

Table S2. Top *B. subtilis* genes up-regulated by PGRP, gentamicin, and CCCP^a.

Genes (regulators)	Function	Gene array						qRT PCR					
		PGRP	Gent	CCCP	<i>P</i> (<i>t</i> -test) ^b		FDR <i>q</i> ^c		PGRP	Gent	CCCP	<i>P</i> (<i>t</i> -test) ^b	
Oxidative stress													
<i>yrkl</i>	Predicted NAD(P)H oxidoreductase	60±30	1±0	1±0	0.0625	0.0625	0.0824	0.0815					
<i>kata</i> (PerR)	Vegetative catalase 1, degrades H ₂ O ₂	54±24	94±26	13±3	0.1623	0.0822	0.1238	0.0908	417±45	469±97	48±6	0.3239	0.0001
<i>nfrA</i> (Spx, σ ^A , σ ^D)	NADPH nitro/flavin reductase, response to thiol stress and oxidative stress	28±1	5±2	4±0	0.0003	0.0000	0.0093	0.0039	14±3	3±1	2±0.5	0.0066	0.0040
<i>ybcF</i>	Carbonic anhydrase-like protein, maintains pH	17±8	2±0	1±0	0.0642	0.0586	0.0834	0.0804	191±49	17±4	8±0.4	0.0061	0.0048
<i>ybcD</i>	Putative aldehyde dehydrogenase, aldehyde oxidation	17±7	3±1	1±0	0.0472	0.0346	0.0743	0.0655	26±5	4±0.5	1±0.2	0.0031	0.0017
<i>mrgA</i> (PerR, σ ^A)	Mini-ferritin, protects from oxidative stress	17±6	68±21	22±5	0.0416	0.2574	0.0701	0.1537					
<i>ndhF</i>	NADH dehydrogenase, respiration	16±6	8±6	1±0	0.1996	0.0348	0.1369	0.0655					
<i>katE</i> (σ ^B)	Catalase 2, degrades H ₂ O ₂	14±4	5±2	5±2	0.0620	0.0511	0.0823	0.0765	22±6	3±1	2±0.2	0.0084	0.0060
<i>ohrB</i> (σ ^B)	Organic hydroperoxide reductase	13±3	3±1	4±1	0.0244	0.0352	0.0567	0.0656					
<i>srfAB</i> (PerR, ComAP)	Surfactin synthetase, thiol stress response	12±9	1±0	15±7	0.1396	0.4004	0.1149	0.1980					
<i>ywcH</i> (σ ^D , σ ^A)	Putative monooxygenase, detoxification	12±0	3±1	4±1	0.0001	0.0001	0.0073	0.0065	20±4	2±0.4	2±0.3	0.0015	0.0014
<i>ycbP</i> (σ ^B)	Putative NAD(P)H-dependent FMN reductase	12±3	2±1	2±0	0.0181	0.0144	0.0497	0.0477					
<i>ahpF</i> (PerR, σ ^A)	Alkyl hydroperoxide reductase, degrades H ₂ O ₂	11±4	9±2	2±0	0.3578	0.0560	0.1982	0.0793	36±10	14±4	2±0.5	0.0484	0.0087
<i>yxnA</i> (σ ^B)	Oxidoreductase, induced in oxidative stress	10±2	2±0	3±1	0.0073	0.0157	0.0326	0.0495	13±4	2±0.5	2±0.6	0.0092	0.0109
<i>yqjM</i> (σ ^A)	Flavin oxidoreductase, reduction of aldehydes and ketones, induced by H ₂ O ₂	10±3	1±0	1±0	0.0160	0.0166	0.0464	0.0503	18±2	1±0.2	1±0.4	0.0000	0.0000
<i>yfkI</i> (σ ^B)	Stress protein, protects from H ₂ O ₂	10±6	5±1	3±1	0.2176	0.1478	0.1439	0.1173					
Copper and zinc efflux and detoxification													
<i>copA</i> (CsoR, σ ^A)	Cu efflux transporting ATPase	53±11	69±5	1±0	0.1193	0.0045	0.1060	0.0306	93±20	136±15	3±0.4	0.0692	0.0021
<i>cadA</i> (CzrA, σ ^A)	Cd, Zn, Cu, Co, Ni efflux ATPase	52±12	77±7	1±0	0.0796	0.0061	0.0907	0.0336	33±9	49±9	1±0.1	0.1711	0.0187
<i>czcD</i> (CzrA, σ ^A)	K/H- Zn, Cu, Co, Ni efflux antiporter	52±17	49±11	5±2	0.4329	0.0268	0.2231	0.0594	34±4	21±6	3±0.8	0.0581	0.0002
<i>copZ</i> (CsoR, σ ^A)	Cu chaperone for Cu efflux	21±3	30±2	9±3	0.0288	0.0218	0.0611	0.0548					
<i>trkA</i> (CzrA, σ ^A)	Cation exporter, resistance to metal ions	12±1	8±2	1±0	0.0939	0.0001	0.0962	0.0056					
Arsenite efflux and detoxification													
<i>arsB</i> (ArsR, σ ^F , σ ^A)	Arsenite efflux pump	151±64	96±33	1±0	0.2448	0.0398	0.1548	0.0685	238±33	73±20	2±0.6	0.0025	0.0002
<i>yqkC</i> (ArsR, σ ^F , σ ^A)	Arsenite efflux pump operon	101±40	71±25	2±0	0.2782	0.0326	0.1686	0.0635					
<i>arsC</i> (ArsR, σ ^F , σ ^A)	Arsenate reductase, reduces arsenate to arsenite	90±39	70±23	1±0	0.3422	0.0435	0.1927	0.0712	220±49	167±34	2±0.2	0.2087	0.0023
Other transporters													
<i>ybcL</i>	MFS-type transporter, unknown function	56±36	4±0	1±0	0.1129	0.1037	0.1036	0.0995					
<i>ytrF</i> (YtrA, σ ^A)	ABC transporter, unknown function	37±4	2±0	2±0	0.0004	0.0004	0.0102	0.0131	45±10	2±0.8	2±0.5	0.0030	0.0031
<i>ytrC</i> (YtrA, σ ^A)	ABC transporter, unknown function	32±11	1±0	2±1	0.0220	0.0259	0.0544	0.0585	62±17	3±0.8	2±0.4	0.0072	0.0071
<i>ytrB</i> (YtrA, σ ^A)	ABC transporter, unknown function	25±10	1±0	2±0	0.0328	0.0370	0.0642	0.0671	37±9	1±0.2	2±0.5	0.0045	0.0055
<i>lctP</i> (Rex, σ ^A)	L-lactate permease	23±9	7±4	27±8	0.0970	0.3606	0.0977	0.1858					
<i>ytrD</i> (YtrA, σ ^A)	ABC transporter, unknown function	21±7	1±0	2±0	0.0212	0.0231	0.0532	0.0559	13±1	1±0.2	2±0.3	0.0001	0.0001
<i>khtT</i>	K/H K ⁺ efflux antiporter, acid stress response	20±2	1±0	1±0	0.0006	0.0006	0.0119	0.0153					
<i>ytrE</i> (YtrA, σ ^A)	ABC transporter, unknown function	19±8	1±0	1±0	0.0428	0.0459	0.0711	0.0727	19±4	1±0.3	2±0.3	0.0013	0.0016
<i>yvdR</i>	Multidrug efflux transporter homolog	13±6	18±6	14±5	0.3144	0.4856	0.1826	0.2219					
<i>yvdS</i>	Multidrug efflux transporter homolog	11±5	18±7	12±6	0.2326	0.4628	0.1497	0.2156					
<i>zosA</i> (PerR, σ ^A)	Zn uptake ATPase, oxidative/thiol stress	11±5	24±6	7±5	0.0821	0.2893	0.0920	0.1634					

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<i>nrgA</i> (TnrA, σ^A)	Ammonium uptake, acid stress response	11±2	36±13	41±23	0.0746	0.1356	0.0881	0.1115						
<i>yhaU</i>	K/H K ⁺ efflux antiporter, acid stress response	11±1	1±0	1±0	0.0004	0.0004	0.0130	0.0131						
Chaperones, protein quality control, thiol stress														
<i>nhaX</i> (σ^B)	Stress protein, protects from oxidative damage	26±2	6±2	3±1	0.0016	0.0004	0.0172	0.0131	15±1	2±0	2±1	0.0000	0.0001	
<i>clpC</i> (CtsR, σ^B , σ^F , σ^A)	Inducer of autolysins (LytC and LytD)	17±4	10±2	2±1	0.1133	0.0092	0.1073	0.0393						
<i>yraA</i> (AdhR, σ^B , σ^M)	Cysteine proteinase, degrades thiol-damaged proteins	15±3	2±1	4±0	0.0063	0.0087	0.0308	0.0388	23±3	2±0	1±0.3	0.0004	0.0003	
<i>htrB</i> (C _{ssRS})	HtrA-like serine protease	14±4	5±0	0±0	0.0390	0.0123	0.0686	0.0456	100±33	19±9	2±0.2	0.0269	0.0118	
<i>mcsB</i> (CtsR, σ^B , σ^F)	Arginine kinase, protein degradation, thiol stress	14±4	14±3	3±1	0.4891	0.0198	0.2380	0.0534						
<i>ctsR</i> (CtsR, σ^B)	Master regulator of protein quality control	14±6	13±6	5±2	0.4612	0.1210	0.2310	0.1061						
<i>ctc</i> (σ^B)	50S ribosomal protein, protein synthesis	13±1	3±1	5±1	0.0032	0.0054	0.0225	0.0317						
<i>mcsA</i> (CtsR, σ^B , σ^F)	Activator of protein degradation, thiol stress	13±5	14±6	5±1	0.4548	0.0735	0.2293	0.0860						
<i>clpE</i> (CtsR, σ^A)	Protease chaperone, protein degradation	12±3	113±25	1±0	0.0077	0.0130	0.0332	0.0465						
<i>queD</i> (preQ1)	Protein synthesis (trRNA modification)	12±4	23±3	6±1	0.0541	0.1389	0.0792	0.1129						
<i>queE</i> (preQ1)	Protein synthesis (trRNA modification)	12±5	25±5	5±1	0.0754	0.1312	0.0884	0.1096						
<i>yyaO</i>	Carboxypeptidase homolog	11±3	3±1	3±0	0.0338	0.0282	0.0651	0.0597						
<i>yfkH</i> (σ^B)	Putative tRNA-processing ribonuclease	11±6	2±0	2±1	0.1026	0.1095	0.0998	0.1018						
<i>yugP</i>	Putative metal-dependent protease	10±1	2±0	2±0	0.0002	0.0002	0.0083	0.0100						
<i>cysS</i> (T-box, σ^A)	Cysteine-tRNA synthetase, protein synthesis	10±3	2±1	1±0	0.0312	0.0246	0.0630	0.0573						
<i>htrA</i> (C _{ssRS} , σ^A)	Serine protease Do (heat shock protein)	9±3	4±0	1±0	0.1023	0.0297	0.0997	0.0607	81±21	15±5	1±0.2	0.0103	0.0041	
Histidine synthesis														
<i>hisI</i>	Histidine synthesis	44±22	1±0	1±0	0.0582	0.0571	0.0811	0.0797	71±22	1±0.7	0.2±0	0.0092	0.0086	
<i>hisF</i>	Histidine synthesis	31±17	1±0	1±0	0.0736	0.0735	0.0878	0.0860	96±15	2±1	0.5±0	0.0004	0.0003	
<i>hisH</i>	Histidine synthesis	26±15	1±0	1±0	0.0891	0.0887	0.0951	0.0936	108±21	1±0.4	0.1±0	0.0012	0.0011	
<i>hisB</i>	Histidine synthesis	24±14	1±0	1±0	0.0902	0.0902	0.0951	0.0936						
<i>hisA</i>	Histidine synthesis	24±14	1±0	1±0	0.0892	0.0894	0.0951	0.0936						
<i>hisD</i>	Histidine synthesis	18±10	1±0	1±0	0.0885	0.0885	0.0948	0.0935						
<i>hisG</i>	Histidine synthesis	16±10	1±0	1±0	0.0998	0.0998	0.0988	0.0976						
Energy														
<i>yrhJ</i> (FatR, σ^M , σ^W , σ^X)	Predicted NADPH-cytochrome reductase, fatty acids	34±8	4±1	1±0	0.0087	0.0067	0.0339	0.0352	46±11	19±5	8±2	0.0326	0.0069	
<i>ldh</i> (Rex, σ^A)	Lactate dehydrogenase, respiration, fermentation	34±20	4±3	46±18	0.1123	0.3446	0.1034	0.1809	33±11	6±2	94±20	0.0226	0.0172	
<i>ptsG</i> (GlcT, σ^A)	Glucose transport and phosphorylation	24±17	4±1	16±1	0.1492	0.3244	0.1183	0.1143						
<i>nasD</i> (ResD, TnrA, σ^A)	Nitrite reductase (nitrite as nitrogen source)	17±8	6±2	6±0	0.1301	0.1241	0.1098	0.1073						
<i>ycdF</i> (σ^B)	Predicted glucose dehydrogenase, generates NADPH	11±2	5±1	8±4	0.0326	0.2646	0.0640	0.1557						
<i>ycnD</i>	NADPH-FMN oxidoreductase, electron transport	11±4	4±1	3±1	0.1117	0.0690	0.1034	0.0841						
<i>yqiG</i>	Predicted flavin oxidoreductase, electron transport	10±3	1±0	2±1	0.0186	0.0301	0.0500	0.0609						
<i>pdhB</i> (stringent resp., σ^A)	Pyruvate dehydrogenase, TCA cycle	9±5	4±1	18±2	0.1915	0.0967	0.1335	0.0957						
<i>gntR</i> (AbrB, σ^A)	Repressor of gluconate operon	9±3	2±0	2±1	0.0553	0.0579	0.0799	0.0803						
Envelope lysis and														

Table S2. Continued

remodeling												
<i>ywbH</i>	Putative holin, regulates murein hydrolases	46±15	7±1	3±0	0.0303	0.0226	0.0624	0.0555				
<i>yrkH</i>	Putative hydrolase	34±17	1±0	1±0	0.0636	0.0636	0.0833	0.0820				
<i>ywbG</i>	Putative peptidoglycan hydrolase	23±8	2±0	2±1	0.0296	0.0292	0.0618	0.0604				
<i>ywoC</i> (σ^A)	Putative hydrolase	9±1	1±0	2±0	0.0002	0.0005	0.0091	0.0148				
DNA repair												
<i>pyrAB</i> (σ^A)	Carbamoyl-phosphate synthetase, pyrimidine synthesis	51±26	46±7	6±3	0.3897	0.0214	0.2226	0.0915				
<i>pyrF</i> (σ^A)	Orotidine-phosphate decarboxylase, pyrimidine synthesis	40±20	45±2	5±2	0.4018	0.0740	0.2138	0.0860				
<i>pyrD</i> (σ^A)	Dihydroorotic acid dehydrogenase, pyrimidine synthesis	37±20	38±1	6±3	0.4766	0.1022	0.2346	0.0989				
<i>pyrC</i> (σ^A)	Dihydroorotase, pyrimidine synthesis	34±24	59±21	20±3	0.2363	0.2892	0.1513	0.1634				
<i>pyrAA</i> (σ^A)	Carbamoyl-phosphate synthetase, pyrimidine synthesis	31±17	84±27	14±2	0.0850	0.1924	0.0933	0.1249				
<i>pyrE</i> (σ^A)	Orotate phosphoribosyltransferase, pyrimidine synthesis	29±7	63±4	4±1	0.0065	0.0136	0.0309	0.0470				
<i>pyrK</i> (σ^A)	Dihydroorotic acid dehydrogenase, pyrimidine synthesis	26±13	45±1	6±3	0.1055	0.0961	0.1010	0.0956				
<i>pyrB</i> (σ^A)	Aspartate carbamoyltransferase, pyrimidine synthesis	25±18	77±22	35±4	0.0680	0.3058	0.0856	0.1693				
<i>purC</i> (σ^A)	phosphoribosylaminoimidazole succinocarboxamide synthase, purine synthesis	11±3	36±12	4±1	0.0599	0.0592	0.0813	0.0806				
<i>purB</i> (σ^A)	adenylsuccinate lyase, purine synthesis	10±2	27±6	7±2	0.0309	0.1761	0.0628	0.1262				
Detoxification and stress-response												
<i>ywzA</i> (σ^B)	General stress protein	34±8	5±2	7±3	0.0118	0.0164	0.0394	0.0500				
<i>ywmE</i> (σ^B)	Ethanol stress and general stress	24±6	4±1	4±1	0.0199	0.0205	0.0520	0.0538				
<i>bmrU</i> (σ^B)	Multidrug resistance protein	23±7	5±2	6±2	0.0337	0.0422	0.0651	0.0703				
<i>ybyB</i> (σ^B)	Survival of ethanol stress	22±9	2±1	6±3	0.0452	0.0802	0.0729	0.0898				
<i>yfhK</i> (σ^B)	General stress protein, ethanol stress	21±8	1±0	6±3	0.0335	0.0795	0.0651	0.0867				
<i>csbD</i> (σ^B)	Survival of salt and temperature stress	12±5	2±1	7±3	0.0513	0.2261	0.0777	0.1412				
<i>ywsB</i> (σ^B)	Survival of ethanol and salt stress	11±1	4±1	5±2	0.0027	0.0139	0.0215	0.0470				
<i>yxbG</i> (σ^B)	General stress response	11±3	3±1	4±1	0.0254	0.0336	0.0575	0.0645				
<i>yjIT</i> (σ^B)	Ethanol and heat stress	9±2	2±1	6±3	0.0165	0.1957	0.0496	0.1306				

^a Bacteria were treated with albumin (100 µg/ml, control), PGRP (PGLYRP4, 100 µg/ml), or gentamicin (5 µg/ml), for 30 min or CCCP (800 µM) for 15 min at 37°C, and gene expression was determined by whole genome expression arrays and qRT-PCR. Genes are listed from the most to the least up-regulated in each group. The numbers are mean ratios ± SEM of the gene expression signals in PGRP-, gentamicin-, or CCCP-treated bacteria to control albumin-treated bacteria, obtained from 3 independent whole genome expression arrays experiments and 3 independent qRT-PCR experiments (as indicated). All genes in PGRP-treated bacteria were expressed significantly higher than in control bacteria at $P < 0.001$ by two sample one-tailed t -test (not shown), and 94% of these genes were expressed significantly higher than in control at FDR $q \leq 0.05$ (not shown). The entire whole genome expression array data have been deposited in NCBI GEO under the accession number GSE44212.

^b P values (two sample one-tailed t -test) for the differences in gene expression in PGRP-treated bacteria *versus* gentamicin- or CCCP-treated bacteria (numbers on the left or on the right, respectively) are shown as indicated, with $P < 0.05$ in bold.

^c FDR (false discovery rate) q values for the differences in gene expression in PGRP-treated bacteria *versus* gentamicin- or CCCP-treated bacteria (numbers on the left or on the right, respectively) are shown as indicated, with $q \leq 0.05$ in bold.