

Table S5. List of differentially expressed genes in a Δ *pamR* strain compared to its parental wild type *B. subtilis* strain

gene	Effect of Δ <i>pamR</i>	Exp. Diff.	Functional category	Function	Regulated by
genes repressed in absence of <i>pamR</i> during exponential growth					
<i>rasP</i>	-	2,67	Cellular processes_Cell division	intramembrane protease; control of cell division, SigV and SigW activity (via FtsL, RsiV and RsiW clivage)	U
<i>gtcA</i>	-	2,21	Cellular processes_Cell wall synthesis and homeostasis	teichoic acid glycosylation protein	CcpA (-)
<i>cpgA</i>	-	2,29	Cellular processes_Cell wall synthesis and homeostasis	GTPase	U
<i>prpC</i>	-	2,95	Cellular processes_Cell wall synthesis and homeostasis	protein phosphatases_PrkC antagonist	U
<i>murF</i>	-	2,22	Cellular processes_Cell wall synthesis and homeostasis_biosynthesis of peptidoglycan	peptidoglycan precursor biosynthesis	SigM SigV
<i>mutSB</i>	-	2,17	Information processing_DNA replication, repair & recombination	probable DNA mismatch repair protein	U
<i>sbcE</i>	-	2,30	Information processing_DNA replication, repair & recombination	DNA double-strand break repair and competence; SMC-like protein	LexA (-)
<i>dnal</i>	-	2,34	Information processing_DNA replication, repair & recombination	primosome component (helicase loader)	U
<i>parE</i>	-	2,55	Information processing_DNA replication, repair & recombination	chromosome segregation_subunit of DNA topoisomerase IV	LexA (-)
<i>mutM/ytaE</i>	-	3,04	Information processing_DNA replication, repair & recombination	formamidopyrimidine-DNA glycosidase	SigE
<i>glxX</i>	-	2,09	Information processing_Protein synthesis	translation; glutamyl-tRNA synthetase	T-box
<i>fmt/yloL</i>	-	2,34	Information processing_Protein synthesis	tRNA modification; methionyl-tRNA formyltransferase	SigA
<i>engA</i>	-	2,41	Information processing_Protein synthesis	ribosome assembly ; essential GTPase for ribosome 50S assembly	U
<i>queA</i>	-	2,45	Information processing_Protein synthesis	tRNA modification; S-adenosylmethionine tRNA ribosyltransferase	U
<i>valS</i>	-	2,58	Information processing_Protein synthesis	translation; valyl-tRNA synthetase	T-box
<i>cca</i>	-	2,63	Information processing_Protein synthesis	tRNA modification; tRNA nucleotidyltransferase	Spx
<i>pheS</i>	-	2,70	Information processing_Protein synthesis	translation; phenylalanyl-tRNA synthetase (alpha subunit)	T-box
<i>trmK</i>	-	2,74	Information processing_Protein synthesis	tRNA modification; tRNA:m1A22 methyl transferase	U
<i>truA/ybaH</i>	-	2,88	Information processing_Protein synthesis	tRNA modification; pseudouridylyl synthase I	RelA (-)
<i>yukB</i>	-	2,39	Information processing_Protein synthesis_secretion	part of the type VII protein secretion system; ATPase	DegU (+)
<i>deaD</i>	-	2,16	Information processing_RNA synthesis and degradation	DEAD-box RNA helicases	U
<i>yxaB</i>	-	2,85	Lifestyle_biofilm formation	putative exopolysaccharide synthase	SigB AbrB (-)
<i>acpK</i>	-	14,40	Lifestyle_Biosynthesis of antibacterial compounds	polyketide biosynthesis, acyl carrier protein	AbrB (-) CodY (+)
<i>cheR</i>	-	2,30	Lifestyle_Motility & chemotaxis	MCPs methyltransferase	U
<i>motA</i>	-	2,36	Lifestyle_Motility & chemotaxis	H+-coupled flagellar stator	SigD
<i>flhG</i>	-	2,59	Lifestyle_Motility & chemotaxis	GTPase activating protein, activates FlhF	SigD CodY DegU Spo0A, SwrAA/1
<i>spoVT</i>	-	2,37	Lifestyle_Sporulation	regulation of forespore gene expression; transcription regulator	SigF/G
<i>sigF</i>	-	2,56	Lifestyle_Sporulation	RNA polymerase forespore-specific (early) sigma factor SigF	AbrB (-) Spo0A (+) SinR (-) SigF/G
<i>yhbB/ygaQ</i>	-	2,67	Lifestyle_Sporulation	spore coat protein, amidase	SigE
<i>ytaF</i>	-	2,72	Lifestyle_Sporulation	U	SigE
<i>thiQ</i>	-	3,14	Lifestyle_Sporulation	U	SigE SpoIIID (-)
<i>tepA</i>	-	2,49	Lifestyle_Sporulation_germination	degradation of SASPs; orphan ClpP-like germination protease	SigG SpoVT (-)
<i>araF</i>	-	2,34	Metabolism_Biosynthesis & acquisition of Aminoacids	chorismate synthase	SigA
<i>tyrA</i>	-	2,50	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of tyrosine; prephenate dehydrogenase	MtrB TRAP (-)
<i>proB</i>	-	2,53	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of proline; glutamate 5-kinase	T-box
<i>trpD</i>	-	2,66	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of tryptophan, anthranilate phosphoribosyltransferase	MtrB TRAP (-)
<i>artQ</i>	-	2,72	Metabolism_Biosynthesis & acquisition of Aminoacids	Arginine uptake; arginine ABC transporter (permease)	casa ac (-)
<i>araB</i>	-	2,74	Metabolism_Biosynthesis & acquisition of Aminoacids	3-dehydroquinate synthase	SigA
<i>thrR</i>	-	2,75	Metabolism_Biosynthesis & acquisition of Aminoacids	TR, control of threonine biosynthesis	U
<i>hisH</i>	-	2,93	Metabolism_Biosynthesis & acquisition of Aminoacids	histidine biosynthesis; imidazole glycerol phosphate synthase (glutaminase subunit)	U
<i>hisA</i>	-	3,07	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of histidine; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	U
<i>trpF</i>	-	3,26	Metabolism_Biosynthesis & acquisition of Aminoacids	synthesis of tryptophan, phosphoribosylanthranilate isomerase	MtrB TRAP (-)
<i>hisB</i>	-	3,70	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of histidine; imidazoleglycerol-phosphate dehydratase	U
<i>mccB</i>	-	4,43	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of cysteine; methionine-to-cysteine conversion; cystathionine lyase/ homocysteine lyase	CymR (-) Spx (+)
<i>mccA</i>	-	4,51	Metabolism_Biosynthesis & acquisition of Aminoacids	biosynthesis of cysteine; methionine-to-cysteine conversion; O-acetylserine-thiol-lyase	CymR (-) Spx (+)
<i>lplJ</i>	-	2,14	Metabolism_Biosynthesis of cofactors	Lipoate:protein ligase	U
<i>moaE</i>	-	2,29	Metabolism_Biosynthesis of cofactors	nitrate respiration; molybdopterin synthase (large subunit)	U
<i>panB</i>	-	2,40	Metabolism_Biosynthesis of cofactors	biosynthesis of coenzyme A; 3-methyl-2-oxobutanoate hydroxymethyltransferase	U
<i>pdxK</i>	-	2,49	Metabolism_Biosynthesis of cofactors	pyridoxal biosynthesis; kinase	U
<i>birA</i>	-	2,50	Metabolism_Biosynthesis of cofactors	Transcriptional regulator; Biotin-protein ligase	BirA (-) Spx (+)
<i>bioW</i>	-	2,86	Metabolism_Biosynthesis of cofactors	Biotin synthesis; pimeloyl-CoA synthase	BirA (-)
<i>thiU</i>	-	2,88	Metabolism_Biosynthesis of cofactors	thiamine transporter (binding protein)	Thi-box
<i>folC</i>	-	2,91	Metabolism_Biosynthesis of cofactors	biosynthesis of folate ; folyl-polyglutamate synthetase	Thi-box
<i>thiS</i>	-	3,43	Metabolism_Biosynthesis of cofactors	biosynthesis of thiamine; sulfur carrier protein	Thi-box
<i>bioF</i>	-	3,70	Metabolism_Biosynthesis of cofactors	Biotin synthesis; 8-amino-7-oxononanoate synthase	BirA (-)
<i>tenI</i>	-	3,97	Metabolism_Biosynthesis of cofactors	biosynthesis of thiamine; thiazole tautomerase	Thi-box
<i>sumT</i>	-	9,87	Metabolism_Biosynthesis of cofactors	siroheme biosynthesis , sulfite reduction;probable uroporphyrin-III C-methyltransferase	CymR (-) S-box
<i>ykuN</i>	-	2,54	Metabolism_Electron transport & ATP synthesis	electron transfer; flavodoxin	Fur (-) NsrR (-) Kre (-) ResD (+)
<i>atpF</i>	-	2,56	Metabolism_Electron transport & ATP synthesis	ATP synthase(Fo complex subunit b)	RelA (-)
<i>atpH</i>	-	2,96	Metabolism_Electron transport & ATP synthesis	ATP synthase(Fo complex subunit d)	RelA (-)
<i>etfB</i>	-	3,22	Metabolism_Electron transport & ATP synthesis	fatty acid degradation, electron transfer flavoprotein (beta subunit)	CcpA (-) FadR (-)

<i>resB/ypxB</i>	-	2,36	Metabolism_Electron transport & ATP synthesis_Respiration	cytochrome c biogenesis; part of the ResB-ResC haem translocase	CcpA (-)	PhoP (+)	ResD (+)
<i>pfkA</i>	-	2,69	Metabolism_Glycolysis	6-phosphofructokinase	Glucose (+)		
<i>dhbB</i>	-	2,24	Metabolism_iron metabolism	isochorismatase; biosynthesis of the siderophore bacillibactin	Fur (-)	AbrB (-)	Kre (-)
<i>sufU</i>	-	2,58	Metabolism_iron metabolism	biosynthesis of iron-sulfur clusters; Fe-S cluster scaffold protein	U		
<i>mobB</i>	-	2,66	Metabolism_Nitrate respiration	molybdopterin-guanine dinucleotide cofactor synthesis protein	U		
<i>dra</i>	-	2,24	Metabolism_nucleotide metabolism	nucleotide catabolism_deoxyribose-phosphate aldolase	CcpA (-)	DeoR (-)	
<i>nupC</i>	-	3,02	Metabolism_nucleotide metabolism	pyrimidine nucleoside transport protein	CcpA (-)	DeoR (-)	
<i>purH</i>	-	2,90	Metabolism_nucleotide metabolism	purine biosynthesis; phosphoribosylaminoimidazole carboxamide formyltransferase	PurR (-)		
<i>pyrF</i>	-	3,63	Metabolism_nucleotide metabolism	pyrimidine biosynthesis, orotidine-5-phosphate decarboxylase	PyrR		
<i>araL</i>	-	4,58	Metabolism_poorly characterized	sugar-P phosphatase	CcpA (-)	AraR (-)	
<i>crh</i>	-	2,43	Metabolism_regulation of carbon flux	CcpA cofactor	CcpA (-)		
<i>rhsA</i>	-	3,09	Metabolism_Sugar uptake	Ribose uptake; ABC transporter (ATP-binding protein)	CcpA (-)	AbrB (+)	
<i>glcK</i>	-	3,14	Metabolism_Sugar uptake	glucose kinase	U		
<i>levG</i>	-	4,59	Metabolism_Sugar uptake	fructose uptake; fructose-specific PTS, EIID component	CcpA (-)	LevR (+)	SigL
<i>rhsD</i>	-	5,13	Metabolism_Sugar uptake	Ribose uptake; ABC transporter	CcpA (-)	AbrB (+)	
<i>levD</i>	-	6,11	Metabolism_Sugar uptake	fructose uptake; fructose-specific PTS, EIIA component	CcpA (-)	LevR (+)	SigL
<i>levF</i>	-	7,25	Metabolism_Sugar uptake	fructose uptake; fructose-specific PTS, EIIC component	CcpA (-)	LevR (+)	SigL
<i>levE</i>	-	7,43	Metabolism_Sugar uptake	fructose uptake; trigger enzyme:fructose PTS EIIB	CcpA (-)	LevR (+)	SigL
<i>cysH</i>	-	2,67	Metabolism_sulfur metabolism	sulfate reduction, phosphoadenosine phosphosulfate sulfotransferase	CymR (-)	S-box	
<i>sat</i>	-	6,52	Metabolism_sulfur metabolism	sulfate activation, sulfate adenyltransferase	CymR (-)	S-box	
<i>cysC</i>	-	7,16	Metabolism_sulfur metabolism	sulfate reduction and activation, adenyllyl-sulfate kinase	CymR (-)		
<i>citZ</i>	-	2,38	Metabolism_TCA cycle	citrate synthase II	CcpA (-)	CcpC (-)	
<i>mdh</i>	-	2,47	Metabolism_TCA cycle	malate dehydrogenase	CcpA (-)	CcpC (-)	
<i>sucC</i>	-	2,58	Metabolism_TCA cycle	TCA cycle,succinyl-CoA synthetase (beta subunit)	CcpA (-)		
<i>icd</i>	-	2,64	Metabolism_TCA cycle	isocitrate dehydrogenase	CcpA (-)	CcpC (-)	
<i>sdhA</i>	-	2,78	Metabolism_TCA cycle	succinate dehydrogenase (flavoprotein subunit)	FsrA (-)		
<i>sucD</i>	-	2,91	Metabolism_TCA cycle	TCA cycle,succinyl-CoA synthetase (beta subunit)	CcpA (-)		
<i>gcvT</i>	-	2,41	Metabolism_utilization of amino acids	glycine utilization; aminomethyltransferase	Gly-box		
<i>gcvPA</i>	-	2,68	Metabolism_utilization of amino acids	glycine utilization; glycine decarboxylase (subunit 1)	Gly-box		
<i>rocG</i>	-	3,43	Metabolism_utilization of amino acids	arginine utilization; controls the activity of GlcT; glutamate deshydrogenase	CcpA (-)	AbrB (-)	RocR (+) AhrC (+) SigL
<i>bgIA</i>	-	2,35	Metabolism_utilization of beta-glucosides	utilization of beta-glucosides; 6-phospho-beta-glucosidase	U		
<i>bgIH</i>	-	3,98	Metabolism_utilization of beta-glucosides	salicin utilization, phospho-beta-glucosidase	CcpA (-)	LicT	
<i>fadF/ywjF</i>	-	3,10	Metabolism_utilization of fatty acids	Fatty acid degradation; function unknown	FadR (-)		
<i>galK</i>	-	2,38	Metabolism_utilization of galactose	galactokinase	CcpA (-)		
<i>iolE</i>	-	3,11	Metabolism_utilization of inositol	myo-inositol catabolism, 2-keto-myo-inositol dehydratase, dehydration of 2-keto-myo-inositol	CcpA (-)	IolR (+)	
<i>iolD</i>	-	3,42	Metabolism_utilization of inositol	myo-inositol catabolism, formation of 5-deoxy-D-glucuronic acid (3rd reaction)	CcpA (-)	IolR (+)	
<i>iolC</i>	-	3,74	Metabolism_utilization of inositol	myo-inositol catabolism, formation of 2-deoxy-5-keto-gluconic acid-6-phosphate (5th reaction)	CcpA (-)	IolR (+)	
<i>iolG</i>	-	3,79	Metabolism_utilization of inositol	myo-inositol catabolism, inositol 2-dehydrogenase	CcpA (-)	IolR (+)	
<i>iolB</i>	-	4,64	Metabolism_utilization of inositol	myo-inositol catabolism; formation of 2-deoxy-5-keto-gluconic acid (4th reaction)	CcpA (-)	IolR (+)	
<i>mtID</i>	-	3,49	Metabolism_utilization of mannitol	mannitol-1-phosphate 5-dehydrogenase	MiTR		
<i>mtIA</i>	-	4,18	Metabolism_utilization of mannitol	mannitol uptake; trigger enzyme: mannitol-specific phosphotransferase system, EIICB of the PTS	MiTR		
<i>mtIF</i>	-	6,38	Metabolism_utilization of mannitol	PTS mannitol-specific enzyme IIA component	MiTR		
<i>acuA</i>	-	3,19	Metabolism_utilization of organic acids	control of AcsA activity; N-acetyltransferase	CcpA (-)		
<i>citT</i>	-	3,99	Metabolism_utilization of organic acids	two-component response regulator, regulation of citrate uptake	CitT		
<i>mall</i>	-	2,80	Metabolism_utilization of other Carbon sources	starch & maltodextrine utilization; alpha-glucosidase	U		
<i>licB</i>	-	4,30	Metabolism_utilization of other Carbon sources	lichenan uptake; trigger enzyme:lichenan PTS EIIB	CcpA (-)	LicR (+)	
<i>mdxE</i>	-	4,71	Metabolism_utilization of other Carbon sources	maltodextrin ABC transporter	U		
<i>xynD</i>	-	2,54	Metabolism_utilization of other polymeric carbohydrates	arabinoxylan degradation; arabinoxylan arabinofuranohydrolase	AbrB (-)		
<i>gmuE/ydhR</i>	-	2,52	Metabolism_utilization of specific C source	glucomannan utilization; mannose kinase	AbrB (+)	CcpA (-)	GmuR (-)
<i>gmuD/ydhP</i>	-	2,53	Metabolism_utilization of specific C source	glucomannan utilization; phospho-beta-mannosidase	AbrB (+)	CcpA (-)	GmuR (-)
<i>gmuF/ydhs</i>	-	2,86	Metabolism_utilization of specific C source	glucomannan utilization; mannose-6-P-isomerase	AbrB (+)	CcpA (-)	GmuR (-)
<i>gmuA/ydhN</i>	-	2,91	Metabolism_utilization of specific C source	glucomannan-specific phosphotransferase system, EIIA component	AbrB (+)	CcpA (-)	GmuR (-)
<i>gmuC/ydhO</i>	-	3,08	Metabolism_utilization of specific C source	glucomannan-specific phosphotransferase system, EIIC component	AbrB (+)	CcpA (-)	GmuR (-)
<i>kdgK</i>	-	3,84	Metabolism_utilization of specific C source	utilization of galacturonic acid, 2-dehydro-3-deoxygluconokinase	CcpA (-)	KgdR (-)	
<i>treA</i>	-	2,98	Metabolism_utilization of trehalose	trehalose utilization_phospho-alpha-glucosidase	CcpA (-)	TreR (-)	PhoP (+)
<i>rhaM</i>	-	3,68	Metabolism_utilization of rhamnose	utilization of rhamnose, mutarotase	CcpA (-)	RhaR (-)	
<i>xtmB</i>	-	2,35	Prophages & mobile genetic elements_PBSX prophage	phage DNA replication; PBSX terminase	Xpf (+)		
<i>xkdE</i>	-	2,69	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		
<i>xtmA</i>	-	2,77	Prophages & mobile genetic elements_PBSX prophage	phage DNA replication; PBSX terminase	Xpf (+)		
<i>xkdQ</i>	-	2,78	Prophages & mobile genetic elements_PBSX prophage	U	U		
<i>xtrA</i>	-	2,83	Prophages & mobile genetic elements_PBSX prophage	U	Xre (-)		
<i>xepA</i>	-	2,86	Prophages & mobile genetic elements_PBSX prophage	phage release, PBSX prophage lytic exoenzyme	U		
<i>xkdG</i>	-	2,98	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		
<i>xkdF</i>	-	3,07	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		
<i>xkdJ</i>	-	3,08	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		
<i>xkdH</i>	-	3,12	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		
<i>xhIA</i>	-	3,13	Prophages & mobile genetic elements_PBSX prophage	host cell lysis upon induction of PBSX	U		
<i>xkdS</i>	-	3,13	Prophages & mobile genetic elements_PBSX prophage	U	U		
<i>xkdI</i>	-	3,14	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)		

<i>xkdX</i>	-	3,21	Prophages & mobile genetic elements_PBSX prophage	U	U
<i>xkdR</i>	-	3,30	Prophages & mobile genetic elements_PBSX prophage	U	U
<i>xkdC</i>	-	3,43	Prophages & mobile genetic elements_PBSX prophage	U	Xre (-)
<i>xhlB</i>	-	3,45	Prophages & mobile genetic elements_PBSX prophage	host cell lysis	U
<i>xkdW</i>	-	3,64	Prophages & mobile genetic elements_PBSX prophage	U	U
<i>xkdK</i>	-	3,65	Prophages & mobile genetic elements_PBSX prophage	U	Xpf (+)
<i>xkdB</i>	-	3,77	Prophages & mobile genetic elements_PBSX prophage	U	Xre (-)
<i>xkdD</i>	-	4,07	Prophages & mobile genetic elements_PBSX prophage	U	Xre (-)
<i>ykzM</i>	-	4,73	Prophages & mobile genetic elements_PBSX prophage	U	U
<i>yzkK</i>	-	5,55	Prophages & mobile genetic elements_PBSX prophage	U	U
<i>psdS</i>	-	2,41	Stress response_Antibiotic resistance	two-component sensor kinase, response to lipid II-binding lantibiotics, such as nisin and gallidermin	PsdR
<i>ylvIA</i>	-	2,14	stress response_cell envelope stress resistance	U	SigW AbrB (-)
<i>yknW</i>	-	2,60	stress response_cell envelope stress resistance	modulates assembly of the YknX-YknY-YknZ ABC transporter for the export of the SdpC toxin	AbrB (-) SigW
<i>yqfA</i>	-	2,76	stress response_cell envelope stress resistance	flotillin-like protein, resistance against sublancin	SigW
<i>floT</i>	-	2,44	Stress response_membrane dynamics	lipid microdomains organization; resistance to cefuroxime	SigW
<i>yuaF</i>	-	2,59	Stress response_membrane dynamics	NfeD2, role in maintaining membrane integrity during conditions of cellular stress	SigW
<i>psdA</i>	-	2,69	Stress response_resistance to antimicrobials	export of lantibiotics, such as nisin and gallidermin	PsdR (+)
<i>yhcY</i>	-	2,13	U	two component sensor kinase	LiaR (+)
<i>ytIR</i>	-	2,25	U	U	SigD
<i>yqeK</i>	-	2,31	U	U	U
<i>yprA</i>	-	2,33	U	putative helicase	U
<i>yloV</i>	-	2,34	U	U	U
<i>ykuO</i>	-	2,34	U	U	Fur (-) NsrR (-) Kre (-) ResD (+)
<i>yloM</i>	-	2,36	U	similar to 5-adenosyl-L-methionine-dependent 16S rRNA m5C967 methyltransferase	SigA
<i>yusY</i>	-	2,37	U	similar to endopeptidase	U
<i>ypgQ</i>	-	2,38	U	Mn2-dependent pyrophosphohydrolase	U
<i>yqjZ</i>	-	2,42	U	U	U
<i>ycnE</i>	-	2,42	U	U	U
<i>yyaE</i>	-	2,43	U	similar to formate deshydrogenase, put electron transport	U
<i>yyzE</i>	-	2,49	U	similar to PTS IIE	U
<i>ylmE</i>	-	2,54	U	poorly charcterized; involved in control of the CoA pool	Spo0A (-)
<i>yloN</i>	-	2,57	U	similar to rRNA methyltransferase	U
<i>ytpQ</i>	-	2,59	U	maybe involved in Fe homeostasis	Spx (+)
<i>ycbM</i>	-	2,71	U	predicted two-component sensor kinase	U
<i>ynbB</i>	-	2,79	U	U	U
<i>ysmA</i>	-	2,82	U	U	U
<i>yrhE</i>	-	2,84	U	U	U
<i>yxil</i>	-	3,20	U	U	U
<i>yhcF</i>	-	3,26	U	putative transcription factor (GntR family)	U
<i>lplA</i>	-	3,44	U	putative ABC transporters	U
<i>yxIM</i>	-	3,80	U	U	U
<i>yvrO</i>	-	2,98	U (put based on regulation: Lifestyle_stationnary phase adaptation)	putative ABC transporters	AbrB (-) ComK (+)
<i>acuB</i>	-	2,71	U (put based on regulation: metabolism)	U	CcpA (-)
<i>yjmB</i>	-	2,86	U (put based on regulation: metabolism)	similar to symporter	CcpA (-) ExuR (-)
<i>msmE</i>	-	3,05	U (put based on regulation: metabolism)	putative melibiose uptake; ABC transporter	CcpA (-)
<i>lrgA</i>	-	3,79	U (put based on regulation: metabolism)	putative pyruvate transporter	CcpA (-) Kre (-) LytT (+)
<i>yjmC</i>	-	4,10	U (put based on regulation: metabolism)	may be involved in galacturonate utilization	CcpA (-) ExuR (-)
<i>yesM</i>	-	4,38	U (put based on regulation: metabolism)	two-component sensor kinase	CcpA (-)
<i>yxkK</i>	-	7,19	U (put based on regulation: metabolism_sulfur metabo)	putative utilization of a modified cystein variant; similar to monooxygenase	CymR (-)
<i>yxkN</i>	-	8,86	U (put based on regulation: metabolism_sulfur metabo)	putative cystein ABC transporter	CymR (-)
<i>yxkL</i>	-	9,47	U (put based on regulation: metabolism_sulfur metabo)	putative sulfur N-acetylase	CymR (-)

genes induced in absence of *pamR* during exponential growth

<i>ydjM</i>	+	5,39	Cellular processes_Cell wall synthesis and homeostasis	May be involved in cell wall metabolism (WalR regulon)	WalR (+) PhoP (+)
<i>tagC</i>	+	3,17	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	unknown function	LexA (-)
<i>tagD</i>	+	3,17	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	Glycerol-3-phosphate cytidylyltransferase	WalR (+) PhoP (-)
<i>ggaB</i>	+	3,31	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	Galactosamine-containing minor teichoic acid biosynthesis	SigA
<i>tagB</i>	+	3,84	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	putative CDP-glycerol:glycerol phosphate glycerophosphotransferase	WalR (+) PhoP (-)
<i>tagA</i>	+	4,24	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	UDP-N-acetyl-D-mannosamine transferase	WalR (+) PhoP (-)
<i>ggaA</i>	+	4,64	Cellular processes_Cell wall synthesis and homeostasis_Biosynthesis of teichoic acid	Galactosamine-containing minor teichoic acid biosynthesis; activity unknown	SigA
<i>mntR</i>	+	2,77	Cellular processes_Trace metal homeostasis (Cu, Zn, Ni, Mn, Mo)	Regulation of manganese transport; transcriptional regulator (DtxR family)	MntR
<i>hbs</i>	+	2,92	Information processing_DNA condensation/segregation	DNA packaging; Non-specific DNA-binding protein	LexA (-) SigH
<i>secE</i>	+	3,16	Information processing_Protein synthesis_secretion	Protein secretion; preprotein translocase	U
<i>rpmGC</i>	+	2,83	Information processing_Protein synthesis_translation	Replaces L33 under conditions of zinc depletion; alternative ribosomal protein	Zur (-)
<i>rpsO</i>	+	2,95	Information processing_Protein synthesis_translation	Ribosomal protein S15	U
<i>rpmB</i>	+	3,45	Information processing_Protein synthesis_translation	Ribosomal protein L28	U
<i>rpmGB</i>	+	3,49	Information processing_Protein synthesis_translation	Ribosomal protein L33b	U
<i>rpsT</i>	+	3,81	Information processing_Protein synthesis_translation	Ribosomal protein S20	U

<i>trnD-Cys/trnR</i>	+	2,97	Information processing_Protein synthesis_tRNA	tRNA-Cys	SigA
<i>trnD-Trp/trnR</i>	+	3,16	Information processing_Protein synthesis_tRNA	tRNA-Trp	SigA
<i>trnD-Ser/trnR</i>	+	3,44	Information processing_Protein synthesis_tRNA	tRNA-Ser	SigA
<i>trnB-Met3</i>	+	3,62	Information processing_Protein synthesis_tRNA	tRNA-Met	SigA
<i>albG</i>	+	3,64	Lifestyle_Biosynthesis of antibacterial compounds	Production of subtilisin; activity unknown	AbrB (-) Rok (-) ResD (+)
<i>ntdR</i>	+	3,73	Lifestyle_Biosynthesis of antibacterial compounds	Activator of ntdABC-glcP operon; transcriptional regulator (LacI family)	AbrB (-) NtdR (+)
<i>comK</i>	+	2,74	Lifestyle_Genetic competence	Competence transcription factor	AbrB (-) Spo0A (+) CodY (-) Rok (-), ComK (+), DegU (+)
<i>comC</i>	+	2,74	Lifestyle_Genetic competence	required for processing and translocation of ComGC, ComGD, ComGE and ComGG; protease	ComK (+)
<i>kre</i>	+	3,31	Lifestyle_Genetic competence	inhibitor of competence; ComK repressor	ComK (-)
<i>sda</i>	+	2,68	Lifestyle_Sporulation	checkpoint coupling replication and sporulation; inhibitor of Spo0A phosphorelay	LexA (-) DnaA (+)
<i>yhfM</i>	+	2,70	Lifestyle_Sporulation	U	SigF
<i>phrE</i>	+	3,48	Lifestyle_Sporulation	Regulator of RapE phosphatase	CcpA (-) AbrB (-) SigH CodY (-), ComA (+)
<i>yozQ</i>	+	3,61	Lifestyle_Sporulation	U	SigG
<i>catM</i>	+	3,87	Lifestyle_Sporulation	spore resistance; spore coat protein	SigE GerE (+) SpoIIID (-)
<i>yknT</i>	+	3,88	Lifestyle_Sporulation	spore protection; spore coat protein	SigE SpoIIID (+)
<i>ypzA</i>	+	4,13	Lifestyle_Sporulation	U	SigG
<i>yisi</i>	+	4,16	Lifestyle_Sporulation	inhibition of phosphorelay; Spo0A-P phosphatase	PchR (+)
<i>cotX</i>	+	5,96	Lifestyle_Sporulation	spore resistance; spore crust assembly	SigE GerE (+) SpoIIID (-)
<i>catC</i>	+	6,28	Lifestyle_Sporulation	spore resistance; spore coat protein	SigK GerE (+) SpoIIID (-)
<i>yckD</i>	+	6,38	Lifestyle_Sporulation	U	SigF/G
<i>yhcN</i>	+	3,05	Lifestyle_Sporulation_germination	efficient spore germination; activity unknown	SigF/G
<i>gerD</i>	+	3,37	Lifestyle_Sporulation_germination	Scaffold of the germinosome	SigF/G
<i>sinR</i>	+	2,76	Lifestyle_stationary phase adaptation	Transcriptional regulator of post-exponential-phase responses genes, control of biofilm formation	AbrB (-) SinR (-) Spo0A (+) ScoC (-)
<i>abrB</i>	+	4,34	Lifestyle_stationary phase adaptation	Transition state regulator_trnscritonal regulator	AbrB (-) Spo0A (-)
<i>lrpB</i>	+	3,51	Metabolism_Biosynthesis & acquisition of Aminoacids	metabolism of glycine; Repression of glyA transcription and KinB-dependent sporulation	U
<i>lrpA</i>	+	5,26	Metabolism_Biosynthesis & acquisition of Aminoacids	metabolism of glycine; Repression of glyA transcription and KinB-dependent sporulation	U
<i>pyrR</i>	+	3,56	Metabolism_Biosynthesis & acquisition of nucleotides	Transcriptional antiterminator of the pyr operon	PyrR
<i>pyrP</i>	+	4,13	Metabolism_Biosynthesis & acquisition of nucleotides	uracil permease	PyrR
<i>tnrA</i>	+	2,45	Metabolism_nitrogen metabolism	control of nitrogen assimilation; transcriptional regulator (MerR family)	GlnR (-) TnrA (+)
<i>nupG</i>	+	2,78	metabolism_nucleotide metabolism	Purine nucleosides transporter	G-box
<i>degR</i>	+	3,58	Metabolism_Regulation of degradative enzyme production	control of DegU; Positive effector of DegU-phosphate stability	SigD
<i>rapI</i>	+	2,96	Prophages & mobile genetic elements_ICEBs1	Control of ICEBs1, ImmR antagonist; response regulator aspartate phosphatase	ComA (+) SigH
<i>ligB</i>	+	2,96	Prophages & mobile genetic elements_ICEBs1	phage SP-beta replication_DNA ligase	U
<i>int</i>	+	3,32	Prophages & mobile genetic elements_ICEBs1	Excision of the conjugative transposon ICEBs1; integrase	U
<i>immA</i>	+	3,40	Prophages & mobile genetic elements_ICEBs1	control of ImmR activity; site-specific protease	U
<i>ydcO</i>	+	3,42	Prophages & mobile genetic elements_ICEBs1	U	ImmR (-)
<i>xis</i>	+	3,54	Prophages & mobile genetic elements_ICEBs1	Excision of the conjugative transposon ICEBs1; excisionase	ImmR (-)
<i>ydcP</i>	+	3,83	Prophages & mobile genetic elements_ICEBs1	Conjugation and replication of ICEBs1; helicase processivity factor	ImmR (-)
<i>immR</i>	+	3,86	Prophages & mobile genetic elements_ICEBs1	Control of transfer of the mobile genetic element ICEBs1; Transcriptional repressor	U
<i>xre</i>	+	3,83	Prophages & mobile genetic elements_PBSX prophage	regulation of PBSX prophage gene expression; Transcriptional repressor	U
<i>ybzH</i>	+	3,84	Prophages & mobile genetic elements_Prophage 1	unknown; putative transcriptional regulator	U
<i>yqaS</i>	+	2,78	Prophages & mobile genetic elements_Skin element	unknown; similar to terminase	SigD
<i>sknR</i>	+	3,04	Prophages & mobile genetic elements_Skin element	repression of yqaF operon of the skin element; transcriptional repressor (Xre family)	U
<i>yqbC</i>	+	3,68	Prophages & mobile genetic elements_Skin element	U	U
<i>yqbG</i>	+	4,94	Prophages & mobile genetic elements_Skin element	U	U
<i>yoyH</i>	+	2,34	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yoqL</i>	+	2,49	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yomO</i>	+	2,49	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yorS</i>	+	2,54	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yotM</i>	+	2,56	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yorB</i>	+	2,58	Prophages & mobile genetic elements_SP-beta prophage	U	CsoR (-) SigE/K
<i>yorE</i>	+	2,61	Prophages & mobile genetic elements_SP-beta prophage	U	LexA (-)
<i>yorM</i>	+	2,64	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yosT</i>	+	2,70	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yonT</i>	+	2,72	Prophages & mobile genetic elements_SP-beta prophage	toxin	as-yonT
<i>yopC</i>	+	2,72	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yorJ</i>	+	2,78	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yonV</i>	+	2,82	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopK</i>	+	2,99	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopQ</i>	+	3,04	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopA</i>	+	3,08	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopE</i>	+	3,10	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yonI</i>	+	3,14	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopP</i>	+	3,17	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yoyJ</i>	+	3,26	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopR</i>	+	3,26	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yokB</i>	+	3,47	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yopM</i>	+	3,52	Prophages & mobile genetic elements_SP-beta prophage	U	U
<i>yorC</i>	+	3,54	Prophages & mobile genetic elements_SP-beta prophage	U	LexA (-)

<i>yokC</i>	+	3,72	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yoyI</i>	+	3,72	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yopN</i>	+	3,73	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yotE</i>	+	3,75	Prophages & mobile genetic elements_SP-beta prophage	U	CsoR (-)	SigE/K
<i>yopO</i>	+	4,12	Prophages & mobile genetic elements_SP-beta prophage	similar to transcriptional regulator (Xre family)	U	
<i>yonsS</i>	+	4,23	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yotD</i>	+	4,25	Prophages & mobile genetic elements_SP-beta prophage	Unknown; similar to acyl-coA synthetase	CsoR (-)	SigE/K
<i>yopF</i>	+	4,33	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yonR</i>	+	5,29	Prophages & mobile genetic elements_SP-beta prophage	Similar to transcriptional regulator (Xre family)	U	
<i>bhlB</i>	+	6,45	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>yosU</i>	+	8,08	Prophages & mobile genetic elements_SP-beta prophage	U	U	
<i>dps</i>	+	3,21	stress response	Fe storage and stress resistance; miniferritin	SigB	
<i>SRS</i>	+	3,99	stress response_Anti-toxin	contro of BsrE toxin expression; Antisense RNA to bsrE	U	
<i>ydjO</i>	+	3,09	stress response_cell envelope stress resistance	U	SigW	SigE
<i>mgsR</i>	+	2,86	Stress response_oxydative stress resistance	Transcriptional regulator of a subset of the SigB general stress regulon; protection vs oxidative stress	SigB	MgsR (+)
<i>yydJ</i>	+	3,00	Stress response_resistance to antimicrobials	control of LiaR-LiaS activity; putative ABC transporter (ATP-binding)	AbrB (-)	Rok (-)
<i>sixX</i>	+	3,07	Stress response_Resistance to antimicrobials	Resistance to cationic antimicrobial peptides; RNA polymerase ECF-type sigma factor	SigX	YvrbH (+)
<i>yydI</i>	+	3,86	Stress response_resistance to antimicrobials	control of LiaR-LiaS activity; putative ABC transporter (permease)	AbrB (-)	Rok (-)
<i>yydG</i>	+	4,50	Stress response_resistance to antimicrobials	control of LiaR-LiaS activity; oxidoreductase	AbrB (-)	Rok (-)
<i>yydH</i>	+	4,86	Stress response_resistance to antimicrobials	control of LiaR-LiaS activity; putative ABC transporter	AbrB (-)	Rok (-)
<i>yobK</i>	+	2,48	Stress response_toxins, antitoxins and immunity against toxins	antitoxin, inhibition of the cytotoxic activity of YobL	U	
<i>yobL</i>	+	2,78	Stress response_toxins, antitoxins and immunity against toxins	Toxin	U	
<i>yxxD</i>	+	2,92	Stress response_toxins, antitoxins and immunity against toxins	Antitoxin; inhibition of cytotoxic YxiD	U	
<i>sdpI</i>	+	3,02	Stress response_toxins, antitoxins and immunity against toxins	protection against SdpC toxin	AbrB (-)	SdpR (-)
<i>sdpA</i>	+	5,21	Stress response_toxins, antitoxins and immunity against toxins	maturation of SdpC toxin	AbrB (-)	Rok (-) Spo0A (+)
<i>ywnA</i>	+	2,29	U	U	U	
<i>yvkN</i>	+	2,33	U	U	U	
<i>yrkD</i>	+	2,53	U	U	U	
<i>yubF</i>	+	2,54	U	U	U	
<i>yceK</i>	+	2,56	U	unknown; putative transcriptional regulator	U	
<i>yozV</i>	+	2,58	U	U	U	
<i>yurQ</i>	+	2,60	U	U	U	
<i>ypbS</i>	+	2,60	U	U	U	
<i>ynaB</i>	+	2,63	U	U	U	
<i>ykvN</i>	+	2,64	U	Unknown; MarR family transcription regulator	U	
<i>yfnC</i>	+	2,65	U	unknown; similar to fosmidmycin resistance protein	U	
<i>ycxB</i>	+	2,67	U	U	U	
<i>yqzF</i>	+	2,68	U	U	U	
<i>ydel</i>	+	2,70	U	U	U	
<i>ywpF</i>	+	2,70	U	U	U	
<i>ybfF</i>	+	2,70	U	U	U	
<i>yqgW</i>	+	2,71	U	U	U	
<i>yrdC</i>	+	2,78	U	U	U	
<i>yydD</i>	+	2,80	U	U	U	
<i>yoeC</i>	+	2,81	U	U	U	
<i>yfzA</i>	+	2,96	U	U	U	
<i>yezA</i>	+	2,96	U	U	U	
<i>yjfB</i>	+	2,97	U	U	SigD	
<i>ypoP</i>	+	3,00	U	Similar to transcriptional regulator (MarR family)	U	
<i>yqkE</i>	+	3,03	U	U	U	
<i>yraH</i>	+	3,05	U	U	U	
<i>pbuO</i>	+	3,06	U	unknown; similar to permease PbuG	PurR (-)	
<i>yncB</i>	+	3,16	U	U	U	
<i>ydeB</i>	+	3,26	U	unknown; putative transcriptional regulator	U	
<i>yeeD</i>	+	3,27	U	U	U	
<i>yaaC</i>	+	3,28	U	putative sporulation protein	U	
<i>ydfL</i>	+	3,30	U	unknown; similar to multidrug efflux transporter regulator of MreR family	U	
<i>ybfE</i>	+	3,33	U	U	U	
<i>yIbN</i>	+	3,39	U	may be required for accumulation of 23S rRNA	U	
<i>yybN</i>	+	3,40	U	U	Rok (-)	DnaA (-)
<i>yxcC</i>	+	3,43	U	U	SigD	TnrA (+)
<i>ynaE</i>	+	3,49	U	U	U	
<i>yxaC</i>	+	3,50	U	Holin-like auxiliary protein	U	
<i>yrzM</i>	+	3,53	U	U	U	
<i>ykzT</i>	+	3,57	U	U	U	
<i>ykvsS</i>	+	3,57	U	U	U	
<i>yjiA</i>	+	3,57	U	U	U	
<i>ypzI</i>	+	3,61	U	U	U	
<i>yjzD</i>	+	3,62	U	U	U	

<i>yybM</i>	+	3,66	U	U	Rok (-)	DnaA (-)
<i>ymzD</i>	+	3,68	U	U	U	
<i>yoyA</i>	+	3,68	U	U	U	
<i>yobD</i>	+	3,69	U	similar to transcriptional regulator (Xre family)	U	
<i>yneF</i>	+	3,73	U	U	Spo0A (+)	
<i>yddK</i>	+	3,76	U	U	U	
<i>yugI</i>	+	3,81	U	U	RelA	
<i>yybL</i>	+	3,82	U	similar to ABC transporter (permease)	Rok (-)	DnaA (-)
<i>yozF</i>	+	3,87	U	U	U	
<i>ybeF</i>	+	3,90	U	putative sporulation protein	U	
<i>ygzA</i>	+	4,10	U	U	U	
<i>yaaQ</i>	+	4,16	U	U	U	
<i>ydzP</i>	+	4,22	U	U	U	
<i>yxIA</i>	+	4,32	U	similar to purine-cytosine permease	U	
<i>yjzI</i>	+	4,47	U	U	U	
<i>yabE</i>	+	4,50	U	unknown; Similar to CW binding prot	sRNA(-)	
<i>ykbB</i>	+	4,99	U	U	TnrA (+)	PhoP (+)
<i>yocC</i>	+	5,47	U	U	U	
<i>yozH</i>	+	5,77	U	U	U	
<i>ykoL</i>	+	6,46	U	U	PhoP (+)	TnrA (+)
<i>ydcG</i>	+	17,56	U	U	U	
<i>ydcF</i>	+	71,73	U	U	U	
<i>yvzA</i>	+	2,72	U (put based on regulation: lifestyle_transition state)	U	AbrB (-)	DegU (+)
<i>yfml</i>	+	2,74	U (put based on regulation: lifestyle_transition state)	unknown, similar to macrolide-efflux transporter	AbrB (-)	Spo0A (+)
<i>ydeH</i>	+	2,89	U (put based on regulation: lifestyle_transition state)	U	AbrB (-)	
<i>yvnA</i>	+	2,97	U (put based on regulation: lifestyle_transition state)	U	AbrB (-)	CcpA (-)
<i>yjcM</i>	+	3,91	U (put based on regulation: lifestyle_transition state)	U	AbrB (-)	SigD
<i>yjdG</i>	+	4,87	U (put based on regulation: lifestyle_transition state)	U	AbrB (-)	
<i>yoZL</i>	+	14,32	U	U	LexA (-)	

