

Supplemental Table S1. Details of Microarrays used in this study.

Microarray	Cy5-labelled probe		Cy3-labelled probe	
	Strain	Pressure (kPa)	Strain	Pressure (kPa)
Fig. 1A	WN624	101	WN624	101
Fig. 1B	WN624	5	WN624	5
Fig. 1C	WN624	5	WN624	101

Supplemental Table S2. *B. subtilis* genes significantly up-regulated by exposure to 5 kPa.

NOTE: Known operons are grouped by colored boxes are used to distinguish adjacent operons and have no further meaning nor imply further grouping.

Accession BSU number	Gene Name	Fold Change	P-value	Known Regulon	Gene Description
BSU00520	ctc	7.18	0.016	SigB	ribosomal protein Ctc, binding 5S RNA
BSU00830	ctsR	11.26	0.004	CtsR	transcriptional regulator
BSU00840	mcsA	8.82	0.009	CtsR, SigF	activator of protein kinase McsB
BSU00850	mcsB	5.29	0.036	CtsR, SigF	protein tyrosine kinase
BSU02100	cypC	7.90	0.013	SigB	fatty acid beta-hydroxylating cytochrome P450
BSU02110	ybyB	76.68	<0.001	?	conserved hypothetical protein
BSU02590	ycbP	14.75	0.002	SigB	putative inner integral membrane protein
BSU02830	ycdF	12.76	0.003	SigB	putative dehydrogenase
BSU02840	ycdG	6.14	0.025	?	putative glycosidase
BSU03050	ldh	9.79	0.007	Rex	L-lactate dehydrogenase
BSU03060	lctP	16.20	0.001	Rex	L-lactate permease
BSU03200	ycgM	6.06	0.026	CodY, PutR, Spo0A	proline oxidase
BSU03300	nasD	5.87	0.028	NsrR, ResD, TnrA	assimilatory nitrite reductase subunit
BSU03760	yclK	4.83	0.044	ResD	two-component sensor histidine kinase [YclJ]
BSU03940	ycnI	4.78	0.045	YcnK	conserved hypothetical protein
BSU03950	ycnJ	4.76	0.046	YcnK	putative copper import protein
BSU03960	ycnK	5.28	0.036	AbrB, YcnK	putative transcriptional regulator (DeoR family)
BSU04190	ydaD	6.73	0.019	SigB	putative dehydrogenase
BSU04200	ydaE	6.93	0.018	SigB	conserved hypothetical protein
BSU04220	ydaG	32.42	<0.001	SigB	putative general stress protein
BSU04240	ydzA	6.06	0.026	?	conserved hypothetical protein
BSU04340	ydaP	19.14	0.001	SigB	putative enzyme with pyruvate as substrate
BSU04370	ydaS	9.33	0.008	SigB	conserved hypothetical protein
BSU04400	gsiB	90.26	<0.001	SigB, SigI	general stress protein
BSU04710	rsbV	36.63	<0.001	SigB	anti-anti-sigma factor (antagonist of RsbW)
BSU04720	rsbW	44.01	<0.001	SigB	switch protein/serine kinase and anti-sigma factor (inhibitory sigma-B binding protein)
BSU04730	sigB	56.94	<0.001	SigB	RNA polymerase sigma-37 factor (sigma(B))
BSU04740	rsbX	49.01	<0.001	SigB	serine phosphatase
BSU05130	ydeB	6.71	0.02	?	putative transcriptional regulator
BSU05790	ydhK	9.13	0.008	SigB	hypothetical protein
BSU05980	tatAY	5.66	0.03	?	component of the twin-arginine pre-protein translocation pathway
BSU05990	tatCY	7.12	0.017	?	component of the twin-arginine pre-protein translocation pathway
BSU06590	yerD	5.50	0.033	SigB	putative flavoenzyme
BSU06640	yerI	8.57	0.01	AbrB	putative kinase
BSU06660	opuE	30.35	<0.001	SigB, CcpA	proline transporter
BSU06710	yerP	5.16	0.038	?	transporter involved in surfactin self-resistance
BSU06830	rapH	5.21	0.037	AbrB, ComK, RghR	response regulator aspartate phosphatase
BSU07380	yfmQ	6.94	0.018	?	conserved hypothetical protein
BSU07550	yfiT	31.64	<0.001	SigB	heat stress induced protein
BSU07750	yfiA	45.79	<0.001	Abh, AbrB, SigB	putative aminoacid transporter
BSU07760	yfkT	24.75	<0.001	SigB	putative spore germination integral inner membrane protein
BSU07770	yfkS	13.26	0.003	SigB	hypothetical protein
BSU07780	yfkR	4.82	0.045	SigG	putative spore germination protein
BSU07850	yfkM	23.91	<0.001	Fur, SigB	general stress protein 18
BSU07880	yfkJ	29.03	<0.001	SigB	protein-tyrosine-phosphatase
BSU07890	yfkI	21.62	<0.001	SigB	conserved hypothetical protein
BSU07900	yfkH	15.34	0.002	SigB	putative integral inner membrane protein with ribonuclease fold
BSU07920	yfkE	14.71	0.002	SigB, SigG	putative H ⁺ /Ca ²⁺ antiporter
BSU07930	yfkD	7.91	0.013	SigB	conserved hypothetical protein
BSU08490	yfhD	9.35	0.008	SigB	conserved hypothetical protein
BSU08500	yfhE	5.70	0.03	SigB	hypothetical protein

BSU08510	yfhF	5.99	0.026	SigB	putative nucleotide binding protein
BSU08570	yfhK	89.64	<0.001	SigB, SigW	conserved hypothetical protein
BSU08580	yfhL	30.83	<0.001	SigB, SigW	SdpC immunity factor
BSU08590	yfhM	15.77	0.001	SigB, SigW	putative hydrolase
BSU08600	csbB	7.21	0.016	SigB, SigX	putative glycosyl transferase
BSU08990	yhbI	8.77	0.009	?	putative transcriptional regulator (MarR family)
BSU09000	yhbJ	10.04	0.006	?	putative integral inner membrane protein; putative exporter subunit
BSU09010	yhcA	6.50	0.021	?	putative exporter
BSU09020	yhcB	5.10	0.039	?	putative oxidoreductase associated to oxygen stress
BSU09140	yhcM	5.05	0.04	SigB, SigF, SigG	hypothetical protein
BSU09190	yhcR	4.95	0.042	?	non specific extracellular endonuclease cleaving RNA and DNA
BSU09230	yhcV	6.23	0.024	SigG	putative oxidoreductase
BSU09530	yhdN	28.76	<0.001	SigF, SigG	aldo/keto reductase specific for NADPH
BSU09690	nhaX	68.38	<0.001	SigB	stress response protein, UspA family
BSU09750	sspB	6.84	0.019	SigG, SpoVT	small acid-soluble spore protein (beta-type SASP)
BSU10130	hemH	5.09	0.039	?	ferrochelatase
BSU10140	hemY	4.80	0.045	?	protoporphyrinogen IX and coproporphyrinogen III oxidase
BSU10150	yhgD	6.40	0.022	?	putative transcriptional regulator
BSU10230	yhfH	4.69	0.047	?	hypothetical protein
BSU10430	yhxD	4.98	0.041	SigB	putative oxidoreductase
BSU11490	yjbC	28.10	<0.001	PerR, SigB, SigM, SigW, SigX	putative thiol oxidation management factor; putative acetyltransferase
BSU11830	yjcE	19.45	0.001	SigB	BG1315:unknown
BSU11990	yjdB	92.88	<0.001	AbrB, PhoP	putative exported protein
BSU12080	ctaO	8.71	0.01	AbrB	protoheme IX farnesyltransferase (heme O synthase)
BSU12160	yjgC	7.65	0.014	SigB	putative oxidoreductase
BSU12270	yjIB	12.31	0.003	?	conserved hypothetical protein ; cupin family
BSU12430	rapA	28.32	<0.001	CodY, ComA, Spo0A	response regulator aspartate phosphatase
BSU12440	phrA	31.67	<0.001	CodY, ComA, Spo0A	secreted inhibitor of the activity of phosphatase RapA
BSU13020	ykgA	38.11	<0.001	SigB	putative aminohydrolase
BSU13160	ykzA	24.31	<0.001	SigB	organic hydroperoxide resistance reductase B
BSU13170	guaD	8.66	0.01	PucR, SigB	guanine deaminase
BSU13850	ykvw	6.99	0.018	PerR	Zn transporter
BSU14660	ykzI	20.32	0.001	SigB	conserved hypothetical protein
BSU14890	ctaC	7.07	0.017	Abh, AbrB, CcpA, ResD	cytochrome caa3 oxidase (subunit II)
BSU14910	ctaE	4.81	0.045	Abh, AbrB, ResD	cytochrome caa3 oxidase (subunit III)
BSU14920	ctaF	5.07	0.04	Abh, AbrB, ResD	cytochrome caa3 oxidase (subunit IV)
BSU14930	ctaG	5.40	0.034	ResD	cytochrome aa(3) assembly factor
BSU15870	recG	7.74	0.013	?	DNA helicase involved in DNA recombination and repair
BSU15880	ylpC	5.70	0.03	ComA, FapR	transcription factor
BSU16180	flgB	5.02	0.04	CodY, SigD, Spo0A	flagellar component of cell-proximal portion of basal-body rod
BSU16190	flgC	5.80	0.029	CodY, SigD, Spo0A	flagellar component of cell-proximal portion of basal-body rod
BSU16200	fliE	5.15	0.038	CodY, SigD, Spo0A	flagellar basal body protein
BSU16210	fliF	5.95	0.027	CodY, SigD, Spo0A	flagellar basal-body M-ring protein
BSU16220	fliG	8.22	0.011	CodY, SigD, Spo0A	flagellar motor switching and energizing component
BSU16230	fliH	7.32	0.016	CodY, SigD, Spo0A	flagellar export apparatus component
BSU16240	fliI	5.91	0.027	CodY, SigD, Spo0A	flagellar-specific ATPase
BSU16250	fliJ	4.78	0.045	CodY, SigD, Spo0A	flagellar synthesis chaperone
BSU17100	pksC	6.25	0.024	AbrB, CodY	malonyl-CoA-acyltransferase involved in polyketide synthesis
BSU17110	pksD	7.65	0.014	AbrB, CodY	enzyme involved in polyketide synthesis
BSU17120	pksE	5.44	0.033	AbrB, CodY	enzyme involved in polyketide synthesis
BSU17130	acpK	4.63	0.049	AbrB, CodY	acyl-carrier protein
BSU17180	pksJ	5.57	0.032	AbrB, CodY	polyketide synthase of type I
BSU17240	ymzB	4.97	0.041	AbrB, SigB	conserved hypothetical protein
BSU17690	yncM	24.09	<0.001	AbrB	conserved hypothetical protein
BSU17710	tatAC	17.94	0.001	?	component of the twin-arginine pre-protein translocation pathway
BSU18110	ynfC	11.12	0.005	?	conserved hypothetical protein
BSU18310	ppsD	4.73	0.047	AbrB	plipastatin synthetase
BSU18320	ppsC	5.15	0.038	AbrB	plipastatin synthetase

BSU18350	dacC	5.85	0.028	SigH	D-alanyl-D-alanine carboxypeptidase
BSU18360	yoxA	5.45	0.033	SigH	putative epimerase
BSU18380	yoeB	7.97	0.012	WalR	inhibitor of cell-separation enzymes
BSU18440	gltB	16.00	0.001	GltC, FsrA, TnrA	glutamate synthase (small subunit)
BSU18450	gltA	57.49	<0.001	GltC, FsrA, TnrA, Efp-dependent	glutamate synthase (large subunit)
BSU18510	yoxC	36.27	<0.001	Proteins	conserved hypothetical protein
BSU18520	yoxB	27.18	<0.001	SigB	conserved hypothetical protein
BSU18530	yoaA	11.67	0.004	SigB	putative N-acetyltransferase
BSU18920	phrK	6.80	0.019	AbrB, SigH	secreted regulator of the activity of phosphatase RapK
BSU19030	yobO	7.09	0.017	AbrB, CcpA	putative phage-related pre-neck appendage protein
BSU19150	yocB	9.65	0.007	SigB	conserved hypothetical protein
BSU19310	dhaS	11.16	0.004	?	putative aldehyde dehydrogenase
BSU19410	yojL	6.53	0.021	Abh, AbrB, CcpA, SigD, SigH	peptidoglycan hydrolase (cell wall-binding d,l-endopeptidase)
BSU23120	resD	5.42	0.034	CcpA, PhoP, ResD	two-component response regulator
BSU23130	resC	4.72	0.047	CcpA, PhoP, ResD	factor required for cytochrome c synthesis
BSU23140	resB	5.96	0.027	CcpA, PhoP, ResD	factor required for cytochrome c synthesis
BSU23270	ribE	6.35	0.023	ResD	riboflavin synthase (alpha subunit)
BSU23280	ribD	6.17	0.024	FMN-box	fused diaminohydroxyphosphoribosylaminopyrimidine deaminase
BSU24000	bmrU	37.25	<0.001	SigB	putative diacylglycerol kinase
BSU24110	yqzF	4.99	0.041	?	conserved hypothetical protein
BSU24550	gcvPB	11.10	0.005	Gly-box	glycine decarboxylase (subunit 2) (glycine cleavage system protein P)
BSU24560	gcvPA	11.44	0.004	Gly-box	glycine decarboxylase (subunit 1) (glycine cleavage system protein P)
BSU24570	gcvT	9.45	0.007	Gly-box	aminomethyltransferase (glycine cleavage system protein T)
BSU24740	yqxL	11.52	0.004	LexA, SigB	putative CorA-type Mg(2+) transporter
BSU24750	yqhB	12.43	0.003	LexA, SigB	putative membrane associated protein
BSU24760	yqhA	22.09	<0.001	SigB	component of the piezosome (stressosome)
BSU24770	yqgZ	94.89	<0.001	SigB, MgsR	transcriptional regulator of stress
BSU25080	yqfX	4.74	0.046	SigG	conserved hypothetical protein
BSU25220	antE	6.28	0.023	AbrB	hypothetical protein
BSU26620	yrdR	6.40	0.022	?	putative efflux transporter
BSU26890	csn	82.13	<0.001	AbrB	chitinase
BSU26900	yraL	4.83	0.044	?	conserved hypothetical protein
BSU26920	yraJ	6.90	0.018	?	conserved hypothetical protein
BSU26930	yraI	6.91	0.018	?	conserved hypothetical protein
BSU28340	ysnF	6.25	0.024	SigB	putative stress response protein
BSU28550	ysiA	5.42	0.034	CcpA, FadR	transcriptional regulator of fatty acids degradation (TetR/AcrR family)
BSU28560	lcfA	6.41	0.022	CcpA, FadR	long chain acyl-CoA ligase (degradative)
BSU29260	ytpI	7.39	0.015	?	conserved hypothetical protein
BSU29760	ytxJ	11.23	0.004	SigB, SigH	conserved hypothetical protein
BSU29770	ytxH	14.48	0.002	SigB, SigH	conserved hypothetical protein
BSU29780	ytxG	17.69	0.001	SigB, SigH	conserved hypothetical protein
BSU30650	dps	11.35	0.004	SigB	DNA-protecting protein, ferritin
BSU30660	ytkA	6.50	0.021	?	putative lipoprotein
BSU30700	rpmE2	19.88	0.001	?	ribosomal protein L31
BSU30930	ytaB	20.41	0.001	SigB	putative receptor
BSU31280	yugU	6.17	0.025	SigB	conserved hypothetical protein
BSU31690	comP	6.50	0.021	?	two-component sensor histidine kinase
BSU31700	comX	7.87	0.013	?	competence pheromone precursor (pheromone peptide aa 46->55)
BSU31710	comQ	5.69	0.03	?	isoprenyl transferase (pre-ComX modification)
BSU31880	yukB	6.65	0.02	DegU	BG1237:unknown; similar to unknown proteins
BSU32890	yusQ	17.57	0.001	?	putative tautomerase
BSU32900	yusR	21.71	<0.001	SigE	putative 3-oxoacyl- acyl-carrier protein reductase
BSU32910	yusS	24.32	<0.001	?	putative 3-oxoacyl- acyl-carrier protein reductase
BSU33200	yvrE	9.00	0.009	SigB	conserved hypothetical protein
BSU33240	oxdC	20.16	0.001	YvrI-YvrHa	oxalate decarboxylase
BSU33410	yvgO	24.86	<0.001	AbrB, SigB	conserved hypothetical protein
BSU33530	yvaA	10.26	0.006	SigB	putative oxidoreductase
BSU33700	opuBD	5.20	0.037	GbsR, OpcR	choline ABC transporter (permease)
BSU33710	opuBC	22.06	<0.001	GbsR, OpcR	choline ABC transporter (choline-binding lipoprotein)
BSU33720	opuBB	12.35	0.003	GbsR, OpcR	choline ABC transporter (permease)
BSU33730	opuBA	5.21	0.037	GbsR, OpcR	choline ABC transporter (ATP-binding protein)
BSU33750	yvaW	5.92	0.027	AbrB, Rok, Spo0A	export of killing factor

BSU33760	yvaX	5.10	0.039	AbrB, Rok, Spo0A	exporter of killing factor SpbC
BSU33770	yvaY	12.75	0.003	AbrB, Rok, Spo0A	killing factor SdpC
BSU35050	yvnA	8.92	0.009	AbrB, CcpA	putative transcriptional regulator
BSU35060	cypX	7.61	0.014	AbrB	putative monooxygenase (cytochrome P450)
BSU35070	yvmC	5.46	0.033	AbrB	conserved hypothetical protein
BSU35180	csbA	10.33	0.006	SigB	putative membrane protein
BSU35310	yvyD	7.69	0.014	SigB, SigH	ribosome-associated sigma 54 modulation protein
BSU35830	ywtG	9.85	0.007	SigB	putative carbohydrate transporter
BSU36460	ywoF	6.60	0.021	Abh, AbrB, CodY, GlnR, PucR, SigH, TnrA	putative pectate lyase
BSU36640	ureC	8.21	0.011	CodY, GlnR, PucR, SigH, TnrA	urease (alpha subunit)
BSU36650	ureB	18.29	0.001	CodY, GlnR, PucR, SigH, TnrA	urease (beta subunit)
BSU36660	ureA	19.35	0.001	TnrA	urease (gamma subunit)
BSU36670	csbD	16.92	0.001	SigB	stress response protein
BSU36720	ywmE	17.57	0.001	SigB	hypothetical protein
BSU37210	ywjC	44.45	<0.001	SigB	conserved hypothetical protein
BSU37240	ywiE	35.33	<0.001	SigB	cardiolipin synthetase
BSU37250	narI	57.08	<0.001	Fnr	nitrate reductase (gamma subunit)
BSU37260	narJ	44.17	<0.001	Fnr	nitrate reductase (protein J)
BSU37270	narH	54.93	<0.001	Fnr	nitrate reductase (beta subunit)
BSU37280	narG	38.15	<0.001	Fnr	nitrate reductase (alpha subunit)
BSU37310	fnr	19.63	0.001	Fnr, NsrR, ResD	transcriptional regulator (FNR/CAP family)
BSU37320	narK	10.14	0.006	Fnr, NsrR	nitrite extrusion permease
BSU37350	sboA	104.74	<0.001	AbrB, ResD, Rok	subtilisin A
BSU37360	sboX	118.20	<0.001	AbrB, ResD, Rok	putative bacteriocin-like product
BSU37370	albA	84.14	<0.001	AbrB, ResD, Rok	putative antilisterial bacteriocin (subtilisin) production enzyme
BSU37380	albB	74.22	<0.001	AbrB, ResD, Rok	putative membrane component involved in subtilisin production
BSU37390	albC	56.75	<0.001	AbrB, ResD, Rok	putative transporter involved in subtilisin production
BSU37400	albD	61.89	<0.001	AbrB, ResD, Rok	integral inner membrane protein involved in subtilisin production and immunity
BSU37410	albE	116.47	<0.001	AbrB, ResD, Rok	putative hydrolase involved in subtilisin production
BSU37420	albF	102.31	<0.001	AbrB, ResD, Rok	putative peptidase involved in subtilisin production
BSU37430	albG	98.90	<0.001	AbrB, ResD, Rok	integral inner membrane protein involved in subtilisin production and immunity
BSU37440	ywhL	24.49	<0.001	?	conserved hypothetical protein
BSU37450	ywhK	5.03	0.04	?	factor interacting with DNA helicase PcrA
BSU37670	ywfI	4.87	0.043	?	putative oxidoreductase/oxygenase/dismutase
BSU38180	ywzA	26.75	<0.001	SigB	conserved hypothetical protein
BSU38430	gspA	69.26	<0.001	SigB	putative glycosyl transferase (general stress protein)
BSU38610	yxzF	5.85	0.028	SigB	hypothetical protein
BSU38630	katX	4.60	0.049	RsfA, SigB, SigF	major catalase in spores
BSU38730	cydD	13.06	0.003	CcpA, ResD, Rex	ABC membrane transporter (ATP-binding protein) required for cytochrome bd function
BSU38740	cydC	48.69	<0.001	CcpA, ResD, Rex	ABC membrane transporter (ATP-binding protein) required for cytochrome bd function
BSU38750	cydB	40.17	<0.001	CcpA, ResD, Rex	cytochrome bd ubiquinol oxidase (subunit II)
BSU38760	cydA	27.64	<0.001	CcpA, ResD, Rex	cytochrome bd ubiquinol oxidase (subunit I)
BSU38920	pepT	4.96	0.042	?	peptidase T (tripeptidase)
BSU38930	yxjJ	5.37	0.035	DegU, SigB	hypothetical protein
BSU39040	ysiS	5.17	0.038	SigB	hypothetical protein
BSU39050	katE	29.22	<0.001	SigB	catalase 2
BSU39330	ysiA	7.22	0.016	?	arabinan endo-1,5-alpha-L-arabinosidase
BSU39810	csbC	20.29	0.001	SigB	putative sugar transporter
BSU39840	yxgG	7.12	0.017	SigB	putative oxidoreductase
BSU39940	yxal	5.66	0.03	AbrB, Rok	membrane associated protein kinase with beta-propeller domain
BSU40000	yxna	10.68	0.005	SigB	putative oxidoreductase
BSU40660	yybF	37.30	<0.001	?	putative permease

Supplemental Table S3. *B. subtilis* genes significantly down-regulated by exposure to 5 kPa.

NOTE: Known operons are grouped by colored boxes are used to distinguish adjacent operons and have no further meaning nor imply further grouping.

Accession BSU number	Gene Name	Fold Change	P-value	Regulon	Gene Description
BSU02120	ybeC	-7.73	0.013	?	putative H ⁺ /amino acid transporter
BSU02130	glpQ	-11.35	0.004	CcpA, GlpP,	glycerophosphoryl diester phosphodiesterase
BSU02140	glpT	-19.12	0.001	PhoP	
BSU02230	purT	-8.36	0.01	CcpA, GlpP	glycerol-3-phosphate permease
BSU02530	yczA	-5.25	0.035	?	phosphoribosylglycinamide formyltransferase 2
BSU02540	ycbK	-6.23	0.023	T-box	anti-TRAP regulator
BSU03270	ycgT	-9.32	0.007	T-box, TRAP	putative efflux transporter
BSU03370	yckA	-4.89	0.042	Fur	putative thioredoxin reductase
BSU03450	hxlB	-6.31	0.022	?	putative ABC transporter (permease)
BSU03460	hxlA	-6.33	0.022	HxlR	6-phospho-3-hexuloisomerase (PHI)
BSU03800	yclN	-11.63	0.004	HxlR	3-hexulose-6-phosphate synthase (HPS)
BSU03810	yclO	-11.41	0.004	Fur	putative iron-siderophore ABC transporter (permease)
BSU03820	yclP	-6.24	0.023	Fur	putative iron-siderophore ABC transporter (permease)
BSU04000	ycaA	-6.57	0.02	Fur	putative iron-siderophore ABC transporter (ATP-binding protein)
BSU04470	dctP	-38.15	<0.001	?	putative tartrate dehydrogenase
BSU05680	ydgK	-5.54	0.031	CcpA, FsrA	C4-dicarboxylate transport protein
BSU06150	gutB	-4.80	0.043	?	putative efflux transporter
BSU06230	ydjK	-33.70	<0.001	GutR	glucitol (sorbitol) dehydrogenase
BSU06380	yebC	-4.81	0.043	IolR	myo-inositol transporter
BSU07150	yetG	-9.77	0.006	?	putative integral inner membrane protein
BSU07160	yetH	-5.37	0.033	Fur	putative monooxygenase
BSU07340	yfnA	-4.86	0.042	?	putative lyase/dioxygenase
BSU07520	yfmC	-6.38	0.022	?	metabolite permease
BSU07610	citM	-27.71	<0.001	Fur	iron-dicitrate ABC transporter (binding lipoprotein)
BSU07620	yfiN	-11.63	0.004	CcpA, CitT	transporter of divalent metal ions/citrate complexes
BSU07700	nagP	-5.29	0.035	CcpA, CitT	putative metal-dependent hydrolase
BSU07800	treP	-43.61	<0.001	NagR	PTS N-acetylglucosamine-specific enzyme IICB component
				CcpA, PhoP,	PTS trehalose-specific enzyme IIBC component
				TreR	
				CcpA, PhoP,	trehalose-6-phosphate hydrolase
				TreR	
				Fur	putative iron(III) dicitrate transporter binding lipoprotein
				Fur	iron(III) siderophore transport permease
				Fur	iron(III) siderophore transport permease
				Fur	putative oxidoreductase (nitroreductase family)
				SigH, SigW	sporulation-control gene
BSU09110	yhcJ	-4.63	0.047	?	putative ABC transporter (binding lipoprotein)
BSU09280	glpF	-26.30	<0.001	AbrB, CcpA,	glycerol permease
BSU09290	glpK	-4.82	0.043	GlpP	
				AbrB, CcpA,	glycerol kinase
				GlpP	
				?	putative sodium-dependent transporter
				?	proton/sodium-glutamate symport protein
				?	putative N-acetyltransferase
				Fur	putative iron(III) dicitrate-binding lipoprotein
				CcpA, ManR	transcriptional antiterminator
				Rex,	conserved hypothetical protein
				Stringent	
BSU12280	yjIC	-4.88	0.042	Response	ATPase possibly involved in protein degradation
BSU12420	yjoB	-4.68	0.046	SigW	putative integral inner membrane protein
BSU13430	ykoX	-5.18	0.036	?	membrane protease
BSU13490	ykrL	-5.22	0.036	Rok, YkrK	
BSU13890	ptsG	-15.70	0.001	GlcT,	PTS glucose-specific enzyme IICBA component
				Stringent	
				Response	putative beta-hydroxyacid dehydrogenase
				?	
				Fur	short-chain flavodoxin
				Fur	conserved hypothetical protein
				Fur	short-chain flavodoxin
				?	tetrahydrodipicolinate N-acetyltransferase
				?	N-acetyl-diaminopimelate deacetylase
				?	conserved hypothetical protein
BSU14480	abh	-5.89	0.027	SigM, SigX	transcriptional regulator
BSU14550	ykrA	-6.61	0.02	?	putative hydrolase
BSU14820	ylaL	-6.65	0.019	?	conserved hypothetical protein
BSU17630	yncC	-9.28	0.008	?	putative sugar transporter
BSU19510	yojB	-11.10	0.004	?	conserved hypothetical protein
BSU19520	yoyA	-15.37	0.001	?	putative H ⁺ /anion permease
BSU22600	aroE	-10.19	0.006	TRAP	5-enolpyruvoylshikimate-3-phosphate synthase
BSU22610	tyrA	-7.11	0.016	TRAP	prephenate dehydrogenase
BSU22620	hisC	-4.73	0.045	TRAP	histidinol-phosphate, tyrosine/phenylalanine aminotransferase
BSU23550	mleA	-21.44	<0.001	AnsR, CcpA	NAD-dependent malic enzyme (conversion of malate into pyruvate)
BSU23560	mleN	-30.54	<0.001	AnsR, CcpA	malate-H ⁺ /Na ⁺ -lactate antiporter

BSU23570	ansA	-18.21	0.001	AnsR	L-aspartase (aspartate ammonia lyase)
BSU23580	ansB	-11.31	0.004	AnsR	exported L-asparaginase
BSU23590	ansR	-5.52	0.031	AnsR	transcriptional regulator of ansAB (Xre family)
BSU27200	yrhG	-12.18	0.003	?	putative formate/nitrite transporter
BSU28080	folC	-4.98	0.04	T-box	folyl-polyglutamate synthase
				T-box, Efp-dependent	
BSU28090	valS	-5.13	0.037	proteins	valyl-tRNA synthetase
BSU28710	cstA	-4.69	0.046	CcpA	carbon starvation-induced membrane protein
BSU28900	ysbB	-21.29	<0.001	?	antiholin factor
BSU28910	ysbA	-27.84	<0.001	?	antiholin factor
BSU28950	thrS	-4.85	0.042	T-box	threonyl-tRNA synthetase
BSU29480	ytxK	-5.56	0.031	?	putative nucleic acid methyltransferase
BSU29490	tpx	-5.07	0.038	Spx	putative peroxiredoxin
BSU29520	yteJ	-7.58	0.014	SigW	putative integral inner membrane protein
BSU29530	sppA	-8.06	0.011	SigW	signal peptide peptidase
BSU29600	braB	-5.20	0.036	?	branched-chain amino acid-Na ⁺ symporter
BSU29990	ytiP	-5.10	0.038	PurR	hypoxanthine/guanine permease
BSU30000	ythQ	-5.34	0.034	SigW	putative ABC transporter (permease)
BSU30260	msmR	-23.08	<0.001	CcpA	transcriptional regulator (LacI family)
BSU30990	yuaJ	-8.24	0.011	Thi-box	thiamin permease
BSU31440	patB	-5.23	0.036	?	C-S lyase
BSU31580	maeN	-9.66	0.007	MalR	Na ⁺ /malate symporter
BSU31600	mrpA	-5.82	0.027	?	Na ⁺ /H ⁺ antiporter
BSU31610	mrpB	-6.80	0.018	?	Na ⁺ /H ⁺ antiporter complex
BSU31620	mrpC	-6.26	0.023	?	component of Na ⁺ /H ⁺ antiporter
BSU31630	mrpD	-5.99	0.025	?	component of Na ⁺ /H ⁺ antiporter
BSU31640	mrpE	-4.90	0.042	?	non essential component of Na ⁺ /H ⁺ antiporter
BSU31960	dhbF	-11.56	0.004	AbrB, Fur	siderophore bacillibactin synthetase
BSU31970	dhbB	-10.66	0.005	AbrB, Fur	isochorismatase
BSU31980	dhbE	-14.72	0.002	AbrB, Fur	2,3-dihydroxybenzoate-AMP liqase (enterobactin synthetase comp E)
BSU31990	dhbC	-18.97	0.001	AbrB, Fur	isochorismate synthase
BSU32000	dhbA	-16.64	0.001	AbrB, Fur	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase

				AbrB, Fur, Efp dependent	
BSU32010	yuiI	-11.58	0.004	proteins	bacillibactin trilactone hydrolase
BSU32040	yuiF	-4.96	0.04	?	amino acid transporter
BSU32940	yusV	-4.57	0.049	Fur	iron(III)-siderophore transporter (ATP binding component)
BSU33290	fhuC	-9.60	0.007	Fur	ferrichrome ABC transporter (ATP-binding protein)
BSU33300	fhuG	-21.51	<0.001	Fur	ferrichrome ABC transporter (permease)
BSU33310	fhuB	-25.37	<0.001	Fur	ferrichrome ABC transporter (permease)
BSU33320	fhuD	-11.30	0.004	Fur	ferrichrome ABC transporter (ferrichrome-binding lipoprotein)
BSU33460	yvgT	-6.20	0.023	?	putative integral inner membrane protein
BSU33560	yvaD	-9.11	0.008	?	putative integral inner membrane protein
BSU33570	yvaE	-11.80	0.004	?	putative metabolite-efflux transporter
BSU33580	yvaF	-7.71	0.013	?	putative transcriptional regulator
BSU33940	gapA	-7.18	0.016	CqqR	glyceraldehyde-3-phosphate dehydrogenase
BSU34190	yvfH	-6.97	0.017	ComA	putative lactate permease
				AbrB, EAR,	
BSU34260	yvfB	-6.20	0.023	RemA, SinR	BG1187:unknown
				AbrB, EAR,	
BSU34270	yvfA	-6.47	0.021	RemA, SinR	BG1186:unknown
				AbrB, EAR,	
BSU34320	yveP	-5.91	0.026	RemA, SinR	glycosyltransferase involved in extracellular matrix formation
				AbrB, EAR,	
BSU34330	yveO	-4.65	0.047	RemA, SinR	putative glycosyltransferase
				AbrB, RemA,	
BSU34360	yveL	-6.76	0.019	SinR	protein tyrosine kinase
				AbrB, RemA,	
BSU34370	yveK	-9.08	0.008	SinR	modulator of protein tyrosine kinase EpsB
BSU35910	rbsR	-5.80	0.028	AbrB, CcpA	transcriptional regulator (LacI family)
BSU36360	mscL	-4.95	0.04	?	large conductance mechanosensitive channel protein
BSU36370	ywpB	-4.99	0.04	?	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
BSU36480	ywoD	-5.70	0.029	YtrA	putative efflux transporter
BSU36610	ywnC	-6.99	0.017	?	putative integral inner membrane protein
BSU37490	speB	-5.98	0.026	?	agmatinase
BSU37570	mmr	-7.87	0.012	?	toxic compound efflux transporter

				AbrB, AhrC, CodY, RocR,	
BSU37780	rocA	-5.65	0.03	SigL	delta-1-pyrroline-5 carboxylate dehydrogenase
BSU37940	ywdJ	-4.56	0.049	TnrA	putative purine/pyrimidine permease
BSU38040	sacA	-5.07	0.038	CcpA, SacT	sucrase-6-phosphate hydrolase
BSU38050	sacP	-6.20	0.023	CcpA, SacT	PTS sucrose-specific enzyme IIBC component
BSU38840	yxkD	-4.86	0.042	?	efflux transporter
BSU39600	yxec	-7.22	0.016	?	putative integral inner membrane protein
BSU39610	yxeb	-20.61	<0.001	Fur	ABC transporter (ferrioxamine binding lipoprotein)
BSU39660	yxkJ	-4.65	0.047	?	two-component response regulator [YxkK]
BSU39670	fbaB	-8.04	0.012	CcpA, IolR	2-deoxy-5-keto-D-gluconic acid 6-phosphate aldolase
BSU39680	iolI	-9.17	0.008	CcpA, IolR	putative sugar-phosphate epimerase/isomerase
BSU39690	iolH	-8.10	0.011	CcpA, IolR	putative sugar-phosphate epimerase/isomerase
BSU39700	idh	-7.02	0.017	CcpA, IolR	myo-inositol 2-dehydrogenase

BSU39710	<u>iolF</u>	-9.80	0.006	CcpA, IolR	inositol transport protein
BSU39720	<u>iolE</u>	-10.20	0.006	CcpA, IolR	2-keto-myo-inositol dehydratase
BSU39730	<u>iolD</u>	-7.84	0.012	CcpA, IolR	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase
BSU39740	<u>iolC</u>	-8.75	0.009	CcpA, IolR	2-deoxy-5-keto-D-gluconic acid kinase
BSU39750	<u>iolB</u>	-8.87	0.009	CcpA, IolR	5-deoxy-D-glucuronic acid isomerase
BSU39760	<u>mmsA</u>	-7.95	0.012	CcpA, IolR	methylmalonate-semialdehyde dehydrogenase
BSU39960	<u>yxaI</u>	-4.79	0.044	?	putative integral inner membrane protein

Supplemental Table S4. Response of General Stress Response genes to LP exposure (5 kPa).

NOTE: Data are expressed as an induction ratio of (expression at 5kPa / expression at ~101 kPa)

^ABSU number are gene identifiers from the Genolist database (<http://genodb.pasteur.fr/>).

^BShaded cells denote genes with ratios either less than 4.5 or with a P-value > 0.05 (i.e., not significantly down-regulated by at least 4.5-fold). Hatched cells denote down-regulated genes.

^CUnderlined genes have been documented to be induced solely by a sigB-dependent promoter (<http://subtiwiki.uni-goettingen.de/wiki>).

BSU number ^A	Gene Name ^{B,C}	Ratio 5 kPa/ ~101 kPa	P-Value	Gene Description
BSU00160	<u>yaaH</u>	1.8	0.2574	spore peptidoglycan hydrolase
BSU00170	<u>yaaI</u>	4.1	0.0641	putative isochorismatase
BSU00520	<u>ctc</u>	7.2	0.0164	ribosomal protein Ctc, binding 5S RNA
BSU00530	<u>spoVC</u>	3.7	0.0799	peptidyl-tRNA hydrolase
BSU00660	<u>yabT</u>	1.8	0.2608	putative serine/threonine-protein kinase
BSU00890	<u>vacL</u>	2.2	0.2019	putative membrane protein
BSU02100	<u>cypC</u>	8	0.0126	fatty acid beta-hydroxylating cytochrome P450
BSU02110	<u>ybyB</u>	76.7	<0.0001	conserved hypothetical protein
BSU02540	<u>ycbK</u>	0.2	0.023	putative efflux transporter
BSU02580	<u>ycbO</u>	1.3	0.3831	putative Na ⁺ -driven exporter or maturation protein
BSU02590	<u>ycbP</u>	14.8	0.0018	putative inner integral membrane protein
BSU02790	<u>ycdB</u>	0.7	0.3238	putative hydrolase
BSU02830	<u>ycdF</u>	12.8	0.0029	putative dehydrogenase
BSU02840	<u>ycdG</u>	6.1	0.0248	putative glycosidase
BSU02900	<u>yceD</u>	0.8	0.3981	putative stress adaptation protein
BSU02910	<u>yceE</u>	0.8	0.3806	putative stress adaptation protein
BSU02920	<u>yceF</u>	0.6	0.2817	putative stress adaptation transporter
BSU02930	<u>yceG</u>	1.4	0.3478	conserved hypothetical protein
BSU03130	<u>nadE</u>	1	0.4807	ammonium-dependent NAD ⁺ synthetase
BSU03910	<u>gabD</u>	1.5	0.3348	succinate-semialdehyde dehydrogenase
BSU04030	<u>ycsD</u>	0.8	0.3977	putative hydroxymyristoyl-(acyl carrier protein) dehydratase
BSU04190	<u>ydaD</u>	6.7	0.0195	putative dehydrogenase
BSU04200	<u>ydaE</u>	6.9	0.0181	conserved hypothetical protein
BSU04220	<u>ydaG</u>	32.4	0.0001	putative general stress protein
BSU04340	<u>ydaP</u>	19.1	0.0007	putative enzyme with pyruvate as substrate
BSU04370	<u>ydaS</u>	9.3	0.0078	conserved hypothetical protein
BSU04380	<u>ydaT</u>	3.9	0.072	conserved hypothetical protein
BSU04400	<u>gsiB</u>	90.3	<0.0001	general stress protein
BSU04420	<u>ydbC</u>	0.7	0.3244	conserved hypothetical protein
BSU04430	<u>ydbD</u>	2.3	0.1806	putative manganese-containing catalase
BSU04710	<u>rsbV</u>	36.6	<0.0001	anti-anti-sigma factor (antagonist of RsbW)
BSU04720	<u>rsbW</u>	44	<0.0001	switch protein/serine kinase and anti-sigma factor (inhibitory sigma-B binding protein)
BSU04730	<u>sigB</u>	56.9	<0.0001	RNA polymerase sigma-37 factor (sigma-B)
BSU04740	<u>rsbX</u>	49	<0.0001	serine phosphatase
BSU05150	<u>ydeC</u>	0.8	0.4186	putative transcriptional regulator (AraC/XylS family)
BSU05360	<u>ydfC</u>	0.9	0.4652	putative permease
BSU05440	<u>nap</u>	1.1	0.4512	carboxylesterase NP
BSU05490	<u>mhqO</u>	1.7	0.2844	putative dioxygenase
BSU05790	<u>ydHk</u>	9.1	0.0083	hypothetical protein
BSU06120	<u>ydjB</u>	0.8	0.3873	hypothetical protein

BSU06220	<i>ydjJ</i>	1.7	0.2869	putative membrane associated potassium channel
BSU06240	<i>ydjL</i>	2.6	0.1513	acetoin reductase/2,3-butanediol dehydrogenase
BSU06310	<i>gabP</i>	0.6	0.2567	gamma-aminobutyrate (GABA) permease
BSU06350	<i>yebA</i>	1.3	0.3846	conserved hypothetical protein
BSU06590	<i>verD</i>	5.5	0.0326	putative flavoenzyme
BSU06660	<i>opuE</i>	30.4	0.0001	proline transporter
BSU06980	<i>yesP</i>	0.8	0.4234	rhamnogalacturonan permease
BSU07260	<i>yfnI</i>	0.8	0.3903	exported glycerol phosphate lipoteichoic acid synthetase and anion-binding protein
BSU07540	<i>yfmA</i>	0.8	0.4076	unknown
BSU07550	<i>yflT</i>	31.6	0.0001	heat stress induced protein
BSU07680	<i>yflH</i>	1.4	0.3544	conserved hypothetical protein
BSU07750	<i>yflA</i>	45.8	<0.0001	putative aminoacid transporter
BSU07760	<i>yfkT</i>	24.8	0.0003	putative spore germination integral inner membrane protein
BSU07770	<i>yfkS</i>	13.3	0.0026	hypothetical protein
BSU07850	<i>yfkM</i>	23.9	0.0003	general stress protein 18
BSU07880	<i>yfkJ</i>	29	0.0001	protein-tyrosine-phosphatase
BSU07890	<i>yfkI</i>	21.6	0.0004	conserved hypothetical protein
BSU07900	<i>yfkH</i>	15.3	0.0015	putative integral inner membrane protein with ribonuclease fold
BSU07920	<i>chaA</i>	14.7	0.0018	putative H ⁺ /Ca ²⁺ antiporter
BSU07930	<i>yfkD</i>	7.9	0.0126	conserved hypothetical protein
BSU08490	<i>yfhD</i>	9.4	0.0077	conserved hypothetical protein
BSU08500	<i>yfhE</i>	5.7	0.0299	hypothetical protein
BSU08510	<i>yfhF</i>	6	0.0264	putative nucleotide binding protein
BSU08570	<i>yfhK</i>	89.6	<0.0001	conserved hypothetical protein
BSU08580	<i>yfhL</i>	30.8	0.0001	SdpC immunity factor
BSU08590	<i>yfhM</i>	15.8	0.0014	putative hydrolase
BSU08600	<i>csbB</i>	7.2	0.0163	putative glycosyl transferase
BSU09140	<i>yhcM</i>	5.1	0.0399	hypothetical protein
BSU09390	<i>ygxB</i>	3.8	0.0735	putative integral inner membrane protein
BSU09450	<i>yhdF</i>	3.5	0.0862	putative NAD(P)-dependent dehydrogenase
BSU09530	<i>yhdN</i>	28.8	0.0001	aldo/keto reductase specific for NADPH
BSU09690	<i>nhaX</i>	68.4	<0.0001	stress response protein, UspA family
BSU10430	<i>yhxD</i>	5	0.0412	putative oxidoreductase
BSU10810	<i>visP</i>	3	0.1198	putative squalene/phytoene synthase
BSU11120	<i>yitT</i>	2.1	0.2126	putative integral inner membrane protein
BSU11490	<i>yjbC</i>	28.1	0.0001	putative thiol oxidation management factor; putative acetyltransferase
BSU11830	<i>yjcE</i>	19.5	0.0006	unknown
BSU12010	<i>manP</i>	0.3	0.1089	phosphotransferase system (PTS) mannose-specific enzyme IIBC component
BSU12070	<i>yjdJ</i>	2.8	0.1363	conserved hypothetical protein
BSU12150	<i>yjgB</i>	1.7	0.283	hypothetical protein
BSU12160	<i>yjgC</i>	7.7	0.0138	putative oxidoreductase
BSU12170	<i>yjgD</i>	4.4	0.0544	conserved hypothetical protein
BSU12560	<i>xpf</i>	1.1	0.4755	putative RNA polymerase PBSX sigma factor-like
BSU12720	<i>xkdS</i>	0.8	0.3887	conserved hypothetical protein; putative PBSX prophage protein
BSU13020	<i>ykgA</i>	38.1	<0.0001	putative aminohydrolase
BSU13160	<i>ohrB</i>	24.3	0.0003	organic hydroperoxide resistance reductase B
BSU13170	<i>guaD</i>	8.7	0.0097	guanine deaminase
BSU14210	<i>ykuT</i>	2.9	0.1256	putative small-conductance mechanosensitive channel
BSU14660	<i>ykzI</i>	20.3	0.0005	conserved hypothetical protein
BSU16640	<i>ylxP</i>	1.9	0.2534	conserved hypothetical protein
BSU17240	<i>ymzB</i>	5	0.0414	conserved hypothetical protein
BSU17850	<i>lexA</i>	0.8	0.3734	transcriptional repressor of the SOS regulon
BSU18110	<i>ynfC</i>	11.1	0.0045	conserved hypothetical protein
BSU18510	<i>voxC</i>	36.3	<0.0001	conserved hypothetical protein
BSU18520	<i>voxB</i>	27.2	0.0002	conserved hypothetical protein
BSU19150	<i>yocB</i>	9.7	0.007	conserved hypothetical protein

BSU19240	<i>yocK</i>	3.8	0.0737	putative general stress protein
BSU20450	<i>yorA</i>	1.9	0.2505	putative capsid component; phage SPbeta
BSU23060	<i>ypzE</i>	1.1	0.4607	hypothetical protein
BSU23830	<i>yqjL</i>	0.9	0.469	putative hydrolase
BSU23970	<i>yqiY</i>	1.3	0.379	High affinity arginine ABC transporter (permease)
BSU24000	<i>bmrU</i>	37.3	<0.001	putative diacylglycerol kinase
BSU24010	<i>bmr</i>	1.5	0.3396	multidrug-efflux transporter
BSU24020	<i>bmrR</i>	2.6	0.1554	transcriptional regulator (MerR family)
BSU24140	<i>mmgD</i>	1.3	0.3795	2-methylcitrate synthase
BSU24490	<i>yqhQ</i>	3.1	0.1127	conserved hypothetical protein
BSU24740	<i>yqxL</i>	11.5	0.0041	putative CorA-type Mg(2+) transporter
BSU24750	<i>yqkB</i>	12.4	0.0032	putative membrane associated protein
BSU24770	<i>yqgZ</i>	94.9	<0.0001	putative transcriptional regulator of stress
BSU25020	<i>sodA</i>	0.5	0.1927	superoxide dismutase
BSU26180	<i>yqBA</i>	1	0.4997	putative phage capsid protein; skin element
BSU26540	<i>yrkE</i>	1	0.4833	conserved hypothetical protein
BSU27020	<i>yraA</i>	1	0.4962	general stress protein
BSU27230	<i>yrhD</i>	1.5	0.3296	conserved hypothetical protein
BSU27640	<i>yrvC</i>	0.5	0.1884	putative potassium transport accessory component
BSU27750	<i>bofC</i>	3.1	0.1121	Bypass of forespore C, intercompartmental signaling factor
BSU27760	<i>csbX</i>	2.1	0.2072	putative permease
BSU28180	<i>ysxD</i>	0.4	0.1874	putative integral inner membrane protein
BSU28340	<i>ysnF</i>	6.3	0.0237	putative stress response protein
BSU28450	<i>sdhC</i>	0.2	0.0508	succinate dehydrogenase (cytochrome b558 subunit)
BSU28590	<i>yshC</i>	1.6	0.3109	DNA polymerase X
BSU28810	<i>abnA</i>	2.7	0.1382	arabinan-endo 1,5-alpha-L-arabinase
BSU28830	<i>ysdB</i>	1.9	0.2434	conserved hypothetical protein
BSU29410	<i>ytkL</i>	0.9	0.4641	putative metal-dependent hydrolase
BSU29760	<i>ytXJ</i>	11.2	0.0044	conserved hypothetical protein
BSU29770	<i>ytXH</i>	14.5	0.0019	conserved hypothetical protein
BSU29780	<i>ytXG</i>	17.69	0.0009	conserved hypothetical protein
BSU30020	<i>ytZE</i>	1.9	0.2459	putative transcriptional regulator (DeoR family)
BSU30230	<i>bioA</i>	1	0.4994	lysine-8-amino-7-oxononanoate aminotransferase
BSU30650	<i>dps</i>	11.4	0.0042	DNA-protecting protein, ferritin
BSU30700	<i>rpmE2</i>	19.9	0.0006	ribosomal protein L31
BSU30930	<i>ytaB</i>	20.4	0.0005	putative receptor
BSU31280	<i>yugU</i>	6.2	0.0245	conserved hypothetical protein
BSU31380	<i>yuzA</i>	2.1	0.2136	conserved hypothetical protein
BSU32320	<i>yutC</i>	1.1	0.465	putative lipoprotein
BSU32520	<i>yurG</i>	0.6	0.2864	putative ureidoglycolate lyase (ureidoglycolase)
BSU32880	<i>yusP</i>	2.3	0.1866	putative multidrug-efflux transporter
BSU33140	<i>yvqJ</i>	0.7	0.3215	putative efflux protein
BSU33200	<i>yvrE</i>	9	0.0087	conserved hypothetical protein
BSU33400	<i>yvgN</i>	0.6	0.3084	glyoxal/methylglyoxal reductase
BSU33410	<i>yvgO</i>	24.9	0.0002	conserved hypothetical protein
BSU33460	<i>yvqI</i>	0.2	0.0233	putative integral inner membrane protein
BSU33530	<i>yvaA</i>	10.3	0.0058	putative oxidoreductase
BSU33610	<i>rnr</i>	1.5	0.3269	ribonuclease R
BSU33620	<i>yvaK</i>	2.4	0.1769	carboxylesterase
BSU33660	<i>yvaN</i>	0.5	0.2084	transcriptional repressor
BSU33710	<i>opuBC</i>	22.1	0.0004	choline ABC transporter (choline-binding lipoprotein)
BSU33720	<i>opuBB</i>	12.4	0.0032	choline ABC transporter (permease)
BSU34240	<i>yvfD</i>	0.3	0.0802	putative O-acetyltransferase
BSU34910	<i>hisD</i>	1.2	0.423	histidinol dehydrogenase
BSU35180	<i>csbA</i>	10.3	0.0057	putative membrane protein
BSU35310	<i>yvyD</i>	7.7	0.0136	ribosome-associated sigma 54 modulation protein

BSU35670	<i>gtaB</i>	1.6	0.3196	UTP-glucose-1-phosphate uridylyltransferase
BSU35690	<i>ggaA</i>	3.1	0.1128	poly(glucosyl N-acetylgalactosamine 1-phosphate) glucosyltransferase
BSU35830	<i>ywtG</i>	9.9	0.0066	putative carbohydrate transporter
BSU35970	<i>ywsB</i>	1.5	0.3426	conserved hypothetical protein
BSU36670	<i>csbD</i>	16.9	0.0011	stress response protein
BSU36720	<i>ywmE</i>	17.6	0.0009	hypothetical protein
BSU36960	<i>ywlB</i>	1.2	0.4134	conserved hypothetical protein
BSU37210	<i>ywjC</i>	44.5	<0.0001	conserved hypothetical protein
BSU37230	<i>ywjA</i>	0.8	0.4016	putative ABC lipid transporter (ATP-binding protein)
BSU37240	<i>ywiE</i>	35.3	0.0001	cardiolipin synthetase
BSU37480	<i>ywhH</i>	1	0.4908	putative RNA-binding protein
BSU37620	<i>rsfA</i>	0.9	0.4589	prespore-specific regulatory gene
BSU37680	<i>ywfH</i>	1.5	0.3262	carrier protein reductase of bacilysin synthesis
BSU38180	<i>ywzA</i>	26.8	0.0002	conserved hypothetical protein
BSU38430	<i>gspA</i>	69.3	<0.0001	putative glycosyl transferase (general stress protein)
BSU38440	<i>ywaF</i>	1	0.4946	putative integral inner membrane protein
BSU38600	<i>licR</i>	1.4	0.3549	transcriptional activator of the lichenan operon
BSU38620	<i>yxkJ</i>	2.3	0.1859	3-alkylated purines and hypoxanthine DNA glycosidase
BSU38630	<i>katX</i>	4.6	0.0494	major catalase in spores
BSU38720	<i>yxkO</i>	1.5	0.3286	putative carbohydrate kinase
BSU38830	<i>aldY</i>	4.2	0.0593	putative aldehyde dehydrogenase
BSU38930	<i>yxjJ</i>	5.4	0.0346	hypothetical protein
BSU38960	<i>yxjG</i>	0.4	0.1865	putative methyltetrahydrofolate methyltransferase
BSU39040	<i>yxiS</i>	5.2	0.0378	hypothetical protein
BSU39050	<i>katE</i>	29.2	0.0001	catalase 2
BSU39810	<i>csbC</i>	20.3	0.0006	putative sugar transporter
BSU39840	<i>yxbG</i>	7.1	0.0168	putative oxidoreductase
BSU40000	<i>yxnA</i>	10.7	0.0052	putative oxidoreductase
BSU40020	<i>yxaC</i>	1.1	0.4497	unknown; similar to unknown proteins
BSU40030	<i>yxaB</i>	1.8	0.2664	putative exopolysaccharide pyruvyl transferase
BSU40450	<i>yycD</i>	1.7	0.2805	conserved hypothetical protein
BSU40570	<i>yybO</i>	1.6	0.3024	putative permease
BSU40810	<i>yyaM</i>	1.4	0.3694	putative efflux transporter