

COMPARATIVE TRANSCRIPTOMICS OF *BACILLUS SUBTILIS* BACILYSIN-
NEGATIVE GENOTYPE WITH PARTICULAR REFERENCE TO BACILYSIN
FORMATION

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NAZ KOCABAY

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**COMPARATIVE TRANSCRIPTOMICS OF *BACILLUS SUBTILIS*
BACILYSIN-NEGATIVE GENOTYPE WITH PARTICULAR REFERENCE
TO BACILYSIN FORMATION**

submitted by **NAZ KOCABAY** in partial fulfillment of the requirements for the degree of **Master of Science in Molecular Biology and Genetics, Middle East Technical University** by,

Prof. Dr. Halil Kalıpçılar
Dean, Graduate School of **Natural and Applied Sciences**

Prof. Dr. Ayşe Gül Gözen
Head of the Department, **Biology**

Prof. Dr. Gülay Özcengiz
Supervisor, **Biology, METU**

Examining Committee Members:

Prof. Dr. Mustafa Akçelik
Biotechnology, Ankara University

Prof. Dr. Gülay Özcengiz
Biology, METU

Assoc. Prof. Dr. Sezer Okay
Vaccine Institute, Hacettepe University

Date: 15.02.2021



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Name, Last name: Naz Kocabay

Signature:

ABSTRACT

COMPARATIVE TRANSCRIPTOMICS OF *BACILLUS SUBTILIS* BACILYSIN-NEGATIVE GENOTYPE WITH PARTICULAR REFERENCE TO BACILYSIN FORMATION

Kocabay, Naz
Master of Science, Molecular Biology and Genetics
Supervisor: Prof. Dr. Gülay Özcengiz

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The Gram-positive model prokaryote *Bacillus subtilis* is a non-pathogenic organism that is known for producing a wide variety of secondary metabolites with pharmacological and antimicrobial activities. The smallest dipeptide antibiotic bacilysin is among the many secondary metabolites that are produced by *B. subtilis*, and it is composed of L-alanine and L-anticapsin. As shown earlier by our research group, the synthesis of bacilysin is regulated by *bacA* operon under the control of quorum sensing and sporulation pathways. Additionally, our findings suggested that bacilysin acts as a pleiotropic molecule and alters the cellular physiology of *B. subtilis*. In the present study, the transcriptomic profiles of mutant OGU1 and its parental strain PY79 were investigated by RNA-Seq and validated with RT-qPCR analyses. While a total of 2369 significantly differentially expressed transcripts were identified by RNA-Seq, only 223 differentially expressed genes (DEGs) were overexpressed in mutant OGU1. The results of previous comparative proteomics studies were integrated with the current transcriptomic (RNA-Seq) analysis, and the results are compared and discussed with respect to their cellular functions. Overall,

this study confirms and expands our earlier studies with a fresh perspective on the pleiotropic changes that emerge from the loss of bacilysin biosynthetic function.

Keywords: *Bacillus subtilis*, bacilysin, RNA-Seq, transcriptome, proteome



ÖZ

BACILLUS SUBTILIS BASİLİSİN-NEGATİF GENOTİPİNİN BASİLİSİN ÜRETİMİNE YÖNELİK KARŞILAŞTIRILMALI TRANSKRİPTOMİK ANALİZİ

Kocabay, Naz
Yüksek Lisans, Moleküler Biyoloji ve Genetik
Tez Yöneticisi: Prof. Dr. Gülay Özcengiz

Şubat 2021, 193 sayfa

Gram pozitif bakteriler için model organizma olan *Bacillus subtilis*, farmakolojik ve antimikrobiyal aktiviteye sahip çok çeşitli ikincil metabolitler üreten ve patojenik olmayan bir organizmadır. Bilinen en küçük dipeptid olan basilisin ise L-alanine ve L-anticapsin'den oluşmakta olan bir antibiyotik olup *B. subtilis* tarafından sentezlenen birçok ikincil metabolitten sadece bir tanesidir. Grubumuz tarafından daha önce gösterildiği üzere, basilisin sentezi çoğunluğu algılama (quorum sensing) ve sporülasyon yollarına bağlı olarak *bacA* operonu tarafından gerçekleştirilmektedir. Basilisinin pleiotropik bir molekül olarak davrandığı ve üretici organizmanın hücrel fizyolojisini etkilediği yine grubumuzca daha önce rapor edilmiştir. Bu çalışmada ise basilisin üretemeyen mutant OGU1 suşu ve ana suş PY79'un transkriptom profilleri RNA dizileme (RNA-Seq) ile incelenmiş ve gerçek zamanlı kantitatif PCR (RT-qPCR) yöntemi ile doğrulanmıştır. RNA dizileme sonucunda farklı ifade edilen 2369 gen belirlenmiştir. 223 genin ifadesi mutant suşta artarken 2146 genin ifadesinin azaldığı gözlemlenmiştir. Grubumuz tarafından daha önce gerçekleştirilmiş olan karşılaştırmalı proteom analizlerinden elde edilen bulgular ile RNA dizileme verileri entegre edilmiş, hücrel

fonksiyonlarına göre gruplandırılmış ve detaylı bir şekilde tartışılmıştır. Bu çalışma grubumuzun önceki bulgularını doğrulamış ve basilisin yokluğundan kaynaklanan pleiotropik değişikliklerin üretici organizma üzerindeki etkilerini yeni bir bakış açısıyla gözlemleme imkânı tanımıştır.

Anahtar Kelimeler: *Bacillus subtilis*, basilisin, RNA-Seq, transkriptom, proteom





To my dearest little sister Alya

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LIST OF ABBREVIATIONS

ABBREVIATIONS

bp(s)	: Base pair(s)
kDa	: Kilo Daltons
GO	: Gene Ontology
KEGG	: Kyoto Encyclopedia of Genes and Genomes
RNA-Seq	: RNA-Sequencing
DEG	: Differentially Expressed Genes
DEP	: Differentially Expressed Proteins
PTM	: Posttranslational Modification
ORF	: Open Reading Frame
RIN	: RNA Integrity Number
Mw	: Molecular Weight
pI	: Isoelectric Point
nanoLC-MS/MS	: nanoLiquid Chromatography-Mass Spectrometry
2DE	: Two-Dimensional Gel Electrophoresis
MALDI-TOF	: Matrix-assisted Laser Desorption Ionization Time of Flight
MS	: Mass Spectrometry
LC	: Liquid Chromatography
PCR	: Polymerase Chain Reaction
qPCR	: Quantitative Polymerase Chain Reaction
RT-qPCR	: Real Time Quantitative Polymerase Chain Reaction

CHAPTER 1

INTRODUCTION

1.1 *Bacillus subtilis*

1.1.1 *Bacillus subtilis* as a model organism

Bacillus subtilis, like other members of the genus *Bacillus*, is a rod-shaped, Gram-positive, motile bacterium. It is very prevalent in nature and can be found in soil and water sources, as well as the gastrointestinal tract of humans and plants. *Bacillus subtilis* is also capable of forming endospores that are resistant to extreme environmental conditions. Given that it is a model organism, *Bacillus subtilis* is the most well-known and extensively studied organism among other *Bacillus* species. *Bacillus subtilis* is a non-pathogenic organism even though some *Bacillus* species such as *B. cereus* and *B. anthracis* are well-known pathogens (Wipat and Harwood, 1999; Sonenshein *et al.*, 2002; Lippolis *et al.*, 2013). In terms of molecular and cell biology, *B. subtilis* is the most prominently studied prokaryote after *Escherichia coli* (Zweers *et al.*, 2008). Due to its developed natural transformation system and versatile genome, *B. subtilis* is very open to genetic manipulation and therefore, it has been widely used by researchers for more than 50 years (Harwood, 1992; Zweers *et al.*, 2008).

B. subtilis is also a chemoorganotroph, which allows the organism to maintain the necessary growth conditions by oxidizing organic compounds. It is mesophilic like numerous other members of its genus and it can produce normal-sized colonies after overnight incubation at 37°C (Harwood and Cutting, 1990). Studies showed that *B.*

subtilis can grow anaerobically despite being classified as a strict aerobe for many years. Fermentation or the usage of nitrate or nitrite as a terminal electron acceptor enables anaerobic growth. It has been revealed that ResDE two-component signal transduction system is the key in anaerobic respiration (Nakano and Zuber, 1998). Additionally, *B. subtilis* is capable of producing several antibiotics, industrial enzymes and secondary metabolites that are used in various chemical, industrial and medical practices (Sonenshein *et al.*, 2002).

In 1997, the whole genome of *B. subtilis* was sequenced and published for the first time as 4.2 Mb in size (Kunst *et al.*, 1997). Subsequent studies revealed that the genome of *B. subtilis* harbors 4106 protein-coding genes as well as 86 tRNA, 30 rRNA and 3 small RNA genes (Ando *et al.*, 2002; Kobayashi and Ogasawara, 2002). For *B. subtilis* to grow in rich medium at moderate temperature in aerobic conditions, which are the optimal experimental conditions for this microorganism, 275 genes are determined as essential although 25 genes are of unknown functions. The genome of *B. subtilis* also contains 17 sigma factors in addition to roughly 250 DNA binding transcriptional regulators (Kobayashi and Ogasawara, 2002).

In 1958, it has been presented for the first time that *B. subtilis* 168, a tryptophan auxotroph, is open to genetic manipulation. Consequently, *B. subtilis* 168 has evolved to be the most widely used strain in the following years and has become the standard strain (Spizizen, 1958; Harwood and Cutting, 1990). *B. subtilis* PY79, the prototrophic derivative of *B. subtilis* 168, is another strain that is commonly used as a wild type strain by researchers (Youngman *et al.*, 1984). However, the reference PY79 is different from our lab-adapted PY79 due to continuous growth and repeated transfers in our laboratory for the past forty years. Unlike the reference strain PY79, the genome of our lab-adapted PY79 possesses one deletion and 5 SNP's.

1.1.2 Primary Metabolism in *B. subtilis*

To be able to continue its life cycle, *B. subtilis* requires energy in the same way as other living organisms do. It was classified as a strict aerobe for many years before eventually reported as a facultative anaerobe by Nakano and Zuber (1998). Either by using nitrate or nitrite as a terminal electron acceptor or by fermentation, it is capable of growing anaerobically. Therefore, *B. subtilis* can adjust its metabolic activity based on the availability of oxygen and alternative electron acceptors.

A sensor kinase, ResE, and a response regulator, ResD, together form a two-component signal transduction system. ResDE is the primary regulator of anaerobic respiration in *B. subtilis* and plays a crucial role in the early stages of anaerobic gene regulation. *fnr* transcription is induced by ResDE upon oxygen limitation. Along with anaerobically induced genes, respiratory nitrate reductase operon, *narGHJI*, is then activated by a transcriptional activator FNR. Since pyruvate dehydrogenase is used for pyruvate metabolization, *B. subtilis* can execute fermentation without any external electron acceptors unlike many anaerobes (Nakano and Zuber, 1998).

It has been reported that the relationship between carbon and nitrogen metabolism also changes based on aerobic or anaerobic respiration. A study conducted by Clements *et al.* showed that anaerobic fermentation induced at least 44 proteins compared with aerobic growth controls, while nitrate respiration induced at least 19 proteins compared with the same aerobic controls. They stated that several metabolic proteins showed an upregulation in response to their environments. While some proteins were induced by both anaerobic processes, numerous other proteins were particularly induced by either fermentation or nitrate respiration (2002).

Shifts in metabolism of energy production play a significant role when it comes to different industrial applications of *B. subtilis*. Various proteases can be synthesized and secreted out of the cell by secretion systems under different environmental conditions. The vitamin riboflavin, the flavor agent ribose, the supplement polyglutamic acid as well as several enzymes, such as proteases and amylases collected from *B. subtilis* are utilized for many industrial appliances (Schallmeyer *et al.*, 2004). Another study revealed that the alteration of the metabolic products might be possible in *B. subtilis* by a shift in environmental conditions, which will then provide secretion of diverse industrial compounds (Renna *et al.*, 1993). Westers *et al.* also reported that *B. subtilis* is an appealing host as it is capable of effortless production and secretion of a variety of industrial enzymes and biopharmaceuticals in immense quantities (2004).

1.1.3 Secondary Metabolites of *B. subtilis*

Biologically active peptides have different functions in cellular physiology due to their structural diversity (Gill *et al.*, 1996). As a result of its distinct metabolism, *B. subtilis* is capable of producing various secondary metabolites with pharmacological or antimicrobial activities. These peptides with antimicrobial activity can be either produced non-ribosomally or with ribosomal synthesis followed by posttranslational modification, such as the formation of lanthionine. Antibiotics that contain lanthionine are named lantibiotics (Schnell *et al.*, 1988; Zuber *et al.*, 1993; Weber and Marahiel, 2001).

It was reported by several studies that acting as antimicrobial agents is not the only function of peptide antibiotics produced by *B. subtilis*. For example, lantibiotics operate as pheromones in quorum-sensing or as killing factors to promote

programmed cell death. Lipopeptides that are non-ribosomally produced are linked to swarming motility and biofilm formation (Stein, 2005). Tables that show the functions and structures of lantibiotics and non-ribosomally produced peptide antibiotics of *B. subtilis* are given below in Table 1.1 and Table 1.2, respectively.

Table 1.1. The functions and structures of lantibiotics of *B. subtilis* (Stein, 2005).

Antibiotic	Function	Structure
Mersacidin	Inhibition of cell wall synthesis	Globular
Ericin	Acting like pheromone, subtilin-like activity	Cyclic
Subtilin	Acting like pheromone	Cyclic
Subtilosin A	Acting against some Gram (+) bacteria	Cyclic

Table 1.2. The functions and structures of non-ribosomally produced peptide antibiotics of *B. subtilis* (Stein, 2005).

Antibiotics	Function	Structure
Bacilysin	Probable pleiotropic molecule	Linear
Bacillibactin	Siderophore	Cyclic
Fengycin	Acting on filamentous fungi specifically	Cyclic
Surfactin	Acting like detergent on biological membranes	Cyclic
Bacillomycin	Hemolytic and antifungal activity	Cyclic lipopeptide
Iturin	Hemolytic and antifungal activity	Cyclic lipopeptide
Mycosubtilin	Hemolytic and antifungal activity	Cyclic lipopeptide

1.2 Gene expression regulation in *Bacillus subtilis*: General overview of quorum sensing, sporulation, and two-component systems

Gene expression and development are regulated by several types of cells through the utilization of cell to cell signaling. The most important example of cell to cell signaling is known as quorum sensing, and it involves a regulatory feedback mechanism to cell density signals. This process involves the secretion of quorum sensing signal molecules. In proportion to cell density, as these molecules reach the threshold concentration, the regulation of gene expression is started by their producers (Fuqua *et al.*, 1994). Though various systems and signaling molecules exist in different microorganisms, quorum sensing systems can be classified in three groups: (i) the acyl homoserine lactone (AHL) in Gram-negative bacteria, which is produced by a LuxI-type synthase and is perceived by a DNA-binding LuxR-type transcriptional activator, (ii) autoinducing peptides (AIP) in Gram-positive bacteria that are sensed by a two-component regulatory systems, and (iii) the autoinducer-2 (AI-2) system that commonly exist in both Gram-negative and Gram-positive bacteria (Brackman and Coenye, 2014).

In *B. subtilis*, quorum sensing takes part in several physiological events such as sporulation, competence development, and production of extracellular enzymes and antibiotics (Comella and Grossman, 2005). As in other prokaryotic organisms, signal transduction involves a two-component histidine kinase system. A histidine protein kinase, the first component, senses autoinducer peptides (AIPs) and after binding, it gets activated by autophosphorylation on its histidine residue. The phosphoryl group is then transferred to a response regulator, the second component, and activates it to regulate gene expression (Stock *et al.*, 2000; Zhang and Dong, 2004).

Three categories of signal peptides were determined in *B. subtilis*: (i) ComX, a 5 to 10 amino-acid peptide that maintains extracellular interaction with its receptor (Magnuson *et al.*, 1994), (ii) Phr peptides, which inhibit the activity of their target Rap proteins by internalizing them into the cell (Lazazzera, 2001; Perego and Brannigan, 2001), and lastly (iii) lantibiotic peptides like subtilin, which shows both signaling and antibiotic activities (Kleerebezem and Quadri, 2001).

A family of 8 Phr peptides (PhrA, PhrC, PhrE, PhrF, PhrG, PhrH, PhrI, and PhrK), and 11 Rap proteins (RapA to RapK) are encoded by *B. subtilis* (Lazazzera, 2001). Each Phr peptide is encoded with its corresponding Rap protein in the same operon. However, an unpaired Rap protein, RapB, gets suppressed by the PhrC peptide, also known as competence and sporulation stimulating factor (CSF) (Parashar *et al.*, 2013; Perego, 1997). It has been reported that other Rap proteins might also be inhibited by unpaired Phr peptides (Auchtung *et al.*, 2006).

As the targets of Rap proteins in *B. subtilis*, three response regulators have previously been identified as Spo0F, ComA and DegU. During the transition to stationary growth phase, regulation of essential processes is executed by Rap and Phr proteins, such as the regulation of sporulation by RapA/PhrA, production of extracellular proteases by RapG/PhrG, and transfer of conjugative DNA elements by RapI/PhrI pairs (Lanigan-Gerdes *et al.*, 2007; Omer Bendori *et al.*, 2015). The functions of Rap proteins and Phr peptides are given in Figure 1.1.

In a concentration dependent manner, PhrC or competence and sporulation stimulating factor (CSF) controls the regulation of the ComA response regulator, which is responsible for the expression of competence related genes. CSF blocks its cognate RapC protein at low extracellular concentrations, also inhibiting the

activation of ComA (Solomon *et al.*, 1996). Yet, by interacting and blocking ComP histidine kinase, CSF is able to block the activity of ComA indirectly in increased extracellular concentrations (Lazazzera and Grossman, 1998; Lazazzera *et al.*, 1997). According to Mirel *et al.* (2000), CSF can also block ComS in the stationary phase and lead to reduced competence gene expression.

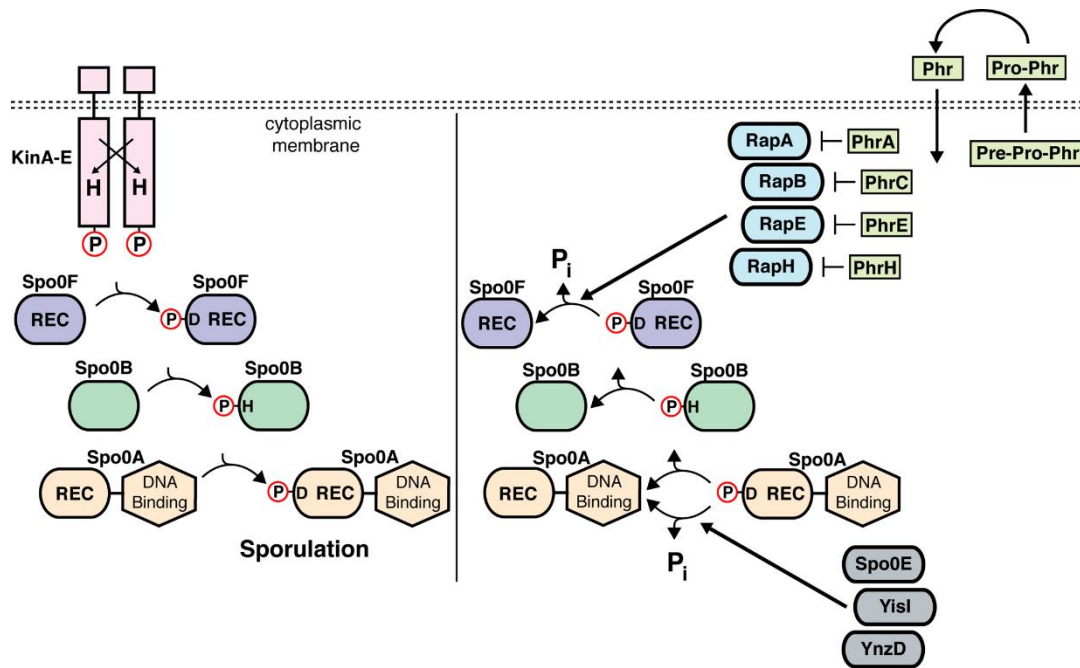


Figure 1.1. Regulation of *B. subtilis* sporulation signal transduction by Rap proteins and Phr peptides. Though the sporulation kinases (KinA-E) are illustrated as membranous proteins for simplicity, it is important to note that they are actually soluble cytoplasmic receptors. Consecutive phosphorylation of Spo0F, Spo0B and eventually Spo0A are shown. On the left, sporulation is triggered when the level of Spo0A reaches a critical level. On the right, Spo0F is dephosphorylated by Rap proteins and sporulation is inhibited as a result. Phr peptides are imported into the cytoplasm by the Spo0K permease (oligopeptide permease A; OppA), which is not pictured, to regulate sporulation positively by binding to Rap proteins and inhibiting

Spo0F dephosphorylation subsequently. Spo0E, YisI and YnzD dephosphorylate Spo0A in *B. subtilis*. REC, Receiver Domain; H, histidine; D, aspartic acid; P, phosphoryl group; Pi, inorganic phosphate (Parashar *et al.*, 2011).

As the main component of the ComQXPA pathway, the transcription factor ComA regulates more than 10% of the genome (Comella and Grossman, 2005). Depending on the accumulation of CSF and ComX pheromone, ComQXPA pathway is activated. As a regulator of the competence development, the expression of both *comX* and *comQ* is essential for the production of ComX (Magnuson *et al.*, 1994). As a summary, ComX activates ComP, a membrane bound receptor protein kinase. After autophosphorylation, ComP donates the phosphate group to the response regulator ComA and leads to the activation of ComA-dependent promoters hence enhancing the expression of genes that control genetic competence development, such as *comS* (*srfA*). At the same time, Spo0K (oligopeptide permease; Opp) imports CSF to inhibit RapC. Thus, inhibition of RapC eliminates the repression on ComA and leads to a negative regulation (Comella and Grossman, 2005; Core and Perego, 2003).

It was reported that other pheromones like PhrF and PhrK increase the activity of ComA in addition to ComX and CSF. By an oligopeptide permease, these pheromones, which block the inhibitory activity of their cognate Rap proteins on ComA, are transported (Pottathil *et al.*, 2008). In total, the regulation of more than 20 genes directly, and more than 150 genes indirectly are under the control of the ComX-ComP-ComA quorum sensing pathway (Claverys *et al.*, 2006).

Along with CheA-CheY (chemotaxis) (Rosario *et al.*, 1994), ResD-ResE (anaerobic gene activation) (Nakano *et al.*, 1996), ComP-ComA (competence) (Grossman, 1995), DegS-DegU (degradative enzyme production) (Dartois *et al.*, 1998) and PhoR-PhoP (phosphate regulation) (Sun *et al.*, 1996), at least 36 histidine kinases

and 36 response regulators have been reported in *B. subtilis* genome (Fabret *et al.*, 1999). However, the sporulation phosphorelay, which includes five histidine kinases (KinA, KinB, KinC, KinD, and KinE) and two crucial response regulators (Spo0B and Spo0F), is the most critical regulatory pathway of *B. subtilis* (Perego and Hoch, 2002). Figure 1.2 shows the sporulation phosphorelay in question.

Sporulation in *B. subtilis* is a multistaged developmental mechanism that regulates the conversion of a growing cell into a dormant cell type that is known as the spore or endospore (Piggot and Losick, 2002; Stragier and Losick, 1996). The coat that encircles and protects the spore is the last structure to be formed. Several genes directly take part in coat assembly, including the *cot* genes that are necessary for 18 structural coat proteins. Other genes that control the assembly of the structural components but are not necessarily part of the final structure also participate in the process, such as TasA. *tasA* is the key component of the biofilm extracellular matrix. Additionally, TasA shows broad-spectrum antibacterial activity that leads to the inhibition of competitor bacteria growth in nature (Branda *et al.*, 2006; Serrano *et al.*, 1999; Stöver and Driks, 1999).

Starvation signals that are sensed by sensory kinases lead to the start of sporulation phosphorelay that eventually ends up with the activation of Spo0A under suitable conditions (Jiang *et al.*, 2000; Sonenshein, 2000). Proteins that regulate histidine kinases like KipI or dephosphorylation of Spo0F by the Rap proteins can inhibit the sporulation phosphorelay shown in Figure 1.2 (Stephens, 1998).

The DNA binding protein Spo0A is the master regulator of entry into sporulation (Hoch, 1993). Once it is activated, the production of additional Spo0A-regulated proteins is also triggered (Fujita and Sadaie, 1998). Indeed, Spo0A regulates the

expression of 520 genes, proving that it is an essential element in the global regulation of gene expression (Liu *et al.*, 2003). 121 of 520 genes are directly under the control of Spo0A. While 81 of these genes are negatively controlled, 40 of them are positively regulated (Molle *et al.*, 2003). It has been shown that Spo0A also regulates the *skf* operon that encodes SkfA, the sporulation killing factor that promotes the lysis of sibling cells that failed to enter the sporulation pathway (Fawcett *et al.*, 2000; Molle *et al.*, 2003).

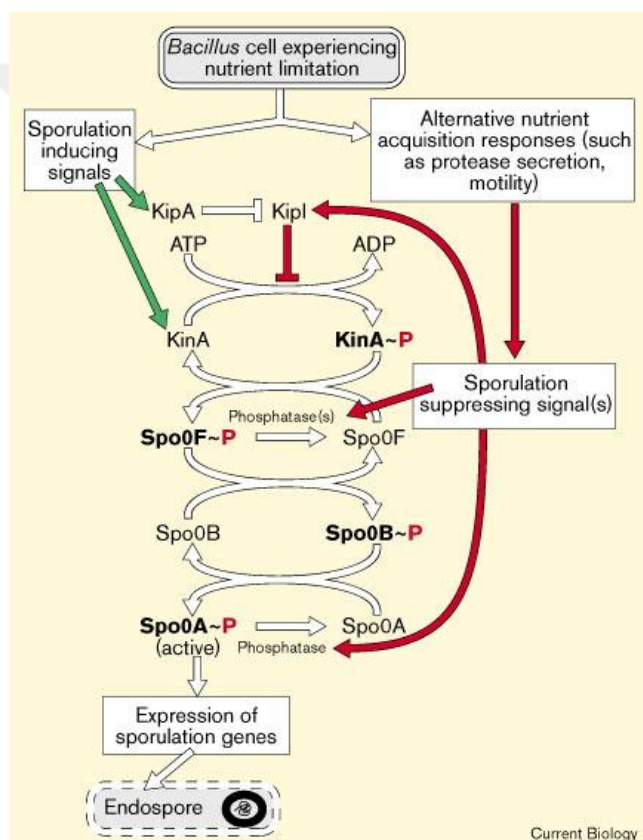


Figure 1.2. Sporulation phosphorelay in *B. subtilis* is illustrated (Stephens, 1998). While sporulation activating signals are shown with green arrows, inhibitory signals are portrayed with red arrows.

In addition, Spo0A represses *abrB* expression. In normal conditions, AbrB inhibits the expression of vital stationary phase genes like *sigH* and *kinA*, and therefore maintains Spo0A inactivation (Robertson *et al.*, 1989; Strauch, 1995). Thus, the negative regulation of AbrB expression by active Spo0A leads to *sigH* and *kinA* production, and eventually Spo0A activation (Veening *et al.*, 2005). A simplified illustration of the regulatory network that controls the initiation of sporulation is shown in Figure 1.3.

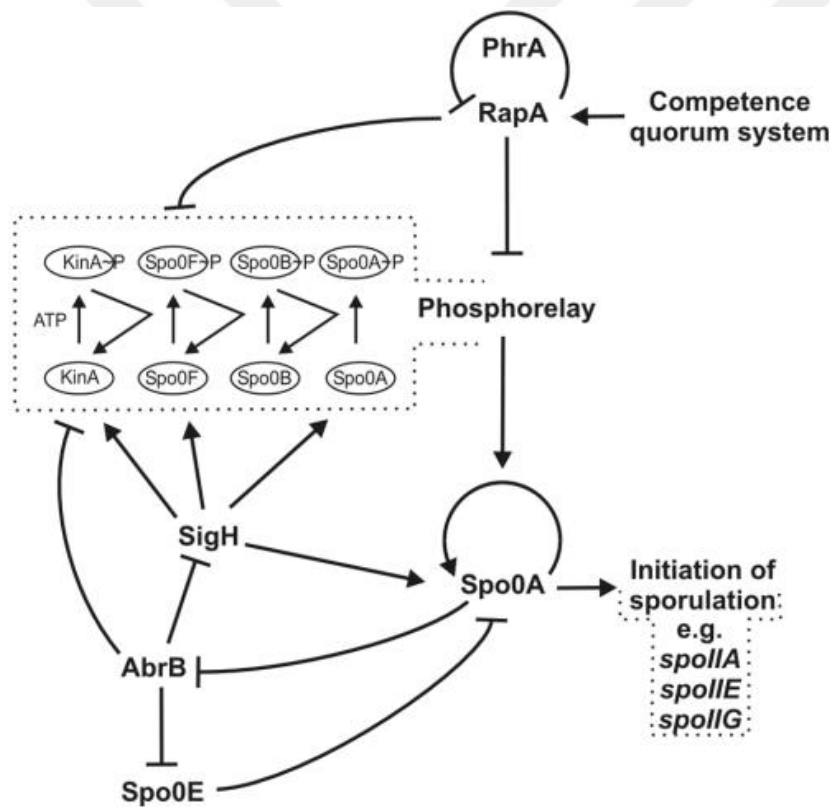


Figure 1.3. The network that regulates the initiation of sporulation is shown. While the negative regulations are displayed by perpendiculars, arrows signify positive actions (Veening *et al.*, 2005).

1.3 Dipeptide antibiotic bacilysin

Bacilysin, the simplest peptide antibiotic known, is composed of L-alanine at its N-terminus and L-anticapsin, a non-proteinogenic amino acid, at its C-terminus (Figure 1.4). As a dipeptide, bacilysin has a molecular weight of 270 Da (Walker and Abraham, 1970).

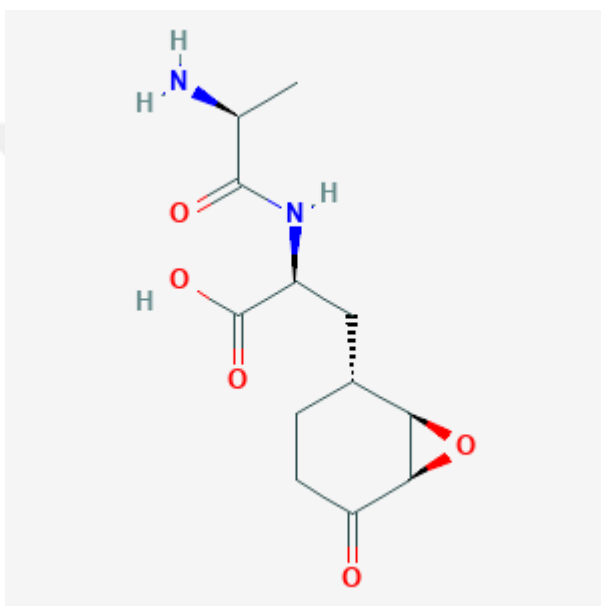


Figure 1.4. Structure of bacilysin (“Bacilysin | C₁₂H₁₈N₂O₅ - PubChem,” 2021).

Bacilysin can inhibit the growth of some bacteria and fungi, including *Staphylococcus aureus* and *Candida albicans* (Kenig and Abraham, 1976). The antibiotic activity of bacilysin depends on its anticapsin moiety. The glucosamine synthetase, which takes part in the bacterial peptidoglycan and fungal mannoprotein biosynthesis, is inhibited by the anticapsin moiety after bacilysin uptake by the target cells. This process then leads to cell lysis (Inaoka *et al.*, 2003).

The mechanism of bacilysin biosynthesis relies on a polycistronic operon named *ywfBCDEF* and a monocistronic gene *ywfG* despite being synthesized nonribosomally (Inaoka *et al.*, 2003). It has been shown that these genes were responsible for the biosynthetic core functions of bacilysin synthesis, and later renamed as *bacABCDE* and *bacF*. While the *bacABC* genes participate in the conversion of prephenate to anticapsin, the *bacDE* genes act in amino acid ligation and bacilysin immunity, respectively (Steinborn *et al.*, 2005). The *ywfH* gene, which was later renamed as *bacG*, is divergently located and transcribed from the opposite DNA strand from *bacABCDE*. *ywfG* was also renamed as *bacF*, for convenience (Parker and Walsh, 2012). The organization of *bac*-operon is given in Figure 1.5.

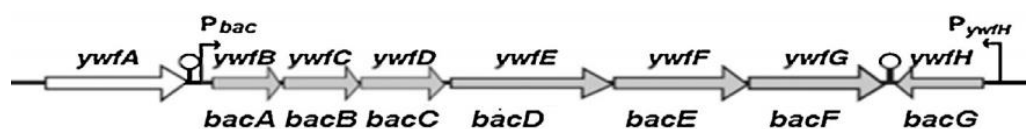


Figure 1.5. Organization of *bac*-operon and *bacG* is shown (Özcengiz and Ögölür, 2015).

The production of bacilysin is parallel to active growth in *B. subtilis* PY79 in synthetic medium. Its production is blocked by specific nutrients like ammonium, casamino acids and glucose, along with specific culture pH and temperatures (Özcengiz and Alaeddinoglu, 1991; Özcengiz *et al.*, 1990). Further studies revealed that quorum sensing global regulation, along with stringent response and feedback regulation together control the production of bacilysin (Inaoka *et al.*, 2003; Özcengiz and Alaeddinoglu, 1991; Yazgan *et al.*, 2001a).

Numerous studies showed that the levels of bacilysin production can be altered. As revealed by Karataş *et al.*, (2003), the disruption of surfactin operon (*srfA*) inhibits the production of bacilysin. Furthermore, four transcriptional regulators control the expression of *bac*-operon (*bacA*): ComA, Spo0A, AbrB and CodY. Both ComA and Spo0A are necessary for transition state induction while ComA activity alone is sufficient for basal level *bac*-operon transcription. However, AbrB and CodY together bind to *bac*-operon promoter region and lead to negative regulation of bacilysin biosynthesis (Karataş *et al.*, 2003; Köroğlu *et al.*, 2011). It has also been shown that no bacilysin production was observed in *phrC* and *comA* deleted mutant strains of *B. subtilis* (Yazgan *et al.*, 2001b). Moreover, bacilysin production was found to be drastically decreased in *comP*-inactive mutants, and completely blocked in *comQ* mutants (Karataş *et al.*, 2003).

DegS/DegU, a two-component signal transduction system that is vital for production of degradative enzymes, positively regulates *bac*-operon and *bacG* (Mariappan *et al.*, 2012). A transition state regulator ScoC (Hpr) is another negative regulator of protease production and sporulation as ScoC directly binds to the promoter region (P_{bac}) of *bacABCDEF* (Inaoka *et al.*, 2009). Additionally, LutR transcriptional repressor was also revealed to be essential for bacilysin biosynthesis since it regulates several physiological events in *B. subtilis* (İrigül-Sönmez *et al.*, 2014). The regulation of bacilysin biosynthesis is shown in Figure 1.6.

1.4 Findings of our group's recent proteomics studies

Our group has previously performed comparative cytosolic proteomic analyses. 2DE MALDI-TOF/MS and nanoLC-MS/MS approaches were utilized in the comparison of our lab-adapted standard strain PY79 and bacilysin non-producer mutant strain OGU1 (Aras-Taşkın, 2010; Demir, 2013; Ertekin *et al.*, 2020).

2DE MALDI-TOF/MS approach discovered more than 1900 proteins within different pH ranges (4-7, 4.5-5.5, 5.5-6.7). However, only 159 proteins that corresponded to 121 distinct open reading frames (ORFs) were differentially expressed between two strains. While 63 proteins were downregulated, 33 proteins were found to be upregulated. Twenty proteins were absent from OGU1 and one protein spot was detected only in mutant OGU1. Additionally, four proteins showed opposing ratios in different 2DE gels within different pH ranges (Aras-Taşkın, 2010; Ertekin *et al.*, 2020).

The nano-LC-MS/MS analysis revealed 1274 proteins in total, but only 76 of them were expressed differentially. Although 18 proteins were overrepresented in the mutant, 58 proteins were either absent or underrepresented in OGU1 (Demir, 2013; Ertekin *et al.*, 2020).

Different functional groups were affected by the loss of bacilysin, such as sporulation-germination, global regulators, secondary metabolite production, stress response, along with many proteins of unknown functions. Based on the findings of both studies, it is possible to say that the loss of bacilysin biosynthetic operon leads to pleiotropic changes in *B. subtilis* (Ertekin *et al.*, 2020).

1.5 RNA-Sequencing

The transcriptome is comprised of a complete set of transcripts in a cell and their quantity. In the light of the central dogma, the transcription of genes into complementary RNAs later lead to a regulation of biological activities of the cell. Hence, these RNA molecules play a very critical part in the interpretation of the genome (Kukurba and Montgomery, 2015; Wang *et al.*, 2009). Due to their coding abilities, mRNAs are the most explored target of transcriptomic studies (Watkins and Arya, 2019). However, all kinds of RNAs, including non-coding RNAs (ncRNAs) and small RNAs (sRNA) play substantial parts in the transcriptome. Other aims of the transcriptomic studies include the discovery of posttranscriptional modifications, the recognition of the transcriptional structure of genes such as their 5' and 3' ends, transcription start sites, splicing models, and most importantly detection and quantification of differentially expressed transcripts under specific conditions (Wang *et al.*, 2009).

Initially, gene expression was analyzed by low-throughput methods like quantitative polymerase chain reaction (qPCR) and northern blots. The limitation of these methods of measuring single transcripts at a time led to a need for more complex, less time-consuming methods. The evolution of technology introduced hybridization or sequence-based methods (Kukurba and Montgomery, 2015; Wang *et al.*, 2009).

Hybridization-based methods consist of incubating fluorescently labelled cDNAs with either custom microarrays or commercial oligo microarrays. While these microarrays are high throughput and usually not expensive, they also come with many limitations such as the requirement of already existing knowledge about genome sequence, problematic high-background levels due to cross-hybridization, and unreliable quantification of transcripts in very low or high abundances.

Additionally, due to the challenges of complex normalization techniques, the comparison of differentially expressed transcripts across separate experiments can be tricky (Kukurba and Montgomery, 2015; Wang *et al.*, 2009).

On the other hand, cDNA sequences can directly be verified by sequence-based methods like Sanger sequencing or EST libraries. However, these methods were more expensive, relatively low throughput and often lacked the quantitative data. As an alternative, tag-based methods were established such as SAGE (serial analysis of gene expression), CAGE (cap analysis of gene expression) and MPSS (massively parallel signature sequencing). These high throughput methods quantified the number of tagged sequences, which correlates directly with the number of mRNA transcripts. Yet, these methods were based on Sanger sequencing technology and found to be highly costly, the majority of the short tags could not be mapped to the reference genome, and isoforms were indistinguishable from each other. Furthermore, these methods were not suitable for novel gene discovery (Kukurba and Montgomery, 2015; Wang *et al.*, 2009).

The development of high throughput next-generation sequencing technologies transformed the world of transcriptomics by allowing global measurement of transcript abundance through the sequencing of complementary DNA (cDNA) (Haas and Zody, 2010; Kukurba and Montgomery, 2015). RNA sequencing (RNA-Seq) offers much more precise, detailed, and quantitative assessment of transcript levels than previous microarray and Sanger sequencing based techniques. The construction of clone libraries is no longer needed since RNA-Seq enables direct sequencing of cDNA fragments, thus requiring fewer RNA samples. The discovery of novel genes as well as detection of alternatively spliced genes and allele-specific expression is also possible with this revolutionary method. RNA-Seq has extremely low background noise and it allows a broader range of expression levels for the detection

of transcripts while showing higher levels of reproducibility. Additionally, RNA-Seq is less expensive and time consuming than previous techniques (Haas and Zody, 2010; Kukurba and Montgomery, 2015; Wang *et al.*, 2009).

The first step in a standard RNA-Seq analysis workflow is the isolation of RNAs from a biological sample. To make sure that the rest of the experiment goes smoothly, it is critical of RNA samples to be of appropriate quality. Therefore, RNA isolation is mostly followed by typical steps that measure the quality and quantity of isolated RNAs. Then, RNA samples are converted to cDNAs by reverse transcription (RT-PCR). Sequencing adaptors are ligated to cDNAs, to the end of the fragments. However, selecting appropriate library protocols and designing the experiment accordingly is extremely crucial since libraries are designed based on the needs of the researcher. For instance, poly-A libraries are used to acquire mRNAs while small RNAs such as micro RNAs (miRNAs) and small interfering RNAs (siRNAs) require different strategies due to their abundance in cells. Lastly, cDNAs are amplified with PCR and RNA-Seq library is ready for sequencing (Figure 1.7) (Kukurba and Montgomery, 2015).

After single-end or paired-end sequencing in a high throughput platform, such as Illumina, RNA-Seq reads are aligned to the reference genome. The mapped reads are then assembled into transcripts, either by reference transcript annotations or *de novo* reconstruction. Gene expression levels are calculated by the number of overlapping transcripts. After normalization of results, statistical comparisons and differential gene expression calculations are achieved between different samples (Figure 1.8) (Kukurba and Montgomery, 2015).

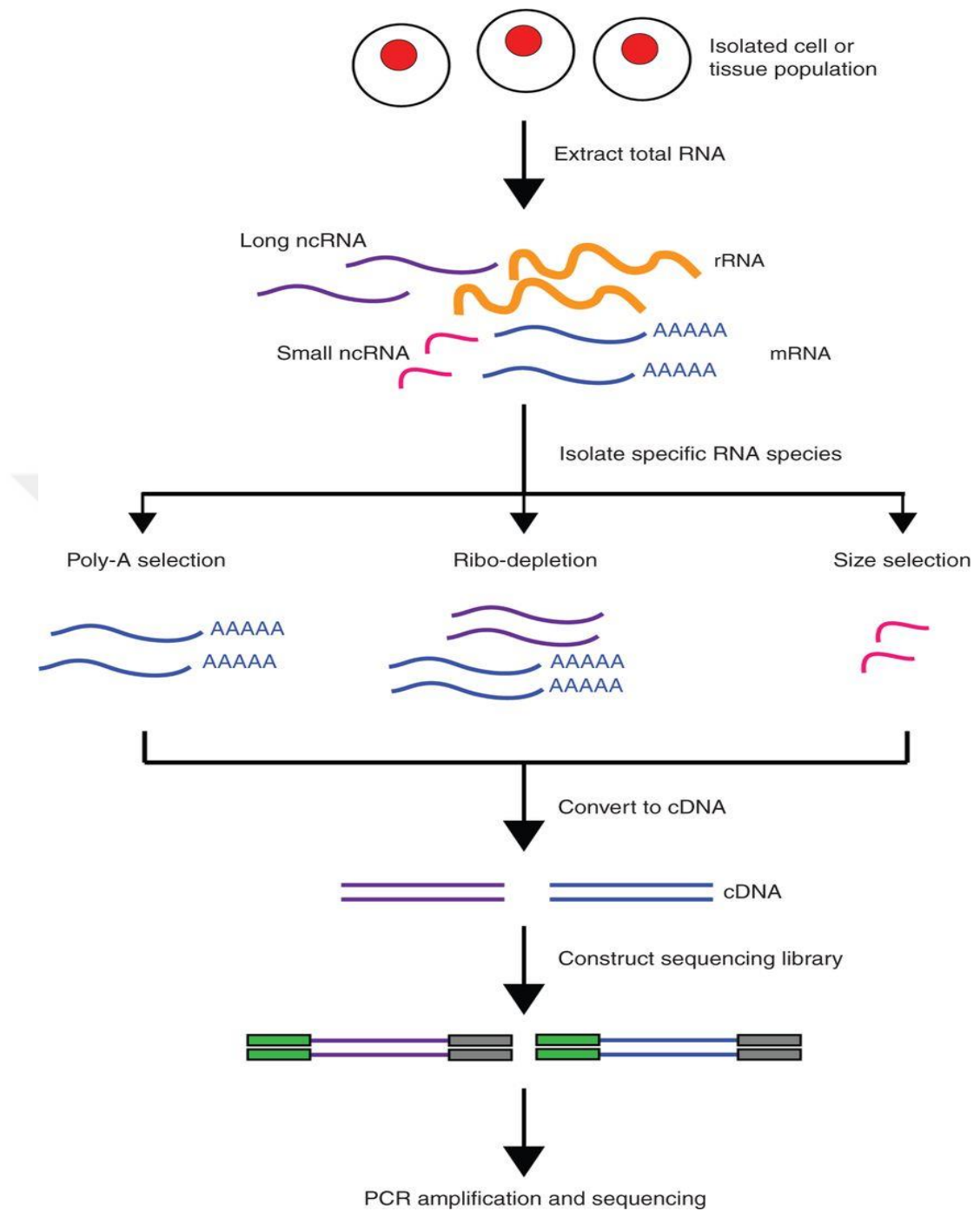


Figure 1.7. RNA-Seq workflow is shown. RNA is extracted, isolated, and converted to cDNA. After PCR amplification, the RNA-Seq library is ready for sequencing (Kukurba and Montgomery, 2015).

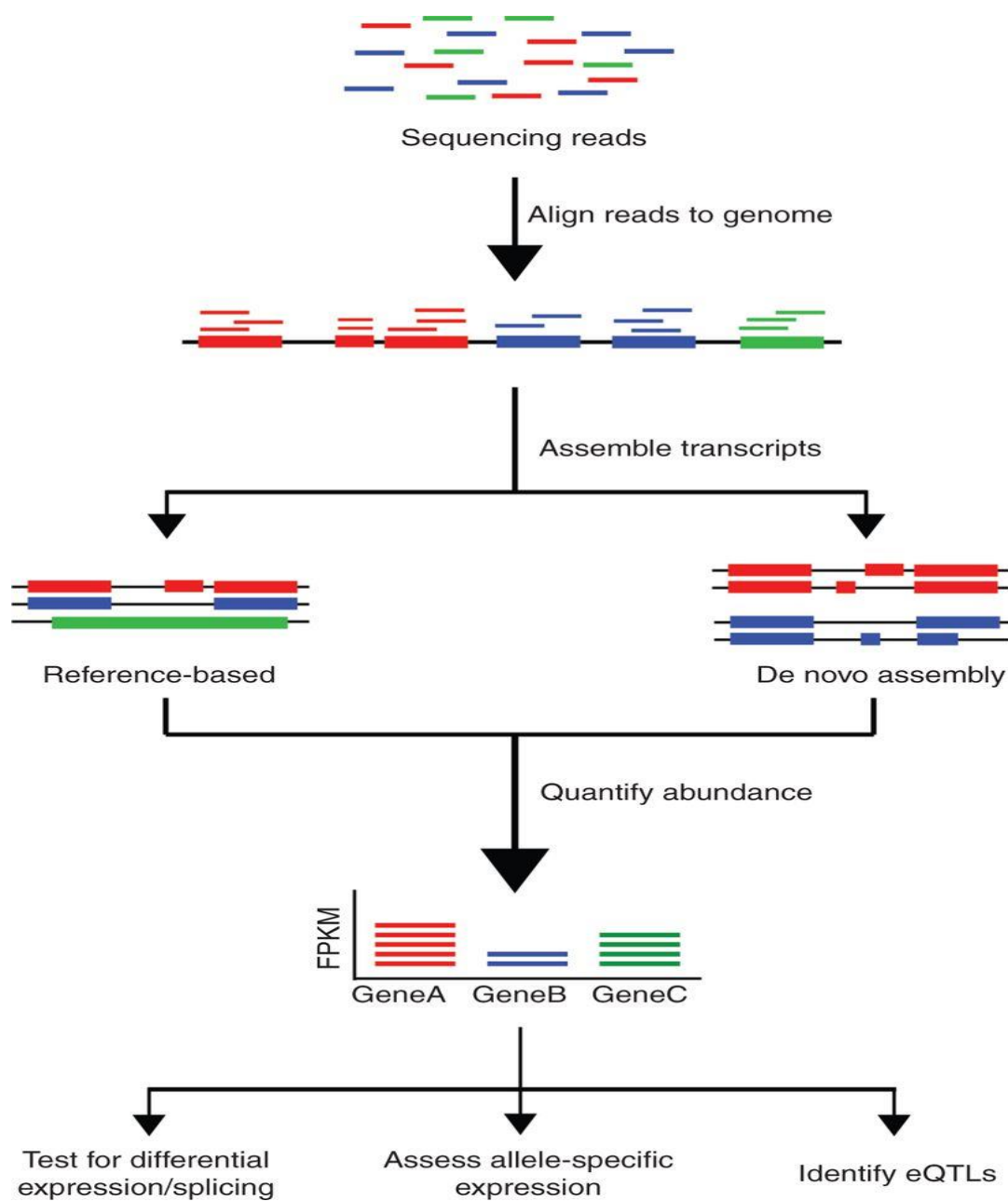


Figure 1.8. RNA-Seq data analysis is shown. After sequencing, reads are aligned to a reference genome. The reads are then assembled into transcripts and gene expression levels are determined. Lastly, downstream analyses are carried out such as determining differential gene expressions between samples and detecting allele-specific expressions (Kukurba and Montgomery, 2015).

1.6 Aim of the Present Study

As mentioned earlier, the cytoplasmic proteomes of bacilysin biosynthetic operon silenced mutant *B.subtilis* OGU1 and its parental strain *B. subtilis* PY79 were analyzed comprehensively in our laboratory by using two complementary proteomic approaches, 2DE MALDI-TOF/MS and nanoLC-MS/MS (Aras-Taşkın, 2010; Demir, 2013). These studies were validated by RT-qPCR analysis of selected differentially expressed genes (Ertekin *et al.*, 2020). The results shed light on the functional role of bacilysin biosynthesis, and implied pleiotropic effects of bacilysin on cellular physiology in *B. subtilis*. On the other hand, posttranscriptional and posttranslational modifications as well as diverse environmental and growth conditions influence the gene expression regulation in many ways. Therefore, transcriptomic analyses play a crucial role to better understand the pleiotropic effects of bacilysin silencing in *B. subtilis*. In the present study, the transcriptomic profiles of mutant OGU1 and its parental strain PY79 were analyzed by RNA-Seq method and RT-qPCR analyses were performed to validate the role of selected genes. Transcriptomic and proteomic data were integrated, compared, and discussed with respect to their cellular functions. Overall, this study provides a fresh perspective to pleiotropic changes that arise from the loss of bacilysin biosynthetic function by confirming and expanding earlier studies.

CHAPTER 2

MATERIALS AND METHODS

2.1 Bacterial Strains

Our lab-adapted *B. subtilis* PY79, the prototrophic derivative of *B. subtilis* 168 (Youngman *et al.*, 1984), and bacilysin non-producer *bacA::lacZ::erm* strain OGU1, which was previously constructed by our group (Köroğlu *et al.*, 2011), were used in this study.

2.2 Culture Media

The composition and preparation of culture media that were used in this study are given in Appendix A.

2.3 Buffers and Solutions

The composition and preparation of buffers and solutions that were used in this study are given in Appendix B.

2.4 Chemicals and Enzymes

The chemicals and enzymes that were used in this study are given in Appendix C.

2.5 Maintenance and Growth of Bacterial Strains

B. subtilis strains were grown in Luria-Bertani (LB) liquid medium and preserved on Luria-Bertani (LB) agar plates. All cultures were stored at 4°C and subcultured

monthly. Additionally, 20% glycerol stocks were prepared for each strain and kept at -80°C for the long-term storage.

For experimental procedures, *B. subtilis* strains that were preserved on Luria-Bertani (LB) agar plates were inoculated into 15 mL of PA medium (Perry and Abraham, 1979) (pH 7.4), and they were grown for 16h at 37°C (200 rpm) in 50 mL falcon tubes (Appendix A). These cultures were then used to inoculate 100 mL of PA medium with an initial optical density of 0.1 at 595 nm (OD₅₉₅). After inoculation, the cultures were cultivated by shaking at 37°C (200 rpm) for 16 hours. As indicated in K  ro  lu *et al.* (2011), lincomycin and erythromycin were added into all LB and PA media for the growth of OGU1 strain.

2.6 RNA-Sequencing (RNA-Seq)

2.6.1 Total RNA Isolation

Total RNA of 16h cultures of *B. subtilis* PY79 and OGU1 were isolated by using Nucleospin[®] RNA Kit (Macherey-Nagel GmbH & Co, Germany). Despite mostly carrying out the procedures according to the manufacturer's protocol, slight modifications were made. 450 µL of lysis buffer RA1 with 4.5 µL of β-mercaptoethanol was used in the cell lysis step, instead of 350 µL and 3.5 µL, respectively. In the next step, 450 µL of 70% (v/v) ethanol, which was previously prepared with DEPC treated water, was used in the experiment instead of 350 µL. The elution of total RNA samples was carried out with nuclease-free water and later kept at -80°C until further usage.

2.6.2 Agarose Gel Electrophoresis

To check the integrity of total RNAs, they were run on 0.8% agarose gel. The preparation of 0.8% agarose gel was made with TAE buffer (Appendix B), and ethidium bromide was added later. Total RNAs were mixed with loading dye (6X) and loaded on the gel. Electrophoresis was performed at 100 Volts for about 45 minutes. Vilber Lourmat Gel Imaging System (Vilber Lourmat, France) was used to capture all RNA bands.

2.6.3 Sample Integrity

The concentration and quality of total RNA samples were checked spectrophotometrically with Nanodrop (BioDrop, United Kingdom) at 260 nm and 280 nm. RNA integrity was once more evaluated and verified by using Bioanalyzer 2100 (Agilent, United States), and five criteria were taken into consideration: (i) concentration (ng/μl), (ii) quantity (μg), (iii) absorbance (OD_{260/280} and OD_{260/230}), (iv) RIN (RNA integrity number), and (v) 23S/16S rRNA ratio. To stabilize the RNAs at room temperature and avoid degradation until further RNA-Seq experiments, RNAsable[®] (Biomatrica, San Diego, CA, USA) was used.

2.6.4 RNA Sequencing

RNA sequencing of *B. subtilis* PY79 and OGU1 was performed on individual colonies on Illumina HiSeq 4000 system (BGI Genomics Co., Ltd., Hong Kong), and paired-end 100 bp libraries were obtained. An average of 3.83 GB data were produced by each sample. Raw sequence reads were deposited at National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under the BioProject accession no. PRJNA655951.

2.6.5 Bioinformatics Analyses

Low-quality reads and linker sequences were removed from the raw data. Clean reads were mapped and compared with the reference genome by using *Bowtie2* (Langmead and Salzberg, 2012) and *HISAT* (Kim *et al.*, 2015). Further detailed analysis of clean data was carried out by *Integrative Genomics Viewer (IGV)* 2.3.32 (Thorvaldsdóttir *et al.*, 2013). Calculation of gene expression levels were achieved by *RSEM* software (Li and Dewey, 2011), and later normalized by FPKM (fragments per kilobase of exon model per million reads). Transcripts were considered significantly differentially expressed when: (i) FDR (false detection rate) ≤ 0.005 and (ii) $|\log_2\text{FoldChange}| \geq 1$. For pathway analysis of significantly differentially expressed genes (DEGs), KEGG database (Kanehisa *et al.*, 2008) was used. Gene ontology (GO) terms were used for functional analyses.

2.7 Real Time Quantitative PCR (RT-qPCR)

2.7.1 Total RNA Isolation

Total RNA extraction was carried out as stated previously in section 2.6.1 of this study.

2.7.2 cDNA Synthesis with Reverse Transcription PCR (RT-PCR)

iScript™ cDNA Synthesis Kit (Bio-Rad Laboratories, United States) was used for cDNA synthesis from total RNA samples. 5X iScript™ Reaction Mix contains random hexamer and oligo(dT) primers as well as salts required for reverse transcriptase. The reaction components and protocol for cDNA synthesis are given in Table 2.1. Newly synthesized cDNAs were stored at -20°C until further analysis.

Table 2.1. RT-PCR Reaction Setup.

Component	Volume per Reaction (μl)
5X iScript™ Reaction Mix	4
iScript™ reverse transcriptase	1
Nuclease-Free Water	Variable (total volume of 20 μl)
RNA template	Variable (100 ng to 1 μg total RNA)
Reaction Protocol	
Annealing	5 minutes at 25°C
Reverse transcription	30 minutes at 46°C
Reverse transcriptase inactivation	5 minutes at 95°C
Cooling	Hold at 4°C

2.7.3 Real Time Quantitative PCR (RT-qPCR)

Synthesized cDNAs were used as templates in real time quantitative PCR (RT-qPCR) reactions that were performed in 0.2 ml PCR tubes with caps (Greiner Bio-One GmbH, Germany). RT-qPCR reactions were performed with SsoAdvanced™ Universal SYBR® Green Supermix (Bio-Rad Laboratories, United States), which contains Sso7d fusion polymerase, MgCl₂, dNTPs, enhancers, stabilizers and SYBR® Green I dye. RT-qPCR master mix components are given in Table 2.2.

Table 2.2. Components of RT-qPCR master mix.

Ingredients	Amount
SsoAdvanced™ Universal SYBR Green Supermix (2X)	10 µL
Forward primer	200 nM
Reverse primer	200 nM
cDNA template	Up to 100 ng
Nuclease-Free Water	4 µL

Two independent qPCR runs were carried out with three biological and two technical replicates each. A no-template control (NTC) sample was also contained in each run, having 2 µL of nuclease-free water instead of *B. subtilis* PY79 and OGU1 cDNAs. To detect possible contaminant PCR products such as primer dimers or non-specific amplification of template, melting curve analyses were also performed for each run. Primers for RT-qPCR analyses were designed using OligoAnalyzer Tool (Integrated DNA Technologies, Inc., United States), and primer sets are shown in Table 2.3. RT-qPCR reactions were performed in Rotor-Gene Q Real-time PCR cycler (QIAGEN, Germany). Reaction protocol for RT-qPCR is given in Table 2.4.

Table 2.3. Primer sets used for real-time quantitative PCR.

Gene	Sense Primer (5'-3')	Antisense Primer (5'-3')
<i>rpoB</i>	TGAACATCGGGCAGGTATTG	GTTTCCCAGACATCCTCTTCTC
<i>degR</i>	TGATTTAGAAGAACTGGCCGAT	CATCTGGATTTCATCGCCAAA
<i>ywpD</i>	CAGTAATCGGCTTGAGGTTCT	CTTGCTGACACCGTGAAGA
<i>ybfI</i>	GCTTGACCCACACCTTCATA	CCAGATACCGTTGCCCTTT
<i>fliJ</i>	CCTTATCCGAATATCAGCAATCAGT	TTGGTAGTGCCTCATTCTTGT
<i>comEA</i>	CAGTGGTGTACATCCCGAAA	ACTCCTCTAAGGTTGCTGTATTG
<i>acoA</i>	TGATGGCGACAGCATTACA	CCCTTGCCTTTGCACAATC
<i>acoR</i>	GCCGATGGTGCTCTGTAATA	CCGTTCTTCAACTCGTACA

Table 2.4. Reaction protocol for RT-qPCR.

1.	Denaturation-Holding stage	95°C	3 minutes	1 cycle
2.	Amplification-Cycling stage	denaturation	95°C	10 seconds
3.	Annealing	62°C	60 seconds	
4.	Extension	---	---	
5.	Return to 2	40 cycles		
6.	Melting curve stage	50°C - 95°C	0,5°C, increment 0.05 sec for each increment	1 cycle
7.	Cooling stage	40°C	30 seconds	1 cycle

2.7.4 Statistical Analysis

The calculation of Ct values was made by using a relative standard curve. Ct values were then used to calculate relative fold changes by implementing the $2^{-\Delta\Delta CT}$ method improved with efficiency correction (Rao *et al.*, 2013). RNA polymerase beta subunit *rpoB* was selected as the internal control (reference gene). Student's t-test was performed on GraphPad Prism 8.0 (Graphpad Software, CA, USA) to evaluate the data obtained. Statistical significance was reported as ns (no significance, $p > 0.05$), * ($p < 0.05$), **($p < 0.01$), and *** ($p < 0.001$).

2.8 Correlation Analysis

The correlation of transcriptomic and proteomic data was investigated by performing non-parametric Spearman's rank-order correlation test via the `cor.test()` and `cor()` functions and visualized with “ggpubr” library v.0.4.0 of R in version 4.0.3.

CHAPTER 3

RESULTS AND DISCUSSION

3.1 RNA-Sequencing (RNA-Seq) Analysis of *B. subtilis* PY79 and OGU1

It is crucial to understand the transcriptomic profile of an organism to be able to interpret the functional elements of the genome. RNA-Seq, a high-throughput technology, allows the detection of even the smallest changes in gene expression levels while also delivering more precise measurement than other currently existing techniques. In recent years, RNA-Seq replaced microarrays and other transcriptomic methods as the more favored approach due to its evident advantages over them (Kumar *et al.*, 2016; Wang *et al.*, 2009).

3.1.1 Quality Control of Total RNA Samples

For a successful RNA-Seq analysis, total RNA samples are required to be of high quality. Spectrophotometric measurement of total RNA samples was first assessed with A260/A230 and A260/A280 ratios. Total RNAs yielded A260/A230 and A260/A280 ratios of around 2.0, signifying pure and contaminant-free samples. Total RNAs were then run on an agarose gel to prove they were intact. The integrity of RNAs were further evaluated by verifying five essential criteria, as shown in Table 3.1.

Table 3.1. The minimum requirements of total RNA samples for a successful RNA-Seq analysis.

Concentration (ng/ μ l)	Quantity (μ g)	Absorbance	RIN value	23S/16S rRNA ratio
≥ 40 ng/ μ l	≥ 1 μ g	OD _{260/280} ≥ 1.8 OD _{260/230} ≥ 1.8	RIN ≥ 7.0	23S/16S ≥ 1.0

3.1.2 General Characterization of the RNA-Seq Data

A total of 40.73 Mb raw data was acquired from each *B. subtilis* strain PY79 and OGU1. background noise, adapter reads and low-quality reads with poor accuracy together interfere with the general reliability and quality of raw data. Thus, their removal from the original data is necessary. Filtering of the low-quality data generated 38.57 Mb (94.71%) and 37.87 Mb (92.98%) clean reads for *B. subtilis* PY79 and OGU1, respectively. An average of 3.83 Gb data were produced by each sample. 53.66% of PY79 and 59.15% of OGU1 were mapped to the reference genome, generating an average mapping ratio of 56.41% as shown in Table 3.2. Additionally, 1442 new transcripts were predicted. Only 10 new transcripts were, however, determined to have protein-coding capacity, resulting in 1432 new non-coding transcripts.

Table 3.2. Statistics of RNA-Seq data.

	<i>B.subtilis</i> PY79	<i>B.subtilis</i> OGU1
Type	Clean data	Clean data
Number of Reads	38,571,272	37,867,838
Data Size	3,857E+09	3,787E+09
N Reads (%)	0.11	0.13
GC (%)	45.56	46.12
Q20 (%)	98.50	98.44
Q30 (%)	95.35	95.29
Clean data/Raw data (%)	94.71	92.98
Total Mapped Reads (%)	53.66	59.15

3.1.3 Gene Expression Profiles of *B. subtilis* PY79 and OGU1

Gene expression analysis of *B. subtilis* PY79 and OGU1 revealed a total of 3814 commonly expressed genes between two strains. The number of specific expression genes was found as 83 and 8 in PY79 and OGU1, respectively (Figure 3.1).

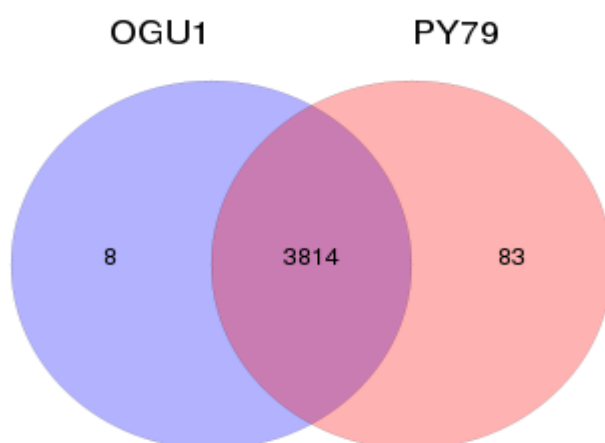


Figure 3.1. Gene expression analysis of *B. subtilis* PY79 and OGU1 are shown in a Venn diagram.

Differential gene expression analysis identified 2369 differentially expressed genes (DEGs) in two strains. While 2146 of DEGs, which corresponds to 54.96% of the whole transcriptome, were downregulated in mutant OGU1 strain compared with PY79, only 223 genes (5.71%) showed an increase in their transcript levels. 1536 transcripts (39.33%) were determined as non-significant either because (i) $|\log_2\text{FoldChange}| < 1$ or (ii) $\text{FDR} > 0.005$. Figure 3.2 below illustrates a volcano plot of differential gene expression analysis.

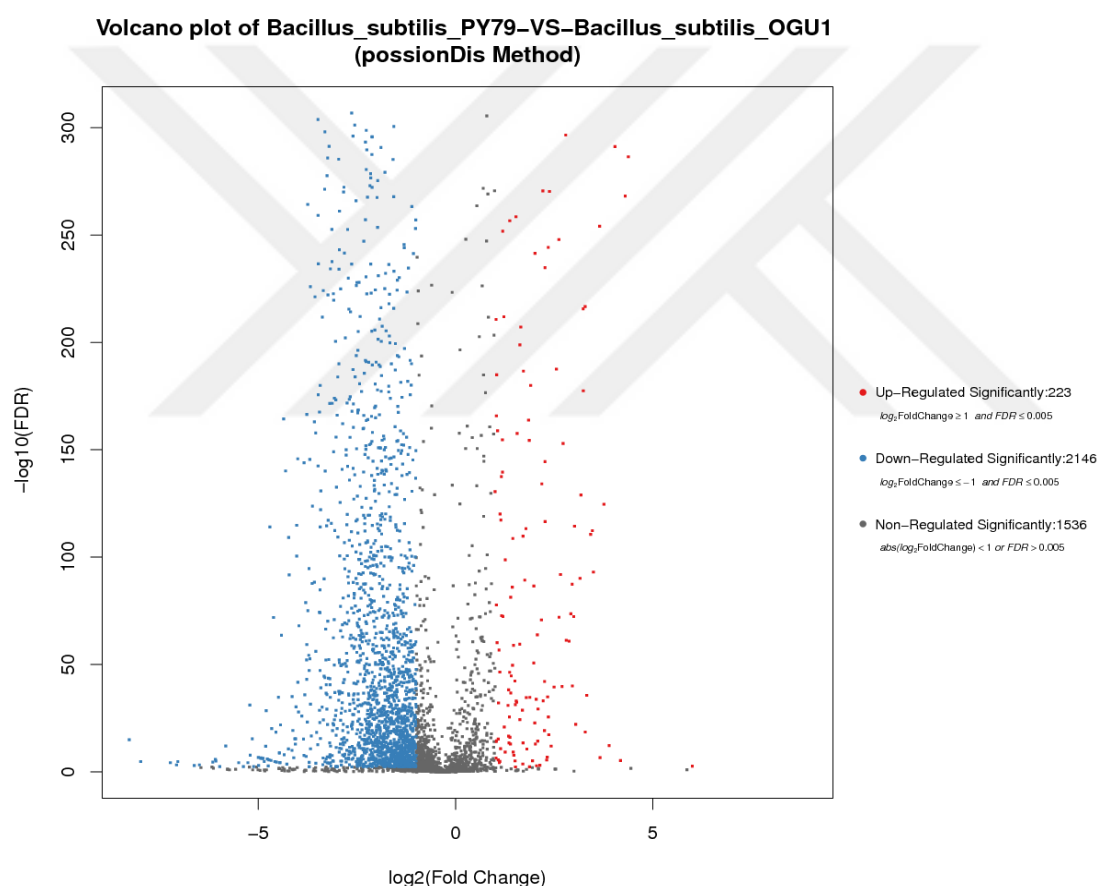


Figure 3.2. Volcano plot of *B. subtilis* PY79 and OGU1 differentially expressed genes. Horizontal axis represents the times of difference after log2 normalization. Vertical axis represents FDR values. Upregulated and downregulated genes are shown in red and blue, respectively. Genes shown in gray are determined as non-significant since they do not conform with previously stated criteria.

3.1.4 KEGG Pathway Analysis

To be able to comprehend how molecular networks and interactions operate under certain conditions, it is essential to understand the roles of genes and their biological functions. Pathway analysis therefore plays one of the most crucial roles in gaining significant insights into how gene expression is regulated in an organism. KEGG (Kyoto Encyclopedia of Genes and Genomes) is the main public database used for pathway analysis, which is divided into five main categories for this study: (i) cellular processes, (ii) environmental information processing, (iii) genetic information processing, (iv) metabolism, and (v) organismal systems.

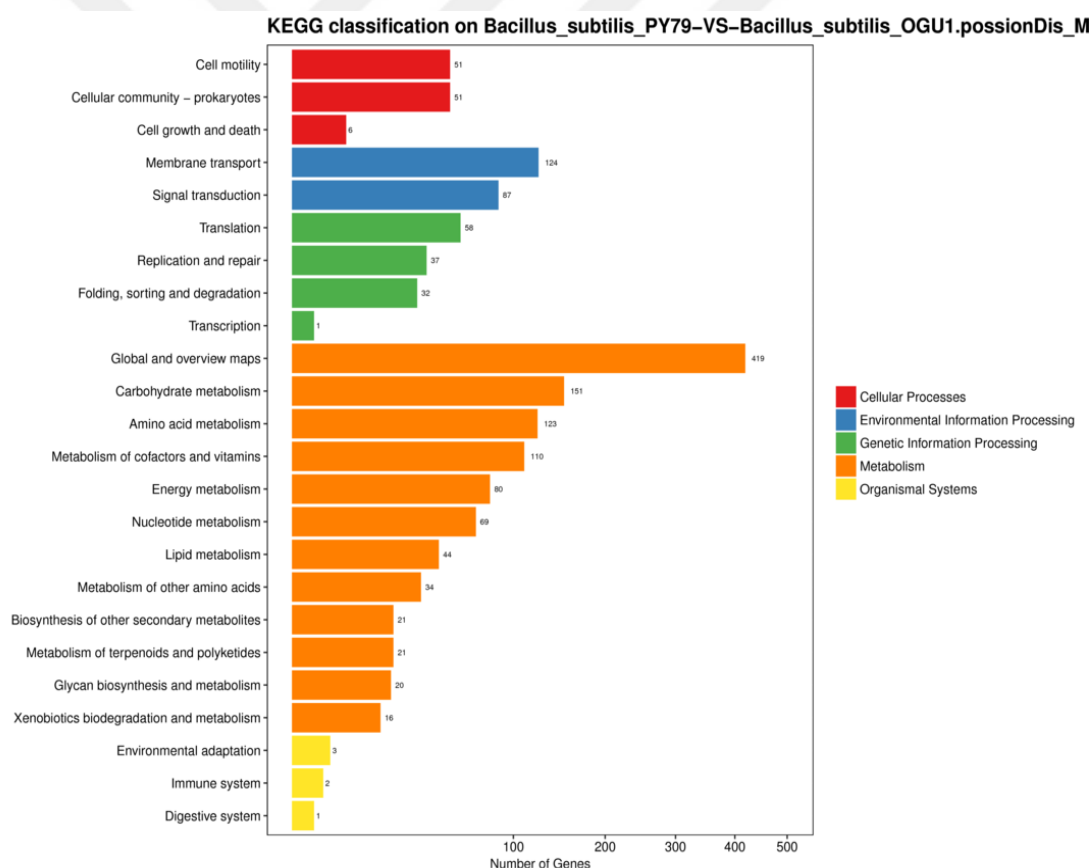


Figure 3.3. DEGs of *B. subtilis* OGU1 distributed into five KEGG pathway categories.

As seen in Figure 3.3, most of the differentially expressed genes belonged to metabolic functions with a total of 1108 genes, followed by environmental information processing with 211 genes, genetic information processing with 128 genes, cellular processes with 108 genes, and lastly organismal systems with only 6 genes. ‘Global and overview maps’ comprised the highest number of DEGs with 419 genes, corresponding to 37.82% of all genes under the category of metabolism. Carbohydrate metabolism with 151 genes (13.63%), and amino acid metabolism with 123 genes (11.10%) were the other two subcategories under metabolism with the highest number of DEGs. It is worth noting that ‘membrane transport’ of environmental information processing also included a significant amount of DEGs.

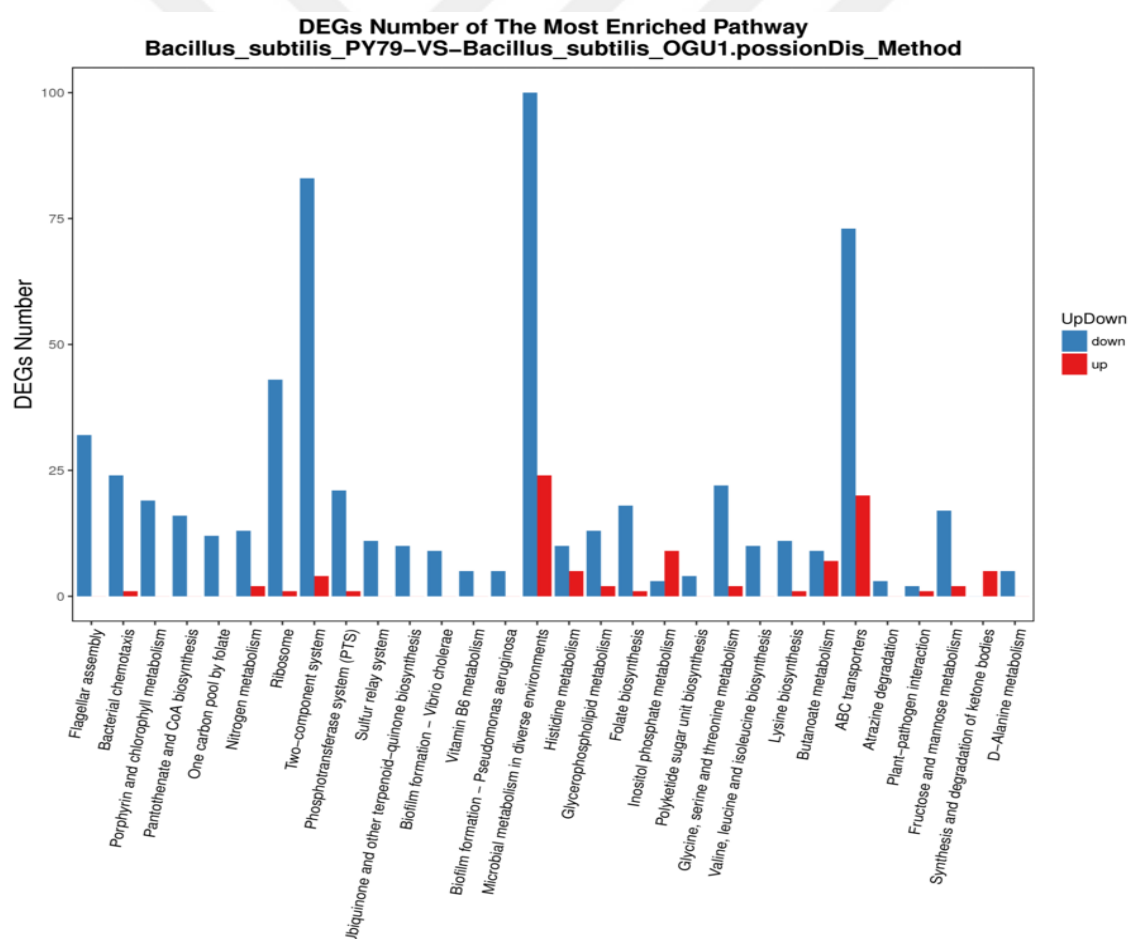


Figure 3.4. The most enriched pathways of *B. subtilis* OGU1 are illustrated. The number of DEGs are shown in red (upregulated) and blue (downregulated).

Figure 3.4 shows the most enriched pathways of OGU1 strain. ‘Microbial metabolism in diverse environments’ of ‘global and overview maps’ was found as the most enriched pathway with a total of 124 DEGs. ‘ABC transporters’ of ‘membrane transport’ (93) and ‘two-component system’ of ‘signal transduction’ (87) were the other two pathways with the highest number of DEGs, respectively.

All of the following enriched pathways belonged to ‘metabolism of cofactors and vitamins’ with a total of 81 DEGs: ‘Porphyrin and chlorophyll metabolism’ (19), ‘pantothenate and CoA biosynthesis’ (16), ‘one carbon pool by folate’ (12), ‘ubiquinone and other terpenoid-quinone biosynthesis’ (10), ‘vitamin B6 metabolism’ (5), and ‘folate biosynthesis’ (19). ‘Global and overview maps’ (microbial metabolism in diverse environments), ‘membrane transport’ (phosphotransferase system (PTS) and ABC transporters), and lastly ‘signal transduction’ (two-component system) were the other top three groups with 124, 115, and 87 DEGs, respectively, in most enriched pathways.

3.1.5 Gene Ontology (GO) Functional Classification

The GO functional classification is an internationally standardized classification system that is extensively used for the interpretation and characterization of genes or gene functions. The three ontological categories of GO are biological process, molecular function, and cellular component.

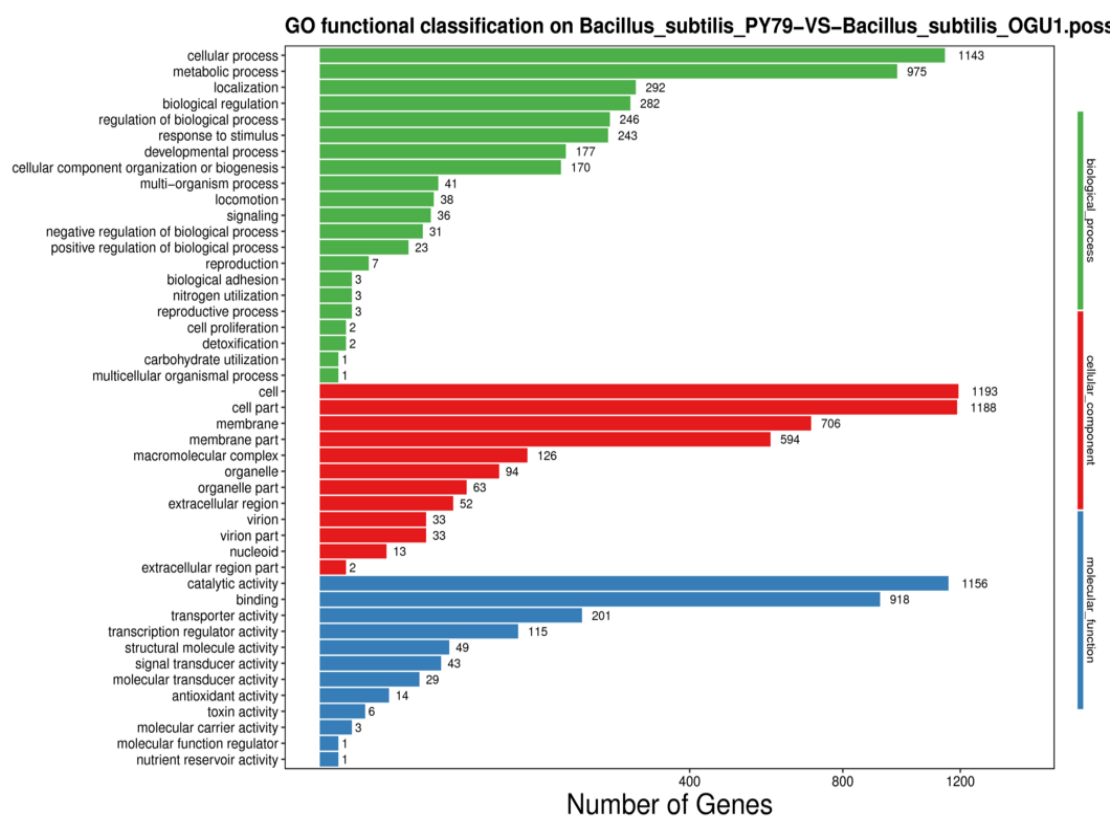


Figure 3.5. GO functional classification map of *B. subtilis* OGU1.

In the biological process category, ‘cellular process’ (1143) and ‘metabolic process’ (975) were the two functional classes with highest number of DEGs, constituting 56.95% of the whole biological process category. ‘Localization’ (292), ‘biological regulation’ (282), ‘regulation of biological process’ (246) and ‘response to stimulus’ (243) were recorded as the other top functional classes in the mentioned category, as shown in Figure 3.5.

‘Cell’ (1193) and ‘cell part’ (1188) of cellular component were found as the classes with highest number of DEGs, forming more than 58% of the whole category. They were followed closely by ‘membrane’ (706) and ‘membrane part’ (594).

Lastly, ‘catalytic activity’ (1156) and ‘binding’ (918) were the top two functional classes with highest number of DEGs in molecular function category, with a total of 81.78% of whole category. ‘Transporter activity’ (201) and ‘transcription regulator activity’ (115) were found as the other two classes with significant amount of DEGs.

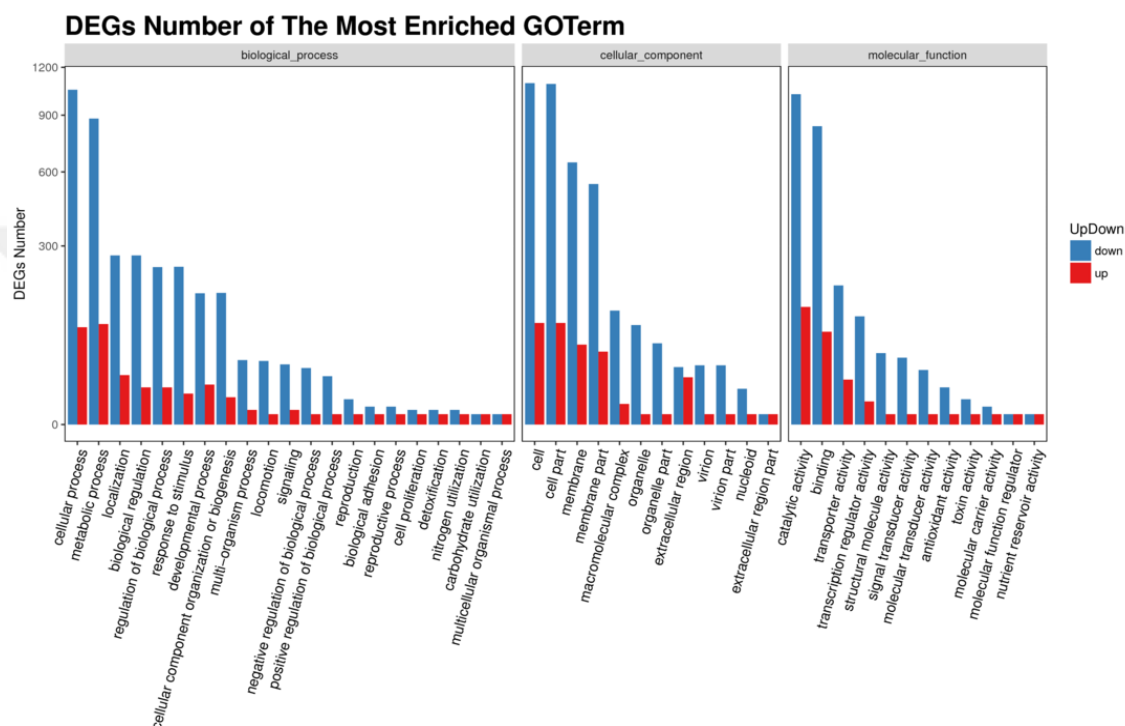


Figure 3.6. The most enriched GO terms of *B. subtilis* OGU1 are given. The number of DEGs are shown in red and blue for upregulated and downregulated DEGs, respectively.

Figure 3.6 confirms the findings of previous Figure 3.5. The most enriched GO terms were ‘cellular process’ and ‘metabolic process’ of biological process, ‘cell’ and ‘cell part’ of cellular component, and finally ‘catalytic activity’ and ‘binding’ of molecular function.

3.2 Validation of RNA-Seq Analysis with Real Time Quantitative PCR

Quantitative PCR (qPCR) is a commonly used validation technique for RNA-Seq analysis as well as complementing proteomic analyses in biological systems (Handler *et al.*, 2018; Wang *et al.*, 2009). However, the accuracy of this technique depends on several variables such as the quality of mRNA, adequate reference genes and amplification efficiency, which in turn may play a considerable role in the interpretation of the results (Pombo *et al.*, 2017).

In this study, 7 selected genes were investigated with RT-qPCR technique to measure their expression levels and validate RNA-Seq data in *B. subtilis* OGU1. The results of qPCR analyses were grouped into two depending on the change in their expression levels in RNA-Seq data. The results of upregulated (*acoA* and *acoR*) and downregulated (*degR*, *ywpD*, *ybfI*, *fliJ* and *comEA*) genes are given in Figure 3.7 and Figure 3.8.

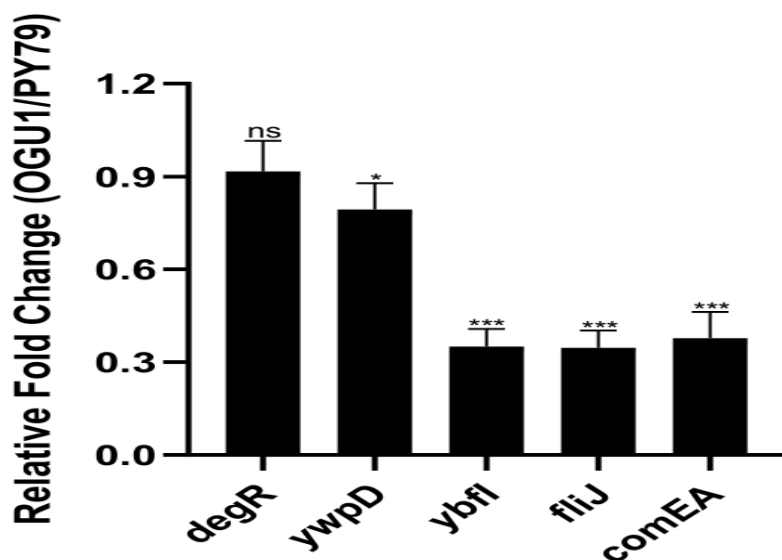


Figure 3.7. RT-qPCR results of selected, downregulated genes. The significance levels are represented as ns (no significance, $p > 0.05$), * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$).

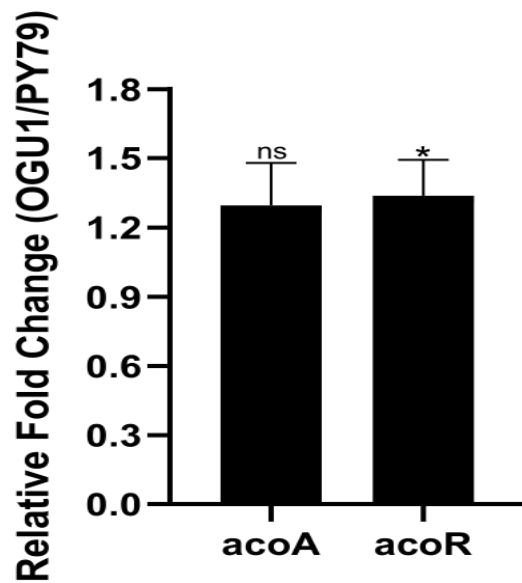


Figure 3.8. RT-qPCR results of selected, upregulated genes. The significance levels are represented as ns (no significance, $p > 0.05$), * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$).

The expression levels of all 7 selected genes were consistent with our RNA-Seq data. Although it is important to note that there were two genes, *degR* and *acoA*, with statistically non-significant results. Melting curve analyses also showed no contaminant PCR products. Overall, it is possible to conclude that RT-qPCR results were accorded well with transcriptomic data.

3.3 Integration of Transcriptomic and Proteomic Approaches

Comparative 2DE MALDI-TOF/MS and nanoLC-MS/MS studies on *B. subtilis* PY79 and OGU1 have been conducted previously by our group. 2DE approach identified 159 differentially expressed proteins that corresponded to 121 distinct ORFs. Although nano-LC-MS/MS analysis discovered 1274 proteins, only 76 of them were expressed differentially. However, only a few proteins were differentially expressed in both studies (Aras-Taşkın, 2010; Demir, 2013; Ertekin *et al.*, 2020).

Diverse environmental and growth conditions affect the transcriptomic and proteomic profiles of an organism and regulate gene expression in several ways. Posttranscriptional and posttranslational modifications create a dynamicity that is challenging to interpret since they bring many possibilities to how molecular patterns can be reflected. Therefore, individual analysis of transcriptomic and proteomic profiles provides limited information regarding actual gene expression regulation (Kumar *et al.*, 2016). Integration of transcriptomic and proteomic data brings a new, fresh perspective into gene expression regulation in *B. subtilis* and offers a more comprehensive and complementary understanding of pleiotropic effects of bacilysin silencing.

3.3.1 Comparative Analysis of Transcriptomic and Proteomic Data

The data obtained from the RNA-Seq analysis and previous proteomics studies of our group (Aras-Taşkın, 2010; Demir, 2013) are discussed in this section with respect to their cellular functions.

3.3.1.1 Sporulation and Germination

More than 30 differentially expressed proteins were detected in this category by our earlier proteomics studies. According to RNA-Seq analysis, the majority of genes that take part in sporulation and germination were downregulated in *bac*-operon silenced OGU1, and most of them belonged to σ^E and σ^K regulons.

spo0A, the master regulator of entry into sporulation (Hoch, 1993), showed -1.46-fold downregulation in OGU1. *spo0B* and *spo0F*, the two crucial response regulators of the sporulation phosphorelay (Perego and Hoch, 2002), displayed a strong 1.94- and 2.30-fold decrease in OGU1, respectively. However, neither of these three transcripts were identified at protein level.

A member of σ^K regulon and the penultimate gene set of hierarchical cascades of sporulation, *gerE* is vital for transcriptional activation of coat protein genes, such as *cotB* and *cotC*. As it also has an influence on the expression of other coat protein genes like *cotA* and *cotD*, *gerE* is responsible for the proper flow of the regulatory cascade (Zheng *et al.*, 1992). In the present study, *gerE* was found to be 2.74-times downregulated at mRNA level despite not being detected in our earlier proteomics work. Though it is worth noting that GerE is a small regulatory protein (8.43 kDa) with a high pI value (9.64).

Many genes that code for spore coat proteins, including *cotA-D*, *cotF-I*, *cotM*, *cotP-Z*, *cotSA*, *oxdD*, *cgeA* showed drastically lower levels of expression in the mutant. Except for *cotC* (-1.69-fold) and *cotF* (-1.83-fold), all mentioned spore coat genes demonstrated at least 2-fold downregulations, ranging from 2.16 to 3.76-fold. However, despite some spore coat genes like *cotE* (-0.86-fold), *cotO* (-0.72-fold), *safA* (-0.60-fold) and *spoVID* (-0.25-fold) exhibiting relatively decreased levels of

expression, they were statistically non-significant. Spore coat polysaccharide synthesis genes like *spsB*, *spsJ* and *spsK* were also found to be significantly downregulated in bacilysin nonproducer OGU1 by 3.23-, 2.11- and 2.41-fold changes. According to Plomp *et al.* (2014), and Zheng *et al.*, (1988), the loss of coat proteins such as CotE, CotH, CotO and SafA would hinder the coat architecture. The significant downregulation of numerous spore coat genes and spore coat polysaccharide synthesis genes confirm that the overall coat architecture of OGU1 is disrupted, and this disruption causes OGU1 to be much more susceptible to lysozyme and chloroform. Moreover, significant underrepresentation of *cotA* leads to the loss of brownish pigmentation (Hullo *et al.*, 2001), which confirms the findings of morphological analyses in our previous study that bacilysin takes part in the regulation of *cotA* gene expression (Ertekin *et al.*, 2020).

ScoC (Hpr), a transition state regulator, directly binds to P_{bac} of *bacABCDEF* and negatively regulates sporulation and protease production (Inaoka *et al.*, 2009). In nanoLC-MS/MS analysis, ScoC showed a non-significant 0.40-fold increment. However, RNA-Seq analysis revealed a substantial decrease (2.55-fold) at the expression levels of *scoC* (*hpr*).

In *Bacillus* species, Dipicolinic acid (DPA) takes up 25% of core dry weight of the spore core along with its divalent cations (Ca-DPA). The accumulation of DPA and calcium has very precise roles in the protection of spore DNA from damage and together they form an essential component of the overall sporulation process (Jamroskovic *et al.*, 2016; Magge *et al.*, 2008; Setlow *et al.*, 2006). The SpoVF protein complex is responsible for the final step in DPA synthesis (Daniel and Errington, 1993). *dpaA* (*spoVFA*) and *dpaB* (*spoVFB*) displayed 2.63- and 2.65-fold downregulation in the current RNA-Seq analysis, respectively. Both DpaA (SpoVFA) and DpaB (SpoVFB) were present at protein level in 2DE MALDI-TOF/MS and nanoLC-MS/MS analyses, respectively, with 2.64- and 2.1- times

lower expression levels. Lack of alterations in DPA content of spores implied no change in spore heat resistance even though dipicolinate synthase subunits were underrepresented in OGU1 (Ertekin *et al.*, 2020). Spores with no DPA or low DPA levels might lack the cortex-lytic enzyme SleB (Magge *et al.*, 2008), which was found in lower abundance at mRNA level (-1.33-fold). SleB was not detected in the proteome of OGU1.

It was previously reported that the inactivation of *opp* (*spo0K*) operon results in the loss of bacilysin biosynthesis (Yazgan *et al.*, 2001a). Oligopeptide ABC transporter OppD (Spo0KD) was 2.47 times underrepresented in OGU1 at proteome level, however almost no change in its transcript was detected in RNA-Seq analysis. *oppA* (*spo0KA*), *oppB* (*spo0KB*), *oppC* (*spo0KC*) and *oppF* (*spo0KE*) exhibited 0.81-, 1.44-, 1.49- and 0.64-fold decrease in OGU1, respectively. They either were not detected at protein level or their abundance was non-significantly low.

3.3.1.2 Global Regulators

In *B. subtilis*, the two-component signal transduction system ResDE is the main regulator of anaerobic respiration. While the response regulator ResD and the histidine sensor kinase ResE are crucial for the early stages of anaerobic gene regulation, they also induce the transcriptional regulator of anaerobic genes (*fnr*) upon oxygen limitation (Nakano and Zuber, 1998). At mRNA level, both *resD* and *resE* were found to be 1.65 and 1.91-fold downregulated. Additionally, *fnr* showed a sharp decrease in its transcript levels in OGU1 (3.86-fold). However, only ResD was significantly detected at protein level and showed a 2-fold decrease.

It was previously reported that biofilm formation and swarming motility relies on LuxS quorum sensing (QS) by Autoinducer-2 (AI-2) in *B. subtilis*. Furthermore, Spo0A has also been revealed as a negative regulator of LuxS/AI-2 system (Duanis-Assaf *et al.*, 2016; Lombardía *et al.*, 2006). *luxS* showed a strong 3.09-fold downregulation as expected in OGU1 at transcriptomic analysis even though it was found at elevated levels in 2DE MALDI-TOF/MS analysis. Our previous study demonstrated that no significant swarming motility or biofilm formation was detected in the mutant (Ertekin *et al.*, 2020).

The global regulator CodY is responsible for the regulation of more than 100 genes in *B. subtilis*. The products of these genes are mostly associated with adaptation to poor growth conditions; they are promoted during nutrient unavailability when the growth rate reduces. Transport systems, antibiotic production, genetic competence, catabolic pathways, extracellular degradative enzymes, flagellin and early sporulation genes are among the targets of global regulator CodY (Sonenshein, 2005). Moreover, CodY is one of the transcriptional regulators of *bac*-operon as it co-binds with AbrB and leads to negative regulation of bacilysin synthesis (Köroğlu *et al.*, 2011). It was revealed that CodY directly inhibits ScoC (Hpr), which in turn causes ScoC (Hpr) to lose its own inhibitory effects. CodY also utilizes ScoC (Hpr) in its regulatory cascade for the suppression of various genes when it loses its own activity, which leads to a creation of several forms of cascade regulations (Belitsky *et al.*, 2015). Intriguingly, the present transcriptomics analysis found that *codY* showed a very non-significant 0.03-fold increase in OGU1. Still, numerous members of CodY regulon were found to be significantly underrepresented in the mutant at both mRNA and protein levels, such as inosine-monophosphate dehydrogenase (*guaB*), acotinase (*citB*), alpha subunit of urease (*ureC*), 3-isopropylmalate dehydratase subunit (*leuC*), and amidohydrolase (*amhX*). Other members of CodY regulon like CodY-activated acetate kinase (*ackA*) and dihydroxy-acid dehydratase (*ilvD*) were significantly downregulated at mRNA level but absent from OGU1 when compared to PY79 at protein level.

Another gene under negative control of CodY regulon is the *ispA* gene that encodes for an intracellular protease (Belitsky and Sonenshein, 2013). In nutrient broth medium, *ispA* expression was found to be negatively controlled by ScoC (Ruppen *et al.*, 1988). In the RNA-Seq analysis, *ispA* showed a strong 2-fold overrepresentation in OGU1, which justifies the solid downregulation of ScoC (Hpr). Interestingly, IspA was not detected in the proteome of OGU1 with the nanoLC-MS/MS approach. Based on our findings of CodY global regulator and other genes under its control, there are still several underlying mechanisms that await further investigations to thoroughly understand the molecular patterns of its pleiotropic effects, especially considering the difference between their transcriptomic and proteomic profiles.

At the end of logarithmic growth, *B. subtilis* enters a transition phase where genes that regulate the search of alternate nutrient sources are expressed. Transition state regulators like AbrB directly control the expression of these genes like proteases and amylases. While AbrB positively regulates the transcription of certain genes including *scoC* (*hpr*), the suppression of *abrB* gene transcription is crucial for the expression of several post-exponential genes. The response regulator protein Spo0A is responsible for the control of *abrB* suppression (Greene and Spiegelman, 1996; Perego and Hoch, 1991). Moreover, AbrB also negatively regulates the regulation of bacilysin biosynthesis by interacting with P_{bac} (Köroğlu *et al.*, 2011). The transcript abundance of *abrB* was found to be decreased by 1.17-fold in our RNA-Seq analysis. Additionally, an extracellular alkaline protease *aprE* that is shown to be repressed by *abrB* (Strauch *et al.*, 1989), *scoC* (*hpr*) (Kallio *et al.*, 1991), and *sinR* (-1.24-fold) (Gaur *et al.*, 1991) displayed a sharp 3.69-fold increase at mRNA level, which is in accordance with our data. However, the regulatory mechanisms between *abrB* and *spo0A* await further analysis.

DnaA, the replication initiation protein, is directly repressed by Spo0A (Molle *et al.*, 2003). *dnaA* showed a sharp 2.78-fold downregulation in the mutant OGU1. RT-

qPCR analysis of *dnaA* also displayed 2.4-fold decrease in its transcript abundance (Ertekin *et al.*, 2020). Yet, DnaA was absent from our proteomic analyses.

CheV, which is responsible for sensory adaptation in response to attractants (Karatan *et al.*, 2001), exhibited 2.11-fold upregulation in the mutant at protein level. Intriguingly, RNA-Seq analysis revealed a 3.43-fold lower abundance of *cheV* at mRNA level.

The DegS/DegU two-component signal transduction system is critical for degradative enzyme production. Moreover, *bac*-operon and *bacG* are positively regulated by this two-component system (Mariappan *et al.*, 2012). Both the response regulator *degU* (-0.93-fold) and the histidine protein kinase *degS* (-1.77-fold) were underrepresented in our RNA-Seq analysis. However, DegU was 1.42-fold overexpressed at protein level. According to Ishii *et al.* (2013), the global carbon catabolite repressor CcpA positively regulates *degU*. *ccpA* showed a 1.26-fold decrease in our RNA-Seq study. RT-qPCR analysis also showed a strong 2.7-fold downregulation of *ccpA* (Ertekin *et al.*, 2020).

3.3.1.3 Stress Response

A large group of stress proteins might have a nonspecific yet crucial and protective roles resulting from stress or nutrient starvation without an actual, particular stress stimulus (Petersohn *et al.*, 2001). Transcription of the general stress genes significantly increases after metabolic or environmental stress, which is then followed by σ^B activation (Bernhardt *et al.*, 1997). For all *Bacillus* species that cannot successfully sporulate, either because of stress conditions like osmotic stress or insufficient oxygen that do not favor sporulation, or the cell density is too low, the

general stress response might be a crucial option (Grossman and Losick, 1988; Hoffmann *et al.*, 1995; Ruzal *et al.*, 1998).

In our RNA-Seq analysis, a significant majority of stress response genes were found at lower levels in bacilysin-nonproducer OGU1, regardless of their regulation. These genes include *yceD* (unknown, similar to tellurium resistance protein; -1.93-fold), *yceE* (unknown, similar to tellurium resistance protein; -1.57-fold), *yceH* (unknown, similar to toxic anion resistance protein; -2.13-fold), *ygaF* (unknown, resistance against oxidative stress; -2.19-fold), *yjID* (NADH dehydrogenase; -2.36-fold), *yfkO* (protection against NaOCl stress; -1.36-fold), *yugI* (unknown, a putative member of stringent response regulon; -2.74-fold), *yppQ* (*msrB*; peptide methionine sulfoxide reductase; -2.04-fold), *ytkL* (unknown, general stress protein; -0.72-fold), *bmrA* (multidrug-efflux transporter; -1.69-fold), *msrA* (peptide methionine sulfoxide reductase; -1.66 fold), *ahpC* (alkyl hydroperoxide reductase; -1.92-fold), *katX* (major catalase in spores; -0.30-fold), *ahpF* (resistance against peroxide stress; -1.65-fold), *yaaN* (unknown, cell envelope stress induced by salt shock; -0.42-fold), *dnaK* (class I heat shock protein; -0.53-fold), and *yvaB* (resistance to 2-methylhydroquinone; -0.26-fold).

Out of the transcripts that were mentioned above, DnaK and YceE were absent from OGU1 in our 2DE MALDI-TOF/MS analysis. Two members of σ^B regulon, YtkL and BmrA, and other stress proteins YugI, YppQ, AhpC and YaaN were overrepresented at OGU1 at protein level.

These findings suggest that general stress proteins might be indeed alternatives of cells that cannot efficiently sporulate as we also discovered lower expression levels of sporulation genes at mRNA level, consistent with our proteomic work. The evident overall downregulation of general stress response genes indicates that upon

the loss of bacilysin biosynthetic function, *B. subtilis* becomes more susceptible to stress. Especially being the alternatives to sporulation genes, the lack of proper regulation of general stress response genes causes *B. subtilis* to become extremely vulnerable to environmental and nutritional stress. These drastic changes in the absence of bacilysin leads to a defense mechanism that involves posttranslational modifications. Some proteins like AhpC, YaaN, YppQ, YugI, BmrA and YtkL showed elevated levels of expression in bacilysin nonproducing strain OGU1 despite exhibiting downregulation at mRNA level. This discrepancy might be due to numerous posttranslational modifications that are crucial for *B. subtilis* to overcome extreme stress resulting from the lack of bacilysin production and to survive.

3.3.1.4 Secondary Metabolite Production and Resistance

In the present study, all *bac* operon genes (*bacA* -2.55-fold; *bacB* -4.00-fold; *bacC* -4.22-fold; *bacD* -2.70-fold; *bacE* -2.85-fold; *bacF* -3.22-fold) and the monocistronic gene *bacG* (-1.45-fold) were found to be significantly downregulated in bacilysin biosynthetic operon silenced mutant OGU1, as expected. However, BacA, BacB, BacC, BacD and BacF were absent from OGU1 in comparison to its parental strain PY79 in our previous proteomics studies. Sharp downregulation of *bacABCDEF* and *bacG* expression as well as the lack of detectable end product proves the loss of bacilysin biosynthesis in *bac*-operon silenced OGU1 strain. Overall, these findings demonstrate that *bacA*-targeted pMutin3 T3 insertion into OGU1 genome indeed generated a *B. subtilis* strain that is unable to produce any detectable bacilysin.

Antilisterial bacteriocin (subtilisin) production is carried out by *albE* gene and is encoded by *sbo-alb* operon. Transcription of *sbo-alb* operon is induced as a response to oxygen unavailability and nutritional stress, which is controlled by both the ResDE two-component signal transduction complex and the transition state regulator

AbrB (Nakano *et al.*, 2000). *albE* was found to be 3.66-fold downregulated, while *resD* was 1.65-fold downregulated at mRNA level. Intriguingly, while ResD was also downregulated at protein level, AlbE was completely absent from PY79 while showing 2.98-fold overrepresentation in OGU1. The upregulation of AlbE did not seem to result from the activity of ResDE signal transduction complex, but rather due to elevated levels of AbrB in OGU1. It would be possible to speculate that there is a more intricate mechanism that is triggered upon the loss of bacilysin biosynthetic function. Furthermore, OGU1 might exhibit a competitive adaptation at increased AlbE expression levels upon the loss of bacilysin biosynthesis, since the secretion of subtilisin, a new antimicrobial, into the environment would compensate for the loss of another (Ertekin *et al.*, 2020).

Proteins that function in pre-subtilisin processing and subtilisin export are encoded by *albABCDEFG* genes that together form the *alb* operon, and *sbo-alb* gene cluster is responsible for the production of mature subtilisin. Based on the comparison of the presubtilisin and mature subtilisin sequences, unlike the regular posttranslational modifications that take place during the synthesis of class I lantibiotics or class II bacteriocins, it was revealed that some residues undergo unusual PTMs. The subtilisin peptide product is constituted from 32 common amino acids along with some unusual residues that are a product of PTMs (Zheng *et al.*, 1999; Zheng *et al.*, 2000). All members of the *alb* operon showed sharp downregulations in our RNA-Seq data, ranging from 2.18-fold to 4.41-fold. As mentioned above, AlbE exhibited the most differential expression at protein level with a 2.98-fold (R_{SC}) increase. However, apart from AlbE, AlbF was also absent from PY79 strain (R_{SC} 1.40-fold). According to Zheng *et al.* (2000), *albA* and *albF* are the most crucial genes for subtilisin production. Additionally, AlbA and AlbC also have more peptide count in OGU1 strain. Based on these findings, it is possible to speculate that subtilisin might be produced and secreted into the environment as a new antimicrobial agent to compensate for the absence of bacilysin, and PTMs might play a significant role in this process.

Interestingly, both BceB (ABC transporter (permease) for the export of bacitracin, plectasin, mersacidin and actagardine) and BmrA (multidrug ABC transporter (ATP-binding protein / multiple antibiotic resistance) were found to be absent from PY79 compared to the mutant OGU1 at protein level. While *bceB* showed only 0.26-fold decreased expression at mRNA level, *bmrA* displayed 1.69-fold downregulation in OGU1, suggesting another possible mechanism of posttranslational modifications.

3.3.1.5 Others

As one of the key components of cell wall synthesis, the *dlt* operon controls the production of D-alanylation of lipoteichoic acids in both *B. subtilis* and numerous other Gram-positive bacteria (Cao and Helmann, 2004). In many Gram-positive or pathogenic bacteria, such as *Staphylococcus aureus*, inactivation of DltA is associated with termination of biofilm production, a higher susceptibility to cationic antibiotics and host defensins, and reduction in their pathogenicity (Collins *et al.*, 2002; Gross *et al.*, 2001; Peschel *et al.*, 1999, Peschel *et al.*, 2001). In our study, all members of this operon (*dltABCDE*) showed significant downregulation in the mutant strain, ranging from 1.60-fold to 2.43-fold. DltA was less abundantly expressed at protein level in OGU1 as well. These findings might suggest that the loss of bacilysin biosynthesis might lead to a more susceptible phenotype to certain agents, lack of biofilm production and defects in teichoic acid synthesis.

glmS (glutamine-fructose-6-phosphate transaminase) takes part in cell wall synthesis, and it was found to be 1.20-fold downregulated in OGU1. It is a glucosamine 6-phosphate (GlcN6P)-responsive small ribozyme with a self-cleavage activity. Binding of GlcN6P as a cofactor triggers the self-cleavage activity for this reaction and leads to a gene that is only expressed in the absence of GlcN6P (Collins *et al.*, 2007). GlmS was 2.06-fold downregulated at protein level. RT-qPCR analysis

also discovered 6.25-fold decreased levels of its transcript (Ertekin *et al.*, 2020). Externalized bacilysin may be partly taken up into the cell, sequestering GlcN6P and GlmS to provide the expression of the latter. However, the significant downregulation of *glmS* ribozyme after bacilysin biosynthetic operon silencing implies elevated levels of GlcN6P and self-cleavage activity of *glmS* since the inhibition of GlcN6P synthase activity by its C-terminal anticapsin moiety provides the antimicrobial activity of bacilysin.

MutT repair protein of mismatch recognition protects growing *B. subtilis* cells against oxidizing agents by playing an anti-mutator role (Castellanos-Juárez *et al.*, 2006). Another protein with the same function, MutS was expressed in OGU1 while it was absent from its parental strain PY79 (R_{SC} 2.09-fold). In our RNA-Seq analysis, *mutS* was found to be 1.82-fold underexpressed in the mutant. Overall, the activation of DNA mismatch repair protein in *bac*-operon silenced OGU1 point to an existence of a more complex mechanism.

Interestingly, three proteins with unknown functions, were found at elevated levels in OGU1. However, all three of them, *ywhD* (-2.21-fold), *ywlG* (-2.31-fold) and *yciC* (-5.21-fold) exhibited opposite behavior at mRNA level.

3.3.2 Correlation Analysis

Even though both transcriptomic and proteomic analyses can individually provide basic information regarding gene expression regulation in an organism, they can only partly explain the genome due to factors such as the rate of mRNA translation, protein degradation and posttranslational modifications. Thus, transcriptomic data should be integrated with proteomic data for the comprehensive understanding of gene expression regulation in an organism (Delmotte *et al.*, 2010; Kumar *et al.*, 2016; Muers, 2011).

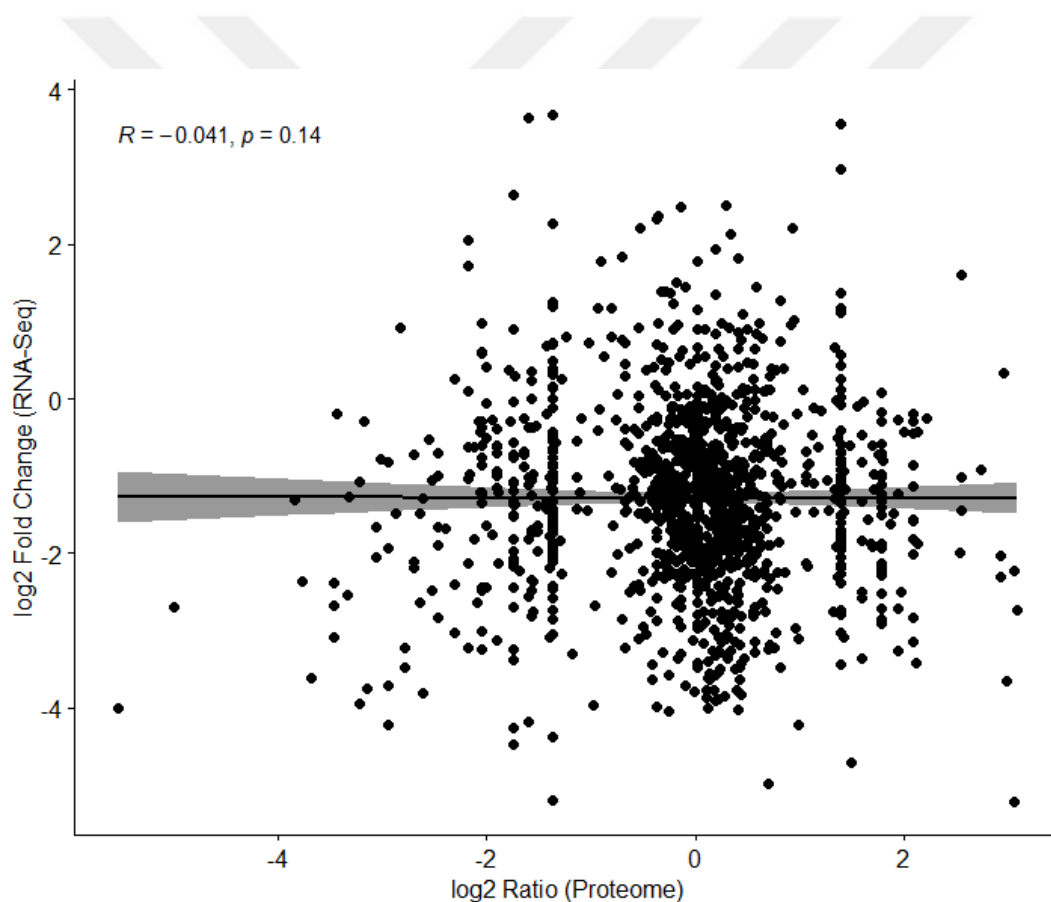


Figure 3.9. Spearman's correlation was calculated between the proteomic and transcriptomic data. The correlation coefficient and the p-value are also shown.

As seen in Figure 3.9, the correlation of transcriptomic and proteomic data was investigated by utilizing Spearman's correlation. The correlation coefficient and p-value were found as -0.041 and 0.14, respectively. These results indicate that there is no correlation between the proteomic and transcriptomic data. Even though correlation coefficients differ among different organisms, they are typically found in the range from 0.2 to 0.47 in bacteria (de Sousa Abreu *et al.*, 2009). However, the correlation between mRNA and protein abundances were recorded to be infamously poor (Gygi *et al.*, 1999; Koussounadis *et al.*, 2015; Maier *et al.*, 2009).

There could be several biological and experimental factors of poor correlation between mRNA and protein levels. Firstly, various posttranslational modifications (PTMs) and regulations can affect protein detection, such as phosphorylation, ubiquitination and cellular localization (Maier *et al.*, 2009). Most bacterial posttranslational modifications are dynamic and reversible, making it easier for the cell to utilize them as regulatory tools. Since bacteria have a remarkable capacity for adaptation and high survival skills in different environmental conditions, PTMs provide necessary vital skills of adaptability (Grangeasse *et al.*, 2015). Different growth conditions and the cell cycle also contribute to the variation of PTMs as well as mRNA and protein levels in the cell (Liu *et al.*, 2016; Soufi *et al.*, 2015). Several PTMs were reported in bacteria, including novel modifications, such as redox regulation via reversible S-thiolation (Loi *et al.*, 2015), protein phosphorylation (Spät *et al.*, 2015), post-translational hydroxylation (van Staalduinen and Jia, 2015), N-glycosylation (Garcia-Quintanilla *et al.*, 2014), arginine phosphorylation and regulated proteolysis (Stannek *et al.*, 2015) and post translationally modified lantibiotics (Zhou *et al.*, 2015). By adding a further level of complexity to gene expression regulation (Grangeasse *et al.*, 2015), PTMs heavily influence the correlation of transcriptomic and proteomic data. As stated by de Sousa Abreu *et al.*, (2009), even though bacteria do not have posttranscriptional regulations the way eukaryotes do, the operon structure of bacterial genome and fine-regulation of gene expression at the level of translation results in a lack of correlation.

Another key posttranslational factor that can impact the correlation between mRNAs and proteins is the difference between mRNA and protein half-lives. Intrinsic protein stability, the first amino-terminal amino acid (N-end rule), the localization of proteins, and posttranslational modifications such as phosphorylation and ubiquitination can profoundly influence the cellular life times of proteins (Maier *et al.*, 2009). There may also be significant heterogeneity even between proteins with similar functions. Besides, experimental error and noise highly affect the transcriptomic and proteomic analyses (Greenbaum *et al.*, 2003). It was proposed that the amount of differentially expressed mRNAs correlate considerably better with their protein products, which leads to higher mRNA-protein correlations (Koussounadis *et al.*, 2015; Rehman *et al.*, 2019).

Importantly, small RNAs (sRNAs) likewise play a crucial role in gene expression regulation in prokaryotic organisms and add another layer of complexity to the mRNA-protein relationship. While they affect the mRNA stability and evolution, they also influence transcription attenuation, translation activation, inhibition, and efficiency (Maier *et al.*, 2009; Watkins and Arya, 2019).

Overall, these findings indicate that mRNA levels can only predict the protein abundance to some extent, and it is highly challenging to determine which biological or experimental factor impacts the mRNA-protein correlation the most (Kumar *et al.*, 2016; Maier *et al.*, 2009).

CHAPTER 4

CONCLUSION

- RNA-Sequencing (RNA-Seq) analysis of *B. subtilis* lab-adapted PY79 and mutant OGU1 revealed 3814 commonly expressed genes between these two strains, and predicted 1442 new transcripts. However, RNA-Seq analysis identified only 2369 transcripts as differentially expressed. While 223 of differentially expressed genes (DEGs) showed an increase in their transcript levels, 2146 of DEGs were underrepresented in bacilysin biosynthetic operon silenced mutant OGU1.
- KEGG pathway term analysis discovered that the majority of DEGs belonged to metabolic functions. Environmental information processing, genetic information processing, cellular processes and organismal systems followed the former category.
- The highest number of DEGs belonged to ‘global and overview maps’ in OGU1, which corresponded to nearly 38% of all genes in the metabolism category as also discovered by KEGG pathway analysis. Along with ‘carbohydrate metabolism’ and ‘amino acid metabolism’ of the main category metabolism, ‘membrane transport’ of environmental information processing obtained a significant amount of DEGs that worth noting.
- According to the most enriched pathway analysis, ‘microbial metabolism in diverse environments’ of ‘global and overview maps’ was found as the most enriched pathway of mutant OGU1. It was followed closely by ‘ABC transporters’ of ‘membrane transport’ and ‘two-component system’ of ‘signal transduction’.

- Based on Gene Ontology functional classification system, ‘cellular process’ and ‘metabolic process’ of biological process category, ‘cell’ and ‘cell part’ of cellular component, and lastly ‘catalytic activity’ and ‘binding’ of molecular function constituted the highest number of DEGs. Likewise, the same GO functional classes were also found as the most enriched GO terms.
- RNA-Seq results were validated with RT-qPCR analysis. The transcript levels of selected seven genes were consistent with their RNA-Seq expression levels.
- The transcriptomic data of this study and proteomic data (2DE MALDI-TOF/MS and nanoLC-MS/MS analyses) from our group’s earlier studies were integrated to get a comprehensive understanding of regulation of gene expression in *B. subtilis* since separate analyses can only provide limited information due to the complexity that arises from biological and experimental elements.
- Many genes of sporulation and germination were downregulated in bacilysin nonproducer strain OGU1 in the present study. The majority of spore coat genes and spore coat polysaccharide synthesis genes were found at much lower abundances in the mutant, which indicates the disruption of general coat architecture of OGU1 strain. Thus, OGU1 is significantly more susceptible to chloroform and lysozyme. Strong downregulation of *cotA* also causes the loss of brownish pigmentation in OGU1. These findings confirm the results of our earlier studies.
- Though the general coat architecture of OGU1 is disrupted, the spores of OGU1 were resistant to heat due to the lack of alterations in DPA levels despite the downregulation of dipicolinate synthase subunits at both mRNA and protein levels.

- Our group's earlier studies revealed that OGU1 strain shows no biofilm formation or swarming motility. However, *luxS*, a gene required for swarming motility and biofilm formation, demonstrated 3-fold downregulation at its transcript levels in RNA-Seq analysis and confirmed our earlier findings.
- Even though the expression levels of the global regulator *codY* were not as significant, many members of the CodY regulon were underrepresented in the mutant strain at mRNA level. The targets of CodY regulatory protein were also detected at protein level at various abundances. These findings of *codY* global regulator and its targets suggest that further investigations are necessary to completely understand the underlying mechanisms of CodY as it regulates more than 100 genes in *B. subtilis*.
- Many global regulators of *B. subtilis* showed opposite behavior at mRNA and protein levels, such as *cheV* and *degU*. This suggests that the absence of bacilysin production strongly impacts the gene expression regulation, and bacilysin might have direct or indirect influence on global regulators in *B. subtilis*.
- A considerable amount of stress response genes was underexpressed in the bacilysin nonproducing strain, which implies that *B. subtilis* indeed becomes more susceptible to general stress upon the loss of bacilysin biosynthetic function. It was previously reported that general stress proteins might be alternatives for cells that are unable to sporulate. Therefore, *B. subtilis* becomes exceptionally vulnerable to nutritional or environmental stress. Considering the fact that some proteins, such as AhpC, BmrA, YaaN, YppQ, YtkL and YugI, demonstrated elevated levels of protein expression despite showing much lower abundances at mRNA level, it might be possible to state

that the loss of bacilysin biosynthetic function leads to a defense mechanism that requires posttranslational modifications as a way of survival.

- As expected, all genes of the *bac* operon (*bacABCDEF*) and the monocistronic *bacG* showed sharp downregulations at mRNA level in bacilysin biosynthetic operon silenced mutant OGU1. Lower transcript abundances, the loss of *bac*-operon encoded proteins (BacABCDEF) in the mutant as well as the lack of detectable end product together confirm the creation of a *B. subtilis* strain that cannot produce bacilysin.
- *albE*, responsible from antilisterial bacteriocin (subtilisin) production, was -3.66-fold downregulated at mRNA level. At protein level, AlbE was absent from the parental strain PY79 while it was found at increased levels in OGU1. Likewise, *albF* showed a similar expression pattern. All members of the *alb* operon (*albABCDEFG*) were strongly underrepresented at mRNA level. AlbA and AlbC were also found to have more peptide count in OGU1. Overall, these findings might point to an existence of a more complex, intricate mechanism like posttranslational modifications that is triggered in the absence of bacilysin. It can be speculated that *B. subtilis* produces subtilisin and secretes it into the environment as a new microbial agent to compensate for the lack of bacilysin.
- At protein level, both BceB and BmrA were absent from PY79 compared to OGU1. Their reduced level of transcripts suggests another possible mechanism of PTMs.
- All members of *dlt* operon (*dltABCDE*), which controls the D-alanylation of lipoteichoic acids, displayed lower abundances in their transcripts in OGU1. Only DltA was identified at our proteomic studies and it showed similar behavior. Since the inhibition of DltA is associated with a higher

susceptibility to cationic antibiotics and host defensins as well as the termination of biofilm production, it can be suggested that the lack of bacilysin might result in a more susceptible phenotype to particular agents, defects in teichoic acid synthesis and lack of biofilm production.

- The lack of correlation between transcriptomic and proteomic data points to the existence of much complex mechanisms such as posttranslational modifications. Additionally, half-life differences between mRNAs and proteins, experimental error and noise, codon usage bias, weak ribosome binding sites, ribosome density and non-coding sRNAs might be influencing the lack of correlation. Still, it is almost impossible to determine which biological or experimental factor affects the mRNA-protein correlation the most.



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APPENDICES

A. Compositions and Preparation of Culture Media

Perry and Abraham (PA) Medium (pH 7.4)

KH ₂ PO ₄	1 g/L
KCl	0.2 g/L
MgSO ₄ .7H ₂ O*	0.5 g/L
Glutamate.Na.H ₂ O	4 g/L
Sucrose*	10 g/L
Ferric citrate**	0.15 g/L
Trace elements**	
CoCl ₂ .6H ₂ O	0.0001 g/L
Ammonium molybdate	0.0001 g/L
MnCl ₂ .4H ₂ O	0.001 g/L
ZnSO ₄ .7H ₂ O	0.0001 g/L
CuSO ₄ .5H ₂ O	0.00001 g/L

*Autoclave separately

**Filter sterilization

Luria Bertani (LB) Medium

Tryptone	10 g/L
Yeast Extract	5 g/L
NaCl	5 g/L

Distilled water was added up to 1000 mL and then autoclaved for 15 minutes.

Luria Bertani (LB) Agar Medium

Tryptone	10 g/L
Yeast Extract	5 g/L
NaCl	5 g/L
Agar	15 g/L

Distilled water was added up to 1000 mL and then autoclaved for 15 minutes.

B. Compositions of Buffers and Solutions

TE Buffer (1X)

Tris	10 mM
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EDTA	1 mM
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pH is adjusted to 8.0 with HCl.

Autoclave for 15 minutes for sterilization if needed.

TE Buffer with lysozyme (1X)

Tris	10 mM
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EDTA	1 mM
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Lysozyme (lyophilized)	2 mg/ml
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pH is adjusted to 8.0 with HCl.

TAE Buffer (50X)

Tris base	242 g
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Glacial acetic acid	57.1 mL
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0.5 M EDTA (pH 8.0)	100 mL
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The final volume is adjusted to 1000 mL with distilled water.

Low Melting Agarose Gel (0.8%)

Agarose 0.8 g

TAE buffer (1X) 100 ml

Before pouring the gel into tray, add 1.5µl EtBr (final concentration: 0.5 µg/ml).



C. Chemicals and Enzymes

<u>Chemicals</u>	<u>Supplier</u>
Agar	Merck
Agarose	Prona
Ammonium Molybdate	Sigma
β – mercaptoethanol	Sigma
CoCl ₂ .6H ₂ O	Merck
CuSO ₄ .5H ₂ O	Merck
EDTA	AppliChem
Erythromycin	Sigma
Ethanol	Sigma
Ethidium Bromide	Sigma
Ferric citrate	Merck
Glacial Acetic Acid	Merck
Glutamate.Na.H ₂ O	Merck
KCl	Merck
KH ₂ PO ₄	Merck
Lincomycin	Sigma
MgSO ₄ .7H ₂ O	Merck
MnCl ₂ .4H ₂ O	Merck
NaCl	Merck

RNAstable	Biomatrica
Sucrose	Merck
Tris Base	Merck
Tryptone	Difco
Yeast Extract	Oxoid
ZnSO ₄ ·7H ₂ O	Sigma

Enzymes

Lysozyme

Supplier

Sigma

D. Comparison of DEGs and DEPs obtained by nanoLC-MS/MS and RNA-Seq analyses.

Locus ID	Gene Name	RNA-Seq (log2FC)	FDR	p-value	R_{SC}	Mw (Da)	pI
BSU38620	<i>aag</i>	0.716631752	0.001354	0.001037	-1.362116	21.9777	6.12
BSU29200	<i>accA</i>	-1.624377077	5.42E-135	1.05E-135	0.13059	36.1784	6.09
BSU24350	<i>accB</i>	-1.765455283	2.94E-53	9.26E-54	0.31835	17.0863	4.39
BSU24340	<i>accC</i>	-0.070449682	5.26E-19	2.61E-19	0.27669	49.4121	4.72
BSU29210	<i>accD</i>	-1.774007296	2.30E-147	4.22E-148	-0.119823	28.7264	5.34
BSU29470	<i>ackA</i>	-1.221295985	3.58E-47	1.20E-47	0.3417	42.9768	5.19
BSU15920	<i>acpA</i>	0.554424308	1.32E-32	5.24E-33	0.0979	8.4543	3.59
BSU29680	<i>acsA</i>	0.987046602	2.67E-271	3.27E-272	-0.357996	64.7168	5.55
BSU10630	<i>addA</i>	-2.252352317	0	0	0.01653	140.85	5.13
BSU10620	<i>addB</i>	-2.44326529	0	0	-2.054123	134.412	5.39
BSU14520	<i>adeC</i>	-0.802418656	0.001447547	0.00111096	-0.182844	62.6418	4.72
BSU26970	<i>adhB</i>	-0.474063237	0.006832134	0.0054972	-1.362116	41.0374	5.66

BSU01370	<i>adk</i>	-1.648691513	0	0	-0.784134	23.9721	4.45
BSU40090	<i>ahpC</i>	-1.915080043	0	0	0.06755	20.4823	4.28
BSU40100	<i>ahpF</i>	-1.646594542	0	0	0.22315	54.7054	4.7
BSU31410	<i>alaR</i>	-2.364913312	2.46E-61	7.26E-62	0.31364	18.6167	4.89
BSU27410	<i>alaS</i>	-0.984615665	5.07E-22	2.38E-22	0.16235	97.0837	4.92
BSU31400	<i>alaT</i>	-2.038319304	2.56E-181	4.02E-182	-0.288392	42.1498	5.11
BSU37370	<i>albA</i>	-2.176005061	0	0	1.07376	51.3482	6.2
BSU37390	<i>albC</i>	-3.037220172	0	0	0.77359	27.0846	5.25
BSU37410	<i>albE</i>	-3.664842152	0	0	2.98056	43.201	6.07
BSU37420	<i>albF</i>	-3.440905585	0	0	1.39517	48.8188	5.42
BSU31930	<i>ald</i>	-0.233787882	0.006329287	0.0050845	0.74636	39.5257	5.12
BSU36000	<i>alsD</i>	-3.396086218	0	0	0.11351	28.6489	4.6
BSU36010	<i>alsS</i>	-3.106733114	0	0	0.29833	61.9454	5.16
BSU03010	<i>amhX</i>	-1.427684423	6.63E-231	8.96E-232	0.01653	42.3702	6.12

BSU14450	<i>ampS</i>	0.107635651	0.000305266	0.000227562	0.68412	45.6366	4.95
BSU02690	<i>ansZ</i>	-1.974662239	8.48E-17	4.35E-17	0.54724	39.9443	6.15
BSU11390	<i>appB</i>	-1.291156894	1.45E-34	5.68E-35	-0.0737	35.2458	9.77
BSU11370	<i>appF</i>	-1.087050893	3.19E-35	1.24E-35	-1.749204	36.957	9.65
BSU17260	<i>aprX</i>	-3.802267086	0	0	-2.616164	47.7419	4.97
BSU27610	<i>apt</i>	-1.16368027	1.03E-17	5.17E-18	0.12759	18.7319	4.7
BSU11210	<i>argB</i>	0.79327372	9.74E-19	4.84E-19	-0.806757	27.5736	6.21
BSU11190	<i>argC</i>	-1.901116392	4.44E-43	1.56E-43	0.01653	37.917	5.17
BSU11220	<i>argD</i>	1.158971118	3.03E-138	5.84E-139	0.01653	40.7351	5.93
BSU11250	<i>argF</i>	1.607103995	0	0	2.55297	34.5086	4.97
BSU29450	<i>argG</i>	-0.869466175	5.12E-32	2.05E-32	0.31118	44.6569	5.03
BSU29440	<i>argH</i>	0.160126691	5.89E-35	2.29E-35	0.01654	51.7619	4.86
BSU11200	<i>argJ</i>	-0.223776966	0.269995705	0.248078	0.01654	43.2023	4.7
BSU37330	<i>argS</i>	-1.314748069	6.90E-153	1.23E-153	0.03844	62.5492	5.11

BSU29750	<i>aroA</i>	-0.680066958	2.27E-22	1.06E-22	-0.41697	39.3822	5.34
BSU22700	<i>aroB</i>	-1.063891967	2.75E-11	1.61E-11	0.05176	40.6583	6.94
BSU22600	<i>aroE</i>	-0.151950554	0.091513184	0.0801004	0.09741	45.0776	6.34
BSU22710	<i>aroF</i>	-1.460049167	2.43E-24	1.10E-24	-0.190256	40.0447	6.58
BSU03150	<i>aroK</i>	-3.041669938	3.32E-201	4.91E-202	-0.468997	21.7176	5.97
BSU23980	<i>artP</i>	-2.263472476	1.89E-299	2.19E-300	-0.035694	28.1615	5.09
BSU23970	<i>artQ</i>	-2.439745925	7.15E-72	1.94E-72	0.68412	23.7513	9.08
BSU23960	<i>artR</i>	-2.013635247	1.68E-191	2.54E-192	-0.26193	26.7999	9.13
BSU16750	<i>asd</i>	-2.570578778	0	0	0.31241	37.6904	4.97
BSU30540	<i>asnB</i>	-0.674956249	2.00E-15	1.05E-15	0.71496	72.4876	5.61
BSU39920	<i>asnH</i>	0.420310128	4.90E-106	1.07E-106	-0.403596	85.6621	5.53
BSU10790	<i>asnO</i>	-0.531701353	6.02E-08	3.86E-08	-2.555581	70.5364	5.7
BSU22360	<i>asnS</i>	-2.242026785	0	0	-0.077324	48.9204	5.12
BSU22370	<i>aspB</i>	-0.403332364	0.142849676	0.1274124	0.34974	42.9278	5.3

BSU27550	<i>aspS</i>	-0.808858513	6.45E-29	2.72E-29	0.0996	65.7995	4.65
BSU36830	<i>atpA</i>	-1.61045049	0	0	0.13606	54.4318	5.04
BSU36870	<i>atpB</i>	-1.354084139	1.34E-95	3.13E-96	-0.324575	26.9047	9.36
BSU36800	<i>atpC</i>	-0.709817121	3.76E-43	1.32E-43	-0.414235	14.0686	5.26
BSU36810	<i>atpD</i>	-0.967442445	0	0	-0.096144	51.2553	4.61
BSU36850	<i>atpF</i>	-1.892779222	1.80E-291	2.12E-292	0.692	19.0643	4.92
BSU36820	<i>atpG</i>	-1.666998901	0	0	0.2741	31.5021	6.64
BSU36840	<i>atpH</i>	-1.95945771	9.36E-232	1.26E-232	0.25771	19.8381	9.57
BSU19230	<i>azoR1</i>	0.447689191	1.86E-15	9.80E-16	-0.052213	22.8305	4.99
BSU33540	<i>azoR2</i>	-0.260112364	0.464769199	0.438466	-0.740523	23.1254	5.11
BSU37740	<i>bacA</i>	-2.547422784	4.08E-30	1.68E-30	-3.334716	23.1794	7.9
BSU37730	<i>bacB</i>	-4.001140921	1.67E-146	3.08E-147	-5.529425	26.69	5.19
BSU37720	<i>bacC</i>	-4.217763502	1.79E-92	4.25E-93	-2.947499	27.1739	4.96
BSU37710	<i>bacD</i>	-2.698357406	4.38E-94	1.03E-94	-4.994989	52.1009	4.68

BSU37690	<i>bacF</i>	-3.22473256	2.37E-44	8.18E-45	-2.791315	44.5423	5.35
BSU24080	<i>bcd</i>	0.168745269	3.83E-05	2.74E-05	0.21604	39.8332	4.94
BSU30380	<i>bceA</i>	-1.068405776	1.55E-07	1.01E-07	0.16601	28.0846	9.29
BSU30370	<i>bceB</i>	-0.257534227	0.521835252	0.495376	2.21845	72.0076	9.79
BSU30400	<i>bceR</i>	-1.706413619	2.56E-17	1.30E-17	0.01653	26.7183	5.29
BSU33480	<i>bdbD</i>	-1.970775278	2.72E-139	5.20E-140	0.15255	24.7582	5.09
BSU06240	<i>bdhA</i>	-1.932169427	0	0	0.60552	37.1855	4.8
BSU30230	<i>bioA</i>	-0.133502206	0.004164057	0.00330672	0.11278	49.9463	5.32
BSU30200	<i>bioB</i>	0.397027454	1.65E-09	1.01E-09	0.31364	36.7703	5.55
BSU30210	<i>bioD</i>	-0.231103059	0.578889893	0.554578	0.50205	25.0123	6.21
BSU24050	<i>bkdAA</i>	-0.385671415	0.44683021	0.420398	-0.67548	36.1773	4.78
BSU24040	<i>bkdAB</i>	-0.138293599	0.063306044	0.0548112	-0.229758	35.7005	4.79
BSU24030	<i>bkdB</i>	-0.089882328	0.000466092	0.00034936	-0.232987	45.6742	5.3
BSU34820	<i>bmrA</i>	-1.686760852	6.70E-36	2.57E-36	2.08718	64.3447	6.47

BSU15300	<i>bpr</i>	3.672198044	0	0	-1.362116	154.34	4.98
BSU21900	<i>bsaA</i>	-2.043439261	1.41E-05	9.88E-06	0.01653	18.1125	5.25
BSU24070	<i>buk</i>	-0.629392602	0.066879695	0.0580252	-0.251562	39.6065	5.47
BSU03180	<i>cah</i>	-1.11528879	5.06E-05	3.64E-05	0.01653	35.6526	5.42
BSU11240	<i>carB</i>	1.225942094	0	0	-0.210367	112.746	4.71
BSU25190	<i>cccA</i>	-0.919021111	3.19E-13	1.77E-13	0.08215	12.6256	5.28
BSU35270	<i>cccB</i>	-2.069227966	2.78E-101	6.25E-102	-1.749204	11.7887	5.01
BSU29740	<i>ccpA</i>	-1.259503501	1.40E-74	3.72E-75	0.10676	36.7842	5.06
BSU14140	<i>ccpC</i>	0.423218847	5.36E-14	2.92E-14	0.19713	33.7595	5.93
BSU25250	<i>ccpN</i>	-0.98327219	2.03E-09	1.25E-09	0.63333	23.7232	7.22
BSU19780	<i>cgeA</i>	-3.620441779	0	0	-3.684885	14.0173	3.98
BSU33950	<i>cggR</i>	-3.99093603	0	0	-0.370561	37.2252	5.68
BSU16430	<i>cheA</i>	-3.626439137	1.77E-124	3.58E-125	-0.419669	74.5864	4.45
BSU22720	<i>cheR</i>	-3.358453971	3.28E-07	2.16E-07	1.60165	29.8017	9.25

BSU14010	<i>cheV</i>	-3.433385673	8.92E-115	1.88E-115	0.5163	34.4794	4.62
BSU16440	<i>cheW</i>	-2.415037499	5.12E-19	2.53E-19	0.22301	17.3625	4.42
BSU16930	<i>cinA</i>	-1.209340342	3.09E-46	1.05E-46	0.01653	45.3749	5.4
BSU18000	<i>citB</i>	-1.381743382	0	0	-0.388263	99.1363	4.9
BSU33040	<i>citG</i>	-1.305552677	3.13E-246	4.06E-247	0.81593	50.3649	5.47
BSU29140	<i>citZ</i>	-0.265578254	0.001998045	0.00154727	-0.023315	41.5693	5.45
BSU00860	<i>clpC</i>	-0.188656289	4.65E-21	2.21E-21	-0.047779	89.9273	5.75
BSU34540	<i>clpP</i>	-0.083938981	1.38E-16	7.08E-17	0.35647	21	5
BSU16150	<i>clpQ</i>	-0.814253553	9.01E-09	5.62E-09	0.17702	19.3333	6.11
BSU28220	<i>clpX</i>	-1.105200833	2.14E-131	4.22E-132	-0.01372	46.2463	4.64
BSU16160	<i>clpY</i>	-1.112004371	4.09E-101	9.21E-102	-0.094701	52.4198	5.31
BSU22890	<i>cmk</i>	-0.389348662	0.267937883	0.24605	0.33362	24.9482	5
BSU16170	<i>codY</i>	0.0310675	1.58E-43	5.50E-44	-0.165711	28.8621	4.75
BSU31680	<i>comA</i>	0.083083102	0.005811483	0.00466258	0.45272	23.9815	4.76

BSU25590	<i>comEA</i>	-3.720413071	4.94E-55	1.54E-55	-1.749204	21.6234	4.82
BSU25580	<i>comEB</i>	-2.489208957	3.71E-129	7.40E-130	-0.52687	20.8234	5.37
BSU25600	<i>comER</i>	-0.204675406	0.007905067	0.00638276	-1.425013	30.0874	6.18
BSU24730	<i>comGA</i>	-2.414933825	0	0	-0.582398	40.3006	8.89
BSU10420	<i>comK</i>	-1.467825214	3.17E-63	9.16E-64	-0.46906	22.2838	7.67
BSU06300	<i>cotA</i>	-2.677273002	0	0	-3.216815	58.3312	5.89
BSU36050	<i>cotB</i>	-2.37403281	0	0	-3.771107	42.8121	9.83
BSU17030	<i>cotE</i>	-0.864366135	2.32E-194	3.48E-195	-2.055268	20.8323	4.14
BSU40530	<i>cotF</i>	-1.833934849	0	0	-1.29532	18.5823	7.37
BSU36060	<i>cotH</i>	-2.443323202	2.69E-64	7.68E-65	-1.749204	42.6537	5.95
BSU30920	<i>cotI</i>	-3.2461719	0	0	-2.054123	41.0872	4.99
BSU06910	<i>cotJC</i>	0.717848185	2.42E-145	4.50E-146	-0.67548	21.5502	4.9
BSU11730	<i>cotO</i>	-0.723848038	1.90E-81	4.82E-82	-1.641039	25.445	6.38
BSU34520	<i>cotQ</i>	-3.052331315	0	0	-1.362116	49.9212	6.1

BSU30900	<i>cotS</i>	-2.817540406	2.67E-242	3.49E-243	-1.568599	40.9261	6.64
BSU30910	<i>cotSA</i>	-3.029305002	1.32E-156	2.28E-157	-2.305726	42.7536	7.81
BSU17670	<i>cotU</i>	-3.757632879	5.95E-24	2.70E-24	-3.154047	11.4246	6.32
BSU11750	<i>cotY</i>	-2.462447242	0	0	-1.362116	17.7409	4.86
BSU27830	<i>coxA</i>	-2.043624839	0	0	-1.373064	19.3942	9.22
BSU15780	<i>cpgA</i>	0.166389088	6.57E-07	4.38E-07	-1.362116	33.6439	4.74
BSU32690	<i>csd</i>	-2.086955812	0	0	0.08967	44.7606	5.2
BSU04580	<i>cshA</i>	-1.446753948	0	0	-1.041449	57.1083	9.89
BSU25140	<i>cshB</i>	-2.503661384	0	0	-0.625244	49.8641	9.89
BSU26890	<i>csn</i>	-1.241193045	0	0	0.613	31.3437	8.89
BSU21930	<i>cspD</i>	-1.178317258	5.87E-98	1.35E-98	1.39517	7.1732	4.31
BSU08930	<i>cspR</i>	-1.66513617	1.49E-41	5.33E-42	0.56411	18.4429	6.05
BSU33010	<i>cssR</i>	-2.288869411	2.20E-96	5.11E-97	0.57305	26.0641	5.07
BSU14890	<i>ctaC</i>	-0.991476896	1.19E-55	3.68E-56	0.01654	39.9365	8.64

BSU14900	<i>ctaD</i>	-0.450435246	1.02E-13	5.60E-14	2.08718	68.9314	6.99
BSU00520	<i>ctc</i>	1.182970212	0	0	-0.800867	21.9097	4.22
BSU19590	<i>ctpA</i>	-1.026293853	4.56E-43	1.60E-43	-0.354031	50.9821	8.86
BSU35240	<i>ctpB</i>	-1.214461562	1.37E-182	2.14E-183	-2.054123	52.6317	8.64
BSU17410	<i>cwIC</i>	-3.942253702	0	0	-3.216815	27.0107	5.94
BSU02600	<i>cwIJ</i>	-0.045607688	9.43E-05	6.88E-05	-1.749204	16.2216	9.35
BSU34800	<i>cwIO</i>	-1.019826344	7.63E-101	1.72E-101	1.78226	50.8659	5.33
BSU27520	<i>cymR</i>	-2.635286475	5.45E-77	1.42E-77	0.40362	11.7507	9.88
BSU35060	<i>cypX</i>	-0.504360705	7.45E-09	4.63E-09	1.37085	45.3118	5.31
BSU15600	<i>cysC</i>	-3.357883024	0	0	0.47126	22.3987	5.08
BSU00930	<i>cysE</i>	-1.957190003	8.94E-51	2.90E-51	1.39517	23.9965	9.49
BSU15570	<i>cysH</i>	-3.148276721	0	0	0.56411	26.8258	5.46
BSU33430	<i>cysI</i>	-1.816963465	0	0	-0.039556	64.634	5.49
BSU33440	<i>cysJ</i>	-2.286189072	5.80E-294	6.79E-295	0.18306	67.0833	4.57

BSU00730	<i>cysK</i>	-3.08680832	0	0	0.03047	32.666	5.49
BSU00940	<i>cysS</i>	-1.943054671	3.01E-190	4.61E-191	-0.075674	53.7406	5.07
BSU00100	<i>dacA</i>	-2.035561974	3.60E-225	4.96E-226	-0.240755	48.4703	5.67
BSU23190	<i>dacB</i>	0.306898717	2.97E-28	1.27E-28	-1.362116	42.92	9.73
BSU23480	<i>dacF</i>	-0.437612065	4.64E-07	3.07E-07	-1.373064	43.1349	9.91
BSU16770	<i>dapA</i>	-1.759415592	0	0	-0.125174	30.8892	4.93
BSU22490	<i>dapB</i>	0.172303724	0.001965123	0.001521272	-0.384138	29.3368	5.06
BSU32170	<i>dapF</i>	-1.393000841	2.12E-19	1.04E-19	0.14781	30.7183	4.51
BSU16760	<i>dapG</i>	-2.114958542	1.71E-296	1.99E-297	-0.190076	42.8176	5.71
BSU09670	<i>dat</i>	-0.897255257	4.72E-81	1.20E-81	-0.018067	31.0308	4.87
BSU00140	<i>dck</i>	-0.741413268	0.00205553	0.001594944	-0.189957	25.2958	5.54
BSU04560	<i>ddl</i>	-1.653653844	1.11E-174	1.79E-175	0.41046	38.973	4.58
BSU14560	<i>ykrB</i>	-1.870970543	3.90E-30	1.61E-30	0.27189	20.511	5.46
BSU35500	<i>degS</i>	-1.770730672	1.01E-105	2.21E-106	0.61067	44.7971	5.99

BSU35490	<i>degU</i>	-0.932363765	4.50E-19	2.22E-19	0.54458	25.7186	5.6
BSU35480	<i>degV</i>	-1.943416472	7.73E-33	3.07E-33	1.78226	31.4279	5.23
BSU19630	<i>deoD</i>	-0.722335182	0.000976479	0.000743424	0.58504	25.2293	4.98
BSU19310	<i>dhaS</i>	2.137442316	0	0	0.33256	53.7138	5.02
BSU05630	<i>dinB</i>	-1.027917718	4.56E-35	1.77E-35	0.01653	19.7599	5.61
BSU22400	<i>dinG</i>	-0.996878408	1.07E-38	3.94E-39	-1.362116	105.832	5.82
BSU00880	<i>disA</i>	-1.401900319	8.37E-65	2.38E-65	0.61942	40.576	5.57
BSU15240	<i>divIB</i>	-1.891598355	4.55E-43	1.60E-43	1.60165	30.0155	9.24
BSU15420	<i>divIVA</i>	-2.120238618	1.23E-154	2.17E-155	0.1818	19.1967	4.85
BSU38500	<i>dltA</i>	-2.264843414	0	0	0.14781	55.6412	4.93
BSU00010	<i>dnaA</i>	-2.775557535	3.27E-148	5.97E-149	0.57305	50.695	6.03
BSU28980	<i>dnaI</i>	-1.797279084	6.58E-43	2.31E-43	0.56411	35.9592	5.74
BSU25470	<i>dnaK</i>	-0.52739671	3.53E-20	1.71E-20	-0.147884	65.8258	4.57
BSU00020	<i>dnaN</i>	-2.625495331	1.17E-168	1.93E-169	0.14492	41.9448	4.72

BSU12920	<i>dppA</i>	-0.282412885	0.583350291	0.559598	-0.227276	30.0909	5.19
BSU12930	<i>dppB</i>	-0.142317905	0.000973725	0.000741078	-0.927084	33.9023	9.94
BSU12960	<i>dppE</i>	0.376232964	0	0	-0.478338	62.4061	5.52
BSU16110	<i>dprA</i>	-0.774156856	1.80E-15	9.48E-16	-0.370561	32.7834	9.76
BSU30650	<i>dps</i>	0.469709342	0	0	0.50232	16.4509	4.44
BSU39420	<i>dra</i>	-2.751286132	1.64E-172	2.65E-173	-0.14397	22.0643	4.93
BSU23500	<i>drm</i>	-0.93401159	1.59E-19	7.82E-20	-0.449265	43.768	4.97
BSU23770	<i>dsdA</i>	-1.186303551	3.73E-10	2.24E-10	-1.362116	49.4959	5.55
BSU24450	<i>efp</i>	-0.779889279	1.57E-24	7.07E-25	0.19727	20.3091	4.84
BSU33900	<i>eno</i>	-2.758195955	0	0	0.0747	46.4179	4.49
BSU34360	<i>epsB</i>	0.891553273	7.87E-56	2.43E-56	-0.214862	24.5273	9.92
BSU34240	<i>epsM</i>	0.216036926	0.000177398	0.000130652	0.19713	22.3369	9.43
BSU25290	<i>era</i>	-1.750469106	0	0	0.01653	33.9216	8.38
BSU28520	<i>etfA</i>	2.486067139	0	0	-0.14397	34.3871	4.65

BSU12370	<i>exuR</i>	-1.217953356	6.52E-26	2.86E-26	1.39517	37.2246	5.85
BSU29610	<i>ezaA</i>	-1.638305698	6.86E-144	1.28E-144	0.13443	64.8212	4.76
BSU15900	<i>fabD</i>	-0.73858569	3.92E-12	2.23E-12	0.27189	33.88	4.51
BSU11340	<i>fabF</i>	-0.977541913	9.36E-83	2.35E-83	-0.210609	43.8424	4.77
BSU15910	<i>fabG</i>	-0.978806858	1.60E-28	6.82E-29	0.23513	26.132	8.09
BSU11330	<i>fabHA</i>	-1.535391324	8.15E-130	1.62E-130	0.28328	33.5767	5.05
BSU10170	<i>fabHB</i>	-0.401324873	0.012139536	0.009951	0.07736	35.2687	5.68
BSU11720	<i>fabI</i>	-1.007593994	2.75E-150	4.98E-151	0.63665	27.7227	5.61
BSU08650	<i>fabL</i>	-0.416889721	0.4481237	0.422074	0.01654	27.0282	5.97
BSU28540	<i>fadB</i>	1.382261972	0	0	-0.324575	27.4035	4.95
BSU32820	<i>fadE</i>	3.637813341	0	0	-1.607243	65.1598	5.15
BSU14060	<i>fadH</i>	0.803199293	2.34E-55	7.25E-56	-1.237521	26.9752	6.49
BSU32840	<i>fadN</i>	1.723725556	0	0	-2.1854	89.9556	6.53
BSU15880	<i>fapR</i>	-1.963399841	3.48E-202	5.14E-203	0.3792	21.2554	5.39

BSU37120	<i>flaA</i>	-1.974426506	0	0	0.23114	30.2482	5.03
BSU15980	<i>ffh</i>	-1.904283771	0	0	-0.180602	49.3756	9.42
BSU33320	<i>fluD</i>	-3.481018481	2.45E-176	3.91E-177	0.01653	34.2721	9.16
BSU16290	<i>flgE</i>	-3.063283788	4.32E-113	9.20E-114	0.30613	27.3184	4.73
BSU35410	<i>flgK</i>	-2.975144111	0	0	0.01653	54.185	4.38
BSU35400	<i>flgL</i>	-2.804606012	0	0	0.01653	32.6057	4.42
BSU16210	<i>fliF</i>	-3.052492123	0	0	0.29223	59.1285	4.37
BSU16220	<i>fliG</i>	-2.945130264	7.95E-244	1.04E-244	-0.504465	38.0351	4.46
BSU35380	<i>fliW</i>	-2.081601901	6.09E-58	1.85E-58	0.01653	16.0277	4.34
BSU16320	<i>fliY</i>	-2.414765061	7.45E-55	2.32E-55	-0.164078	40.8935	4.12
BSU15730	<i>fml</i>	-1.238519846	1.04E-24	4.66E-25	0.14781	34.4802	5.62
BSU24310	<i>folD</i>	-1.330260543	1.29E-83	3.22E-84	0.26241	30.5336	5.6
BSU00790	<i>folK</i>	-2.089677262	4.91E-57	1.50E-57	-0.14397	18.9149	4.53
BSU16520	<i>frr</i>	-0.666216135	3.71E-08	2.36E-08	0.81961	20.6213	5.33

BSU14400	<i>fruA</i>	-2.761839283	0	0	0.35957	67.0059	5.24
BSU06170	<i>fruC</i>	-2.253959466	0	0	0.8552	34.1017	4.62
BSU14390	<i>fruK</i>	-2.473835315	0	0	0.39856	32.6382	4.89
BSU14380	<i>fruR</i>	-2.422933566	0	0	0.01653	27.667	5.68
BSU15280	<i>ftsA</i>	-0.767446556	4.00E-52	1.28E-52	0.55442	47.9395	5.09
BSU35260	<i>ftsE</i>	-3.098469137	2.12E-223	2.96E-224	0.9919	25.4721	8.42
BSU00690	<i>ftsH</i>	-1.303209547	0	0	-0.040398	70.7596	5.84
BSU35250	<i>ftsX</i>	-2.150670103	3.52E-237	4.67E-238	0.27189	32.9468	10.02
BSU15950	<i>ftsY</i>	-0.608144251	8.23E-05	5.98E-05	0.68412	36.1872	5.08
BSU15290	<i>ftsZ</i>	-1.015492329	8.81E-254	1.13E-254	0.28892	40.1954	4.81
BSU23520	<i>fur</i>	-1.589003892	1.05E-74	2.77E-75	0.40362	17.2572	5.37
BSU01120	<i>fusA</i>	-1.660327372	0	0	-0.100533	76.3604	4.61
BSU03910	<i>gabD</i>	-0.174815437	0.005727732	0.00459392	0.19168	50.0967	4.76
BSU06310	<i>gabP</i>	-0.864630261	1.24E-20	5.95E-21	-0.379498	50.93	9.45

BSU38860	<i>galE</i>	-1.892278233	7.40E-217	1.05E-217	0.49558	36.8523	4.78
BSU38200	<i>galK</i>	-0.92664318	1.08E-14	5.80E-15	0.45272	43.36	5.15
BSU38190	<i>galT</i>	-0.28374664	0.563927695	0.538078	1.78226	58.4362	5.62
BSU33940	<i>gapA</i>	-3.263227857	0	0	0.16352	35.6762	5.03
BSU06680	<i>gatA</i>	-0.40000299	0.110524505	0.0977314	0.23296	52.4973	5.24
BSU06690	<i>gatB</i>	-0.447814102	0.000122863	9.01E-05	-0.01404	53.2397	4.9
BSU00500	<i>gcaD</i>	-1.480340767	8.60E-133	1.68E-133	0.44057	49.2897	5.65
BSU05940	<i>gcp</i>	-0.505570157	0.218953163	0.1991044	0.01653	36.6858	5.02
BSU32800	<i>gcvH</i>	-0.564846309	2.81E-07	1.85E-07	0.58232	14.1129	3.89
BSU24560	<i>gcvPA</i>	-1.97533539	2.91E-254	3.71E-255	-1.749204	49.3326	6.95
BSU24550	<i>gcvPB</i>	-1.797371921	1.00E-225	1.38E-226	0.2159	54.2593	5.28
BSU24570	<i>gcvT</i>	-2.22829488	9.04E-165	1.52E-165	-0.055651	39.6216	5.73
BSU03930	<i>gdh</i>	-1.242871636	1.58E-156	2.74E-157	-1.569114	27.9398	5.08
BSU01550	<i>gerD</i>	-1.496673705	1.79E-28	7.61E-29	-1.749204	20.971	4.86

BSU28380	<i>gerM</i>	0.834939976	0	0	0	0.18835	39.4144	4.68
BSU10700	<i>gerPC</i>	-2.161192265	0	0	0	-1.749204	24.0935	4.76
BSU37920	<i>gerQ</i>	-0.416537274	7.28E-07	4.86E-07	4.86E-07	-1.061959	20.1319	7.01
BSU15090	<i>gerR</i>	0.545924939	4.09E-57	1.25E-57	1.25E-57	-0.871457	22.2201	7.11
BSU19490	<i>gerT</i>	-2.110675144	3.49E-190	5.35E-191	5.35E-191	-1.362116	18.3998	6.34
BSU35680	<i>ggaB</i>	-0.756505781	0.094445997	0.0827642	0.0827642	-1.362116	106.955	9.48
BSU41010	<i>gidA</i>	-2.081953318	0	0	0	-0.173727	69.5754	6.33
BSU24850	<i>glcK</i>	-1.294881945	1.56E-17	7.87E-18	7.87E-18	0.01653	33.3907	5.99
BSU30960	<i>glgD</i>	0.231624024	6.76E-11	3.98E-11	3.98E-11	-1.568599	39.0746	6.56
BSU30940	<i>glgP</i>	0.133904811	3.28E-08	2.09E-08	2.09E-08	-1.362116	91.564	6.28
BSU01770	<i>glmM</i>	-0.853454701	1.30E-11	7.55E-12	7.55E-12	0.35777	48.2681	4.68
BSU01780	<i>glmS</i>	-1.204944838	0	0	0	-2.06461	65.1628	4.8
BSU17460	<i>glnA</i>	-2.751943433	0	0	0	0.13742	50.1133	4.87
BSU27440	<i>glnH</i>	-0.346658771	0.254989841	0.233572	0.233572	-1.533205	29.6041	8.55

BSU27430	<i>glnQ</i>	0.009456256	8.98E-12	5.17E-12	-1.568599	27.0196	6.43
BSU09300	<i>glpD</i>	0.987684987	0	0	-2.054123	62.3578	8
BSU09290	<i>glpK</i>	1.258056456	0	0	-1.362116	54.9104	4.99
BSU09270	<i>glpP</i>	-0.132216963	0.030418558	0.0255734	-0.14397	21.4639	8.1
BSU37090	<i>glpX</i>	-1.29649102	2.28E-116	4.75E-117	0.28384	33.7959	5.07
BSU18450	<i>gltA</i>	-1.576968452	0	0	-0.336599	168.613	5.47
BSU18440	<i>gltB</i>	-0.81690431	7.27E-71	1.99E-71	0.26813	54.7796	7.7
BSU18460	<i>gltC</i>	-2.688807083	1.37E-136	2.64E-137	0.56411	33.8666	5.62
BSU10220	<i>gltT</i>	-3.01369384	0	0	-2.054123	45.7585	9.03
BSU00920	<i>gltX</i>	-2.000384094	0	0	0.40738	55.5552	5.02
BSU36900	<i>glyA</i>	-1.990081786	3.62E-268	4.50E-269	0.08711	45.3284	5.47
BSU25270	<i>glyQ</i>	-1.842430017	8.82E-54	2.77E-54	-0.079718	33.8259	4.8
BSU25260	<i>glyS</i>	-1.165177912	1.45E-56	4.44E-57	-0.061057	76.0509	4.97
BSU15680	<i>gmk</i>	-1.090309219	9.66E-35	3.77E-35	-0.384138	23.0716	4.62

BSU23860	<i>gndA</i>	-1.567578948	1.42E-268	1.77E-269	0.38852	51.6091	5.08
BSU25540	<i>gpr</i>	0.099047369	4.51E-12	2.57E-12	-2.1854	40.1248	5.2
BSU22830	<i>gpsA</i>	-0.919234586	4.33E-29	1.82E-29	0.17702	37.2792	6.23
BSU27320	<i>greA</i>	-0.912114432	6.56E-10	3.98E-10	0.57857	17	4
BSU06030	<i>groEL</i>	-0.070251389	2.93E-68	8.12E-69	-0.01306	57.2519	4.53
BSU25480	<i>grpE</i>	-0.412850143	0.026664548	0.0223354	0.44411	21.5373	4.26
BSU08710	<i>gsaB</i>	-1.269273834	4.04E-31	1.64E-31	-0.357996	46.039	5.64
BSU35670	<i>gtbB</i>	0.058772142	2.92E-72	7.92E-73	0.39844	32.9174	4.91
BSU06360	<i>guaA</i>	-1.249978253	3.18E-64	9.08E-65	-0.252548	57.7821	4.75
BSU00090	<i>guaB</i>	-1.106372961	3.31E-94	7.77E-95	0.28281	52.8236	6.17
BSU32130	<i>guaC</i>	-3.326071162	0	0	0.31364	35.6633	6.08
BSU22960	<i>gudB</i>	-1.914058212	0	0	0.14401	47.0484	5.58
BSU00070	<i>gyrA</i>	-1.51159479	0	0	-0.370561	91.9051	5.22
BSU00060	<i>gyrB</i>	-1.293492647	0	0	0.01653	71.324	5.38

BSU35360	<i>hag</i>	-2.107509013	0	0	0	0.09348	32.472	4.78
BSU22790	<i>hbs</i>	1.121547998	0	0	0	1.39517	9.7464	9.5
BSU10380	<i>hemAT</i>	-1.007093782	3.27E-32	1.31E-32	-0.190016	48.6041	5.44	
BSU28130	<i>hemB</i>	-2.891212599	0	0	0.3062	36.0536	4.98	
BSU10120	<i>hemE</i>	-2.027248435	1.24E-165	2.07E-166	-0.317988	39.4899	5.26	
BSU10130	<i>hemH</i>	-2.103955645	0	0	0.08871	35.1937	4.62	
BSU28120	<i>hemL</i>	-2.638328742	0	0	0.63963	46.2862	5.05	
BSU10140	<i>hemY</i>	-2.48440946	0	0	0.26813	51.0374	8.04	
BSU17340	<i>hfq</i>	-1.200248277	2.01E-29	8.36E-30	-1.749204	8.3777	8.7	
BSU34880	<i>hisA</i>	-3.498651933	0	0	0.23484	26.3794	4.84	
BSU34900	<i>hisB</i>	-3.612262816	0	0	0.11966	21.4028	5.6	
BSU22620	<i>hisC</i>	-0.032783827	3.09E-09	1.91E-09	0.49213	39.9272	5.01	
BSU34910	<i>hisD</i>	-3.424497829	0	0	0.44203	46.094	4.78	
BSU34870	<i>hisF</i>	-3.628711108	0	0	0.42339	27.1444	5.24	

BSU34920	<i>hisG</i>	-3.188254039	2.68E-172	4.36E-173	0.42005	23.4739	4.53
BSU34890	<i>hisH</i>	-3.49365055	0	0	0.3792	23.1558	5.72
BSU34860	<i>hisI</i>	-3.57232179	0	0	-0.258692	23.7535	4.63
BSU27560	<i>hisS</i>	-1.067142857	6.63E-10	4.02E-10	0.231	47.9681	5.23
BSU34930	<i>hisZ</i>	-3.545015066	1.67E-158	2.87E-159	0.21948	43.3445	5.15
BSU10030	<i>hit</i>	-0.409352138	0.265747075	0.243834	0.01653	16.1568	6.13
BSU13040	<i>hmp</i>	-2.27364808	1.46E-152	2.59E-153	-0.169948	44.5693	5.7
BSU32260	<i>hom</i>	-1.954270286	0	0	-0.084205	47.3317	4.9
BSU35000	<i>hprK</i>	-0.911231692	2.60E-11	1.52E-11	-0.314805	34.5473	4.91
BSU00680	<i>hprT</i>	-1.044457754	6.96E-17	3.56E-17	0.20508	20.095	4.6
BSU39820	<i>htpG</i>	-1.151498143	5.05E-52	1.62E-52	0.09372	72.0777	4.67
BSU12900	<i>htrA</i>	-1.906928506	4.05E-120	8.30E-121	0.1509	47.5497	4.7
BSU33000	<i>htrB</i>	-1.284116626	7.91E-60	2.37E-60	0.22301	48.5529	4.63
BSU39340	<i>hutP</i>	-1.32809259	1.85E-18	9.20E-19	-1.362116	16.4345	6.06

BSU29130	<i>icd</i>	-0.417614739	2.72E-11	1.59E-11	-0.01793	46.255	4.83
BSU15430	<i>ileS</i>	-0.98644268	7.46E-42	2.66E-42	-0.322295	104.584	5.19
BSU21770	<i>ilvA</i>	-1.929023614	5.18E-113	1.11E-113	0.07669	46.4895	5.54
BSU28310	<i>ilvB</i>	-2.24869949	0	0	0.79061	62.4166	5.18
BSU28290	<i>ilvC</i>	-0.875900435	2.50E-89	6.03E-90	0.14455	37.3022	5.37
BSU21870	<i>ilvD</i>	-1.32285192	7.05E-80	1.80E-80	0.28741	59.3758	5.32
BSU28300	<i>ilvH</i>	-2.265945108	4.02E-128	8.03E-129	0.01653	19.309	10.3
BSU16630	<i>infB</i>	-1.384357979	0	0	-0.261549	78.3519	5.19
BSU28870	<i>infC</i>	-2.8367267	0	0	0.33157	19.5877	10.34
BSU39770	<i>ioIR</i>	-0.823516136	0.000708968	0.000536492	1.39517	28.2549	6.33
BSU39780	<i>ioIS</i>	-1.301138589	3.48E-82	8.75E-83	-0.103911	35.0139	5.38
BSU32680	<i>iscU</i>	-2.35247995	0	0	-1.568599	16.0232	4.71
BSU18380	<i>iseA</i>	-2.137064339	0	0	0.50205	19.9848	10.18
BSU13190	<i>ispA</i>	2.049248509	0	0	-2.1854	33.6946	4.52

BSU16550	<i>ispC</i>	-0.833469526	1.43E-07	9.27E-08	1.39517	43.1234	5.8
BSU00460	<i>ispE</i>	-1.882537191	1.59E-27	6.84E-28	1.78226	31.5666	6.35
BSU00910	<i>ispF</i>	-2.042813084	0.000272117	0.000202224	1.39517	16.9836	5.4
BSU25070	<i>ispG</i>	-0.545383611	2.69E-05	1.90E-05	-0.365502	40.4239	6.8
BSU25160	<i>ispH</i>	-2.16286189	0	0	0.36813	34.7701	5.61
BSU41030	<i>jag</i>	-1.142766733	1.21E-30	4.95E-31	0.32145	23.0157	10.04
BSU19690	<i>kamA</i>	0.904205229	0	0	-1.749204	53.908	6.04
BSU08820	<i>katA</i>	-1.015978562	0	0	-1.141273	54.5667	6.15
BSU38630	<i>katX</i>	-0.298493241	0.607674483	0.585266	-2.082409	62.1924	5.34
BSU22140	<i>kduD</i>	-0.714806521	9.87E-09	6.17E-09	0.01653	27.0363	6.5
BSU22130	<i>kduI</i>	-0.699632444	7.52E-10	4.56E-10	0.10541	30.9827	5.11
BSU13530	<i>kinE</i>	-1.982748668	3.66E-116	7.65E-117	0.01653	85.3245	5.49
BSU00420	<i>ksgA</i>	-1.146618462	2.70E-13	1.49E-13	-0.14397	32.5687	5.71
BSU14510	<i>ktrC</i>	-2.417026052	1.12E-133	2.18E-134	0.09251	24.2008	5.63

BSU03050	<i>ldh</i>	-4.182949149	0	0	0.15291	34	5.394
BSU25510	<i>lepA</i>	-1.494580814	7.57E-142	1.42E-142	-0.521353	68.4097	4.98
BSU28280	<i>leuA</i>	-1.230224668	3.79E-224	5.27E-225	-0.182964	56.7419	5.66
BSU28270	<i>leuB</i>	-1.292127798	1.46E-127	2.93E-128	0.42743	39.7867	4.74
BSU28260	<i>leuC</i>	-1.012097676	1.71E-137	3.29E-138	0.09251	52.2252	6.13
BSU28250	<i>leuD</i>	-0.879342119	1.33E-31	5.37E-32	0.35763	22.8759	4.58
BSU30320	<i>leuS</i>	-0.595434414	2.78E-17	1.41E-17	0.05588	91.3508	4.86
BSU27070	<i>levD</i>	-3.840570511	0	0	0.43612	16.1146	4.48
BSU27060	<i>levE</i>	-3.471991099	0	0	0.42591	17.941	9.44
BSU27040	<i>levG</i>	-3.779319999	0	0	0.3967	29.9354	9.94
BSU34990	<i>lgt</i>	-1.351730847	6.00E-24	2.73E-24	0.40362	30.4685	8.96
BSU33120	<i>liaH</i>	-0.138370482	0.006131622	0.00492414	0.01653	25.5487	6.17
BSU06620	<i>ligA</i>	-0.937518666	1.34E-24	6.01E-25	0.09251	74.6936	4.71
BSU02700	<i>lip</i>	-0.457019949	0.557079079	0.531258	-0.259171	22.6449	10.06

BSU32330	<i>lipA</i>	-1.257119574	5.81E-61	1.72E-61	-0.449265	33.7664	8.25
BSU04110	<i>lipC</i>	-3.482856159	3.80E-143	7.09E-144	-2.791315	23.4586	5.84
BSU28200	<i>lonA</i>	-0.222680107	0.042133539	0.0358216	0.01653	86.4176	5.77
BSU24060	<i>lpdV</i>	-0.629656523	0.004995767	0.0039851	-0.041215	48.5104	4.89
BSU34050	<i>lutA</i>	-1.132506267	8.81E-46	3.00E-46	-0.190016	26.2428	6.25
BSU34040	<i>lutB</i>	-0.655414019	3.03E-53	9.56E-54	-0.106882	53.3066	5.85
BSU34030	<i>lutC</i>	-0.227217949	1.12E-05	7.81E-06	0.18781	26.1283	5.16
BSU30670	<i>luxS</i>	-3.089505361	2.30E-220	3.25E-221	0.10676	17.5714	5.17
BSU23380	<i>lysA</i>	-1.450685041	6.31E-61	1.87E-61	0.01653	48.4107	5.01
BSU28470	<i>lysC</i>	-2.329556935	8.70E-161	1.48E-161	0.71967	43.6459	4.64
BSU00820	<i>lysS</i>	-1.365363992	4.43E-153	7.84E-154	-0.290146	57.3704	5.03
BSU35630	<i>lytB</i>	-3.434628228	5.93E-48	1.97E-48	-0.408969	76.546	9.84
BSU35620	<i>lytC</i>	-2.863169218	7.91E-51	2.57E-51	-0.697426	52.4583	10.11
BSU09420	<i>lytE</i>	-0.567698652	2.82E-06	1.92E-06	-0.67548	37.1632	10.71

BSU35650	<i>lytR</i>	-2.374239207	0	0	0	0.01653	34.4316	9.53
BSU28050	<i>maf</i>	-1.633269298	7.00E-147	1.29E-147	1.29E-147	-0.052213	21.15	5.71
BSU08190	<i>malR</i>	1.783320131	5.27E-114	1.12E-114	1.12E-114	0.01653	29.1469	5.45
BSU29880	<i>malS</i>	0.927897526	0	0	0	-2.823487	61.9763	4.89
BSU01380	<i>map</i>	-1.887394694	0	0	0	0.26813	27.2605	6.39
BSU36410	<i>mbl</i>	-1.205498592	1.61E-148	2.94E-149	2.94E-149	0.56199	35.7049	5.67
BSU27250	<i>mccB</i>	-3.905151361	0	0	0	0.19713	40.7264	5.22
BSU31240	<i>mcpA</i>	-3.102430147	0	0	0	-0.539995	72.2166	4.99
BSU31260	<i>mcpB</i>	-2.332670475	3.46E-88	8.41E-89	8.41E-89	-0.106389	71.7036	5.13
BSU13950	<i>mcpC</i>	-1.914927915	1.26E-76	3.28E-77	3.28E-77	0.39106	71.9315	5.17
BSU00840	<i>mcsA</i>	0.435482428	2.66E-61	7.86E-62	7.86E-62	1.39517	20.8774	6.62
BSU00850	<i>mcsB</i>	-0.316762189	0.825741621	0.8139	0.8139	-0.086597	40.9655	5.07
BSU29120	<i>mdh</i>	-0.501006569	6.20E-36	2.38E-36	2.38E-36	-0.141326	33.4897	4.73
BSU11520	<i>mecA</i>	-1.063600461	7.46E-97	1.72E-97	1.72E-97	1.39517	25.6155	4.21

BSU30800	<i>menB</i>	-1.168801285	6.94E-68	1.93E-68	0.41276	29.748	5.34
BSU21910	<i>metA</i>	-1.754105342	5.88E-21	2.81E-21	0.01653	25.8523	6.41
BSU11880	<i>metC</i>	1.100881981	1.87E-57	5.68E-58	0.45272	42.3318	5.76
BSU13180	<i>metE</i>	1.451144519	2.02E-109	4.37E-110	-0.091909	86.6411	4.84
BSU11870	<i>metI</i>	0.250117417	0.000169361	0.000124603	0.55442	41.5462	5.02
BSU30550	<i>metK</i>	-0.704042085	3.32E-37	1.25E-37	0.14975	43.882	5.03
BSU32750	<i>metQ</i>	-2.090354108	1.49E-43	5.17E-44	0.18465	37.7294	7.3
BSU00380	<i>metS</i>	-0.856995269	4.72E-42	1.68E-42	0.07893	76.0072	4.96
BSU00550	<i>mfd</i>	-0.548460022	5.31E-16	2.76E-16	-0.359842	133.593	5.37
BSU12870	<i>mhqA</i>	-0.663097754	0.001204781	0.000920632	0.01653	35.2333	5.4
BSU19560	<i>mhqD</i>	-0.657137014	0.051018089	0.0436626	-1.362116	22.2868	5.62
BSU28000	<i>minC</i>	-1.722485824	9.28E-75	2.45E-75	-0.094535	24.8501	6.26
BSU27990	<i>minD</i>	-1.75603841	9.42E-141	1.79E-141	0.30627	29.2558	4.98
BSU23550	<i>mleA</i>	-0.916430488	3.85E-11	2.25E-11	0.01653	45.7267	4.89

BSU16710	<i>mlpA</i>	0.046941137	1.46E-06	9.85E-07	-0.288392	45.8008	5.28
BSU24140	<i>mmgD</i>	2.265612679	1.65E-235	2.20E-236	-1.362116	41.9466	6.2
BSU24130	<i>mmgE</i>	2.644059946	0	0	-1.749204	52.7376	6.11
BSU35660	<i>mnaA</i>	-1.810289218	1.13E-29	4.67E-30	0.32145	42.4755	5.47
BSU30770	<i>mntA</i>	-3.134101449	0	0	-0.027217	33.2644	6.16
BSU30760	<i>mntB</i>	-3.273002786	0	0	0.33276	27.7326	9.41
BSU24520	<i>mntR</i>	-1.708899312	4.20E-52	1.34E-52	-1.568599	16.6033	5.63
BSU14300	<i>moaE</i>	-1.580852256	2.45E-07	1.60E-07	0.01653	17.6388	4.75
BSU14280	<i>moeA</i>	-1.327009425	1.91E-17	9.66E-18	0.16095	46.457	5.61
BSU13690	<i>motA</i>	-3.149067294	2.05E-116	4.28E-117	2.08718	29.1881	5.01
BSU13680	<i>motB</i>	-2.913164298	1.34E-225	1.85E-226	1.78226	29.3316	6.65
BSU02240	<i>mpr</i>	0.111875344	3.15E-197	4.70E-198	0.50205	33.6877	8.97
BSU15140	<i>mraW</i>	-1.15469972	2.07E-38	7.66E-39	-0.370561	35.1516	6.03
BSU28030	<i>mreB</i>	-0.708988685	6.49E-12	3.72E-12	0.11351	35.7896	4.9

BSU28020	<i>mreC</i>	-1.009153955	1.19E-42	4.20E-43	0.47126	32.0027	6.25
BSU32990	<i>mrgA</i>	-1.550669435	0	0	-0.468997	17.1895	4.6
BSU38810	<i>msmX</i>	-0.752984075	9.88E-67	2.76E-67	-2.054123	41.2075	7.39
BSU13550	<i>mtnA</i>	0.645680344	7.91E-05	5.73E-05	0.22301	38.7026	5
BSU13610	<i>mtnB</i>	-1.234280911	7.17E-08	4.60E-08	1.78226	23.3419	5.69
BSU13620	<i>mtnD</i>	-0.834886411	1.31E-05	9.18E-06	-0.114806	20.6798	4.41
BSU13560	<i>mtnK</i>	-0.311201688	0.987493759	0.986988	0.01653	45.1867	4.86
BSU27270	<i>mtnN</i>	-2.444784843	1.21E-228	1.65E-229	0.27382	25.1165	4.84
BSU13590	<i>mtnW</i>	-2.147883627	1.01E-31	4.07E-32	1.39517	44.8876	5.28
BSU13600	<i>mtnX</i>	-0.959255983	0.001543453	0.001188518	-0.288392	26.8522	4.66
BSU07340	<i>mtrA</i>	-1.531230517	6.54E-13	3.65E-13	-0.079718	48.7417	9.82
BSU36760	<i>murAA</i>	-2.02798739	0	0	-0.114749	46.537	5.45
BSU37100	<i>murAB</i>	-1.024157122	2.46E-46	8.35E-47	0.01653	45.853	5.83
BSU15230	<i>murB</i>	-1.102119659	3.94E-45	1.35E-45	1.12651	32.6546	6.09

BSU29790	<i>murC</i>	-1.567217362	1.51E-216	2.14E-217	-0.063672	48.2015	5.31
BSU15200	<i>murD</i>	-0.847304302	6.58E-17	3.36E-17	-0.493891	49.4866	5.57
BSU15180	<i>murE</i>	-0.96055859	1.67E-21	7.89E-22	-0.483236	54.1571	5.56
BSU04570	<i>murF</i>	-1.109194155	1.10E-38	4.07E-39	0.2449	49.5575	5.34
BSU15220	<i>murG</i>	-0.959455459	1.37E-18	6.83E-19	-1.362116	39.8198	9.57
BSU17040	<i>mutS</i>	-1.815832412	1.20E-96	2.78E-97	2.08718	97.394	5.19
BSU28580	<i>mutSB</i>	-1.203123339	2.41E-58	7.28E-59	-1.105787	87.2271	5.79
BSU30630	<i>mutTA</i>	-2.745992293	2.23E-101	4.98E-102	1.39517	18.3693	5.95
BSU27850	<i>nadA</i>	-1.170193252	4.21E-140	8.01E-141	-0.292673	41.3332	5.72
BSU27860	<i>nadC</i>	-2.084582458	2.26E-75	5.93E-76	0.54724	31.2396	5.18
BSU25640	<i>nadD</i>	-1.572635462	3.31E-24	1.50E-24	-1.362116	22.0115	5.12
BSU03130	<i>nadE</i>	0.422761465	2.10E-156	3.65E-157	0.80922	30.2441	4.89
BSU11610	<i>nadF</i>	-1.790915811	3.13E-27	1.36E-27	0.01653	29.8619	5.99
BSU27890	<i>nadR</i>	-1.485678848	3.74E-25	1.66E-25	1.39517	19.5756	5.76

BSU35010	<i>nagA</i>	-3.357503999	0	0	-0.164078	42.4616	5.28
BSU07700	<i>nagP</i>	-1.80891362	2.35E-139	4.49E-140	-1.749204	48.4166	7.13
BSU05440	<i>nag</i>	-1.895609971	3.11E-118	6.42E-119	-1.362116	33.7999	5.8
BSU37280	<i>narG</i>	-3.966423796	0	0	-0.973725	138.862	6.06
BSU37270	<i>narH</i>	-4.053553506	0	0	-0.259171	55.3032	5.11
BSU37260	<i>narJ</i>	-3.772827796	0	0	0.17702	21.0646	4.61
BSU03320	<i>nasB</i>	-3.288042101	7.41E-53	2.35E-53	-0.312938	84.5655	5.48
BSU03310	<i>nasC</i>	-3.541893779	7.46E-57	2.28E-57	-1.179668	78.391	6.73
BSU03300	<i>nasD</i>	-2.747558631	0	0	0.5602	88.2395	4.95
BSU03290	<i>nasE</i>	-2.632883343	0	0	0.01653	11.7559	4.8
BSU03280	<i>nasF</i>	-2.884747706	0	0	0.08528	53.703	6.52
BSU12290	<i>ndh</i>	-2.359698562	0	0	0.18251	41.7942	6.29
BSU22730	<i>ndk</i>	-0.97646409	1.39E-23	6.33E-24	0.62674	16.8161	5.57
BSU38110	<i>nfrA</i>	0.157179552	3.29E-30	1.35E-30	-0.197661	28.1696	5.73

BSU03420	<i>nin</i>	-3.796597941	0	0	-0.008798	14.8558	4.92
BSU40990	<i>noc</i>	-1.672585767	3.96E-223	5.56E-224	0.32982	32.6422	5.81
BSU07630	<i>nos</i>	-0.901517424	0.003436906	0.00271608	0.01653	38.5942	5.53
BSU17380	<i>nrdE</i>	-1.564049054	1.97E-65	5.55E-66	-0.114749	80.5024	5.93
BSU17390	<i>nrdF</i>	-1.574396553	3.15E-42	1.12E-42	0.63333	38.2218	4.66
BSU36520	<i>nrgB</i>	-0.777582253	6.76E-14	3.69E-14	0.16289	12.6823	8.82
BSU29250	<i>nrnA</i>	-0.866733469	0.000259165	0.0001922	0.14781	34.9299	4.67
BSU09380	<i>nsrR</i>	-1.854987569	1.44E-50	4.68E-51	0.32145	16.4671	7.75
BSU10550	<i>ntdA</i>	2.495310815	3.22E-40	1.17E-40	0.29223	49.9774	5.97
BSU10540	<i>ntdB</i>	3.154044874	7.05E-91	1.69E-91	1.39517	33.0473	5.35
BSU23610	<i>nudF</i>	-1.861297877	3.54E-55	1.10E-55	0.50219	20.835	4.59
BSU16600	<i>nusA</i>	-1.475758595	1.34E-194	2.00E-195	0.31767	41.567	4.58
BSU01010	<i>nusG</i>	-1.456854062	3.20E-45	1.10E-45	0.51275	19.9815	5.25
BSU27920	<i>obg</i>	-0.806543812	1.51E-19	7.41E-20	-0.046236	47.526	4.86

BSU19370	<i>odhA</i>	-0.544034755	1.52E-85	3.79E-86	-0.015933	105.54	5.87
BSU19360	<i>odhB</i>	-0.060577147	2.14E-87	5.24E-88	-0.050986	45.8267	4.86
BSU13540	<i>ogt</i>	-1.245694602	4.77E-25	2.13E-25	1.78226	18.6089	7.09
BSU11430	<i>oppA</i>	-0.814852945	1.40E-154	2.46E-155	0.16124	61.3181	5.72
BSU11440	<i>oppB</i>	-1.435652333	7.10E-47	2.40E-47	-1.362116	33.9214	9.86
BSU11460	<i>oppD</i>	-1.00039016	1.89E-48	6.27E-49	0.41255	39.6068	6.03
BSU11470	<i>oppF</i>	-0.639626296	2.88E-20	1.39E-20	-1.362116	34.5942	6.95
BSU02980	<i>opuAA</i>	-1.153813478	7.26E-39	2.67E-39	-0.236808	46.2761	5.11
BSU03000	<i>opuAC</i>	-0.272792759	0.442670885	0.416258	-0.417685	32.061	8.02
BSU33830	<i>opuCA</i>	-1.45742971	5.44E-30	2.25E-30	0.96014	43.0884	6.55
BSU33810	<i>opuCC</i>	-1.712935908	4.76E-34	1.87E-34	0.35763	33.8028	5.69
BSU33240	<i>oxdC</i>	-0.086261813	5.03E-224	7.01E-225	0.15899	43.4065	5.1
BSU18670	<i>oxdD</i>	-2.158688377	1.75E-96	4.05E-97	-2.1854	43.3949	5.36
BSU00750	<i>pabA</i>	-1.573385354	1.36E-66	3.81E-67	0.25215	21.5392	4.78

BSU00740	<i>pabB</i>	-3.239278525	0	0	-0.67548	53.0851	5.23
BSU00760	<i>padC</i>	-2.151099979	4.99E-103	1.11E-103	-0.370561	33.362	6.12
BSU32140	<i>paiB</i>	-1.928067222	2.00E-29	8.32E-30	-1.362116	23.9572	5.03
BSU22430	<i>panB</i>	-1.296117245	2.63E-23	1.20E-23	0.22301	29.6072	5.28
BSU14000	<i>patA</i>	-0.995616922	1.58E-100	3.59E-101	-0.184323	43.2888	6.01
BSU15160	<i>pbpB</i>	-1.348309539	2.61E-47	8.76E-48	-1.749204	79.121	9.23
BSU04140	<i>pbpC</i>	-0.712003199	3.75E-23	1.72E-23	0.01654	74.2255	6.2
BSU31490	<i>pbpD</i>	-2.503353855	1.37E-228	1.87E-229	1.60165	70.4479	9.31
BSU34440	<i>pbpE</i>	0.23027015	3.47E-49	1.14E-49	0.20301	51.2717	4.84
BSU13980	<i>pbpH</i>	-2.201226011	1.85E-191	2.81E-192	1.78226	76.9839	8.89
BSU16950	<i>pbpX</i>	-2.225802683	5.62E-23	2.59E-23	0.56411	43.6979	9.71
BSU02650	<i>pcp</i>	-1.366992721	7.41E-18	3.73E-18	-1.749204	23.6276	6.42
BSU06610	<i>pcrA</i>	-1.013128761	1.94E-23	8.88E-24	-0.190016	83.3676	5.77
BSU07980	<i>pdaA</i>	-0.989371213	7.01E-18	3.52E-18	-1.909701	29.9187	7.32

BSU01570	<i>pdaB</i>	-0.116950286	0.003249685	0.0025623	-0.539995	28.1739	9.18
BSU14580	<i>pdhA</i>	-0.559933584	5.59E-25	2.50E-25	0.04602	41.3896	5.84
BSU14590	<i>pdhB</i>	-0.771393462	1.04E-91	2.48E-92	-0.381547	35.3197	4.55
BSU14600	<i>pdhC</i>	-1.459563665	0	0	-0.244678	47.3758	4.86
BSU14610	<i>pdhD</i>	-1.539305316	0	0	0.20937	49.5669	4.76
BSU39400	<i>pdp</i>	-0.649481143	2.84E-10	1.70E-10	-0.312938	46.0434	4.76
BSU38020	<i>thiD</i>	-1.703519111	3.62E-35	1.40E-35	0.26115	28.8658	4.92
BSU00110	<i>pdxS</i>	-1.972919364	4.88E-276	5.89E-277	-0.041523	31.4574	5.09
BSU00120	<i>pdxT</i>	-1.925762046	1.52E-211	2.19E-212	-0.179515	21.3014	4.98
BSU07560	<i>pel</i>	-1.626068571	0	0	1.87123	45.336	8.42
BSU11540	<i>pepF</i>	-0.646633983	1.11E-39	4.05E-40	0.21898	69.9659	5.13
BSU38920	<i>pepT</i>	-0.119457646	4.44E-06	3.05E-06	0.47029	45.3469	4.54
BSU29190	<i>pflkA</i>	-0.861059887	1.96E-12	1.11E-12	0.46119	34.0998	6.14
BSU09310	<i>pgcA</i>	-0.946807784	5.03E-67	1.41E-67	0.57614	62.7281	4.91

BSU31350	<i>pgi</i>	-1.561468798	6.98E-234	9.37E-235	0.5695	50.362	4.85
BSU33930	<i>pgk</i>	-2.832103393	0	0	-0.057953	42.0301	4.77
BSU33910	<i>pgm</i>	-2.956420898	0	0	0.05246	56.1401	5.21
BSU27910	<i>pheB</i>	-0.642830323	0.03469912	0.0293232	0.01653	16.5171	6.36
BSU28640	<i>pheS</i>	-1.7180153	5.59E-39	2.05E-39	0.30146	38.5177	5.08
BSU28630	<i>pheT</i>	-0.084482252	5.54E-09	3.43E-09	0.0328	87.7556	4.86
BSU09410	<i>phoA</i>	-1.028462955	1.80E-26	7.86E-27	-1.568599	50.1066	9.93
BSU25340	<i>phoH</i>	-0.873064084	1.57E-38	5.82E-39	0.07428	35.4159	6.12
BSU29110	<i>phoP</i>	-0.196677515	0.147375685	0.131638	0.01653	27.5336	5.07
BSU29100	<i>phoR</i>	-0.543463871	1.84E-05	1.30E-05	-1.141273	64.9465	5.96
BSU17100	<i>pksC</i>	-1.031722015	4.62E-12	2.64E-12	0.37926	32.3111	5.33
BSU17110	<i>pksD</i>	-0.887790496	0.001670946	0.001289688	0.32145	33.9116	5.78
BSU17120	<i>pksE</i>	0.109465979	0.000475156	0.000356276	0.08528	85.6072	7.38
BSU17140	<i>pksF</i>	1.369150554	4.12E-47	1.39E-47	1.39517	44.9745	5.37

BSU17150	<i>pksG</i>	1.503636931	4.88E-43	1.71E-43	-0.182844	46.6167	5.14
BSU17170	<i>pksI</i>	0.88718017	0.02817296	0.0236422	-0.235075	27.8049	5.61
BSU17180	<i>pksJ</i>	2.374399872	0	0	-0.360018	562	5
BSU17190	<i>pksL</i>	1.777537882	0	0	-0.909901	505.847	5.2
BSU17200	<i>pksM</i>	1.177113115	0	0	-0.939357	475.312	5.31
BSU17220	<i>pksR</i>	0.464734655	0	0	-0.260861	284.727	5.44
BSU17230	<i>pksS</i>	-0.97333032	1.29E-09	7.90E-10	0.77359	43.2574	6.12
BSU09540	<i>plsC</i>	-1.219947622	4.01E-67	1.12E-67	0.42339	21.7776	9.98
BSU15890	<i>plsX</i>	-1.338293731	3.65E-94	8.57E-95	-0.229758	35.6068	5.49
BSU18070	<i>plsY</i>	-2.281005676	2.74E-88	6.67E-89	1.78226	20.8222	10.41
BSU34390	<i>pnbA</i>	-0.562004239	6.83E-05	4.94E-05	0.48232	53.8193	4.78
BSU31760	<i>pncA</i>	-1.176064376	2.68E-13	1.48E-13	0.20301	20.3786	5.6
BSU31750	<i>pncB</i>	-1.652242752	2.29E-119	4.71E-120	-0.060489	56.0109	5.09
BSU16690	<i>pnpA</i>	-0.713237874	2.38E-58	7.21E-59	-0.146102	77.2803	4.89

BSU29090	<i>polA</i>	-1.286269484	1.91E-95	4.46E-96	-0.085765	98.8949	4.92
BSU16580	<i>polC</i>	-1.179235851	1.72E-107	3.73E-108	-1.362116	162.424	5.14
BSU28590	<i>polX</i>	-1.527771161	9.76E-55	3.04E-55	-0.293908	63.9454	5.31
BSU22320	<i>ponA</i>	-1.46649798	0	0	0.03749	99.3625	4.75
BSU40550	<i>ppaC</i>	-2.440062432	0	0	0.00177	33.8344	4.51
BSU23360	<i>ppiB</i>	-0.938261088	2.33E-14	1.26E-14	0.01653	15.1145	5.47
BSU18830	<i>pps</i>	0.139779838	2.50E-06	1.71E-06	-0.539995	96.9978	5.29
BSU18340	<i>ppsA</i>	-0.191019257	1.75E-07	1.14E-07	-0.126843	288.864	5.22
BSU18330	<i>ppsB</i>	-0.890541934	1.26E-106	2.76E-107	-0.378544	289.842	5.06
BSU18320	<i>ppsC</i>	-0.679374564	2.53E-54	7.90E-55	-0.138286	287.185	5.35
BSU18310	<i>ppsD</i>	-0.392306294	0.000105035	7.68E-05	0.06135	406.415	5.35
BSU18300	<i>ppsE</i>	-0.861662386	2.03E-121	4.13E-122	0.37002	144.393	5.66
BSU37010	<i>prfA</i>	-1.663872199	1.70E-200	2.52E-201	0.37182	40.0746	4.82
BSU35290	<i>prfB</i>	-1.843191853	0	0	0.295	41.9132	4.85

BSU08970	<i>prkA</i>	0.255640898	2.74E-151	4.90E-152	-1.28768	72.7069	5.46
BSU15770	<i>prkC</i>	0.051201081	2.89E-05	2.05E-05	-0.079718	71.6872	4.83
BSU13130	<i>proA</i>	-0.549298099	0.002004673	0.001552916	-0.186959	45.1748	5.1
BSU13120	<i>proB</i>	-1.32332133	4.31E-09	2.67E-09	1.60165	39.299	6.01
BSU12910	<i>proG</i>	-1.818529998	9.89E-17	5.08E-17	1.39517	30.0506	4.91
BSU23800	<i>proI</i>	-1.05081379	0.023787056	0.01985808	1.39517	30.2435	6.7
BSU16570	<i>proS</i>	-0.881953336	5.33E-41	1.92E-41	0.15761	63.1314	5.01
BSU15760	<i>prpC</i>	-0.00737246	0.011409567	0.0093351	-1.362116	27.5236	4.36
BSU00510	<i>prs</i>	-1.655123019	7.93E-118	1.65E-118	0.31295	34.7141	5.89
BSU09950	<i>prsA</i>	-1.804149377	0	0	-0.19184	32.3561	9.12
BSU06180	<i>pspA</i>	-1.133900093	1.07E-20	5.12E-21	0.83393	24.9911	5.78
BSU37660	<i>pta</i>	-1.86428199	3.60E-141	6.80E-142	0.79768	34.6355	4.65
BSU24090	<i>ptb</i>	-0.900136106	0.001428137	0.001095332	0.01653	31.6198	7.94
BSU13890	<i>ptsG</i>	-2.599598404	0	0	-0.145619	75.3446	5.41

BSU13910	<i>ptsI</i>	-1.955750395	0	0	0.38287	62.9038	4.59
BSU32450	<i>pucL</i>	-1.453717967	4.27E-29	1.79E-29	-0.655107	56.3905	5.48
BSU23490	<i>pupG</i>	-0.780633155	6.54E-18	3.28E-18	0.17702	28.9755	4.86
BSU40420	<i>purA</i>	-2.504452694	0	0	0.39654	47.5093	5.46
BSU06440	<i>purB</i>	-3.174298571	0	0	0.08056	49.3195	5.82
BSU06450	<i>purC</i>	-3.140222705	0	0	0.37573	27.311	4.88
BSU06530	<i>purD</i>	-3.636505011	0	0	0.13649	45.1182	4.6
BSU06420	<i>purE</i>	-2.446353224	9.59E-52	3.08E-52	0.24203	17.0307	5.2
BSU06490	<i>purF</i>	-3.190941342	0	0	0.70706	51.4533	5.87
BSU06520	<i>purH</i>	-3.030472449	0	0	0.41782	55.5711	5.13
BSU06430	<i>purK</i>	-3.140384095	0	0	0.2499	42.0043	5.12
BSU06480	<i>purL</i>	-3.2799763	0	0	0.24251	80.1048	4.55
BSU06500	<i>purM</i>	-3.364105166	0	0	0.31364	36.8959	4.59
BSU06510	<i>purN</i>	-3.487345104	0	0	0.81322	21.6309	6.18

BSU06470	<i>purQ</i>	-3.766712938	0	0	0.10145	24.6361	4.63
BSU00470	<i>purR</i>	-1.791846764	7.62E-101	1.72E-101	0.01653	31.0765	5.77
BSU06460	<i>purS</i>	-4.231549361	6.91E-110	1.49E-110	0.98209	9.6177	4.59
BSU02230	<i>purT</i>	-1.827712635	1.01E-14	5.41E-15	0.23072	41.9336	4.72
BSU14860	<i>pycA</i>	0.108100855	1.78E-125	3.57E-126	-0.35659	127.721	5.41
BSU29180	<i>pyk</i>	-0.682299754	6.88E-91	1.65E-91	0.23377	61.9991	4.88
BSU15510	<i>pyrAA</i>	-3.862385033	0	0	0.10823	39.9606	5.82
BSU15520	<i>pyrAB</i>	-3.296380036	0	0	-0.141664	117.44	4.78
BSU15490	<i>pyrB</i>	-3.430438472	1.11E-180	1.75E-181	0.01653	34.0161	5.34
BSU15500	<i>pyrC</i>	-3.584693115	0	0	0.18913	46.4451	5.43
BSU15540	<i>pyrD</i>	-3.2583841	2.55E-278	3.07E-279	1.94275	32.9376	4.94
BSU15560	<i>pyrE</i>	-3.564627702	0	0	0.13945	23.3751	5.63
BSU15550	<i>pyrF</i>	-3.853662334	0	0	0.27641	25.8434	5.84
BSU37150	<i>pyrG</i>	-1.387445072	3.94E-182	6.17E-183	0.3989	59.5478	5.16

BSU16510	<i>pyrH</i>	-0.297231665	0.903677294	0.896272	0.09157	25.9335	5.1
BSU15530	<i>pyrK</i>	-3.084820441	0	0	0.22301	27.9501	5.58
BSU15470	<i>pyrR</i>	-1.870376789	1.00E-103	2.22E-104	0.42654	20.1188	4.99
BSU22560	<i>qcrA</i>	-0.270170132	0.566602092	0.54092	0.18166	18.5929	6.08
BSU22550	<i>qcrB</i>	-0.335310307	0.455325122	0.42909	0.01653	25.3409	7.44
BSU22540	<i>qcrC</i>	-0.272128382	0.207886818	0.1886686	-0.240755	28.0118	7.17
BSU38170	<i>qoxA</i>	-2.755678141	0	0	0.24983	36.0989	4.8
BSU38160	<i>qoxB</i>	-2.996300646	0	0	0.18166	73.6567	8.85
BSU27720	<i>queA</i>	-0.974027621	9.56E-17	4.91E-17	-0.288392	38.3547	5.05
BSU13720	<i>queC</i>	-2.822001698	1.07E-43	3.72E-44	0.55579	24.3809	5.15
BSU13740	<i>queE</i>	-2.713717844	1.07E-88	2.58E-89	1.94275	26.9731	4.96
BSU13750	<i>queF</i>	-2.937751559	2.45E-101	5.50E-102	0.32145	19.2306	4.93
BSU37030	<i>racA</i>	3.560969645	0	0	1.39517	20.9251	9.51
BSU34430	<i>racX</i>	0.34557218	6.70E-88	1.64E-88	-1.362116	25.1387	5.4

BSU12430	<i>rapA</i>	0.443225876	0	0	0	-0.680369	44.8132	4.85
BSU36690	<i>rapB</i>	-2.786800666	0	0	0	0.32697	44.8772	4.87
BSU03770	<i>rapC</i>	-2.248305574	2.34E-290	2.76E-291	0.15636	0.15636	45.4744	5.02
BSU37460	<i>rapF</i>	-0.364536239	0.177713526	0.1598284	0.39106	0.39106	45.4484	5.18
BSU40300	<i>rapG</i>	-1.33890643	1.39E-63	4.00E-64	1.39517	1.39517	42.6827	4.81
BSU06830	<i>rapH</i>	-0.336076528	0.088695887	0.0775436	-0.254869	-0.254869	49.9558	6.12
BSU18910	<i>rapK</i>	-1.462928411	3.69E-18	1.85E-18	1.13951	1.13951	43.6828	5.06
BSU16050	<i>rbgA</i>	-1.237201107	2.77E-22	1.30E-22	-0.103798	-0.103798	31.834	9.53
BSU16940	<i>recA</i>	-2.23248485	0	0	-0.119708	-0.119708	37.9336	4.88
BSU27600	<i>relA</i>	-1.625912356	1.05E-190	1.61E-191	-0.161381	-0.161381	84.6521	6.96
BSU23150	<i>resA</i>	-1.069678816	1.83E-07	1.19E-07	1.06409	1.06409	20.7631	8.37
BSU23130	<i>resC</i>	-1.410999649	7.61E-86	1.89E-86	1.78226	1.78226	39.6087	9.56
BSU23120	<i>resD</i>	-1.654331926	8.71E-101	1.97E-101	0.08292	0.08292	27.3361	5.63
BSU23110	<i>resE</i>	-1.914084209	0	0	-0.103798	-0.103798	66.595	5.34

BSU37080	<i>rho</i>	-0.578433064	8.46E-11	5.00E-11	0.19713	48.5132	6.86
BSU23270	<i>ribE</i>	0.952987638	6.54E-39	2.40E-39	-0.164078	23.3328	5.84
BSU23250	<i>ribH</i>	-0.096841951	0.002620771	0.00205098	-0.214862	16.1439	5.2
BSU16020	<i>rimM</i>	-1.114840943	1.00E-07	6.46E-08	0.19713	20.0589	5.22
BSU23160	<i>rluB</i>	-1.866644966	4.74E-86	1.17E-86	-1.362116	25.8778	10.25
BSU15930	<i>rnc</i>	-1.088917456	4.34E-43	1.52E-43	-0.127895	28.2763	8.08
BSU14530	<i>rnjA</i>	-1.687767368	0	0	0.15583	61.3447	5.9
BSU16780	<i>rnjB</i>	-1.527350357	7.28E-188	1.12E-188	0.66893	56.673	9.18
BSU33610	<i>rnr</i>	-0.556744693	1.25E-22	5.82E-23	-1.343135	88.5594	5.7
BSU16960	<i>rny</i>	-1.460096362	0	0	0.27112	58.748	5.39
BSU37780	<i>rocA</i>	1.810780397	0	0	0.40362	56.1505	5.58
BSU40340	<i>rocD</i>	0.97236653	4.44E-204	6.51E-205	0.24792	43.6011	4.89
BSU40320	<i>rocF</i>	0.896017644	1.80E-130	3.56E-131	0.08871	32.0006	4.93
BSU16910	<i>rodZ</i>	-0.678527653	3.21E-09	1.98E-09	1.05433	23.4788	4.68

BSU14240	<i>rok</i>	-2.139499812	1.24E-223	1.73E-224	1.05433	21.6945	9.7
BSU28370	<i>rph</i>	0.370631896	1.57E-06	1.06E-06	-0.288392	26.5318	4.89
BSU01030	<i>rplA</i>	-1.869846099	0	0	-0.232469	24.7749	9.73
BSU01190	<i>rplB</i>	-1.274019816	0	0	-0.62916	30.1812	11.01
BSU01160	<i>rplC</i>	-1.694449155	0	0	-0.243783	22.5374	10.31
BSU01170	<i>rplD</i>	-1.581750758	0	0	-0.224696	22.2451	10.5
BSU01280	<i>rplE</i>	-1.019916332	0	0	-0.148828	20.0029	9.96
BSU01310	<i>rplF</i>	-0.976443693	0	0	0.15553	19.3655	9.92
BSU40500	<i>rplI</i>	-1.878715212	1.89E-105	4.15E-106	0.63333	16.2104	9.96
BSU01040	<i>rplJ</i>	-1.6147083	0	0	0.30445	17.8852	5.49
BSU01020	<i>rplK</i>	-1.726350971	0	0	-0.061057	14.7759	9.72
BSU01050	<i>rplL</i>	-1.499870351	0	0	1.39517	12.6105	4.36
BSU01490	<i>rplM</i>	-2.230178806	0	0	0.6583	16.1499	10.18
BSU01260	<i>rplN</i>	-0.842691806	4.55E-132	8.93E-133	1.08526	13.0144	10.4

BSU01350	<i>rplO</i>	-1.099237352	0	0	0	0.39106	15.241	10.79
BSU01230	<i>rplP</i>	-0.924233435	1.76E-185	2.73E-186	2.73945	16.0481	10.88	
BSU01440	<i>rplQ</i>	-1.117071248	9.03E-191	1.37E-191	1.78226	13.61	10.27	
BSU01320	<i>rplR</i>	-0.947086015	1.08E-224	1.49E-225	-1.909701	12.8779	10.46	
BSU28850	<i>rplT</i>	-2.794406116	0	0	0.01653	13.4979	11.9	
BSU27960	<i>rplU</i>	-1.475311421	1.01E-229	1.38E-230	-0.67548	11.1368	10.16	
BSU01210	<i>rplV</i>	-1.066125935	4.14E-242	5.44E-243	1.39517	12.3201	11.23	
BSU01270	<i>rplX</i>	-0.821723388	1.34E-114	2.85E-115	-0.593688	11.004	10.55	
BSU01430	<i>rpoA</i>	-1.243089347	0	0	0.47644	34.6448	4.59	
BSU01070	<i>rpoB</i>	-0.531913143	8.75E-130	1.74E-130	-0.125666	133.376	4.73	
BSU01080	<i>rpoC</i>	-0.61613603	0	0	-0.135445	133.92	8.86	
BSU37160	<i>rpoE</i>	0.070248712	3.39E-15	1.80E-15	0.09251	20.254	3.65	
BSU16490	<i>rpsB</i>	-1.44541504	0	0	0.23486	27	6	
BSU01220	<i>rpsC</i>	-1.025190777	0	0	0.24371	24	10	

BSU29660	<i>rpsD</i>	-2.189868653	0	0	0.3348	22.6898	10.24
BSU01330	<i>rpsE</i>	-0.989019709	0	0	0.28704	17.4798	10.45
BSU40910	<i>rpsG</i>	-2.309568175	0	0	-0.078166	10.9861	4.99
BSU01110	<i>rpsH</i>	-1.596509204	0	0	0.2449	17	10
BSU01300	<i>rpsI</i>	-1.01074202	9.62E-258	1.22E-258	-1.568599	14.7025	10.3
BSU01500	<i>rpsK</i>	-2.014908977	0	0	-0.317988	14	11
BSU01100	<i>rpsL</i>	-1.693848778	0	0	-0.092465	15	11
BSU01410	<i>rpsM</i>	-1.627315208	0	0	0.32145	13.6611	11.55
BSU04670	<i>rsbR</i>	-1.735681201	3.28E-20	1.58E-20	0.23072	30.8983	4.73
BSU13200	<i>rsbRB</i>	-1.06160512	3.17E-24	1.43E-24	0.11445	32.2345	4.79
BSU19450	<i>rsbRC</i>	-2.012293276	3.92E-15	2.08E-15	0.40362	31.9575	5.51
BSU04720	<i>rsbW</i>	-0.1115753169	3.36E-16	1.74E-16	1.13885	17.8496	4.28
BSU37620	<i>rsfA</i>	0.923926823	0	0	-0.539995	29.5772	5.13
BSU41000	<i>rsmG</i>	-2.848414293	1.05E-81	2.66E-82	-1.362116	26.8049	6.6

BSU27840	<i>safA</i>	-0.603913255	3.91E-171	6.38E-172	0.16601	43.071	5.75
BSU01540	<i>salA</i>	-0.773380163	1.09E-71	2.96E-72	-3.019681	38.4819	5.23
BSU15590	<i>sat</i>	-3.332542598	0	0	0.19197	42.7251	5.65
BSU10650	<i>sbcC</i>	-1.788198094	6.19E-280	7.42E-281	0.36813	128.699	5.29
BSU10640	<i>sbcD</i>	-2.525461489	4.10E-103	9.08E-104	1.78226	43.2472	5
BSU09990	<i>scoC</i>	-2.545243546	1.16E-184	1.80E-185	0.40362	23.5659	5.19
BSU15860	<i>sdaAA</i>	-1.07539307	4.79E-20	2.32E-20	0.16095	30.7811	4.87
BSU15850	<i>sdaAB</i>	-0.703955131	0.001276638	0.000976522	1.78226	23.6723	5.1
BSU28440	<i>sdhA</i>	-1.905003734	0	0	0.12699	65.1739	5.71
BSU28430	<i>sdhB</i>	-1.776385604	0	0	0.105	28.2666	7.99
BSU28450	<i>sdhC</i>	-2.127499933	1.02E-138	1.96E-139	1.78226	22.7852	9.83
BSU33750	<i>sdpA</i>	-1.278535499	4.60E-25	2.05E-25	0.14781	18.5078	9.77
BSU33770	<i>sdpC</i>	0.384533434	0	0	0.73049	22.0747	9.61
BSU35300	<i>secA</i>	-0.252406887	1.59E-05	1.12E-05	-0.105149	95.3335	5.34

BSU27650	<i>secDF</i>	-1.876250436	0	0	-0.006027	81.4693	9.52
BSU01360	<i>secY</i>	-1.294926663	0	0	1.39517	47.0818	10.21
BSU15390	<i>sepF</i>	-1.499532788	6.20E-81	1.58E-81	1.78226	17.013	4.86
BSU23070	<i>serA</i>	-1.877724627	2.90E-185	4.51E-186	0.4181	56.9457	5.62
BSU10020	<i>serC</i>	-2.049977115	2.73E-132	5.35E-133	0.3129	39.9768	5.52
BSU00130	<i>serS</i>	-0.958462903	5.28E-28	2.26E-28	0.12665	48.6778	5.19
BSU25200	<i>sigA</i>	-0.974824787	2.21E-240	2.92E-241	0.01653	42.7976	4.63
BSU15320	<i>sigE</i>	1.39786729	1.83E-37	6.88E-38	-0.288392	27.5498	9.21
BSU23450	<i>sigF</i>	0.745221997	0	0	0.81322	29.2227	5.08
BSU00980	<i>sigH</i>	-2.41789381	8.91E-213	1.28E-213	0.01653	25.2991	5.15
BSU23100	<i>sigX</i>	-0.847213046	5.26E-07	3.49E-07	-1.362116	23.0335	6.09
BSU01730	<i>sigW</i>	0.012077335	5.05E-64	1.45E-64	1.39517	21.5682	8.61
BSU23310	<i>sipS</i>	-1.825099001	1.70E-82	4.29E-83	-0.139653	20.9024	9.72
BSU14410	<i>sipT</i>	-2.299276218	6.60E-119	1.36E-119	0.57305	21.7086	9.85

BSU24630	<i>sipW</i>	-0.210921124	0.328633905	0.30406	0.6688	20.5329	5.49
BSU01920	<i>skfB</i>	1.447056774	0	0	0.58711	45.5926	4.93
BSU01935	<i>skfC</i>	0.966009433	4.74E-158	8.18E-159	0.91468	56	8
BSU01950	<i>skfE</i>	0.652908327	1.35E-62	3.93E-63	0.40362	26.746	6.34
BSU01970	<i>skfG</i>	-0.265848735	0.781083519	0.766882	1.94275	14.3353	5.19
BSU22930	<i>sleB</i>	-1.339644975	5.33E-47	1.80E-47	-2.054123	33.8481	9.51
BSU15940	<i>smc</i>	-0.634495886	2.48E-10	1.48E-10	-2.1854	135.289	5.27
BSU25020	<i>sodA</i>	0.923124776	0	0	0.32575	22.4288	5.2
BSU19330	<i>sodF</i>	0.263639524	1.15E-25	5.08E-26	-2.305726	33.3245	6.17
BSU37500	<i>speE</i>	-0.60591144	0.003881573	0.00307842	0.35763	31.1844	5.07
BSU24220	<i>spo0A</i>	-1.463401657	6.37E-171	1.04E-171	0.18412	29.5402	5.99
BSU40960	<i>spo0J</i>	-2.149771454	2.85E-277	3.44E-278	0.13945	32.0588	8.42
BSU08760	<i>spo0M</i>	-2.113984063	0	0	-0.265874	29.5574	4.28
BSU28060	<i>spoIIB</i>	0.629457929	6.57E-36	2.52E-36	-0.127895	35.7664	4.8

BSU24360	<i>spoIIAH</i>	0.674169397	5.12E-227	7.01E-228	-0.30974	23.5849	4.63
BSU41040	<i>spoIIJ</i>	-1.094024774	1.36E-19	6.65E-20	-0.335072	29.3714	9.99
BSU36550	<i>spoIIQ</i>	1.274150662	0	0	0.81322	30.9606	4.47
BSU22800	<i>spoIVA</i>	0.061358912	0	0	-0.749225	55.0071	4.55
BSU23410	<i>spoVAD</i>	-1.062120613	8.71E-60	2.61E-60	-1.568599	35.8437	5.24
BSU00530	<i>spoVC</i>	2.213720081	0	0	-0.531058	20.7267	5.58
BSU15170	<i>spoVD</i>	0.384511668	8.52E-46	2.90E-46	-1.362116	71.0839	8.85
BSU16740	<i>spoVFB</i>	-2.645814234	0	0	-2.099759	21.723	6.15
BSU28110	<i>spoVID</i>	-0.247759091	1.03E-08	6.46E-09	-1.093791	64.8012	4
BSU09400	<i>spoVR</i>	-0.203236658	0.027835317	0.0233446	-3.443715	55.4603	5.44
BSU16980	<i>spoVS</i>	-0.269002454	0.85892204	0.849464	-0.75755	8.6592	6.47
BSU00560	<i>spoVT</i>	-1.148831818	1.77E-58	5.33E-59	-0.766171	19.598	4.68
BSU29530	<i>sppA</i>	-0.33722104	0.732722979	0.715648	0.83981	36.5156	7.31
BSU37910	<i>spsA</i>	-3.2433149	1.44E-286	1.71E-287	-1.749204	30.0329	5.36

BSU37900	<i>spsB</i>	-3.225144849	0	0	-2.1854	54.1566	5.04
BSU37880	<i>spsD</i>	-3.132697681	2.60E-238	3.43E-239	-1.909701	32.9884	6
BSU37830	<i>spsJ</i>	-2.114463301	2.19E-296	2.56E-297	-2.706394	35.3844	6.29
BSU37820	<i>spsK</i>	-2.408738746	0	0	-2.305726	31.4305	6.08
BSU03480	<i>srfAA</i>	-0.676872657	0	0	-0.182959	401.682	4.87
BSU03490	<i>srfAB</i>	-0.744204515	0	0	-0.160644	400.856	4.9
BSU03510	<i>srfAC</i>	-0.606205221	0	0	-0.06019	143.592	4.97
BSU03520	<i>srfAD</i>	-0.609199212	2.33E-227	3.18E-228	0.22688	27.4721	5.22
BSU09650	<i>srtN</i>	-1.881275494	7.03E-63	2.04E-63	0.29223	27.2677	5.13
BSU40900	<i>ssb</i>	-2.151624394	0	0	0.15316	18.5988	4.82
BSU08660	<i>sspE</i>	-0.342718264	3.13E-17	1.59E-17	-0.46906	9.1308	8.94
BSU08850	<i>sucC</i>	-2.353636955	0.214091955	0.1945194	0.19439	30.0898	10.48
BSU08860	<i>sucD</i>	-0.797086587	0.229622341	0.209218	0.01656	41.6438	5.37
BSU00770	<i>sul</i>	-2.056834568	1.89E-136	3.65E-137	0.01653	30.8491	5.36

BSU06710	<i>swrC</i>	-0.802655553	3.08E-78	7.95E-79	0.38875	114.791	4.76
BSU35770	<i>tagC</i>	-2.332852482	2.25E-37	8.46E-38	-0.293908	50.6603	7.34
BSU35730	<i>tagE</i>	-1.793879372	8.27E-76	2.16E-76	-0.374484	78.1215	6.03
BSU35720	<i>tagF</i>	-1.727329908	1.01E-79	2.58E-80	-0.370561	87.8745	9.4
BSU35700	<i>tagH</i>	-1.848466916	4.22E-87	1.04E-87	1.39517	59.0725	9.45
BSU24620	<i>tasA</i>	2.200990468	0	0	0.93109	28.1539	5.44
BSU03610	<i>tcyA</i>	-1.247975969	1.58E-48	5.22E-49	-0.579927	29.3185	9.12
BSU11650	<i>tenA</i>	-0.737923877	3.66E-05	2.61E-05	0.75426	27.267	4.99
BSU16790	<i>tepA</i>	-1.03437278	3.26E-27	1.41E-27	-2.1854	24.0982	5.57
BSU31270	<i>tgl</i>	-2.734401489	0	0	-1.362116	28.1465	6.69
BSU27710	<i>tgt</i>	-1.291117357	3.41E-44	1.18E-44	0.12759	43.55	6.15
BSU41020	<i>thdF</i>	-2.523911436	1.08E-266	1.34E-267	0.14781	50.8089	4.64
BSU08790	<i>thiC</i>	0.378258406	6.08E-72	1.65E-72	0.7757	65.7405	5.26
BSU38290	<i>thiE</i>	-1.129438555	9.13E-16	4.77E-16	2.08718	23.5333	5.06

BSU11700	<i>thiF</i>	-0.376878559	0.161731079	0.1448746	0.48232	36.2435	5.62
BSU11690	<i>thiG</i>	-0.442573251	0.020213258	0.01678658	0.72228	26.8726	4.72
BSU38300	<i>thiM</i>	-1.987095665	1.70E-36	6.48E-37	-0.357996	28.0625	5.39
BSU11670	<i>thiO</i>	-1.014932348	3.54E-24	1.60E-24	2.55297	40.778	5.9
BSU13240	<i>thiU</i>	-0.644721941	0.018562895	0.0153542	0.19713	21.8774	6.05
BSU32240	<i>thrB</i>	-2.125190318	0	0	0.01653	33.1706	4.74
BSU32250	<i>thrC</i>	-2.123728987	0	0	0.6886	37.3067	5.18
BSU28950	<i>thrS</i>	-2.056689946	0	0	0.07762	73.3352	5.21
BSU17680	<i>thyA</i>	-2.073186055	1.34E-34	5.23E-35	0.01653	32.6548	5.5
BSU21820	<i>thyB</i>	-1.859251682	1.79E-59	5.38E-60	0.40362	30.3873	6.27
BSU28230	<i>tig</i>	-1.149866519	2.45E-176	3.92E-177	0.19847	47	4
BSU36260	<i>tkmA</i>	-2.926838355	3.44E-126	6.91E-127	0.01653	26.4909	4.61
BSU17890	<i>tkt</i>	-0.314345848	0.949420329	0.945044	0.12422	72.1632	4.8
BSU31250	<i>tlpA</i>	-3.229246092	6.54E-118	1.36E-118	0.75379	72.0947	4.91

BSU31230	<i>tlpB</i>	-2.141355849	2.58E-18	1.29E-18	1.39517	71.3551	4.73
BSU00280	<i>tmk</i>	-1.789403057	2.62E-28	1.12E-28	-0.370561	23.7298	4.87
BSU33920	<i>tpi</i>	-2.750607224	0	0	0.67198	26.8796	4.79
BSU29490	<i>tpx</i>	-1.07063923	7.95E-54	2.49E-54	0.79049	18.0722	4.7
BSU29900	<i>trmB</i>	-1.412420195	6.19E-18	3.11E-18	-0.288392	24.3565	6.35
BSU16130	<i>trmFO</i>	-1.18063656	3.29E-29	1.38E-29	-0.314805	47.8991	5.77
BSU25180	<i>trmK</i>	-1.181312527	5.65E-08	3.61E-08	0.22301	23.5581	5.27
BSU27500	<i>trmU</i>	-2.451764926	0	0	-0.14397	42.2048	4.73
BSU22630	<i>trpA</i>	0.112758355	4.15E-14	2.26E-14	1.03758	29.2995	4.82
BSU22640	<i>trpB</i>	0.141565005	1.66E-10	9.84E-11	0.45236	43.4192	5.53
BSU22660	<i>trpC</i>	-0.368594207	0.670433126	0.651376	0.22301	27.6893	5.53
BSU22670	<i>trpD</i>	-0.543228742	0.014069366	0.01156174	0.56411	35.8656	4.9
BSU22680	<i>trpE</i>	-2.092227292	6.00E-60	1.79E-60	0.54724	57.9457	5.25
BSU11420	<i>trpS</i>	-1.571376949	1.83E-58	5.51E-59	0.31364	37.0408	6.54

BSU34790	<i>trxB</i>	-1.279629461	2.12E-61	6.22E-62	0.79923	34.3642	4.99
BSU16500	<i>tsf</i>	-0.376163752	0.012814271	0.0105205	0.63692	32	4
BSU01130	<i>tufA</i>	-1.217587422	0	0	-0.29858	43.432	4.72
BSU22610	<i>tyrA</i>	0.027415458	0.071491963	0.0621916	0.24792	41.2761	5.47
BSU29670	<i>tyrS</i>	-0.248173225	0.466553767	0.440508	-0.235197	47.5741	5.21
BSU27330	<i>udk</i>	-1.857920984	1.30E-65	3.67E-66	0.01653	24.3407	5.38
BSU37970	<i>ung</i>	-2.383805923	1.19E-31	4.81E-32	1.39517	25.8995	8.78
BSU36890	<i>upp</i>	-1.143577429	2.55E-21	1.21E-21	-0.595849	22.8907	5.86
BSU36660	<i>ureA</i>	-1.691978818	1.25E-39	4.57E-40	0.47029	11.3164	4.98
BSU36640	<i>ureC</i>	-1.903318239	0	0	-0.211643	61.0128	5.09
BSU35160	<i>uvrA</i>	-1.213887004	0	0	0.42339	105.831	5.84
BSU35170	<i>uvrB</i>	-1.525363877	3.62E-200	5.38E-201	-0.384138	76.1454	5.26
BSU28090	<i>valS</i>	-0.739514976	3.30E-14	1.79E-14	-0.029101	101.547	4.87
BSU40410	<i>walR</i>	-2.274439169	2.21E-107	4.82E-108	0.50212	27.0773	4.88

BSU39230	<i>wapA</i>	0.699425363	1.89E-272	2.31E-273	-0.370237	258.022	6.13
BSU10770	<i>wprA</i>	1.944443177	0	0	0.19763	96.2898	9.58
BSU22070	<i>xpt</i>	-4.706761876	9.45E-115	2.00E-115	0.04863	20.8937	5.84
BSU00160	<i>yaaH</i>	0.692566687	0	0	-1.206317	48.4743	5.62
BSU00260	<i>yaaN</i>	-0.420646146	0.005919302	0.0047506	0.58232	43.6704	5.6
BSU00290	<i>yaaQ</i>	-2.413985852	2.19E-62	6.39E-63	-0.539995	11.8279	6.09
BSU00320	<i>yaaT</i>	-2.9633315721	5.20E-286	6.20E-287	0.01653	31.0671	4.84
BSU00390	<i>yabD</i>	-0.634395861	0.056000195	0.0480268	0.01653	29.0812	4.81
BSU00650	<i>yabS</i>	1.1861549	0	0	-1.362116	26.6261	4.72
BSU00710	<i>yacC</i>	-1.6252372	1.16E-38	4.28E-39	-0.224575	31.6583	4.66
BSU00720	<i>yacD</i>	-0.435570132	0.603002282	0.579994	0.35763	33.942	4.95
BSU00890	<i>yacL</i>	-0.817304531	1.55E-37	5.80E-38	1.60165	40.7014	4.97
BSU00960	<i>yacO</i>	-1.105447332	7.95E-17	4.07E-17	-0.288392	27.3591	8.63
BSU01460	<i>ybaE</i>	-1.885360758	5.99E-178	9.52E-179	0.17702	30.4265	5.82

BSU01700	<i>ybbI</i>	-0.411208781	0.061930124	0.0534296	-0.93479	32.5456	5.4
BSU01750	<i>ybbP</i>	-1.610655998	7.33E-29	3.09E-29	1.39517	30.4228	8.07
BSU01760	<i>ybbR</i>	-1.466651607	9.55E-74	2.55E-74	-1.362116	52.7782	4.72
BSU02200	<i>ybfG</i>	-2.476438044	5.05E-197	7.55E-198	-2.519916	79.0464	4.69
BSU02220	<i>ybfI</i>	-4.473232941	0	0	-1.749204	32.2874	6.1
BSU02330	<i>ybfQ</i>	-1.480777723	4.60E-225	6.36E-226	0.35763	37.1087	4.91
BSU02390	<i>ybgE</i>	-1.695765145	1.51E-59	4.52E-60	0.24792	39.5193	4.95
BSU02410	<i>ybgG</i>	-0.1111645356	0.538942543	0.512858	-1.362116	34.5807	4.86
BSU01450	<i>ybxA</i>	-1.682211471	3.17E-124	6.41E-125	-1.362116	31.3091	4.77
BSU01060	<i>yxB</i>	-1.290906302	1.60E-31	6.47E-32	0.01653	22.3677	6.12
BSU02520	<i>ycbJ</i>	-1.53419389	1.82E-161	3.07E-162	0.76625	34.327	4.57
BSU02770	<i>yccK</i>	-0.629162305	0.00011679	8.55E-05	0.16095	34.6469	5.01
BSU02780	<i>ycdA</i>	-0.557338479	1.21E-07	7.83E-08	-0.292508	39.0216	4.71
BSU02850	<i>ycdH</i>	-2.302217232	2.72E-116	5.69E-117	1.36081	35.5054	5.15

BSU02890	<i>yceC</i>	-1.910641844	1.05E-151	1.87E-152	0.19182	21.6776	5.31
BSU02900	<i>yceD</i>	-1.930257091	0	0	0.33079	20.5487	4.29
BSU02910	<i>yceE</i>	-1.566378781	2.93E-301	3.37E-302	0.18465	20.8031	4.39
BSU02940	<i>yceH</i>	-2.12514039	5.79E-206	8.45E-207	0.1207	41.5128	5.75
BSU03210	<i>ycgN</i>	1.148767903	5.33E-118	1.10E-118	0.01653	56.32	5.37
BSU03360	<i>yciC</i>	-5.212699025	7.26E-32	2.92E-32	3.05274	45.1452	4.4
BSU03380	<i>yckB</i>	-2.374670921	1.82E-63	5.23E-64	-0.419669	31.5669	8.49
BSU03790	<i>yclM</i>	-1.4735424	7.99E-66	2.25E-66	-0.144028	49.6606	4.78
BSU03830	<i>yclQ</i>	-3.270751887	2.50E-115	5.26E-116	0.22308	34.6376	6.63
BSU03860	<i>ycnD</i>	-1.215357158	2.38E-18	1.19E-18	0.01653	27.7184	5.08
BSU03940	<i>ycnI</i>	-2.846921934	0	0	0.2449	21.9666	4.83
BSU04040	<i>ycsE</i>	-1.337347141	2.19E-25	9.67E-26	-0.414235	27.9172	4.49
BSU04050	<i>ycsF</i>	-2.008004617	8.07E-22	3.80E-22	0.13686	27.391	5.58
BSU04150	<i>ycsN</i>	-0.808213414	3.39E-39	1.24E-39	0.19713	33.986	5.28

BSU04210	<i>ydaF</i>	-0.722517884	0.014322159	0.01178048	0.27189	20.8797	5.56
BSU04220	<i>ydaG</i>	-0.339562918	0.250890241	0.229624	0.01653	15	5.195
BSU04490	<i>ydbJ</i>	-1.935446219	2.44E-24	1.10E-24	1.39517	34.1222	4.73
BSU04520	<i>ydbM</i>	-1.006111998	2.57E-61	7.57E-62	0.55993	41.9805	5.72
BSU04590	<i>ydbS</i>	-0.592310045	0.000277844	0.000206764	1.39517	17.9803	8.13
BSU04630	<i>ydcC</i>	0.296275285	9.78E-162	1.65E-162	-0.676498	42.0293	9.6
BSU04780	<i>ydcI</i>	-1.052985765	2.88E-25	1.28E-25	-0.593688	81.2273	6.77
BSU05170	<i>ydeE</i>	-1.333100024	5.69E-07	3.78E-07	-0.67548	33.1032	7.22
BSU05210	<i>ydeI</i>	-1.196965571	0.000257408	0.000190831	-1.362116	22.9145	7.17
BSU05280	<i>ydeO</i>	-1.881436803	3.87E-30	1.60E-30	1.39517	31.2766	8.67
BSU05300	<i>ydeQ</i>	-1.045003494	0.001091303	0.0008328	-1.362116	22.6857	6.06
BSU05320	<i>ydeS</i>	-1.368061883	0.000222869	0.000164826	-0.14397	21.9973	7.18
BSU05420	<i>ydfI</i>	1.156725504	0.006947224	0.00559336	1.39517	23.8264	5.38
BSU05400	<i>ydfG</i>	0.085679521	0.000122059	8.95E-05	1.78226	17.1714	5.94

BSU05580	<i>ydgC</i>	-1.968038962	9.76E-11	5.78E-11	-1.362116	21.9205	5.57
BSU05600	<i>ydgE</i>	-0.99116414	0.010848675	0.00885952	1.39517	18.2296	5.09
BSU05660	<i>ydgl</i>	-1.319442831	3.07E-05	2.19E-05	-0.531058	23.2122	4.65
BSU05710	<i>ydhd</i>	0.721999208	2.74E-43	9.58E-44	-1.025584	48.8014	9.07
BSU05720	<i>ydhe</i>	-2.271668288	6.30E-151	1.13E-151	-0.288392	42.8663	5.09
BSU05790	<i>ydhk</i>	1.164633365	1.78E-73	4.77E-74	1.39517	22.3889	7.41
BSU05910	<i>ydiB</i>	-0.698383132	0.298686942	0.275358	1.78226	17.7629	4.6
BSU05920	<i>ydiC</i>	0.254264196	0.016354548	0.01347732	1.39517	25.0953	5.76
BSU05770	<i>ydhi</i>	-5.204571144	1.73E-08	1.09E-08	-1.362116	17.7571	5.06
BSU05950	<i>ydiF</i>	-1.893809203	6.29E-98	1.45E-98	0.50212	73.2737	4.87
BSU06090	<i>ydiR</i>	-2.336015407	9.75E-43	3.44E-43	0.11285	35.156	4.39
BSU06100	<i>ydiS</i>	-1.381802717	3.14E-11	1.83E-11	0.41255	39.8758	8.7
BSU06200	<i>ydiH</i>	-1.770931514	1.08E-08	6.74E-09	0.01653	28.0123	5.93
BSU06210	<i>ydiI</i>	-2.380042695	2.68E-65	7.58E-66	0.09673	35.924	4.94

BSU06260	<i>ydjN</i>	-0.763765654	1.76E-05	1.24E-05	0.61942	39.5531	7.35
BSU06280	<i>ydjP</i>	-0.863833398	3.04E-45	1.04E-45	2.08718	30.3582	4.62
BSU06770	<i>yeeB</i>	-2.289506617	3.00E-25	1.33E-25	-0.370561	67.7871	5.28
BSU06812	<i>yeeF</i>	-0.418669704	0.174081692	0.1562946	0.01653	74	8.942
BSU06630	<i>yerH</i>	-1.109357387	2.04E-30	8.34E-31	-0.158621	44.3554	4.88
BSU06640	<i>yerI</i>	-2.141419931	0	0	0.41255	39.1805	4.87
BSU06920	<i>yesJ</i>	0.712229329	9.73E-120	2.00E-120	-1.362116	20.1979	4.87
BSU06860	<i>yezE</i>	-1.785378944	4.49E-25	2.00E-25	-0.164078	21.7411	4.89
BSU06811	<i>yezG</i>	0.386454541	0.007279699	0.0058685	0.85081	18	4
BSU08470	<i>yfhB</i>	-1.752673484	2.44E-67	6.79E-68	0.51542	31.9764	5.19
BSU08480	<i>yfhC</i>	-1.823612873	3.14E-62	9.16E-63	0.23344	22.309	9.16
BSU08580	<i>yfhL</i>	0.41684704	2.00E-47	6.70E-48	0.40362	11.8629	11.02
BSU08590	<i>yfhM</i>	0.539280983	2.58E-264	3.23E-265	-0.158621	32.6065	6.06
BSU08300	<i>yfiK</i>	-0.693757833	0.041665491	0.035413	1.39517	24.2232	4.67

BSU08370	<i>yfiR</i>	-2.009206146	4.96E-19	2.45E-19	0.57857	23.5371	5.02
BSU08390	<i>yfiT</i>	-2.185272966	1.39E-50	4.53E-51	1.39517	20.5221	6.61
BSU08440	<i>yfiY</i>	-2.259776789	5.47E-21	2.61E-21	0.6583	36.1484	7.17
BSU08150	<i>yfiC</i>	-1.931391557	4.62E-08	2.95E-08	0.01653	29.0952	4.86
BSU08140	<i>yfiD</i>	-0.680159239	0.142292503	0.126879	1.39517	21.5405	9.6
BSU08030	<i>yfiN</i>	-1.740339194	1.73E-16	8.91E-17	-1.362116	36.8345	5.38
BSU07990	<i>yfiR</i>	-0.471544595	0.36245832	0.33749	1.11646	27.715	4.78
BSU07930	<i>yfkD</i>	-0.979396983	2.70E-48	8.94E-49	-1.909701	29.437	10.16
BSU07840	<i>yfkN</i>	2.327439079	0	0	-0.364329	159.467	5.02
BSU07830	<i>yfkO</i>	-1.360430728	3.77E-175	6.06E-176	-0.625244	25.4805	5.67
BSU07690	<i>yfiG</i>	-2.383582613	7.33E-178	1.17E-178	0.24258	27.0615	5.58
BSU07650	<i>yfiK</i>	-0.185685065	0.461352252	0.434888	2.08718	24.687	7.76
BSU07520	<i>yfmC</i>	-1.426406313	5.22E-30	2.16E-30	0.24792	34.8659	7.88
BSU07480	<i>yfmG</i>	0.651632563	2.25E-157	3.89E-158	0.56444	56.3743	5.18

BSU07450	<i>yfmJ</i>	-0.502044231	0.017847787	0.01474442	0.67734	36.5073	4.75
BSU07440	<i>yfmK</i>	-1.085846545	3.96E-07	2.61E-07	0.01653	17.1688	4.35
BSU07420	<i>yfmM</i>	-0.657676684	4.88E-06	3.36E-06	-1.909701	59.0237	5.11
BSU07390	<i>yfmP</i>	-2.905439922	3.36E-50	1.10E-50	0.01653	16.3608	5.23
BSU07380	<i>yfmQ</i>	-2.977054124	0	0	0.96014	16.7239	7.17
BSU07370	<i>yfmR</i>	-1.510697852	2.22E-67	6.18E-68	0.28585	70.9415	5
BSU07360	<i>yfmS</i>	-2.394106841	1.18E-86	2.90E-87	0.4172	30.1719	4.53
BSU07350	<i>yfmT</i>	-2.820602246	7.99E-100	1.82E-100	0.43747	53.1541	5.08
BSU07280	<i>yfnG</i>	-3.715360556	0	0	-2.947499	33.9563	5.34
BSU07270	<i>yfnH</i>	-4.254564177	0	0	-1.749204	28.5205	5.49
BSU08680	<i>ygaC</i>	-0.261626336	0.596602884	0.573686	-0.214862	21.0107	5.18
BSU08720	<i>ygaF</i>	-2.192143041	3.57E-24	1.62E-24	0.35763	17.9657	5.86
BSU08750	<i>ygaA</i>	-1.235056863	1.57E-42	5.55E-43	1.94275	34.2436	5.81
BSU10070	<i>yhaA</i>	-1.280733166	2.67E-101	6.00E-102	-0.133617	43.1094	5.86

BSU09930	<i>yhaM</i>	-1.928817406	4.88E-167	8.09E-168	-0.635743	35.5284	5.85
BSU09900	<i>yhaP</i>	0.657593131	1.90E-29	7.90E-30	0.01653	45.2674	5.31
BSU09890	<i>yhaQ</i>	0.050255692	0.001477176	0.001134456	0.14781	33.6891	6.1
BSU09830	<i>yhaX</i>	-0.153695381	7.56E-08	4.86E-08	-0.127895	32.2554	8.07
BSU08950	<i>yhbE</i>	-1.617415689	3.73E-06	2.56E-06	-1.362116	24.5739	4.82
BSU08980	<i>yhbH</i>	-1.155662848	3.69E-104	8.15E-105	-1.388316	45.1712	6.1
BSU09020	<i>yhcB</i>	-0.402228573	0.200143501	0.1813336	1.39517	18.8711	4.64
BSU09090	<i>yhcI</i>	-0.652658194	0.177928425	0.1601128	1.39517	34.7257	6.34
BSU09110	<i>yhcJ</i>	-0.761033354	0.153146878	0.136989	-1.749204	29.0356	5.09
BSU09140	<i>yhcM</i>	-0.908024467	3.24E-78	8.36E-79	-0.531058	16.8883	9.9
BSU09150	<i>yhcN</i>	-1.107616137	5.85E-264	7.34E-265	-1.606334	20.8428	5.36
BSU09180	<i>yhcQ</i>	-0.703582639	7.44E-48	2.48E-48	-1.903889	24.6435	5.74
BSU09190	<i>yhcR</i>	0.712638476	9.79E-148	1.79E-148	-1.362116	132.465	4.69
BSU09200	<i>yhcS</i>	0.568922372	2.03E-20	9.78E-21	1.39517	21.8306	7.17

BSU09240	<i>yhcW</i>	-1.00049671	9.77E-06	6.79E-06	1.39517	24.5273	4.63
BSU09340	<i>yhdA</i>	-1.278594963	3.23E-20	1.56E-20	0.6688	18.7601	6.51
BSU09510	<i>yhdL</i>	-1.725781856	3.41E-86	8.39E-87	1.39517	40.4218	6.18
BSU09550	<i>yhdP</i>	-1.767670359	1.90E-141	3.58E-142	0.48879	49.6915	4.4
BSU09570	<i>yhdR</i>	-1.098879456	6.96E-07	4.63E-07	0.91613	43.7282	5.01
BSU09780	<i>yheC</i>	-0.732230296	3.08E-30	1.26E-30	-2.706394	41.7118	9.22
BSU09730	<i>yheG</i>	-1.073076874	0.001408998	0.001080292	-1.362116	22.6599	5.81
BSU10200	<i>yhfE</i>	-0.487696835	0.03115206	0.026214	-0.285285	38.5791	5.88
BSU10240	<i>yhfI</i>	-0.083159497	0.240607993	0.219782	1.39517	26.3765	5.61
BSU10250	<i>yhfJ</i>	-0.885440236	1.60E-07	1.04E-07	-0.504465	37.8646	5.84
BSU10260	<i>yhfK</i>	-0.556982513	0.0004967	0.000372684	-1.749204	22.6126	5.18
BSU10280	<i>yhfM</i>	-0.611496213	1.51E-06	1.02E-06	0.01653	14.8665	8.43
BSU10310	<i>yhfO</i>	-4.382469637	0.010347315	0.00841034	-1.362116	16.6057	7.9
BSU10320	<i>yhfP</i>	-0.648175166	1.06E-05	7.38E-06	0.01653	34.6025	4.72

BSU10340	<i>yhfR</i>	-1.429377367	1.92E-12	1.08E-12	0.23571	21.8478	5.16
BSU10390	<i>yhfW</i>	0.352711887	1.35E-27	5.81E-28	-1.568599	56.9411	5.66
BSU10100	<i>yhgC</i>	0.545656301	1.04E-48	3.43E-49	0.26813	18.6849	5.22
BSU10450	<i>yhjB</i>	-1.527564981	1.93E-30	7.91E-31	1.39517	52.5962	9.63
BSU09260	<i>yhxA</i>	-0.423272714	0.020118931	0.01669794	0.32145	49.7071	5.64
BSU10400	<i>yhxC</i>	-0.286537235	0.66081667	0.641356	-2.054123	30.6945	7.26
BSU10750	<i>yisK</i>	-1.053027364	9.49E-12	5.47E-12	1.26088	32.9925	5.45
BSU10860	<i>yisT</i>	0.865394127	2.22E-161	3.77E-162	0.41255	19.344	5.73
BSU10900	<i>yisY</i>	-0.817895417	1.88E-06	1.27E-06	-0.531058	30.408	6.89
BSU10920	<i>yitA</i>	-2.123437738	3.46E-288	4.09E-289	-1.749204	43.0947	7.55
BSU10940	<i>yitC</i>	-2.706978189	4.26E-71	1.16E-71	-1.749204	24.5132	5.22
BSU10950	<i>yitD</i>	-2.475957976	6.07E-112	1.30E-112	-2.054123	28.2066	4.38
BSU11010	<i>yitJ</i>	0.299403322	9.82E-08	6.34E-08	0.71343	67.7508	5.34
BSU11020	<i>yitK</i>	-1.86748987	1.13E-23	5.17E-24	0.27382	18.0594	9.65

BSU11030	<i>yitL</i>	-0.231068252	0.508930224	0.482604	-0.370561	33.899	4.81
BSU11110	<i>yitS</i>	-1.522696091	2.00E-76	5.21E-77	-1.362116	31.1246	5.63
BSU11140	<i>yitU</i>	-1.075673761	5.55E-12	3.18E-12	-1.749204	30.4819	4.67
BSU11150	<i>yitV</i>	-0.971430848	0.000140098	0.00010293	0.41255	28.914	5.56
BSU11490	<i>yjbC</i>	-0.673139325	7.07E-29	2.98E-29	-0.468997	22.9557	5.14
BSU11600	<i>yjbM</i>	-1.647818863	4.05E-15	2.15E-15	-0.164078	24.5575	6.71
BSU11850	<i>yjcG</i>	-1.475841487	3.48E-113	7.40E-114	0.0668	19.5178	5.57
BSU11860	<i>yjcH</i>	-1.940179706	2.27E-130	4.50E-131	-0.049089	27.7681	5.99
BSU11890	<i>yjcK</i>	-0.132702537	0.365550077	0.340556	0.19713	20.78	5.46
BSU12050	<i>yjdH</i>	-0.376681668	0.172934123	0.15522	-2.054123	15.1996	5.11
BSU12060	<i>yjdI</i>	-1.826239936	8.38E-07	5.62E-07	1.39517	17.1164	8.76
BSU12180	<i>yjhA</i>	-1.584962501	1.03E-05	7.14E-06	0.26813	23.831	5.29
BSU12220	<i>yjiC</i>	0.127199702	1.21E-06	8.12E-07	0.70854	43.8269	4.65
BSU12230	<i>yjiA</i>	-1.696930932	1.12E-19	5.48E-20	0.30613	29.6849	5.14

BSU12280	<i>yjIC</i>	-2.955199795	8.04E-235	1.08E-235	-0.137626	15.4411	4.26
BSU12410	<i>yjoA</i>	0.674410294	1.40E-63	4.03E-64	0.20508	17.6501	5.81
BSU12420	<i>yjoB</i>	-1.778688228	8.35E-152	1.49E-152	1.39517	48.6122	4.73
BSU12490	<i>yjqC</i>	-1.334494446	1.41E-23	6.44E-24	-2.616164	31.1472	5.15
BSU12850	<i>ykaA</i>	-2.150497586	2.60E-93	6.15E-94	-0.296757	23.6966	4.91
BSU12980	<i>ykfB</i>	0.57955264	1.42E-46	4.82E-47	-2.054123	39.3136	5.91
BSU13000	<i>ykfD</i>	1.357229639	0	0	0.19713	36.83	9.34
BSU13010	<i>ykgB</i>	-0.011396183	2.27E-15	1.20E-15	0.56675	38.2551	5.15
BSU13110	<i>ykkE</i>	-1.319406548	5.62E-21	2.68E-21	1.78226	34.3376	5.95
BSU14250	<i>yknT</i>	-0.890403282	5.60E-48	1.86E-48	0.01653	37.5135	7.16
BSU14340	<i>yknW</i>	-1.681910438	0	0	0.41046	24.028	6.94
BSU14350	<i>yknX</i>	-0.811541784	5.04E-15	2.68E-15	0.82737	41.5489	5.18
BSU14360	<i>yknY</i>	-0.380731377	0.397078983	0.370946	0.44729	25.1236	5.82
BSU14370	<i>yknZ</i>	-0.324753685	0.818909054	0.806746	0.24792	41.9636	4.68

BSU14430	<i>ykpA</i>	-1.915644151	0	0	0.47317	60.8832	4.98
BSU14440	<i>ykpB</i>	-1.239680378	5.36E-20	2.60E-20	0.01653	33.419	6.14
BSU14500	<i>yqA</i>	-2.270528942	2.11E-24	9.50E-25	1.39517	31.507	6.22
BSU14550	<i>ykrA</i>	-0.490701769	0.414218231	0.388018	0.32145	28.7552	4.57
BSU13480	<i>ykrK</i>	-2.29825805	7.20E-33	2.86E-33	0.56411	26.7162	6.15
BSU13490	<i>ykrL</i>	-1.785154704	0	0	0.01653	32.7125	10.16
BSU14650	<i>yktB</i>	-1.385441977	1.67E-11	9.73E-12	0.23072	24.4691	6.43
BSU14670	<i>yktC</i>	0.459187752	4.17E-30	1.72E-30	0.55442	29.6083	5.09
BSU14090	<i>ykuI</i>	-0.625183936	5.73E-05	4.13E-05	0.01653	47.7953	4.46
BSU14180	<i>ykuQ</i>	-1.031407449	4.50E-13	2.50E-13	0.79672	24.8383	4.68
BSU14190	<i>ykuR</i>	-0.591595593	0.024545612	0.0205102	0.6583	41.3985	5.1
BSU14220	<i>ykuU</i>	-0.584017916	9.50E-08	6.13E-08	0.60964	20.302	4.49
BSU14230	<i>ykuV</i>	-1.175306405	4.34E-45	1.49E-45	-0.164078	17.6596	6.33
BSU13860	<i>ykvY</i>	-1.357143626	1.23E-40	4.42E-41	0.68817	40.176	5.17

BSU13960	<i>ykwC</i>	-2.882692567	0	0	-0.168637	30.558	5.11
BSU14770	<i>ylaG</i>	-1.563440249	0	0	0.09128	68.2119	4.97
BSU14800	<i>ylaJ</i>	-1.004417318	1.57E-39	5.73E-40	-0.831664	23.2378	4.83
BSU14810	<i>ylaK</i>	-0.602093582	4.47E-08	2.85E-08	-1.909701	49.1683	5.42
BSU15050	<i>yblL</i>	-0.787986724	1.64E-05	1.16E-05	1.39517	38.6105	5.85
BSU15070	<i>yblN</i>	-1.570017641	1.69E-69	4.66E-70	0.19713	19.8496	4.31
BSU15120	<i>yllA</i>	-0.127401377	0.02641806	0.0221154	0.24343	62.4386	5.25
BSU15340	<i>yImA</i>	0.182932346	0.082959428	0.0724222	0.6583	29.5763	5.13
BSU15350	<i>yImB</i>	-0.609966507	0.120279637	0.1066962	-0.651059	47.0191	4.98
BSU15370	<i>yImD</i>	-0.844804079	2.14E-13	1.18E-13	-1.362116	30.7917	6.18
BSU15620	<i>yImE</i>	-3.279140744	0	0	0.57305	28.6855	6.06
BSU15650	<i>yloB</i>	0.75902492	2.97E-177	4.74E-178	-0.702023	97.0961	8.71
BSU15660	<i>yloC</i>	-1.85239181	1.69E-119	3.47E-120	-0.214862	33.4769	4.87
BSU15700	<i>yloI</i>	-1.677373433	5.90E-31	2.40E-31	0.68412	43.8166	6.01

BSU15750	<i>yloN</i>	-1.238060875	7.03E-40	2.55E-40	-0.370561	41.4105	6.79
BSU15840	<i>yloV</i>	-0.105723886	0.000194234	0.00014345	0.0793	59.3238	4.28
BSU16260	<i>yIxF</i>	-4.026604151	1.44E-115	3.03E-116	0.40362	22.8023	9.74
BSU16590	<i>yIxS</i>	-1.790340768	1.16E-53	3.65E-54	0.01653	17.4814	4.48
BSU15460	<i>ylyB</i>	-1.18706836	7.04E-14	3.85E-14	-1.362116	33.5001	5.43
BSU17400	<i>ymaB</i>	-2.009741394	3.88E-10	2.33E-10	2.08718	23.2407	4.51
BSU17250	<i>ymaE</i>	-0.855957296	7.79E-06	5.39E-06	-0.182844	26.4282	9.29
BSU17010	<i>ymcB</i>	-1.343316021	0	0	0.01653	57.9992	6.87
BSU16970	<i>ymdB</i>	-1.459494763	3.71E-26	1.63E-26	0.68412	29.1381	6.5
BSU16845	<i>ymfF</i>	-0.75636438	1.71E-22	7.98E-23	0.01653	48	5.263
BSU16860	<i>ymfH</i>	-0.523799701	4.30E-12	2.45E-12	-0.186412	47.0394	4.94
BSU17240	<i>ymzB</i>	-0.692357966	6.55E-07	4.36E-07	-1.362116	13.2543	4.44
BSU17430	<i>ynbA</i>	-0.705663983	5.09E-05	3.67E-05	0.01653	37.5059	9.24
BSU17640	<i>yncD</i>	-1.144738373	9.02E-62	2.64E-62	-1.909701	43.4873	9.59

BSU17660	<i>yncF</i>	-0.968464427	0.266428837	0.244596	0.40362	16.2675	5.1
BSU17690	<i>yncM</i>	-0.549339115	4.07E-52	1.30E-52	0.68412	26.4477	9.97
BSU17730	<i>yndB</i>	-1.733968335	8.92E-69	2.47E-69	-1.568599	15.9782	4.6
BSU17910	<i>yneF</i>	-2.08506185	6.58E-19	3.26E-19	0.32145	8.162	11.04
BSU17950	<i>yneJ</i>	-2.81831747	1.77E-107	3.86E-108	1.39517	18.3139	10.47
BSU17960	<i>yneK</i>	-0.974263864	3.52E-10	2.11E-10	1.78226	16.8472	9.66
BSU18080	<i>yneT</i>	-0.727231079	6.20E-12	3.56E-12	-1.749204	14.8483	5.28
BSU18530	<i>yoaA</i>	-0.128526028	0.078738979	0.068637	0.57305	18.8929	5.92
BSU18560	<i>yoaD</i>	-2.561878888	0.006702726	0.00539136	0.22301	38.4731	5.62
BSU18570	<i>yoeE</i>	-1.097485116	2.44E-11	1.43E-11	-0.197661	76.0553	7.33
BSU18970	<i>yobI</i>	-2	3.94E-26	1.73E-26	0.32145	140.397	5.39
BSU18980	<i>yobJ</i>	-1.860092303	9.54E-29	4.05E-29	0.32145	33.5961	9.49
BSU18990	<i>yobK</i>	-0.304854582	0.994196596	0.993942	-0.189957	17.5724	3.97
BSU19010	<i>yobM</i>	-2.005656051	2.01E-20	9.64E-21	-1.362116	19.0036	4.07

BSU19170	<i>yocD</i>	-1.103025043	8.21E-13	4.58E-13	0.01653	36.2546	5.58
BSU19550	<i>yodC</i>	-0.611419697	0.000950243	0.00072199	0.01653	22.1943	5.27
BSU19580	<i>yodF</i>	-0.986019245	6.83E-06	4.72E-06	0.17702	53.599	9.68
BSU19620	<i>yodJ</i>	-1.902585959	8.95E-49	2.95E-49	0.70854	30.7015	5.84
BSU19710	<i>yodQ</i>	0.598887379	2.92E-94	6.84E-95	-2.054123	48.3923	5.41
BSU19730	<i>yodS</i>	0.11075268	1.06E-06	7.12E-07	1.39517	24.2627	4.44
BSU18360	<i>yoxA</i>	-1.810621431	9.21E-156	1.61E-156	0.11966	37.0732	5.6
BSU18500	<i>yoxD</i>	-1.209748212	9.82E-12	5.66E-12	0.05665	25.1503	5.33
BSU22030	<i>ypbR</i>	-1.057737291	5.44E-15	2.90E-15	-2.519916	137.161	5.72
BSU22950	<i>ypdA</i>	-2.46746789	8.74E-206	1.28E-206	0.78724	36.1822	6.08
BSU22920	<i>ypeB</i>	-1.082487454	5.61E-146	1.04E-146	-3.216815	51.0198	6.31
BSU21970	<i>ypeP</i>	-1.332150317	5.86E-32	2.36E-32	-1.749204	13.58	5.24
BSU22880	<i>ypfD</i>	-0.877731387	1.26E-122	2.55E-123	-0.04834	42.2443	4.57
BSU21890	<i>ypgQ</i>	-1.252525655	6.14E-05	4.44E-05	0.19713	22.9759	5.51

BSU21880	<i>ypgR</i>	-1.562095218	2.47E-63	7.11E-64	0.45864	42.4086	4.77
BSU22840	<i>ypbC</i>	-1.192316292	3.96E-55	1.23E-55	0.50225	48.6059	5.25
BSU22810	<i>ypbF</i>	-1.366049357	1.54E-25	6.81E-26	0.01653	27.599	5.63
BSU21860	<i>ypbP</i>	-1.324802627	6.13E-18	3.07E-18	-0.265998	15.7321	4.62
BSU22590	<i>ypbA</i>	-0.45320841	0.010252675	0.00832554	-0.539995	48.1574	4.11
BSU22580	<i>ypbB</i>	-0.03913661	2.02E-29	8.44E-30	0.22301	21.2195	5.88
BSU22570	<i>ypbF</i>	0.503011481	0.000326674	0.000244106	-0.324575	17.1246	5.09
BSU21830	<i>ypjQ</i>	-2.117736315	6.60E-273	8.03E-274	0.36813	19.7577	4.5
BSU22380	<i>ypmB</i>	-1.597763783	1.52E-35	5.85E-36	1.39517	17.7529	9.24
BSU21750	<i>ypmQ</i>	-2.128316039	3.30E-77	8.57E-78	0.29223	21.5005	4.81
BSU21740	<i>ypmR</i>	-1.694960919	3.64E-51	1.18E-51	1.39517	28.7719	6.78
BSU21730	<i>ypmS</i>	-1.993060617	3.33E-34	1.31E-34	0.22301	20.9434	5.26
BSU21700	<i>ypoP</i>	-2.263907142	2.61E-164	4.38E-165	1.78226	16.7242	9.26
BSU22230	<i>ypqE</i>	-1.446816208	1.01E-23	4.59E-24	2.55297	17.7922	5.29

BSU23370	<i>ypuA</i>	-1.139626696	4.80E-60	1.43E-60	0.01653	31.1415	4.51
BSU22080	<i>ypwA</i>	-0.292109463	0.804992791	0.792418	0.295	58.0058	4.77
BSU26230	<i>yqaP</i>	-3.238398013	0	0	0.69922	34.6269	4.8
BSU26160	<i>yqbC</i>	-2.824975844	5.03E-08	3.22E-08	2.08718	25.1034	5.16
BSU25870	<i>yqcF</i>	-0.985172582	3.20E-06	2.19E-06	-0.101368	21.3306	4.27
BSU25860	<i>yqcG</i>	-1.27323199	2.92E-24	1.32E-24	-2.054123	59.4965	8.81
BSU25820	<i>yqcI</i>	-1.557323819	2.11E-23	9.66E-24	-1.362116	29.9542	5.03
BSU25730	<i>yqeC</i>	-0.554716214	0.174405518	0.15663	-1.362116	32.6154	5.82
BSU25670	<i>yqeH</i>	-1.715813468	3.56E-45	1.22E-45	0.40362	40.8413	6.01
BSU25630	<i>yqeK</i>	-1.367149276	3.46E-13	1.92E-13	-0.164078	21.1373	5.97
BSU25450	<i>yqeT</i>	-0.837194982	1.21E-08	7.57E-09	-0.468997	34.4405	4.6
BSU25400	<i>yqeY</i>	-1.4902473	0	0	-0.549262	16.6237	5.53
BSU25390	<i>yqeZ</i>	-1.917167274	0	0	-0.189957	46.2999	5.64
BSU25380	<i>yqfA</i>	-2.231859447	0	0	-0.242099	35.4849	4.92

BSU25330	<i>yqfF</i>	-1.177046239	1.13E-52	3.59E-53	0.23072	78.9826	7.7
BSU25320	<i>yqfG</i>	-0.912801558	1.37E-05	9.54E-06	1.39517	17.6145	4.19
BSU25240	<i>yqfL</i>	-1.521193783	3.36E-43	1.17E-43	-0.370561	30.1984	5.78
BSU25170	<i>yqfO</i>	-1.344678605	4.96E-45	1.71E-45	0.33276	40.7618	5.39
BSU25050	<i>yqgA</i>	-0.789325559	3.11E-08	1.98E-08	-0.14397	15.1397	10.23
BSU24540	<i>yqhL</i>	-2.494864802	2.09E-88	5.07E-89	0.01653	14.4505	10.37
BSU24530	<i>yqhM</i>	-1.569792066	7.81E-09	4.85E-09	2.08718	32.0885	5.93
BSU24500	<i>yqhP</i>	-0.744131732	4.86E-16	2.52E-16	0.01653	14.427	11.89
BSU24470	<i>yqhS</i>	-1.163774106	8.92E-18	4.49E-18	0.01653	16.2903	5.12
BSU24460	<i>yqhT</i>	-0.994747234	4.34E-67	1.21E-67	1.05864	37.963	4.83
BSU24330	<i>yqhY</i>	-0.0219214	4.53E-20	2.19E-20	0.1647	14.5458	4.41
BSU24210	<i>yqiG</i>	-1.18193645	2.72E-48	9.01E-49	0.22301	40.6472	5.18
BSU23990	<i>yqiW</i>	-1.344791005	1.08E-30	4.41E-31	-0.224575	16.0538	4.81
BSU23910	<i>yqjE</i>	-0.828582719	3.90E-35	1.51E-35	0.45568	39.4979	4.76

BSU23820	<i>yqjM</i>	0.532208701	1.18E-16	6.08E-17	0.01653	37.4273	5.14
BSU23690	<i>yqjY</i>	-1.941079282	4.24E-10	2.55E-10	0.01653	17.7097	7.91
BSU23620	<i>yqkF</i>	0.096189646	2.90E-05	2.06E-05	0.66893	34.5627	5.13
BSU24940	<i>yqzC</i>	-2.306060273	0	0	-0.17201	16.8835	9.01
BSU24930	<i>yqzD</i>	-2.183204833	4.78E-153	8.48E-154	1.78226	13.1834	5.05
BSU27020	<i>yraA</i>	-1.440844965	1.25E-48	4.11E-49	1.27058	18.3687	4.73
BSU26780	<i>yrdA</i>	-0.822429829	5.71E-10	3.45E-10	-2.947499	18.7739	5.72
BSU26760	<i>yrdC</i>	-4.01282404	0.010344056	0.00841034	0.11966	21.1043	5.07
BSU27160	<i>y rhJ</i>	-1.689106878	1.03E-218	1.45E-219	0.52362	118.467	6.02
BSU26610	<i>yrkA</i>	-2.413962065	0	0	-0.539995	48.8218	4.92
BSU26560	<i>yrkC</i>	-2.480681992	7.38E-168	1.22E-168	-1.568599	21.1103	7.35
BSU26470	<i>yrkL</i>	-2.137979936	8.65E-28	3.71E-28	0.40362	19.949	5.36
BSU26820	<i>y rpD</i>	0.764218135	0	0	0.44057	24.7277	9.96
BSU27360	<i>y rrM</i>	-2.583831419	1.62E-36	6.15E-37	1.60165	24.9157	5.57

BSU27350	<i>yrnN</i>	-1.854308261	8.65E-52	2.78E-52	0.14781	34.9234	4.64
BSU27300	<i>yrnS</i>	-0.377976546	0.192056736	0.1730232	0.01653	25.1844	4.73
BSU27630	<i>yrnD</i>	-0.460383076	0.677542163	0.659324	1.60165	12.0954	8.72
BSU27540	<i>yrnM</i>	0.034302653	3.88E-12	2.21E-12	0.01653	28.0188	8.19
BSU27510	<i>yrnO</i>	-2.595968081	0	0	0.32145	41.0326	5.46
BSU28940	<i>ysaA</i>	-2.109178521	1.67E-115	3.52E-116	-0.036938	29.3577	4.67
BSU28830	<i>ysdB</i>	-0.086734391	8.17E-05	5.93E-05	1.39517	15.4315	9.41
BSU28820	<i>ysdC</i>	-0.029098814	2.15E-08	1.36E-08	-0.238824	39.0591	5.55
BSU28420	<i>ysmA</i>	-1.292430662	1.27E-15	6.66E-16	-0.189957	16.9306	5.54
BSU28360	<i>ysnA</i>	-0.378648681	0.617244539	0.596538	0.40362	21.7864	4.95
BSU28350	<i>ysnB</i>	-0.293713443	0.94352803	0.938454	2.08718	19.0108	5.32
BSU28190	<i>ysxC</i>	-0.8699262	8.01E-12	4.61E-12	-0.259171	21.8809	9.71
BSU29060	<i>ytaG</i>	-2.230041201	2.52E-108	5.48E-109	-0.495291	21.8672	4.86
BSU29000	<i>ytcG</i>	-1.555950591	8.51E-16	4.44E-16	-1.362116	17.7694	8.05

BSU29560	<i>ytcI</i>	-0.398387556	0.284097447	0.261326	-0.584121	59.4003	6.18
BSU29540	<i>yt dI</i>	1.830963557	0	0	-0.702023	30.1021	6.49
BSU29500	<i>ytfJ</i>	-0.287569346	0.828908499	0.817446	-2.305726	16.204	4.99
BSU30690	<i>ytiB</i>	-0.686329006	0.015391726	0.01266812	-0.114749	20.9662	6.17
BSU29980	<i>ytfP</i>	-1.105812844	9.50E-53	3.02E-53	-0.158621	50.8869	4.66
BSU30660	<i>ytkA</i>	-0.587483122	0.001540493	0.001185844	1.78226	15.7146	4.74
BSU29410	<i>ytkL</i>	-0.721827958	4.13E-17	2.10E-17	0.67734	24.6838	5.01
BSU29970	<i>ytkP</i>	-2.048147796	4.42E-45	1.52E-45	-0.370561	32.9118	4.93
BSU30595	<i>ytIA</i>	-2.130617504	2.79E-166	4.66E-167	-2.1854	38	4.998
BSU30610	<i>ytIC</i>	-2.184595182	6.34E-62	1.85E-62	-2.706394	29.1525	5.43
BSU29270	<i>ytoI</i>	-1.621891718	1.68E-56	5.17E-57	-1.362116	48.8736	6.59
BSU29860	<i>ytoP</i>	-1.097814791	2.61E-11	1.52E-11	-0.103798	39.0791	5.65
BSU29850	<i>ytoQ</i>	-0.811136563	0.01067733	0.00870592	0.46419	16.6487	5.77
BSU30510	<i>ytpA</i>	-1.429621461	3.88E-28	1.66E-28	0.19713	29.4156	6.77

BSU29830	<i>ytpQ</i>	-1.313739288	2.71E-42	9.62E-43	-0.324575	30.8913	5.3
BSU29820	<i>ytpR</i>	-1.529717562	1.93E-43	6.71E-44	-0.370561	21.5509	4.27
BSU30490	<i>y tqB</i>	-0.840263288	9.26E-06	6.42E-06	0.01653	21.1381	5.56
BSU30410	<i>ytrF</i>	-0.780457066	7.37E-06	5.09E-06	1.39517	48.2557	8.29
BSU29220	<i>ytsJ</i>	-1.679103507	1.03E-203	1.51E-204	0.40199	43.5057	5.05
BSU29640	<i>ytsP</i>	-1.415740592	6.59E-13	3.68E-13	0.01653	8.6003	6.09
BSU30360	<i>yttA</i>	-0.62680256	0.172248736	0.1545166	1.17433	27.5265	7.75
BSU30340	<i>ytvA</i>	-1.29689321	5.54E-17	2.82E-17	1.39517	29.044	4.69
BSU29780	<i>ytxG</i>	0.903155607	0	0	0.01653	15.6007	9.98
BSU29770	<i>ytxH</i>	0.907121753	0	0	0.49407	16.5427	5.11
BSU29870	<i>ytzB</i>	-2.572277819	1.10E-81	2.79E-82	-0.370561	11.5279	8.09
BSU30035	<i>ytzG</i>	-2.016820165	1.13E-14	6.07E-15	2.08718	27	5.619
BSU31070	<i>yuaC</i>	-1.677756596	0.000120305	8.81E-05	0.01653	20.9246	4.62
BSU31030	<i>yuaE</i>	-1.425761463	2.43E-108	5.28E-109	-1.141273	18.9673	6.2

BSU31010	<i>yuaG</i>	-1.057015221	0	0	-0.242957	55.8235	5.14
BSU31000	<i>yuaI</i>	-2.208718594	0	0	-0.103798	19.6988	5.14
BSU31160	<i>yubA</i>	-1.740157606	3.78E-48	1.25E-48	1.39517	43.4526	9.76
BSU31150	<i>yubB</i>	-1.476730969	3.51E-58	1.07E-58	-2.871518	30.194	7.9
BSU31860	<i>yueB</i>	-0.691142948	8.26E-10	5.02E-10	0.67734	119.769	4.3
BSU31840	<i>yueD</i>	-1.202785845	1.88E-24	8.45E-25	0.24792	26.9593	6.43
BSU31540	<i>yufN</i>	-1.359741691	1.13E-138	2.18E-139	-0.013406	37.1919	4.82
BSU31550	<i>yufO</i>	-1.176999486	4.77E-35	1.85E-35	-0.419669	56.1315	7.5
BSU31390	<i>yugI</i>	-2.739421815	0	0	-1.362116	14.1427	5.92
BSU31370	<i>yugJ</i>	-0.108808462	3.89E-05	2.78E-05	0.24258	42.5723	5.22
BSU31360	<i>yugK</i>	-0.366073469	0.643149989	0.622892	0.01653	43.2452	4.64
BSU31310	<i>yugP</i>	-0.886486922	6.30E-16	3.28E-16	-1.362116	24.5477	9.16
BSU31290	<i>yugT</i>	0.481976897	1.44E-38	5.33E-39	-1.362116	63.8216	4.97
BSU32050	<i>yuiE</i>	-1.306308287	5.60E-65	1.59E-65	-0.234567	53.4886	4.55

BSU31875	<i>yukB</i>	-0.367224181	0.32961917	0.305056	0.32145	172	5.462
BSU31890	<i>yukC</i>	-0.902214108	4.36E-05	3.13E-05	0.29906	51.9963	4.68
BSU31945	<i>yukJ</i>	0.109695609	1.50E-29	6.22E-30	0.57305	26	4.615
BSU31170	<i>yulF</i>	-1.613123793	1.99E-24	8.97E-25	0.17702	36.3587	5.15
BSU32100	<i>yumB</i>	-0.283998639	0.496744715	0.47054	-1.775404	44.7721	6.62
BSU32110	<i>yumC</i>	-1.890501635	2.30E-51	7.40E-52	0.17871	36.6848	5.57
BSU32570	<i>yurL</i>	-2.620506618	1.32E-12	7.43E-13	-0.960496	30.834	4.91
BSU32600	<i>yurO</i>	-2.245435812	4.87E-19	2.41E-19	-0.8045	47.8634	5.67
BSU32610	<i>yurP</i>	-2.284891125	7.76E-99	1.78E-99	-0.258281	36.7203	5.44
BSU32660	<i>yurT</i>	-1.599099753	8.27E-11	4.89E-11	-1.362116	14.2969	4.61
BSU32670	<i>yurU</i>	-1.725955115	0	0	0.20759	52.5618	4.96
BSU32700	<i>yurX</i>	-2.250727684	0	0	0.23365	48.1301	4.95
BSU32710	<i>yurY</i>	-2.222947263	0	0	0.24233	28.8793	4.62
BSU32300	<i>yutE</i>	-1.437239135	2.54E-12	1.44E-12	0.01653	16.5082	4.58

BSU32290	<i>yutF</i>	-0.646835582	0.001925646	0.001490218	0.01653	27.8059	4.55
BSU32200	<i>yutJ</i>	-0.796658663	2.69E-08	1.71E-08	-0.468997	36.7537	5.82
BSU32230	<i>yuxL</i>	-0.559147659	0.003543904	0.00280336	-0.288392	73.5339	5.1
BSU33530	<i>yvaA</i>	0.783254964	6.45E-248	8.34E-249	0.6403	39.9543	5.46
BSU33590	<i>yvaG</i>	0.32040356	1.14E-31	4.62E-32	0.16095	28.8574	4.76
BSU33620	<i>yvaK</i>	-0.096964463	0.021380164	0.01778304	-0.052213	28.2611	4.99
BSU33840	<i>yvbF</i>	-0.178632036	0.704247543	0.685672	1.78226	21.6051	5.84
BSU33860	<i>yvbH</i>	-1.112377979	6.11E-05	4.42E-05	0.52362	23.6554	4.93
BSU33880	<i>yvbJ</i>	-1.835099913	5.09E-13	2.83E-13	-0.144028	67.0974	4.85
BSU33890	<i>yvbK</i>	-0.988878527	0.001397818	0.001071362	0.01653	17.6025	4.55
BSU34850	<i>yvcA</i>	-1.979666998	1.04E-22	4.85E-23	0.01653	27.7209	6.83
BSU34780	<i>yvcI</i>	-2.727295674	1.39E-91	3.31E-92	1.39517	18.0708	4.99
BSU34770	<i>yvcJ</i>	-2.271246438	9.54E-192	1.44E-192	0.01653	33.6973	6.7
BSU34760	<i>yvcK</i>	-2.666648485	0	0	-0.189957	34.5333	5.41

BSU34720	<i>yvcP</i>	-1.525941987	5.97E-11	3.51E-11	-1.749204	27.3655	4.68
BSU34700	<i>yvcR</i>	-1.43837603	1.10E-15	5.79E-16	0.45272	28.8877	6.34
BSU34680	<i>yvcT</i>	-1.092339844	3.47E-28	1.48E-28	0.27189	36.4632	5.09
BSU34640	<i>yvdD</i>	-0.195750989	0.624330366	0.603546	0.97372	20.9082	5.09
BSU34480	<i>yvdT</i>	-2.385425598	1.11E-97	2.56E-98	1.39517	22.0815	5.3
BSU33380	<i>yvgL</i>	-2.864985468	1.45E-63	4.16E-64	-0.370561	28.205	5.1
BSU33400	<i>yvgN</i>	-1.011278689	1.50E-41	5.37E-42	0.50932	31.5114	5.07
BSU35520	<i>yvhJ</i>	-2.066211392	1.72E-92	4.10E-93	0.50205	43.0498	9.14
BSU35190	<i>yvkC</i>	-1.152936143	1.15E-11	6.63E-12	-0.335072	94.254	4.62
BSU35120	<i>yvIB</i>	-1.872969435	0	0	-0.089519	40.9223	5.39
BSU35080	<i>yvmB</i>	-3.899376542	9.54E-27	4.16E-27	0.22301	19.5376	8.09
BSU34970	<i>yvoE</i>	-1.525399268	3.13E-36	1.20E-36	0.24792	23.8556	4.49
BSU33150	<i>yvqK</i>	-0.294782765	0.965773855	0.963548	-0.370561	21.3444	5.21
BSU33180	<i>yvrC</i>	-0.013756902	0.002371633	0.00184872	1.35265	34.0842	4.93

BSU33190	<i>yvrD</i>	-1.539797505	2.35E-19	1.15E-19	0.32697	28.0707	4.68
BSU33221	<i>yvrHb</i>	-1.010779839	0.094889104	0.0831768	0.01653	27	5.235
BSU33260	<i>yvrN</i>	-0.732814313	3.15E-15	1.67E-15	1.78226	44.9495	4.86
BSU33270	<i>yvrO</i>	-2.006789166	8.40E-20	4.10E-20	-0.754185	25.3298	9.7
BSU33280	<i>yvrP</i>	-2.062862801	2.59E-80	6.61E-81	0.20853	43.3322	4.61
BSU35310	<i>yvyD</i>	0.977343111	0	0	0.60885	21.8337	5.18
BSU35420	<i>yvyG</i>	-2.724788952	0	0	1.78226	18.0381	8.81
BSU38550	<i>ywaA</i>	-2.310124236	0	0	0.11594	40.1643	4.95
BSU37680	<i>ywfH</i>	-1.450257869	2.55E-63	7.35E-64	0.40097	27.8708	6.6
BSU37670	<i>ywfI</i>	-2.97233298	0	0	0.41858	29.3545	4.97
BSU37520	<i>ywhD</i>	-2.21554007	2.52E-60	7.50E-61	-1.362116	19.313	6.51
BSU37340	<i>ywiB</i>	-1.332237194	0.000102817	7.51E-05	1.78226	16.0152	5.61
BSU37140	<i>ywjG</i>	-2.707672864	2.08E-36	7.93E-37	0.01653	18.9214	4.32
BSU37110	<i>ywjH</i>	-1.810727676	0	0	0.17943	22.7669	5.88

BSU36950	<i>ywIC</i>	-0.614558424	0.005134229	0.00409818	-0.235075	36.8517	5.82
BSU36920	<i>ywIF</i>	-2.77281402	1,03E-138	1,86E-145	0.16095	16.0678	5.42
BSU36910	<i>ywIG</i>	-2.31368183	2,26E-172	3,50E-182	0.29223	19.2331	6.48
BSU36620	<i>ywnB</i>	-1.747962666	1,87E+07	1,22E-01	-1.362116	23.0496	5.16
BSU36560	<i>ywnH</i>	-0.964103343	1,48E+07	9,63E-03	0.22301	18.2201	5.28
BSU36490	<i>ywoC</i>	-0.636350536	3,68E+09	2,63E+00	-1.362116	20.9709	4.62
BSU36370	<i>ywpB</i>	-0.531604253	0.368771464	0.343746	0.32145	14.6276	9.36
BSU36290	<i>ywpJ</i>	-1.743311884	4,48E-49	1,30E-57	0.01653	31.8022	4.88
BSU36230	<i>ywqF</i>	-0.595859955	0.00012105	8.87E-05	-2.054123	47.62	5.03
BSU36210	<i>ywqH</i>	-1.388030928	4,96E-11	2,91E-11	0.01653	15.7245	4.82
BSU36190	<i>ywqJ</i>	-1.165458526	1.12E-47	3,75E-48	-0.7206	66.5134	5.91
BSU36180	<i>ywqK</i>	-1.553977255	2.16E-13	1.19E-13	0.01653	18.0737	4.49
BSU36080	<i>ywrF</i>	-1.400829597	5.77E-11	3.39E-11	-0.370561	22.4384	5
BSU36040	<i>ywrJ</i>	-2.43146436	1.11E-99	2.53E-100	-1.362116	25.4487	5.96

BSU35990	<i>ywrO</i>	-2.692591509	3.33E-174	5.37E-175	-0.139653	19.8109	5.2
BSU35850	<i>ywtE</i>	-1.344172104	1.60E-11	9.29E-12	0.40362	31.4352	4.76
BSU35840	<i>ywtF</i>	-2.860211096	7.61E-163	1.28E-163	1.78226	35.6537	9.55
BSU40040	<i>yxαA</i>	-0.781833116	0.000698996	0.000528588	0.56411	39.2401	4.53
BSU39890	<i>yxβB</i>	0.841990845	0	0	0.58159	28.0723	4.57
BSU39880	<i>yxβC</i>	0.338091991	0	0	0.33009	37.3028	4.59
BSU39870	<i>yxβD</i>	-0.973320669	0.000486385	0.00036482	-2.166421	17.9268	4.9
BSU39520	<i>yxεK</i>	-3.104662361	3.00E-23	1.38E-23	1.39517	49.1754	5.67
BSU39500	<i>yxεM</i>	-2.238159737	1.72E-11	1.00E-11	0.53752	29.1598	9.09
BSU39470	<i>yxεP</i>	-2.205530204	3.69E-14	2.01E-14	0.01653	41.4375	5.32
BSU39250	<i>yxιE</i>	-1.881262433	0	0	-0.555667	15.8005	6.34
BSU38960	<i>yxjG</i>	-1.50657535	5.49E-64	1.57E-64	0.51539	42.9561	5.01
BSU38950	<i>yxjH</i>	-0.733877727	2.01E-07	1.31E-07	-0.033251	38.1416	5.09
BSU38940	<i>yxjI</i>	-1.016916348	7.64E-12	4.39E-12	-1.362116	18.6826	4.47

BSU38850	<i>yxkC</i>	-3.714851952	2.19E-95	5.11E-96	-0.100599	22	9.292
BSU39910	<i>yxnB</i>	1.016842872	0	0	0.94991	18.8956	5.11
BSU39290	<i>yxxD</i>	-4.993544978	0.000971484	0.000739124	0.70038	17.5218	3.93
BSU40920	<i>yyaF</i>	-2.754552017	0	0	-0.428029	39.9103	4.66
BSU40710	<i>yybA</i>	-3.183471533	9.09E-09	5.67E-09	-1.362116	17.4417	9.81
BSU40630	<i>yybI</i>	-0.385260285	0.555758174	0.529856	-1.909701	29.9989	5.91
BSU40620	<i>yybJ</i>	-1.41814341	0.158513735	0.1419114	0.46419	24.125	8.68
BSU40390	<i>yycH</i>	-1.845007464	8.03E-73	2.16E-73	0.01653	52.0498	5.59
BSU40290	<i>yycN</i>	-0.504291986	0.11206649	0.0991236	-1.362116	18.0221	6.83
BSU40230	<i>yydA</i>	-0.994266887	5.34E-05	3.85E-05	-0.288392	17.9298	9.31
BSU40220	<i>yydB</i>	-1.739138874	4.40E-24	1.99E-24	0.01653	56.2917	4.99
BSU40200	<i>yydD</i>	-1.040833718	0.003240135	0.00255394	0.36183	68.9301	6.56
BSU40170	<i>yydG</i>	-0.012383724	0.228161375	0.20777	0.29223	37.0552	5.86
BSU40150	<i>yydI</i>	-2.23665899	1.96E-32	7.81E-33	0.08215	23.7364	8.39

BSU13850	<i>zosA</i>	-0.902076461	5.75E-133	1.13E-133	0.01653	68.3859	4.93
BSU23850	<i>zwf</i>	-1.584715814	7.08E-286	8.45E-287	0.55877	55.492	5.28

E. Comparison of DEGs and DEPs obtained by 2DE MALDI-TOF/MS and RNA-Seq analyses.

Locus ID	Gene Name	RNA-Seq (log2FC)	FDR	p-value	OGU1/PY79 (log2)	Mw (Da)	pI
BSU16690	<i>pnpA (comR)</i>	-0.713237874	2.38E-58	7.21E-59	-2.473931188	77.28	4.89
BSU01130	<i>tufA</i>	-1.217587422	0	0	-1.888968688	43.43	4.72
BSU38500	<i>dltA</i>	-2.264843414	0	0	-1.286304185	55.64	4.93
BSU18000	<i>citB</i>	-1.381743382	0	0	-1.514573173	99.14	4.9
BSU19390	<i>yojN/ dat</i>	-0.622222119	0.008290998	0.00670074	-2.120294234	33.33	4.95
BSU32700	<i>yurX (sufD)</i>	-2.250727684	0	0	Not detected in OGU1	48.13	4.95
BSU32700	<i>yurX (sufD)</i>	-2.250727684	0	0	Not detected in OGU1	48.13	4.95

BSU29980	<i>ytjP</i>	-1.105812844	9.50E-53	3.02E-53	Not detected in OGU1	50.89	4.66
BSU40090	<i>ahpC</i>	-1.915080043	0	0	1.35614381	20.48	4.28
BSU25470	<i>dnaK</i>	-0.52739671	3.53E-20	1.71E-20	Not detected in OGU1	65.83	4.57
BSU01430	<i>rpoA</i>	-1.243089347	0	0	Not detected in OGU1	34.64	4.59
BSU28290	<i>ilvC</i>	-0.875900435	2.50E-89	6.03E-90	-1.64385619	37.3	5.37
BSU22230	<i>ypqE (ptsA)</i>	-1.446816208	1.01E-23	4.59E-24	Not detected in OGU1	17.79	5.29
BSU34870	<i>hisF</i>	-3.628711108	0	0	Not detected in OGU1	27.14	5.24
BSU31930	<i>ald (spoVN)</i>	-0.233787882	0.006329287	0.0050845	Not detected in OGU1	39.53	5.12
BSU24060	<i>lpdV (bfmBC)</i>	-0.629656523	0.004995767	0.0039851	Not detected in OGU1	48.51	4.89
BSU36800	<i>atpC</i>	-0.709817121	3.76E-43	1.32E-43	Not detected in OGU1	14.07	5.26
BSU01780	<i>glmS (gcaA, ybxD)</i>	-1.204944838	0	0	Not detected in OGU1	65.16	4.8
BSU21870	<i>ilvD</i>	-1.32285192	7.05E-80	1.80E-80	Not detected in OGU1	59.38	5.32
BSU34910	<i>hisD</i>	-3.424497829	0	0	Not detected in OGU1	46.09	4.78
BSU37710	<i>bacD (ywfE)</i>	-2.698357406	4.38E-94	1.03E-94	Not detected in OGU1	52.1	4.68

BSU01120	<i>fusA</i>	-1.660327372	0	0	Not detected in OGU1	76.36	4.61
BSU01540	<i>ybaL (salA)</i>	-0.773380163	1.09E-71	2.96E-72	Not detected in OGU1	38.48	5.23
BSU29470	<i>ackA</i>	-1.221295985	3.58E-47	1.20E-47	Not detected in OGU1	42.98	5.19
BSU02910	<i>yceE</i>	-1.566378781	2.93E-301	3.37E-302	Not detected in OGU1	20.8	4.39
BSU15500	<i>pyrC</i>	-3.584693115	0	0	Not detected in PY79	46.45	5.43
BSU29750	<i>aroA</i>	-0.680066958	2.27E-22	1.06E-22	-1.64385619	39.38	5.34
BSU37720	<i>bacC (ywfD)</i>	-4.217763502	1.79E-92	4.25E-93	-1.556393349	27.17	5.96
BSU02900	<i>yceD</i>	-1.930257091	0	0	-2.943416472	20.55	4.29
BSU28440	<i>sdhA (citE)</i>	-1.905003734	0	0	1.691534165	65.17	5.71
BSU23070	<i>serA</i>	-1.877724627	2.90E-185	4.51E-186	1.687060688	56.95	5.62
BSU40420	<i>purA</i>	-2.504452694	0	0	1.970853654	47.51	5.46
BSU23860	<i>gndA (yqjI)</i>	-1.567578948	1.42E-268	1.77E-269	1.655351829	51.61	5.08
BSU36900	<i>glyA (glyC)</i>	-1.990081786	3.62E-268	4.50E-269	-3.058893689	45.33	5.47
BSU28820	<i>ysdC</i>	-0.029098814	2.15E-08	1.36E-08	1.613531653	39.06	5.55

BSU15380	<i>ylmE</i>	-1.47090742	5.62E-82	1.42E-82	1.422233001	25.56	5.55
BSU35490	<i>degU</i>	-0.932363765	4.50E-19	2.22E-19	1.422233001	25.72	5.6
BSU16100	<i>sucD</i>	-0.091765943	2.42E-23	1.11E-23	1.555816155	31.23	5.59
BSU30800	<i>menB</i>	-1.168801285	6.94E-68	1.93E-68	1.443606651	29.75	5.34
BSU29410	<i>ytkL</i>	-0.721827958	4.13E-17	2.10E-17	1.757023247	24.68	5.01
BSU14010	<i>cheV</i>	-3.433385673	8.92E-115	1.88E-115	2.114367025	34.48	4.62
BSU16090	<i>sucC</i>	-0.597479576	4.93E-31	2.01E-31	1.695993813	41.21	4.85
BSU39880	<i>yxbC (yxaQ)</i>	0.338091991	0	0	2.95419631	37.3	4.59
BSU00120	<i>yadE (pdxT)</i>	-1.925762046	1.52E-211	2.19E-212	1.389566812	21.3	4.98
BSU06520	<i>purH (purHJ)</i>	-3.030472449	0	0	1.389566812	55.57	5.13
BSU30670	<i>luxS (ytiB)</i>	-3.089505361	2.30E-220	3.25E-221	1.422233001	17.57	5.17
BSU31030	<i>bstB (yuaE)</i>	-1.425761463	2.43E-108	5.28E-109	-0.785875195	18.97	6.2
BSU29850	<i>ytoQ</i>	-0.811136563	0.01067733	0.00870592	1.794935663	16.65	5.77
BSU12410	<i>bstD (yjaA)</i>	0.674410294	1.40E-63	4.03E-64	1.339137385	17.65	5.81

BSU28420	<i>ysmA</i>	-1.292430662	1.27E-15	6.66E-16	1.339137385	16.93	5.54
BSU31390	<i>yugI</i>	-2.739421815	0	0	3.08236197	14.14	5.92
BSU39420	<i>dra (deoC)</i>	-2.751286132	1.64E-172	2.65E-173	1.321928095	22.06	4.93
BSU29880	<i>malS</i>	0.927897526	0	0	-1.358453971	61.98	4.89
BSU00160	<i>yaaH (sleL)</i>	0.692566687	0	0	-1.434402824	48.47	5.62
BSU02940	<i>yceH</i>	-2.12514039	5.79E-206	8.45E-207	-1.888968688	41.51	5.75
BSU37120	<i>fbaA</i>	-1.974426506	0	0	-1.514573173	30.25	5.03
BSU27990	<i>minD (divIVB)</i>	-1.75603841	9.42E-141	1.79E-141	-1.943416472	29.26	4.98
BSU12920	<i>dppA (dciAA)</i>	-0.282412885	0.583350291	0.559598	-1.943416472	30.09	5.19
BSU33930	<i>pgk</i>	-2.832103393	0	0	-2.473931188	42.03	4.77
BSU36810	<i>atpD</i>	-0.967442445	0	0	-1.556393349	51.26	4.61
BSU17460	<i>glnA</i>	-2.751943433	0	0	-1.556393349	50.11	4.87
BSU36640	<i>ureC</i>	-1.903318239	0	0	-2.473931188	61.01	5.09
BSU29120	<i>mdh (citH)</i>	-0.501006569	6.20E-36	2.38E-36	-2	33.49	4.73

BSU03130	<i>nadE (outB)</i>	0.422761465	2.10E-156	3.65E-157	-2	30.24	4.89
BSU40550	<i>ppaC (yybQ)</i>	-2.440062432	0	0	-2	33.83	4.51
BSU24310	<i>folD (yqiA)</i>	-1.330260543	1.29E-83	3.22E-84	-1.395928676	30.53	5.6
BSU00730	<i>cysK</i>	-3.08680832	0	0	-1.395928676	32.67	5.49
BSU29210	<i>accD (yttI)</i>	-1.774007296	2.30E-147	4.22E-148	-1.395928676	28.73	5.34
BSU16500	<i>tsf</i>	-0.376163752	0.012814271	0.0105205	-1.59946207	32	4
BSU33540	<i>azoR2 (yvaB)</i>	-0.260112364	0.464769199	0.438466	-1.64385619	23.13	5.11
BSU29500	<i>gerW (yrfJ)</i>	-0.287569346	0.828908499	0.817446	-3.184424571	16.2	4.99
BSU37110	<i>ywjH</i>	-1.810727676	0	0	-2.120294234	22.77	5.88
BSU37920	<i>ywdL (gerQ)</i>	-0.416537274	7.28E-07	4.86E-07	-2.058893689	20.13	7.01
BSU21690	<i>msrA (yppP)</i>	-1.656435442	2.56E-24	1.16E-24	-3.058893689	20.04	5.71
BSU27890	<i>nadR (yrxA)</i>	-1.485678848	3.74E-25	1.66E-25	1.906890596	19.58	5.76
BSU11720	<i>fabI (yjbW)</i>	-1.007593994	2.75E-150	4.98E-151	-1.395928676	27.72	5.61
BSU00510	<i>prs</i>	-1.655123019	7.93E-118	1.65E-118	-2.473931188	34.71	5.89

BSU17250	<i>ymaE</i>	-0.855957296	7.79E-06	5.39E-06	1.070389328	26.43	9.29
BSU22600	<i>aroE</i>	-0.151950554	0.0915113184	0.0801004	1.201633861	45.08	6.34
BSU16130	<i>gid (ylyC, trmFO)</i>	-1.18063656	3.29E-29	1.38E-29	1.339137385	47.9	5.77
BSU36950	<i>tsaC (ywlC)</i>	-0.614558424	0.005134229	0.00409818	1.480265122	36.85	5.82
BSU22070	<i>xpt</i>	-4.706761876	9.45E-115	2.00E-115	1.49057013	20.89	5.84
BSU31760	<i>yueJ (pncA)</i>	-1.176064376	2.68E-13	1.48E-13	1.704871964	20.38	5.6
BSU15910	<i>fabG (ylpF)</i>	-0.978806858	1.60E-28	6.82E-29	1.704871964	26.13	8.09
BSU09260	<i>yhxA</i>	-0.423272714	0.020118931	0.01669794	2.007195501	49.71	5.64
BSU03010	<i>amhX</i>	-1.427684423	6.63E-231	8.96E-232	-1.434402824	42.37	6.12
BSU00260	<i>yaaN</i>	-0.420646146	0.005919302	0.0047506	2.12763328	43.67	5.6
BSU35120	<i>yvIB</i>	-1.872969435	0	0	2.12763328	40.92	5.39
BSU28000	<i>minC</i>	-1.722485824	9.28E-75	2.45E-75	-1.514573173	24.85	6.26
BSU21680	<i>yppQ (msrB)</i>	-2.042227297	3.86E-49	1.12E-63	2.931683057	16.46	5.84
BSU36910	<i>ywlG</i>	-2.31368183	2.26E-186	3.50E-187	2.931683057	19.23	6.48

BSU37520	<i>ywhD</i>	-2.21554007	2.52E-60	7.50E-61	3.058316496	19.31	6.51
BSU25180	<i>trmK (yqfN)</i>	-1.181312527	5.65E-08	3.61E-08	Not detected in OGU1	23.56	5.27
BSU33040	<i>citG (fumC)</i>	-1.305552677	3.13E-246	4.06E-247	-3.836501268	50.36	5.47
BSU06300	<i>cotA (pig)</i>	-2.677273002	0	0	-3.473931188	58.33	5.89
BSU07690	<i>yflG (mapB)</i>	-2.383582613	7.33E-178	1.17E-178	-3.473931188	27.06	5.58
BSU15530	<i>pyrK (pyrDII, ylxD)</i>	-3.084820441	0	0	-3.473931188	27.95	5.58
BSU10070	<i>sndC (yhaA)</i>	-1.280733166	2.67E-101	6.00E-102	-3.321928095	43.11	5.86
BSU11850	<i>yjcG</i>	-1.475841487	3.48E-113	7.40E-114	-2.64385619	19.52	5.57
BSU10020	<i>serC (yhaF)</i>	-2.049977115	2.73E-132	5.35E-133	-3.058893689	39.98	5.52
BSU19370	<i>odhA (citK)</i>	-0.544034755	1.52E-85	3.79E-86	-1.358453971	105.54	5.87
BSU16730	<i>spoVFA (dpaA)</i>	-2.627167306	0	0	-2.64385619	31.8	5.89
BSU14530	<i>ykqC (rnjA)</i>	-1.687767368	0	0	-2.395928676	61.34	5.9
BSU23120	<i>resD (ypxD)</i>	-1.654331926	8.71E-101	1.97E-101	-2	27.34	5.63
BSU19360	<i>odhB (citM)</i>	-0.060577147	2.14E-87	5.24E-88	-2	45.83	4.86

BSU07830	<i>hypO (yfkO)</i>	-1.360430728	3.77E-175	6.06E-176	-1.736965594	25.48	5.67
BSU40250	<i>yycR</i>	0.378968245	2.89E-15	1.53E-15	-1.785875195	42.79	5.79
BSU23280	<i>ribD (ribG)</i>	0.297401832	9.12E-24	4.15E-24	-1.736965594	39.15	6.08
BSU12980	<i>ykfB</i>	0.57955264	1.42E-46	4.82E-47	-1.689659879	39.31	5.91
BSU24570	<i>gcvT (yqhI)</i>	-2.22829488	9.04E-165	1.52E-165	-1.689659879	39.62	5.73
BSU18360	<i>yoxA (galM)</i>	-1.810621431	9.21E-156	1.61E-156	-1.59946207	37.07	5.6
BSU03050	<i>ldh (lctE)</i>	-4.182949149	0	0	-1.59946207	34	5.39
BSU09180	<i>yhcQ</i>	-0.703582639	7.44E-48	2.48E-48	-1.59946207	24.64	5.74
BSU28260	<i>leuC</i>	-1.012097676	1.71E-137	3.29E-138	-1.59946207	52.23	6.13
BSU00090	<i>guaB (guaA)</i>	-1.106372961	3.31E-94	7.77E-95	-1.59946207	52.82	6.17
BSU12290	<i>ndh (yjiD)</i>	-2.359698562	0	0	-1.556393349	41.79	6.29
BSU11700	<i>thiF (yjbU)</i>	-0.376878559	0.161731079	0.1448746	-1.556393349	36.24	5.62
BSU30820	<i>menD</i>	-1.646651434	1.14E-104	2.51E-105	-1.514573173	63.92	5.66
BSU14280	<i>moeA</i>	-1.327009425	1.91E-17	9.66E-18	-1.434402824	46.46	5.61

BSU08720	<i>ygaF (bcp)</i>	-2.192143041	3.57E-24	1.62E-24	-1.395928676	17.96	5.86
BSU11460	<i>oppD</i>	-1.00039016	1.89E-48	6.27E-49	-2.473931188	39.6	6.03
BSU35020	<i>nagB</i>	-2.555431231	4.82E-139	9.24E-140	-1.59946207	26.84	5.72