

Gene expression regulation in the plant growth promoting *Bacillus atrophaeus* UCMB-5137 stimulated by maize root exudates

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Abstract

Despite successful use of Plant Growth Promoting Rhizobacteria (PGPR) in agriculture, little is known about specific mechanisms of gene regulation facilitating the effective communication between bacteria and plants during plant colonization. Active PGPR strain *B. atrophaeus* UCMB-5137 was studied in this research. RNA sequencing profiles were generated in experiments where root exudate stimulations were used to mimic interactions between bacteria and plants. It was found that the gene regulation in *B. atrophaeus* UCMB-5137 in response to the root exudate stimuli differed from the reported gene regulation at similar conditions in *B. amyloliquefaciens* FZB42, which was considered as a paradigm PGPR. This difference was explained by hypersensitivity of UCMB-5137 to the root exudate stimuli impelling it to a sessile root colonization behavior through the CcpA-CodY-AbrB regulation. It was found that the transcriptional factor DegU also could play an important role in gene regulations during plant colonization. A significant stress caused by the root exudates on *in vitro* cultivated *B. atrophaeus* UCMB-5137 was noticed and discussed. Multiple cases of conflicted gene regulations showed scantiness of our knowledge on the regulatory network in *Bacillus*. Some of these conflicted regulations could be explained by interference of non-coding RNA (ncRNA). Search through differential expressed intergenic regions revealed 49 putative loci of ncRNA regulated by the root exudate stimuli. Possible target mRNA were predicted and a general regulatory network of *B. atrophaeus* UCMB-5137 genome was designed.

Highlights

- Plant colonizing PGPR *Bacillus* responded differently to the root exudate stimuli;
- In UCMB-5137 the CcpA-CodY-AbrB regulation caused fast cell immobilization;
- DegU regulon is important for plant colonization behavior in PGPR *Bacillus*;
- ncRNA involved in regulation of plant colonization were identified;
- A comprehensive model of gene regulation in UCMB-5137 was developed;

Keywords Plant growth promoting rhizobacteria; transcriptomics; RNA sequencing; transcriptional regulatory network; non-coding RNA

Abbreviations

GABA, gamma-aminobutyric acid; mRNA, messenger RNA; ncRNA, non-coding RNA; PGPR, Plant Growth Promoting Rhizobacteria; (p)ppGpp, guanosine pentaphosphate; rRNA, ribosomal RNA.

1. Introduction

Diverse group of bacteria inhabiting plant rhizosphere and directly or indirectly enhancing the plant growth was termed in the literature as Plant Growth Promoting Rhizobacteria (PGPR) (Lugtenberg & Kamilova, 2009). Rhizosphere provided these bacteria with a source of energy and organic compounds from plants (Sivasakthi et al., 2014). In return, bacteria supplied plants with certain nutrients and protection from plant pathogens (Glick 1995). Successful plant colonization by PGPR relied on multiple factors including but not limited to withstanding environmental stress (Reva et al., 2004), efficient chemotaxis (Yssel et al., 2011), effective communication within the bacterial communities and between bacteria and plants carried out by synthesized plant hormones and quorum sensing autoinducers (Lengeler & Postma 1999; Farag et al., 2013). All the factors are directly or indirectly related to effective sensing of environmental signals and proper regulation of gene expression.

Utilizing PGPR for plant growth promotion was recognized as a potential alternative to chemical preparations. In contrast to chemical fertilizers and pesticides, PGPR were considered to be safe to humans and friendly to the environment and resident soil microorganisms (Vessey 2003; Bashan & de-Bashan, 2005; Sivasakthi et al., 2014). For an effective usage of biofertilizers and biopesticides based on PGPR, it is important to understand better the genetic mechanisms underlying the interactions of these bacteria with the host plants at early stages of rhizosphere colonization.

Bacillus strains are common in rhizosphere communities (Podile & Kishore 2007; Fan et al., 2013). However, only a few studies on gene regulation in PGPR *Bacillus* have been reported. Differential gene expression regulations caused by the maize root exudates were reported previously on *Bacillus amyloliquefaciens* FZB42 that was proposed as paradigm of PGPR *Bacillus* (Fan et al., 2012; Kierul et al., 2015). Gene regulation in *Bacillus subtilis* BSB1 under abiotic stresses was reported by Kohlstedt *et al.* (2014). It was not clear whether these reports could be extended to other PGPR *Bacillus*, as it had been found that the activities of biotechnological importance were strain specific (Safronova et al., 2012). There was little knowledge regarding plant colonization behavior of other bacteria of the *B. subtilis* group, such as *B. atrophaeus*. The strain *B. atrophaeus* UCMB-5137 was isolated from rhizosphere

in Ukraine in 1989 and at first, based solely on the phenotype; it was identified as *B. subtilis*. In an array of bioassays, *B. atrophaeus* UCMB-5137 showed ability to protect plants and crops from bacterial and fungal phytopathogens, and to promote the plant growth (Lapa & Reva, 2005). Complete genome sequence of *B. atrophaeus* UCMB-5137 has been achieved recently (Chan et al., 2013). *B. atrophaeus* is a common soil inhabitant. Spores of *B. atrophaeus* have been used in biotechnology to control sterilization processes because of the resistance of the spores to extreme temperatures and chemical detergents (Pinzón-Arango et al., 2009). Except for UCMB-5137, the strains of *B. atrophaeus* were not reported in the literature as active plant associated growth promoters or protectors, in contrast to the strains of the closely related species *B. amyloliquefaciens* and *B. subtilis*. This brought our interest to study this bioactive strain UCMB-5137 to contribute to the knowledge on the gene regulation in PGPR *Bacillus*. Current knowledge on this issue is biased towards the paradigm examples of *B. amyloliquefaciens* ssp. *plantarum* (Reva et al., 2004; Chen et al., 2007; Fan et al., 2011; 2012; 2013; 2015).

In various studies it was demonstrated that the maize root exudates were useful to mimic *in vitro* interactions between different plants and PGPR by initiating a range of biological responses within the bacteria (Mark et al., 2005; Broeckling et al., 2008; Fan et al., 2012; Kierul et al., 2015). It was therefore interesting to study further the gene expression regulation in *B. atrophaeus* UCMB-5137 under the standard laboratory conditions by simulation with the root exudates, to compare the gene expression profile with the published results for other PGPR *Bacillus*. Differential transcription regulation stimulated by the root exudates in *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42 revealed substantial differences between these bacteria. To identify other transcription factors and genes specifically involved in root colonization by *B. atrophaeus* UCMB-5137, the obtained gene regulation profiles were superimposed over known regulatory networks in *B. subtilis* (Kohlstedt et al., 2014; Michna et al., 2015). Possible involvement of non-coding RNA (ncRNA) in gene regulations during plant colonization was studied.

2. Materials and methods

2.1 Root exudate preparation

Root exudates were extracted from maize roots as it was described by Fan et al. (2012). Seeds of the maize breed 5Q-751BR were surface sterilized by treating the seeds with 70% ethanol for 3 min and then with 5% (v/v) sodium hypochlorite for 3 min followed by rinsing 5 times with sterile distilled water. The seeds were germinated at 28°C until the main root was at least 2 cm long before transferring into test tubes with sterilized water in a way that only the roots were submerged into water. The test tubes were kept in plant growth chamber (16-h light/8-h dark) at 24°C for 8 days. Water aliquots were collected daily from the third to eighth day and the tubes were refilled with the same amount of fresh sterilized water. Each collection was kept separate, and 100 µL from each sample were spread on the nutrient agar to check for contamination. Contaminated root exudate samples were discarded and the clean samples were pooled, freeze dried and stored at minus 20°C. The lyophilized exudates were weighted, dissolved in 100 µL of water and centrifuged. The supernatant was filter sterilized. Concentrations of the root exudates were adjusted to 0.25 g/L and the solutions were kept as the stock at minus 80°C.

2.2 Bacterial growth conditions and RNA preparation

Bacillus atrophaeus UCMB-5137 was obtained from the Ukrainian collection of microorganisms at Danylo Zabolotny Institute of Microbiology and Virology, National Academy of Science of Ukraine, Kyiv, Ukraine.

Bacterial cultures were inoculated from a frozen stock culture and incubated at 37°C overnight on solid Luria agar medium (MERCK). Colonies from the overnight culture were inoculated into 1C medium and cultivated at 24°C for 14 hours with shaking at 180 rpm. Composition of the 1C medium was the same as suggested by Fan et al. (2012): 0.7% w/v pancreatic digest of casein, 0.3% w/v papain digest of soya flour, 0.5% w/v NaCl and 0.1% glucose (all the mentioned reagents were purchased from MERCK). 1 ml aliquots of the overnight cultures were inoculated into conical flasks with 20 ml of fresh 1C medium in control, and supplemented with 0.25 mg/ml of the maize root exudates in treatment. Control and treatment cultures were grown at 24°C for 14 hours 30 min with shaking at 180 rpm to achieve the transition to stationary growth phase, which was controlled by the medium opacity of $OD_{600} \approx 1.0$ units. Growth curve analysis showed that the bacterial cultures reached the transition to stationary phase in average after 14 hr 30 min of cultivation at 24°C with shaking ($OD_{600} \approx 1.0$ units) at both treatment and control conditions. Bacterial cells were harvested for the total RNA extraction by mixing with 2 volumes of the ice cold killing buffer (20 mM Tris-HCl from BDH Laboratory, 5 mM $MgCl_2$ from MERCK and 20 mM NaN_3 from SIGMA; pH was adjusted to 7.5) (Völker et al., 1994). The mixture was centrifuged at 5,000 rpm for 3 minutes at room temperature. The final pellet was washed with 1 ml of the killing buffer and immediately frozen at minus 80°C until the RNA extraction. Six RNA samples (3 controls and 3 treatments) were obtained from three independent experiments. However, one sample of the treated bacteria did not pass the RNA quality control and was discarded.

2.3 Total RNA extraction and sequencing

Total RNA were isolated using ZR Fungal/Bacteria RNA Mini Prep kit from Zymo research Corp. according to the manufacturer's instruction. Concentration and quality of RNA samples were checked by NanoDrop. Ribolock Ribonuclease inhibitor (Thermo Scientific) was added to prevent RNA degradation. Paired-end RNA sequencing was performed on the MiSeq Illumina platform in Inqaba Biotech (Pretoria, South Africa, <http://www.inqababiotec.co.za/>). RNA-Seq datasets and the results of the statistical analysis by CLC Genomics Workbench 7 were deposited in NCBI GEO database under the accession number GSE68543.

The RNA-Seq reads were trimmed from the adapter sequences and mapped against the predicted coding and non-coding loci of the reference genome sequence of *B. atrophaeus* UCMB-5137 (CP011802) using CLC Genomics Workbench 7.0.3 (currently this program is distributed by QIAGEN – <http://www.clcbio.com/products/clc-genomics-workbench/>). Estimated Degree of Gene Expression statistics approach (Magoc et al., 2013) was used to identify up- and down-regulated genes. Different cutoff values of the fold change and p-values were applied as explained below.

2.4 Complete genome sequence of *B. atrophaeus* UCMB-5137

A draft genome sequence of *B. atrophaeus* UCMB-5137 (NZ_CM001847.1) comprising 21 contigs was obtained recently by Illumina HiSeq sequencing (Chan et al., 2013). DNA reads obtained by RNA-Seq for the current work were used for gap closing and resolving ambiguities in the previous assembly by mapping reads to contigs by CLC

Genomics Workbench 7.0.3. Prediction of coding genes in the complete genome sequence was performed by using the RAST Genome annotation robot (Aziz et al., 2008) and then checked manually. Nomenclature of the gene names, where it was possible, was adopted from that of *B. subtilis* 168 (NC_000964). Locations of prophages and other horizontally transferred genomic islands were identified in the genome by using the SeqWord Genome Island Sniffer program (Bezuidt et al., 2009).

2.5 Gene orthology and phylogenetic studies

Orthologous genes in the genomes of *B. atrophaeus* UCMB-5137, *B. amyloliquefaciens* ssp. *plantarum* FZB42 (NC_009725), *B. amyloliquefaciens* ssp. *plantarum* Y2 (NC_017912), *B. amyloliquefaciens* ssp. *plantarum* CAU B946 (NC_016784), *B. amyloliquefaciens* ssp. *plantarum* IT-45 (NC_020272), *B. amyloliquefaciens* ssp. *amyloliquefaciens* DSM7 (NC_014551), *B. subtilis* ssp. *subtilis* 168 (NC_000964), *B. subtilis* ssp. *subtilis* BSn5 (NC_014976), *B. subtilis* ssp. *spizizenii* TU-B-10 (NC_016047), *B. atrophaeus* 1942 (NC_014639), *B. atrophaeus* C89, *B. atrophaeus* 9372-1, *B. atrophaeus* 9372-2, *B. atrophaeus* Dugway, *B. atrophaeus* Detrick-1, *B. atrophaeus* Detrick-2, *B. atrophaeus* Detrick-3, *B. atrophaeus* 1013-1, *B. atrophaeus* 1013-2, *B. atrophaeus* 49822-1, *B. atrophaeus* 49822-2, *B. atrophaeus* BACI051-E and *B. atrophaeus* BACI051-N were identified by EDGAR software platform (Blom et al., 2009). The strains with NC (RefSeq) accession numbers were downloaded from the NCBI database (<ftp://ftp.ncbi.nih.gov/genomes/Bacteria/>) and the genomes of other strains were obtained from PATRIC (Wattam et al., 2014; <http://patricbrc.vbi.vt.edu/portal/portal/patric/Home>). The identified groups of orthologous genes were used for superimposition of the gene regulation profiles obtained in this work and those known from the literature. A super-alignment of 856,373 amino acid residues of concatenated alignments of orthologous proteins was used to determine the phylogenetic position of the strain UCMB-5137 by the neighbor-joining clustering algorithm implemented in MEGA 6.0.6 (Tamura et al., 2013).

2.6 Gene co-expression analysis

Operons were predicted as synteny of genes transcribed in the same direction with the spacer regions between genes smaller than 200 bp. It was assumed that the operon was regulated, if it comprised at least one gene regulated by more than 2 folds in comparison to the control condition with a calculated p-value ≤ 0.05 and without contradictions to the regulations of other genes in the operon. The 2 folds threshold was used in this case to make the results comparable with the stress response regulation patterns published by Sappa et al. (2013) and Kohlstedt et al. (2014). Operon predictions and their transcriptional regulations were checked by using the SubtiWiki Web-based resource (Michna et al., 2015). Putative transcription regulation binding sites were identified by using the software tools provided by DBTBS server (Sierro et al., 2008; <http://dbtbs.hgc.jp/>). Loci of 200 bp upstream of the first gene in the operons were searched for transcriptional factor (TF) binding sites by the DBTBS tools.

Co-regulation of genes at different conditions was estimated as four folds phi-correlation (Fleiss et al., 2013):

$$\phi = \frac{n_{11}n_{22} - n_{12}n_{21}}{\sqrt{(n_{11} + n_{21})(n_{12} + n_{22})(n_{11} + n_{12})(n_{21} + n_{22})}}$$

where n_{11} – number of genes activated at both conditions; n_{12} – number of genes activated at the first condition, but repressed at the second condition; n_{21} – number of genes repressed at the first condition, but activated at the second condition; and n_{22} – number of genes repressed at both conditions.

The whole genome regulation network was constructed and visualized using Cytoscape 3.2.1 for Windows (64 bit) (<http://www.cytoscape.org/cy3.html>). Metabolic pathways for regulated genes were identified using the Pathway Tools software version 13.0 for 64-bit Windows 7 (Karp et al., 2010).

2.7 Identification of differentially expressed non-coding RNA

Non-coding RNA (ncRNA) loci were identified by differential density of Illumina reads aligned against the intergenic spacer regions of the genome of *B. atrophaeus* UCMB-5137. They were considered as regulated by the root exudates, if their level of differential transcription exceeded the 3 folds threshold with at least 50 reads mapped to the region in the sample with the highest expression. To avoid false-positive identification of untranslated regions (5'-UTR) as ncRNA, only the loci flanked by oppositely regulated genes were considered in this work. Identified sequences were compared to the records of ncRNA in SubtiWiki database (Michna et al., 2015) and those reported by Fan *et al.* (2015) in *Bacillus amyloliquefaciens* FZB42. The level of sequence conservation of predicted ncRNA was checked by BLASTN search through the complete genome DNA sequences of *B. subtilis* ssp. *subtilis* 168 (NC_000964), *B. amyloliquefaciens* ssp. *plantarum* FZB42 (NC_009725), *B. licheniformis* ATCC 14580 (NC_006270), *B. pumilus* SAFR-032 (NC_009848), *B. halodurans* C-12 (NC_002570) and *B. cereus* ATCC 14579 (NC_004722). If the conserved regions were found at least in 3 different genomes, possible mRNA targets for predicted ncRNA then were identified by using CopraRNA (Wright et al., 2014). Predictions of the target mRNA with p-value of $\leq 1 \times 10^{-5}$ were considered reliable.

3. Results and Discussion

3.1 Complete genome sequence of the strain UCMB-5137 and its phylogeny

In total, 2,233,142 paired-end Illumina MiSeq reads were generated from the RNA samples obtained from two bacterial cultures treated with the root exudates and 5,555,122 reads were obtained from the untreated cultures. The previously published complete genome sequence of *B. atrophaeus* UCMB-5137 (Chan et al., 2013) was updated by closing the gaps with the newly generated reads. A new version of the genome was deposited in the GenBank database under the accession number CP011802 (RefSeq NZ_CP011802.1, NCBI ASM38596v2).

BLASTP search through the sequences of genomes of 22 other publicly available microorganisms belonging to the *B. subtilis* group revealed 3,025 clusters of orthologous protein coding genes. To clarify the phylogenetic position of the strain UCMB-5137 within the *B. subtilis* taxonomic group, a super-alignment of all orthologous genes was analyzed by the Neighbor-Joining algorithm implemented in MEGA 6.0. The phylogenetic position of the strain UCMB-5137 is shown in Fig. 1. The strain UCMB-5137 was grouped together with the reference strain of *Bacillus atrophaeus*. However, it was separated from the cluster of other multiple sequenced strains of this species. It was hypothesized that UCMB-5137 might represent a sub-species of *B. atrophaeus* but this hypothesis was not further analyzed in this study.

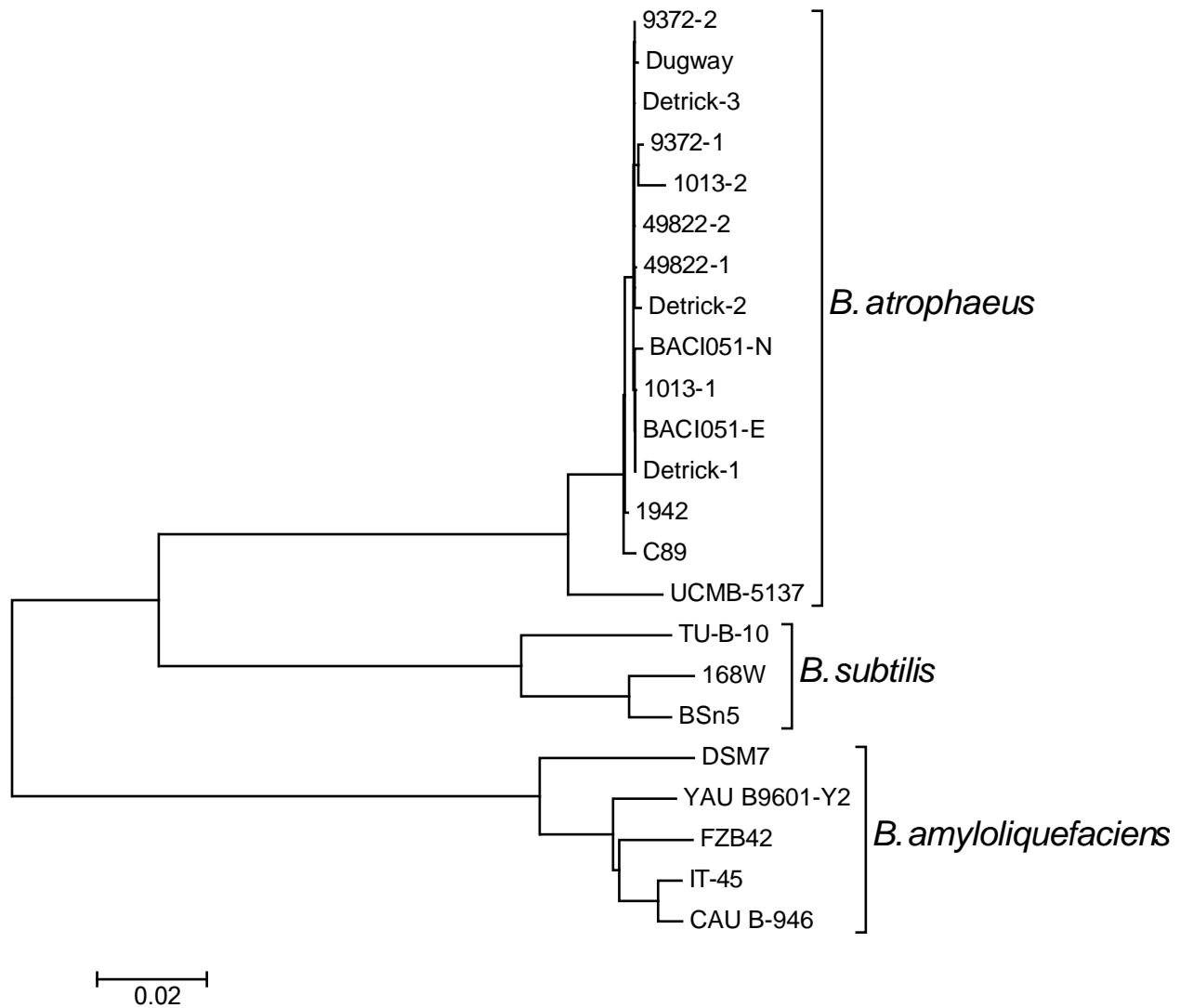


Fig. 1. Neighbor-joining species tree constructed for the selected organisms of the *B. subtilis* group based on concatenated alignments of amino acid sequences of orthologous proteins.

3.2 Gene expression profiling

Up- and down-regulated genes in samples treated by the root exudates compared to the control samples were determined with the fold difference exceeding the factor of 3 and $p\text{-value} \leq 0.05$. The detected genes were grouped by their functional associations (supplementary Table S1). A ratio of 54 up-regulated versus 152 down-regulated genes was observed in the total set of samples. Particularly: amino acid, nucleotide, carbohydrate and fatty acid biosynthetic pathways, anaerobic respiration pathway and also the associated ABC-transport systems were mainly down-regulated by the root exudates. It was also true for all genes associated with identified prophages and horizontally transferred genomic islands. Contrary, several genes for cell surface protein biosynthesis and post-translational processing, aerobic respiration genes and also multiple transcriptional regulators were stimulated by the root exudates. Genes involved in DNA replication and cell division processes were mostly up-regulated by the root

exudates that. However, the bacteria treated with the root exudates did not show any increase in the rate of growth. More details on metabolic pathway regulation may be found in Table S1.

Many of the genes activated by the root exudates were associated with the stress response and detoxification. Activation of the GABA shunt and spermidine biosynthesis indicated a preparation to oxidative and/or acidic stresses (Feehily & Karatzas, 2013). Activation of the stress response genes in PGPR organisms by the root exudates was reported in a previous study (Matilla et al., 2007). Through the observed up-regulation of the SasA alarmone biosynthesis pathway it was hypothesized that the level of (p)ppGpp might be increased in bacteria treated with the root exudates. The alarmone (p)ppGpp could trigger a stringent response in bacteria experiencing nutrient exhaustion. No signs of the stringent response were observed at the control conditions when the medium was the same but without the root exudates. We therefore concluded that there should be no real nutrient exhaustion in the medium. According to Braeken et al. (2006), (p)ppGpp alarmone was also involved in many physiological processes including adaptation to changed environmental conditions and interactions between bacteria and eukaryotic cells.

Aligning of the DNA reads against non-coding intergenic loci of the complete genome sequence of *B. atrophaeus* UCMB-5137 showed multiple differently expressed regions, which could not be translated to any putative proteins. A search for differentially regulated intergenic spacer regions revealed at least 49 loci of putative ncRNA. Genomic location of the identified ncRNA, their neighboring genes, possible mRNA targets and known ncRNA orthologs are listed in Table 1. Out of these 49 ncRNA loci, 40 were up-regulated by the root exudates. There were many other down-regulated intergenic spacer loci; however, since it was difficult to distinguish them from putative 5'-UTR as they were surrounded by down-regulated neighbor genes, these loci were not considered in this study.

Table 1. Non-coding loci regulated by the root exudates. Locations of loci are given as in CP011802.

Name	Location	Upstream gene	Fold change	Predicted targets	Orthologs*
ncr20	22230..22278	D068_03770	19.94	Y11B MraZ protein; SpoIVB peptidase;	
ncr23	25176..25569	D068_03810	3.96	No conservation;	
ncr28	28250..28322	D068_03850	3.1	NagP component of PTS system;	
ncr63	67120..67569	D068_04240	5.99	No conservation;	
ncr86	95107..95160	D068_04490	3.29	No conservation;	<i>bsrF</i>
ncr299	4000114..4000377	D068_19000	15.39	PucD xanthine dehydrogenase;	<i>scr</i> small cytoplasmic scRNA
ncr409	377769..378299	D068_07850	3.35	No conservation;	
ncr628	599457..599519	D068_09620	-inf	Downstream gene: CueR transcriptional regulator;	
ncr818	777740..777830	D068_11560	-2.44	Downstream gene: tryptophan-tRNA ligase TrpS;	<i>trpS-oppA</i> , <i>bar094</i>
ncr912	853200..853261	D068_12600	4.27	Y1bQ 2-dehydropantoate reductase; YeaB transporter;	

ncr1014	939698..939779	D068_13670	5.6	YkrV, MtnE transaminase; CotE spore coat protein;	
ncr1068	997865..998060	D068_14210	-inf	No conservation;	
ncr1092	1020314..1020360	D068_14450	-47.94	SpoIVB peptidase;	<i>ykwD-pbpH</i>
				YqjI 6-phosphogluconate dehydrogenase;	
ncr1258	1108507..1180808	D068_16150	3.03	No significant match found;	
ncr1305	1226294..1226547	D068_16630	12.04	NatB sodium efflux ABC transporter permease; RpoA DNA-directed RNA polymerase;	
ncr1509	1477643..1478293	D068_18730	4.1	No conservation;	
ncr1648	1625065..1625385	D068_20480	3.06	No conservation;	
ncr1827	1821647..1822003	D068_22450	14.59	YfhS and YgzB hypothetical proteins;	
ncr1829	1823159..1823313	D068_22470	7.92	YlIB MraZ protein; YetA hypothetical protein; YesN transcriptional regulator; SpoIVB peptidase;	
ncr1891	1877568..1877676	D068_23110	3.44	MiaA tRNA dimethylallyltransferase;	
ncr1947	1925995..1926105	D068_23670	5.55	No conservation;	
ncr2198	2143072..2143195	D068_26260	3.4	Downstream gene: YqeG hypothetical protein; YlIB MraZ protein; SpoIVB peptidase	
ncr2239	2178179..2178362	D068_01700	3.29	CotE spore coat protein;	<i>glmM-glmS</i>
ncr2499	2463009..2463121	D068_31760	22.34	No significant match found;	<i>bsrC</i>
ncr2755	2697733..2697777	D068_29190	-inf	AhpF NADH dehydrogenase;	<i>bar067</i>
ncr2792	2734908..2735126	D068_28810	4.2	YqgL hypothetical protein;	
ncr2833	2779026..2779093	D068_28380	12.28	RpsD 30S ribosomal protein S4; NhaX stress response protein;	<i>trxA-xsa</i>
ncr2852	2795834..2795898	D068_28200	-inf	No conservation;	
ncr2853	2796437..2796600	D068_28190	3.59	YdiK lipoprotein; TcyP L-cystine uptake protein;	
ncr2893	2839504..2839767	D068_27790	6.14	No significant match found;	
ncr3022	2955963..2956313	D068_26460	3.42	No conservation;	
ncr3198	3034438..3034536	D068_33310	3.61	Downstream gene: DegQ transcriptional regulator;	
ncr3267	3105503..3105823	D068_34020	3.85	No conservation;	
ncr3314	3150551..3150665	D068_34530	5.04	No significant match found;	
ncr3409	3244049..3244404	D068_35490	15.74	YjlA possible transporter;	<i>ssrA tmRNA</i>
ncr3458	3290801..3290900	D068_36020	3.56	RpsG 30S ribosomal protein S7; YkoQ metallophosphoesterase; YqjP and YtnM hypothetical	

ncr3519	3349197..3349330	D068_36640	2.37	proteins; Downstream gene: YvcI Nudix hydrolase;	<i>yvcI-trxB</i>
ncr3522	3351953..3352333	D068_36670	7.75	TenA thiaminase; No conservation;	
ncr3526	3356453...3356663	D068_36720	3.46	No conservation;	
ncr3628	3460797..3460941	D068_37800	-inf	No conservation;	
ncr3736	3555042..3555497	D068_38890	-8.92	No conservation;	bar073
ncr3772	3583861..3583995	D068_39260	2.03	GpsB cell cycle protein;	bar096
ncr3826	3637975..3638305	D068_39820	3.52	No conservation;	
ncr3877	3685045..3685132	D068_40350	4.2	Downstream gene: QoxA quinol oxidase subunit;	
ncr3952	3752185..3752625	D068_41140	3.03	No conservation;	
ncr4000	3793213..3793326	D068_41680	-inf	CysB cyclodextrin-binding protein;	bar084
ncr4136	3931507..3931653	D068_43080	3.42	YlIB MraZ protein;	
ncr4157	3956921..3957068	D068_43320	3.57	RapC aspartate phosphatase C response regulator and 10 other paralog genes;	
ncr4176	3973567..3973915	D068_43510	6.56	XhIA phage-like protein; YlIB MraZ protein;	

*Orthologous ncRNA were searched by sequence similarity among sequences of ncRNA found in *B. amyloliquefaciens* FZB42 (Fan et al., 2015) and indicated as bar0###, and in SubtiWiki database. In the later database ncRNA found in *B. subtilis* 168 were presented either by names, or by names of flanking genes: *trpS-oppA* for example.

3.3 Superimposition of the gene regulation profile in *B. atrophaeus* over the regulatory network of *B. subtilis*

B. atrophaeus is the closest relative of *B. subtilis*. The gene regulation network was studied in *B. subtilis* by many researches and summarized in SubtiWiki (Michna et al., 2015) and DBTBS databases (Sierro et al., 2008). Both species belonged to the same group of related organisms, which were not easily distinguished even by the 16S rRNA sequences (Safronova et al., 2012). We concluded that the transcription regulatory network known for *B. subtilis* might be fully applied to study the regulation of the orthologous genes in *B. atrophaeus*. Supplementary Table S1 presented known activators and repressors associated with the regulated genes. A visualization of the superimposition of the gene regulations in UCMB-5137 under the root exudate stimuli over the regulatory network of *B. subtilis* is shown in Fig. 2. Clusters of co-regulated genes in Fig. 2 were titled by the corresponding TFs or sigma-factors. Inconsistence in regulation of the protein coding genes and the corresponding TFs was depicted by red edges linking the nodes of the genes and TFs. For example, if a gene encoding a transcriptional activator was up- or down-regulated, it was expected that all the genes dependent on this activator would be regulated accordingly. On the contrary, regulation of a repressor should cause an opposite regulation of all the related genes. If a gene was regulated by several TFs, this regulation was accepted as consistent if there was consistency in the regulation at list with one TF. Contradictions depicted in Fig. 2 might indicate shortage of our knowledge on TFs involved in the gene regulation at the given condition.

The biggest number of the conflicted gene repressions was observed among the genes regulated by SigB (stressosome), SigF (sporulation regulon), AhrC (arginine metabolism regulon), FadR (fatty acid degradation regulon), FapR (fatty acid biosynthesis regulon), Fnr (anaerobiosis and overflow metabolism) and TnrA (nitrogen assimilation). Conflicted gene activations were observed in YwaC (ppGpp associated regulon independent from stringent response) and SigW (resistance and detoxification) regulons. The majority of the genes controlled by the up-regulated Spo0A (sporulation initiation) were activated or repressed oppositely to what might be expected. It was supposed that all these genes were additionally controlled either by other TFs, or Spo0A was somehow inactivated by other regulatory factors triggered by the treatment with the root exudates. An interference of the regulatory ncRNA molecules in this process was assumed.

Many general stress response genes were up-regulated by the root exudates, especially those controlled by the SigB stressosome (Fig. 2A). To identify specific regulations not associated with the general stress response, the pattern of gene regulation observed in the current study was compared to the stress response patterns reported earlier (Sappa 2013; Kohlstedt et al., 2014). Significant correlation was observed between the gene regulation patterns triggered by the root exudates and those under nutrient stringency and high temperature stresses, while the congruence with the low temperature growth and osmotic stress conditions was lower. It might be explained in a way that the nutrient stringency, higher temperature growth and plant root colonization were all associated with an increased oxidative stress resulted from accumulation of free radicals (Lamb & Dixon, 1997). Majority of the genes activated at the stress conditions and in the current experiment were controlled by SigB and partly by SigW (Table 2). Down-regulations of gene expression at all these conditions was controlled by CodY and several other repressors. The genes regulated oppositely to the patterns of the general stress response were of interest for us as they most likely were associated with the specific response of *B. atrophaeus* UCMB-5137 to the root exudate stimuli. In total, 250 operons were identified comprising 426 protein coding genes. All these genes were controlled by multiple TFs and sigma-factors (Table 2), particularly by AbrB and Abh (transition to stationary phase), PerR (peroxide response), CggR (glycolysis activator) and WalR (synthesis of cell wall proteins). However, regulation of many of these genes in *Bacillus* was

Table 2. Co-regulation of gene expression by the root exudates and different stress conditions.

Stress conditions	Up-regulated genes		Down-regulated		Pearson correlation coefficient
	Up-regulated	Down-regulated	Up-regulated	Down-regulated	
Stationary growth	25	23	5	64	0.505
Growth at 51°C	11	24	0	26	0.404
Growth at 16°C	20	20	8	27	0.280
Growth with 1.2M NaCl	3	11	4	20	0.059
Regulatory TFs	SigB, SigW	PutR, CodY, AbrB, SigE, SifF, SpoIIID, ScoC, TnrA, Fur, Spo0A	SigD, SinR, SigB, CggR, ResD, Fnr, NsrR, Spo0A	CodY, SigD, SigK, SigW, AbrB, CcpA, TnrA, KipR, FapR, MntR, Spo0A	

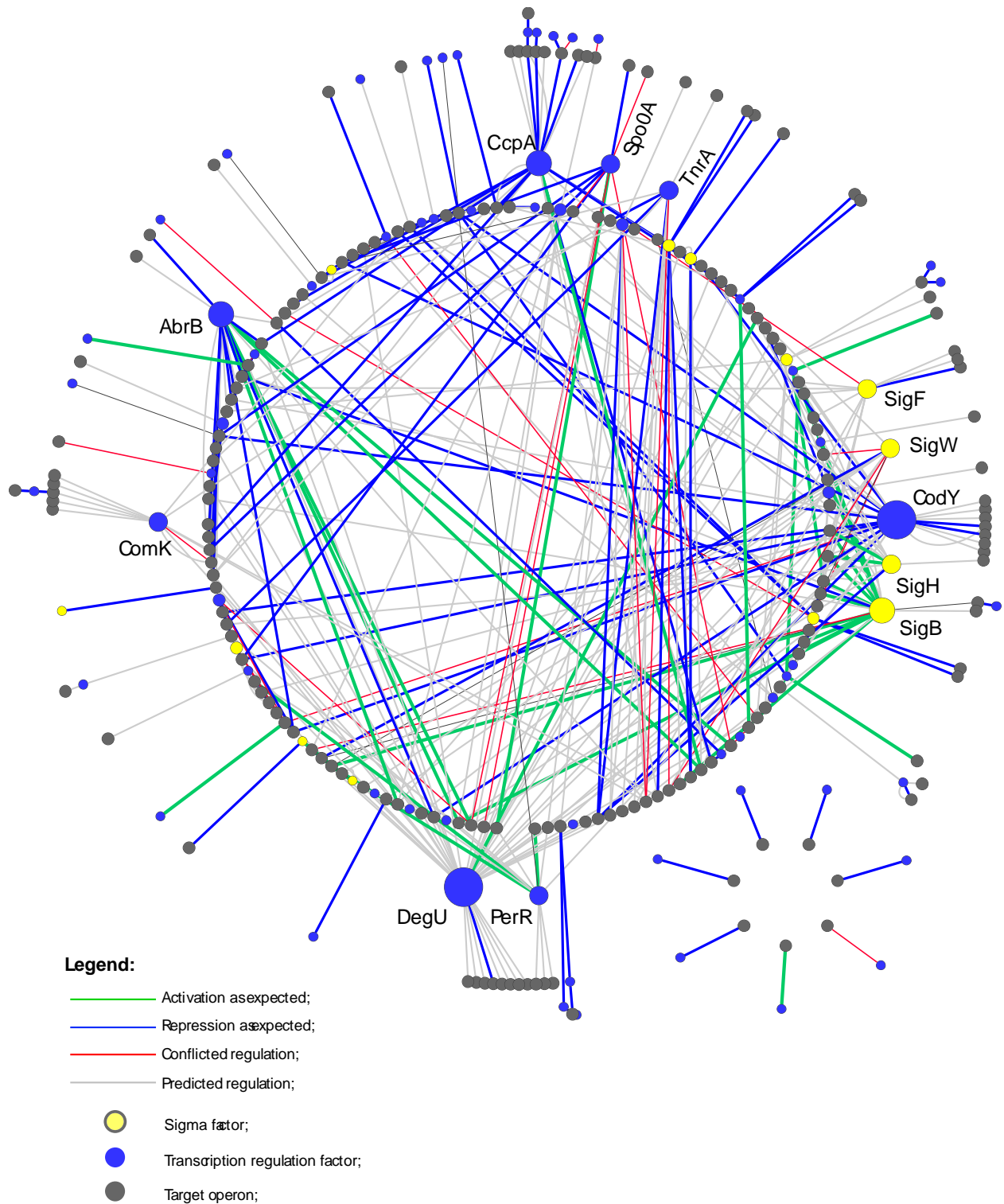


Fig. 3. Regulatory network of the genes, which regulation by the root exudates was incongruent to the general stress response regulation. The nodes representing transcriptional factors were sized according to the numbers of regulated genes. Labeled TFs were involved in regulation of at least 5 protein coding genes.

obscured. Search for possible TF binding sites in 200 bp flanking regions up-stream to the operon start codons was performed. Identified TFs are listed in supplementary Table S2. A combined overview of known and predicted TFs involved in regulation of these operons is shown in Fig. 3. The major repressors activated by the root exudate stimuli were CcpA (mediated carbon catabolite repressor), CodY (pleiotropic repressor), TnrA (nitrogen assimilation regulator) and Spo0A. However, the role of the latter regulator should be taken cautiously as at the treatment condition the effect of Spo0A most likely was modulated by other unknown transcriptional factors (see Fig. 2 and the discussion above). The major activators were AbrB and SigH (both regulated the transition to stationary phase and the cell growth rate), SigB and PerR (general stress and oxidative stress response, respectively).

Fig. 3 highlighted a possible crucial role of DegU in regulation of the plant root colonization by *Bacillus*. The DegU binding sites were identified in front of almost all regulated operons; however, only some of them were reported in the literature as parts of the DegU regulon. It is known that DegU in *B. subtilis* is an important regulator of many processes including chemotaxis, motility, extracellular secretion, quorum sensing and biofilm formation (Msadek et al., 1991; Murray et al., 2009; Gupta & Rao, 2014; Omer et al., 2015). It was reported that inactivation of DegU in *B. amyloliquefaciens* FZB42 led to impairing in efficient root colonization (Budiharjo et al., 2014). Finding of DegU binding sites in front of the operons specifically regulated by the root exudates confirmed the importance of this TF for plant colonization behavior.

3.4 Role of ncRNA in gene regulation under root exudate stimuli

It was known that many TFs were controlled by ncRNA. For example, it was reported for AhrC regulator (Brantl & Brückner, 2014). Conflicted regulation of the genes controlled by AhrC was observed in this study. Also, conflicts were observed in the regulation of genes controlled by SigB, SigW, SigF, YwaC, Spo0A, FadR and several other TFs (Fig. 2).

The majority of ncRNA identified so far in *B. subtilis* were antisense translational inhibitors including dual-function genes encoding both regulatory RNA and small regulatory proteins. One example of the dual-function genes was SR1 (Brantl & Brückner, 2014). In *B. atrophaeus* UCMB-5137, SR1 corresponded to the predicted protein coding gene D068_15140, which was not regulated by the root exudates. Two other genes D068_34490 and D068_15550 predicted in UCMB-5137 as small unknown proteins had shared sequence similarities with *bsrI* and *csfG* regulatory RNA of *B. subtilis*, respectively. These genes were repressed by the root exudates. Multiple cis-encoded phage related antitoxins were repressed by the root exudates together with all the phage related genes.

Many ncRNA predicted in this study had showed significant sequence conservation in different species of *Bacillus* despite being located in variable intergenic spacer regions. This conservation allowed prediction of possible target mRNA by using CopraRNA Web-service (Table 1). Contributions of the found ncRNA to the gene regulatory network of *B. atrophaeus* UCMB-5137 were summarized in Fig. 2A. Six predicted ncRNA, – ncr628, ncr818, ncr2198, ncr3198, ncr3519 and ncr3877, – were located near the promoter regions of the genes, which were their most likely targets. Other six ncRNA, – ncr20, ncr628, ncr1092, ncr1829, ncr2198 and ncr3198, – aimed at different transcriptional regulators. Particularly, the genes of the SpoIVB regulon including *mraZ*, which was reported in

several studies as a new TF inhibiting the cell division (Meile et al., 2006; Eraso et al., 2014), most likely were under control of the predicted ncRNA (Fig. 2A).

Among other potential targets of the predicted ncRNA, there were several genes, which have not been associated with any TF regulons in SubtiWiki. In Table 1, these genes were depicted by the bold typeface. In general, ncRNA were considered in the literature as translational inhibitors. However, several ncRNA were reported to be able to prolong the lifetime of mRNA (Wagner & Romby, 2015). It may explain the observed differences in RNA abundance of several genes, which presumably were controlled in *B. atrophaeus* UCMB-5137 exclusively by ncRNA under the root exudate stimuli.

3.5 Comparison of the gene expression profiles of *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42 stimulated by the root exudates

It was interesting to study to which extent the gene regulation by the root exudate stimuli in *B. atrophaeus* UCMB-5137 was congruent to that reported previously for the paradigm PGPR *B. amyloliquefaciens* FZB42. The gene expression profile of *B. atrophaeus* UCMB-5137 from the current research was compared to the microarray and proteomics profiles of *B. amyloliquefaciens* FZB42 published earlier (Fan et al., 2012; Kierul et al., 2015). The transcriptional profiles appeared to be substantially different (Table 3). For example, the chemotaxis and motility genes were down regulated in *B. atrophaeus* (see also the supplementary Table S1) in contrast to what was reported for *B. amyloliquefaciens*. All the mentioned genes were under control of SigD, which was two folds down-regulation by the root exudates in the current experiment. While SigD was down-regulated, its repressor CodY was two folds up-regulated by the root exudates in *B. atrophaeus* UCMB-5137. From the literature it is known that the sporulation repressor CodY is activated in *Bacillus* by the catabolic repressor CcpA (Ratnayake-Lecamwasam et al., 2001). It implied a possible role of CcpA in gene regulation by the root exudates.

The similarity between *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42 was in activation of the genes *ymcA* and *luxS* controlling biofilm formation (Nicolas et al., 2012). It is known that *luxS* is also an activator of synthesis of the quorum sensing autoinducer AI-2 (Ruzheinikov et al., 2001). Activation of *ylbF*, which is an antagonist of the biofilm repressor SinR (Kearns et al., 2005), was also observed in *B. atrophaeus* UCMB-5137 treated by the root exudates. FlaA flagella protein synthesis was activated by the root exudates in both organisms. It was reported in a study on *Bacillus cereus* that FlaA was important for biofilm formation and had nothing to do with other flagellin proteins (Houry et al., 2010), which were down-regulated by the root exudates in *B. atrophaeus* UCMB-5137. These observations confirmed the activation of the quorum sensing triggered biofilm formation in *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42 in response to the root exudate stimuli.

The most striking and unexpected effect on gene expression in *B. atrophaeus* UCMB-5137 treated by the root exudates was the strong stringent response presumably triggered by the alarmone (p)ppGpp. Summarized scheme of interactions between the key TFs and the regulated genes is shown in Fig. 4. Similarities in the responses to the treatment with root exudates in *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42 were represented on the right part of the Fig. 4, and the dissimilar regulations were shown on the left part of the figure. The stringent response and general catabolic repression by CcpA could explain all the differences between the expression profiles of these two microorganisms. The stringent response was known to be accompanied by the general stress response

Table 3. Comparison of the gene expression profiles observed in *B. atrophaeus* UCMB-5137 and reported for *B. amyloliquefaciens* FZB42.

Genes, pathway and/or metabolic processes	UCMB-5137		FZB42
	RNA-Seq (this work)	Microarray hybridization data (Fan et al., 2012)	Proteomics data (Kierul et al., 2015)
<i>Similar response to root exudate in both organisms</i>			
Biofilm and quorum sensing: <i>ymcA</i> and <i>luxS</i> genes.	Up-regulated	Up-regulated	Not reported
Proteins secreted in late exponential phase: SodA (superoxide dismutase), Tpx (thiol peroxidase), AhpC (alkyl hydroperoxide reductases C), YodJ (D-Alanine carboxypeptidase), CysK (cysteine synthase A) and FbaA (fructose 1,6-bisphosphate hydrolase)	Up-regulated	Not reported	Up-regulated
PenP (beta-lactamase precursor)	Down-regulated	Not reported	Down-regulated
All phage-associated genes	Down-regulated	Not reported	Down-regulated (associated with the late exponential phase)
Cold shock protein CspA	Up-regulated	Not reported	Up-regulated
<i>Dissimilar response to root exudate</i>			
Genes involved in carbon and nitrogen utilization	Down-regulated	Up-regulated	Not reported
Genes involved in mobility and chemotaxis	Down-regulated	Up-regulated	Not reported
Non-ribosomal synthesis of secondary metabolites with antimicrobial action such as surfactin synthetase	Down-regulated	Up-regulated	Up-regulated
Inositol metabolism IolFGEDBC	Down-regulated	Up-regulated	Not reported
Lipids metabolism: FabI enoyl-(acyl-carrier-protein) reductase and FabF acyl carrier protein synthase II	Down-regulated	Not reported	Up-regulated
ChbA chitin-binding protein	Down-regulated	Not reported	Up-regulated
Tricarboxylic acid (TCA) cycle	Differentially regulated but below statistical reliability	Up-regulated	Not reported
Oligopeptide ABC transporters OppADF	Down-regulated (p > 0.05)	Up-regulated	Not reported
Phosphotransferase system (PTS)	Down-regulated	Up-regulated	Not reported

(Eyman et al., 2002) and by activation of the SigB stressosome that caused up-regulation of many general stress response genes (Hecker et al. 2007). The results of our study were in agreement with the previous publications that reported significant down-regulation of the SigD activator of motility and chemotaxis by different stress conditions (Sappa 2013; Kohlstedt et al., 2014). This effect might be linked to the activation of the CodY repressor, which also repressed the amino acid metabolism and many other metabolic pathways at the time of transition from the exponential to stationary growth phases in response to shortage of nutrients (Serror & Sonenshein, 1993; Bergara et al., 2003).

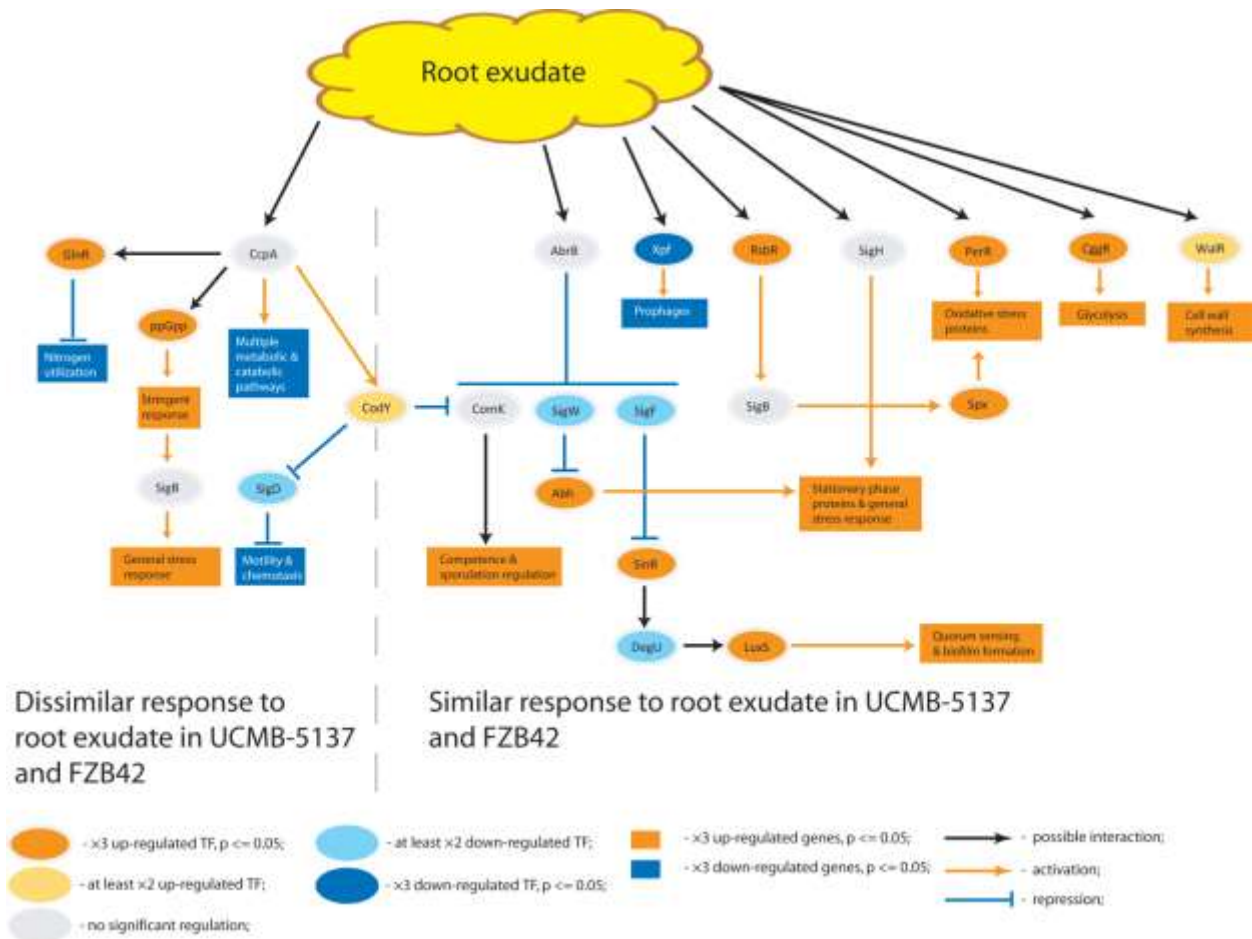


Fig. 4. Schematic representation of involvement of the top level transcriptional factors, which may explain the observed differences and similarities in the gene expression profiles of *B. atrophaeus* UCMB-5137 and *B. amyloliquefaciens* FZB42.

It remained unclear which factors could trigger such strong stress on *B. atrophaeus* UCMB-5137 resulted from an addition to the medium of a tiny amount of the root exudates. It was hypothesized that the stress could be associated with the metabolic repression caused by CcpA. The major function of the CcpA repressor is to optimize the carbon and nitrogen metabolism by repressing the pathways of utilization of less convenient sources of nutrients, when there is an abundance of easily accessible sugars and ammonium (Wacker et al., 2003; Görke & Stülke, 2008). Normally CcpA is activated by glucose, which is a major component of the root exudates (Fan et al., 2012). However, other components, i.e. organic acids, melibiose and traces of amino acids, might intensify this response. The amount of the root exudates added to the medium could not provide any sufficient increase in the amount of nutrients, but it could mislead the bacteria by signaling the presence of plant roots suitable for colonization in the close vicinity, which could be a source of surplus of plant sugars (Dennis et al., 2010). The strong carbon metabolism repression without any supply of additional sugars could cause an abrupt shortage of energy and nutrients that led to accumulation of uncharged tRNA molecules, which in their turn had triggered the stringent response through ppGpp alarmone activation (Eymann et al., 2002) and further repression of many metabolic pathways by ppGpp activation of the CodY repressor (Wünsche et al., 2012; Geiger & Wolz, 2014).

4. Conclusion

The current study showed limitations of our knowledge of the gene regulatory network in *B. subtilis* and related organisms. The whole dimension of the gene regulations by small non-coding RNA is still to be discovered. Significant alterations in the gene regulation profiles between *B. atrophaeus* UCMB-5137 and the paradigm PGPR strain *B. amyloliquefaciens* FZB42 demonstrated that PGPR could use different strategies for plant colonization. It may be important to count for these differences to achieve an optimal performance of the biopesticides and biofertilizers based on PGPR. It was concluded in this work that these differences could be explained by hypersensitivity of UCMB-5137 to the root exudate stimuli impelling it to a sessile root colonization behavior through the CcpA-CodY-AbrB and probably DegU regulations. It was found that the general stress response genes were significantly up-regulated in UCMB-5137 by the root exudates that might result from the repression of catabolism by CcpA activated by chemicals components of root exudates. Regulation of many genes by the root exudates was inconsistent with our knowledge on the gene regulation in *B. subtilis*. It was demonstrated that ncRNA interfered with the gene expression regulation at the time of rhizosphere colonization.

Competing interests

The authors declare that they have no competing interests.

Author contributions

LM and WYC performed the experiment; ONR and SLL designed the experiment and analyzed the data; TP worked with plants; SVL and LVA worked with the bacterial culture; LM and ONR wrote the manuscript. All authors read and approved the manuscript.

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Table S1. Functional grouping of genes of *Bacillus atrophaeus* UCMB-5137 regulated by maize root exudate (fold change ≥ 3 ; $p \leq 0.05$).

Functional groups and reactions		Up-regulated	Down-regulated	Activator*	Repressor*
Aerobic respiration					
<i>ctaA</i>	cytochrome oxidase biogenesis, heme A synthase	D068_15390		ResD, SigE	
<i>ykuU</i>	alkyl hydroperoxide reductase	D068_14700			AbrB
<i>qcrB</i>	menaquinol-cytochrome c reductase cytochrome b		D068_22850	ResD	AbrB
Anaerobic respiration					
<i>nfrA</i>	nitrate respiration	D068_40270		SigD, Spx	Spo0A
<i>narG</i>	respiratory nitrate reductase alpha chain		D068_39480	Fnr	
<i>yyaE</i>	selenocysteine-containing anaerobic dehydrogenases		D068_43360		
Amine and polyamine metabolism					
<i>speD</i>	spermidine biosynthesis I	D068_28960			CcpN
<i>gubD</i>	4-aminobutyrate degradation II and III; GABA shunt	D068_32090		GabR, SigB	
Amino acid biosynthesis, degradation and transportation					
<i>cysE</i>	cystein biosynthesis I		D068_00800		
<i>hisA</i>	histidine/imidazole biosynthesis		D068_36810		
<i>hisD</i>			D068_36840		
<i>hisF</i>			D068_36800		
<i>hisH</i>			D068_36820		
		homocystein biosynthesis		D068_36350	
<i>proB</i>	proline biosynthesis I		D068_13560		
<i>ycgM</i>	proline dehydrogenase/oxidase		D068_03140	PutR, Spo0A	CodY
<i>ycgN</i>	delta-1-pyrroline-5-carboxylate dehydrogenase		D068_03150	PutR, Spo0A	CodY
<i>cysC</i>	sulfate activation for sulfonation		D068_16200		CymR
<i>hutU</i>	histidine degradation I		D068_41790		CcpA, CodY
<i>hutM</i>	histidine transport permease		D068_41820		CcpA, CodY
<i>yckJ</i>	TcyB L-cystine ABC transporter		D068_32510		
<i>ydgF</i>	D-serine/D-alanine/glycine transporter		D068_42470		
<i>yxen</i>	amino acid ABC transporter		D068_32320		CymR
<i>ycsG</i>	branched chain amino acids transporter		D068_31920	TnrA	KipR
<i>ycgO</i>	PutP proline/sodium symporter		D068_03160	PutR	
Antibiotic and bacteriocin biosynthesis					

<i>yshB</i>	colicin V biosynthesis	D068_28480			
<i>pksE-R</i>	bacillaene biosynthesis operon		D068_17790-17890		
<i>ycbN</i>	bacitracin transporters		D068_02530		
<i>ycbO</i>			D068_02540		
<i>plpC</i>	plipastatin/fengycin synthetase		D068_20095		
<i>srfAA</i>	surfactin synthetase		D068_03520	ComA, PerR	Abh, CodY, Spx
<i>srfAB</i>			D068_03530		
<i>yuil</i>	trilactone hydrolase, bacillibactin siderophore biosynthesis		D068_33600		AbrB, Fur
<i>ybdB</i>	SkfF cannibalism toxin		D068_01840	PhoP, Spo0A	AbrB
Aromatic compound biosynthesis and degradation					
<i>yitW</i>	aromatic ring hydroxylating enzyme	D068_11280			
Biofilm formation and regulation					
<i>luxS</i>	S-adenosyl-L-methionine cycle I; autoinducer AI-2 biosynthesis	D068_30750			
<i>ymcA</i>	biofilm formation regulation	D068_17660			
<i>yugO</i>	putative K ⁺ channel protein		D068_32890		
<i>ywqE</i>	protein dephosphorylation		D068_38300		AbrB
Carbohydrate biosynthesis and degradation					
<i>sacA</i>	sucrose degradation III (sucrose invertase)		D068_40170		CcpA
<i>yfnG</i>	galactose degradation I (Leloir pathway); galactose degradation III; UDP-D-galactose biosynthesis		D068_07090	SigK	
<i>ycbC</i>	D-glucarate/D-galactarate degradation II		D068_02410		YcbG
<i>ycbD</i>			D068_02420		YcbG
<i>pelB</i>	pectin synthesis/degradation		D068_41580		
<i>lich</i>	arbutin/salicin-6-phosphate hydrolysis		D068_27630	LicR	CcpA
<i>glgC</i>	glycogen biosynthesis I (from ADP-D-glucose)		D068_31080	SigE	
<i>xynD</i>	cellulose and hemicellulose degradation (cellulolosome)		D068_19950		AbrB
<i>yveB</i>	levanase		D068_36400	DegU	
<i>RhiN</i>	rhamnogalacturonides degradation protein		D068_06760		
	chitin binding protein		D068_21820		
<i>yyaE</i>	RpiR sialic acid utilization regulator		D068_01620		
<i>yisS</i>	myo-inositol degradation II, myo-, chiro- and scillo-inositol degradation		D068_04260		

<i>lolF</i>	myo-inositol transporter		D068_42110		CcpA, lolR
<i>iolI</i>	inosose isomerase		D068_42080		CcpA, lolR
<i>rbsK</i>	alpha-D-ribofuranose phosphorylation to D-ribose 5-phosphate		D068_37920	AbrB	CcpA
<i>acoB</i>	transketolase		D068_07970	AcoR, SigL	CcpA
<i>yufO</i>	unspecified monosaccharide		D068_33130		CodY
<i>yufP</i>	ABC transporters		D068_33140		CodY
Carbon metabolism and glycolysis					
<i>ywkA</i>	gluconeogenesis I; glycolysis III; heterolactic fermentation; sucrose biosynthesis I, glycerol degradation to butanol	D068_39220		MalR	
<i>gapA</i>		D068_35950			CggR
<i>yqiK</i>	glycerophosphoryl diester, phosphodiesterase	D068_24670			
<i>glpD</i>	aerobic glycerol-3-phosphate dehydrogenase	D068_09280		AbrB	CcpA
<i>pdhA</i>	pyruvate dehydrogenase E1 component alpha subunit		D068_15080		ppGpp, YwaC
<i>pyrC</i>	dihydroorotase		D068_16080	PyrR	ppGpp
<i>iolS</i>	oxidoreductase, aldo/keto reductase		D068_06830		lolR
Cell division					
<i>divIVA</i>	cell division initiation protein	D068_16000			Spo0A
<i>yyaA</i>	ParB chromosome partitioning protein	D068_43440		ComK	
<i>ftsW</i>	cell division protein	D068_40290		SigM	
<i>gpsB</i>	cell division protein	D068_22460			
Cell wall biosynthesis and membrane proteins					
<i>yocA</i>	antigen A homolog; putative transposon-related lytic enzyme	D068_20960			
<i>tagD</i>	teichoic acid biosynthesis	D068_37680		WalR	PhoP
<i>tagO</i>	peptidoglycan biosynthesis I and V (beta-lactam resistance)	D068_37460			
<i>secG</i>	preprotein translocase subunit	D068_35560			
<i>yoch</i>	cell wall binding protein	D068_21050		Spo0A, WalR	AbrB
<i>yfmQ</i>	holin associated protein, membrane protein	D068_23710			
<i>yneJ</i>	integral inner membrane proteins	D068_19650			
<i>yoZB</i>		D068_20970			
<i>yqjG</i>		D068_24390		MifM	
<i>yuiD</i>		D068_33670			
<i>gtab</i>	sucrose degradation II, UDP-glucose biosynthesis	D068_37620		SigB	
<i>tuaA</i>	undecaprenyl-phosphate		D068_37540	PhoP	

	galactosephosphotransferase				
<i>yubE</i>	N-acetylmuramoyl-L-alanine amidase (cell wall degradation/ turnover)		D068_05240		
<i>ykfC</i>	cell wall endopeptidase NLP/P60		D068_13420		CodY
	LysM domain containing peptidoglycan-binding protein (horizontally acquired)		D068_05530		
			D068_05540		
Chemotaxis and motility					
<i>flaA</i>	FlaA flagellin protein	D068_37280		SigD	CodY, CsrA, ScoC
<i>flbD</i>	flagellin proteins		D068_16900		
<i>flhB</i>			D068_16990	SigD	CodY, Spo0A
<i>fliY</i>			D068_16930	SigD	CodY, Spo0A
<i>flhA</i>			D068_17000	SigD	CodY, Spo0A
<i>tlpA</i>	methyl-accepting chemotaxis protein		D068_32780	SigD	AbrB
Co-factor biosynthesis and utilization					
<i>ppnK</i>	NAD kinase	D068_29420			
<i>ywfl</i>	HemQ hemoprotein	D068_39940			
<i>atpI</i>	ATP synthase protein I2	D068_39040			ppGpp, YwaC
<i>moaC</i>	molybdenum cofactor biosynthesis	D068_04680			
<i>ribT</i>	vitamin B synthesis, acetyltransferase	D068_23580			
<i>yqeY</i>	GatB transamidase	D068_25960			
<i>ytaP</i>	biotin biosynthesis; fatty acid biosynthesis		D068_30330		
<i>bioD</i>			D068_30270		BirA
<i>bioB</i>			D068_30260		BirA
<i>yqjQ</i>			D068_03660		
<i>tenI</i>	thiamin biosynthesis and salvage		D068_11830		
<i>thiC</i>			D068_08720		
<i>thiF</i>			D068_42760		
<i>yaaD</i>	PdxST pyridoxine biosynthesis glutamine amidotransferases		D068_18930		Spo0A
<i>yaaE</i>			D068_18940		Spo0A
Fatty acid biosynthesis					
<i>glpQ</i>	glycerophosphoryl diester, phosphodiesterase		D068_02080	PhoP	CcpA
<i>pcrB</i>	S-3-O-geranylgeranyl glyceryl phosphate synthase		D068_06290		
<i>ypxA</i>	glycerate kinase		D068_42360		AbrB

<i>yusK</i>	fatty acid beta-oxidation pathway		D068_34610	SdpR	CcpA, FadR
<i>yqjQ</i>	short-chain dehydrogenase/reductase		D068_03670		
<i>pgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase		D068_17520		
<i>yqiD</i>	ThiJ/Pfpl family protein, biosynthesis of lipids		D068_36480		
Iron metabolism					
<i>yvrA</i>	adenosylcobalamin salvage from cobinamide II, iron metabolism		D068_34950		
<i>dhbC</i>	1,4-dihydroxyl-2-naphthoate biosynthesis I; 2,3-dihydrobenzoate biosynthesis		D068_33580		AbrB, Fur
<i>dhbA</i>			D068_33590		AbrB, Fur
<i>dhbE</i>	vibriobactin biosynthesis		D068_33570		AbrB, Fur
Nitrogen utilization					
<i>nasA</i>	nitrate/nitrite transporter		D068_03270	TnrA	
<i>ureA</i>	urea degradation II		D068_38790	PucR, SigH, TnrA	CodY, GlnR
<i>ureB</i>			D068_38780	PucR, SigH, TnrA	CodY, GlnR
Nucleotide biosynthesis and degradation					
<i>guaC</i>	nucleotide biosynthesis/acquisition		D068_33750	CodY	PurR
<i>purA</i>	adenosine ribonucleotides de novo biosynthesis		D068_42840		PurR
<i>purN</i>	5-aminoimidazole ribonucleotide biosynthesis; tetrahydropholate salvage		D068_06180		PurR
<i>purS</i>	5-aminoimidazole ribonucleotide biosynthesis		D068_06130		PurR
	pyrimidine deoxyribonucleotides biosynthesis		D068_04970		
<i>pyrB</i>	UMP biosynthesis; pyruvate decarboxylation to acetyl CoA		D068_16070	PyrR	
	adenine/guanine phosphoribosyltransferases		D068_02880		
	ATP/GTP-binding protein		D068_02890		
Protein translation, maturation, activation and utilization					
<i>yfhP</i>	cysteinyl-tRNA synthetase related protein	D068_08500			
<i>ppiB</i>	protein folding acceleration	D068_23750			
<i>prfA</i>	peptide chain release factor 2	D068_37200			

<i>yflG</i>	N-terminal amino acid release	D068_07470			
<i>sipT</i>	leader sequence cleavage, signal peptidase	D068_14890		DegU	
<i>sipS</i>		D068_23650			
<i>ykuE</i>	protein kinases	D068_14540			
<i>yjbH</i>		D068_11720			
<i>yrzF</i>		D068_27510			
<i>prkC</i>			D068_16370		
Ribosomal proteins					
<i>rbfA</i>	ribosome-binding factor A	D068_17260			ppGpp, YwaC
<i>rpsB</i>	SSU ribosomal protein S2p	D068_17100			ppGpp, YwaC
<i>rpsL</i>	SSU ribosomal protein S9p	D068_01340			ppGpp, YwaC
<i>rpsT</i>	SSU ribosomal protein S20p	D068_26110			
<i>rpsU</i>	SSU ribosomal protein S21p	D068_25970			
<i>rplT</i>	LSU ribosomal protein L20p	D068_28780			ppGpp, YwaC
<i>ytiA</i>	LSU ribosomal protein L31p	D068_30790		SigB	Zur
<i>rpmF</i>	LSU ribosomal protein L32p	D068_15640			ppGpp, YwaC
<i>ylnN</i>	ribosomal protein clustered with L32p	D068_15630			ppGpp, YwaC
<i>yvyD</i>	ribosomal subunit interface protein	D068_37220		SigB, SigH	
<i>rplB</i>	LSU ribosomal protein L2p		D068_01060		ppGpp, YwaC
<i>rplP</i>	LSU ribosomal protein L16p		D068_01080		ppGpp, YwaC
<i>rimM</i>	16S rRNA processing protein		D068_16620		
<i>ybxB</i>	ribosomal RNA small subunit methyltransferase		D068_00930		ppGpp, YwaC
Replication, repair, recombination					
<i>dnaN</i>	DNA polymerase III beta subunits	D068_00020			Spo0A
<i>dinG</i>		D068_26790			
Resistance to antibiotics and toxins					
<i>yvaE</i>	ethidium bromide-methyl viologen resistance protein EmrE		D068_04110		
<i>pbpE</i>	beta-lactamase		D068_05680	SigW	
<i>lmrB</i>	drug resistance transporter EmrB/QacA		D068_02650		LmrA
<i>yoaV</i>	drug/metabolite transporter DMT		D068_41730		
Sporulation					
<i>yraG</i>	spore coat protein F	D068_08690		SigG	
<i>sspJ</i>	spore protein	D068_35180		SigG	
<i>yndM</i>	sporulation protein	D068_19520			
<i>yqfU</i>	sporulation protein	D068_25650		SigG	

<i>yraF</i>	sporulation protein		D068_01970		
<i>yisY</i>	chlorination of organic molecules		D068_29590	SigG	
<i>spsG</i>	CMP-N-acetylneuraminate biosynthesis II, spore coat protein		D068_38680	SigK	
<i>spsC</i>	PglE 4-keto-6-deoxy-N-Acetyl-D-hexosaminyL-Lipid carrier aminotransferase		D068_35870	SigK	
<i>ytCA</i>	UDP-alpha-D-glucuronate biosynthesis from UDP-glucose		D068_35880		
<i>cotJC</i>	spore coat protein		D068_06660	SigE, SpoIIID	
<i>yesJ</i>	GNAT family acetyltransferase		D068_06670	SigE, SpoIIID	
<i>ypjB</i>	spore formation membrane associated protein		D068_22820	SigE	
<i>gerKA</i>	spore germination protein		D068_37880	SigG	SpoVT
<i>ybbE</i>	nylon-6 oligomer degradation		D068_01600		
Stress response, detoxication, antibiotic resistance					
<i>nfrA</i>	oxygen-insensitive NADPH nitroreductase (oxidative stress)	D068_40270		SigD, Spx	Spo0A
<i>hxlB</i>	thiaminase II, resistance against oxidative stress	D068_03470		HxIR	
<i>ywbC</i>	lactoylglutathione lyase, oxidative stress resistance	D068_40560			
<i>ygaF</i>	thiol peroxidase antioxidant proteins, resistance against oxidative stress	D068_08610			
<i>yjbC</i>		D068_11650		SigB, SigM, SigW, SigX	PerR
<i>yjbL</i>	thiol management oxidoreductase component	D068_11730			
<i>ykuV</i>	thiol-disulfide isomerase	D068_14710			AbrB
<i>sodA</i>	superoxide radicals degradation	D068_25560		SigB	
<i>trxA</i>	thioredoxin pathway	D068_28370		SigB, Spx	CtsR
<i>trxA</i>		D068_31340			
<i>trxB</i>		D068_36650		Spx	
<i>yusE</i>		D068_34550		Spo0A	
<i>mrgA</i>	metal ion oxidation for incorporation into corresponding proteins	D068_34740			PerR
<i>yock</i>	general stress protein	D068_21090		SigB	
<i>ytXJ</i>	NAD kinase, general stress response	D068_29850		SigB, SigH	
<i>cspC</i>	cold-shock proteins	D068_03770			
		D068_23670			
<i>ykrL</i>	HtpX heat shock protein	D068_13940			Rok, YkrK
<i>yfIT</i>	heat stress induced protein	D068_07310		SigB	

<i>yzkA</i>	OhrB organic hydroperoxide resistance protein	D068_13600		SigB	
<i>ylmG</i>	YggT integral membrane protein involved in response to extracytoplasmic stress osmotic shock	D068_15980			Spo0A
<i>nhaX</i>	stress response protein	D068_09730		SigB	
<i>yfkM</i>	ThiJ/Pfpl family protein	D068_07580		SigB	Fur
<i>ytxH</i>	general stress response proteins	D068_29860		SigB, SigH	
<i>ytxG</i>		D068_29870		SigB, SigH	
<i>ydaG</i>		D068_31760		SigB	
<i>gsiB</i>		D068_31500		SigB, SigI	
<i>gspA</i>		D068_40610		SigB	
<i>yugI</i>		D068_32960			ppGpp, YwaC
<i>yxiE</i>		D068_41660			CcpA
<i>yfhL</i>	SdpC immunity factor	D068_08450		SigB, SigW	
<i>ywsB</i>		D068_37970		SigB	
<i>clpP</i>	proteolysis and hydrolysis, general stress response	D068_36470		SigB	CtsR
<i>yfhM</i>		D068_08460		SigB, SigW	
<i>clpX</i>		D068_28080			CtsR
<i>ydiL</i>	stress protection CAAX amino terminal protease	D068_04730			
<i>yvgN</i>	stress response protein	D068_01940		SigB	SinR
		D068_35260		SigB	SinR
<i>ydaM</i>	general stress protein		D068_31640		
<i>dnaJ</i>	chaperone protein DnaJ		D068_26020		HrcA
<i>ydfO</i>	MhqO glyoxalase/dioxygenase		D068_29690	SigB	MhqR
<i>ispF</i>	methylerythriol phosphate pathway, lipid biosynthesis, stress response		D068_00770	SigB	
Transcriptional regulation					
<i>ywaC</i>	SasA protein, stringent response, ppGpp biosynthesis	D068_40690		SigM, SigW	
<i>perR</i>	peroxide stress regulator PerR	D068_08620			PerR
<i>spo0A</i>	stage 0 sporulation two-component response regulator	D068_24730		SigH	Spo0A
<i>lexA</i>	LexA SOS-response repressor	D068_19550			LexA
<i>yoZG</i>	Cro/Ci family transcriptional regulator	D068_21840			
<i>ydeB</i>	CarD-like transcriptional regulator	D068_03780			
<i>ypdC</i>	anti-sigW regulation	D068_23280			
<i>ytvA</i>	positive sigma-B regulator, blue light GTP-binding	D068_30400		Spx	

	receptor				
<i>paiB</i>	sporulation negative regulatory protein PAI-2	D068_03850			
<i>sinR</i>	SinR regulator of post-exponential-phase responses genes competence and sporulation	D068_25150			AbrB, ScoC, Spo0A
<i>bmrU</i>	transcription regulator, stress response, resistance against toxins and antibiotics	D068_24490		SigB	
<i>yqgZ</i>	MgsR transcriptional regulator of stress response	D068_25310		MgsR, SigB	
<i>dps</i>	non-specific DNA-binding protein Dps, iron-binding ferritin-like antioxidant protein	D068_30720		SigB	
<i>ydhC</i>	GntR transcriptional regulator	D068_43070			
<i>ykvE</i>	MhqR transcriptional regulator, resistance to methyl-hydroxyquinone	D068_14120			
<i>ykoM</i>	MarR family transcriptional regulator	D068_13800			
<i>ypoP</i>		D068_21940			
<i>yvnA</i>		D068_35190			AbrB, CcpA
<i>mecA</i>	MecA negative regulator	D068_11680			
<i>yphH</i>		D068_23310			
<i>glnR</i>	GlnR transcriptional regulator of nitrogen metabolism	D068_18140			GlnR, TnrA
<i>fnr</i>	Fnr transcriptional regulator	D068_39520		Fnr, ResD	NsrR
<i>yvdT</i>	TetR transcriptional regulator	D068_36420			
<i>yvaP</i>	CatR/HxlR transcriptional regulator, viability in the presence of catechol	D068_35610			
<i>cggR</i>	CggR glycolytic genes regulator	D068_35960			CggR
<i>yhdE</i>	NsrR nitrite-sensitive transcriptional repressor, resistance against nitric oxide, phenolic acids, flavonoids, oxalate	D068_09360			
<i>ykmA</i>	OhrR organic hydroperoxide resistance transcriptional regulator	D068_13590			
<i>hrcA</i>	HrcA heat-inducible transcription repressor	D068_26050			HrcA
<i>ykoB</i>	RsbRB piezosome protein	D068_13690			
<i>abh</i>	Abh transcriptional regulator, transition from	D068_14960		SigM, SigX	

	growth to stationary phase				
<i>ylbF</i>	ComK regulatory protein, antagonist of biofilm repression by SinR	D068_15530			
<i>tnrA</i>	TnrA transcriptional regulator, regulation of nitrogen assimilation	D068_13790		TnrA	GlnR
<i>fur</i>	Fur regulation of iron homeostasis By repression of transcription of ferri-siderophore uptake genes	D068_23940		PerR	
<i>zur</i>	Zur transcriptional regulator, trace metal homeostasis	D068_25630			
<i>yjbD</i>	Spx transcriptional regulator	D068_11660		SigB, SigM, SigW, SigX	PerR
<i>xpf</i>	Xpf transcriptional regulator, prophage transcription activator		D068_12870		ppGpp
<i>yvrL</i>	YvrL regulator, controls acid stress proteins		D068_35050	YvrHa, YvrHb, Yvrl	
Transport and uptake (in addition to mentioned above amino acid, hydrocarbon and secondary metabolite transporters)					
<i>ycaA</i>	RibU riboflavin ECF transporter	D068_23390			
	siderophore Fe-uptake	D068_09870			
<i>expZ</i>	ABC-transporters	D068_34750			
<i>yfiM</i>			D068_08200		
<i>yfiL</i>			D068_08190		
<i>yhcG</i>			D068_09020		
<i>yvrO</i>			D068_35100	ComK	AbrB
<i>yclI</i>			D068_32270	YclI	
<i>fhuG</i>		ABC-type Fe ³⁺ -siderophore transports		D068_35130	
<i>fhuB</i>			D068_35140		Fur
<i>ycdI</i>	zinc ABC transporter		D068_02790		Zur
<i>ssuA</i>	aliphatic sulfonate ABC transporters		D068_08760		CymR
<i>ssuC</i>			D068_08770		CymR
<i>ybbF</i>	PTS transporters		D068_01610		
<i>mtIA</i>			D068_32010		
<i>sacP</i>			D068_40180		CcpA
<i>appB</i>	OppB oligopeptide transport system permease protein		D068_11530		CodY, ScoC
<i>pstA</i>	PstA phosphate ABC transporter		D068_25510	PhoP	
<i>yqeW</i>	sodium-dependent Na ⁺ /anion phosphate transporter		D068_25980		
<i>glpP</i>	proton/glutamate-aspartate symport protein		D068_02290		
<i>glpP</i>	glycerol-3-phosphate		D068_02100		CcpA

	transporter				
<i>yclF</i>	di-/tripeptide transporter		D068_32430		ScoC
<i>dctP</i>	aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate and succinate		D068_31430		CcpA
Other enzymes					
	acetylxylin esterase	D068_19930			
<i>tatCY</i>	R-CoA hydrolysis, twin-arginine translocation pathway	D068_13460			
<i>yneT</i>	succinyl-CoA synthetase	D068_19790			
<i>yfmJ</i>	putative oxidoreductase		D068_07240	Spo0A	
<i>yxel</i>	putative acetyltransferase		D068_32340		CymR
<i>yxek</i>	nitrilotriacetate monooxygenase		D068_32350		CymR
<i>yurQ</i>	endo/excinuclease amino terminal domain protein		D068_34420		

*Information about gene repressors and activators was taken from SubtiWiki (http://subtiwiki.uni-goettingen.de/wiki/index.php/Main_Page) and DBTBS (<http://dbtbs.hgc.jp/>).

Table S2. Operons of *Bacillus atrophaeus* UCMB-5137 regulated by maize root exudate differently from the patterns of stress response.

#	Operon and genes	Orthologs in Bs168	Annotation	Regulation by root exudate		Overall regulation	Regulation at stress conditions*				TF		
				Fold Change	p-value		1.2M-NaCl	51°C	Stationary growth	16°C	Known [†]	Predicted [‡]	
1:	[cgs_D068_00770; cds_D068_00760; cds_D068_00750]												
	cds_D068_00770	BSU00910	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase EC 4.6.1.12	-30.77	4.27E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	SigB, SigM	DegU, RocR	
	cds_D068_00760	BSU00900	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase EC 2.7.7.60;	-1.36	0.73								
	cds_D068_00750	BSU00890	pilT; Pili retraction protein pilT;	-1.65	0.81								
2:	[cgs_D068_00800]												
	cds_D068_00800	BSU00930	Serine acetyltransferase EC 2.3.1.30	-8.42	2.47E-04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			
3:	[cgs_D068_01060; cds_D068_01050; cds_D068_01040; cds_D068_01030; cds_D068_01020]												
	cds_D068_01060	BSU01190	LSU ribosomal protein L2p L8e	-4.57	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	YwaC		
	cds_D068_01050	BSU01180	LSU ribosomal protein L23p L23Ae;	-3.14	0.09								
	cds_D068_01040	BSU01170	LSU ribosomal protein L4p L1e;	-3.31	0.08								
	cds_D068_01030	BSU01160	LSU ribosomal protein L3p L3e;	-2.16	0.48								
	cds_D068_01020	BSU01150	SSU ribosomal protein S10p S20e;	-1.85	0.78								
4:	[cgs_D068_01290]												
	cds_D068_01290	BSU01450	ATPase component of general energizing module of ECF transporters	-4.81	5.07E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			
5:	[cgs_D068_01620; cds_D068_01630]												
	cds_D068_01620	BSU01690	Sialic acid utilization regulator, RpiR family N-acetylmuramic acid 6-phosphate etherase EC 4.2.-.-;	-19.93	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		ComK	
	cds_D068_01630	BSU01700		-4.98	0.28								
6:	[cgs_D068_01790]												
	cds_D068_01790	BSU01890	major facilitator MFS superfamily protein	-50.76	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			
7:	[cgs_D068_01970]												
	cds_D068_01970		LrgA; Antiholin-like protein LrgA	inf	0.03	DOWN						ComK	
8:	[cgs_D068_02080; cds_D068_02090; cds_D068_02100]												
	cds_D068_02080	BSU02130	Glycerophosphoryl diester phosphodiesterase, periplasmic EC 3.1.4.46	-14.41	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	CcpA, PhoP	CcpA	
	cds_D068_02090		hypothetical protein;		0.58								
	cds_D068_02100	BSU02140	Glycerol-3-phosphate transporter;	-65.27	2.08E-04						CcpA		
9:	[cgs_D068_02130; cds_D068_02140]												
	cds_D068_02130	BSU02200	FIG01249079: hypothetical protein	-22.84	3.45E-07	DOWN	Not regulated	UP	Not regulated	Not regulated		CodY	
	cds_D068_02140		hypothetical protein;	-1.59	0.86								
10:	[cgs_D068_02290]												
	cds_D068_02290	BSU02340	Proton/glutamate symport protein @ Proton/aspartate symport protein	inf	0.03	DOWN	Not regulated	Not regulated	UP	Not regulated		CcpA, DegU, SigH	
11:	[cgs_D068_02410]												
	cds_D068_02410	BSU02460	5-dehydro-4-deoxyglucarate dehydratase EC 4.2.1.41	-76	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	YcbG, F912	SigA	
12:	[cgs_D068_02530; cds_D068_02520; cds_D068_02510]												
	cds_D068_02530	BSU02570	bacitracin ABC transporter, ATP-binding protein	-12.53	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			
	cds_D068_02520	BSU02560	sensor histidine kinase;	-22.47	0.2								
	cds_D068_02510	BSU02550	DNA-binding response regulator;	-3.05	0.69								
13:	[cgs_D068_02690]												
	cds_D068_02690	BSU02770	oxidoreductase, aldo/keto reductase family	-3.59	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		CodY, DegU, SigB	
14:	[cgs_D068_02790; cds_D068_02780]												
	cds_D068_02790	BSU02860	ZnuC; Zinc ABC transporter, ATP-binding protein ZnuC	-17.06	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	Zur	SigE	
	cds_D068_02780	BSU02850	znuA; Zinc ABC transporter, periplasmic-binding protein ZnuA;	-2.25	0.81								
15.1:	[cgs_D068_02880; cds_D068_02870]												
	cds_D068_02880		COG0503: Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	-5.31	2.52E-03	DOWN						DegU, FNR, SigW, SigX	
	cds_D068_02870		Citrate lyase beta chain EC 4.1.3.6;	-3.1	0.1								
15.2:	[cgs_D068_02860; cds_D068_02850; cds_D068_02840; cds_D068_02830]												
	cds_D068_02860	BSU02920	TerC-like integral membrane protein;	-1.1	0.5						SigB, SigM, SigW, SigX		
	cds_D068_02850	BSU02910	terDC; Tellurium resistance protein TerDC;	-1.79	0.66								
	cds_D068_02840	BSU02900	terDB; Tellurium resistance protein TerDB;	-1.93	0.51								
	cds_D068_02830	BSU02890	terDA; Tellurium resistance protein TerDA;	-3.04	0.09								
16:	[cgs_D068_03140]												
	cds_D068_03140	BSU03200	Proline dehydrogenase EC 1.5.99.8 Proline oxidase	-4.75	0.01	DOWN	UP	Not regulated	Not regulated	UP	CodY, PutR, Spo0A	ResD	
17:	[cgs_D068_03270]												
	cds_D068_03270	BSU03330	Nitrate/nitrite transporter	-7.78	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	TnrA	ComK, GlnR	
18:	[cgs_D068_03520]												
	cds_D068_03520		Surfactin synthetase SrfAA	-5.48	6.96E-03	DOWN							
19:	[cgs_D068_03660]												
	cds_D068_03660	BSU23780	3-oxoacyl-[acyl-carrier protein] reductase EC 1.1.1.100; putative metabolite dehydrogenase, NAD-binding; Possible ortholog: BSn5_02410 from <i>Bacillus subtilis</i>	-25.64	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			
20:	[cgs_D068_03670]												
	cds_D068_03670	BSU23780	oxidoreductase, short-chain dehydrogenase/reductase family; short-chain dehydrogenase/reductase family; Possible ortholog: GYO_0717 from <i>Bacillus subtilis</i>	-8.8	9.33E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			

21: [cids_D068_04110; cids_D068_04100]											
cids_D068_04110	BSU33570	Emre; Ethidium bromide-methyl viologen resistance protein EmrE; spermidine export protein mdJ; Possible ortholog: BACAU_3793 from Bacillus	inf	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		
cids_D068_04100		Transcriptional regulator, TetR family; TetR family transcriptional regulator; Possible ortholog: BATR1942_06460 from Bacillus;		-2.9	0.81						
22: [cids_D068_04260]											
cids_D068_04260	BSU10850	Myo-inositol 2-dehydrogenase EC 1.1.1.18; putative inositol 2-dehydrogenase; Possible ortholog: BSUW23_02820 from Bacillus	inf	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		CodY, RocR
23: [cids_D068_04790]											
cids_D068_04790	BSU26340	Repressor cro-like [Bacteriophage A118]; BSn5_14575; putative xre family transcriptional; BSn5_14575; putative xre family transcriptional	inf	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	SknR	ComK
24: [cids_D068_04810]											
cids_D068_04810	BSU20670	Phage Rha protein; hypothetical protein; Possible ortholog: BSn5_14585 from Bacillus subtilis		-9.71	5.55E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	CodY, LevR, Zur
25: [cids_D068_04860; cids_D068_04850]											
cids_D068_04860		hypothetical protein; Possible ortholog: BAXH7_02364 from Bacillus		-92.4	1.37E-05	DOWN					DegU, HrcA
cids_D068_04850		hypothetical protein; hypothetical 6.8Kb protein; Possible ortholog: BSn5_14605 from Bacillus;	inf		0.25						
26: [cids_D068_04880]											
cids_D068_04880	BSU26270	unknown; LL3_00593; putative DNA-binding protein; skin; LL3_00593; putative DNA-binding protein; skin		-52.8	2.02E-05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	SknR
27: [cids_D068_04890]											
cids_D068_04890	BSU12530	Dnac: DNA replication protein DnaC; hypothetical protein; Possible ortholog: BAMTA208_11545 from Bacillus	inf	4.95E-07	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	Xre	CodY
28: [cids_D068_04910]											
cids_D068_04910		Hypothetical protein, Lmo2306 homolog from Bacteriophage A118; hypothetical protein; Possible ortholog: BSn5_14650 from Bacillus subtilis		-36.63	4.40E-03	DOWN					
29: [cids_D068_04940; cids_D068_04930; cids_D068_04920]											
cids_D068_04940		hypothetical protein; Possible ortholog: BAXH7_02356 from Bacillus	inf	2.98E-04	DOWN						BkdR
cids_D068_04930	BSU26240	hypothetical protein; BAXH7_02357; hypothetical protein; skin element;; BAXH7_02357; hypothetical protein; skin element;;	inf		0.24						
cids_D068_04920		hypothetical protein; Possible ortholog: BACAU_0576 from Bacillus;	inf		0.43						
30: [cids_D068_05010]											
cids_D068_05010		hypothetical protein; Uncharacterized protein yqgA; Possible ortholog: BAMF_0572 from Bacillus	inf	1.75E-03	DOWN						GlnR
31: [cids_D068_05030; cids_D068_05020]											
cids_D068_05030	BSU11930	hypothetical protein; Possible ortholog: BSU11930 from Bacillus subtilis	inf	5.47E-03	DOWN	Not regulated	Not regulated	Not regulated	UP		
cids_D068_05020		hypothetical protein; Possible ortholog: BSn5_14710 from Bacillus subtilis;		1	1						
32: [cids_D068_05050]											
cids_D068_05050		hypothetical protein; unknown; unknown	inf	0.02	DOWN						CcpA
33: [cids_D068_05070; cids_D068_05060]											
cids_D068_05070		Hypothetical protein; overlaps prophage gene, possible frameshift mutation;		-25.83	1.21E-04	DOWN					PurR, SigF
cids_D068_05060		hypothetical protein; unknown; unknown;	inf		0.15						
34: [cids_D068_05090]											
cids_D068_05090		Phage terminase small subunit; hypothetical protein; Possible ortholog: BACAU_1835 from Bacillus	inf	7.32E-10	DOWN						
35: [cids_D068_05220]											
cids_D068_05220	BSU26030	Phage tail length tape-measure protein; SPBc2 prophage-derived transglycosylase Yom; Possible ortholog: BACAU_1821 from		-111.55	1.09E-09	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	PurR
36: [cids_D068_05310]											
cids_D068_05310	BSU25910	FIG1237406: hypothetical protein; putative holin lysis protein; Possible ortholog: BACAU_0613 from Bacillus	inf	2.59E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		SigF
37: [cids_D068_05470]											
cids_D068_05470		hypothetical protein; unknown; unknown		-17.18	0.03	DOWN					DegU, GlnR
38: [cids_D068_05520]											
cids_D068_05520		conserved hypothetical protein;		-31.58	0.04	DOWN					SigF
39: [cids_D068_05950]											
cids_D068_05950	BSU06320	Cobalt-zinc-cadmium resistance protein; YeaB; Possible ortholog: BATR1942_00675 from Bacillus	inf	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		DegU, PucR

52: [cids_D068_10330]																				
cids_D068_10330	BSU10240	Ribonuclease Z EC 3.1.26.11; putative metal-dependent hydrolase; Possible ortholog: BATR1942_02730 from Bacillus	inf	-4.73	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated										CodY
53: [cids_D068_10380]																				
cids_D068_10380	BSU10290	peptidase, M48 family; putative membrane metalloprotease; Possible ortholog: BATR1942_02755 from Bacillus		-5.37	0.05	DOWN	Not regulated	Not regulated	Not regulated	UP										
54: [cids_D068_11530; cids_D068_11520; cids_D068_11510; cids_D068_11500]																				
cids_D068_11530	BSU11390	Oppb; Oligopeptide transport system permease protein OppB TC 3.A.1.5.1; AppB; Possible ortholog: BATR1942_03330 from Bacillus		-6.85	0.04	DOWN	Not regulated	Not regulated	Not regulated	UP										CodY, ScoC
cids_D068_11520	BSU11380	oppA; Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA TC 3.A.1.5.1; AppA; Possible ortholog: BATR1942_03325 from Bacillus;		1.05	0.23															
cids_D068_11510	BSU11370	oppF3; Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1; oligopeptide ABC transporter ATP-binding protein; Possible ortholog: BATR1942_03320 from Bacillus;		-3.22	0.6															
cids_D068_11500	BSU11360	oppD3; Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1; oligopeptide ABC transporter ATP-binding protein; Possible ortholog: BSn5_17590 from Bacillus subtilis;		-4.55	0.49															
55: [cids_D068_11550]																				
cids_D068_11550	BSU11410	FIG01234419: hypothetical protein; putative nucleic acid binding protein; Possible ortholog: BATR1942_03340 from Bacillus	inf		0.05	DOWN	Not regulated	Not regulated	UP	UP									SigF	TnrA
56: [cids_D068_11590; cids_D068_11580]																				
cids_D068_11590	BSU11440	OppB1; Oligopeptide transport system permease protein OppB TC 3.A.1.5.1; hypothetical protein; Possible ortholog: BATR1942_03355 from Bacillus		-4.36	0.04	DOWN	Not regulated	Not regulated	Not regulated	UP									ScoC, TnrA	SigH
cids_D068_11580	BSU11430	oppA1; Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA TC 3.A.1.5.1; oligopeptide ABC transporter binding lipoprotein; Possible ortholog: BATR1942_03350 from Bacillus;		-1.92	0.54															
57: [cids_D068_11830; cids_D068_11820]																				
cids_D068_11830	BSU11660	Thiamin-phosphate pyrophosphorylase EC 2.5.1.3; transcriptional regulator TenI; Possible ortholog: BATR1942_03475 from Bacillus		-6.14	5.31E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated										DegU
cids_D068_11820	BSU11650	Thiaminase II EC 3.5.99.2 involved in salvage of thiamin pyrimidine moiety; transcriptional activator TenA; Possible ortholog: BATR1942_03470 from Bacillus;		-3.82	0.19															
58: [cids_D068_12750]																				
cids_D068_12750	BSU12460	N-acetylmuramoyl-L-alanine amidase EC:3.5.1.28; BATR1942_03870; N-acetylmuramoyl-L-alanine amidase;; BATR1942_03870; N-acetylmuramoyl-L-alanine		-9.52	9.46E-04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated										
59: [cids_D068_12820; cids_D068_12810]																				
cids_D068_12820	BSU12520	Xkdb; Phage-like element PBSX protein xkdb; hypothetical protein; Possible ortholog: BATR1942_03900 from Bacillus		-42.5	4.93E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated									Xre	DegU, Xre
cids_D068_12810		hypothetical protein; Possible ortholog: BATR1942_03895 from Bacillus;		1	1															
60: [cids_D068_12870]																				
cids_D068_12870	BSU12560	RNA polymerase sigma-70 factor; positive control sigma-like factor; Possible ortholog: BATR1942_03930 from Bacillus	inf		2.71E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated										
61: [cids_D068_12880]																				
cids_D068_12880	BSU12570	Phage terminase small subunit; PBSX defective prophage terminase small subunit; Possible ortholog: BATR1942_03935 from Bacillus		-36.12	2.42E-06	DOWN	Not regulated	UP	Not regulated	Not regulated										Xpf
62: [cids_D068_13020]																				
cids_D068_13020	BSU12680	Phage tail length tape-measure protein; hypothetical protein; Possible ortholog: BSU12680 from Bacillus subtilis		-177.75	2.72E-11	DOWN	Not regulated	UP	Not regulated	Not regulated										Xre
63: [cids_D068_13420; cids_D068_13410; cids_D068_13400]																				
cids_D068_13420	BSU12990	NLP/P60 family protein; cell wall endopeptidase; Possible ortholog: BATR1942_04180 from Bacillus		-9.08	0.02	DOWN	Not regulated	Not regulated	UP	Not regulated									CodY	CodY
cids_D068_13410	BSU12980	Muconate cycloisomerase EC 5.5.1.1; L-Ala-D/L-Glu epimerase; Possible ortholog: BATR1942_04175 from Bacillus;		-5.93	0.13															
cids_D068_13400	BSU12970	Muramoyltetrapeptide carboxypeptidase EC 3.4.17.13; putative L,D-carboxypeptidase; Possible ortholog: BATR1942_04170 from Bacillus;		-5.09	0.23															
64: [cids_D068_14060; cids_D068_14050; cids_D068_14040]																				

cds_D068_14060	BSU13610	Methylthioribulose-1-phosphate dehydratase EC 4.2.1.109; methylthioribulose-1-phosphate dehydratase; Possible ortholog: BATR1942_04560 from Bacillus	-3.8	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	BkdR, SpoIIID
cds_D068_14050	BSU13600	2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate phosphatase related protein; 2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate; Possible ortholog: BATR1942_04555 from Bacillus;	-2.91	0.13						
cds_D068_14040	BSU13590	2,3-diketo-5-methylthiopentyl-1-phosphate enolase; Possible ortholog: BATR1942_04550 from Bacillus;	-3.83	0.06						
65: [cgs_D068_14100; cds_D068_14090]										
cds_D068_14100	BSU13650	small membrane protein; putative small membrane protein; Possible ortholog: BATR1942_04580 from Bacillus	inf	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	AbrB, Rok, SigB
cds_D068_14090	BSU13640	Spo0E regulatory protein, specific dephosphorylation of Spo0A-P stage 0 sporulation; BATR1942_04575; negative regulatory phosphatase; BATR1942_04575; negative regulatory phosphatase;	inf	0.11						
66: [cgs_D068_16310; cds_D068_16300; cds_D068_16290; cds_D068_16280; cds_D068_16270; cds_D068_16260; cds_D068_16250]										
cds_D068_16310	BSU15710	PriA; Helicase PriA essential for oriC/DnaA-independent DNA replication; primosome assembly protein PriA; Possible ortholog: BATR1942_05650 from Bacillus	-5.57	8.14E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	SigF
cds_D068_16300	BSU15700	Phosphopantothencycysteine decarboxylase EC 4.1.1.36 / Phosphopantothencycysteine synthetase EC 6.3.2.5; BATR1942_05645; Coenzyme A biosynthesis bifunctional protein CoaBC; phosphopantothencycysteine; BATR1942_05645; Coenzyme A biosynthesis; DNA-directed RNA polymerase omega subunit EC 2.7.7.6; BATR1942_05640; DNA-directed RNA polymerase subunit; BATR1942_05640; DNA-directed RNA polymerase;	-2.63	0.23						
cds_D068_16290	BSU15690	Guanylate kinase EC 2.7.4.8; guanylate kinase; Possible ortholog: BATR1942_05635 from Bacillus;	-1.65	1						
cds_D068_16280	BSU15680	FIG003307: hypothetical protein; UPF0296 protein yizA; Possible ortholog: LL3_01727 from Bacillus;	1.37	0.02						
cds_D068_16270	BSU15670	yicC; Protein YicC; hypothetical protein; Possible ortholog: BATR1942_05625 from Bacillus;	-1.27	0.51						
cds_D068_16260	BSU15660	Ca ion P-type ATPase; P-type calcium transport ATPase; Possible ortholog: BATR1942_05620 from Bacillus;	-1.02	0.19						
cds_D068_16250	BSU15650	BATR1942_05620 from Bacillus;	-5.49	0.49						
67: [cgs_D068_16610]										
cds_D068_16610	BSU16010	FIG01228237: hypothetical protein; YlqD; Possible ortholog: BATR1942_05795 from Bacillus	-5.6	2.76E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	
68: [cgs_D068_16900; cds_D068_16890; cds_D068_16880; cds_D068_16870; cds_D068_16860; cds_D068_16850; cds_D068_16840; cds_D068_16830; cds_D068_16820; cds_D068_16810; cds_D068_16800; cds_D068_16790; cds_D068_16780]										
cds_D068_16900		FliB; Flagellar protein FliB; putative flagellar protein; Possible ortholog: BATR1942_05945 from Bacillus	-4.66	0.01	DOWN					CodY, SigD, Spo0A
cds_D068_16890	BSU16290	flgG; Flagellar basal-body rod protein FlgG; flagellar basal body rod protein FlgG; Possible ortholog: BATR1942_05940 from Bacillus;	-4.03	0.03						DegU
cds_D068_16880	BSU16280	flgD; Flagellar basal-body rod modification protein FlgD; flagellar basal body rod modification protein; Possible ortholog: BATR1942_05935 from Bacillus;	-3.4	0.06						
cds_D068_16870	BSU16270	fliK; Flagellar hook-length control protein FliK; flagellar hook-length control protein; Possible ortholog: BATR1942_05930 from Bacillus;	-2.14	0.41						
cds_D068_16860	BSU16260	fliB; Flagellar protein FliB; putative kinesin-like protein; Possible ortholog: BATR1942_05925 from Bacillus;	-2.81	0.15						
cds_D068_16850	BSU16250	fliJ; Flagellar protein FliJ; flagellar biosynthesis chaperone; Possible ortholog: BATR1942_05920 from Bacillus;	-3.01	0.11						
cds_D068_16840	BSU16240	ATP synthase beta chain EC 3.6.3.14; flagellum-specific ATP synthase; Possible ortholog: BATR1942_05915 from Bacillus;	-2.93	0.13						
cds_D068_16830	BSU16230	fliH; Flagellar assembly protein FliH; flagellar assembly protein H; Possible ortholog: BATR1942_05910 from Bacillus;	-3.76	0.05						
cds_D068_16820	BSU16220	fliG; Flagellar motor switch protein FliG; flagellar motor switch protein G; Possible ortholog: BATR1942_05905 from Bacillus;	-3.28	0.08						
cds_D068_16810	BSU16210	fliF; Flagellar M-ring protein FliF; flagellar M-ring protein; Possible ortholog: BATR1942_05900 from Bacillus;	-3.05	0.1						
cds_D068_16800	BSU16200	fliE; Flagellar hook-basal body complex protein FliE; flagellar hook-basal body protein FliE; Possible ortholog: BATR1942_05895 from Bacillus;	-3.19	0.08						
cds_D068_16790	BSU16190	flgC; Flagellar basal-body rod protein FlgC; flagellar basal body rod protein FlgC; Possible ortholog: BATR1942_05890 from Bacillus;	-2.42	0.25						

		flgB; Flagellar basal-body rod protein FlgB; flagellar basal body rod protein FlgB; Possible ortholog: BATR1942_05885 from Bacillus;	-1.26	0.58									
69: [cgs_D068_17140]													
		Undecaprenyl pyrophosphate synthetase EC 2.5.1.31; undecaprenyl pyrophosphate synthase; Possible ortholog: BATR1942_06065 from Bacillus	-3.69	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			AbrB, GlnR, SigF	
70: [cgs_D068_17220; cgs_D068_17210; cgs_D068_17200]													
		COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination; YlxR; Possible ortholog: BATR1942_06110 from Bacillus nusA; Transcription termination protein NusA; transcription elongation factor NusA; Possible ortholog: BATR1942_06105 from Bacillus;	-4.03	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		YwaC	SpolIID	
			-2.03	0.49									
		COG0779: clustered with transcription termination protein NusA; hypothetical protein; Possible ortholog: BATR1942_06100 from Bacillus;	-1.54	0.98									
71: [cgs_D068_17520; cgs_D068_17510; cgs_D068_17500]													
		CDP-diacylglycerol-glycerol-3-phosphate 3- phosphatidyltransferase EC 2.7.8.5; CDP- diacylglycerol-glycerol-3-phosphate; Possible ortholog: BATR1942_06260 from Bacillus	-8.42	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			DegU	
		Transcriptional regulator in cluster with unspecified monosaccharide ABC transport system; hypothetical protein; Possible ortholog: BATR1942_06255 from Bacillus; ACT domain protein; hypothetical protein; Possible ortholog: BATR1942_06250 from Bacillus;	1.58	0.03									
			-1.33	0.59									
72: [cgs_D068_17860; cgs_D068_17850; cgs_D068_17840; cgs_D068_17830; cgs_D068_17820; cgs_D068_17810; cgs_D068_17800]													
		Bat2; polyketide synthase of type I; Possible ortholog: BATR1942_06400 from Bacillus bat1, Long-chain-fatty-acid-CoA ligase EC 6.2.1.3; polyketide synthase of type I; Possible ortholog: BATR1942_06395 from Bacillus;	-3.78	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated			ResD	
			-4.01	0.04									
		batE; Enoyl-CoA hydratase EC 4.2.1.17; polyketide biosynthesis enoyl-CoA hydratase; Possible ortholog: BATR1942_06390 from Bacillus;	-5.5	0.01	-								
		batD; Methylglutaconyl-CoA hydratase EC 4.2.1.18; polyketide biosynthesis enoyl-CoA hydratase; Possible ortholog: BATR1942_06385 from Bacillus;	-9.69	1.19E-03	-								
		batC; Hydroxymethylglutaryl-CoA synthase EC 2.3.3.10; acetyl-S-AcpK beta- ketothioester polyketide; Possible ortholog: BATR1942_06380 from Bacillus;	-10.9	2.01E-04	-								
		batB; 3-oxoacyl-[acyl-carrier-protein] synthase, KASII EC 2.3.1.41; polyketide beta- ketoacyl:acyl carrier protein; Possible ortholog: BATR1942_06375 from Bacillus; batA; Acyl carrier protein; acyl carrier protein; Possible ortholog: BATR1942_06370 from Bacillus;	-5.31	5.73E-03	-								
			-5.51	0.03	-								
73: [cgs_D068_18000]													
		unknown; Ymaf; Possible ortholog: BATR1942_06470 from Bacillus	inf	0.05	DOWN	Not regulated	Not regulated	UP	UP				
74: [cgs_D068_18410; cgs_D068_18400]													
		DNA polymerase IV EC 2.7.7.7; lesion bypass phage DNA polymerase; Possible ortholog: BAXH7_01248 from Bacillus BAXH7_01247; hypothetical protein; phage SPbeta;; BAXH7_01247; hypothetical protein; phage SPbeta;;	-116.25	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		LexA	LexA	
			1	1									
75: [cgs_D068_19950]													
		Endo-1,4-beta-xylanase A precursor EC 3.2.1.8; endo-1,4-beta-xylanase xylanase D; Possible ortholog: BATR1942_07120 from Bacillus	-14.5	7.58E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		AbrB	CodY, DegU	
76: [cgs_D068_20095; cgs_D068_20150a; cgs_D068_20150]													
		PipC, Long-chain-fatty-acid-CoA ligase EC 6.2.1.3; pipastatin synthetase	-4.55	0.03	DOWN							CodY, DegU, GlnR, PerR	
77: [cgs_D068_20440; cgs_D068_20450]													
		hypothetical protein; Possible ortholog: BAXH7_02352 from Bacillus	inf	0.02	DOWN								
		hypothetical protein; Possible ortholog: Bsn5_14675 from Bacillus subtilis;	inf	0.77									
78: [cgs_D068_20590]													
		Long-chain-fatty-acid-CoA ligase EC 6.2.1.3; Mycosubtilin synthase subunit C; Possible ortholog: BATR1942_07345 from Bacillus	-4.58	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		Abh, CodY, ComA, PerR, Spx	LevR	
79: [cgs_D068_21820]													

			Acetyl-coenzyme A carboxyl transferase beta chain EC 6.4.1.2; acetyl-CoA carboxylase subunit beta; Possible ortholog: BATR1942_12390 from Bacillus;	-2.69	0.15									
93:	[cgs_D068_29590]													
			Non-heme chloroperoxidase EC 1.11.1.10; bromoperoxidase; Possible ortholog: BATR1942_12570 from Bacillus	-22.4	1.81E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				SigG
94:	[cgs_D068_29690]													
			Glyoxalase family protein; putative dioxxygenase; Possible ortholog: BATR1942_12615 from Bacillus	-23.92	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				MhqR, SigB
95:	[cgs_D068_30030; cgs_D068_30040; cgs_D068_30050]													
			Transcription regulator containing diacylglycerol kinase catalytic domain; putative phospholipid kinase; Possible ortholog: BATR1942_12775 from Bacillus	-4.16	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				
			FIG01233842: hypothetical protein; putative hydrolase; Possible ortholog: BATR1942_12780 from Bacillus;	-2.45	0.31									
			2'-5' RNA ligase; Possible ortholog: BATR1942_12785 from Bacillus;	-1.65	1									
96:	[cgs_D068_30330]													
			FIG01232743: hypothetical protein; putative hydrolase; Possible ortholog: BATR1942_12915 from Bacillus	inf	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				
97:	[cgs_D068_31080; cgs_D068_31090]													
			Glucose-1-phosphate adenylyltransferase EC 2.7.7.27; glucose-1-phosphate adenylyltransferase; Possible ortholog: BATR1942_13290 from Bacillus	-23.41	0.02	DOWN	Not regulated	Not regulated	UP	UP				SigE CcpA, ComK
			1,4-alpha-glucan glycogen branching enzyme, GH-13-type EC 2.4.1.18; glycogen branching enzyme; Possible ortholog: BATR1942_13295 from Bacillus;	-13.22	0.09									
98:	[cgs_D068_31320; cgs_D068_31330]													
			UDP-N-acetylmuramoylalanine-D-glutamyl-2,6-diamino pimelate--D-alanyl-D-alanine ligase EC 6.3.2.10; UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine; Possible ortholog: BATR1942_21020 from Bacillus	-4.11	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				SigM
			D-alanine--D-alanine ligase A EC 6.3.2.4; D-alanyl-alanine synthetase A; Possible ortholog: BATR1942_21015 from Bacillus;	1.15	0.07									
99:	[cgs_D068_31430]													
			Aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate, succinate; C4-dicarboxylate transporter DctA; Possible ortholog: BATR1942_20965 from Bacillus	-14.22	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				CcpA, FsrA CcpA, Zur
100:	[cgs_D068_31640; cgs_D068_31650; cgs_D068_31660; cgs_D068_31670]													
			glycosyl transferase, group 2 family protein; putative glycosyltransferase associated to biofilm; Possible ortholog: BATR1942_20880 from Bacillus	-18.99	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				
			FIG01238801: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_20875 from Bacillus;	-23.8	7.25E-03	-								
			GGDEF domain protein; putative membrane protein with diguanylate cyclase; Possible ortholog: BATR1942_20870 from Bacillus;	-13.26	0.05									
			FIG01227714: hypothetical protein; putative glycosyl hydrolase lipoprotein; Possible ortholog: BATR1942_20865 from Bacillus;	-11.03	0.14									
101:	[cgs_D068_31750]													
			FIG01101636: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_20830 from Bacillus	-88.37	4.64E-03	DOWN								CcpA
102:	[cgs_D068_32010; cgs_D068_32020]													
			PTS system, mannitol-specific IIA component EC 2.7.1.69; Mannitol-specific phosphotransferase enzyme IIA; Possible ortholog: BATR1942_20705 from Bacillus	inf	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				CcpA, ResD
			PTS system, mannitol-specific IIB component EC 2.7.1.69 / PTS system, mannitol-specific IIC component EC 2.7.1.69; hypothetical protein; Possible ortholog: BATR1942_20700 from Bacillus;	-90.05	0.07									
103:	[cgs_D068_32080]													
			glucose uptake protein; GlcU; Possible ortholog: BATR1942_20670 from Bacillus	inf	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				SigG, SpoVT MntR, SigG, Xre
104:	[cgs_D068_32270; cgs_D068_32260]													
			ABC transporter, permease protein; hypothetical protein; Possible ortholog: BSU03740 from Bacillus subtilis	inf	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated				YclJ
			hypothetical protein;	1	1									

	cds_D068_38300	BSU36240	Manganese-dependent protein-tyrosine phosphatase EC 3.1.3.48 epsD; Tyrosine-protein kinase EpsD EC 2.7.10.2;		-9.21	7.12E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	AbrB	CcpA, DegU, RocR
	cds_D068_38310	BSU36250	2.7.10.2;		-8.14	0.03	-						
	cds_D068_38320	BSU36260	epsC1; Tyrosine-protein kinase transmembrane modulator EpsC;		-2.83	0.49							
127:	[cds_D068_38340]												
	cds_D068_38340	BSU36270	FIG01230320: hypothetical protein		-6.96	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		
128:	[cds_D068_38500; cds_D068_38490]												
	cds_D068_38500	BSU36450	major facilitator family transporter		-4.23	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		
	cds_D068_38490	BSU36440	Transcriptional regulator, MarR family;		-1.79	0.89							
129:	[cds_D068_38680; cds_D068_38670; cds_D068_38660; cds_D068_38650; cds_D068_38640]												
	cds_D068_38680	BSU37850	Pseudaminic acid cytidyltransferase EC 2.7.7.43 spsF; Spore coat polysaccharide biosynthesis protein spsF;		-24.76	0.01	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	SigE, SigK	SigK
	cds_D068_38670	BSU37860	PglE; Bacillosamine/Legionaminic acid biosynthesis aminotransferase PglE; 4-keto-6-deoxy-N-Acetyl-D-hexosaminyL-lipid carrier		-10.31	0.08							
	cds_D068_38660	BSU37890	aminotransferase;		-6.34	0.16							
	cds_D068_38650	BSU37830	UDP-glucose 4-epimerase EC 5.1.3.2;		-10.52	0.14							
130:	[cds_D068_38780; cds_D068_38790]												
	cds_D068_38780	BSU36650	Urease beta subunit EC 3.5.1.5		-7.07	2.32E-03	DOWN	Not regulated	Not regulated	UP	Not regulated	CodY, GlnR, PucR, SigH, TnrA	DegU
	cds_D068_38790	BSU36660	Urease gamma subunit EC 3.5.1.5;		-6.55	0.01	-					CodY, GlnR, PucR, SigH, TnrA	
131:	[cds_D068_39120]												
	cds_D068_39120	BSU36950	YrdC; YrdC/Sua5 family protein, required for threonylcarbamoyladenosine t6A formation in tRNA		-4.85	0.05	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	DnaA	
132:	[cds_D068_39480]												
	cds_D068_39480	BSU37280	Respiratory nitrate reductase alpha chain EC 1.7.99.4		-27.35	0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	Fnr	FNR, SigW
133:	[cds_D068_39950]												
	cds_D068_39950	BSU37750	FIG01240693: hypothetical protein	inf		0.04	DOWN	Not regulated	Not regulated	Not regulated	UP		GlnR, TnrA
134:	[cds_D068_40170; cds_D068_40180; cds_D068_40190]												
	cds_D068_40170	BSU38040	Sucrose-6-phosphate hydrolase EC 3.2.1.26		-57.73	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	CcpA	BkdR
	cds_D068_40180	BSU38050	PTS system, sucrose-specific IIB component EC 2.7.1.69 / PTS system, sucrose-specific IIC component EC 2.7.1.69;	inf		2.66E-03	-						
	cds_D068_40190		hypothetical protein;		1	1							
135:	[cds_D068_40930; cds_D068_40940]												
	cds_D068_40930	BSU38690	YxlC; Uncharacterized protein yxlC		-6.04	0.04	DOWN	Not regulated	Not regulated	UP	Not regulated	SigY	AbrB, DegU
	cds_D068_40940	BSU38700	RNA polymerase sigma-70 factor;		-2.58	0.46						SigY	
136:	[cds_D068_41580]												
	cds_D068_41580	BSU18650	Pectin lyase EC 4.2.2.10	inf		0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		
137:	[cds_D068_41670; cds_D068_41680]												
	cds_D068_41670	BSU39260	Beta-glucosidase EC 3.2.1.21; 6-phospho-beta-glucosidase EC 3.2.1.86		-3.45	0.05	DOWN	Not regulated	Not regulated	UP	Not regulated	CcpA	
	cds_D068_41680	BSU39270	PTS system, beta-glucoside-specific IIB component EC 2.7.1.69 / PTS system, beta-glucoside-specific IIC component EC 2.7.1.69 / PTS system, beta-glucoside-specific IIA component EC 2.7.1.69;		-7.95	0.07						CcpA	
138:	[cds_D068_41700; cds_D068_41710; cds_D068_41720; cds_D068_41730]												
	cds_D068_41700		FIG01249520: hypothetical protein		-5.53	2.35E-03	DOWN						
	cds_D068_41710	BSU37740	FIG01225345: hypothetical protein;		-2.57	0.23						AbrB, CodY, ScoC	
	cds_D068_41720	BSU37710	FIG01233033: hypothetical protein;		-3.78	0.04							
	cds_D068_41730	BSU18770	Permease of the drug/metabolite transporter DMT superfamily;		-6.11	8.48E-04	-						
139:	[cds_D068_41790; cds_D068_41780]												
	cds_D068_41790	BSU39360	Urocanate hydratase EC 4.2.1.49		-45.16	0.02	DOWN	Not regulated	Not regulated	UP	Not regulated	CcpA, CodY	
	cds_D068_41780	BSU39350	Histidine ammonia-lyase EC 4.3.1.3;		-38.59	0.06							
140:	[cds_D068_42000; cds_D068_42010; cds_D068_42020]												
	cds_D068_42000	BSU39620	DUF1093 domain-containing protein yvcS2; ABC transporter permease protein	inf		0.04	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	YxdJ	
	cds_D068_42010	BSU39630	YvcS;		-6.71	0.08							
	cds_D068_42020	BSU39640	yvcR2; ABC transporter ATP-binding protein YvcR;		-8.62	0.25							
141:	[cds_D068_42080; cds_D068_42090; cds_D068_42100; cds_D068_42110; cds_D068_42120; cds_D068_42130; cds_D068_42140; cds_D068_42150; cds_D068_42160]												
	cds_D068_42080	BSU39680	Inosose isomerase EC 5.3.99.- Glyceraldehyde-3-phosphate ketol-isomerase EC 5.3.1.1;		-29.99	0.03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	CcpA, IolR	CcpA
	cds_D068_42090	BSU39690			-4.86	0.44							
	cds_D068_42100	BSU39700	Myo-inositol 2-dehydrogenase 1 EC 1.1.1.18;		-5.26	0.2							
	cds_D068_42110	BSU39710	IolF; Minor myo-inositol transporter IolF;		-8.49	0.03	-						
	cds_D068_42120	BSU39720	Inosose dehydratase EC 4.2.1.44;		-3.53	0.18							
	cds_D068_42130	BSU39730	Epi-inositol hydrolase EC 3.7.1.-;		-4.62	0.14							
	cds_D068_42140	BSU39740	5-keto-2-deoxygluconokinase EC 2.7.1.92;		-4.65	0.14							
	cds_D068_42150	BSU39750	5-deoxy-gluconate isomerase EC 5.3.1.-; Methylmalonate-semialdehyde dehydrogenase, inositol metabolism EC 1.2.1.27;		-3.24	0.31							
	cds_D068_42160	BSU39760			-1.63	0.89							
142:	[cds_D068_42360; cds_D068_42370]												
	cds_D068_42360	BSU40040	Glycerate kinase EC 2.7.1.31		-5.69	0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	AbrB	
	cds_D068_42370		D-glycerate transporter predicted;		-9.58	0.08							
143:	[cds_D068_42470]												
	cds_D068_42470	BSU05620	D-serine/D-alanine/glycine transporter	inf		0.02	DOWN	Not regulated	Not regulated	Not regulated	Not regulated		SigH

144: [cds_D068_42630] cgs_D068_42630	BSU40280	unknown	inf	0.04	DOWN	Not regulated	Not regulated	UP	Not regulated	PhoP	DegU
145: [cgs_D068_42660] cgs_D068_42660	BSU40330	RocE; Arginine permease RocE		-3.76	0.03	DOWN	Not regulated	Not regulated	Not regulated	AhrC, CodY, RocR, SigL, Spo0A	
146: [cgs_D068_42730; cds_D068_42740; cds_D068_42750; cds_D068_42760] cgs_D068_42730 cgs_D068_42740 cgs_D068_42750 cgs_D068_42760	BSU05950 BSU39930 BSU27540	ABC transporter, ATP-binding protein transport protein; FIG01239712: hypothetical protein; thIF; Sulfur carrier protein adenylyltransferase ThIF;		-4.45 -2.76 -23.9	9.66E-03 0.38 0.14	DOWN	Not regulated	Not regulated	Not regulated	AbrB, CodY	GitC, GitR
147: [cgs_D068_43050] cgs_D068_43050	BSU40630	FIG01244235: hypothetical protein		-38.24	0.02	DOWN	Not regulated	Not regulated	Not regulated	UP	SigE
148: [cgs_D068_43360; cds_D068_43370] cgs_D068_43360 cgs_D068_43370	BSU40930	Anaerobic dehydrogenases, typically selenocysteine-containing FIG001891: protein involved in chromosome partitioning;	inf	-21.43	6.23E-03	DOWN	Not regulated	Not regulated	Not regulated	Not regulated	DegU, TnrA
149: [cgs_D068_00020] cgs_D068_00020	BSU00020	DNA polymerase III beta subunit EC 2.7.7.7		2.17	3.74E-04	UP	Not regulated	Not regulated	DOWN	Not regulated	Spo0A SigH
150: [cgs_D068_01940] cgs_D068_01940	BSU33400	oxidoreductase of aldo/keto reductase family, subgroup 1		2.02	8.44E-04	UP	Not regulated	Not regulated	Not regulated	DOWN	SigB, SinR DegU
151: [cgs_D068_03770] cgs_D068_03770	BSU05120	CspA; Cold shock protein CspA; cold-shock protein; Possible ortholog: BATR1942_00145 from Bacillus		4.28	5.72E-07	UP	Not regulated	Not regulated	Not regulated	Not regulated	Fur
152: [cgs_D068_04680] cgs_D068_04680	BSU05960	Moac; Molybdenum cofactor biosynthesis protein MoaC; molybdenum cofactor biosynthesis protein MoaC; Possible ortholog: BATR1942_00500 from Bacillus		2.03	5.44E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	
153: [cgs_D068_04730] cgs_D068_04730	BSU06010	CAAX amino terminal protease family protein; putative membrane protease; Possible ortholog: BATR1942_00525 from Bacillus		2.1	3.72E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated	
154: [cgs_D068_05350] cgs_D068_05350		hypothetical protein; Possible ortholog: Bsn5_14910 from Bacillus subtilis		3.82	2.80E-05	UP					
155: [cgs_D068_05370] cgs_D068_05370	BSU19890	unknown; hypothetical protein; Possible ortholog: BSU19890 from Bacillus subtilis		3.02	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	
156: [cgs_D068_05910] cgs_D068_05910	BSU06290	YeaA; conserved protein YeaA; hypothetical protein; Possible ortholog: BATR1942_00655 from Bacillus		2.68	3.37E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigE, SigW SigW
157: [cgs_D068_07460] cgs_D068_07460	BSU07680	FIG01242431: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_01445 from Bacillus		5.32	3.34E-08	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigB Xre
158: [cgs_D068_07470] cgs_D068_07470	BSU07690	Methionine aminopeptidase EC 3.4.11.18; methionine aminopeptidase; Possible ortholog: BATR1942_01450 from Bacillus		2.31	1.80E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	
159: [cgs_D068_08500] cgs_D068_08500	BSU08620	Hypothetical protein SAV1869; YfhP; Possible ortholog: BATR1942_01880 from Bacillus		2.29	5.58E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	
160: [cgs_D068_08570] cgs_D068_08570	BSU08680	CysteinyI-tRNA synthetase related protein; hypothetical protein; Possible ortholog: BATR1942_01915 from Bacillus		2.57	5.30E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated	
161: [cgs_D068_08620] cgs_D068_08620	BSU08730	Perr; Peroxide stress regulator PerR, FUR family; PerR; Possible ortholog: BATR1942_01940 from Bacillus		3.19	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	PerR Fur, PerR
162: [cgs_D068_08690; cds_D068_08700] cgs_D068_08690	BSU26950	Spore coat protein F; putative spore coat protein; Possible ortholog: BATR1942_01975 from Bacillus; overlaps CDS with the same product name, possible frameshift mutation; inf	inf		0.04	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigG BkdR
163: [cgs_D068_09280] cgs_D068_09280	BSU09300	Aerobic glycerol-3-phosphate dehydrogenase EC 1.1.5.3; glycerol-3-phosphate dehydrogenase; Possible ortholog: BATR1942_02250 from Bacillus		5.47	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	AbrB, CcpA SigF, SigK
164: [cgs_D068_09360] cgs_D068_09360	BSU09380	NsrR; Nitrite-sensitive transcriptional repressor NsrR; NO-dependent activator of the ResDE regulon; Possible ortholog: BATR1942_02290 from Bacillus		5.36	6.61E-07	UP	Not regulated	Not regulated	Not regulated	Not regulated	

165: [cgs_D068_09830; cds_D068_09820]											
cgs_D068_09830	BSU09800	Hypothetical protein SAV1845; hypothetical protein; Possible ortholog: BATR1942_02520 from Bacillus	2.12	2.70E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		
cgs_D068_09820	BSU09790	Hypothetical protein SAV1846; hypothetical protein; Possible ortholog: BATR1942_02515 from Bacillus;	-1.1	0.24							
166: [cgs_D068_09870]											
cgs_D068_09870		Siderophore biosynthesis protein, monooxygenase; putative lysine/ornithine N-monooxygenase; Possible ortholog: BATR1942_02540 from Bacillus	2.21	1.04E-04	UP						SigB, SigF, TnrA
167: [cgs_D068_10010; cds_D068_10020]											
cgs_D068_10010		FIG01227217: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_02605 from Bacillus	2.15	5.88E-04	UP						
cgs_D068_10020	BSU09960	Hypothetical protein SAV1840; putative bacteriocin; Possible ortholog: BATR1942_02610 from Bacillus;	1.6	0.01							
168: [cgs_D068_10450]											
cgs_D068_10450	BSU10340	Predicted broad substrate specificity phosphatase; phosphatase; Possible ortholog: BATR1942_02790 from Bacillus	3.08	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		
169: [cgs_D068_11280; cds_D068_11270]											
cgs_D068_11280	BSU11160	probably aromatic ring hydroxylating enzyme, evidenced by COGnitor; PaaD-like protein DUF59 involved in Fe-S cluster assembly; hypothetical protein; Possible ortholog: BATR1942_03205 from Bacillus	3.1	9.88E-06	UP	Not regulated	Not regulated	Not regulated	Not regulated		SigA
cgs_D068_11270	BSU11150	Putative hydrolase of the alpha/beta superfamily; putative hydrolase; Possible ortholog: BATR1942_03200 from Bacillus;	-2.22	0.67							
170: [cgs_D068_11660]											
cgs_D068_11660	BSU11500	Arsenate reductase family protein; transcriptional regulator Spx; Possible ortholog: BAXH7_02421 from Bacillus	5.13	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		PerR, SigB, SigM, SigW, SigX
171: [cgs_D068_11680]											
cgs_D068_11680	BSU11520	Meca; Negative regulator of genetic competence Meca; adaptor protein; Possible ortholog: BATR1942_03400 from Bacillus	4.48	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		DegU, HrcA, SigB
172: [cgs_D068_11720; cds_D068_11730]											
cgs_D068_11720	BSU11550	YjbH-like, GTP pyrophosphokinase domain; YjbH; Possible ortholog: BATR1942_03420 from Bacillus	2.57	5.48E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated		
cgs_D068_11730	BSU11560	hbO; Hemoglobin-like protein HbO; putative thiol management oxidoreductase component; Possible ortholog: BATR1942_03425 from Bacillus;	1.7	2.79E-03	+						
173: [cgs_D068_12440]											
cgs_D068_12440	BSU12150	YjgB; Uncharacterized protein yjgB precursor; YjgB; Possible ortholog: BATR1942_03725 from Bacillus	5.27	1.53E-08	UP	Not regulated	Not regulated	Not regulated	Not regulated		SigB, SigF
174: [cgs_D068_12700; cds_D068_12710]											
cgs_D068_12700	BSU12410	FIG01232970: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_03850 from Bacillus	3.2	1.22E-05	UP	DOWN	Not regulated	Not regulated	DOWN		
cgs_D068_12710		hypothetical protein;	inf	0.77							
175: [cgs_D068_13310]											
cgs_D068_13310		unknown; unknown	2.73	1.09E-05	UP						SigB
176: [cgs_D068_13460]											
cgs_D068_13460	BSU13030	Acyl-CoA hydrolase EC 3.1.2.20; YkhA; Possible ortholog: BATR1942_04200 from Bacillus	2.06	8.47E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		
177: [cgs_D068_13590]											
cgs_D068_13590	BSU13150	Organic hydroperoxide resistance transcriptional regulator; OhrR; Possible ortholog: BATR1942_04265 from Bacillus	2.59	2.05E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated		DegU
178: [cgs_D068_13790]											
cgs_D068_13790	BSU13310	transcriptional regulator	5.04	7.74E-06	UP	Not regulated	Not regulated	Not regulated	Not regulated	GlnR, TnrA	AbrB, ComK, GlnR, TnrA
179: [cgs_D068_13940]											
cgs_D068_13940	BSU13490	heat shock protein HtpX	2.02	8.27E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	Rok, YkrK	DegU
180: [cgs_D068_14120]											
cgs_D068_14120	BSU13670	Transcriptional regulator, MarR family; transcriptional regulator MarR family protein; Possible ortholog: BATR1942_04590 from Bacillus	2.44	8.47E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated		
181: [cgs_D068_14700]											
cgs_D068_14700	BSU14220	Alkyl hydroperoxide reductase subunit C-like protein; putative 2-cys peroxiredoxin; Possible ortholog: BATR1942_04875 from Bacillus	3.06	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	AbrB	FNR, GltC, RocR, SigA
182: [cgs_D068_14890]											
cgs_D068_14890	BSU14410	Signal peptidase I EC 3.4.21.89; type I signal peptidase; Possible ortholog: BATR1942_04970 from Bacillus	2.58	1.06E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	DegU	CodY

183: [cds_D068_14960]			Abh; Putative transition state regulator Abh; transcriptional regulator; Possible ortholog: BATR1942_05005 from Bacillus	3.09	2.18E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigM, SigX	SigW, SigX
184: [cds_D068_15170]			FIG01108286: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_05100 from Bacillus	2.6	5.69E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated		
185: [cds_D068_15630]			COG1399 protein in cluster with ribosomal protein L32p, Firmicutes subfamily; hypothetical protein; Possible ortholog: BATR1942_05325 from Bacillus	2.45	0	UP	Not regulated	Not regulated	DOWN	Not regulated	YwaC	CodY, DegU, SigA
186: [cds_D068_15980; cds_D068_15970; cds_D068_15960; cds_D068_15950]			YggT; Integral membrane protein YggT, involved in response to extracytoplasmic stress osmotic shock; YlmG; Possible ortholog: BATR1942_05495 from Bacillus	2.49	1.17E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated	Spo0A	
			FIG001960: FtsZ-interacting protein related to cell division; cell division machinery factor; Possible ortholog: BATR1942_05490 from Bacillus;	1.32	0.05							
			Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC; hypothetical protein; Possible ortholog: BATR1942_05485 from Bacillus;	-1.37	0.77							
			FIG01197458: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_05480 from Bacillus;	-2.42	0.25							
187: [cds_D068_17100]			SSU ribosomal protein S2p SAe; 30S ribosomal protein S2; Possible ortholog: BATR1942_06045 from Bacillus	2.13	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	YwaC	DegU
188: [cds_D068_17660; cds_D068_17650; cds_D068_17640]			YMCA protein; master regulator for biofilm formation; Possible ortholog: BATR1942_06315 from Bacillus	2.54	3.31E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		DegU
			tRNA- <i>i</i> 6A37 methyltransferase; dimethylallyladenine tRNA methyltransferase;	1.03	0.21							
			Chloramphenicol acetyltransferase EC 2.3.1.28; hypothetical protein; Possible ortholog: BATR1942_06305 from Bacillus;	-1.35	0.46							
189: [cds_D068_17910]			FIG01239751: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_06425 from Bacillus	2.67	1.50E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated	AbrB, SigB	CodY, RocR
190: [cds_D068_19520]			FIG01228874: hypothetical protein; putative integral inner membrane protein; Possible ortholog: BATR1942_06940 from Bacillus	2.04	2.62E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated		
191: [cds_D068_19610; cds_D068_19600]			Yoxg; alternate gene name: yoxG; unknown; unknown	2.09	1.01E-03	UP					Spo0A	PerR
			yoxF; alternate gene name: yoxF; hypothetical protein; Possible ortholog: BATR1942_06980 from Bacillus;	1.35	0.04							
192: [cds_D068_19650; cds_D068_19640; cds_D068_19630]			FIG01108097: hypothetical protein; putative integral inner membrane protein; Possible ortholog: BATR1942_07005 from Bacillus	2.21	6.92E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		
			Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY; hypothetical protein; Possible ortholog: BATR1942_07000 from Bacillus;	-2.54	0.68							
			ccdA; Cytochrome c-type biogenesis protein CcdA DsbD analog; cytochrome c-type biogenesis protein CcdA; Possible ortholog: BATR1942_06995 from Bacillus;	-10.75	0.13							
193: [cds_D068_19790]			Succinyl-CoA synthetase, alpha subunit-related enzymes; putative CoA-binding protein; Possible ortholog: BATR1942_07075 from Bacillus	2.46	9.28E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated		HrcA, ResD
194: [cds_D068_20880]			hypothetical protein	6.12	0.03	UP						Hpr
195: [cds_D068_20960]			Pneumococcal vaccine antigen A homolog; putative transposon-related lytic enzyme; Possible ortholog: BATR1942_08235 from Bacillus	2.28	1.36E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated		CodY
196: [cds_D068_20970]			FIG01234361: hypothetical protein; putative integral inner membrane protein; Possible ortholog: BATR1942_08240 from Bacillus	3.35	1.24E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		

	cds_D068_24670	BSU24180	Glycerophosphoryl diester phosphodiesterase EC 3.1.4.46; glycerophosphoryl diester phosphodiesterase; Possible ortholog: BATR1942_10395 from Bacillus	2.2	2.55E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		CodY, SigH, SigW
213:	[cgs_D068_25080]											
	cds_D068_25080	BSU24540	Rhodanese-like domain protein; putative sulfur transferase; Possible ortholog: BATR1942_10585 from Bacillus	2.32	1.79E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated		
214:	[cgs_D068_25150; cds_D068_25140]											
	cds_D068_25150	BSU24610	SinR; SinR, regulator of post-exponential-phase responses genes competence and sporulation; HTH-type transcriptional regulator slrR; Possible ortholog: BACAU_2306 from Bacillus	3.13	1.40E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated	AbrB, ScoC, Spo0A	RocR, SigH
	cds_D068_25140	BSU24600	SinI; SinI protein, antagonist of SinR; antagonist of SinR; Possible ortholog: BATR1942_10615 from Bacillus;	inf	0.4							
215:	[cgs_D068_25470]											
	cds_D068_25470	BSU24930	unknown; hypothetical protein; Possible ortholog: BATR1942_10780 from Bacillus	2.3	4.96E-03	UP	Not regulated	Not regulated	Not regulated	DOWN	Spo0A	DegU
216:	[cgs_D068_25560]											
	cds_D068_25560	BSU25020	Manganese superoxide dismutase EC 1.15.1.1; superoxide dismutase; Possible ortholog: BATR1942_10825 from Bacillus	2.96	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigB	SigE
217:	[cgs_D068_25630]											
	cds_D068_25630	BSU25100	Zinc uptake regulation protein ZUR; transcriptional regulator Fur family protein; Possible ortholog: BATR1942_10860 from Bacillus	2.31	9.26E-04	UP	Not regulated	Not regulated	Not regulated	Not regulated		LexA
218:	[cgs_D068_25930; cds_D068_25940; cds_D068_25950]											
	cds_D068_25930	BSU25370	FIG01232279: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_10995 from Bacillus	2.13	1.04E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigW	SigG, SigW
	cds_D068_25940	BSU25380	DUF1432 domain-containing protein; hypothetical protein; Possible ortholog: BATR1942_11000 from Bacillus;	1.17	0.2							
	cds_D068_25950	BSU25390	FIG01107945: hypothetical protein; putative membrane bound hydrolase; Possible ortholog: BATR1942_11005 from Bacillus;	-1.17	0.61							
219:	[cgs_D068_25960; cds_D068_25970]											
	cds_D068_25960	BSU25400	GatB ; Transamidase GatB domain protein; hypothetical protein; Possible ortholog: BATR1942_11010 from Bacillus	2.87	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		SigA, SpoIIID
	cds_D068_25970	BSU25410	SSU ribosomal protein S21p; 30S ribosomal protein S21; Possible ortholog: BAXH7_02662 from;	2.25	6.71E-04	+						
220:	[cgs_D068_26050; cds_D068_26060; cds_D068_26070]											
	cds_D068_26050	BSU25490	HrcA; Heat-inducible transcription repressor HrcA; heat-inducible transcription repressor; Possible ortholog: BATR1942_11055 from Bacillus	2.03	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	HrcA	
	cds_D068_26060	BSU25500	Putative coproporphyrinogen III oxidase of BS HemN-type, oxygen-independent EC 1.3.99.22, in heat shock gene cluster; coproporphyrinogen III oxidase; Possible ortholog: BATR1942_11060 from Bacillus;	-3.11	0.1							
	cds_D068_26070	BSU25510	lepA; Translation elongation factor LepA; GTP-binding protein LepA; Possible ortholog: BATR1942_11065 from Bacillus;	-1.3	0.48							
221:	[cgs_D068_26110]											
	cds_D068_26110	BSU25550	SSU ribosomal protein S20p; 30S ribosomal protein S20; Possible ortholog: BATR1942_11085 from Bacillus	2.29	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		
222:	[cgs_D068_26400]											
	cds_D068_26400	BSU31030	unknown; hypothetical protein; Possible ortholog: BATR1942_13330 from Bacillus	4.42	0	UP	Not regulated	Not regulated	Not regulated	Not regulated		PerR
223:	[cgs_D068_27510]											
	cds_D068_27510	BSU27780	FIG01233475: hypothetical protein; putative serine/threonine-protein kinase; Possible ortholog: BATR1942_11620 from Bacillus	2.43	9.68E-05	UP	Not regulated	Not regulated	Not regulated	Not regulated		
224:	[cgs_D068_28080]											
	cds_D068_28080	BSU28220	ClpX; ATP-dependent Clp protease ATP-binding subunit ClpX; ATP-dependent protease ATP-binding subunit ClpX; Possible ortholog: BATR1942_11880 from Bacillus	2.21	0	UP	Not regulated	Not regulated	Not regulated	Not regulated	CtsR	
225:	[cgs_D068_28370]											
	cds_D068_28370	BSU28500	Thioredoxin reductase EC 1.8.1.9; thioredoxin; Possible ortholog: BATR1942_12010 from Bacillus	4.15	5.91E-07	UP	Not regulated	Not regulated	Not regulated	Not regulated	CtsR, SigB, Spx	DegU, SigF
226:	[cgs_D068_28760]											
	cds_D068_28760	BSU28830	FIG01231657: hypothetical protein; hypothetical protein; Possible ortholog: BATR1942_12195 from Bacillus	2.19	2.23E-03	UP	Not regulated	Not regulated	Not regulated	Not regulated	SigB, SigW	PerR, SigW, Xre

	cds_D068_37280	BSU35360	FlaA; Flagellin protein FlaA	2.15	0.01 UP	DOWN	Not regulated	Not regulated	Not regulated	CodY, CsrA, ScoC, SigD	SigD
248:	[cgs_D068_37460]										
	cgs_D068_37460	BSU35530	Phospho-N-acetylmuramoyl-pentapeptide-transferase EC 2.7.8.13	2.12	1.55E-03 UP	Not regulated	Not regulated	Not regulated	Not regulated		
249:	[cgs_D068_37680]										
	cgs_D068_37680	BSU35740	Glycerol-3-phosphate cytidyltransferase EC 2.7.7.39	3.19	0 UP	Not regulated	Not regulated	Not regulated	Not regulated	PhoP, WalR	CodY
250:	[cgs_D068_38410]										
	cgs_D068_38410	BSU36330	unknown	3.52	1.96E-06 UP	Not regulated	Not regulated	Not regulated	Not regulated		DegU

*Patterns of gene regulation at stress was as published in Sappa (2013) [55].

[†]Known transcription regulation binding sites were taken from SubtiWiki database (http://subtiwiki.uni-goettingen.de/wiki/index.php/Main_Page)

[‡]New putative transcription regulation binding sites were identified in 200 bp loci up-stream of the first gene in the operon by using the software tools provided by DBTBS server ([Shttp://dbtbs.hgc.jp/](http://dbtbs.hgc.jp/)). Genes of operons are shown in brackets. Leading 'r' means that the operon is located on the reverse strand. Gene IDs are as in the genome submission to NCBI with accession CP011802.