite oxidase subunit	Energy metabolism
YPTB3649	<i>pgi</i>		1.9			glucose-6-phosphate isomerase	C metabolism
YPTB3731	<i>argD</i>		2			succinylornithine transaminase family	aa metabolism
YPTB3740	<i>nirB</i>	2.4				nitrite reductase (NAD(P)H), large subunit	Energy metabolism
YPTB3762	<i>pckA</i>		4			phosphoenolpyruvate carboxykinase (ATP)	C metabolism
YPTB3783	<i>glgP-1</i>		3.4			glycogen/starch/alpha-glucan phosphorylase	C metabolism
YPTB3784	<i>glgA</i>		2.7			glycogen/starch synthase, ADP-glucose type	C metabolism
YPTB3785	<i>glgC</i>		3			glucose-1-phosphate adenylyltransferase	C metabolism
YPTB3786	<i>glgX</i>		2.2			glycogen debranching enzyme GlgX	C metabolism
YPTB3787	<i>glgB</i>		1.8			1,4-alpha-glucan branching enzyme	C metabolism
YPTB3803	<i>fbaA-2</i>		2.4			fructose-bisphosphate aldolase, class II	C metabolism Glycolysis
YPTB3813	<i>gdhA</i>	1.9				glutamate dehydrogenase (NADP(+))	vitamin/cofactor
YPTB3818	<i>gor</i>		1.8			glutathione-disulfide reductase	aa metabolism
YPTB3829	<i>praC</i>	1.8	2.6			4-oxalocrotonate tautomerase family enzyme	Xenobiotics degradation
Transport							
Downregulated loci							
YPTB0180	<i>yfiK</i>		-1.9			amino acid permease-associated region	
YPTB1061	<i>yapC</i>		-2.3			pectatin family virulence factor/autotransporter	transport
YPTB1110	<i>corC</i>		-1.8		-2	magnesium/cobalt efflux protein CorC	transport
YPTB1341	<i>yiuA</i> ,	-2				iron siderophore/cobalamin ABC transporter substrate-binding protein	transport
YPTB1352	<i>sdaC</i>		-3.9	-1.9	-1.8	serine transporter	transport
YPTB1390	<i>macA-2</i>	-1.9	-3.1			macrolide transporter subunit	transport
YPTB1391	<i>macB-2</i>		-2.2			macrolide transporter ATP-binding/permease	transport
YPTB1397	<i>cydC</i>		-1.8			cysteine/glutathione ABC transporter membrane /ATP-binding protein	transport, LPS synthesis
YPTB1508	<i>ybiT</i>		-1.9			ABC transporter ATP-binding protein	transport
YPTB1522	<i>mglB</i>		-2.8		-1.8	periplasmic binding protein/LacI transcriptional regulator	transport
YPTB1524	<i>mglC</i>		-2			Monosaccharide-transporting ATPase	transport
YPTB1724	<i>putP</i>		-2.5			sodium/proline symporter	transport
YPTB2117	<i>tonB</i>	-1.8				transporter	transport
YPTB2165	<i>rfnC</i> , <i>rsxC</i>		-1.9			electron transport complex protein RnfC	transport
YPTB2252	<i>qacE</i>		-1.9			small multidrug resistance protein	transport
YPTB3383	<i>exbH</i>	-1.8				tonB-system energizer ExbB	transport
YPTB3600	<i>yjcD</i>		-1.9			xanthine/uracil/vitamin C permease	transport
YPTB3642	<i>lamB</i>				-2.2	porin, 8amb type	
YPTB3643	<i>malk</i>				-2.5	ABC transport related	
YPTB3644					-2.4	glycosidase	
YPTB3737	<i>oprC</i>	-2	-2.7			TonB-dependent copper receptor /iron siderophore receptor	transport
YPTB3832	<i>dctA</i>		-2.6			sodium:dicarboxylate symporter	transport, two component system
YPTB3936	<i>mdfA</i>		-1.9			major facilitator superfamily MFS_1	transport
Upregulated loci							
YPTB1022	<i>copA</i>		2.4			copper translocating P-type ATPase	transport
YPTB1261	<i>ompC</i>	2.9	2			outer membrane pore protein ompC	transport
YPTB1632	<i>manZ</i>		1.9			PTS system, mannose specific, IID subunit	C metabolism, PTS
YPTB1633	<i>manY</i>		2			PTS system, mannose specific IIC subunit	C metabolism, PTS
YPTB1634	<i>manX</i>		1.8			PTS system, mannose specific IIB subunit	C metabolism, PTS
YPTB2258	<i>mppA</i> , <i>oppA</i>		1.9			murein peptide-ABC transporter substrate-binding protein	transport

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB2365	<i>gltP</i>		1.9			sodium:dicarboxylate symporter	transport
YPTB2410	<i>mgtB</i>				12.8	magnesium-translocating P-type ATPase	transport
YPTB2411	<i>mgtC-1</i>				4.3	MgtC/SapB transporter	transport
YPTB2491	<i>yceE</i>		1.8			amino acid/peptide transporter	transport
YPTB2706	<i>nupC-1</i>		2.1			CNT family H+/nucleoside symporter	transport
YPTB2770	<i>afuC, fbpC</i>			2.9	2.9	iron(III) transport system, ATP-binding protein	transport
YPTB2771	<i>afuB, fbpB</i>			2.2	2	iron(III) transport system, permease protein	transport
YPTB2772	<i>afuA, fbpA</i>			4	3.2	iron(III) transport system, substrate binding protein	transport
YPTB2934	<i>kch</i>		3.5			voltage gated potassium channel	transport
YPTB2946	<i>yntD, ddpD-1</i>		3			nickel/di-oligopeptide ABC transporter ATP-binding protein	transport
YPTB2947	<i>yntC, ddpC-1</i>		1.8			nickel/di-oligopeptide ABC transporter permease	transport
YPTB2948	<i>yntB, dppB-1</i>		2.4			nickel/di-oligopeptide ABC transporter permease	transport
YPTB2949	<i>yntA, ddpA-1</i>		2.6			nickel/di-oligopeptide ABC transporter substrate-binding protein	transport
YPTB2975	<i>metQ-1</i>		2			DL-methionine transporter substrate-binding subunit	transport
YPTB3194	<i>mscS</i>		2.1			mechanosensitive ion channel	transport
YPTB3669	<i>mscL</i>		3			large conductance mechanosensitive channel protein	transport
YPTB3842	<i>dppA</i>			1.9		dipeptide ABC transporter substrate-binding protein	transport
YPTB3959	<i>phoU</i>		2			phosphate uptake regulator, PhoU	transport
YPTB3960	<i>pstB-2</i>		2.1			phosphate transporter ATP-binding protein	transport
YPTB3961	<i>pstA-2</i>		2.2			phosphate transporter permease subunit	transport
YPTB3962	<i>pstC-2</i>		2.2			phosphate ABC transporter permease	transport
YPTB3963	<i>pstS-2</i>		3.3			phosphate ABC transporter, periplasmic phosphate-binding protein	transport
General membrane transport,secretion, and structural proteins							
Downregulated loci							
YPTB0260	<i>tatC</i>	-2	-2.3	-3.6	-2.4		
YPTB0477	<i>secG</i>		-2			preprotein translocase subunit SecG	protein export
YPTB0697	<i>secA</i>		-1.8			preprotein translocase, subunit SecA	protein export
YPTB1090	<i>tatE</i>				-2.5	Sec-independent protein translocase subunit TatE	protein export
YPTB0930	<i>secD</i>		-2.3			protein-export membrane protein SecD	protein export
YPTB0931	<i>secF</i>		-2			protein-export membrane protein SecF	protein export
YPTB3948	<i>yidC</i>		-2.5			inner membrane protein translocase component	protein export
Others							
Downregulated loci							
YPTB0025	<i>typA, bipA</i>		-1.8			GTP-binding protein TypA	
YPTB0114	<i>hasA</i>		-2			Heme-binding A family protein	
YPTB0444	<i>fkIB</i>		-2		-1.9	peptidylprolyl isomerase FKBP-type	
YPTB0780	<i>ydjJ</i>		-3.5			alcohol dehydrogenase zinc-binding domain	
YPTB0781			-2.8			short-chain dehydrogenase/reductase SDR	
YPTB0887	<i>nqrA</i>		-2.3			NADH:ubiquinone oxidoreductase, subunit A	
YPTB0888	<i>nqrB</i>		-2.1			NADH:ubiquinone oxidoreductase, subunit B	
YPTB0889	<i>nqrC</i>		-2.2			NADH:ubiquinone oxidoreductase, subunit C	
YPTB0890	<i>nqrD</i>		-2			NADH:ubiquinone oxidoreductase, subunit D	
YPTB0891	<i>nqrE</i>		-1.8			NADH:ubiquinone oxidoreductase, subunit E	

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB0892	<i>nqrF</i>		-2			NADH:ubiquinone oxidoreductase, subunit F	
YPTB0928	<i>tgt</i>		-2.2			queuine tRNA-ribosyltransferase	
YPTB0936	<i>nusB</i>		-2.2			NusB antitermination factor	
YPTB0958	<i>tig</i>		-2			trigger factor	
YPTB1034	<i>ppiB</i>				-2.1	peptidyl-prolyl cis-trans isomerase cyclophilin type	
YPTB1125	<i>fldA</i>				-1.9	flavodoxin	
YPTB1127	<i>ybfE</i>	-1.8				LexA regulated protein	
YPTB1256	<i>gyrA</i>		-2			DNA gyrase, A subunit	
YPTB1258	<i>rcsB</i>				-1.8	transcriptional regulator	
YPTB1298	<i>ndpA</i>		-1.8			nucleoid-associated protein	
YPTB1355			-2.4			undecaprenyl pyrophosphate phosphatase	
YPTB1433	<i>ycbL</i>				-1.8	metallo-beta-lactamase superfamily protein	
YPTB1568	<i>yeeF</i>		-3.2			APC family amino acid permease	
YPTB1621	<i>aroP</i>		-1.8			amino acid APC transporter	
YPTB1652	<i>dbpA</i>		-2			ATP-dependent RNA helicase DbpA	
YPTB1660	<i>copC</i>		-2.5			copper resistance protein C	
YPTB1661	<i>copD</i>		-1.8			copper resistance protein D	
YPTB1935	<i>ansP</i>		-2.1			amino acid permease-associated region	
YPTB1998	<i>ychF, engD</i>		-2			GTP-binding protein YchF	
YPTB2031	<i>cutC</i>	-1.9				copper homeostasis protein	
YPTB2037	<i>ntpA</i>		-2.2			NUDIX hydrolase	
YPTB2048	<i>hexR</i>		-2			transcriptional regulator	
YPTB2084	<i>mrsB</i>		-2.2			methionine-R-sulfoxide reductase	
YPTB2135	<i>rluB</i>		-1.8			23S rRNA pseudouridylate synthase B	
YPTB2433			-3.8			lipoprotein	
YPTB2434	<i>phoP</i>		-2.2			two component transcriptional regulator	
YPTB2693			-1.9			lipoprotein	
YPTB2694			-1.8			lipoprotein	
YPTB3576			-2.4			tRNA-dihydrouridine synthase B	
Upregulated loci							
YPTB0434	<i>aidB</i>		2.4			acyl-coA dehydrogenase domain protein	
YPTB0600	<i>creA</i>		2			CreA family protein	
YPTB0621	<i>tnp</i>		1.8			transposase for the IS1541 insertion element	
YPTB1052			4.4			aldo/keto reductase	
YPTB1053			4.6			2,5-didehydrogluconate reductase	
YPTB1167	<i>psiF</i>		4.5			starvation inducible protein	
YPTB1240	<i>adiC</i>		6.8			arginine agmatine antiporter	
YPTB1309	<i>spr</i>		1.8			NLP/P60 protein	
YPTB1345	<i>yliJ, gst</i>		2.1			glutathione S-transferase	
YPTB1728	<i>wrbA</i>		3.3			flavoprotein WrbA	
YPTB2073	<i>ycgB, spoVR</i>		1.9			stage 5 sporulation protein R	
YPTB2080	<i>prkA, yeaG</i>		2.3			putative serine protein kinase	
YPTB2124			3.7			lipoprotein	
YPTB2261	<i>tpx</i>		2.3			thiol peroxidase	
YPTB2281	<i>gst</i>		2.8			glutathione S-transferase	
YPTB2303	<i>cfa</i>		2.7	1.8		cyclopropane-fatty-acyl-phospholipid synthase	
YPTB2335	<i>ihfA</i>		2.4			integration host factor, alpha subunit	
YPTB2352	<i>yniA</i>		2.1			fructosamine kinase	

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB2395	<i>cwlA</i> , <i>xylA</i> , <i>xylB</i>		2.3			N-acetylmuramyl-L-alanine amidase	
YPTB2416			1.9			NAD(P)H quinone oxidoreductase, PIG3 family	
YPTB2494	<i>mdoG</i>		1.9			periplasmic glucan biosynthesis protein MdoG	
YPTB2902	<i>yplA</i>		1.8			putative phospholipase A accessory protein	
YPTB2903	<i>gcrA</i>	3.6	2			formate C-acetyltransferase glycine radical	
YPTB2932	<i>crcB-2</i>		2.8			CrcB protein	
YPTB2933	<i>crcB-1</i>		2.7			camphor resistance CrcB protein	
YPTB3387	<i>yqhD</i>		2.1			iron-containing alcohol dehydrogenase	
YPTB3008		2				flavodoxin/nitric oxide synthase	
YPTB3388	<i>dkgA-1</i>		2.2			2,5-dihydrogluconate reductase	
YPTB3489	<i>yqjG</i>		2.9			glutathione S-transferase	
YPTB3498	<i>elbB</i>		2.2			isoprenoid biosynthesis protein	
YPTB3590	<i>yghU</i>		3			glutathione S-transferase	
YPTB3659			2.3			transferase	
Hypothetical							
Downregulated loci							
pYptb0043			-1.9			hypothetical protein	
YPTB0237			-1.9			hypothetical protein	
YPTB0478			-1.9			hypothetical protein	
YPTB0610	<i>yaaH</i>		-1.8			hypothetical protein	
YPTB0953	<i>yfeN</i>		-1.8			hypothetical protein	
YPTB1062			-1.8			hypothetical protein	
YPTB1099			-1.8			hypothetical protein	
YPTB1227		-1.9	-2.6			hypothetical protein	
YPTB1242		-1.8				hypothetical protein	
YPTB1257			-1.9			hypothetical protein	
YPTB1296	<i>yejM</i>		-1.8			hypothetical protein	
YPTB1389	<i>virK</i> , <i>ybjX</i>		-2		-2	hypothetical protein	
YPTB1410			-1.9			hypothetical protein	
YPTB1432	<i>ycbK</i>		-1.8			hypothetical protein	
YPTB1570			-2.5			hypothetical protein	
YPTB1623			-2			hypothetical protein	
YPTB1723			-2.2			hypothetical protein	
YPTB1985			-2.4			hypothetical protein	
YPTB2002			-2.7			hypothetical protein	
YPTB2038			-2.7			hypothetical protein	
YPTB2085			-2.2			hypothetical protein	
YPTB2101			-1.9			hypothetical protein	
YPTB2102			-1.8			hypothetical protein	
YPTB2114			-3			hypothetical protein	
YPTB2148					-1.8	hypothetical protein	
YPTB2155			-2.2			hypothetical protein	
YPTB2184		-1.8				hypothetical protein	
YPTB2207			-1.8			hypothetical protein	
YPTB2215		-2	-3.6			hypothetical protein	
YPTB2344			-2.1			hypothetical protein	
YPTB3947	<i>yidD</i>		-2.9			hypothetical protein	
Upregulated loci							
YPTB0030	<i>yihX</i>		2.2			hypothetical protein	

Gene Locus	Gene Name	FC ^a 26°C Exp.	FC 26°C Stat	FC 37°C Exp.	FC 37°C Stat.	Description	Category-Class
YPTB0094		2	3.1			hypothetical protein	
YPTB0216	<i>yhhN</i>		1.9			hypothetical protein	
YPTB0449	<i>ytfK</i>		1.9			hypothetical protein	
YPTB0577			5.7			hypothetical protein	
YPTB0639			5.2			hypothetical protein	
YPTB0649			1.8			hypothetical protein	
YPTB0651			1.9			hypothetical protein	
YPTB0652			1.9			hypothetical protein	
YPTB1104			2.2			hypothetical protein	
YPTB1222		1.8	7.8			hypothetical protein	
YPTB1312			1.8			hypothetical protein	
YPTB1577			2			hypothetical protein	
YPTB1615			3.4			hypothetical protein	
YPTB1654	<i>yqfB</i>		2.5			hypothetical protein	
YPTB1655			2.8			hypothetical protein	
YPTB1940			3.3			hypothetical protein	
YPTB1954			3.6			hypothetical protein	
YPTB2056	<i>slp,</i> <i>yeaY</i>		1.8			hypothetical protein	
YPTB2079			1.9			hypothetical protein	
YPTB2279			2.3			hypothetical protein	
YPTB2285			1.8			hypothetical protein	
YPTB2387			4			hypothetical protein	
YPTB2413	<i>dsrB</i>		2			hypothetical protein	
YPTB2420			2.2			hypothetical protein	
YPTB2425			2.2			hypothetical protein	
YPTB2484	<i>bssS</i>		3.2			hypothetical protein	
YPTB2562	<i>rhiA</i>		2			hypothetical protein	
YPTB2563	<i>elaB</i>		4.5			hypothetical protein	
YPTB2606	<i>yfcH</i>		2.2			hypothetical protein	
YPTB2745	<i>ygiW</i>		4			hypothetical protein	
YPTB2819	<i>yegP</i>		3.5			hypothetical protein	
YPTB2901			1.8			hypothetical protein	
YPTB2982		1.8	2.1			hypothetical protein	
YPTB3007			1.8			hypothetical protein	
YPTB3192	<i>yggE</i>		2.2			hypothetical protein	
YPTB3260			1.8			hypothetical protein	
YPTB3434			2.8			hypothetical protein	
YPTB3435			2			hypothetical protein	
YPTB3485	<i>yqiD</i>	1.8	3.1			hypothetical protein	
YPTB3486		2.3	3.2			hypothetical protein	
YPTB3487	<i>yqiK</i>		1.8			hypothetical protein	
YPTB3488	<i>yphA,</i> <i>yqiF</i>		2.8			hypothetical protein	
YPTB3534			3.1			hypothetical protein	
YPTB3711	<i>syIX</i>		2			hypothetical protein	
YPTB3770		2.1	11.5	1.8		hypothetical protein	
YPTB3827	<i>yhjG</i>		2.1			hypothetical protein	
YPTB3917	<i>yiaF</i>		2			hypothetical protein	
YPTB3922			2.9			hypothetical protein	

^a Fold Change

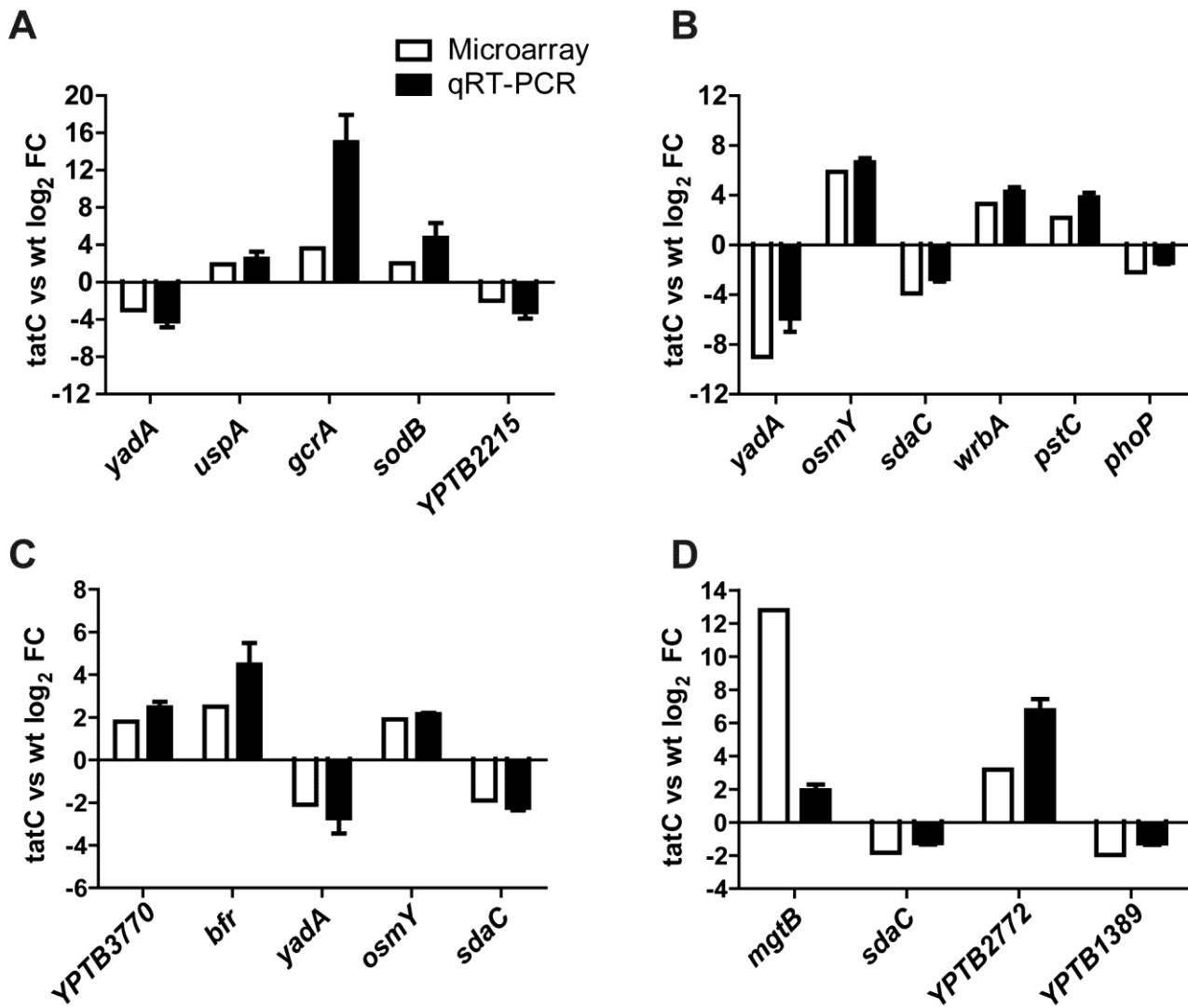


Figure S1. Comparison of microarray results with qRT-PCR with selected differentially regulated genes at 26°C exponential (A) and stationary phase (B), 37°C exponential (C) and stationary phase (D).