An explorative study of *Enterococcus faecalis* transcriptional responses to infection-relevant growth environments

Et eksplorativt studium av de transkripsjonelle responsene til *Enterococcus faecalis* under infeksjonsrelevante vekstbetingelser

Philosophiae Doctor (PhD) Thesis

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SUMMARY

Enterococcus faecalis is commonly found in the gastrointestinal tract of humans. It is also an opportunistic pathogen and one of the leading causes of nosocomial infections worldwide. The treatment of *E. faecalis* infections is often difficult due to its innate and acquired antibiotic resistance. Several functional studies have been performed to link genetic traits to antibiotic resistance and virulence. However, there are still many unanswered questions regarding the importance of virulence factors, and the global regulation of these and other genes in the pathogenicity of this bacterium. Therefore, a more comprehensive understanding of the global gene regulation of *E. faecalis* in response to different growth environments is needed, as well as an understanding of how this gene regulation affects the establishment of an infection.

This thesis focuses on the importance of *E. faecalis*' gene regulation in response to the infection-relevant growth conditions blood, urine and exposure to erythromycin. The effect of a small percentage (10%) of blood on the transcriptome of *E. faecalis*, as well as the different transcriptional profiles of three diverse *E. faecalis* isolates grown in urine were also examined.

The work in this thesis showed that erythromycin inhibits the growth of the resistant V583 strain and affects the transcription of several genes, but not the constitutively expressed *erm*(B) gene that confers erythromycin resistance. Furthermore, we discovered that growth in blood and urine resulted in several similar transcriptional responses despite the use of four diverse isolates. Important responses to blood and urine include a reduced transcription of genes involved in the production of cell wall polysaccharides, enhanced transcription of several stress genes, including many involved in oxidative stress, and enhanced transcription of genes encoding iron- and manganese-uptake systems. Each environment also activated a unique subset of genes, an effect that was particularly evident for genes related to metabolism. The enhanced transcription of *lrgAB* was unique to growth in blood. The function of these two genes is so far unknown in *E. faecalis* and could be interesting to study more closely. Growth in urine revealed a strain specific enhanced regulation of the virulence related *fsr*-operon, which could give an indication to the isolates pathogenic potential. All three studies revealed that the modulation of the *E. faecalis* cell envelope is important for the adaptation to growth in these three infection-relevant environments.

SAMMENDRAG

Enterococcus faecalis finnes ofte som en del av menneskets tarmflora. Den er også en opportunistisk patogen, og er en av hovedårsakene til sykehusinfeksjoner verden over. Behandlingen av *E. faecalis* infeksjoner er ofte vanskelige på grunn av bakteriens nedarvede og tilegnede antibiotikaresistens. Mange funksjonelle studier har blitt utført for å koble genetiske egenskaper mot antibiotikaresistens og virulens. Imidlertid er det fortsatt ukjent hvor stor betydning antatte virulens faktorer, og den globale reguleringen av disse og andre gener, faktisk har for denne bakteriens patogenisitet. Derfor er det behov for en mer inngående forståelse av hvordan den globale genreguleringen i *E. faecalis* responderer på ulike vekstbetingelser, og hvordan denne genreguleringen influerer etableringen av infeksjoner.

Denne avhandlingen fokuserer på hvordan genreguleringen i *E. faecalis* påvirkes av de infeksjonsrelevante vekstbetingelsene blod, urin og vekstmedium tilsatt antibiotikumet erythromycin. Effekten av en liten prosentandel (10%) blod på transkripsjonen, samt forskjeller i transkripsjonsprofilene til tre ulike *E. faecalis* isolater dyrket i urin ble også undersøkt.

Arbeidet i denne avhandlingen viste at erythromycin hemmer veksten av den resistente V583-stammen og påvirker transkripsjonen av mange gener, men ikke det konstitutivt uttrykte erythromycinresistensgenet *erm*(B). Videre oppdaget vi at vekst i blod og urin ga mange liknende transkripsjonsprofiler, selv om fire ulike isolater ble undersøkt. Viktige responser i blod og urin omfatter redusert transkripsjon av gener involvert i produksjon av celleveggpolysakkarider, økt transkripsjon av mange stress-gener blant annet flere involvert i oksidativt stress og økt transkripsjon av gener som koder for jern- og mangan-opptakssystemer. Begge vekstbetingelsene aktiverer også et unikt sett med gener, og denne effekten var spesielt tydelig for gener relatert til metabolisme. En unik respons ved vekst i blod var en økt transkripsjon av *lrgAB*, to gener med hittil ukjent funksjon i *E. faecalis* som kan være interessante å studere videre. Ved vekst i urin fant vi et stammespesifikt uttrykk av det virulensrelaterte *fsr*-operonet, noe som dermed kan gi en indikasjon på isolatets patogene potensial. Alle tre studiene viste at forandringer i celleveggen/cellemembranen til *E. faecalis* er viktig for tilpasningen til vekst i disse tre infeksjonsrelevante betingelsene.

LIST OF PAPERS

Paper I

Aakra, Å., Vebø, H., Snipen, L., Hirt, H., Aastveit, A., Kapur, V., Dunny, G., Murray, B. E. & Nes, I. F. (2005). Transcriptional Response of *Enterococcus faecalis* V583 to Erythromycin. *Antimicrobial Agents and Chemotherapy,* 49:2246-2259.

Paper II

Vebø, H. C., Snipen, L., Nes, I. F. & Brede, D. A. (2009). The Transcriptome of the Nosocomial Pathogen *Enterococcus faecalis* V583 Reveals Adaptive Responses to Growth in Blood. *PLoS ONE,* 4(11):e7660.

Paper III

Vebø, H. C., Soheim, M., Snipen, L., Nes, I. F. & Brede, D. A. Comparative genomic analysis of pathogenic and probiotic *Enterococcus faecalis* isolates, and their transcriptional responses to growth in human urine. (Manuscript)

List of related papers by the author, not included in the thesis

Berget, I., Mevik, B.-H., Vebø, H., Næs, T. (2005). A strategy for finding relevant clusters; with an application to microarray data. *Journal of Chemometrics*, 19(9):482-491.

Solheim, M., Aakra, Å., Vebø, H., Snipen, L. & Nes, I. F. (2007). Transcriptional Responses of *Enterococcus faecalis* V583 to Bovine Bile and Sodium Dodecyl Sulfate. *Applied and Environmental Microbiology,* 73(18):5767-74.

Aakra, Å., Vebø, H., Indahl, U., Snipen, L., Gjerstad, Ø. Hjorthaug, H. S., Lunde, M. & Nes, I. F. The response of *Enterococcus faecalis* V583 to chloramphenicol treatment. (Submitted)

1. INTRODUCTION

This thesis describes the use of microarrays as a tool to study the transcriptional responses of *Enterococcus faecalis* when exposed to different infection-relevant growth environments such as blood, urine, and the antibiotic erythromycin. This organism is among the leading causes of hospital acquired infections, which are often difficult to treat due to high level antibiotic resistance [12, 98]. Hence, it is of great importance to understand how this opportunistic pathogen responds and adapts to growth in infectious environments in order to gain further knowledge about its virulence, and to come up with new therapeutic strategies to be able to treat infections caused by *E. faecalis*.

1.1 The *Enterococcus* genus

The term "enterococcal group" was first used by Sherman [137] to describe group D streptococci that grew at 10 and 45°C, and could survive heating at 60°C for 30 minutes. Furthermore, this group grew in environments with broad pH values and could tolerate high salt concentrations (6.5% NaCl) [53]. Although this group of bacteria, described the first time in 1899 [159] was different from the other members of the *Streptococcus* genus, a separate *Enterococcus* genus was not established until almost a century later, in 1984 [130]. The *Enterococcus* genus now comprises of 40 different species [32], and an overview of some of the enterococcal species, and their relatedness to each other is shown in the phylogenetic tree in Figure 1.

Enterococci are Gram-positive, catalase-negative cocci which most often occur in pairs or short chains. They are found in several different environments such as soil, food and in the intestinal flora of most birds and mammals including humans. However, they are also opportunistic pathogens often involved in nosocomial infections. Enterococci are facultative anaerobes with an optimum growth temperature of 35°C and can utilize a wide variety of nutrients such as diverse carbohydrates, arginine, agmatine, many α-keto acids, glycerol, lactate, malate and citrate [56]. Under most conditions enterococci, like other lactic acid bacteria perform fermentative carbohydrate metabolism with lactate as the major end product [75]. It has also been demonstrated that certain enterococci are able to perform respiration utilizing oxygen as terminal electron acceptor in the presence of heme [127]. Their versatile

metabolism combined with their tolerance of extremely harsh growth conditions most likely enhances the enterococcal competitiveness in diverse environments.

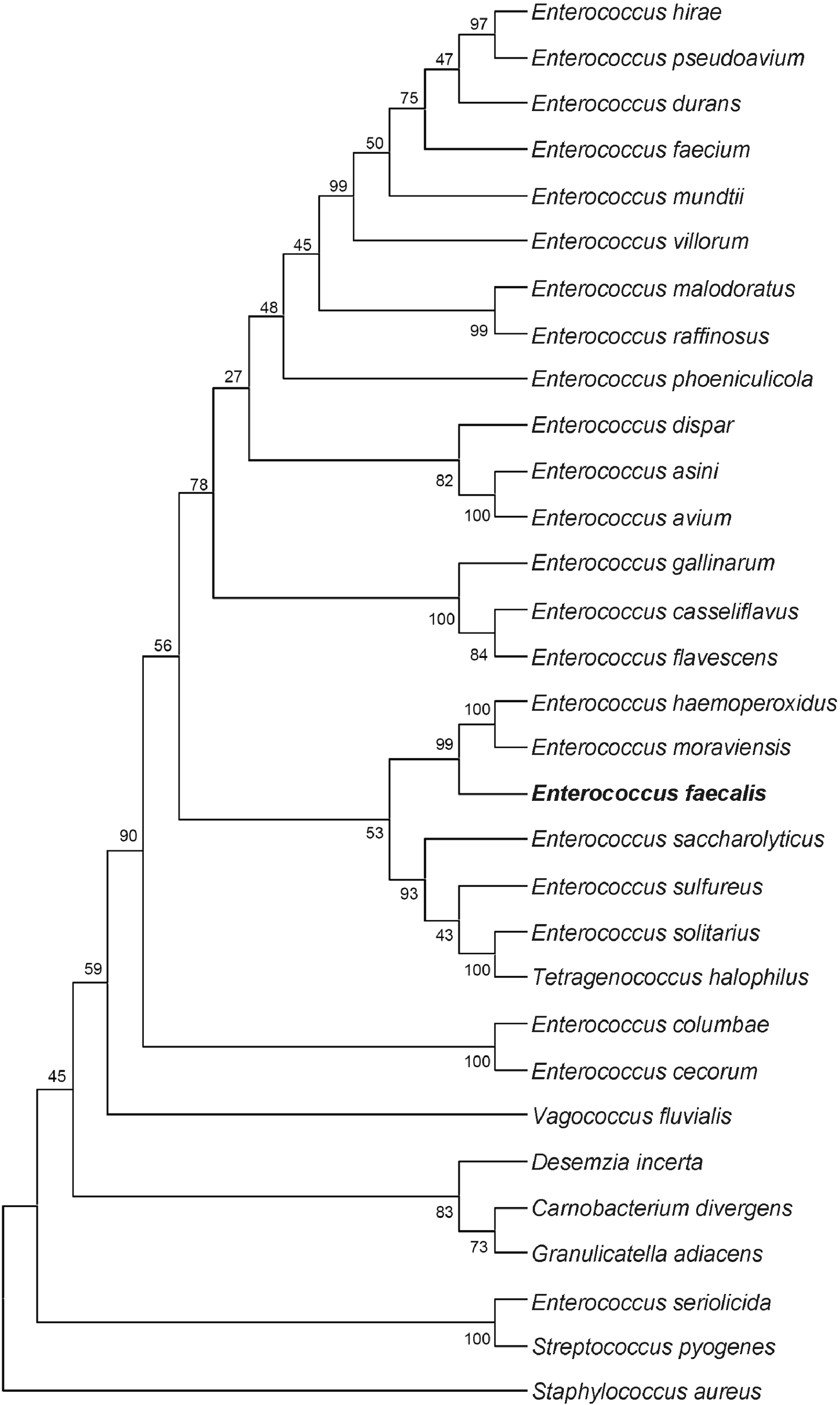

Figure 1: Unrooted phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between *Enterococcus faecalis* and other enterococci and lactic acid bacteria. The sequence of the 16S rRNA gene of *Staphylococcus aureus* was used as an outgroup. (Modified from [74])

1.1.1 *Enterococcus faecalis*

The name *Streptococcus faecalis* was fist used by Andrewes and Horder in 1906 to identify an organism of faecal origin [2]. *Enterococcus faecalis* and *Enterococcus faecium* were the first two enterococcal species suggested to comprise the new *Enterococcus* genus [130]. Both species can be found throughout the gastro intestinal (GI) tract in humans, although in low numbers in the oral cavity [85]. *E. faecalis* is normally found in higher numbers (10^5-10^7 per gram feces) in the GI tract than *E. faecium* (10^4-10^5 per gram feces) [12]. Although often found in the same habitats, there are some phenotypic characteristics that separate these two species (Table 1). Based on these differences there are several rapid test such as API Rapid ID 32 [38] that separates *E. faecalis* from other enterococci by 88.6% accuracy, and *E. faecium* by 67% accuracy [167].

Table 1: Differentiation of *E. faecalis* and *E. faecium* (modified from [130])

Characteristics	*E. faecalis*	*E. faecium*
Acid produced from:		
Arabinose	–	+
Tagatose	+	–
Energy from:		
Pyruvate	+	–
Citrate	+	–
Malate	+	–
Serine	+	–
Tolerance to:		
0.04% Tellurite	+	–
0.01% Tetrazolium	+	–

One enterococcal strain intensively studied in this thesis is the V583 strain, since it was the first fully sequenced *E. faecalis* strain [112]. Its chromosome contains 3093 genes, and more than 25% of these genes are within mobile elements such as prophages, conjugative transposons and integrated plasmid remnants [112]. Furthermore, it contains three plasmids, the pAD1-like pTEF1, the pCF10-like pTEF2 and pTEF3 that belongs to the family of pAM$^{\beta}$1 broad host range plasmids [112]. V583 was also the first vancomycin resistant clinical isolate reported in the United States [129], and is resistant to several other antibiotics. This strain was isolated from a patient suffering from a persistent bloodstream infection, and is

included in the clonal complex 2 consisting mainly of infection derived isolates [128]. Another member of the clonal complex 2 studied in this thesis is the MMH594 strain. This was the first *E. faecalis* strain reported to contain a complete *E. faecalis* pathogenicity island (PAI) [134]. It was involved in a hospital outbreak in the middle of the 1980s, causing more than 30 infections and with an elevated mortality rate compared to infections by other nosocomial *E. faecalis* strains [60].

The important laboratory *E. faecalis* strain, OG1RF was also studied in this thesis. It has commonly been used for molecular manipulations and virulence studies, and its sequence was published recently [4]. The sequencing of this strain revealed that it contains only a few mobile elements. This has been suggested to be due to the presence of two CRISPR (comprised of regularly interspaced short palindromic repeats) loci and the *cas*-genes cognate to one of the two CRISPR loci, which prevent establishment of invading phages or plasmids ([4] and references therein). It has 39 unique regions comprising 127 new genes compared to the V583 genome, and OG1RF does not contain a PAI like the two above mentioned strains. Finally, the forth strain that has been studied more closely in this thesis is Symbioflor 1. This is a probiotic strain isolated from a healthy human adult around 1950 [25]. It has been used as part of a commercially available probiotic product for over 50 years without any reports of it causing infections or other unwanted effects. Symbioflor 1 is susceptible to all clinically relevant antibiotics employed to treat enterococcal infections including ampicillin [25]. About 75% of the Symbioflor 1 genome is identical to the V583 genome [25]. Furthermore, the strain is devoid of any PAI-like structure and is missing the virulence factors cytolysin, enterococcal surface protein (Esp) and gelatinase (coccolysin) [25]. However, the genome sequence of Symbioflor 1 is not publicly available, thus it is not known which traits this strain possess other than what is found in V583. A genome atlas representation [48] of comparative genome hybridization analysis of the latter three strains illustrates the genomic similarities and differences compared to V583 (Figure 2).

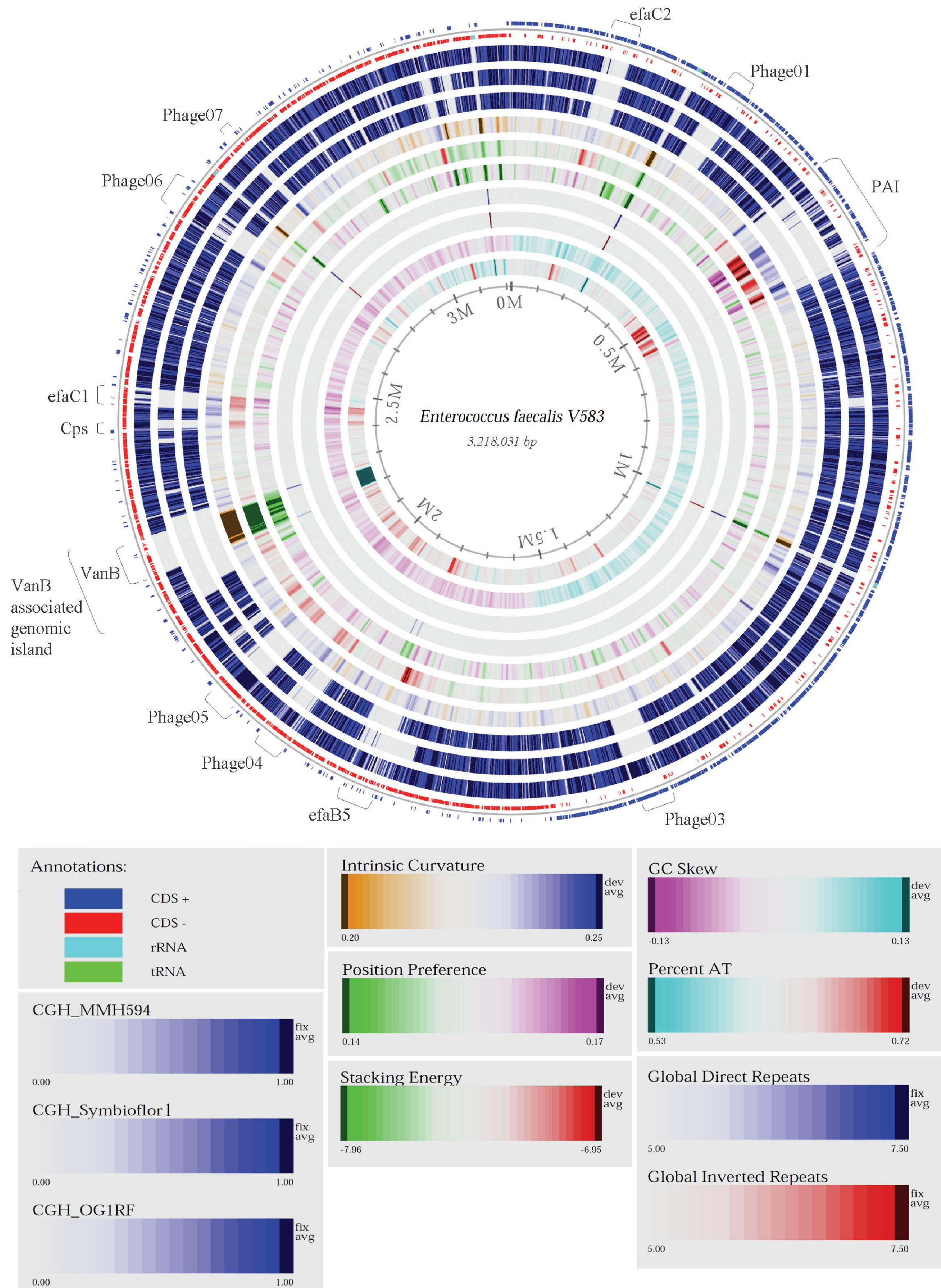

Figure 2: Genome atlas showing comparative genome hybridization of MMH594, Symbioflor 1 and OG1RF compared to the V583 genome. Putative mobile genetic elements predicted in the V583 genome are indicated around the genome atlas.

1.2 Antibiotics and antibiotic resistance in enterococci

Antibiotics were fist described in 1929 by Alexander Fleming [35], in the form of penicillin. Since the mid 1940's antibiotics have been extensively used to treat infections, however in the last decades the usage of antibiotics has exploded. Besides the treatment of human infections, antimicrobial agents are used for laboratory purposes, in plant production, for industrial purposes, and in animals, both for treatment of disease and to improve growth. Approximately 35 tons of antibiotics were used to treat human infections in Denmark in 1997 [1]. In comparison, 53 tons were used for animal therapy and 107 tons were used as growth promoters [1]. This extensive usage of antibiotics has led to a massive distribution of antimicrobial agents in the environment, which consequently have promoted a natural selection for bacteria that possess antibiotic resistance genes.

Enterococci are intrinsically resistant to a broad range of antimicrobial agents, such as low concentrations of clindamycin and aminoglycosides, cephalosporins and penicillins [97] and are also able to acquire antibiotic resistance through the exchange of plasmids or transposons [59]. For more than 30 years the glycopeptides vancomycin and teicoplanin were used to treat serious infections caused by resistant Gram-positive organisms, without observing any development of resistance towards these antibiotics. However, in 1986 the first vancomycin resistant *E. faecium* isolates were reported from patients in France and England [78, 166]. The resistance against this widely used antibiotic quickly spread to a large population of enterococci (mainly *E. faecium*) [14], and in 1998, 20% of the enterococcal isolates in the United States (US) were resistant to vancomycin [39]. The rapid spread of vancomycin resistance among enterococci in the US in the 1990s, leading to infections which were extremely difficult to treat raised a newfound interest in enterococci [98]. The number of vancomycin resistant enterococci in Europe was low compared to in the US, but has increased dramatically in the last ten years, apparently following the trend in the US with a ten year delay [178].

Once vancomycin resistant enterococci have colonized a patient, they often persist in the GI tract and may be spread to other patients [98]. Furthermore, *E. faecium* (and to a lesser extent *E. faecalis*) can act as a reservoir for the spread of vancomycin resistance to other more pathogenic species, and the transfer of vancomycin resistance from enterococci to methicillin-resistant *Staphylococcus aureus* (MRSA) has been observed [10, 155]. The increasing spread

of antibiotic resistance other than vancomycin (*e.g.* ampicillin resistance) primary among *E. faecium* in the US [43, 67], and in the recent years also in Europe [165] rise further concerns about therapeutic options to treat enterococcal infections. Hence, it is a race against time to find new targets for novel antibiotics that the bacteria have not developed resistance against, which can be used to treat infections caused by multi resistant enterococci.

1.2.1 Erythromycin resistance in enterococci

Erythromycin is a macrolide antibiotic that inhibits protein synthesis by binding to the 50S subunit of the bacterial 70S ribosomal RNA complex [151, 169]. This binding interferes with the translocation of the peptidyl tRNA from the A to the P site, blocking the binding of an incoming tRNA and its attached amino acid to the nascent polypeptide chain (Fig. 3), and hence inhibiting production of functional proteins [156].

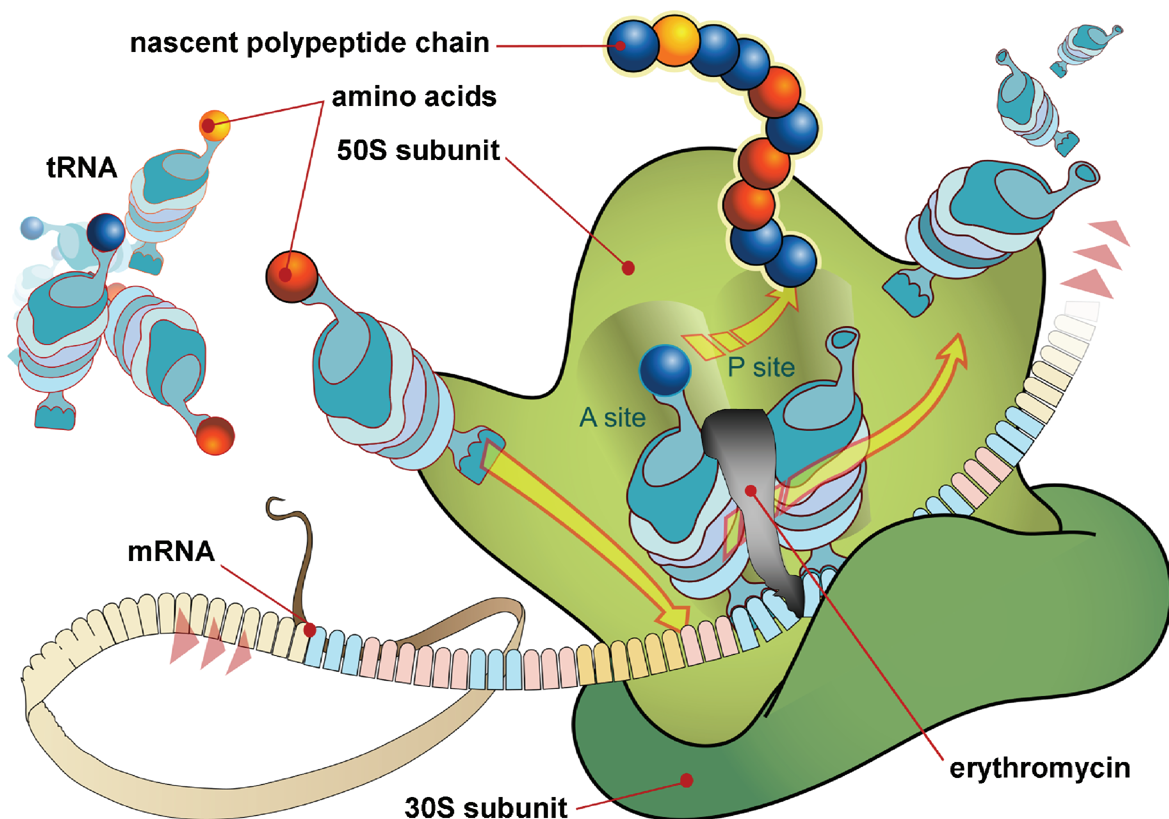

Figure 3. An illustration of prokaryote translation inhibited by binding of erythromycin to the large ribosomal subunit.

(Modified from http://en.wikipedia.org/wiki/File: Ribosome_mRNA_translation_en.svg)

Erythromycin (and other macrolides) are effective against beta-hemolytic streptococci, pneumococci, staphylococci and enterococci [77]. However, resistance to macrolides is very common in enterococci isolated from humans [24, 30, 121]. Three different mechanisms account for the acquired resistance to macrolide antibiotics (and also to lincosamide and streptogramin B antibiotics, hence referred to as MLS-resistance) in Gram-positive bacteria: (i) modification of the drug target, (ii) inactivation of the drug, (iii) and active efflux of the antibiotic [116]. Among enterococci, resistance to erythromycin is most commonly mediated by a series of structurally related erythromycin-resistant methylase (*erm)* genes. These genes encode enzymes that methylate an adenine residue in the 50S ribosomal subunit leading to a reduced binding of erythromycin and most other macrolides to the ribosomal subunit [150].

The expression of *erm* can either be inducible or constitutive; constitutive *erm* expression provides resistance to several macrolide, lincosamide and streptogramin B antibiotics, while inducible expression of *erm* only provides resistance to 14- and 15-membered-ring macrolides [77]. The inducible form of *erm* contains a leader sequence, which in the absence of erythromycin causes translational attenuation due to a stem-loop structure that makes the initiation codon of the *erm*-gene inaccessible for the ribosomes [77, 175]. In the presence of erythromycin, this antibiotic binds the ribosomes causing them to stall, which induces a conformational change of the mRNA that expose the initiation codon, and the translation of the methylase can proceed [77, 175]. The constitutive form does not contain a leader sequence, or has modifications in the leader sequence, such as point mutations, deletions or tandem repeats [92]. The most common *erm* variant in enterococci is *erm*(B) [64, 91, 116], which also is the variant found in V583 (EFA0007). The *erm*(B) gene in V583 does not contain the inducible leader sequence and hence is constitutively expressed. Other mechanisms of erythromycin resistance reported in enterococci include membrane bound efflux proteins encoded by the *mef*(A/E) and *msr*(C) genes [83, 116].

1.3 Enterococcal infections

Although infections due to enterococci were reported already in the mid-20th century [120], it is during the last decades that enterococci have received most attention due to the large increase of nosocomial infections [12, 97], which mainly have been attributed to the emergence of multiple antibiotic resistant strains [12, 98]. The enterococci now rank among the top three leading causes of hospital acquired infections where *E. faecalis* is responsible for

around 80% of these [59, 126]. However, in the last two decades the number of infection caused by *E. faecium* resistant to vancomycin and ampicillin has increased dramatically as described in section 1.2 [39, 165, 178], and with the continuing selective pressure of antibiotics it is possible that *E. faecium* and *E. faecalis* will account for equal numbers of enterococcal infections in the near future.

Before the emergence of vancomycin and aminoglycoside resistant *E. faecium* the number of infections caused by *E. faecium* was relatively low compared to infection caused by *E. faecalis*, and there are different theories around this lower frequency. Several studies have examined the ability of different infection derived isolates of *E. faecalis* and *E. faecium* to produce biofilm. These studies showed that while up to 100% of the *E. faecalis* isolates tested were biofilm producers, less than 50% of the *E. faecium* isolates produced biofilm [94]. A biofilm is formed when planktonic cells colonize a surface, aggregate and/or grow into multicellular colonies, surrounded by an exopolysaccharide matrix [26, 46]. More than 60% of all microbial infections in the human body involve bacteria within biofilms [80]. Bacteria within biofilms represent a therapeutic challenge since they are more protected compared to their planktonic counterparts, and hence more resistant against antibiotics and clearance by effectors of the host immune system [22]. It has been speculated that the larger number of *E. faecalis* involved in enterococcal infections compared to *E. faecium* is due to their differences in biofilm producing ability. However, as mentioned in section 1.1.1 *E. faecalis* is normally more abundant in the GI tract than *E. faecium* and hence the human body has a larger reservoir of *E. faecalis* which might explain the higher ratio of *E. faecalis* infections [34, 36]. There are also a larger number of virulence factors associated with *E. faecalis* than *E. faecium* [34], which will be described in further detail in section 1.4.

Antibiotic resistant *E. faecalis* has been isolated from surfaces in the hospital patient wards, thus the hospital can therefore serve as a reservoir of antibiotic resistant bacteria [12]. *E. faecalis* can be transmitted from patient to patient on the hands of healthcare workers, or on medical instrumentation such as thermometers [12]. Transmission of enterococci from the hands of healthcare workers can involve direct inoculation onto e.g. urinary catheters, but is more likely to result in colonization of the GI tract with the acquired strain, which becomes part of the patient's endogenous flora [85]. When *E. faecalis* has colonized the intestine of a patient, it can translocate through the epithelial cells of the intestine and can cause infection by further spreading to other locations within the body via the lymph nodes or blood stream

[69, 177]. Transmission of enterococcal strains can occur within a unit, between hospitals and even across borders, often due to a persistent colonization of the patients intestine, also after discharge of the patient from the hospital [85].

E. faecalis is associated with a variety of different infections, and some of its most common types of infections will be described in more detail below.

1.3.1 Urinary tract infection

In young healthy women, enterococci accounts for less than 5% of all urinary tract infections (UTI) [12]. However, enterococci are the second most common cause of hospital acquired UTIs world-wide [12] and UTI is the most common infection caused by enterococci [85]. Risk factors for enterococcal UTI are structural abnormalities, urinary tract instrumentation, catheterization, genitourinary tract pathology, as well as prior antibiotic treatment [44, 81, 96]. Enterococcal UTIs acquired in the hospital or long-term care units are likely to be caused by strains resistant to several different antibiotics [157, 158].

The ability to form biofilm has been proposed as an especially important trait for the bacterium's ability to cause UTI. A study of UTI caused by *E. faecalis* over a 12-year period showed that more than 60% of the isolates were medium to strong biofilm producers [133]. It has been shown that *E. faecalis* adhere to urinary tract epithelial cells, and that isolates from UTI adhere better to these cells than endocarditis isolates [45]. Several virulence factors such as Epa, Esp, Ace and Ebp (described in more detail in section 1.4.2) have been shown to be important for *E. faecalis* ability to cause infection in various UTI models [76, 135, 141].

1.3.2 Bacteremia

Enterococci constitute the third most prevalent pathogens isolated from bloodstream infections [24, 126]. Translocation across an intact epithelial barrier is thought to lead to many blood stream infections with no identifiable source [177], whereas identifiable sources include intravenous lines, abscesses and UTIs [65]. Even though an identifiable source of infection is known, the overall mortality rate from enterococcal bacteremia has been reported to be between 12-50% [171, 174]. Risk factors for developing enterococcal bacteremia are

high age, combined with multiple underlying diseases such as diabetes, cancer, heart disease and prior surgery [84, 111, 158]. Infections by cytolysin producing strains, such as MMH594 have been shown to worsen the outcome of the bacteremia [60].

1.3.3 Other enterococcal infections

Enterococci are the third leading cause of infective endocarditis, which is also one of the most therapeutic challenging infections caused by enterococci [89]. Even for antibiotic susceptible enterococci the treatment is difficult, and in situations with endocarditis caused by vancomycin or high-level aminoglycoside resistant strains, surgery is often necessary to remove the infected valve [85]. Enterococci are also frequently found in intra-abdominal, pelvic and soft tissue infections, although they rarely have been shown to cause monomicrobial infections at these sites [85]. The treatment for such infections, besides the use of antibiotics, is drainage of abscesses and debridement of infected tissue [85]. The importance of the intra-abdominal, pelvic and soft tissue infections has been debated, however these infections are sources to enterococcal bacteremia and surgical-site infections [85]. In fact, enterococci represent the most frequent cause of surgical-site infections in intensive care units [126]

1.4 Enterococcal virulence factors

Virulence factors can be defined as the gene products of a pathogen that enhance its ability to cause disease [11]. Virulence factors include secreted proteins, such as bacterial toxins and enzymes, and cell-surface structures, such as cell surface carbohydrates or proteins that mediate bacterial attachment or protect the pathogen from host defense mechanisms [11]. The importance of distinct virulence factors in enterococci has been under debate since they, besides being present in invasive isolates, also often are found in food- and community-derived isolates [23, 28, 37, 86]. However, patients infected with the MMH594 strain, which contains several of the known virulence genes, had an increased risk of death compared to patients infected with other nosocomial *E. faecalis* strains [60]. This suggests that several virulence genes together provide additional challenges for the host immune system. The *E. faecalis* virulence factors can be divided into two groups: secreted factors and cell envelope bound factors (Table 2).

Table 2. List of the major *E. faecalis* virulence factors (modified from [50])

Virulence factor	Description	Reference(s)
Secreted		
Cyl	Cytolysin, Hemolysin/bacteriocin; lyses a broad range of eukaryotic and gram-positive cells	[13, 19, 63, 66]
GelE	Gelatinase, zinc metalloprotease	[31, 118, 138]
SprE	Serine protease	[31, 118, 138]
Toxic metabolites	Reactive oxygen species; extracellular superoxide, hydrogen peroxide	[57]
Cell envelope bound		
Esp	Enterococcal surface protein; enhances biofilm formation and bladder epithelium colonization	[135]
Aggregation substance	Involved in conjugation and adhesion to eukaryotic cells	[13, 54, 71, 131]
Ace	Collagen-binding protein	[102, 125, 164]
Epa	Enterococcal polysaccharide antigen; antiphagocytic cell wall polysaccharide	[141, 152, 154]
Cps	Capsular polysaccharide, antiphagocytic cell wall polysaccharide	[49, 52, 55]
Ebp	Endocarditis and biofilm-associated pili	[104, 142]

1.4.1 Secreted virulence factors

Three important secreted proteins have been identified in *E. faecalis*: cytolysin, gelatinase and a serine protease. Cytolysin displays both hemolytic and bactericidal activity. Its importance for virulence in *E. faecalis* has been extensively studied in several animal models, showing that cytolysin producing strains are up to 10 times more toxic than non-cytolysin producers [13, 63, 66]. The cytolysin operon is either encoded on large pheromone-responsive plasmids [15, 62], or within the *E. faecalis* PAI [134]. The operon consists of six genes; $cylL_L$ and $cylL_S$ encoding the toxin, and *cylM*, *cylB*, *cylA*, and *cylI* playing a role in peptide modification, secretion, activation, and immunity, respectively [41, 42]. Transcription of the *cyl*-operon is repressed by CylR1 and CylR2, the products of a second operon responding by quorum-sensing to the level of $CylL_S$ [61]. The accumulation of fully processed $CylL_S$ releases the repression on the *cyl*-operon, and hence stimulates the production of more toxin as the cell density increases [61].

Regarding the secreted proteases they first of all provide peptide nutrients to the organism, but might also cause direct or indirect damage to host tissues making them potential virulence factors. The two proteases gelatinase (GelE, a zinc metalloprotease) and serine protease

(SprE) have been shown to be important for virulence in *E. faecalis* in various animal models [31, 118, 138]. It has also been shown that GelE confers immune system evasion by degradation of complement peptide C3, which makes *E. faecalis* less susceptible to phagocytosis [110]. Both proteases are regulated by the *fsr* quorum-sensing locus, which encodes a response regulator FsrA that is phosphorylated by the histidine kinase FsrC [119]. FsrC is autophosphorylated when sensing the accumulation of a peptide lactone molecule encoded by *fsrD* [99, 100]. The *fsr* system also regulates several other genes [5], and provides an additional effect on virulence in *E. faecalis* [31, 95, 138].

Potential virulence factors in *E. faecalis* can also be the production of toxic metabolites such as reactive oxygen species, which can damage cells or organs of the infected host [57]. Although the vast majority of *E. faecalis* strains produce superoxide, Huycke *et al.* showed that invasive *E. faecalis* isolates displayed an increased production of superoxide compared to non-invasive isolates [58], further emphasizing its role for virulence in *E. faecalis*. Due to its superoxide production, *E. faecalis* also has a large battery of genes encoding oxidative stress management [124]. This has been shown to be an advantage for its virulence potential [40, 73, 172, 173], since bacteria are exposed to massive oxidative stress by the hosts immune system during an infection [70, 160].

1.4.2 Cell envelope bound virulence factors

Factors that enhance the bacterium's ability to produce biofilm, adhere to host cells and extracellular matrix proteins such as collagen fibronectin etc. are considered important for the bacterium's ability to cause infection [11]. There are several factors that have been shown to contribute to biofilm formation, *e.g.* the involvement of Fsr and GelE (mentioned in section 1.4.1) in biofilm production [51, 72, 95, 115]. Another important biofilm enhancing factor is the enterococcal surface protein (Esp). Esp is highly associated with *E. faecalis* ability to form biofilm on polystyrene surfaces [163]. Esp has also been shown to be involved in adhesion of *E. faecalis* during colonization of the urinary tract; strains producing Esp were recovered in higher amounts from the bladder and urine compared to the isogenic mutant [135]. The *esp* gene is found within the *E. faecalis* PAI, in close association with the *cyl*-operon (see section 1.4.1) [134]. A locus (e*bpABC*) encoding pilus-like structures has been shown to be important in the initial attachment step of biofilm production [104]. The *ebp*-locus has also been shown to be important for endocarditis and urinary tract infection [104, 142]. Furthermore, the *ebp*-

locus is found in most of the *E. faecalis* strains examined, indicating an essential role for this pili in *E. faecalis* [17, 104, 139].

Two other enterococcal adhesins have also been found to be important for virulence in *E. faecalis*: an aggregation substance (pheromone-responsive plasmid encoded) and an adhesin to collagen in *E. faecalis* (ace). The main role of the aggregation substance is to aid the formation of mating aggregates during bacterial conjugation [16], however this factor also mediates binding to eukaryotic cells [71, 149, 168]. Ace has been shown to bind to collagen and laminin [47, 102, 103], although this binding can only be seen in gelatinase negative strains (or at 46°C), since the heat labile gelatinase can cleave these proteins [164]. Ace was recently shown to be involved in urinary tract infection in a mouse peritonitis model [76] and to be important for experimental endocarditis [143].

Other cell surface bound virulence factors that have received attention the recent years are two serotype-determining cell wall polysaccharides called the enterococcal polysaccharide biosynthesis cluster (*epa*) and the serotype 2 (also known as serotype C) capsular polysaccharide (*cps*). Both exopolysaccharides have been shown to be important for biofilm formation [95, 152]. Furthermore, the two cell wall polysaccharides have been found to be important for *E. faecalis* adherence/colonization and for evasion of the host immune system [49, 52, 55, 95, 141, 152, 154, 182]. The *epa* locus is widespread among *E. faecalis* and has been designated the *E. faecalis* group antigen [152], whereas *cps* is serotype determining and is more abundant among clinical isolates [49]. The cell wall polysaccharides are interesting as they have a potential of being targets in anti-enterococcal vaccines, hence providing an alternative to combat infections caused by antibiotic resistant *E. faecalis*. Furthermore, Cps encapsulated *E. faecalis* have been shown to mask the presence of enterococcal lipoteichoic acids (LTA) [161, 162], which are known to stimulate the immune response [132].

1.4.3 Other potential virulence factors

The composition of the *E. faecalis* PAI is characterized by its plasticity as revealed by inter strain differences, and especially the region surrounding the *cyl*-locus has been shown to be associated with a high frequency deletion [87, 88, 105, 134]. Within the PAI few genes other than the once encoding Esp and cytolysin production and the transcriptional regulator *araC* have been found to contribute to *E. faecalis* virulence [18, 63, 135]. Even so, the other genes

within the PAI might also contribute to the fitness of the strain, although no specific virulence function has so far been assigned, and this can be supported by the high frequency of the PAI in infection derived isolates [88, 134]. Factors that contribute to the robustness and survival of the bacterium during an infection can also be considered as virulence factors. These can be stress survival mechanisms, specialized metabolic features, manganese/iron uptake mechanisms etc. In fact, several other genes have been shown to contribute to the virulence of *E. faecalis*, *e.g.* the general stress protein Gls24, the superoxide dismutase (SodA) and a manganese scavenging system encoded by *efaCBA* [106, 140, 153, 172].

1.5 DNA microarray technology

In the past decade, a paradigm shift has emerged from the step-by-step studies of expression of individual genes to the analysis of thousands of genes in one experiment. This was made possible by the development of DNA microarrays [181]. Microarrays contain small probe sequences (typically 25- to 70-mer oligonucleotide probes) that are immobilized to specific positions on a glass slide [29]. Target sequences can be labeled in different ways [148], but labeling with two different fluorophores such as Cy3 and Cy5 is widely used. The use of two different fluorophores allows a co-hybridization of two different samples (such as treated-untreated) on one microarray slide. The number of targets bound to their respective probes is quantified by scanning the microarrays and measuring the fluorescence emitted by the hybridized fluorescence-labeled targets when exited by the light from the lasers [148]. Microarrays have many applications, but gene expression profiling, where the transcription of thousands of genes in one state is compared to their transcription in a different state (*e.g.* treated versus untreated, different growth phases, wild type versus mutant) is the most common application in microbiology, followed by comparative genome hybridizations (CGH) [29].

1.5.1 Experimental design and data analysis

Although microarrays provide a powerful tool, the design of a microarray transcription experiment is of utmost importance in order to gain reproducible and meaningful data. Important steps include knowledge about growth conditions and growth rate, accurate sample preparations; especially time from cell harvest to transcriptional stop/mRNA release due to rapid mRNA decay, and applying an appropriate statistical analysis [20, 122]. There are many critical steps from cell harvest to the data analysis, all which can bias the final results.

Therefore certain control points such as RNA quality control, measurement of amount of cDNA produced, and labeling efficiency are important steps in quality insurance of the final results [20]. A well designed and performed experiment will also reduce the unwanted experimental variance; the variance which is not due to the biological differences in the study, and hence, which only introduce noise to the final data [20, 108].

Due to all the steps that can affect the results, it is crucial to repeat the experiment. In general the more replicates, the more reliable data, although the usual limitation is the cost of each replicate [68, 179]. The number of biological replicates needed depends on the type of experiment performed, where bacterial cultures give a more uniform response from experiment to experiment compared to *e.g.* cancer cell from different individuals [108]. For cell culture studies, a minimum of three biological replicates are normally needed in order to get reliable estimates of the amount of differential gene expression [79]. Before a statistical analysis is carried out, normalization needs to be performed to adjust the microarray data for effects which arise from variation in the technology, rather than from biological differences between the samples or between the printed probes [145].

Microarray results are challenging with regards to statistical analysis due to the complex datasets consisting of several regulated genes compared to relatively few experiments [147]. There are different statistical methods available that are developed to analyze these specific types of data. In this thesis we have analyzed the data using two types of mixed models which accommodate for the two types of effects that arise from microarray experiments, fixed and random effects. Effects modeled as fixed effects are typically those we are interested in finding (*e.g.* the effect of the treatment) or effects that are expected to have a small number of outcomes and that we are interested to learn more about (dye-effect). Random effects are different types of noise (*e.g.* the effect of the array used, variation between replicated spots) [144, 179]. These mixed models, or similar methods are used to test for whether genes are expressed differentially at a certain significance level by providing a p-value. As a measure for reduction of false positive differentially expressed genes, p-values are often adjusted [147]. In this thesis two different methods for corrections of the p-values have been employed; (i) the very strict Bonferroni correction and (ii) the correction to control the false

discovery rate (FDR). The latter method is a less stringent correction and is commonly accepted as a standard in the microarray data analysis community [113].

One of the biggest challenges with microarray transcriptional analysis is to make sense out of the large amount of data produced, and to extract hypotheses and conclusions that are biologically meaningful [82]. Helpful tools for this purpose are online databases (such as KEGG[a] and BioCyc[b]) which can provide clues about regulatory mechanisms and biochemical pathways the regulated genes are involved in.

1.5.2 DNA microarray technology in the future

The use of microarrays, especially for CGH has in some extent been caught up by the more advanced and rapid genome sequencing, and some have been speculating whether this technique will take over several microarray applications [21, 180]. For example in the last two years the number of sequenced *E. faecalis* strains has increased from one strain to the currently 24[c] strains with available complete or annotated draft genome sequences. Nonetheless, CGH has so far the advantage of being a fast and relatively inexpensive way to gain information about differences in the genome of *e.g.* different bacterial strains. The disadvantage with this method is that one can only gain knowledge about which genes are divergent in the strain of interest compared to the reference strain, and not any knowledge about the genes that are unique in the strain examined [27]. Then again, it is now possible to add more genomes to one microarray slide, since development in the production of microarrays allow a much higher density of probes on a slide [93], compared to only a few years back. The use of pan-genome arrays will allow a rapid screen of *e.g.* a strain collection, which can provide a better characterization of new strains, including emerging pathogens, and which also can provide insights into phylogenetic relationships between strains [180].

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[a] http://www.genome.jp/kegg/
[b] http://biocyc.org/
[c] http://www.ncbi.nlm.nih.gov/sites/entrez?db=genomeprj&cmd=search&term=txid1351[orgn]

2. OBJECTIVES OF THIS STUDY

The main objectives of the work presented in this thesis were to investigate how *E. faecalis* grow and survive in different infection-relevant environments, and how these different environments affected its transcription. To accomplish this, DNA microarrays were used to study the global transcriptome.

This work included the following tasks:

- Investigate how treatment with the clinically relevant antibiotic erythromycin affect the global transcription of an erythromycin resistant nosocomial *E. faecalis* isolate, and identify new traits potentially implicated in intrinsic antibiotic resistance of *E. faecalis*.
- Investigate the transcriptional responses of an *E. faecalis* bacteremia isolate to blood as a biological cue and growth environment. Characterize the transcriptional responses of potential virulence traits, and examine *E. faecalis*' immediate responses as well as its adaptations to a prolonged existence in blood.
- Examine the gene expression of different *E. faecalis* isolates in response to growth in urine, and identify common genes important for the survival in urine as well as strain specific genes, possibly related to its pathogenic potential.

3. MAIN RESULTS AND DISCUSSIONS

E. faecalis is found in several different environments, but it is its ability to cause infections combined with its resistance against antibiotics, that give rise to the concern regarding this bacterium. Several virulence factors have been identified in *E. faecalis* (reviewed in [50]), and although mutants with deletions of the different virulence genes have been impaired in their ability to cause infections compared to the wild type strains, none of these virulence genes have been shown to be absolutely necessary for the ability of *E. faecalis* to cause infection (reviewed in [50]). The importance of the known virulence factors is therefore controversial, and it is likely that the interplay between several (virulence) genes is just as important for the pathogenic potential of a strain as each separate virulence factor. This thesis reveals clues about potential important global regulation in infection-relevant growth environments; when exposed to the commonly used antibiotic erythromycin (paper I), in blood and in the presence of trace amounts of blood (paper II), and finally in human urine (paper III). In the three papers different microarrays, different strains and different statistical analyses have been used; hence a comparison of the results in the three papers is not straightforward. However, some general comments about similarities and/or differences between the three papers will be discussed in the following sections.

Erythromycin is commonly used to treat Gram-positive bacterial infections when a patient is allergic to penicillin [77]. In paper I, gene regulation of *E. faecalis* V583 in response to sub-lethal concentrations of erythromycin was examined. Initial experiments showed that the growth of V583 was impeded by 50 µg/ml erythromycin. This indicated that although bearing an erythromycin resistance genes (*erm*(B)), V583 was affected by erythromycin treatment. We wanted to investigate the effect of erythromycin treatment on the global gene regulation in V583 and to examine the adaptation of the bacterium to this treatment over time. Furthermore, we wanted to uncover genes important for erythromycin treatment besides the *erm*(B) gene.

We discovered a drastic change in the gene expression of around 600 genes, which clearly indicated an effect of the erythromycin treatment on V583 although being erythromycin resistant. Many of the affected genes were related to changes in growth conditions/rate between treated and non-treated cells. Other genes were involved in modifications of the cell envelope, *e.g.* genes involved in fatty acid and phospholipid metabolism, which possibly can alter the uptake of erythromycin into the bacterial cells due to

changed cell wall/cell membrane properties. Erythromycin also affected genes related to the erythromycin target site, such as an up-regulation of several genes encoding ribosomal proteins and the down-regulation of several tRNA synthase genes. Previous studies have observed similar effects on genes encoding ribosomal proteins and tRNA synthase genes in response to translation inhibitors [33, 107]. This indicated that although the *erm*(B) gene was expressed, the bacterium was affected by the antibiotic treatment. Apparently, V583 compensated for the erythromycin-effect by an enhanced production of ribosomes, while the production of tRNA was decreased to accommodate the protein synthesis activity. Interestingly, six genes involved in (multi)drug resistance/transport, including a gene encoding an MsrC-like macrolide efflux pump were among the genes showing an enhanced expression at most or all time points tested. Hence, several genes other than *erm*(B) seem to be involved in erythromycin tolerance in *E. faecalis*, and one mechanism to overcome erythromycin stress can possibly be transport of erythromycin out of the bacterial cell by specialized transport systems/pumps.

Compared to the enhanced expression of several stress genes seen in *E. faecalis* during growth in blood or urine (paper II and III), erythromycin treatment did not trigger a general stress in the bacterium, as most of the genes related to stress management were either not regulated or down-regulated. Furthermore, the effect of erythromycin on the MsrC-like macrolide efflux pump is very interesting, as the gene encoding this pump was not expressed/not regulated in any strain/timepoint in paper II and III.

In paper II the gene regulation of V583 in response to growth in blood and also in the presence of 10% blood (YTB) was examined. It has previously been shown that *E. faecalis* modulates the expression of virulence genes during growth in serum, and that this regulation also is growth phase dependent [136]. Furthermore, *E. faecalis* strains isolated from urinary tract infections (UTIs) and endocarditis showed enhanced adherence to different human cell cultures after growth in serum [45], and 46 strains from different origins showed an enhanced binding to fibrinogen, fibronectin and collagen after growth in the presence of 40% serum [101]. These previous reports indicated that *E. faecalis* responds to growth in serum by changing its virulence and adherence properties, making it more suited to colonize organs of the infected host. We wanted to investigate what effect growth in blood and YTB had on the global gene expression in *E. faecalis*. Furthermore, we chose to use whole blood, instead of serum since this would better mimic the conditions encountered during bacteraemia.

Growth in blood resulted in a modulation of several genes. Surprisingly we only found an enhanced expression of a few of the virulence genes examined by Shepard and Gilmore [136]. However, several differences in the experimental setup, *e.g.* choice of *E. faecalis* strains, whole blood versus serum, and sampling at differences time points and different growth stages could lead to such discrepancies. Another surprising observation was the down-regulation of both exopolysaccharide genes clusters (*epa* and *cps*) found in V583. Several studies have shown that the cell wall polysaccharides are important for biofilm formation, adherence and virulence of *E. faecalis* in several different studies [49, 52, 55, 95, 141, 152, 182]. However, although capsule formation is crucial for virulence in *Streptococcus pneumonia* [176], the transcription of its capsular polysaccharide gene-cluster was not enhanced in blood during *in vivo* infection in mice [109]. Furthermore, the expression of a number of virulence traits in *S. pneumonia* was shown to be body site dependent [109]. Hence, it is possible that the transcription of the *epa* and *cps* loci, and other virulence genes in *E. faecalis* would be enhanced in contact with host cells, and warrants further investigation.

The expression of several genes in V583 was affected immediately (5-15 minutes) after exposure to YTB, including genes related to the cell envelope and stress mechanisms. Some genes such as the fatty acid biosynthesis cluster (FASII) and *lrgAB* showed an enhanced expression throughout the experiment indicating an important role of these genes for the ability of V583 to grow in blood/YTB. The exact function of LrgAB has not been established, but two genes homologous to *lrgAB* were up-regulated in *Streptococcus agalactiae* in a similar study [90]. This previous observation combined with the continuously high level transcription shown in paper II suggest that the role of these genes in blood stream infection of *Enterococcus* and also *Streptococcus* should be investigated further. Interestingly, although growth in blood and urine triggered several common transcriptional changes, no enhanced expression of *lrgAB* was found in either of the strains examined in paper III, implying that this is a specific response to blood.

The work in paper III presents a slightly different perspective, where not only the transcriptional responses caused by growth in urine were examined, but more interestingly an investigation of different transcriptional responses of three *E. faecalis* strains from diverse origins were investigated. UTI is the most common infection caused by enterococci [85], and is also becoming exceedingly difficult to treat due to the antibiotic resistance among enterococci [157, 158]. Hence, to gain further knowledge about genes and processes

important for enterococcal UTI is essential in order to come up with alternative therapies. In paper III we used fresh human urine as a growth medium to partly mimic the conditions of the urinary tract. Growth of *E. faecalis* in urine has previously been shown to modulate several genes related to virulence in *E. faecalis* [9, 136]. Furthermore, we wanted to examine if there were any clear differences between the transcriptional responses in isolates from diverse origins. An initial growth experiment showed that the six strains examined grew equally good in urine, consistent with observations by Carlos and co-workers [8]. We therefore decided to further examine three strains from diverse origins, the pathogenic strains MMH594 and OG1RF, and the probiotic strain Symbioflor 1. Comparative genome hybridization (CGH) was performed to ensure that the oligos presented on the microarrays could reproduce the differences between these three strains and the V583 strain previously established [4, 25, 87, 88].

Similarly to what was found in the growth experiment, the transcriptional responses of the three different strains were also very comparable, hence there were no large differences in the transcriptional profiles of pathogenic and probiotic *E. faecalis* which could indicate crucial traits for causing UTI. Furthermore, the results obtained in paper III, revealed a number of similarities to the transcriptional responses of V583 in blood (paper II). In both paper II and III we found an enhanced expression of the FASII system. It is possible that the modulation of the fatty acid composition is important for virulence in *E. faecalis*. However, a previous study showed that the FASII genes also were modulated in response to the detergent SDS (sodium dodecyl sulphate), bovine bile, and a combination of SDS and bovine bile, suggesting that modulation of the fatty acid composition is a general response in *E. faecalis* to stressful conditions. The regulation of many other general stress genes, such as *gls24* and *gspA1-2* were also enhanced under both conditions, and notably several genes connected to oxidative stress were up-regulated both during growth in urine and blood, suggesting that oxidative stress management is important for growth in these environments. Furthermore, the experiments in both paper II and III suggests that iron- and manganese-uptake is important for growth in both blood and urine, while regulation of genes involved in metabolism was slightly different in urine compared to blood.

Counter-intuitively, similar to what was found in paper II we observed a down-regulation of the cell wall polysaccharide (*epa*) in all three strains. This exopolysaccharide was specifically shown to be important for infection in a UTI model [141]. Interestingly, we also found a reduced transcription of the *cps*-locus in MMH594, which was the only strain

containing these genes. These results may further indicate that the expression of the cell wall polysaccharides could be body-site dependent. The most intriguing results found during growth in urine was however an enhanced regulation of one of the most studied virulence determinants in *E. faecalis*, *fsrABC* in MMH594, but not in OG1RF (these genes are not present in Symbioflor 1). The seemingly higher expression of the *fsr*-regulon in urine by MMH594 compared to by OG1RF could imply a more virulent potential during a UTI of the former strain. However, OG1RF did cause an increased mortality in a mouse peritonitis model compared to V583, and outnumbered V583 in a mouse UTI model showing that OG1RF is equally virulent as/more virulent than V583 [4]. V583 and MMH594 are closely related, although MMH594 contains more virulence genes than V583 [134]. To our knowledge the ability of MMH594 to cause UTI compared to other *E. faecalis* strains has not previously been examined, and hence we can only speculate that the enhanced expression of *fsr* in MMH594, but not in OG1RF, will make it more potent to cause UTI. Most of the other virulence genes, including those involved in adherence were not significantly regulated in either strain during growth in urine.

The implication of a differential expression of genes such as *fsrABC*, the *epa*-cluster etc. is hard to predict since transcript levels detected by microarray do not reflect all regulatory processes in the cell, like post-transcriptional/post-translational processes that can alter the amount of active protein. Proteomics does however suffer from several constraints in terms of resolution and sensitivity, and to date no complete prokaryote or eukaryote proteome has been resolved [170]. Therefore, a combination of transcriptomic- and proteomic-approaches is needed to improve our knowledge on gene expression and cell performance. Even so, it is known that most conditions influence the transcription of several genes, not directly involved in the process studied. One example is the sigma factor B-dependent stress response of *Bacillus subtilis*, which not only is induced by various environmental stressors such as heat or carbon starvation [114, 117], but also by various antibiotics [3, 7]. An increased insight of the transcriptional networks existing in the organism of interest is of great importance in order to be able to extract the biological relevant responses arising from the conditions tested. Besides the work presented in this thesis there are currently only 4 publications devoted to *E. faecalis*' global transcriptional analysis [5, 6, 123, 146]. The results presented in this thesis therefore not only give an insight into the responses of *E. faecalis* to the infection related growth environments examined, but also contribute to the general understanding of *E. faecalis* global transcriptional regulation.

4. MAIN CONTRIBUTIONS AND FUTURE WORK

The work presented in this thesis has provided new insight into the adaptation *E. faecalis* undergoes to be able to grow and survive in infection-relevant growth environments. We have shown the importance of a rapid regulation of genes involved in metabolism, stress mechanisms and cell envelope modification in response to infection-relevant growth environments. Microarray data can point to new potentially interesting genes, not previously connected to virulence, as well as provide clues about global regulation of genes and operons important for virulence and survival. Besides providing much needed information about the global regulation of *E. faecalis* to various growth environments, the most interesting observations in this thesis were:

- The possible involvement of two ABC-transporters (EF1733-2) and a putative MsrC protein in the efflux of erythromycin in V583.
- A potential important role of LrgAB (EF3194-3) for growth of V583 in blood.
- Strain dependent expression of the *fsr*-system might contribute to the pathogenic potential during UTI.
- The involvement of cell envelope modifications, especially the modifications effectuated by the FASII pathway in stress management and survival in various infection-relevant growth environments.

In order to fully exploit the new information provided in this thesis, follow-up studies are needed. The erythromycin study has already been followed up by a study of the transcriptional responses of *E. faecalis* to another translation inhibiting antibiotic, chloramphenicol, and the responses have been compared with those of *E. faecalis* to erythromycin. Further experiments to enhance our understanding of *E. faecalis* resistance and tolerance to antibiotics have not been planned.

To extract more information from the already produced data in paper II and III, a study of the transcriptional responses of *E. faecalis* in a minimal medium performed in a similar manner would provide clues about which of the observed effects are relevant as responses to biological cues/infection-relevant growth environments, and which responses are due to a sudden transfer to a low nutrient growth environment. The extraction of these responses will probably reduce the number of genes important for the specific growth environments, and their relevance for growth and infection can be studied further by *e.g.* knock out studies.

Since we did not observe any large differences between isolates from different sources it would be interesting to examine the virulence potential of these and other strains in infection models, such as *Caenorhabditis elegans*. The importance of the different genes found in this thesis for virulence could also be tested in animal models.

The most intriguing experiments would however be *in vivo* infection studies of *E. faecalis*, either in animal models, but even more relevant in *E. faecalis* found in human infections such as UTIs. The use of pan-genome arrays based on all the sequenced *E. faecalis* strains would be most useful to be able to extract as much information as possible.

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PAPER I

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Transcriptional Response of *Enterococcus faecalis* V583 to Erythromycin

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A transcriptional profile of *Enterococcus faecalis* V583 (V583) treated with erythromycin is presented. This is the first study describing a complete transcriptional profile of *Enterococcus*. *E. faecalis* is a common and nonvirulent bacterium in many natural environments, but also an important cause of nosocomial infections. We have used a genome-wide microarray based on the genome sequence of V583 to study gene expression in cells exposed to erythromycin. V583 is resistant to relatively high concentrations of erythromycin, but growth is retarded by the treatment. The effect of erythromycin treatment on V583 was studied by a time course experiment; samples were extracted at five time points over a period of 90 min. A drastic change in gene transcription was seen with the erythromycin-treated cells compared to the untreated cells. Altogether, 260 genes were down-regulated at one or more time points, while 340 genes were up-regulated. Genes encoding hypothetical proteins and genes encoding transport and binding proteins were the two most dominating groups of differentially expressed genes. The gene encoding *ermB* (EFA0007) was expressed, but not differentially, which indicated that other genes are important for the survival and growth maintenance of V583 treated with erythromycin. One of these genes is a putative MsrC-like protein, which was up-regulated at all time points studied. Other specific genes that were found to be up-regulated were genes encoding ABC transporters and two-component regulatory systems, and these may be genes that are important for the specific response of V583 to erythromycin.

Enterococci are commonly found in the gastrointestinal tracts of humans and animals. Most enterococci are not virulent, and some are frequently found in artisan fermented foods, in which they contribute to longer shelf life, flavor, and texture. However, enterococci are best known as antibiotic-resistant opportunistic pathogens that are commonly recovered from patients who have received multiple courses of antibiotics and have been hospitalized for prolonged periods. Innate resistance to many antibiotics is a common trait among enterococci (see, e.g., reference 7 and the references therein). They also acquire antibiotic resistance determinants, including resistance to vancomycin, very rapidly from the environment (see, e.g., references 16–18). The two species best known to be involved in infections in human and animal bodies are *Enterococcus faecalis* and *E. faecium* (6).

The complete genome sequence of the vancomycin-resistant *E. faecalis* V583 (V583) is now available (20). Access to the genome sequence opens new possibilities to gain basic information on the molecular biology of the organism, and one of the tools that can be used to exploit the genome sequence experimentally is the DNA microarray technology. Microarrays give us the opportunity to study all transcriptional events going on in a cell and identify which genes are involved in certain cell processes in one experiment. The main advantage of the microarray technology is the ability to study the transcription of thousands of genes in one experiment. By nature, the microarray technology is explorative and hypothesis generating. The results of microarray experiments are, in principle, snapshots of the transcriptional activities of the cell. Moreover, since transcription and translation are coupled processes in prokaryotes, the transcriptome should reflect the proteome well. Indeed, it has been shown that regulation of the majority of genes parallels the level of proteins produced (2). On a genome-wide scale, it is difficult to speculate about which bacterial genes are regulated or not during certain conditions, and it is also hard to gain such information through the use of traditional low-throughput methods. By the use of microarrays, one can relatively quickly obtain information about gene expression levels and thereby explore the responses of the cells to changing growth conditions.

V583 survives and grows in media containing relatively high levels of the commonly used macrolide antibiotic erythromycin, but the addition of erythromycin to the culture retards cell growth. In sensitive cells, erythromycin inhibits protein synthesis by binding to the large ribosomal subunit close to the peptidyl transfer center. Protein synthesis is thereby aborted during early rounds of translation, since access to the nascent peptide channel is prevented (29). In gram-negative bacteria,

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intrinsic resistance to erythromycin is due to the impermeability of the cellular outer membrane to this hydrophobic macrolide. Two main mechanisms of erythromycin resistance that have been identified in gram-positive bacteria are as follows: (i) Target modification by the *erm* (erythromycin resistant methylase) genes that encode enzymes which methylate rRNA has been described. The rRNA methylation causes conformational changes in the P site of the rRNA and prevention of macrolide binding. (*erm*-mediated resistance in enterococci has been described. The pAD1-like plasmid pTEF1 of V583 encodes ErmB, an rRNA adenine dimethylase family protein.) (ii) A macrolide efflux resistance mechanism, which is an energy-dependent pump, has been described for both gram-positive and gram-negative bacteria (22).

This paper describes the use of a genome-wide amplicon-based microarray based on the genome sequence of V583 to obtain a profile of the transcriptional events in V583 cells treated with erythromycin. The aim of the work was to obtain an overview of how erythromycin affects transcriptional events and bacterial growth, aside from described resistance mechanisms, and how this bacterium tolerates stress. Taking into account the observed phenotypic effects of erythromycin on V583, it was expected that genes involved in general stress responses, genes involved in protein synthesis, and genes encoding (multi)drug resistance would be among the genes affected by the antibiotic treatment.

MATERIALS AND METHODS

Bacterial strain and growth conditions. The bacterium studied was *E. faecalis* V583 (V583), which was the first vancomycin-resistant clinical isolate reported in the United States (24) and whose genome sequence has been completed (20). V583 samples were grown overnight in flasks with brain heart infusion (BHI) medium (Difco) at 37°C on a rotary shaker (300 rpm). Cultures were then diluted 50× and grown in BHI, as described above, for 1 h. Cultures were split in two, and erythromycin (Sigma) was added to one of the cultures. The final concentration of erythromycin was 50 μg/ml. The two cultures (BHI and BHI plus erythromycin) were then incubated further, and 3-ml samples of each culture were collected immediately after the addition of erythromycin (*t*0), and after 15 (*t*15), 30 (*t*30), 60 (*t*60), and 90 (*t*90) min. Growth of the cultures was monitored spectrophotometrically (optical density at 600 nm [OD_{600}]). Samples were centrifuged for 5 min at 4°C, and pellets were flash frozen in liquid N_2 prior to RNA extraction.

Construction of V583 microarrays. PCR primers for all V583 open reading frames (The Institute for Genomic Research, May 2002 update) were designed using Primer3 (freeware; http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi), which has commonly been used for primer design during microarray construction (3, 13). Primers were designed to amplify full-length or ~500-bp amplicons from genomic DNA. PCRs (50-μl reaction volume) were run with 50 mM KCl; 10 mM Tris-HCl (pH 9.0); 0.1% Triton X-100; 2.5 mM $MgCl_2$; 2 μM of each primer; 0.2 mM of each dATP, dCTP, dGTP, and dTTP; 10 to 20 ng genomic DNA; and 1.25 U *Taq* polymerase (Promega). Amplifications were performed with Perkin-Elmer 9600 thermocyclers with an initial denaturation at 94°C for 3 min and then 35 cycles of denaturation at 94°C for 1 min, annealing at 54 to 56°C for 1 min (the annealing temperature varied depending on the melting temperatures of the primers), and an extension at 74°C for 1 min. The PCR was finalized with incubation at 74°C for 10 min. The quality of the PCR products was assessed by agarose gel electrophoresis. The PCR products were cleaned up using a QIAquick 96 PCR purification kit (QIAGEN). Of a total of 3,337 predicted open reading frames in the V583 genome, 3,160 PCR products were obtained. The purified PCR products were eluted in 3× SSC (1× SSC is 0.15 M NaCl plus 0.015 M sodium citrate)-0.01% sodium dodecyl sulfate (SDS) and printed on Corning UltraGaps slides. All PCR products, representing the predicted V583 open reading frames, were printed in five copies on the slides. In addition, negative controls (three genes from *Arabidopsis thaliana*, buffer [3× SSC, 0.01% SDS], and empty spots) and digested genomic DNA from V583 (positive control) were spotted on the arrays. Altogether, 3,502 samples were spotted on the slides.

RNA isolation. Total RNA extractions from the samples collected at the time points described above were performed with RNeasy Mini columns (QIAGEN), with DNA digestions being done on the columns by the addition of 82 Kunitz units of RNase-free DNase (QIAGEN) and incubation at room temperature for 15 min. The integrity of and concentration of RNA samples were measured using a RNA 600 Nano LabChip kit and a Bioanalyzer 2100 (Agilent Technologies). For both strains, 10 μg of each RNA sample was used in separate hybridization experiments on identical arrays.

cDNA synthesis, fluorescent labeling, hybridization, and microarray data analysis. For reverse transcription and cDNA synthesis, 30 μg of random hexamers (Amersham) and 10 μg of total RNA was initially preheated at 70°C for 10 min and was incubated for 10 min at 4°C and then for 2 h at 42°C in an Eppendorf Mastercycler. The reverse transcription (RT)-PCR mix was 1× first-strand buffer, 10 mM dithiothreitol; 380 units of Superscript II RT; 500 μM concentrations of dATP, dCTP, and dGTP; 300 μM dTTP (all from Invitrogen), and 200 μM amino-allyl-labeled dUTP (Sigma). After hydrolysis with 10 μl of 1 M NaOH and 10 μl of 0.5 M EDTA for 15 min at 65°C, the samples were neutralized with the addition of 25 μl of 1 M Tris-HCl (pH 7.4) and cleanup was performed with Microcon 30 filters (Millipore). The fluorescent monofunctional *N*-hydroxysuccinimide-ester dyes cyanine-3 and cyanine-5 (Amersham) were coupled to the cDNAs originating from cultures grown without erythromycin and with erythromycin, respectively, for 1 h, quenched with 1.5 M hydroxylamine (Sigma), mixed, and finally cleaned with a QIAquick PCR purification kit (QIAGEN). The samples (30 μl) were then dried and used for hybridization within 12 h. Hybridizations to the microarrays were conducted as follows. Slides were prehybridized by incubation at 50°C for 30 min in a solution containing 1% bovine serum albumin (Calbiochem), 3.5× SSC, and 0.1% (wt/vol) SDS. The dried fluorescently labeled cDNA samples were resuspended in the following hybridization solution (40 μl): 5× SSC, 0.1% (wt/vol) SDS, 1.0% (wt/vol) bovine serum albumin, 50% (vol/vol) formamide, and 0.01% (wt/vol) single-stranded salmon sperm DNA. The resuspended probes were added to the arrays and incubated, in darkness, at 42°C for 6 h. After hybridization, excess hybridization solution and unspecific bound probe were washed away by four washing steps and gentle shaking, in darkness, for 2 min in 2× SSC-0.1% SDS, 1 min in 1× SSC, 1 min in 0.2× SSC, and 30 seconds in 0.05× SSC. Immediately after washing, the arrays were dried by centrifugation at 600 rpm for 5 min in an Eppendorf 5810R tabletop centrifuge. Three replicate hybridizations were performed with two separate batches of RNA. The two batches of RNA were obtained in two separate growth experiments.

Hybridized arrays were scanned at wavelengths of 532 nm (cyanine-3) and 635 nm (cyanine-5) at a 10-μm resolution to obtain two TIFF images with a ScanArrayExpress Microarray scanner (Packard Bioscience). Fluorescent intensities and spot morphologies were analyzed using the QuantArray program ver. 3.0 (Packard BioScience), and spots were excluded based on slide or morphology abnormalities.

Raw data from each array was preprocessed independently. A Lowess smoothed background was subtracted from all foreground intensities, and a cross-validated Lowess method was used in an intensity-dependent normalization of every array. The $\log_2$ ratios for each spot were further analyzed using a mixed model (30) to detect differentially expressed genes. A mixed model was fitted to the data for each of the five sample times (0, 15, 30, 60, and 90 min) separately. Data for the three arrays at every sample time were described by $y_{ijk} = \mu_i + u_{ij} + e_{ijk}$ where y_{ijk} is the observed $\log_2$ ratio of gene i (1, . . ., 3,502) on array j (1, 2, 3) and in spot k (1, . . ., 5) on that array, μ_i is the expected $\log_2$ ratio for gene i, u_{ij} is a random effect of gene i on array j, and e_{ijk} is the remaining noise. The variance components were estimated under the assumption of Gaussian errors using a restricted maximum likelihood approach coping with the unbalanced data due to missing spots. Differentially expressed genes were identified by testing the hypothesis H_0, defined as $\mu_i = 0$, against H_1, defined as $\mu_i \neq 0$. A chi-square test for every gene resolves this for the model in the y_{ijk} equation (4), and a Bonferroni-corrected rejection level of a P value of <0.01 was used throughout. If H_0 ($\mu_1 = 0$) was rejected, and μ_i is >0, genes were considered to be up-regulated in the erythromycin-treated cells. If H_0 was rejected, and μ_i is <0, genes were considered to be down-regulated. All data analysis algorithms were programmed by using Matlab (MathWorks, Inc.), but a subset of the data was also analyzed by the SAS system (SAS Institute, Inc.) to check the validity of the code.

Confirmation of expression levels of specific genes by real-time RT-PCR. To confirm independently the differential gene expression observed by microarray experiments, four genes were selected for analysis by real-time quantitative RT-PCR (RTQ). Primers and probes for the RTQ were designed using the Assays-

By-Design file builder (ver. 2.0; http://www.appliedbiosystems.com/support/software/assaysbydesign/installs.cfm?prod_id=1541; Applied Biosystems). Primers and probes were synthesized by and purchased from Applied Biosystems. The genes selected for RTQ analyses were EF0633 (*tryS-1*, encoding tyrosyl-tRNA synthetases), EF2653 (encoding a transcriptional regulator of the Cro/CI family), and EF0105 (*argF-1*, encoding ornithine carbamoyltransferase). EF1964 (*gap-2*, encoding glyceraldehyde-3-phosphate dehydrogenase), which is constitutively expressed, was used to normalize the *Taq*Man data. The RTQ analyses were run on an ABI PRISM 7700 sequence detector (Applied Biosystems). cDNA was synthesized as above, with 15 ng RNA as template. Real-time PCR was performed using the *Taq*Man Universal PCR Master Mix (Applied Biosystems), according to the manufacturer's instructions. To ensure that the cDNA was not contaminated by genomic DNA, reactions without reverse transcriptase were also included. Differential expression was determined by calculating the change in threshold cycle (ΔC_t) for each gene, with RNA isolated from cells grown with and without erythromycin and harvested at the five time points mentioned above.

RESULTS

We have studied the transcriptional responses of *E. faecalis* V583 to treatment with the macrolide antibiotic erythromycin through a time course experiment utilizing a genome-wide microarray based on the V583 genome sequence. By applying a time course experiment in this manner, we were able to investigate both an immediate response to this stress and the cells' adaptation to a more permanent presence of erythromycin. In the following, we focus on genes that were differentially expressed in the untreated and the erythromycin-treated cells.

We applied a stringent confidence level (a P value of <0.01 plus Bonferroni correction for multiple comparisons) for the determination of significant differential transcription. Genes were "scored" as significantly up- or down-regulated as described above, with a threshold P value of <0.01 and the conservative Bonferroni correction for multiple comparisons, ensuring a very low number of false negatives.

Circa 600 (18%) of the predicted V583 genes were found to be differentially transcribed at one or more of the five time points examined during the 90-min time course experiment. Obviously, the erythromycin exposure seriously affected the transcriptional events in these enterococci: 260 genes were found to be significantly up-regulated (induced; $\log_2$ ratios of stressed cells/nonstressed cells were different from and higher than 0) and 340 genes down-regulated (repressed; $\log_2$ ratios of stressed cells/nonstressed cells were different from and lower than 0) at one or more time points. Among the up-regulated genes, four were plasmid encoded, while 27 plasmid-encoded genes were down-regulated. The numbers of differentially expressed genes, sorted by their cellular roles, are shown in Table 1. The total number of V583 genes represented on the array was 3,160 (out of total of 3,337 genes in the V583 genome), which means that ca. 8% of all V583 genes were up-regulated and ca. 10% down-regulated in the erythromycin-exposed cells. This shows that transcriptional events in these enterococcal cells are strongly altered by erythromycin exposure. During the 90-min time course, the number of down-regulated genes is higher than the number of induced genes at all time points except *t*90 (the last time point) (Tables 2 and 3), which indicates a general decrease in transcriptional activity by exposure to erythromycin.

Growth of erythromycin-treated *E. faecalis* V583. Cell samples were collected at five time points after the addition of erythromycin (50 μg/ml) to one of the cultures. We chose this level of erythromycin in the cultures on the basis of preliminary experiments (results not shown), where we found that growth of V583 was retarded but still significant. (V583 does grow in medium with >400 μg erythromycin/ml.) Our time course experiment was performed over a period of 90 min, and in this first part of the growth, the erythromycin-treated cells grow more slowly than the untreated cells. Thus, this work describes

TABLE 1. Number of genes that were differentially expressed at one or more time points, sorted by cellular role[a]

Cellular role	No. of differentially expressed genes	
	Down-regulated	Up-regulated
Amino acid biosynthesis	5	2
Biosynthesis of cofactors/prosthetic groups/carriers	6	1
Cell envelope	24	12
Cellular processes	28	8
Central intermediary metabolism	5	3
DNA metabolism	5	16
Energy metabolism	30	11
Fatty acid and phospholipid metabolism	1	6
Hypothetical proteins	118	83
Other categories	8	1
Protein fate	9	8
Protein synthesis	14	13
Purine/pyrimidine/nucleoside/nucleotide	11	8
Regulatory functions	17	14
Signal transduction	17	9
Transcription	3	3
Transport and binding protein	40	49
Unknown function	23	17
Viral functions	1	0

[a] Differentially expressed plasmid-encoded genes are also included. Genes that were up-regulated at some time points and down-regulated at other time points are counted twice. Likewise, genes that have been assigned more than one cellular role were counted twice.

TABLE 2. Number of up-regulated genes in each functional category at all time points studied

Cellular role	No. of up-regulated genes at time point indicated				
	*t*0	*t*15	*t*30	*t*60	*t*90
Amino acid biosynthesis	2	0	0	0	0
Biosynthesis of cofactors/prosthetic groups/carriers	0	1	1	0	0
Cell envelope	1	4	5	5	5
Cellular processes	0	2	6	5	7
Central intermediary metabolism	2	2	3	1	0
DNA metabolism	1	7	6	11	6
Energy metabolism	0	1	3	2	7
Fatty acid and phospholipid metabolism	0	4	5	2	3
Hypothetical protein	4	25	45	36	48
Other categories	0	0	1	0	0
Protein fate	0	2	4	5	5
Protein synthesis	0	8	9	5	3
Purine/pyrimidine/nucleoside/nucleotide	0	3	4	1	4
Regulatory functions	0	4	7	7	9
Signal transduction	0	2	4	2	5
Transcription	0	1	1	1	1
Transport and binding protein	6	18	24	21	28
Unknown function	2	5	9	11	9
Viral functions	0	0	0	0	0
Total	18	89	137	115	140

TABLE 3. Number of down-regulated genes in each functional category at all time points studied

Cellular role	No. of down-regulated genes at time point indicated				
	*t*0	*t*15	*t*30	*t*60	*t*90
Amino acid biosynthesis	1	1	2	3	4
Biosynthesis of cofactors/prosthetic groups/carriers	1	4	4	0	1
Cell envelope	5	10	16	10	9
Cellular processes	1	10	10	7	10
Central intermediary metabolism	1	2	2	1	1
DNA metabolism	0	4	4	0	1
Energy metabolism	3	4	12	21	11
Fatty acid and phospholipid metabolism	0	0	0	0	1
Hypothetical protein	29	59	47	35	43
Other categories	0	2	3	2	3
Protein fate	0	2	2	4	4
Protein synthesis	0	6	6	5	6
Purine/pyrimidine/nucleoside/nucleotide	0	4	3	6	5
Regulatory functions	2	7	6	3	4
Signal transduction	1	2	4	11	3
Transcription	0	1	2	0	0
Transport and binding protein	6	11	18	16	12
Unknown function	6	8	9	6	9
Viral functions	0	1	1	0	0
Total	56	138	151	130	127

the response of V583 to erythromycin during the first cycles of growth. We chose a relatively low level of erythromycin for the experiments, according to the observation by Hutter et al. (11) that lower concentrations are better for obtaining good microarray results. During the experiments, growth was measured spectrophotometrically. After 15 min, the OD of the erythromycin-treated culture was approximately 82% of the OD of the untreated (control) culture; after 30 min, the OD of the erythromycin-treated culture was approximately 69% of that of the untreated culture; after 60 min, the OD of the erythromycin-treated culture was approximately 54% of that of the untreated culture; and after 90 min, the OD of the treated culture was 40% of the OD of the untreated culture. The growth curves of erythromycin-treated and untreated V583 are shown in Fig. 1.

EFA0007, the *ermB* gene. EFA0007, which was referred to as an rRNA adenine dimethylase family protein encoded on pTEF1 (20) is, in fact, ErmB (>99% identity with ErmB from *Bacillus cereus*, *Streptococcus pyogenes*, *E. faecium* [BlastP]). This gene was expressed in cultures both with and without erythromycin, but the gene was not differentially expressed at any time point. This is in accordance with earlier observations that the *ermB* is constitutively expressed in enterococci (B. Murray, unpublished results). The retarded cell growth in the presence of erythromycin confirms that EFA0007 does not fully protect the bacterium against this antimicrobial compound and suggests that additional genes are involved in the cells' protection against this stress factor. Alternatively, the apparent lack of differential expression may be explained by posttranscriptional regulation of this gene; *ermB* may be posttranscriptionally regulated by a stalling on the ribosome during translation.

Up-regulated (induced) genes. The number of up-regulated genes in each functional category at various time points is shown in Table 2. Among the up-regulated genes, the genes encoding hypothetical proteins represented the highest percentage (85 genes; around 32% of all up-regulated genes), while genes related to transport and binding functions represented around 17% (44 genes) of the genes induced by the erythromycin stress. Moreover, genes encoding proteins involved in energy metabolism (10 genes), protein synthesis (13 genes), synthesis of cell envelope components (12 genes), and regulatory functions (13 genes) were up-regulated. The majority of up-regulated genes related to protein synthesis are genes encoding ribosomal proteins. In addition, genes classified in the category of genes of unknown function represent a considerable part of the induced genes (17 genes).

Among the up-regulated genes, three genes encoded drug

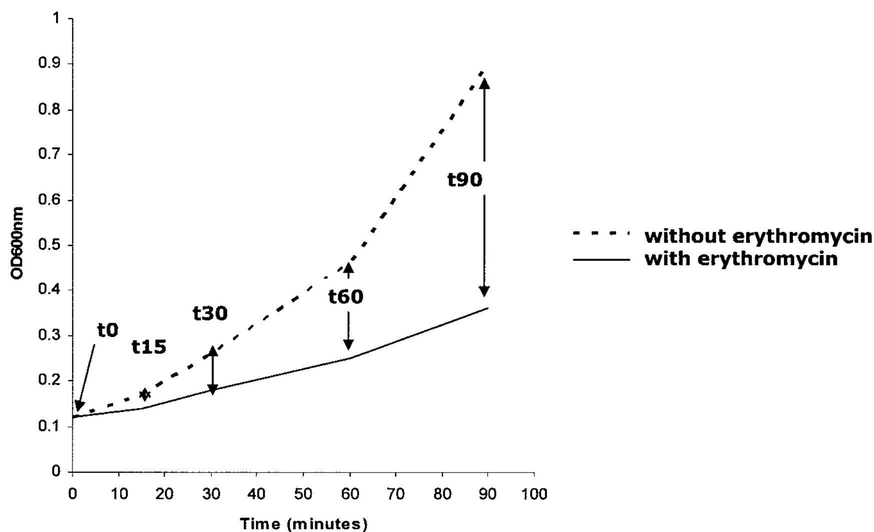

FIG. 1. Growth of *E. faecalis* V583 treated with erythromycin (50 μg/ml; solid line) and of untreated *E. faecalis* V583 (broken line). Growth was measured spectrophotometrically at a λ of 600 nm. Arrows indicate time points at which samples were collected for RNA extraction and microarray experiments.

resistance proteins. These genes were EF0420 (up-regulated at *t*30 and *t*60), EF1370 (up-regulated at *t*30, *t*60, and *t*90), and EF1078 (up-regulated at *t*15, *t*30, *t*60, and *t*90). Four genes only were induced at all time points. These genes were EF1400 (predicted to encode a cadmium-translocating ATPase), EF1413, EF1916 (encoding a GTP-binding protein), and EF2720 (encoding an ABC transporter). The gene encoding a putative MsrC-like protein (EF1413) is of particular interest. MsrC is widely spread among *Enterococcus faecium*, and MsrC is believed to be an efflux pump involved in low-level macrolide resistance in this species (23, 25). However, the EF1413 is only 40% identical (60% similar) to the *E. faecium* MsrC, and it is therefore not clear whether the EF1413 encodes a functional MsrC-like protein. Table 4 gives the full list of genes found to be induced (up-regulated), with $\log_2$ ratios. Genes predicted to encode hypothetical proteins and plasmid encoded genes are excluded from this list.

Down-regulated (repressed) genes. The numbers of down-regulated genes in each functional category at various time points are shown in Table 3. Among the down-regulated genes, those encoding hypothetical proteins are the dominant category (115 genes; 35%), followed by genes encoding transport and binding proteins (38 genes; 11%), genes with unknown function (23 genes), genes encoding cell envelope-related proteins (24 genes), and genes involved in energy metabolism (29 genes), regulatory function (13 genes), protein synthesis (14 genes), and cellular processes (23 genes). The majority of down-regulated genes related to protein synthesis are eight tRNA synthetases (cysteinyl-tRNA synthetase, tyrosyl-tRNA synthetase, alanyl-tRNA synthetase, aspartyl-tRNA synthetase, tryptophanyl-tRNA synthetase [EF2228], threonyl-tRNA synthetase, valyl-tRNA synthetase, and seryl-tRNA synthetase). The tryptophanyl-tRNA synthetase gene encoded by EF2679 (*trpS*) was significantly up-regulated at all time points except *t*0. Transcription was found to be repressed at all five time points examined for 10 genes. Table 5 lists all of the down-regulated genes, with $\log_2$ ratios. Genes encoding hypothetical proteins and plasmid genes are not included.

Validation of microarray data by real-time quantitative RT-PCR analyses of selected genes. Verifications of the expression levels of four genes observed by microarrays were performed by real-time quantitative RT-PCR analyses (*Taq*Man assays). The genes selected for these RTQ analyses represented various functional categories and different patterns of expression. The transcription profiles of the genes examined by RTQ correlated well with the transcription profiles observed by the use of microarrays ($r = 0.83$).

DISCUSSION

The present study focuses on functional genomics of *Enterococcus faecalis* V583, applying a genome-wide microarray based on the genome sequence of V583. In general, the knowledge of gene expression in enterococci is scarce. This is the first paper describing a global transcriptional profile of *Enterococcus*, and more studies are definitely needed to obtain a deeper understanding of gene expression in this species. We used a microarray to study the transcriptional responses of V583 to the macrolide antibiotic erythromycin. V583 is resistant to relatively high levels of erythromycin, but exposure to erythromycin retards its growth. The work was performed to (i) gain insight into the mechanisms involved in resistance to erythromycin by V583, (ii) obtain clues about transcriptional responses to general stress in bacteria, and (iii) generate hypotheses for subsequently gaining deeper knowledge on antibiotic resistance and general stress in this bacterium.

In the experiments, V583 was treated with erythromycin (50 μg/ml), which decreased the growth of the cells significantly compared to the untreated control during the 90-min time course experiment. The concentration of antibiotic to apply in such experiments is, of course, a matter of discussion. Hutter et al. (11) claimed that compound concentrations should be at concentrations that are just low enough not to affect the growth of the organism. This probably varies with the strains and compounds being studied.

We chose a stringent confidence level plus Bonferroni correction to score for significant differential expression, in the data analysis. Consequently, the number of false positives is, per definition, very low. We preferred this method, although some information might have been lost. Moreover, we decided to score for significant up- and down-regulation instead of using the common fold change cutoff values. Thus, the conclusions are based on experimental data precision (noise levels and number of replicates); this is appropriate since microarrays probably underestimate actual mRNA induction ratios (2). Also, treating each array as a random sample from a population of all possible arrays makes all conclusions more general. Even our simple mixed model gives a quite accurate description of the variance structure of normalized microarray data from repeated experiments and allows for an extended information extraction from every experiment. Our analysis differs from that by Wernisch et al. (30) in that we have excluded the array main effect. Our argument for this is that all arrays have been normalized separately, and thus any array main effects will be ignorable, which is also the conclusion drawn by Wernisch et al. (30) in analyzing similar data. Another variant of our mixed model approach is taken by Wolfinger et al. (31). They use one variance component per gene, which makes the model much more complex. More research must be done in this area of bioinformatics before we can come to a conclusion as to which strategy is appropriate. For now, we have chosen to use a simple model, in line with the principle of parsimony.

The target of erythromycin and other macrolides is protein synthesis, more specifically the 50S (large) ribosomal subunit. These antibiotics block the ribosome exit tunnel, which prevents the movement and release of the nascent peptide chain. The *ermB* gene (EFA0007) was not found to be significantly up- or down-regulated at any time point. Hence, this gene is probably constitutively expressed and contributes to the erythromycin resistance of V583. However, based on the high level of differential transcription and slow growth observed for erythromycin-exposed cells compared to untreated cells, it appears that a battery of other genes respond expressionally to the presence of erythromycin. These responses are not necessarily all due to resistance, but rather an adaptation to changes in growth conditions. Thus, these genes contribute to maintenance of the growth during erythromycin exposure. Three genes encoding drug resistance proteins (EF0420, EF1078, and EF1370), on the other hand, appear to play a role

TABLE 4. Log_2 ratios of genes whose transcription increased at one or more of the five time points (altogether 90 min) at which the effect of erythromycin treatment was studied, sorted by functional category (cellular role)

Protein encoded by gene	Cellular role(s)	ORF	Log_2 ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
Cystathionine beta-lyase (*metC*)[a]	Amino acid biosynthesis	EF0290	0.71	0	0	0	−1.05
Prephenate dehydrogenase	Amino acid biosynthesis	EF1565	0.71	0	0	0	0
Cobyric acid synthase, putative	Biosynthesis of cofactors/prosthetic groups/carriers	EF2586	0	0.87	0.86	0	0
Alanine racemase (*alr*)	Cell envelope	EF0849	0	0	0.78	0.87	1.11
Membrane protein, putative	Cell envelope	EF0860	0	0	0	0	0.77
Glycosyl transferase, group 2 family protein	Cell envelope	EF0887	0	0.61	0	0.98	0
Extracellular protein, putative	Cell envelope	EF0944	0	0.72	0	0	0
UDP-*N*-acetylglucosamine–*N*-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol *N*-acetylglucosamine transferase (*murG*)	Cell envelope	EF0994	0	0.64	0	0	0
Membrane protein, putative	Cell envelope	EF1384	0	0	0	0.79	0.81
Bacterial sugar transferase	Cell envelope	EF2177	0	0.75	0.71	0	0
Glycosyl transferase, group 1 family protein	Cell envelope	EF2890	0	0	0.60	0	0
Glycosyl transferase, group 1 family protein	Cell envelope	EF2891	0	0	0.69	0.83	0
Membrane protein	Cell envelope	EF3176	0.74	0	0	0	0
Adhesion lipoprotein	Cell envelope/cellular processes	EF3206	0	0	0	0.96	0.70
NAD-dependent epimerase/dehydratase family protein	Cell envelope/energy metabolism	EF2165	0	0	0.74	0	0.71
Cell division protein, FtsW/RodA/SpovE family	Cellular processes	EF1300	0	0	0	0.86	1.23
MsrC protein, putative	Cellular processes	EF1413	1.88	2.96	3.24	3.36	3.44
Beta-lactamase, putative	Cellular processes	EF1502	0	0	0.62	0	0
Competence protein (*comG3*)	Cellular processes	EF2044	0	0	0.65	0	0.76
Competence protein (*comG2*)	Cellular processes	EF2045	0	0	0	0.73	0.85
Competence protein (*comG1*)	Cellular processes	EF2046	0	0	0.73	0.90	0
Chromosome partitioning protein ParB	Cellular processes	EF3298	0	0	0	0	0.69
ATPase, ParA family	Cellular processes	EF3299	0	0	0	0	0.89
Drug resistance transporter, EmrB/QacA family protein	Cellular processes/transport and binding protein	EF0420	0	0	0.69	0.98	0
Multidrug resistance protein, putative	Cellular processes/transport and binding protein	EF1078	0	0.78	1.24	1.18	0.93
Drug resistance transporter, EmrB/QacA family protein	Cellular processes/transport and binding protein	EF1370	0	0	0.83	0.97	0.68
Cell division ABC transporter, permease protein FtsX, putative	Cellular processes/transport and binding protein	EF1760	0	0.80	1.13	0.72	0.69
Glycerol dehydrogenase, putative	Central intermediary metabolism	EF1358	0	0	0.66	0	0
Alkaline phosphatase (*phoZ*)	Central intermediary metabolism	EF2973	0.79	0.85	0.62	0.70	0
Heptaprenyl diphosphate synthase, component II, putative	Central intermediary metabolism	EF3260	0.83	0.84	0.84	0	0
Chromosomal replication initiator protein DnaA	DNA metabolism	EF0001	0	0	0	0	0.65
MutT/nudix family protein	DNA metabolism	EF0780	0	0.70	0	0.95	0
DNA repair exonuclease family protein	DNA metabolism	EF0972	0	0	0	1.01	0
DNA polymerase III, alpha subunit (*dnaE*)	DNA metabolism	EF1044	0	0.65	0	0.71	0
Endonuclease III (*nth*)	DNA metabolism	EF1155	0	0	0.66	0	0
ATP-dependent DNA helicase RecQ	DNA metabolism	EF1545	0	0.76	0.88	1.00	1.08
MutT/nudix family protein	DNA metabolism	EF1587	0	0	0	0	0.78
Site-specific recombinase, phage integrase family	DNA metabolism	EF1648	0	0	0	0.73	0.81
Endonuclease IV (*nfo*)	DNA metabolism	EF1736	0	0.61	0.75	0.67	0
Site-specific recombinase, phage integrase family	DNA metabolism	EF2043	0	0	0	0.66	0
Toprim domain protein	DNA metabolism	EF2305	0	0	0	0.76	0.76
A/G-specific adenine glycosylase (*mutY*)	DNA metabolism	EF2704	0	0.65	0.68	0	0
Regulatory protein RecX, putative	DNA metabolism	EF2705	0	0.65	0	0.94	0
Exonuclease	DNA metabolism	EF2736	0.91	0	0.97	0	0
ATP-dependent DNA helicase RecG	DNA metabolism	EF3113	0	0.60	0	0.74	0.69
Beta-phosphoglucomutase (*pgmB*)	Energy metabolism	EF0956	0	0	0	−0.90	1.27
Glycosyl hydrolase, family 65	Energy metabolism	EF0957	0	0	0	−1.12	1.36
Galactose-1-phosphate uridylyltransferase (*galT*)	Energy metabolism	EF1071	0	0	0.60	0	0
Glycosyl hydrolase, family 13	Energy metabolism	EF1347	0	0	0	−0.99	0.80
Glucan 1,6-alpha-glucosidase, putative	Energy metabolism	EF1348	0	0	0	−1.01	0.77
Glycosyl hydrolase, family 13	Energy metabolism	EF1349	0	0	0	−0.99	0.93
Glycosyl hydrolase, family 4	Energy metabolism	EF1411	0	0	0	0	0.87
Ferredoxin (*fer*)	Energy metabolism	EF1543	0	0	0.60	0.79	0
Glycosyl hydrolase, family 1	Energy metabolism	EF1606	0	0.69	0.70	0.70	0
Glycerate kinase, putative	Energy metabolism	EF2646	0	0	0	−1.65	0.70
3-Oxoacyl-(acyl-carrier-protein) synthase II (*fabF-1*)	Fatty acid and phospholipid metabolism	EF0283	0	0.83	0	0	0
Holo-(acyl-carrier-protein) synthase (*acpS*)	Fatty acid and phospholipid metabolism	EF0848	0	0	0.69	0.67	0.91
Cardiolipin synthetase, putative	Fatty acid and phospholipid metabolism	EF1608	0	0.71	0.63	0	0
1-Acyl-sn-glycerol-3-phosphate acyltransferase, putative	Fatty acid and phospholipid metabolism	EF2691	0	1.06	0.65	0.74	1.09
Enoyl-(acyl-carrier-protein) reductase II (*fabK*)	Fatty acid and phospholipid metabolism	EF2883	0	0.67	0.72	0	0.89
Fatty acid/phospholipid synthesis protein PlsX	Fatty acid and phospholipid metabolism	EF3112	0	0	0.64	0	0
TraE protein, putative	Other categories	EF2320	0	0	0.61	0.69	0

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TABLE 4—*Continued*

Protein encoded by gene	Cellular role(s)	ORF	Log$_2$ ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
ATP-dependent Clp protease, ATP-binding subunit ClpE	Protein fate	EF0706	0	0	0.79	0	0
DnaJ protein	Protein fate	EF1310	0	0	0	0	0.79
Heat shock protein HslV	Protein fate	EF1647	0	0	0	0.74	0
Signal recognition particle protein (*ffh*)	Protein fate	EF1700	0	0.74	0.80	0.81	1.05
Preprotein translocase, SecE subunit	Protein fate	EF2730	0	0	0.75	1.17	0.71
Signal peptidase I	Protein fate	EF3073	0	0.64	0	0	0.72
Ribosomal protein L18 (*rplR*)	Protein synthesis	EF0223	0	0.66	0.75	0	0
Ribosomal protein S5 (*rpsE*)	Protein synthesis	EF0224	0	0.58	0.64	0	0
Ribosomal protein L30 (*rpmD*)	Protein synthesis	EF0225	0	0.60	0.61	0	0
Ribosomal protein L15 (*rplO*)	Protein synthesis	EF0226	0	0.66	0.92	0	0
Ribosomal protein L27 (*rpmA*)	Protein synthesis	EF0970	0	0.73	0	0	0
Ribosomal protein S16 (*rpsP*)	Protein synthesis	EF1694	0	0	0.73	0	0
Ribosome recycling factor (*frr*)	Protein synthesis	EF2395	0	0	0.81	0.77	0
Translation elongation factor Ts (*tsf*)	Protein synthesis	EF2397	0	0.72	0.82	0	0
Ribosomal-protein-alanine acetyltransferase, putative	Protein synthesis	EF2473	0	0.63	0	0.75	0
Ribosomal-protein-alanine acetyltransferase, putative	Protein synthesis	EF2474	0	0	0	0	0.66
Tryptophanyl-tRNA synthetase (*trpS*)	Protein synthesis	EF2679	0	0.86	1.23	1.01	0.82
Ribosomal protein L33 (*rpmG-2*)	Protein synthesis	EF2731	0	0	0.62	0.99	1.17
Ribosomal protein S4 (*rpsD*)	Protein synthesis	EF3070	0	0	0	0.66	0
Dihydroorotate dehydrogenase (*pyrD-1*)	Purine/pyrimidine/nucleoside/nucleotide	EF0285	0	0.82	0.67	0	0
Dihydroorotate dehydrogenase (*pyrD-2*)	Purine/pyrimidine/nucleoside/nucleotide	EF1714	0	0.71	0	0	0
Dihydroorotase (*pyrC*)	Purine/pyrimidine/nucleoside/nucleotide	EF1718	0	0	0	0	0.66
Phosphoribosylaminoimidazole carboxylase, ATPase subunit (*purK-2*)	Purine/pyrimidine/nucleoside/nucleotide	EF2362	0	0	0	0	0.68
Xanthine phosphoribosyltransferase (*xpt*)	Purine/pyrimidine/nucleoside/nucleotide	EF2365	0	0	0.79	1.04	0
Uridylate kinase (*pyrH*)	Purine/pyrimidine/nucleoside/nucleotide	EF2396	0	0.76	0.68	0	0
Inosine-uridine preferring nucleoside hydrolase	Purine/pyrimidine/nucleoside/nucleotide	EF2587	0	0	0.79	0	0.90
2′,3′-Cyclic-nucleotide 2′-phosphodiesterase, putative	Purine/pyrimidine/nucleoside/nucleotide	EF2902	0	0	0	0	0.80
Transcriptional regulator, DeoR family	Regulatory functions	EF0719	0	0	0	1.78	0
Transcriptional regulator, PemK family	Regulatory functions	EF0850	0	0	0.67	0.84	0.95
DNA-binding response regulator	Regulatory functions	EF1050	0	0	0.76	0	0
Transcriptional regulator, Cro/CI family	Regulatory functions	EF1369	0	0.68	1.18	1.40	1.13
Transcription antiterminator BglG family protein	Regulatory functions	EF1515	0	0.69	0.62	0	0.89
Protease synthase and sporulation negative regulatory protein pai 1	Regulatory functions	EF1590	0	0.70	0.65	0.66	0.87
Sucrose operon repressor ScrR (*scrR-1*)	Regulatory functions	EF1604	0	0	0.65	1.05	0.75
Transcriptional regulator (*codY*)	Regulatory functions	EF1645	0	0	0.69	0.73	0.78
Transcriptional regulator, TetR family	Regulatory functions	EF2066	0	0	0	0.68	0
Phosphosugar-binding transcriptional regulator, putative	Regulatory functions	EF2259	0	0	0	0	0.70
Transcriptional regulator, Cro/CI family	Regulatory functions	EF2653	0	0	0	0	0.94
Transcriptional regulator, Cro/CI family	Regulatory functions	EF2852	0	0	0	0	0.93
Zinc-binding transcriptional regulator, Cro/CI family	Regulatory functions	EF3272	0	0.84	0	0	0
PTS system component, mannose-specific IIC component	Signal transduction	EF0021	0	0	0	−1.22	1.04
PTS system, mannose-specific IID component	Signal transduction	EF0022	0	0	0	−1.34	1.04
PTS system, fructose-specific family, IIABC component	Signal transduction	EF0717	0	0	0	0.90	0
PTS system, IIABC component	Signal transduction	EF0958	0	0	0	−1.27	0
Sensor histidine kinase	Signal transduction	EF1051	0	0	0.69	0	0
Sensor histidine kinase	Signal transduction	EF1261	0	0	0.65	0	0
PTS system, IIABC component	Signal transduction	EF1516	0	1.13	1.44	1.06	1.06
PTS system, IIC component	Signal transduction	EF2978	0	0	0	0	0.66
PTS system, IIB component	Signal transduction	EF2979	0	0.69	0.72	0	0.94
ATP-dependent RNA helicase, DEAD/DEAH box family	Transcription	EF0846	0	0	0	0.68	0
Transcription termination factor Rho	Transcription	EF1170	0	0	0.68	0	0.84
ATP-dependent helicase, DEAH-box family, putative	Transcription	EF3214	0	0.62	0	0	0
Iron compound ABC transporter, substrate-binding protein	Transport and binding protein	EF0188	0	0	0	0	0.82
Na^+/H^+ antiporter (*nhaC-2*)	Transport and binding protein	EF0636	0	0.64	0	1.01	0
Sodium/dicarboxylate symporter family protein	Transport and binding protein	EF0744	0	1.44	1.20	0.87	0.71
Amino acid ABC transporter, ATP-binding protein	Transport and binding protein	EF0760	0	0	0.63	0	0
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF0789	0	0.70	1.08	1.09	0
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF0790	0	0	0.75	0.96	0
Potassium uptake protein	Transport and binding protein	EF0872	0	0.65	0	0	0
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF0941	0	0	0	0.72	0
Amino acid permease family protein	Transport and binding protein	EF1103	0	0	0.84	0.93	0.66
ABC transporter, ATP-binding protein	Transport and binding protein	EF1255	0.94	0.75	0	0	0
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF1341	0	0.69	0	0	0
Sugar ABC transporter, permease protein	Transport and binding protein	EF1344	0	0.62	0	−0.93	1.25
Cadmium-translocating P-type ATPase	Transport and binding protein	EF1400	0.65	0.71	0.86	0.78	1.09
V-type ATPase, subunit B	Transport and binding protein	EF1499	0	0	0	0	0.79
Iron compound ABC transporter, ATP-binding protein	Transport and binding protein	EF1639	0	0	0.62	0	0.95
Iron compound ABC transporter, permease protein	Transport and binding protein	EF1640	0	0.60	0.74	0.67	1.04

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TABLE 4—*Continued*

Protein encoded by gene	Cellular role(s)	ORF	Log$_2$ ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
ABC transporter, ATP-binding/permease protein, MDR family	Transport and binding protein	EF1732	0	1.18	0.86	0.78	1.69
ABC transporter, ATP-binding/permease protein, MDR family	Transport and binding protein	EF1733	0	1.13	0.95	0.81	1.54
Amino acid permease family protein	Transport and binding protein	EF2047	0	0	0.90	1.21	0
Transport ATP-binding protein CydD, putative	Transport and binding protein	EF2058	0	0	0.68	0	0
Transport ATP-binding protein CydC, putative	Transport and binding protein	EF2059	0	0	0.61	0	0.83
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF2226	0	0	0	1.00	0.70
Xanthine permease	Transport and binding protein	EF2364	0.73	0	0.97	1.07	0
Amino acid permease	Transport and binding protein	EF2377	0	0.63	0.74	0.92	0
ABC transporter, permease protein	Transport and binding protein	EF2485	0	0	0.62	0	0
AzlC protein	Transport and binding protein	EF2509	0	0	0	0.75	0
Glycine betaine/L-proline transport ATP binding subunit	Transport and binding protein	EF2641	0	0	0	1.30	0
Glycine betaine/L-proline ABC transporter, glycine betaine/L-proline-binding/permease protein	Transport and binding protein	EF2642	0	0	0.82	1.75	0.86
Permease, GntP family	Transport and binding protein	EF2647	0	0	0	−2.31	1.32
Spermidine/putrescine ABC transporter	Transport and binding protein	EF2649	0	0	0	0	1.05
Spermidine/putrescine ABC transporter	Transport and binding protein	EF2650	0	0	0	0	0.92
Spermidine/putrescine ABC transporter	Transport and binding protein	EF2651	0	0	0	0	0.94
Spermidine/putrescine ABC transporter	Transport and binding protein	EF2652	0	0	0	0	0.67
ABC transporter, ATP-binding protein	Transport and binding protein	EF2720	0.93	0.69	1.12	0.86	0.80
ABC transporter, ATP-binding protein	Transport and binding protein	EF2769	0	0	−0.60	0	0.72
Ion transporter, putative	Transport and binding protein	EF2854	0	0	0	0	0.72
Potassium uptake protein TrkA	Transport and binding protein	EF2910	0	0.65	0.84	0.86	1.15
ABC transporter, ATP-binding protein	Transport and binding protein	EF2986	0	0	0.62	0	0
Cytosine/purines, uracil, thiamine, allantoin permease family protein	Transport and binding protein	EF3000	0	0	0	0	0.82
Formate/nitrite transporter family protein	Transport and binding protein	EF3069	0.82	0.87	0	0.73	0.66
Iron compound ABC transporter, permease protein	Transport and binding protein	EF3085	0	0	0	0	0.69
ABC transporter, permease protein	Transport and binding protein	EF3199	0	0	0.98	0	1.26
ABC transporter, ATP-binding protein	Transport and binding protein	EF3200	0	0.70	0.86	0	0.94
ABC transporter, permease protein	Transport and binding protein	EF3208	0	0.71	0.98	0	0
Oxidoreductase, DadA family	Unknown function	EF0414	0	0	0	0.72	0
LysM domain protein	Unknown function	EF0443	0.85	1.21	1.30	1.03	0
Glyoxalase family protein	Unknown function	EF0666	0	0.71	0	0	0
Methyltransferase, putative	Unknown function	EF0691	0	0	0	0.75	0
Type 2 phosphatidic acid phosphatase family protein	Unknown function	EF0796	0	0	0	0.69	0
DegV family protein	Unknown function	EF1191	0	0	0	0	0.77
Metallo-beta-lactamase YycJ	Unknown function	EF1197	0	0	0.90	0.93	0.92
GTP-binding protein	Unknown function	EF1527	0	0	0.77	0.68	0.74
GTPase, putative	Unknown function	EF1549	0	0	0.71	0	0
Acetyltransferase, GNAT family	Unknown function	EF1589	0	0	0	0	1.00
LacX protein, putative	Unknown function	EF1644	0	0.64	0.70	0.81	0
Lipase/acylhydrolase, putative	Unknown function	EF1683	0	0	0.69	0	0.67
GTP-binding protein	Unknown function	EF1916	0.99	1.02	1.39	1.09	1.18
GTP-binding protein LepA	Unknown function	EF2352	0	0	0.63	1.04	0
Diacylglycerol kinase catalytic domain protein	Unknown function	EF2661	0	0	0	0.86	0.92
Oxidoreductase, pyridine nucleotide-disulfide family	Unknown function	EF2899	0	0.75	0.73	1.06	1.02
Glucose-inhibited division protein B (*gidB*)	Unknown function	EF3300	0	0	0	0	0.67

[a] Gene names in parentheses.

for the ability of V583 to survive erythromycin treatment. Their influence must, however, be limited, since the growth of V583 is so retarded by erythromycin.

It was expected that the exposure of V583 to erythromycin would affect genes involved in protein synthesis, despite the expression of *ermB*. The induction of eight genes encoding ribosomal proteins (r-proteins), along with two r-protein-Ala-acetyltransferases, might be an indication that the overproduction of ribosomal proteins is one way to evade the effect of erythromycin. To balance the number and function of the ribosomes, the cells may have to compensate by up-regulation of these genes. Five of the induced r-protein genes and one of the r-protein-Ala-acetyltransferase genes are induced after 15 min of growth, i.e., their induction is a quick response. Closely related to the known target of erythromycin in sensitive cells is the fact that eight tRNA synthetase genes are repressed. The repression of tRNA synthetase genes may be seen as a logical consequence of the reduced ability of a cell's capacity to synthesize proteins, when an antibiotic binds a ribosomal subunit. The up-regulation of genes encoding r-proteins and two translation elongation factors, as well as down-regulation of tRNA synthetase genes, in response to translation inhibitors, has been noticed also by other authors (5, 19, 28).

Although the V583 cells are defined as resistant to erythromycin and will survive in the presence of relatively high levels of erythromycin, the cell growth is impaired, and, as shown above, the transcriptional activities are greatly altered. The differential transcription reflects the effect of erythromycin as well as the adaptation of V583 to the general stress. The retarded growth follows as a consequence of a slow-down of

TABLE 5. Log_2 ratios of genes whose transcription decreased at one or more of the five time points (altogether 90 min) at which the effect of erythromycin treatment was studied, sorted by functional category

Protein encoded by gene	Cellular role(s)	ORF	Log_2 ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
Ornithine carbamoyltransferase (*argF-1*)[a]	Amino acid biosynthesis	EF0105	0	0	−1.37	−2.81	−2.19
Cysteine synthase B, putative	Amino acid biosynthesis	EF0289	0	0	0	0	−0.75
Cystathionine beta-lyase (*metC*)	Amino acid biosynthesis	EF0290	0.71	0	0	0	−1.05
Arginine repressor (*argR*)	Amino acid biosynthesis	EF0676	0	0	0	−0.94	0
Aspartate aminotransferase, putative	Amino acid biosynthesis	EF0891	−1.00	−1.08	−0.96	−0.74	−1.03
Phosphomevalonate kinase	Biosynthesis of cofactors/prosthetic groups/carriers	EF0902	−0.75	−0.73	0	0	0
Thiamin biosynthesis ApbE, putative	Biosynthesis of cofactors/prosthetic groups/carriers	EF1225	0	0	−0.92	0	0
NH_3-dependent NAD^+ synthetase (*nadE*)	Biosynthesis of cofactors/prosthetic groups/carriers	EF2625	0	0	0	0	−0.88
Phosphomethylpyrimidine kinase (*thiD*)	Biosynthesis of cofactors/prosthetic groups/carriers	EF2775	0	−0.83	−0.95	0	0
Thiamine-phosphate pyrophosphorylase (*thiE*)	Biosynthesis of cofactors/prosthetic groups/carriers	EF2776	0	−0.75	−0.76	0	0
Hydroxyethylthiazole kinase, putative	Biosynthesis of cofactors/prosthetic groups/carriers	EF2777	0	−0.63	−0.72	0	0
Adhesion lipoprotein	Cell envelope	EF0055	0	0	−0.84	0	0
Glycosyl hydrolase, family 20	Cell envelope	EF0114	0	0	0	−0.87	0
Surface exclusion protein, putative	Cell envelope	EF0146	−0.84	−0.85	−0.72	0	0
Chitinase, family 2	Cell envelope	EF0361	0	0	0	−0.86	−0.86
Chitin binding protein, putative	Cell envelope	EF0362	0	0	0	−1.09	−0.96
LemA protein	Cell envelope	EF0468	0	0	−1.11	0	0
Penicillin-binding protein, putative	Cell envelope	EF0746	0	−0.73	−1.39	0	−0.87
Gram-positive anchor protein, putative	Cell envelope	EF0775	−0.95	−1.10	−0.81	−0.67	−0.91
Membrane protein, putative	Cell envelope	EF1027	0	0	−0.60	0	0
Pheromone cAM373 precursor lipoprotein	Cell envelope	EF1340	0	−0.79	0	0	0
Coccolysin	Cell envelope	EF1818	0	0	0	−0.85	0
Endocarditis specific antigen	Cell envelope	EF2076	0	−0.76	−0.77	−1.12	−1.51
DltD protein	Cell envelope	EF2746	0	0	−0.65	0	0
D-Alanyl carrier protein (*dltC*)	Cell envelope	EF2747	−0.86	−0.79	−1.22	0	0
Basic membrane protein DtlB	Cell envelope	EF2748	0	0	−0.65	0	0
D-Alanine-activating enzyme, putative	Cell envelope	EF2749	0	0	−0.74	0	0
Sortase family protein	Cell envelope	EF3056	0	0	−0.77	−1.56	−1.32
Rod shape-determining protein MreD	Cell envelope	EF3061	0	0	0	−0.93	−1.28
Rod shape-determining protein MreC	Cell envelope	EF3062	0	0	0	−1.01	−1.21
Pheromone cAD1 precursor lipoprotein	Cell envelope	EF3256	0	−0.68	−0.73	0	0
Gls24 protein	Cellular processes	EF0079	0	−1.04	−0.97	−1.16	−1.39
Gls24 protein	Cellular processes	EF0080	0	−0.98	−1.20	−1.28	−1.87
Regulatory protein, putative (*pfoR*)	Cellular processes	EF0097	0	0	−0.78	0	0
Superoxide dismutase, Mn (*sodA*)	Cellular processes	EF0463	0	−0.65	0	0	0
Low-temperature requirement C protein, putative	Cellular processes	EF0639	0	0	0	0.96	−1.21
Polysaccharide lyase, family 8	Cellular processes	EF0818	0	−0.70	−0.89	0	−1.24
Universal stress protein family	Cellular processes	EF1058	0	−1.20	−1.28	−1.44	−2.27
Streptomycin 3-adenylyltransferase, putative	Cellular processes	EF1076	−0.71	−0.97	−0.64	−0.88	−0.77
Autoinducer-2 production protein LuxS	Cellular processes	EF1182	0	−0.68	−0.66	0	−0.99
Cold shock protein CspC	Cellular processes	EF1991	0	−0.98	0	0	0
Negative regulator of genetic competence MecA, putative	Cellular processes	EF2677	0	0	0	0	−0.66
Alkyl hydroperoxide reductase, C subunit (*ahpC*)	Cellular processes	EF2739	0	−0.70	−0.68	−0.68	−0.68
Dps family protein	Cellular processes	EF3233	0	0	−0.70	0	0
Nucleotidyltransferase family protein	Central intermediary metabolism	EF0137	0	−0.69	−0.87	0	−0.77
Hydrolase, alpha/beta hydrolase fold family	Central intermediary metabolism	EF1028	0	0	−0.70	0	0
6-Aminohexanoate-cyclic-dimer hydrolase, putative	Central intermediary metabolism	EF1033	0	0	0	−0.95	0
Microcompartment protein	Central intermediary metabolism	EF1623	−0.66	−0.76	0	0	0
Chromosomal replication initiator protein DnaA	DNA metabolism	EF0001	0	0	0	0	0.65
Thermonuclease precursor (*nuc-1*)	DNA metabolism	EF0511	0	0	0	0	−0.70
Exonuclease RexB	DNA metabolism	EF1112	0	−0.67	−0.64	0	0
MutT/nudix family protein	DNA metabolism	EF1141	0	−0.58	−0.59	0	0
L-Serine dehydratase, iron-sulfur-dependent, beta subunit (*sdhB-1*)	Energy metabolism	EF0098	0	0	−1.08	0	0
L-Serine dehydratase, iron-sulfur-dependent, alphasubunit (*sdhA-1*)	Energy metabolism	EF0099	0	0	−0.67	0	0
Arginine deiminase (*arcA*)	Energy metabolism	EF0104	0	−0.65	−1.73	−3.16	−2.55
Carbamate kinase (*arcC-1*)	Energy metabolism	EF0106	0	0	−0.92	−1.99	−1.26
Phosphoglycerate mutase 1 (*gpm*)	Energy metabolism	EF0195	0	0	−0.62	0	−0.65
Aldehyde dehydrogenase	Energy metabolism	EF0253	−0.74	−0.82	−0.90	−0.72	−0.91
L-Lactate dehydrogenase (*ldh-2*)	Energy metabolism	EF0641	0	0	0	−0.78	−0.75
Phosphoglucomutase/phosphomannomutase family protein	Energy metabolism	EF0677	0	0	0	−1.16	0

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TABLE 5—*Continued*

Protein encoded by gene	Cellular role(s)	ORF	Log$_2$ ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
Aldehyde-alcohol dehydrogenase (*adhE*)	Energy metabolism	EF0900	0	0	−0.77	0	0
Methylglyoxal synthase (*mgsA*)	Energy metabolism	EF0939	−0.88	−1.10	−0.96	−0.85	−0.96
Beta-phosphoglucomutase (*pgmB*)	Energy metabolism	EF0956	0	0	0	−0.90	1.27
Glycosyl hydrolase, family 65	Energy metabolism	EF0957	0	0	0	−1.12	1.36
Glycosyl hydrolase, family 1	Energy metabolism	EF1020	0	0	0	−1.93	0
Aldose 1-epimerase (*galM*)	Energy metabolism	EF1068	−0.84	−1.07	−0.72	0	−0.75
Iron-sulfur cluster binding protein	Energy metabolism	EF1109	0	0	−0.78	0	0
NADH peroxidase (*npr*)	Energy metabolism	EF1211	0	0	−0.59	0	−0.73
Glycosyl hydrolase, family 13	Energy metabolism	EF1347	0	0	0	−0.99	0.80
Glucan 1,6-alpha-glucosidase, putative	Energy metabolism	EF1348	0	0	0	−1.01	0.77
Glycosyl hydrolase, family 13	Energy metabolism	EF1349	0	0	0	−0.99	0.93
Glyceraldehyde 3-phosphate dehydrogenase (*gap-1*)	Energy metabolism	EF1526	0	0	0	0	−0.98
Pyruvate formate-lyase activating enzyme (*pflA*)	Energy metabolism	EF1612	0	0	0	−0.73	0
Formate acetyltransferase (*pflB*)	Energy metabolism	EF1613	0	0	0	−0.86	0
Alcohol dehydrogenase, zinc containing	Energy metabolism	EF1826	0	0	−0.84	−0.70	−1.01
Mannose-6-phosphate isomerase, class I (*manA*)	Energy metabolism	EF2589	0	0	0	−0.69	0
Glycerate kinase, putative	Energy metabolism	EF2646	0	0	0	−1.65	0.70
Endo-beta-*N*-acetylglucosaminidase	Energy metabolism	EF2863	0	0	0	−1.39	0
Ribokinase (*rbsK*)	Energy metabolism	EF2961	0	0	0	−1.32	−1.16
Glycosyl hydrolase, family 65	Energy metabolism	EF3157	0	0	0	−1.34	0
Lipase/acylhydrolase	Fatty acid and phospholipid metabolism	EF0169	0	0	0	0	−1.00
IS*1216*, transposase	Other categories	EF0514	0	0	−0.63	−0.81	−0.81
Transposase, putative	Other categories	EF0913	0	−0.69	0	0	0
Aminopeptidase C (*pepC*)	Protein fate	EF0302	0	0	0	0	−0.82
Rotamase family protein	Protein fate	EF0685	0	−0.60	−0.75	−0.80	−1.01
Preprotein translocase, YajC subunit, putative	Protein fate	EF0897	0	0	0	0	−0.83
Signal peptidase I	Protein fate	EF1111	0	−0.66	0	0	0
Serine proteinase, V8 family	Protein fate	EF1817	0	0	0	−0.86	0
Serine protease DO (*htrA*)	Protein fate	EF3027	0	0	0	−0.67	0
Peptidase, M20/M25/M40 family	Protein fate	EF3178	0	0	−0.62	−0.80	−1.32
Cysteinyl-tRNA synthetase (*cysS*)	Protein synthesis	EF0045	0	0	−0.59	0	0
RNA methyltransferase, TrmH family	Protein synthesis	EF0047	0	−0.60	−0.61	0	0
Tyrosyl-tRNA synthetase (*tryS-1*)	Protein synthesis	EF0633	0	0	0	−0.67	−1.61
Glutamyl-tRNA (Gln) amidotransferase, C subunit (*gatC*)	Protein synthesis	EF0724	0	−0.65	−0.68	0	0
Ribosomal protein L25 (*rplY*)	Protein synthesis	EF0820	0	0	0.68	−1.01	−2.07
Alanyl-tRNA synthetase (*alaS*)	Protein synthesis	EF1379	0	0	0	0	−0.69
Ribosomal subunit interface protein (*yfiA*)	Protein synthesis	EF1764	0	−0.78	0	0	0
Aspartyl-tRNA synthetase (*aspS*)	Protein synthesis	EF1970	0	0	0	0	−0.77
Tryptophanyl-tRNA synthetase	Protein synthesis	EF2228	0	0	−0.62	0	0
Ribosomal protein L33 (*rpmG-3*)	Protein synthesis	EF2856	0	−0.98	0	0	0
Threonyl-tRNA synthetase (*thrS*)	Protein synthesis	EF2858	0	−0.72	−0.64	−0.90	−1.20
Valyl-tRNA synthetase (*valS*)	Protein synthesis	EF2931	0	0	0	−0.67	0
Seryl-tRNA synthetase (*serS-2*)	Protein synthesis	EF3292	0	0	0	−0.67	−0.83
Ribosomal protein L34 (*rpmH*)	Protein synthesis	EF3333	0	−0.61	0	0	0
Adenylosuccinate synthetase (*purA*)	Purine/pyrimidine/nucleoside/nucleotide	EF0014	0	−0.73	−0.73	0	−0.70
Phosphopentomutase (*deoB*)	Purine/pyrimidine/nucleoside/nucleotide	EF0185	0	0	−0.69	0	0
Ribonucleoside-diphosphate reductase 2, beta subunit (*nrdF*)	Purine/pyrimidine/nucleoside/nucleotide	EF0470	0	0	0	−0.80	0
Ribonucleoside-diphosphate reductase 2, alpha subunit (*nrdE*)	Purine/pyrimidine/nucleoside/nucleotide	EF0471	0	0	0	−0.69	−0.79
Ribonucleoside-diphosphate reductase 2, NrdH-redoxin (*nrdH*)	Purine/pyrimidine/nucleoside/nucleotide	EF0473	0	−0.59	0	−0.80	−0.83
Aspartate carbamoyltransferase (*pyrB*)	Purine/pyrimidine/nucleoside/nucleotide	EF1719	0	−0.63	0	0	0
Pyrimidine operon regulatory protein PyrR (*pyrR*)	Purine/pyrimidine/nucleoside/nucleotide	EF1721	0	−0.82	0	0	0
Inosine-uridine-preferring nucleoside hydrolase	Purine/pyrimidine/nucleoside/nucleotide	EF1921	0	0	0	−0.92	0
Anaerobic ribonucleoside-triphosphate reductase (*hrdD*)	Purine/pyrimidine/nucleoside/nucleotide	EF2754	0	0	0	−0.96	−0.83
Anaerobic ribonucleoside-triphosphate reductase activating protein (*nrdG*)	Purine/pyrimidine/nucleoside/nucleotide	EF2755	0	0	0	−0.96	−1.14
Transcriptional regulator, Cro/CI family	Regulatory functions	EF0129	0	−0.69	−0.73	0	0
Transcriptional regulator, Cro/CI family	Regulatory functions	EF0869	0	−0.64	0	0	0
Transcriptional regulator, DeoR family	Regulatory functions	EF1124	−0.79	−0.84	−0.68	0	−0.71
Transcriptional regulator, LysR family	Regulatory functions	EF1303	0	0	−0.87	0	0
Transcriptional regulator, Cro/CI family	Regulatory functions	EF2142	−0.67	0	−0.67	0	0
Transcriptional regulator, Cro/CI family	Regulatory functions	EF2338	0	−0.79	−0.60	0	−0.88
Transcriptional regulator, Cro/CI family	Regulatory functions	EF2544	0	−0.75	0	0	0
Transcriptional regulator	Regulatory functions	EF2703	0	−0.65	−0.84	0	0
Transcriptional regulator, AraC family	Regulatory functions	EF2711	0	0	0	−1.00	0
Transcriptional antiterminator, bglG family	Regulatory functions	EF2966	0	0	0	−1.08	−1.28
DNA-binding response regulator	Regulatory functions	EF3289	0	0	0	0	−0.84

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TABLE 5—*Continued*

Protein encoded by gene	Cellular role(s)	ORF	Log$_2$ ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
PTS system, mannose-specific IIAB component	Signal transduction	EF0020	0	0	0	−0.88	0
PTS system, mannose-specific IIC component	Signal transduction	EF0021	0	0	0	−1.22	1.04
PTS system, mannose-specific IID component	Signal transduction	EF0022	0	0	0	−1.34	1.04
PTS system, mannitol-specific IIBC component	Signal transduction	EF0411	0	0	0	0	−0.73
PTS system, IID component	Signal transduction	EF0553	0	0	0	−0.73	0
PTS system, IIABC component	Signal transduction	EF0958	0	0	0	−1.27	0
PTS system, IIB component	Signal transduction	EF1012	0	0	0	−2.91	0
PTS system, IIB component	Signal transduction	EF1017	0	0	0	−2.75	0
PTS system, IIA component	Signal transduction	EF1018	0	0	0	−2.68	0
PTS system, IIC component	Signal transduction	EF1019	0	0	0	−3.28	0
Response regulator	Signal transduction	EF1336	0	−0.79	−0.60	0	0
Response regulator	Signal transduction	EF1633	−0.80	−1.06	−0.92	−0.80	−0.86
PTS system, IIA component	Signal transduction	EF1801	0	0	−0.69	0	0
PTS system, IIBC component	Signal transduction	EF2213	0	0	0	−1.83	0
PTS system, IID component	Signal transduction	EF3029	0	0	−0.66	0	0
Sensor histidine kinase	Signal transduction	EF3290	0	0	0	0	−0.97
RNA polymerase sigma-54 factor (*rpoN*)	Transcription	EF0782	0	−0.76	−0.64	0	0
RNA polymerase sigma-70 factor, ECF subfamily	Transcription	EF3180	0	0	−1.12	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF0056	0	0	−0.75	0	0
ABC transporter, permease protein	Transport and binding protein	EF0179	0	−0.59	0	0	0
Amino acid ABC transporter, amino acid-binding/ permease protein	Transport and binding protein	EF0247	0	0	−0.68	0	0
Na^+/H^+ antiporter (*nhaC-1*)	Transport and binding protein	EF0402	0	0	0	−1.10	−0.98
Cation ABC transporter, permease protein	Transport and binding protein	EF0576	0	0	−0.62	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF0793	−0.85	−0.92	−0.86	0	−0.75
Amino acid ABC transporter, ATP-binding protein	Transport and binding protein	EF0892	0	−0.61	0	0	0
Peptide ABC transporter, peptide-binding protein	Transport and binding protein	EF0907	0	0	0	−0.67	−1.39
ABC transporter, ATP-binding/TOBE domain protein	Transport and binding protein	EF0938	0	0	0	−1.39	0
$Mn2^+/Fe2^+$ transporter, NRAMP family	Transport and binding protein	EF1057	0	−1.13	−1.12	−1.23	−1.78
ABC transporter, ATP-binding/permease protein	Transport and binding protein	EF1100	−0.76	−0.86	−0.70	0	0
Phosphotransferase enzyme II, B component SgaB (*sgaB*)	Transport and binding protein	EF1128	−0.86	−0.74	0	0	0
ABC transporter, permease protein	Transport and binding protein	EF1254	0	0	0	0	−0.88
Cation-transporting ATPase, E1-E2 family	Transport and binding protein	EF1268	0	−0.64	−0.72	0	0
Magnesium-translocating P-type ATPase	Transport and binding protein	EF1304	−0.84	−1.01	−1.31	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF1331	0	−0.79	−0.69	0	0
Sugar ABC transporter, permease protein	Transport and binding protein	EF1344	0	0.62	0	−0.93	1.25
Sugar ABC transporter, sugar-binding protein	Transport and binding protein	EF1345	0	0	0	−1.39	0
Magnesium-translocating P-type ATPase	Transport and binding protein	EF1352	0	0	−0.62	0	0
V-type ATPase, subunit F	Transport and binding protein	EF1492	0	0	−0.86	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF1673	−0.65	0	−0.82	0	0
Uracil permease	Transport and binding protein	EF1720	0	−0.60	0	0	0
Phosphate ABC transporter, phosphate-binding protein	Transport and binding protein	EF1759	0	0	−0.61	0	0
ABC transporter, permease protein, putative	Transport and binding protein	EF2049	0	0	−1.18	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF2050	0	0	−1.16	0	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF2074	0	0	0	−0.70	−0.76
ABC transporter, permease protein	Transport and binding protein	EF2081	0	0	0	−0.68	0
ABC transporter, ATP-binding protein	Transport and binding protein	EF2394	0	0	−0.61	0	0
Permease, GntP family	Transport and binding protein	EF2647	0	0	0	−2.31	1.32
ABC transporter, ATP-binding protein	Transport and binding protein	EF2769	0	0	−0.60	0	0.72
Ribose uptake protein, putative	Transport and binding protein	EF2959	0	0	0	−1.19	−0.77
Ribose transporter protein RbsD	Transport and binding protein	EF2960	0	0	−0.70	−1.48	−1.30
Peptide ABC transporter, peptide-binding protein	Transport and binding protein	EF3106	0	0	0	−1.88	−1.13
Peptide ABC transporter, permease protein	Transport and binding protein	EF3107	0	0	0	−1.75	−0.82
Peptide ABC transporter, permease protein	Transport and binding protein	EF3108	0	0	0	−2.19	−0.87
Peptide ABC transporter, ATP-binding protein	Transport and binding protein	EF3109	0	0	0	−1.33	0
Peptide ABC transporter, ATP-binding protein	Transport and binding protein	EF3110	0	0	0	−1.65	−0.86
Cytosine permease, putative	Transport and binding protein	EF3277	−0.80	−0.74	0	0	0
AMP-binding family protein	Unknown function	EF0452	0	0	−0.61	0	0
OsmC/Ohr family protein	Unknown function	EF0453	0	0.95	−1.05	−1.16	−1.67
Acetyltransferase, GNAT family	Unknown function	EF0678	0	0	0	−1.32	0
Oxidoreductase, aldo/keto reductase 2 family	Unknown function	EF0877	0	0	0	−0.67	0
Pentapeptide repeat family protein	Unknown function	EF0905	−0.81	−1.04	−0.92	0	−0.75
N-acyl-D-amino-acid deacylase family protein	Unknown function	EF1062	−0.92	−1.02	0	0	0
Acetyltransferase, GNAT family	Unknown function	EF1075	−0.87	−0.97	−0.79	0	−0.78
Acetyltransferase, GNAT family	Unknown function	EF1077	−0.64	−0.92	−0.64	0	0
YkgG family protein	Unknown function	EF1110	−0.67	−0.71	0	0	0
Oxidoreductase, aldo/keto reductase family	Unknown function	EF1138	0	0	0	0	−0.77
HesA/MoeB/ThiF family protein	Unknown function	EF1329	0	−0.58	−0.64	0	0
CelC-related protein	Unknown function	EF2440	0	0	0	−1.31	0
PDZ domain protein	Unknown function	EF2450	0	0	0	0	−0.68
HD domain protein	Unknown function	EF2470	0	0	0	0	−0.80

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TABLE 5—*Continued*

Protein encoded by gene	Cellular role(s)	ORF	Log$_2$ ratio at:				
			*t*0	*t*15	*t*30	*t*60	*t*90
Aldehyde oxldoreductase, putative	Unknown function	EF2570	0	0	−0.80	0	0
Hydrolase, haloacid dehalogenase-like family	Unknown function	EF2681	0	−0.86	0	0	0
Oxidoreductase, Gfo/Idh/MocA family	Unknown function	EF2734	0	0	0	0	−0.76
Thioredoxin reductase/glutathione-related protein	Unknown function	EF2738	0	0	−0.62	0	0
DNA-binding protein, putative	Unknown function	EF2933	0	0	−0.69	0	0
Glyoxalase family protein	Unknown function	EF3092	0	0	0	−0.71	0
Hydrolase, haloacid dehalogenase-like family	Unknown function	EF3158	0	0	0	−1.16	−0.72
Cell-envelope-associated acid phosphatase	Unknown function	EF3245	0	0	−0.78	0	0
Gp35	Viral functions	EF2143	0	−0.59	−0.59	0	0

[a]Gene names in parentheses.

many cellular activities when important processes, such as protein synthesis, apparently are repressed. In our experiments, we found that a lower number of genes was induced than repressed at all time points except for *t*90 (see Tables 1 to 5). At *t*90, it is tempting to look upon the altered transcriptional activity in the stressed cells as a consequence of an adaptation to the presence of erythromycin. At this point, the cells may have adapted to the stressing conditions and may have overcome the critical effects of the drug.

Ng et al. (19) report the induction of several genes related to purine biosynthesis in *Streptococcus pneumoniae* R6 exposed to various translation inhibitors, including erythromycin. This effect on purine synthesis is not clear for V583; only *purK* is up-regulated, and *purA* is down-regulated. Three genes related to pyrimidine biosynthesis (*pyrD-1*, *pyrD-2*, and *pyrC*) are induced, however. Similarly to what was found with *S. pneumoniae* R6 (19), the purine salvage gene *xpt* had a relative increase in transcription in V583 in response to the erythromycin treatment. Therefore, it looks as if the responses of the two relatively closely related bacteria *E. faecalis* and *S. pneumoniae* to erythromycin have common themes, but most of the transcriptional responses appear distinct.

Transport and binding proteins represent the second most dominant group of differentially expressed genes (Tables 1 to 5). This group of genes appears to be heavily influenced by various stressors in many bacteria (see, e.g., references 19, 21, and 26). The altered transcription of transport and binding proteins indicates that altered transport is an important part of general stress response mechanisms. The large number of differentially expressed genes encoding ABC transporters and permeases emphasizes the importance of such genes in stress responses.

Another interesting group of induced genes are those related to fatty acid and phospholipid metabolism (six genes). As mentioned briefly above, erythromycin resistance in gram-negative bacteria is usually mediated by a low permeability of the outer membrane to the hydrophobic macrolide. One may speculate as to whether a slightly altered cell membrane may have contributed also to the erythromycin adaptation in the gram-positive V583 cells.

In time course experiments like ours, one should draw attention to genes that are differentially expressed at all time points examined. Our results showed that 14 genes were regulated, 4 up and 10 down, at all five time points. Among these, the most interesting gene is EF1413, which encodes a putative MsrC protein, although the sequence identity with the described MsrC is not more than ca. 40%. EF1413 was up-regulated at all time points and showed the strongest differential expression of all genes on the microarray (Table 4). EF1413 was not differentially expressed in experiments with chloramphenicol treatment of V583 (Å. Aakra, unpublished results). The *msrC* is distributed in many isolates of *E. faecium* and has even been suggested to be specific for this species (23, 25). Comparative genomic hybridizations with five *E. faecalis* strains indicate the presence of the putative *msrC* in these genomes, as well (Aakra, unpublished). Singh et al. (25) found that the *msrC* conferred an increased resistance to macrolides among *E. faecium* isolates. Our observation of strong induction of EF1413 (log$_2$ ratio of 1.88 at *t*0; log$_2$ ratio of 3.44 at *t*90) in erythromycin exposed *E. faecalis* V583 support the involvement of an MrsC homologue in macrolide resistance in this species as well.

EF1732 and EF1733 encode two ABC transporters belonging to the MDR family. These two genes were up-regulated at all time points except *t*0. (In a similar study, the same two genes were also strongly up-regulated in response to chloramphenicol treatment [Aakra, unpublished].) Taken together, these results make it tempting to speculate that the efflux of erythromycin by proteins encoded by EF1413, EF1732, and EF1733 is an important part of the survival mechanism for V583 when exposed to this antibiotic.

At *t*0, i.e., immediately after the addition of erythromycin, 18 genes were up-regulated and 56 genes were down-regulated, which were considerably fewer genes than those regulated at the other time points under study. It must be assumed that the genes that show an immediate response also are crucial for the growth and survival of erythromycin-exposed V583 cells.

Several studies on stress responses (and genes involved therein) of *E. faecalis* have been published (e.g., see references 1, 8, 9, 14, and 15). Some papers focus on two-component signal transduction pathways, which commonly are related to bacterial stress (10, 15). A few of the genes found to have a significantly differential expression in our work have been discussed in these papers, e.g., genes encoding the Gls24 proteins (EF0079 and EF0080), two histidine kinases and their cognate response regulators (EF3290 and EF3289, EF1051 and EF1050), L-lactate dehydrogenase (EF0641), L-serine dehydratase (EF0098, EF0099), carbamate kinase (EF0106), and superoxide dismutase (EF0463). In this work, we found that the *gls24* genes (EF0079, EF0080) were repressed at all time points except *t*0, which is in contrast with the hypotheses of Giard et al. (9) that these genes are induced under stress. The

repression of the *gls24* genes was also found in our study of the transcriptional responses of V583 to chloramphenicol treatment (Aakra, unpublished). Similarly to Giard et al. (9), the EF0604 which encodes another Gls24 protein was not found to be differentially expressed at any time point of our study. Therefore, the role of Gls24 in stress responses in *E. faecalis* is not obvious. Regarding the two-component signal transduction pathways, the histidine kinase (HK) EF3290 and the cognate response regulator (RR) EF3289 were both down-regulated at *t*90. The function of this HK-RR pair is not known (10), and it remains to be seen whether the repression of EF3290/EF3289 at *t*90 in this study is stress related. The other pair of differentially expressed HK-RR (EF1051/EF1050) is similar to known HK-RR systems in *Listeria monocytogenes* and *S. pneumoniae* (10). EF1051 and EF1050 were both induced at *t*30. Recently, the EF1051/EF1050 pair was described by Teng et al. (27), who named this pair of genes *etaRS* (enterococcal two-component system a). Teng et al. (27) showed the involvement of EtaRS in both stress responses and virulence, and our results support their hypothesis on the function of *etaRS*. EF0641 encoding L-lactate dehydrogenase (*ldh*) was down-regulated at *t*60 and *t*90. Previously, it was shown that *ldh* was induced under stress (8), and it was speculated that also this gene could be involved in stress responses (8), but the function is unclear. The repression of *ldh* in this study indicates that the possible involvement of this gene in stress is not general. Likewise, *sodA* (encoding superoxide dismutase), *arcC* (encoding carbamate kinase), and *sdhA* and *sdhB* (encoding L-serine dehydratase) were down-regulated in our work, while they were induced in the study by Giard et al. (8). Based on these comparisons, it appears that a considerable number of the genes affected by environmental stress in *E. faecalis* are not general stress genes but, rather, are specified by certain conditions.

Interestingly, EF1078, which was induced at all time points except *t*0, is identical to *emeA* (enterococcal multidrug resistance efflux), which was characterized by Jonas et al. (12). *emeA* is probably a homolog of the *norA* found in *Staphylococcus aureus* (12). Jonas et al. (12), showed that *emeA* is involved in resistance to many toxic compounds, among them erythromycin (12). Thus, our study also supports the results of Jonas et al. on the function of *emeA*.

We have presented the transcriptional profile of erythromycin-exposed *E. faecalis* V583. The addition of erythromycin to this bacterium causes numerous events of differential transcription. Efflux of the macrolide molecules from the cells may be an important part of the survival mechanism, in addition to the resistance conferred by ErmB. This work adds information to the growing archive of condition-specific bacterial transcription signatures, which, in the future, will aid the elucidation of microbial physiology, metabolism, ecology, pathogenesis, etc. With a comprehensive archive of such transcription signatures, it will also be possible to pay more attention to all genes encoding hypothetical proteins or putative genes. This group represents a significant part of prokaryotic genomes and a dominant group of regulated genes in many microarray studies published so far. Profiling of transcriptional events in V583 under other stress conditions is in progress. Hopefully, this will lead to a deeper understanding of the biology of this bacterium.

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PAPER II

The Transcriptome of the Nosocomial Pathogen *Enterococcus faecalis* V583 Reveals Adaptive Responses to Growth in Blood

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Abstract

Background: *Enterococcus faecalis* plays a dual role in human ecology, predominantly existing as a commensal in the alimentary canal, but also as an opportunistic pathogen that frequently causes nosocomial infections like bacteremia. A number of virulence factors that contribute to the pathogenic potential of *E. faecalis* have been established. However, the process in which *E. faecalis* gains access to the bloodstream and establishes a persistent infection is not well understood.

Methodology/Principal Findings: To enhance our understanding of how this commensal bacterium adapts during a bloodstream infection and to examine the interplay between genes we designed an *in vitro* experiment using genome-wide microarrays to investigate what effects the presence of and growth in blood have on the transcriptome of *E. faecalis* strain V583. We showed that growth in both 2xYT supplemented with 10% blood and in 100% blood had a great impact on the transcription of many genes in the V583 genome. We identified several immediate changes signifying cellular processes that might contribute to adaptation and growth in blood. These include modulation of membrane fatty acid composition, oxidative and lytic stress protection, acquisition of new available substrates, transport functions including heme/iron transporters and genes associated with virulence in *E. faecalis*.

Conclusions/Significance: The results presented here reveal that cultivation of *E. faecalis* in blood *in vitro* has a profound impact on its transcriptome, which includes a number of virulence traits. Observed regulation of genes and pathways revealed new insight into physiological features and metabolic capacities which enable *E. faecalis* to adapt and grow in blood. A number of the regulated genes might potentially be useful candidates for development of new therapeutic approaches for treatment of *E. faecalis* infections.

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Introduction

Enterococcus faecalis is a common resident of the gastrointestinal tract of humans [1]. This bacterium displays a rough physiology that enables it to withstand oxidative stress [2] and harsh conditions such as high pH and salt concentrations [3]. *E. faecalis* is also an opportunistic pathogen, ranked among the leading causes of nosocomial infections worldwide [4]. Enterococci constitute the third most prevalent pathogens isolated from bloodstream infections, and represent the most frequent cause of surgical-site infections in intensive care units [4]. In the United States, *E. faecalis* accounts for approximately 80% of all enterococcal nosocomial infections [5].

E. faecalis V583 (referred to as V583 hereafter) originates from a patient suffering from a persistent bloodstream infection, and it was the first vancomycin-resistant clinical isolate reported in the United States [6]. V583 is part of the high risk clonal complex 2 [7,8], which comprises mostly of isolates derived from hospital infections world wide. The genome of V583 contains several virulence related genes [8], including several antigens such as *E. faecalis* antigen A (EfaA) [9], and two well characterized antigenic exopolysaccharides; the serotype 2 capsular polysaccharide (*cps*) [10,11], and the enterococcal polysaccharide antigen biosynthesis cluster (*epa*) [12,13]. It has been acknowledged that *E. faecalis* acquires genetic traits by horizontal gene transfer, which includes virulence and antibiotic resistance determinants, to survive and persist in complex environments such as different infection sites (reviewed in [14]). However, *E. faecalis* pathogenesis most likely involves an orchestrated interplay between the regulation of virulence factors and multiple genetic traits that govern adaptation of the bacterial cell physiology during the process of infection. Several functional studies have been performed to link genetic traits to virulence [10,15–21], but few studies have examined such genome wide transcriptional interplay in *E. faecalis*.

Even though *E. faecalis* is a clinically significant pathogen implicated in different types of infections, little is known regarding

the molecular mechanisms involved in the adaptive process this bacterium undertakes to permit survival and growth in e.g. the bloodstream of an infected patient. Several studies have demonstrated that *E. faecalis* has evolved opportunistic strategies to sense and respond to entrance into the bloodstream of a host [22–26]. To improve the current understanding of *E. faecalis*' ability to cause bloodstream infections, we performed a genome wide transcriptional analysis of V583 during growth in 2xYT supplemented with 10% blood (YTB). We have employed a biphasic approach, performing a time-course experiment to examine the immediate responses of *E. faecalis* to blood as a biological cue, but also to explore the adaptation of *E. faecalis* in the presence of blood. Secondly, to increase our knowledge regarding the initial phase of an *E. faecalis* bloodstream infection, growth capacity and transcriptome responses in 100% blood were assessed. These experiments revealed that both growth in the presence of a small percentage (10%) of blood, and pure blood alters the transcription of the bacterium extensively. The results presented here provide new insights into processes essential for the survival and growth of *E. faecalis* in the complex blood environment.

Results

Growth of V583 in Blood and YTB Compared to 2xYT-Culture Medium

E. faecalis is able to establish a persistent infection in the bloodstream and internal organs of an infected host [27,28], and it is of utmost importance to understand the mechanisms that enable *E. faecalis* to survive in this complex growth environment. A rich laboratory medium (2xYT) was selected as the reference culture medium since it is considered to contain minuscule amounts of infection relevant biological cues [24]. Initial experiments were performed to assess growth and behavior of V583 in 2xYT, in 2xYT supplemented with different concentrations of blood, and in pure blood. Based on these experiments it was decided to use 10% blood in 2xYT (YTB) and 100% blood in the subsequent transcriptome profiling experiments. Since *E. faecalis* is known to sense and respond to target cells such as erythrocytes, e.g. by expressing virulence factors like the toxin cytolysin [23], we decided to use whole blood rather than serum or plasma to mimic the *in vivo* environment and to examine other responses possibly modulated by erythrocytes.

The morphology of V583 was examined by light microscopy, revealing that it grew in chains consisting of up to 8 cells in 2xYT. It was also evident that in the presence of blood, bacterial cells aggregated, probably due to agglutination. In order to obtain reliable colony forming units (CFU) counts, gentle sonication was applied to break up aggregates and long chains of V583 cells. Several tests were performed to ensure that the aggregates and chains were properly dissolved without affecting the viability of the cells. V583 was cultivated in 2xYT until mid-exponential growth phase (cell density $\sim 1\times10^8$ CFU/ml), prior to exposing the cells to the test conditions; pre-warmed 2xYT, YTB or blood, as described in the Materials and Methods section. The average growth curves of V583 grown in 2xYT, YTB and blood measured by CFU counts are presented in Fig. 1.

The doubling time (Td) of V583 was similar for growth in 2xYT and YTB, with a Td of 39.7 and 36.8 minutes respectively. However, growth of V583 in blood was constrained compared to in 2xYT with a Td of 80.5 minutes. When grown in 2xYT or YTB, V583 reached a maximum cell density of 1×10^9 CFU/ml, whereas in blood V583 reached approximately 2×10^8 CFU/ml.

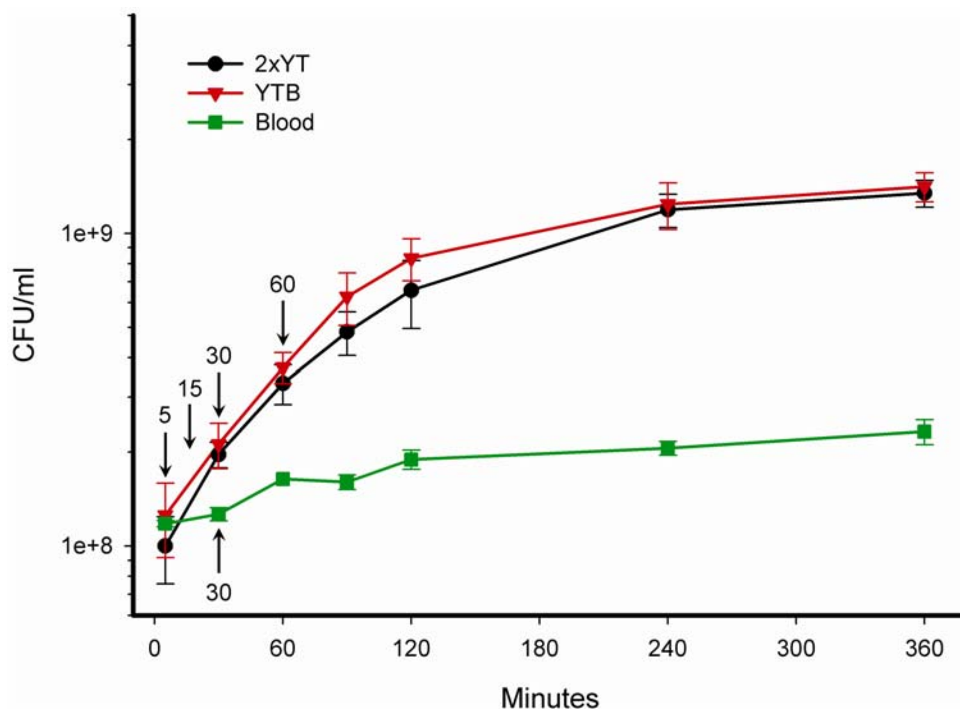

Figure 1. Characterization of *E. faecalis* V583 growth in 2xYT, YTB and blood. Growth of *E. faecalis* V583 was determined from cultures pre-cultivated in 2xYT, and transferred to a fresh medium (either 2xYT, YTB or blood). The growth curves are represented by colony forming units per millilitre (CFU/ml) on the Y-axis, and minutes as indicated on the X-axis. The growth curves correspond to the mean ± STD of three individual experiments. Arrows indicate the time points when samples were harvested prior to RNA extraction. Samples from 2xYT were harvested either only after 30 minutes (when compared to blood), or after 5, 15, 30 and 60 minutes (when compared to YTB).
doi:10.1371/journal.pone.0007660.g001

Based on these results, it was decided to investigate transcriptional responses after 5, 15, 30 and 60 minutes growth in YTB, and after 30 minutes growth in blood as indicated in Fig. 1.

Global Adaptation of the V583 Transcriptome Reveals Changes Comprising Most Functional Gene Categories

To examine *E. faecalis*' immediate response to blood as a biological cue and adaptation to a prolonged existence in blood, a time-course experiment was carried out. The time points for cell harvesting followed by RNA isolation (within 60 minutes after addition of blood), were carefully chosen to reflect the actively growing V583 cells in both 2xYT and in YTB (Fig. 1), as well as to portray the different stages of adaptation that V583 undergo upon the first encounter of blood. To further examine the *E. faecalis* adaptation towards persistence in blood, the transcriptional response of V583 grown for 30 minutes in blood was assessed. The obtained log_2-ratios and p-values for all the V583 genes found during exposure to YTB and blood compared to 2xYT are listed in Table S1. Statistical analysis using a mixed model [29] combined with a stringent Bonferroni corrected confidence level of $p<0.05$, identified 148 significantly regulated genes during growth of *E. faecalis* in YTB. Of these, 72 genes were up-regulated, 73 where down-regulated and 3 genes where both up- and down-regulated at one or more time points. The most pronounced transcriptional responses to YTB occurred after 15 and 30 minutes. When V583 was grown in blood for 30 minutes, a total of 549 genes were differentially expressed (225 genes were up-regulated and 324 were down-regulated). The heat map in Fig. 2 presents an overview of the regulated genes within each functional category in the YTB and blood experiments. This revealed similarities in the expression patterns of a number of genes between the YTB and the blood experiments, e.g. genes involved in fatty acid and phospholipid metabolism, energy metabolism, transcription, genes with a regulatory function and genes encoding proteins with binding and/or transport functions (Fig. 2). Growth in pure blood caused additional transcriptional responses within several gene categories such as the cell envelope, protein synthesis and amino acid biosynthesis, which can be seen as a distinct pattern in the heat map (Fig. 2). The down-regulation of several genes within the latter two functional groups most likely reflects the reduced growth rate in blood compared to in 2xYT (Fig. 1).

Stress Response of V583 Caused by Blood Exposure

Several of the V583 genes associated with stress protection mechanisms in enterococci were found to respond to blood, while only a few stress-related genes were regulated in response to

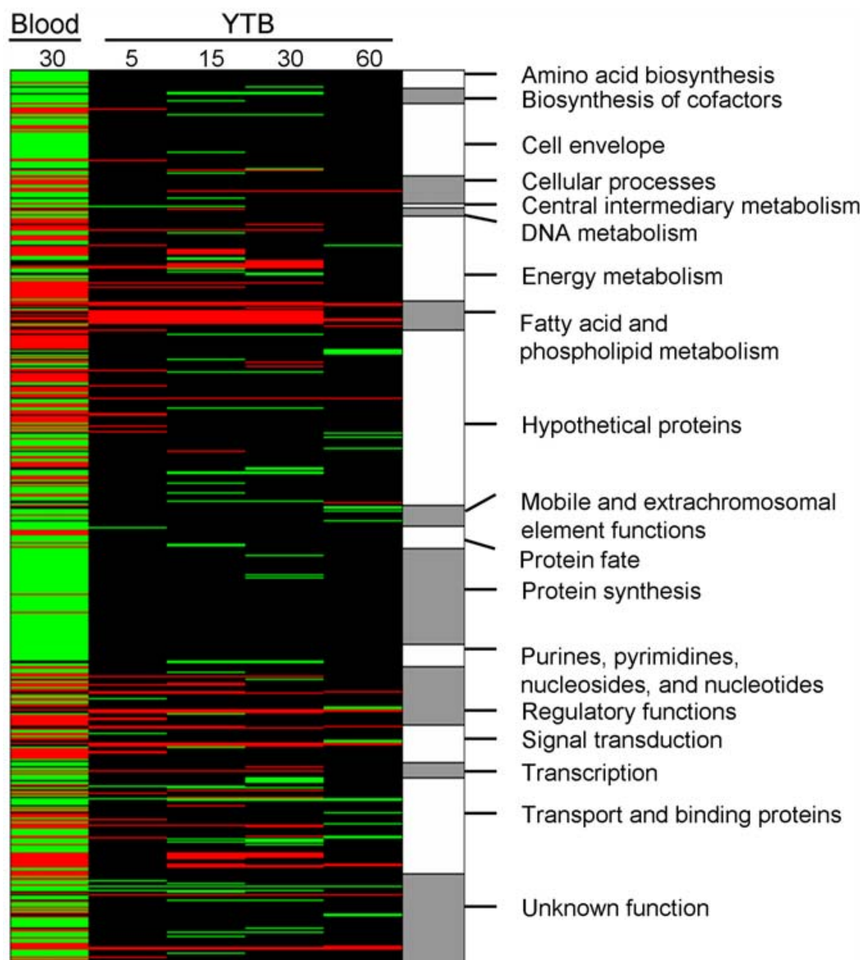

Figure 2. Heat map visualizing regulated genes in V583 grown in blood and YTB compared to growth in 2xYT. Genes found to be significantly regulated are indicated by either red (up-regulated), or green (down-regulated). Genes regulated after growth for 30 minutes in blood, compared to in 2xYT are listed in column 1. Genes regulated during growth in YTB compared to 2xYT are listed in columns 2–4, time-points in minutes indicated on the top of each column. The genes are sorted alphabetically by functional categories (column 5).
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growth in YTB as expected. For growth in blood an operon (EF0076-81) which includes the *gls24* and *glsB* genes [30,31], was up-regulated (Table 1 and S1). The Gls24 protein appears to be implicated in both stress protection and virulence of *E. faecalis* [30,32]. Exposure to blood also mounted universal stress protection genes, including EF1084 and the general stress operon *gspA1-2* (EF1810-11). A gene encoding a cold shock protein *cspC* (EF1991) was found to be up-regulated in both blood and in YTB after 15, 30 and 60 minutes, which indicates that this gene might be important for V583 to overcome the stress triggered by growth in blood. Interestingly, in response to growth in blood we also observed an up-regulation of EF1560, a hypothetical gene that has been reported to show an enhanced transcription under six different stress conditions in previous studies [33,34].

During the course of infection, bacteria are exposed to massive oxidative stress [35,36]. The microarray results revealed that the expression of several genes associated with oxidative stress response in *E. faecalis* was affected by blood exposure. Interestingly, previous studies have established a relationship between the oxidative stress response and virulence in *E. faecalis* [37–40]. A total number of nine oxidative stress protection genes [41] were regulated during growth in YTB or blood (Table 1 and S1). Five of these genes were up-regulated in response to growth in blood, including an organic hydroperoxide resistance gene *ohr* (EF0453) [42], the *dps* gene (EF0606) predicted to protect DNA from oxidative damage [8], the NADH peroxidase *npr* (EF1211), the peptide methionine reductase *msrB* (EF3164), and the superoxide dismutase gene *sodA* (EF0463). The *sodA* gene is important for *E. faecalis* to survive ingestion by macrophages [38] and was also up-regulated in *Streptococcus agalactiae* during growth in blood [43]. Four genes related to oxidative stress were found to be down-regulated in response to growth in blood (Table 1 and S1). Two of these genes, an oxidoreductase (EF3257) and a thioredoxin reductase *ahpF* (EF2738), were down-regulated both during growth in blood and YTB. An NADH oxidase *nox* (EF1586) was also found to be down-regulated during growth in blood, and an alkyl hydroperoxide reductase *ahpC* (EF2739) showed a reduced expression after 15 minutes growth in YTB.

Exposure to Blood Induces Modifications to the Cell Envelope

The integrity and composition of the cell envelope of an invading bacterium is important to evade the challenges evoked by the host defense systems [44,45]. A number of changes in the transcriptome of *E. faecalis* imply extensive adaptations in the cell membrane composition and surface related structures (Table S1). A particularly pronounced change was detected in two gene clusters (EF0282-84 and EF2886-75), responsible for type II fatty acid biosynthesis (FASII) and isomerization of membrane phospholipids. These loci were up-regulated throughout the time-course of the YTB experiment and also in response to growth in blood. Interestingly, these gene clusters have previously been shown to be regulated in response to exposure to the cell membrane detergents SDS and bovine bile [46], indicating that remodeling of the fatty acid composition in the cell membrane might be an important response to a broad range of external stressors. Furthermore, the up-regulation of the cardiolipin synthase gene EF1608 (Table 1 and S1), which modulates the phosphatidylglycerol content in the cell membrane, also suggests that exposure to blood affects the membrane composition of *E. faecalis*. Evidence of lipolytic activity in response to growth in blood was substantiated by the up-regulation of two lipases (EF0169 and EF3191) (Table 1 and S1). The latter gene did also show an enhanced expression after 60 minutes growth in YTB and it has been proposed by Paulsen *et al* [8] as a potential virulence factor.

The *lrgAB* operon (EF3194-93) that encodes a putative lysis inhibitory system was highly up-regulated in response to blood (Table S1) with a log_2-value of 7.9 for *lrgB* and 5.6 for *lrgA*. The two genes were also found to be highly up-regulated throughout the time-course experiment in YTB. The rapid induction and consistently high level of transcription of the *lrgAB* operon, in addition to its putative function suggests a role in modification of the cell wall structure, which might be propitious for growth in blood. Noticeably, the synonymous genes (gbs0182-83) in *S. agalactiae* showed an increased expression during growth in blood [43]. The expression of *lrgAB* in *Staphylococcus aureus* is regulated by the closely located LytSR two-component system [47]. In V583, a two-component system (EF3197-96) homologous to the LytSR system in *S. aureus*, resides directly upstream from *lrgAB*. It is possible that this system is involved in the regulation of *lrgAB*, but only a modest enhanced expression (not statistically significant) of this two-component system was observed.

E. faecalis contains two gene clusters responsible for the production of two serotype-determining exopolysaccharides: the serotype 2 capsular polysaccharide (*cps*) [10], and the enterococcal polysaccharide antigen biosynthesis cluster (*epa*) [13]. It has previously been shown that the *cps* and *epa* clusters affect virulence in mice [48–50] and also contribute to resistance against phagocytic killing [10,20,51]. In our experiments most of the genes within the *epa* cluster (EF2200-2189 and EF2184-77) and the *cps* cluster (EF2492-84) were down-regulated during growth in blood (Table 1 and S1). In addition, some of the *cps* genes were also down-regulated after 15 and 30 minutes growth in YTB. These results are consistent with previous work on *E. faecalis* FA2-2, which showed that genes in the *cps* locus were down-regulated during growth in serum [11].

The V583 genome contains an operon, *dltABCD* (EF2749-46), responsible for incorporating d-alanine into cell-wall associated teichoic acids and lipoteichoic acids [52]. The first two genes of this operon, *dltA* and *dltB*, were found to be down-regulated in response to growth in blood (Table 1 and S1). Reduced content of D-alanine esters in the teichoic acid results in an increased net negative charge on the bacterial cell surface, which in turn can affect several bacterial properties such as susceptibility to cationic antimicrobial peptides and biofilm formation [52]. In addition, the expression of a genetic locus known to be involved in biofilm formation and maltose metabolism [53,54] showed an enhanced expression in response to growth in blood (Table 1 and S1). This locus includes one operon, the *bopABCD/malPBMR* operon (EF0957-54), and a phosphoenolpyruvate phosphotransferase system (PTS) *malT* (EF0958) of which the genes *malT* and *bopAB/malPB* were up-regulated in blood. The genes *bopCD/malMR* showed the same trend, although not statistically significant. Furthermore, the secreted antigen *salB* (EF0394) showed reduced expression during growth in blood, and after 5 minutes growth in YTB (Table 1 and S1). This gene has also been demonstrated to be important for biofilm formation [55].

It has been proposed that lipoproteins are implicated in virulence in *E. faecalis* [56]. Interestingly, we found that the transcription of nine genes encoding lipoproteins were regulated (five up-regulated and four down-regulated). Among these, the cAD1 conjugation pheromone precursor (EF3256) showed decreased expression in blood and after 15 minutes in YTB (Table 1 and S1), while transcription of an operon encoding an ABC-transporter and an YaeC family lipoprotein (EF3200-EF3198) was elevated in blood and after 15 and 30 minutes in YTB (Table 1 and S1). The cAD1 conjugation pheromone

Table 1. Genes proven or predicted to be important for virulence in V583 found to be regulated during growth in blood.

ORF #	Function (Gene name)	Characteristic	log_2	Reference
EF0079	*gls24*	Stress response	3.9	[30,32]
EF0169	lipase/acylhydrolase	Fatty acid and phospholipid degradation	2.9	[97]
EF0361	chitinase, family 2	Cell envelope	4.2	[8]
EF0362	chitin binding protein, putative	Cell envelope	4.4	[8]
EF0373	sensor histidine kinase	Signal transduction	3.0	[12]
EF0394	secreted antigen, putative (*salB*)	Protein fate	−1.6	[8]
EF0453	OsmC/Ohr family protein (*ohr*)	Oxidative stress response	3.2	[41,42]
EF0463	superoxide dismutase, Mn (*sodA*)	Oxidative stress response	1.7	[38]
EF0606	Dps family protein (*dps*)	Oxidative stress response	2.2	[41]
EF0956	beta-phosphoglucomutase (*malB/bopB*)	Energy metabolism	2.5	[54]
EF0957	glycosyl hydrolase, family 65 (*malA/bopA*)	Energy metabolism	2.5	[54]
EF0958	PTS system, IIABC components (*malT*)	Signal transduction	2.2	[54]
EF1051	sensor histidine kinase (*etaS*)	Signal transduction	−2.6	[70]
EF1211	NADH peroxidase (*npr*)	Oxidative stress response	2.8	[41]
EF1586	NADH oxidase (*nox*)	Oxidative stress response	−2.4	[41]
EF1608	cardiolipin synthetase, putative	Fatty acid and phospholipid biosynthesis	2.5	[98]
EF2074	ABC transporter, ATP-binding protein (*efaC*)	Transport and binding proteins	3.6	[9,12]
EF2075	ABC transporter, permease protein (*efaB*)	Transport and binding proteins	2.4	[9,12]
EF2076	endocarditis specific antigen (*efaA*)	Cellular processes	1.4*	[9,12]
EF2167	glycosyl transferase, group 2 family protein	Cell envelope	−2.1	[8]
EF2170	glycosyl transferase, group 2 family protein	Cell envelope	−2.2	[8]
EF2174	conserved domain protein	Hypothetical proteins	−1.7	[8]
EF2177	bacterial sugar transferase (*epaR*)	Cell envelope	−2.7	[8,20]
EF2178	membrane protein, putative (*epaQ*)	Cell envelope	−2.8	[8,20]
EF2179	conserved hypothetical protein (*epaP*)	Hypothetical proteins	−3.1	[8,20]
EF2180	glycosyl transferase, group 2 family protein (*epaO*)	Cell envelope	−3.0	[8,20]
EF2181	glycosyl transferase, group 2 family protein (*epaN*)	Cell envelope	−2.9	[8,20]
EF2182	ABC transporter, ATP-binding protein (*epaM*)	Transport and binding proteins	−2.5	[8,20]
EF2183	ABC transporter, permease protein (*epaL*)	Transport and binding proteins	−1.9	[8,20]
EF2189	conserved hypothetical protein (*epaJ*)	Hypothetical proteins	−2.0	[8,20]
EF2190	glycosyl transferase, group 2 family protein (*epaI*)	Cell envelope	−1.9	[8,20]
EF2192	dTDP-glucose 4,6-dehydratase (*epaG*)	Cell envelope	−1.7	[8,20]
EF2194	glucose-1-phosphate thymidylyltransferase (*epaE*)	Cell envelope	−2.2	[8,20]
EF2195	glycosyl transferase, group 2 family protein (*epaD*)	Cell envelope	−1.9	[8,20]
EF2197	glycosyl transferase, group 2 family protein (*epaB*)	Cell envelope	−1.8	[8,20]
EF2198	glycosyl transferase, group 4 family protein (*epaA*)	Cell envelope	−2.1	[8,20]
EF2439	undecaprenol kinase, putative	Toxin production and resistance	−3.2	[8]
EF2485	ABC transporter, permease protein (*cpsK*)	Transport and binding proteins	−2.9	[10]
EF2486	ABC transporter, ATP-binding protein (*cpsJ*)	Transport and binding proteins	−3.5	[10]
EF2487	UDP-galactopyranose mutase (*cpsI*)	Cell envelope	−2.4	[10]
EF2488	lipoprotein, putative (*cpsH*)	Cell envelope	−2.5	[10]
EF2489	MurB family protein (*cpsG*)	Cell envelope	−2.9	[10]
EF2490	conserved hypothetical protein (*cpsF*)	Hypothetical proteins	−3.2	[10]
EF2491	glycosyl transferase, group 2 family protein (*cpsE*)	Cell envelope	−1.9	[8,10]
EF2492	glycosyl transferase, group 2 family protein (*cpsD*)	Cell envelope	−2.1	[8,10]
EF2658	FemAB family protein	Toxin production and resistance	−1.7	[8]
EF2713	cell wall surface anchor family protein	Cell envelope	2.8	[8]
EF2738	thioredoxin reductase (*ahpF*)	Oxidative stress response	−1.8	[41]
EF2748	basic membrane protein DtlB (*dltB*)	Cell envelope	−2.2	[52]
EF2749	D-alanine-activating enzyme, putative (*dltA*)	Cell envelope	−2.9	[52]

Table 1. Cont.

ORF #	Function (Gene name)	Characteristic	log_2	Reference
EF2795	LysM domain lipoprotein	Cell envelope	−2.0	[8]
EF3082	iron compound ABC transporter (*fatB*)	Transport and binding proteins	3.5	[8]
EF3106	peptide ABC transporter, peptide-binding protein	Transport and binding proteins	6.1	[8]
EF3164	PilB family protein (*msrB*)	Oxidative stress response	2.1	[41]
EF3191	lipase, putative	Fatty acid and phospholipid degradation	2.3	[8]
EF3198	lipoprotein, YaeC family	Cell envelope	3.2	[8]
EF3245	cell-envelope associated acid phosphatase	Enzymes of unknown specificity	−1.8	[8]
EF3256	pheromone cAD1 precursor lipoprotein	Cell envelope	−2.9	[8]
EF3257	oxidoreductase	Oxidative stress response	−4.4	[41]
EFC0001	pheromone binding protein (*prgZ*)	Transport and binding proteins	1.6	[8]

*The corresponding p-value was above the chosen level of statistical significance. However the up-regulation of this gene was confirmed by real-time QPCR (Fig. 3).
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precursor and the YaeC family lipoprotein have both been predicted by Paulsen *et al* to contribute to virulence in V583 [8]. Furthermore, twelve putative membrane-protein encoding genes were affected by growth in blood (six up-regulated and six down-regulated), and three glycosyl transferase genes were down-regulated. We also found a down-regulation of eight genes involved in peptidoglycan biosynthesis. Noticeably, we observed an up-regulation of two genes encoding chitin binding proteins (EF0361and EF0362) and a gene encoding a cell wall surface anchor family protein, EF2713 (Table 1 and S1), all three proposed as potential virulence factors by Paulsen *et al* [8].

Adaptive Metabolic Shift during Whole Blood Exposure

A massive transcriptional response was observed for genes involved in metabolism when V583 was grown in blood or YTB compared to 2xYT, which could be expected from the results of the growth experiments (Fig. 1). Accordingly, the transcriptome analysis portrayed rapid adjustments of gene expression to accommodate the changed nutritional conditions. The results revealed changed expression of genes involved in pathways in the central metabolism of V583 indicating that a wide range of alternative energy sources were utilized (Table S1).

After 30 minutes of growth in YTB or blood we found a reduced transcription of the main uptake system of glucose in *E. faecalis*, the mannose PTS *mptBACD* (EF0019-22) [57], signifying exhaustion of the glucose reservoir at this stage of the experiment. This notion was supported by the down-regulation of the *ptsHI* operon (EF0709-10), which constitutes the signal transduction components that mediate carbon catabolite repression (CCR) [58]. Furthermore, the observed down-regulation of *pfk-pyk* (EF1045-46) and *fba* (EF1167) involved in the first steps of the glycolysis is also consistent with depletion of intracellular glucose catabolic intermediates. Simultaneously, glycolysis genes *gap-1* (EF1526), glycerate kinase (EF2646) and *pgm* (EF2982) were up-regulated, indicating increased carbon flux from sources other than hexose sugars. Interestingly, the glycerol catabolic pathway (EF1929-27), was highly up-regulated in response to growth in blood, and was also found to be up-regulated after 5, 15 and 30 minutes growth in YTB, suggesting that glycerol and other C3-glycerides from blood serves as a source of energy.

Several metabolic systems subject to catabolite control protein A (CcpA) mediated CCR [58] were also regulated during growth in blood, indicating the use of certain amino acids and available sugars as alternative energy sources. Of these, the gene cluster responsible for citrate catabolism (EF3327-15) and three genes involved in arginine catabolism, *argF-1* (EF0105), *arcC-1* (EF0106) and EF0108 were up-regulated, while the gene-cluster involved in serine degradation (EF0097-100) showed a reduced expression. After 30 minutes growth in YTB we also found an enhanced expression of catabolism of branched chain amino acids (*ptb, buk, bdkDAB*, EF1663-59), and the same trend was found during growth in blood. Furthermore, derepression of four PTS systems regulated by CCR mediated binding of CcpA to cis-acting catabolite-responsive elements (*cre*) [58] was observed. These include the predicted cellobiose (EF0292-91), N-acetyl galactoseamine (EF0456), lactose/galactose (EF1801) and gluconate (EF3139-36) PTS systems. The latter is part of a predicted metabolic pathway consisting of two operons (EF3142-37 and EF3136-34) that facilitates gluconate uptake and catabolism via the mannonate route [58]. The expression of both operons was enhanced during growth in blood, whereas only some of these genes showed a significantly enhanced expression during growth in YTB.

Significantly altered expression was observed for six PTS systems that probably are regulated by a sigma 54 dependent PTS regulation domain (PRD) and/or Bgl antiterminator mechanisms. Induced transcription of such PTS systems requires both release of CCR and availability of the specific sugars [58]. Two sigma 54 dependent PRD controlled PTS systems, *mphAD* (EF1953-50) [57], and a putative N-acetylglucosamine PTS (EF1516), were down-regulated in YTB and blood respectively. Also, the *mpoAD* PTS system (EF2980-76) [57] was found to be up-regulated and appeared to be co-regulated with EF2982-81. Similarly, the inferred sorbitol metabolism operon (EF3310-04) was up-regulated during growth in blood. Moreover, an indication of co-metabolism of glucose and other sugars in blood was seen by several up-regulated PTS systems for which no CCR mechanism has been identified. This includes the ascorbate PTS *sgaB* (EF1128), during growth in blood and mannitol (EF0411-12) during growth in YTB. The fructose PTS system (EF0717), was up-regulated in blood, but down-regulated in YTB. The PTS mannose/fructose/sorbose (EF3029) showed a reduced expression during growth in both blood and YTB.

The observed changes in substrate utilization and metabolism influenced the pyruvate metabolic pathways. An increased expression of L-lactate dehydrogenase (*ldh-1*; EF0255) was observed in YTB, whereas the *pflAB* genes (EF1612 and EF1613) involved in formate formation were reduced during growth in blood, and after 15 minutes growth in YTB. Furthermore, a reduced expression of *adhE* (EF0900) signifies low contribution of ethanol fermentation in blood. The pyruvate dehydrogenase complex gene-cluster *pdhAB, aceF* and *lpdA*

(EF1353-56) involved in acetyl-CoA biosynthesis was up-regulated during growth in blood and also after 15 minutes growth in YTB. The cell can harvest an additional ATP from acetyl-CoA by oxidation to acetate, but no change was detected in transcription of the involved genes *eutD* (EF0949) or *ackA* (EF1983). We previously mentioned up-regulation of the fatty acid biosynthesis pathway FASII, and since acetyl-CoA also serves as the precursor of the FASII pathway, it is possible that acetyl-CoA is funneled to fatty acid biosynthesis.

Blood Specific Components Influence Transport and Biosynthesis Pathways

Iron uptake is a crucial factor in bacterial virulence and in gut colonization of commensal bacteria [59,60]. The mechanisms that enable bacteria to acquire iron from the surroundings have thus received a lot of attention [61]. Our data reveal a potentially important role of iron acquisition and homeostasis during growth in blood. Six genes involved in iron transport, including *feuA* (EF0188), *feoB* (EF0476), *ceuBCD* and *fatB* (EF3085-82) were up-regulated in YTB. The latter four genes comprise an operon that also was up-regulated during growth in blood (Table 1 and S1). The *hrtB* (EF0793) ABC-transporter gene, which homologue in *S. aureus* facilitates expulsion of toxic surplus of heme [60] was up-regulated after 15 minutes growth in YTB. Another scarcely available co-factor is manganese, which also is essential for growth of *E. faecalis in vitro* [62,63]. Notably, a gene cluster, *efaCBA* (EF2074-76) originally identified to encode the endocarditis associated antigen is responsible for Mn^{2+} acquisition in manganese depleted environments [64]. The notion that the ability to acquire manganese is important for growth of *E. faecalis* was sustained by the observed up-regulation of *efaCB* in blood (Table 1 and S1).

The presence of blood also changed the transcription of a number of genes encoding other transport systems in the cell. For example the up-regulation of genes encoding two sugar ABC-transporters (EF1345 and EF1344-43), further supports that V583 utilizes alternative sugars from the blood. Certain transport system encoding genes were down-regulated during growth in blood including a major facilitator ABC transporter (EF0082), amino acid ABC-transporters (EF0761-60, EF2642 & EF2649), a cell division ABC-transporter (EF1760) and a phosphate ABC-transporter (EF1756). Thirteen additional genes encoding ABC-transporters with unknown substrates showed altered transcription in response to growth in blood (3 up-regulated and 10 down-regulated), indicating the requirement for balancing numerous solutes to maintain the cell homeostasis.

Previous studies on the biosynthetic capacities and nutritional requirements of *E. faecalis* have shown that all strains investigated, including the sequenced OG1RF [65], require histidine, isoleucine, methionine, and tryptophan for growth, and that arginine, glutamate, glycine, leucine, or valine was essential for growth of some strains [66]. By comparing the genome sequences of V583 and OG1RF they appear to have similar requirements for amino acids. Since our data show that the transcription of several genes encoding oligo-peptide ABC-transporters (EF0907 and EF3110-06) was up-regulated, and the transcription of two amino acid importer genes (EF0440 and EF0635) was down-regulated (Table S1), it is possible that V583 meets its demand for amino acids by acquiring oligo-peptides when growing in the host bloodstream. This is analogous to what was observed in *Streptococcus pyogenes* in a similar study [67]. Furthermore, the increased expression of *cysK* (EF1584) implies that cysteine is not abundant in blood. Glutamine and glutamate on the other hand seems to be readily available in blood, since we observed a reduced expression of the glutamine synthase operon *glnRA* (EF2160-59), glutamate synthase *gltA* (EF2560) and transamination of aspartate to glutamate by *aspB* (EF2372) during growth in blood and/or in YTB.

During growth in blood we noticed up-regulation of an isochorismatase gene (EF3192). This coincided with a down-regulation of the EF1561-68 operon, responsible for biosynthesis of chorismate, which is a precursor of aromatic amino acids, folate and quinones. In agreement with this observation we also noticed a reduced transcription of several genes responsible for biosynthesis of cofactors, prosthetic groups, and carriers including menaquinone and ubiquinone (EF0446-50, EF3255-54 and EF3260). Noticeably, modulation of chorismate acquisition was also observed in similar experiments in *S. pyogenes* and *S. agalactiae* [43,67], suggesting that chorismate might be involved in virulence development of these bacteria.

E. faecalis is prototrophic for purines and pyrimidines [66]. The down-regulation of several genes involved in biosynthesis of these compounds (e.g. EF0014, EF0058, EF1547, EF2362-61 and EF3293) might imply that the requirement for nucleotides was covered by scavenging (Table S1). However, no evidence of modulation of ribose/deoxyribose metabolism was observed, which suggests a lowered demand for nucleotides, most likely as a result of the reduced growth rate (Fig. 1).

Virulence Traits and Regulatory Genes

Several virulence traits have been identified in *E. faecalis* [10,15–21]. The origin of V583 as a nosocomial isolate, causing a persistent bloodstream infection made this strain suitable for investigating responses of virulence traits by growth in blood. As previously described, the expression of several of the loci that contribute to *E. faecalis* virulence, such as oxidative and nutritional stress management genes, capsule formation genes and genes involved in acquisition of biometals, were affected by blood. In addition, some genes predicted to be involved in virulence in *E. faecalis* were found to be regulated, and a summary of these genes can be found in Table 1.

A number of regulatory genes showed altered expression in blood-containing growth environment, in particular regulators of carbohydrate metabolism. In addition, several genes encoding TetR-repressors and other unassigned regulators were found to be differentially expressed (Table S1). V583 inherits 4 sigma factors, of which the *sigA* (EF1522) and *sigV* (EF3180) showed a changed expression in blood. The sigma factor *sigV* was up-regulated, but only one (EF0315) of its five potential target genes [68] showed an altered transcription. The fact that *sigA*, the primary sigma factor of the cell was down-regulated after 30 minutes in blood, is consistent with the observed down-regulation of the entire transcription and protein synthesis apparatus, which in turn can be ascribed the lowered growth rate in blood compared to 2xYT (Fig. 1).

Of the 18 two-component systems present in V583 [8,69], only two of the sensor histidine kinase genes were found to be significantly regulated in blood. Transcription of *etaS* (EF1051) a sensor histidine kinase involved in stress and virulence [70] was reduced, and the expression of a sensor histidine kinase gene (EF0373) previously identified as antigenic (antigen yx84) during infection in humans [12], was highly elevated (Table 1 and S1). However, the exact functions of these two-component systems are not well characterized. The *fsr* locus is an important virulence determinant in *E. faecalis* shown to contribute to virulence in mouse peritonitits models [17]. Due to microarray spot abnormalities, regulation of selected genes including the *fsr* locus was assessed by real-time quantitative RT-PCR (described in further detail below). The RT-PCR revealed that both *fsrB* and *gelE* were down-regulated both in blood and YTB.

Table 2. List of genes and primers (5′→ 3′) used for real-time quantitative RT-PCR.

ORF	Gene	Forward primer	Reverse primer	Reference
EF0282	*fabI*	TGATGGTTTCCTATTAGCACAAG	GTTAGGAATCGCACGTTCGG	This work
EF0957	*bopA*	CAGCGACATGGACAGCCTAC	TTGCAGGACCGTCGAGTAAA	This work
EF1099	*ace*	CGGCGACTCAACGTTTGAC	TCCAGCCAAATCGCCTACTT	[24]
EF1818	*gelE*	CGGAACATACTGCCGGTTTAGA	TGGATTAGATGCACCCGAAAT	[24]
EF1821	*fsrB*	TGCTCAAAAAGCAAAGCCTTATAA	GATGACGAGACCGTAGAGTATTACTGAA	[24]
EF2076	*efaA*	TGGGACAGACCCTCACGAATA	CGCCTGTTTCTAAGTTCAAGCC	[24]
EF2493	*cpsC*	GGTTGATGCCAAGAGCTCAG	GTCCCATGCCACGTCTGTAT	This work
EF2749	*dltA*	ACGCGTTTGCCACAATTAAC	GCGCAGTGCTGGTAGATGTT	This work
EF2883	*fabK*	GCTGGATTGCCTGCACCTGTCG	GGTAGCCGATGCTTCATTAGCAAGTGC	This work
EF2886	*fabT*	ACTACACGTCGATCATCTTCACTACGC	CATTACGGAGATGCACACAATCGAAGC	This work
EF3192	-	GAACTGACGGGCGTAATCTG	GTCCAAATCCGTGCCACTAA	This work
EF3193	*lrgB*	CGACAGTAGCGTTTGCGATT	ACAGCCACTAGCGAACCAAA	This work
EF3198	-	GCTGATTTAGTGGCTGTGCAA	AGCACGACCTTCATTGGTTG	This work
	23S	CCTATCGGCCTCGGCTTAG	AGCGAAAGACAGGTGAGAATCC	[24]

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Gene Regulation Examined by Real-time Quantitative RT-PCR

In order to confirm the results from the microarray experiments and to investigate the transcription of a few genes of special interest (excluded from the microarray results due to spot abnormalities), real-time quantitative RT-PCR (QPCR) was performed on 13 genes listed in Table 2. We only examined the 30 minutes time point from the YTB experiment, which is most comparable to the blood experiment. The QPCR results were consistent with the results obtained by the microarray experiments (Fig. 3). For most of the genes the QPCR produced similar or greater $\log_2$ ratios than the corresponding microarray results. One gene, *efaA*, showed a $\log_2$-ratio of 1.4 during growth in blood, but with a p-value indicating non-significance. However, the QPCR showed a $\log_2$-ratio identical to the microarray results supporting that this gene is in fact up-regulated. Most of the genes tested by QPCR were not found to be significantly regulated in YTB using microarrays. However, the QPCR-analysis showed equal to larger

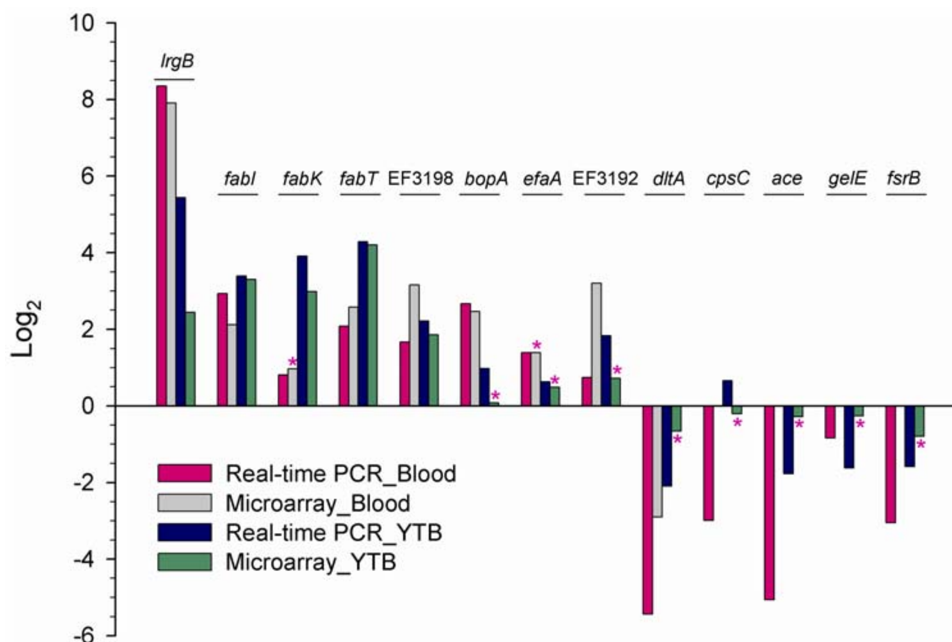

Figure 3. Gene regulation ($\log_2$) after 30 minutes growth in either blood or YTB compared to 2xYT analyzed by microarray or real-time quantitative RT-PCR. The asterisks indicate values from the microarray experiments that were found to be outside the rejection level. The corresponding orf-numbers for the genes tested are: *lrgB*; EF3193, *fabI*; EF0285, *fabK*; EF2883, *fabT*; EF2886, *bopA*; EF0957, *efaA*; EF2076, *dltA*; EF2749, cpsC; EF2493 ace; EF1099, *gelE*; EF1818, *fsrB*; EF1821.
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responses in terms of fold change of these genes. An exception was the gene *cpsC* which showed a slightly reduced expression when examined by microarrays, while a slightly enhanced expression was seen using QPCR. Thus, the QPCR analysis confirmed the reliability of the transcriptional data obtained from the microarray experiments, indicating that the rejection level applied on the microarray data was adequate. Furthermore, the four genes which were excluded from the microarray results due to spot abnormalities (*cpsC*, *ace*, *gelE* and *fsrB*) were all found to be down-regulated in blood when examined by QPCR.

Discussion

In the present study we describe the first microarray analysis of the global transcriptional response of *E. faecalis* to blood. Although certain aspects of *E. faecalis* virulence development in blood have been studied [23–25], the global gene regulation and interplay during adaptation to the blood environment remained largely unaddressed. However, *in vivo* mouse infection models in which *E. faecalis* was intravenously injected, showed that the bacterial cell number initially dropped before stabilizing at about 10^3 CFU/ml blood for at least 7 days [27]. This indicates that *E. faecalis* has to adapt to overcome serious challenges upon entering the bloodstream of a host. With the present study we provide novel information about the gene regulation relevant to such an adaptation process.

Transcriptomics has been successfully employed for studying adaptation to blood *ex vivo* of the closely related pathogens *S. pyogenes* [67] and *S. agalactiae* [43]. As emphasized in these studies [43,67], it is important to note that *in vitro* experiments like the one we present here, can not entirely reproduce the environment encountered by the bacterium during *in vivo* infections with respect to oxygen tension, interaction with the host immune system, the potential depletion of nutrients etc. Consequently, our results have been cautiously interpreted with respect to inherent constraints. Hence, we have used this *in vitro* model to investigate the initial adaptation phase needed for dissemination of an infection, and to explore molecular mechanisms that might be involved in the complex host-bacterium interaction in blood.

The most significant transcriptional changes found in this study include genes relevant for cell envelope structures. In the cell membrane both the fatty acid (FASII) and phosphatidylglycerol biosynthesis genes were up-regulated. This suggests that *E. faecalis* adjusts its fatty acid composition and membrane fluidity to accommodate stress imposed by blood constituents, and possibly also by involving phospholipids from the blood. A recent study demonstrated the ability of *S. agalactiae, S. pyogenes, S. pneumoniae* and *E. faecalis* to utilize free phospholipids in serum and thus overcome the FASII pathway inhibiting antibiotics [71]. Brinster *et al* [71] also showed by QPCR that growth of *S. agalactiae* in serum results in a down-regulation of the eight FASII genes tested. Moreover, other studies have shown by microarray that the gene clusters involved in FASII were down-regulated in *S. pyogenes*, but not significantly regulated in *S. agalactiae* or *S. pneumniae* during growth in blood [43,67,72]. Although *E. faecalis* and the three streptococcal species mentioned above show a similar phenotype when grown in serum containing FASII inhibiting drugs, it appears that the regulation of the FASII pathway is different during growth in blood. This might be due to the differences in the genetic organization of the FASII pathway between enterococci and streptococci. Another possible explanation is that *E. faecalis* processes the unsaturated fatty acids from blood in order to accommodate a lipid composition compatible with its membrane. The observed increased transcription of two lipase genes during growth in blood might imply a connection between the modulation of fatty acid and phospholipid metabolism and lipolysis/tissue tropism. A recent study showed that 71% of the invasive *E. faecalis* isolates examined produced lipase, whereas only 35% of the noninvasive isolates produced lipase indicating that lipase activity might be important for the pathogenicity of *E. faecalis* [73].

It has been shown that orally administered or intravenously injected *E. faecalis* in mice can colonize internal organs of the host [27,28]. Moreover, Guzman and co-workers [74] showed that growth of *E. faecalis* in serum enhanced its ability to bind Girardi Heart cells, an interaction which in a later study was shown to be inhibited by incubation of the target cells with specific sugar residues. This indicated that carbohydrate antigens were responsible for the enhanced binding [75]. We observed that transcription of two capsular polysaccharides encoded by *epa* and *cps* were down-regulated during growth in blood. Inactivation of these carbohydrate antigen loci cause reduced biofilm formation [20,76], increased susceptibility to phagocytosis [20,51], and attenuated virulence in mice [48]. More interestingly, these exopolysaccharides appear to play a role in adherence/colonization of tissues and organs, and in immune system evasion [10,11,20,50,51]. The involvement of carbohydrate antigens in binding has been further investigated by Singh *et al*, who showed that the *epa* locus is important for adherence/colonization of tissues and organs [50]. Capsule formation is crucial for virulence in *S. pneumonia*, which undergoes phase variation in order to establish infection [77]. However, an *in vivo* transcriptome analysis of *S. pneumonia* infection in mice has revealed that the *cps* transcription was not enhanced in blood. Furthermore, this study also demonstrated that the expression of a number of virulence traits in *S. pneumonia* was body site dependent [72]. Hence, it is possible that the transcription of the *E. faecalis epa* and *cps* loci might be more pronounced in colonized organs.

The effect of serum on *E. faecalis* adherence has been studied further by Nallapareddy and Murray [78], who found that 46 different *E. faecalis* strains all showed enhanced binding to fibronectin and fibrinogen after exposure to 40% horse serum. This property was eliminated by protease treatment, which indicated that adherence was mediated by surface exposed proteins [78]. In our study most genes encoding identified or putative adhesive proteins (such as microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), the collagen adhesin *ace* and aggregation substances) were either not regulated or down-regulated during growth in blood. However, we observed enhanced transcription of several genes encoding membrane proteins or lipoproteins. It is tempting to speculate that these cell envelope bound proteins also might play a role in promoting the adherence of *E. faecalis* during infection.

Analysis of the V583 transcriptome revealed signs of lytic stress in response to blood. Particularly interesting was the immense up-regulation of the *lrgAB* operon. In *S. aureus* it has been shown that the transcription of *lrgAB* is affected by carbohydrate metabolism, acid production or cell wall active antibiotics. LrgAB inhibit murein hydrolase activity, and thus counteract lysis of the cell [79,80]. The exact function of *lrgAB* in *E. faecalis* remains elusive. Even so, the immediate and continuously high level transcription of this operon observed in the present study, and the fact that the homologous genes in *S. agalactiae* also showed an enhanced transcription during growth in blood [43], suggests an important role for *lrgAB* upon blood exposure.

Biometal limitation constitutes a significant obstacle for bacterial pathogens to establish infection in vertebrate hosts [59,60,64]. Lactic acid bacteria (LAB) comprise one of the very

few groups of bacteria for which iron is not an essential growth factor [63,81]. In contrast, manganese is essential to the fermentative metabolism of LAB [62,63]. The enhanced transcription of the main manganese scavenging mechanism encoded by *efaCBA* is a clear indication that *E. faecalis* experiences manganese constraints that might restrict its growth in blood. The strong increase in the superoxide dismutase (*sodA*) expression further emphasizes the importance of an effective manganese uptake during growth in blood. These observations are particularly interesting as both *efaCBA* and *sodA* have been shown to be implicated in virulence [38,82]. In addition, our microarray data show that genes related to iron metabolism constituted one of the major changes of *E. faecalis* adaptation to blood, although iron is not an essential requirement for growth. This suggests a potential role of iron acquisition in virulence development of *E. faecalis*. Examination of the V583 genome has revealed approximately 53 genes with an apparent function in iron homeostasis and metabolism. It was recently demonstrated that many LAB can utilize heme to perform respiratory metabolism [83,84], and that the pathogen *S. agalactiae* requires heme for full virulence [85]. Thus, the significance of the biometals manganese and iron/heme in virulence of *E. facealis* warrants further investigation.

Previous studies have demonstrated the ability of *E. faecalis* to sense its environment and modulate cytolysin production upon blood encounter [23]. The V583 strain is deficient of cytolysin production, but is classified as a pathogen since it was isolated from a patient with a persistent bloodstream infection [6] and belongs to a high risk clonal complex consisting of nosocomial isolates [7]. Consequently, it was relevant to look at the response of virulence related genes. The V583 strain harbors an incomplete (partially deleted) *E. faecalis* pathogenicity island (PAI) [86]. From the PAI of V583 only one gene, *dps* (EF0606) involved in oxidative stress management, was up-regulated. A few genes involved in pantothenate biosynthesis, amino acid metabolism and a transposase were down-regulated, while transcription of the remaining genes within the PAI were unaffected. It is important to note that most genes in the PAI were indeed expressed, and hence might contribute to the fitness of V583, but in the experimental growth conditions examined here, no major responses in transcription of PAI-genes were revealed.

A number of pathogens employ master regulatory systems to coordinate expression of virulence factors during infection e.g. *prfA* in *Listeria monocytogenes* [87], *agr* in *S. aureus* [88] and *covRS* in *S. pyogenes* [89]. The equivalent system in *E. faecalis* is the *fsr* quorum sensing system, which controls the expression of several genes including *gelE* (encoding a gelatinase) and *sprE* (encoding a serine proteinase) [17,90,91]. It has previously been shown that expression of this system is sensitive to environmental conditions [24], and that its level of expression varies between different bacterial strains [92]. In our study we readily detected the *fsrB* and *gelE* transcripts by QPCR, but growth in blood caused a moderate down-regulation of these genes in V583. This appears to be the opposite effect from growth in serum by the MMH594 strain [24]. Our results demonstrate that blood did not act as a cue to enhance *fsr* expression, but rather interfered with its expression. It has been shown that the cytolysin quorum sensing pheromones interact with blood cells in a positive manner [23]. It is possible that the down-regulation was caused by the presence of blood cells in our experiments, which might have adsorbed the quorum sensing signaling pheromone. It has been proposed that the GelE and SprE proteases contribute to virulence by degrading infected tissue [93], and it is possible that *fsr* expression is more pronounced in colonized organs.

In conclusion, this study provides new insights into the adaptive process of *E. faecalis* to growth and persistence in blood. Bacteremia caused by *E. faecalis* represents a major clinical problem, thus the results presented here could be valuable for future studies devoted to the development of new therapeutic approaches for preventing or treating enterococcal infections.

Materials and Methods

Cultivation and Growth Measurement

The strain used in this study was the sequenced *E. faecalis* clinical isolate, V583 ([6,8]). For all experiments V583 was streaked on a 2xYT (1% (w/v) yeast extract, 1.6% (w/v) tryptone and 1% (w/v) NaCl) agar plate and incubated at 37°C o/n. Four individual colonies from the 2xYT plate were inoculated into the same tube of 5 ml 2xYT medium and grown for 17 hours without shaking at 37°C. The culture was then diluted 1000x in 2xYT medium (pre-warmed to 37°C) and incubated until the culture reached an optical density at 600 nm (OD_{600}) of 0.1.

Growth of the bacterium was monitored by counting colony forming units (CFU). A 150 ml culture grown to an OD_{600} of 0.1 as described above was split in three and centrifuged at 8000 x *g* for 3 minutes at 37°C. The cells were resuspended in either (i) 50 ml defibrinated horse blood (TCS Biosciences Ltd.), (ii) 45 ml 2xYT medium and 5 ml blood (10% (v/v) blood) or (iii) 50 ml 2xYT medium (all pre-warmed to 37°C). After thorough mixing 5 ml from each culture was immediately transferred to a fresh tube and placed on ice and the remaining culture was incubated further at 37°C without shaking. The 5 ml cultures were sonicated at an amplitude of 25% 25 seconds (5 seconds on and 5 seconds off) using a Vibra-Cell VCX-500 ultrasonic processor (Sonics) with a microtip. Immediately after sonication 500 µl of each culture was serially diluted in 0.9% (w/v) NaCl (pre-chilled) and plated on 2xYT agar plates. The whole process was repeated after 30, 60, 90, 120, 240 and 360 minutes and the experiment was performed on three consecutive days.

Cultivation and Sampling Prior to Microarray Analysis

A pre-culture of V583 was prepared as described above. After 17 hours the culture was diluted 1000x in 450 ml 2xYT medium and incubated at 37°C until the culture reached an OD_{600} of 0.1, when the culture was split in two. A volume of 25 ml pre-warmed 2xYT medium (37°C) was added to the control culture whereas 25 ml pre-warmed blood was added to the test culture, resulting in a final concentration of 10% (v/v) blood. Samples (25 ml) from each culture were collected by centrifugation (8000 x *g* for 2 minutes at 37°C) after 5, 15, 30 and 60 minutes, and the cell-pellets were immediately frozen in liquid Nitrogen and stored at −80°C prior to RNA extraction.

A parallel experiment was designed to investigate the transcriptional response in pure blood. A pre-culture of V583 was diluted 1000x in 200 ml 2xYT medium and incubated at 37°C until the culture reached an OD_{600} of 0.1, when the culture was split in two and centrifuged (8000 x *g* for 3 minutes at 37°C). For the control culture the cells were resuspended in 100 ml pre-warmed 2xYT (37°C) whereas for the test culture the cells were resuspended in 100 ml pre-warmed blood (37°C), resulting in a final concentration of 100% (v/v) blood in the test culture. Samples (35 ml) of each culture were collected by centrifugation (8000 x *g* for 2 minutes at 37°C) 30 minutes after addition of blood, and the cell-pellets were immediately frozen in liquid Nitrogen and stored at −80°C prior to RNA extraction.

RNA Isolation

The bacterial cells were washed with 50 ml cold 0.1xTE (for 10% blood) and 3×50 ml cold 0.1xTE (for 100% blood) to remove blood constituents prior to RNA extraction. Then samples suspended in 700 µl RLT buffer (Qiagen) were transferred to a 2 ml screw cap FastPrep tube (Qbiogene) containing 0.6 g of glass beads (≤106 µm) (Sigma) and 300 µl chloroform (Merck). Cells were lysed by vigorous shaking for 20 seconds at 6.0 m/s in a FP120 FastPrep cell disruptor (Qbiogene). After lysis the samples were placed on ice for 5 minutes before glass beads and chloroform were removed by a brief centrifugation. The aqueous phase was transferred to a new tube and centrifuged at ~8000 x *g* for 2 minutes to remove cell debris and unlysed cells. The supernatants were removed and kept on ice in separate tubes, while the pellets were suspended in 350 µl RLT buffer, transferred to new FastPrep tubes and subjected to another round of homogenization. The two supernatants from each sample were merged and added 750 µl 96% EtOH. Total RNA was then isolated using the RNeasy Mini kit (Qiagen) according to the manufacturer's protocol. The integrity of the RNA samples was analyzed using the RNA 600 Nano LabChip kit and a Bioanalyzer 2100 (Agilent Technologies). The concentration and purity of the total RNA was measured using a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Inc.).

cDNA Synthesis and Fluorescent Labeling

Total RNA was reversed transcribed using a modified version of protocol #M007 from the Pathogen Functional Genomic Resource center at The Institute for Genomic Research (TIGR: http://pfgrc.tigr.org/protocols/M007.pdf). Accordingly, 5 µg of total RNA and 20 µg of random hexamers (Invitrogen) in a reaction volume of 17.3 µl were denatured at 70°C for 10 minutes and cooled on ice for 5 minutes. Then, 6 µl of 5x First Strand buffer (Invitrogen), 3 µl of 0.1 M dithiothreitol, 20 U rRNasin (Promega), 1.2 µl of a 12.5 mM dNTP (Invitrogen) and aminoallyl-dUTP (Ambion) labeling mixture (aa-dUTP-dTTP 2:3), and 400 U of SuperScript III reverse transcriptase (Invitrogen) were added in a total volume of 30 µl. The labeling reaction mixture was incubated at 25°C for 5 minutes and then at 42°C for 16 hours. The RNA was hydrolyzed by adding 10 µl of 0.5 M EDTA and 10 µl of 1 M NaOH. The reaction mixture was incubated at 65°C for 15 minutes, and then neutralized by adding 25 µl of 1 M Tris-HCl (pH 7.0). Purification of the cDNA was performed using Microcon YM-30 filters (Millipore) according to the manufacturer's protocol. The cDNA was dried in a vacuum centrifuge and stored at −20°C. Coupling of aminoallyl-labeled cDNA to Cy3 and Cy5 (Amersham Biosciences) was done by resuspending the cDNA in 9 µl 0.1 M sodium carbonate buffer pH 9.3. The cDNA samples were transferred to dried Cy-dye aliquots (dissolved in DMSO and dried in a vacuum centrifuge prior to labeling), mixed and incubated for 1 hour. A volume of 35 µl 100 mM sodium acetate pH 5.2 was added and unincorporated dye was removed using QIAquick PCR purification kit (Qiagen) according to the manufacturer's protocol. Finally the Cy3- and Cy5-labeled samples were mixed and dried in a vacuum centrifuge.

Hybridization and Microarray Data Analysis

Microarray experiments were performed using whole genome *E. faecalis* V583 PCR-based microarrays described by Aakra et al [94]. Prior to hybridization, the Ultra Gaps slides (Corning) were prehybridized according to the manufacturer's recommendations. Briefly, the arrays were incubated in a prehybridization solution (3x SSC, 0.1% (wt/vol) sodium dodecyl sulphate (SDS), 0.1 mg/ml Bovine Serum Albumin (BSA), Sigma) at 50°C for 30 minutes. After prehybridization, the arrays were washed twice in distilled water (RT) for 1 minute, then at 95°C in distilled water for 2 minutes, followed by a 1 minute wash in isopropanol and the slides were dried by centrifugation (70 x *g* for 5 minutes) in an Eppendorf 5810R tabletop centrifuge. The Cy3- and Cy5-labeled cDNA samples were resuspended in 40 µl hybridization solution (3x SSC, 0.1% (wt/vol) SDS, 1 mg/ml BSA, 0.1 mg/ml Salmon Sperm DNA (Invitrogen), 50% (vol/vol) Formamide), denatured by boiling for 2 minutes and cooled at room temperature for 5 minutes. The samples were centrifuged briefly and applied to the prehybridized microarray under a 25×60 mm LifterSlip (Erie Scientific Company). The microarrays were hybridized at 42°C for 16 hours. After hybridization, the slides were washed in 2x SSC buffer with 0.1% (wt/vol) SDS for 2 minutes, followed by a wash in 1x SSC for 2 minutes, then in 0.2x SSC for 2 minutes and finally in 0.05x SSC for 1 minute, each at room temperature. The slides were dried by centrifugation (70 x *g* for 5 minutes). Three biological replicates with one dyeswap were performed for all experiments. Microarray slides were scanned at 10 µm resolution using a Model G2505B (Agilent) microarrayscanner. Fluorescent intensities and morphologies were analyzed using GenePix Pro ver. 6.0 (Axon).

Normalization and Data Analysis

Raw data from each array was preprocessed independently. A lowess-smoothed background was subtracted from all foreground intensities, and a cross-validated lowess-method was used in an intensity-dependent normalization of every array. The $\log_2$ ratios for each spot were further analyzed using a mixed model [29] to detect differentially expressed genes. For YTB a mixed model was fitted to the data for each of the four sample times (5, 15, 30 and 60 minutes) separately and for blood a mixed model was fitted to the data from the 30 minutes time point. Data for the three arrays at every sample time were described by

$$y_{ijk} = \mu_i + u_{ij} + e_{ijk} \tag{1}$$

Where y_{ijk} is the observed $\log_2$ ratio of gene i (1,…,3502) on array j (1,2,3) and in spot k (1,…,5) on that array, μ_i is the expected $\log_2$ ratio for gene i, u_{ij} is a random effect of gene i on array j and e_{ijk} is the remaining noise. The variance components were estimated under the assumption of gaussian errors using a restricted maximum likelihood approach coping with the unbalanced data due to missing spots. Differentially expressed genes were identified by testing the hypothesis H_0: $\mu_i = 0$ against H_1: $\mu_i \neq 0$. A chi-square test for every gene resolves this for the model in [1,95], and a Bonferroni-corrected rejection level of $p < 0.05$ was used throughout. If H_0: $\mu_I = 0$ was rejected, and $\mu_i > 0$, genes were considered to be up-regulated in the cells grown in YTB and blood. If H_0: $\mu_i = 0$ was rejected, and $\mu_i < 0$, genes were considered to be down-regulated. All data analysis algorithms were programmed in MATLAB (MathWorks inc). A gene was discarded from the final results (designated NA in Table S1) if it was replicated in less than 8 spots after filtering of the data.

Microarray Data Accession Number

The microarray data obtained in this study has been deposited in the ArrayExpress database (http://www.ebi.ac.uk/arrayexpress/) according to the MIAME standard. The accession number is E-TABM-541.

Real-time Quantitative RT-PCR

Real time quantitative RT-PCR (QPCR) was used to validate the expression levels for selected genes. QPCR was performed on a Rotor-Gene 6000 centrifugal amplification system (Corbett Research). The genes of interest and the corresponding primers are listed in Table 2. Total RNA used for cDNA synthesis was the same as described above (RNA samples harvested after 30 minutes growth in YTB or blood and their corresponding control samples). Synthesis of cDNA was performed using 1 μg total RNA, 6 μg random primers (Invitrogen) and 40 U RNase OUT (Invitrogen) in a reaction volume of 12.5 μl. The reaction mixture was denatured at 65°C for 10 minutes and cooled at 4°C for 5 minutes. The reaction mixture was then added 4 μl of 5x First Strand buffer (Invitrogen), 1 μl of 0.1 M dithiothreitol (Invitrogen), 1 μl of 10 μM dNTP (Invitrogen) and 140 U of SuperScript III reverse transcriptase (Invitrogen) to a total volume of 20 μl. The reaction mixture was incubated at 25°C for 5 minutes, 2 hours at 50°C, and then for 15 minutes at 70°C. Finally, 20 ng RNaseA (Sigma-Aldrich) was added to the reaction followed by an incubation at 37°C for 20 minutes. PCR amplification was performed using the recommendation by the manufacturer (with an annealing temperature of 60°C) with 2.5 μl 100x diluted cDNA in a 25-μl reaction mixture containing 12.5 μl FastStart SYBR green Master (Roche) and 7.5 μM of each primer. Standard curves with four dilutions were made in duplicates for each primer pair to calculate the amplification efficiency, and all genes were quantified in triplicates. Since the standard curves indicated a slight difference in amplification efficiencies of the different target genes and reference, differential expression was calculated by the Pfaffl method. This is an optimal method to use for calculating relative gene expression when the amplification efficiencies of the target gene and the reference gene are different since the amplification efficiency is included in the calculation [96]. The obtained C_T value for 23S from each sample was used as a reference for each gene in the corresponding samples.

Supporting Information

Table S1 Microarray expression data from *E. faecalis* strain V583 during incubation in blood or 2xYT supplemented with 10% blood (YTB). Gene expression after 30 minutes (blood) or 5, 15, 30 and 60 minutes (YTB) of incubation is relative to the expression during growth in 2xYT for the corresponding time length. a) Genes comprising putative operon structures predicted by http://biocyc.org [1,2] are marked with one color (red or light red for genes on the leading strand, blue or light blue for genes in on the lagging strand). b) Log2-values greater than 1 or less than -1 are highlighted in red or green respectively. Genes for which less than 8 spots were present were discarded from the analysis and are denoted "NA". c) A significantly regulated gene (bonferroni corrected level of $p<0.05$) has the corresponding p-value written in bold. 1.Paley SM, Karp PD (2002) Evaluation of computational metabolic-pathway predictions for *Helicobacter pylori*. Bioinformatics 18: 715–724. 2. Romero PR, Karp PD (2004) Using functional and organizational information to improve genome-wide computational prediction of transcription units on pathway-genome databases. Bioinformatics 20: 709–717.
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Author Contributions

Conceived and designed the experiments: HCV DAB. Performed the experiments: HCV. Analyzed the data: HCV LS IFN DAB. Contributed reagents/materials/analysis tools: LS IFN. Wrote the paper: HCV LS IFN DAB.

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PAPER III

Comparative genomic analysis of pathogenic and probiotic *Enterococcus faecalis* isolates, and their transcriptional responses to growth in human urine.

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Abstract

Background:

Urinary tract infection (UTI) is the most common infection caused by enterococci, and *Enterococcus faecalis* accounts for the majority of enterococcal infections. Although a number of virulence related traits have been established, no comprehensive genomic or transcriptomic studies have been conducted to investigate how to distinguish pathogenic from non-pathogenic *E. faecalis* in their ability to cause UTI.

Methodology/Principal Findings:

In order to identify potential genetic traits or gene regulatory features that distinguish pathogenic from non-pathogenic *E. faecalis* with respect to UTI, we have preformed comparative genomic analysis, and investigated growth capacity and transcriptome profiling in human urine *in vitro*.

Six strains of different origins were cultivated and all grew readily in human urine. The three strains chosen for transcriptional analysis showed an overall similar response with respect to energy and nitrogen metabolism, stress mechanism, cell envelope modifications, and trace metal acquisition. Our results suggest that citrate and aspartate are significant for growth of *E. faecalis* in human urine, and manganese appear to be a limiting factor. The majority of virulence factors were either not differentially regulated or down-regulated. Notably, the *fsrABC* operon important for virulence in *E. faecalis* was significantly up-regulated in the pathogenic MMH594 strain.

Conclusions/Significance:

Strains from different origins have similar capacity to grow in human urine. The overall similar transcriptional responses imply that the pathogenic potential of a certain *E. faecalis* strain is to a great extent determined by presence of fitness and virulence factors, rather than the level of expression of such traits. However, the significant differential expression of the *fsr*-system between MMH594 and OG1RF implies that the amount produced of certain virulence factor(s) can contribute to differences in virulence potential between strains.

Introduction

Once considered as harmless commensals of the intestinal tract, enterococci now rank among the leading causes of infections among hospital patients [1,2]. *Enterococcus faecalis* is among the most prevalent agents isolated from nosocomial urinary tract infections (UTIs), and is a common cause of chronic and recurrent UTIs, especially those associated with structural abnormalities and medical devices, such as urinary catheters [3]. The ability of *E. faecalis* to cause infection has been linked to inherent enterococcal traits, enabling the bacterium to tolerate harsh and diverse environments. In addition, several factors that may contribute to enterococcal virulence have been characterized (reviewed in [4]), and the role of these factors in pathogenicity have been further established in various animal models [5-8] and cultured cell lines [9,10]. However, a widespread distribution of putative virulence determinants in enterococcal isolates independent of origin has been reported [11-16], and to date, no single virulence factor has been demonstrated to be essential for enterococcal infections. The ability of *E. faecalis* to cause infection is therefore likely to involve an orchestrated interplay between the regulation of these putative virulence factors and various genetic determinants that govern adaptation of the bacterial cell physiology during the infection process. Cultivation in urine partly mimics the urinary tract environment, and identification of differentially expressed genes *in vitro* may therefore represent a potential means to identify novel fitness factors required for this particular ecological niche.

Shepard and Gilmore previously examined the effect of growth in urine on the expression of known and suspected enterococcal virulence factors by quantitative real-time PCR [17], and significant changes in *E. faecalis* virulence-associated gene expression were observed in response to the biological cues present in urine, compared to laboratory medium-growth. Furthermore, studies of other pathogens causing UTI have reported responses involving iron acquisition systems and genes involved in sugar and amino acid metabolism [18,19], which may indicate that bacteria suffer from glucose and iron limitation during growth in human urine.

In this report, we compare the global expression profiles of three *E. faecalis* strains during growth in human urine *in vitro*. The three strains were chosen based on their origins; the

Symbioflor 1 strain, included in a commercial probiotic product used for more than fifty years without any reports of infection [20], the hospital outbreak strain MMH594 holding most known virulence genes in its genetic repertoire [21,22], and finally the laboratory strain OG1RF which harbors some important virulence traits like *fsr* and *epa*, but is devoid of mobile genetic elements (MGEs) [23,24]. This latter strain is however capable of causing infection in *e.g.* mice [23,25], and has been extensively used as a model organism to investigate virulence ([4] and references therein) . The aim of this work was to gain insight into genetic factors that make *E. faecalis* such a potent cause of human UTI. The study was designed to identify traits that distinguish pathogenic from non-pathogenic *E. faecalis*. Identification of such traits may ultimately contribute to development of strategies for prevention and treatment of *E. faecalis* UTI.

Results and Discussion

Growth capacity of different *E. faecalis* strains in urine and 2xYT

Escherichia coli associated with UTI normally grow well in urine, while non-uropathogenic strains do not [26]. To examine whether this also could be true for *E. faecalis*, six strains of nosocomial, UTI, commensal or probiotic origin were cultivated in urine and colony forming unit (CFU) counts performed (Fig. 1). Only minor differences in growth capacity were observed between the various isolates, with generation times of around 48 minutes. MMH594 and V583 reached a slightly higher final cell density (~$2.0x10^8$ CFU/ml) compared to OG1RF and Symbioflor 1 (~$1.2x10^8$ CFU/ml), and even more so compared to Baby isolate 62 and 179Vet (~$6.5x10^7$ CFU/ml). These observations are consistent with a recent study by Carlos *et al.* [27], where strains from diverse origins, such as food and clinical strains, did not grow significantly different in urine. Furthermore, the growth capacity of MMH594 observed in the present study was in agreement with previous reports [17].

Comparative genomic hybridization

Since the initial growth experiments did not reveal any strains with a distinctively enhanced or reduced growth capacity in urine, two pathogenic strains MMH594 and OG1RF, and the

probiotic strain Symbioflor 1 were selected for further investigation by comparative genome hybridization and transcriptional analysis.

Comparative genome hybridization was performed to assess the variation in gene content between the three test strains, using V583 as reference (Fig. 2, Fig. 3 and Table S1). A total of 2284 genes were classified as present in all the strains tested. Not surprisingly, the clinical bacteremia isolate MMH594 showed the highest similarity to the reference strain V583 (94.7% genes in common). In addition, the CGH data confirmed the presence of all the ten additional enterococcal pathogenicity island (PAI) genes, covering a 17-kb deletion in V583, in MMH594 [22,28]. For the two other test stains the similarity to the reference strain was significantly lower, with 74.1 and 73.7% of V583 genes represented on the array classified as present in OG1RF and Symbioflor 1, respectively. The CGH analysis indicated that 12 PAI genes without apparent function in virulence were present in Symbioflor1, whereas three PAI genes were found in OG1RF (Fig. 3 and Table S1), but inspection of the published genome sequence [23] showed that these were false positive results. As expected, none of the additional PAI genes seemed to be present in the latter two strains. Altogether, MMH594 contains 596 genes that appear to be divergent in OG1RF and Symbioflor 1. Major variations in the presence of all the previously defined mobile genetic elements (MGEs) were observed between the three test strains. Except for *phage01* and *vanB*, all the MGEs seemed to be present in MMH594. *phage02* appear to be part of the *E. faecalis* core genome, but none of the other elements were found in OG1RF. This observation is consistent with the genome sequence available for OG1RF [23]. Symbioflor 1 appeared to contain certain genes/modules from *phage06*, but not the entire element. The rest of the MGEs were divergent by CGH in Symbioflor 1, which is consistent with previous reports [20]. Notably, Symbioflor 1 contains two major deletions in proximity to the *vanB* associated island and the efaB5 element (Fig. 3 and Table S1). The latter deletion extends in the 5' direction of efaB5 to EF1811 including the *fsr-gelE-sprE* virulence locus.

The number of on-going *E. faecalis* sequencing projects is rapidly increasing, and the recent publication of the OG1RF genome revealed a total of 2474 genes that were common for V583 and OG1RF. This number was based on the homology at the DNA level with the ORFs described for V583, with a BLASTN cutoff e-value of $1x10^{-5}$ [23]. The number of common

genes revealed by sequencing is slightly higher than the number of present genes obtained by CGH in this present study. When comparing the list of common genes between OG1RF and V583 obtained by Bourgogne *et al*. to the data presented here, a total of 168 genes deviate in their classification as present and divergent in OG1RF. In addition, 20 of 2474 genes identified as common to V583 and OG1RF by Bourgogne *et al*. were not represented on the array used in the present study. Moreover, the numbers reported by Bourgogne *et al*. did not include blasting with any of the plasmid ORFs described for V583, while 47 plasmid genes were classified as present in OG1RF by CGH. An interactive Genewiz map [29] of OG1RF CGH and BlastN (Genbank ABPI00000000) analysis compared with V583 is accessible at; http://ws.cbs.dtu.dk/cgi-bin/gwBrowser-0.91/edit.cgi?hexkey=6561d07e713b77fe75aa3403798e36c1.

Transcriptional analysis

A rich laboratory medium (2xYT) was used as the reference culture medium since it is considered to contain a minimum of infection relevant biological cues [17]. The growth capacity in urine was compared to that in the 2xYT medium by CFU counts (Fig. S1). We found that growth in urine was slightly slower, and the cell density obtained was about one log lower than in 2xYT. For the transcriptional analysis, the three strains were grown in 2xYT to a cell density ~$1x10^7$ before exposure to either pre-warmed urine or 2xYT (control). Samples were collected after 5 (t_5) and 30 (t_{30}) minutes growth. The obtained log_2-ratios and *q*-values found in the three strains during growth in urine compared to 2xYT are listed in Table S1.

Growth in urine vs. 2xYT triggers global transcriptional changes for both pathogenic and probiotic *E. faecalis*

The microarray results revealed changed expression in most functional gene categories for all three strains. At t_5, 713 genes were differentially expressed in MMH594, 735 in OG1RF and 730 in Symbioflor 1. 344 of these regulated genes were common for all three strains (Fig. 4A). At t_{30}, the number of regulated genes increased dramatically to 1212 genes in MMH594 and 979 in Symbioflor 1. However, in OG1RF the number of regulated genes decreased to 574 after 30 minutes growth in urine. It is possible that the reduced number of

regulated genes in OG1RF at t_{30} reflects a more rapid adjustment to the new growth environment, which potentially can be advantageous for the establishment of an infection. A total of 378 differentially expressed genes were common for MMH594, OG1RF and Symbioflor 1 at t_{30} (Fig. 4B). Of the 596 genes that appeared unique to MMH594, 153 were differentially expressed at one or both time points during growth in urine. None of the genes unique to OG1RF or Symbioflor 1 were differentially expressed.

The heat map in Figure 5 presents an overview of the regulated genes within each functional category for the three strains. The figure shows large similarities in the expression pattern between the strains, but also reveals an individual transcriptional signature for each strain. The similarities were particularly evident by the down-regulation of several genes involved in transcription and cell envelope functions, and in the up-regulation of several genes involved in fatty acid and phospholipid metabolism, energy metabolism, amino acid biosynthesis, and genes with a regulatory function. For OG1RF, it seems that the down-regulation of several genes involved in protein synthesis occurs at t_5, while most of the down-regulation occurs at t_{30} in the two other strains. We also found several genes encoding proteins with a transport and/or binding function that are regulated in only two of the three strains, however, without any two strains showing a more similar pattern to each other. An overview of the number of regulated genes within each functional category is given in Figure S2.

Transcription of metabolic pathways during exponential growth in urine.

As described in Figure 1, all the investigated *E. faecalis* strains were capable of rapid growth (doubling time of 48.6 ± 3.7 min) in urine, with most strains reaching final cell densities of ~$1x10^8$ cfu/mL (mean growth $1.3x10^8 \pm 0.6x10^8$). Prior to the current study, no comprehensive investigation regarding which substrates or metabolic processes that confer growth of *E. faecalis* in urine existed. The transcriptome data (Table S1) was thus examined to identify metabolic pathways that showed specific responses during exponential growth in urine.

With respect to carbon metabolism the genes encoding the main glucose uptake-system, mannose phosphoenolpyruvate phosphotransferase (PTS) *mptBACD* (EF0019-22) [30] were down-regulated in all three strains. This is consistent with a recent metabolomic investigation which showed that urine from healthy adults contains glucose concentrations in the range of 0.2-0.6 mM [31]. Such concentrations of glucose is below the threshold for release of carbon catabolite repression (CCR), and the cells thus initiate use of less preferred carbon and energy sources [32]. This implied that substrates besides glucose might play a role for growth of *E. faecalis* in urine. However, of the loci known to be subject to catabolite control protein A (CcpA) mediated CCR, only the genes encoding citrate metabolism (EF3322-15) [33] were positively modulated in MMH594 and OG1RF at both time points and at t_5 in Symbioflor1. At t_{30} EF3322-15 only showed a slightly (not statistically significant) enhanced expression in Symbioflor 1. The content of citrate in human urine is in the range of 1-2 mM [34], which suggests that citrate metabolism is important for *E. faecalis* during growth in urine.

PTS systems facilitate uptake of diverse sugars in *E. faecalis*. Two genes encoding PTS systems with unknown substrates (EF2438 and EF2603) showed an enhanced expression in all three strains. Both EF2438 and EF2603 are part of the *E. faecalis* core genome, and might be important for growth of *E. faecalis* in urine. Furthermore, two operons encoding a sucrose uptake PTS-system (EF1602-01) and sucrose metabolism (EF1603-04) showed consistent up-regulation in all three strains. Dietary sucrose is normally degraded in the intestinal lumen and absorbed as glucose and fructose, but a previous study has shown that even healthy individuals have µM sucrose content in their urine [35]. Moreover, the sugar content in urine increases with high sugar diet. Once sucrose is present in the bloodstream it is not metabolized further, but removed from the blood via the renal capillaries and excreted into the urine, reaching concentrations of 70 to 200 µM [35]. Interestingly, EF1603-04 knock-out mutants show reduced virulence in a *Caenorhabditis elegans* infection model [36,37]. All three strains showed elevated expression of the major facilitator family transporter (EF0082) proposed to function in import of phosphorylated sugars [38] and glycerol [39], which implies that such substrates might contribute to growth in urine.

Transcriptome analysis conducted on an *E. coli* asymptomatic bacteriuria strain revealed an important role of amino sugar and amino acids present in urine as growth substrates [40]. The

transcription of *nagB* (EF0466) and *nagA-1* (EF1317) involved in N-acetyl glucosamine metabolism was highly elevated, implying that these substrates were utilized by *E. faecalis* during growth in urine. A massive down-regulation of *glmS* (EF2151), which is responsible for conversion of fructose-6P into glucosamine-6P using glutamine as a nitrogen source, could signify glutamine constraints.

Growth in urine also had an impact on pyruvate metabolic pathways and certain changes were strain specific. For OG1RF and Symbioflor 1, we observed increased expression of L-lactate dehydrogenase (*ldh*-1; EF0255), whereas expression of *adhE* (EF0900), involved in ethanol formation was reduced. The *pflAB* (EF1612 and EF1613) genes responsible for formate formation were reduced in MMH594 and Symbioflor 1. In all strains the *lutABC* operon (EF1108-1110), involved in metabolism of L-lactate like substrates was up-regulated. The pyruvate dehydrogenase complex gene-cluster *pdhAB, aceF* and *lpdA* (EF1353-56) involved in acetyl-CoA biosynthesis showed consistent up-regulation in all three strains. Moreover, the *ackA* gene (EF1983) responsible for conversion of acetyl-phosphate to acetate and ATP was significantly down-regulated, perhaps as a consequence of increased acetate production due to elevated activity of the citrate metabolism (EF3322-15) [33]. It is thus conceivable that the increased acetyl-CoA formation serves to supply either the FASII biosynthesis, or the citrate metabolism.

Transport and biosynthesis

Compared to the rich 2xYT medium the growth rates were significantly lower in urine, and moreover, the growth halted one order of magnitude below that in 2xYT (Fig. S1). For *E. coli* it has been demonstrated that growth in urine is restricted by availability of one specific cofactor, namely iron [40]. We were thus interested to see whether the transcriptional responses with respect to transport and biosynthesis processes in *E. faecalis*, could reveal candidate nutrients or co-factors whose availability restrict growth of *E. faecalis* in urine.

Human urine contains significant amounts of creatine, creatinine, and glycine, while other amino acids like histidine, glutamine, methionine, proline, glutamate, arginine and branched chain amino acids (bcaa) are present at lower concentrations [41]. The CGH-results indicate

that MMH594 and Symbioflor 1 have similar requirements for amino acids as OG1RF, which was shown to be auxotrophic for amino acids like histidine, isoleucine, methionine, and tryptophan [24]. Also, some *E. faecalis* strains require arginine, glutamate, glycine, leucine, or valine [24], and are capable of utilizing certain amino acids as energy and carbon source [42,43]. However, transcription of the genes encoding catabolism of arginine (EF0104-7 and EF0108) and serine (EF0097-100) was significantly reduced, indicating a shift towards protein synthesis rather than energy metabolism.

According to our data, the transcription of several genes encoding oligo-peptide ABC-transporters (EF0907, EF0909-12 and EF3110-06) was enhanced at t_{30}, and the transcription of three amino acid permease genes (EF0635, EF0929 and EF2377) and two operons encoding amino acid transporters (EF0247-46 and EF0761-60) was reduced in all three strains (Table S1). These observations indicate that *E. faecalis* meets its demand for certain amino acids by acquiring oligo-peptides during growth in urine. However, the *gln*-operon encoding glutamine/glutamate transport system (EF1120-17) [44] were up-regulated in all strains at both time points, suggesting that glutamate/glutamine from urine were utilized. This was further supported by the observed reduced expression of the glutamine synthase operon *glnRA* (EF2160-59) and glutamate synthase *gltA* (EF2560). On the contrary, the increased expression of *cysK* (EF1584) implies that cysteine is scarce in urine, which also is in accordance to the metabolomic analysis of human urine [41].

An operon comprising a putative amino acid ABC transporter (EF0893-92) and a putative aspartate aminotransferase (EF0891) was highly up-regulated in all strains. The latter gene is predicted to facilitate the conversion of aspartate and alpha-ketoglutarate to oxaloacetate and glutamate, which may also in turn explain the down-regulation of the above mentioned *gltA*. Furthermore, the transcription of a gene encoding methionine synthase (EF0395) was enhanced in all three strains. These results are consistent with the metabolomic analysis of human urine which showed that aspartate is 5-fold more abundant than methionine [41]. These observations imply that aspartate might serve a key role for nitrogen metabolism of *E. faecalis* in urine.

We observed an enhanced transcription of an isochorismatase gene (EF3192) in all strains at t_{30}, and also a second isochorismatase gene (EF3090) in MMH594. This coincided with a down-regulation of the EF1561-68 operon in MMH594 and Symbioflor 1, responsible for biosynthesis of chorismate, which is a precursor of aromatic amino acids, folate and quinones. In agreement with this observation, we also noticed a reduced transcription of several genes responsible for biosynthesis of cofactors, prosthetic groups, and carriers including menaquinone and ubiquinone (EF3255-54 and EF3260). Interestingly, the genes encoding chorismate biosynthesis were not down-regulated in OG1RF. Moreover, another gene cluster encoding menaquinone biosynthesis (EF0446-50) showed a reduced transcription in MMH594 and Symbioflor 1, while an enhanced transcription in OG1RF, although the regulation of some of the genes were not statistically significant.

Thus, it appears that *E. faecalis* scavenge available peptides and amino acids, which in turn are sequentially hydrolyzed and transaminated in order to fuel the pool of depleted amino acids.

Urinary tract pathogenic bacteria like *E. coli* (UPEC), have pathogenic islands dedicated to acquisition of limited nutrients and biometals [45]. Manganese is one such factor which is essential for the fermentative metabolism of lactic acid bacteria (LAB) [46,47]. The up-regulation of the main manganese scavenging mechanism encoded by *efaCBA* (EF2074-76), accompanied by two other genes (EF1057 and EF1901) encoding Mn^{2+}/Fe^{2+} transporters in all strains at both time points is a clear indication that *E. faecalis* scavenged manganese. The content of manganese in human urine is in the nano molar range [48], while the optimal concentration for *E. faecalis* is in the micro molar range [49]. Thus manganese may be restrictive for the growth of *E. faecalis*. This in turn can affect the virulence of the bacterium and *efaCBA* has indeed been shown to be implicated in virulence [50]. Notably, for MMH594 a potential auxiliary Mn-uptake system (EF 0575-78) [51], located within the PAI also showed highly elevated expression, indicating that PAI harboring strains might be better equipped to cope with manganese deplete environments.

Furthermore, our experiments revealed an enhanced expression of several other genes involved in iron transport; the *feoAB* (EF0475-76) and *ceuBCD* and *fatB* (EF3085-82) operons were up-regulated in all strains at t_{30}. Another gene involved in iron transport, *feuA*

(EF0188) was down-regulated in all strains at t_5, but was up-regulated in MMH594 and OG1RF at t_{30}. Interestingly, in OG1RF a third iron transport encoding operon (EF0191-93) was only up-regulated at t_{30}. Iron is one of the main limiting factors for *E. coli* growth in urine and the addition of iron to urine increased the maximum growth extensively [18,19]. LAB, on the other hand comprise one of the very few groups of bacteria for which iron is not an essential growth factor [47]. Even so, our data suggest a potentially important role of iron acquisition and metabolism during growth in urine.

Stress response of V583 towards exposure to urine

Proteomic analyses with systematic exposure to various stresses have previously identified six genes encoding general stress response proteins (GSPs) which were up-regulated in *E. faecalis* by a wide variety of environmental stimuli [52]. The enhanced expression of all the GSP-encoding genes at one or both time points in the present study indicates that the bacterium experienced a multitude of stress factors upon the encounter with urine. This impression was further substantiated by the significantly differential transcription of a large number of genes with a proven or predicted function in other stress responses in *E. faecalis* (Table 1 and S1).

The gene encoding Gsp62 (EF0770; hypothetical protein) was the only GSP which showed a significantly enhanced expression in all strain at both time points. The stress- and starvation inducible *gls24* operon (EF0076-81) was significantly up-regulated at both time points in OG1RF and Symbioflor 1, while partly up-regulated in MMH594. Inactivation of *gls24* and *glsB* (EF0079 and -80, respectively) has been reported to have a pleiotrophic effect on cell morphology and stress tolerance in *E. faecalis* [53]. A *gls24* disruption mutant has also been shown to be highly attenuated in animal infection models [54,55]. MMH594 contains two additional *gls24*-like genes within the PAI (EF0604 and PAIef0055). Both gene were up-regulated at t_{30} and might possibly contribute to the fitness of MHH594 during growth in urine.

An organic hydroperoxide resistance protein, *ohr* (Gsp65; EF0453) was up-regulated in MMH594 at t_5, and in all three strains at t_{30}. An *ohr* mutant has previously been shown to be

less resistant to the oxidative stress generated by 20 mM Tertiary-Butylhydroperoxide, suggesting that Ohr may be implicated in oxidative stress resistance in *E. faecalis* [56]. Interestingly, the microarray data revealed differentially expression of an arsenal of genes holding putative roles in oxidative stress response in *E. faecalis* (Table 1 and S1). Verneuil and co-workers previously reported the expression of *ahpCF* (EF2738 and -39), *sodA* (EF0463), *katA* (EF1597) and *gor* (EF3270) to be positively controlled by the transcriptional regulator *hypR* (EF2958) [57]. Indeed, *hypR* showed augmented expression in Symbioflor 1 at both t_5 and t_{30}. However, the lack of significant enhanced expression of *hypR* in the two remaining test strains, may suggest that that these genes are under more complex regulation. In fact, *fur* (EF1525), *perR* (EF1585) and *zur* (EF2417), encoding other putative regulators of oxidative response in *E. faecalis* [58,59] were also up-regulated at t_{30} in MMH594, in all three strains and in Symbioflor 1, respectively. In addition, *ers* (EF0074), encoding another regulator involved in survival during oxidative stress [60] showed reduced transcription in OG1RF at t_5 and in Symbioflor 1 at both t_5 and t_{30}. The enhanced transcription of genes involved in oxidative stress response during exposure to urine is interesting. Especially in light of an observed adaptation to lethal challenges of H_2O_2 by pretreatment with sublethal concentrations of H_2O_2 [61], and a reported link between oxidative stress response and survival within macrophages in enterococci [60,62,63]. Furthermore, it has been demonstrated that purified lipoteichoic acids from *E. faecalis* induced proliferation and production of nitrous oxides and cytokines by a subpopulation of basal urothelial cells [64,65]. It is thus tempting to speculate that urine act as a cue to trigger oxidative stress-protection by *E. faecalis*, in order to render increased resistance against certain host defense mechanisms in the urinary tract.

Modifications to the cell envelope caused by growth in urine

When infecting a host, the integrity and composition of the cell envelope of the bacterium is important to avoid damage by the host defense systems [66,67]. In the case of *E. faecalis*, it has been demonstrated that important processes in the interaction with the host *e.g.* recognition by immune system mechanisms and innate immune evasion, involve specific cell envelope structures like lipotechioc acids [68], and cell wall and capsular polysaccharide determinants [69,70].

During growth in urine, signs of adaptation to this new growth environment were evident for several genes important for the cell membrane composition and surface related structures (Table S1). We observed an immediate response to urine by the up-regulation of two gene clusters (EF0282-84 and EF2886-75) responsible for type II fatty acid biosynthesis (FASII) and isomerization of membrane phospholipids. Most of these genes were up-regulated in all strains at t_5 and t_{30}. Interestingly, these gene clusters have previously been shown to be up-regulated in response to growth in blood [71] and to exposure to the cell membrane detergent SDS [72]. Furthermore, the FASII genes were down-regulated in response to exposure to NaCl (Solheim *et al*, in preparation), bovine bile, and SDS and bovine bile in combination [72], indicating that several different external stressors triggers remodeling of the fatty acid composition in the cell membrane.

In addition to the FASII pathway, a regulation of three genes encoding lipases and two genes encoding cardiolipin synthetases further indicates both degradation and processing of fatty acids (Table S1). The cardiolipin synthetase gene (EF0631) was down-regulated in MMH594 and Symbioflor 1 at both t_5 and t_{30}, and in OG1RF at t_5, whereas another cardiolipin synthetase gene (EF1608) was up-regulated at both time points in Symbioflor 1, at t_5 in OG1RF and t_{30} in MMH594. Of the lipase encoding genes, EF0169 was up-regulated in all strains at both time points, EF3191 was up-regulated in MMH594 and Symbioflor 1 at t_{30}, and EF1683 was only up-regulated in Symbioflor 1 at t_{30}. It is possible that the lipolytic activity is connected to a modulation of the FASII genes, as it recently was demonstrated that *E. faecalis* can utilize available fatty acids from the environment in their membrane biogenesis [73]. However, there are only trace amounts of free fatty acids in urine [34], and it is therefore more likely that the remodeling of the fatty acid composition in the cell membrane is a more general stress response in *E. faecalis*, while the lipases may play a more specialized role in virulence. A recent study by Walecka and co-workers revealed that a higher percentage of invasive *E. faecalis* isolates produce lipases compared to non-invasive isolates [74], indicating a central role for lipase activity during invasive infection. Notably, Symbioflor 1 showed a more enhanced expression of genes encoding lipases compared to the pathogenic strains.

The ability of *E. faecalis* to adhere to and develop biofilm is thought to be important for its potential to cause UTI and other infections [75]. In our experimental design, the cells were cultivated planktonically. We were thus interested in assessing whether genes implicated in

adherence or biofilm formation would be modulated by human urine. The gene encoding the maltose PTS system *malT* (EF0958) and the cognate operon *bopABCD*/*malPBMR* (EF0957-54), which are involved in biofilm formation [76,77], were partly up-regulated in OG1RF at t_5. Another gene important for biofilm production and the initial attachment stage for binding to abiotic surfaces is a sortase A encoding gene, *srtA* (EF3056) [78,79]. This gene showed an enhanced expression in MMH594 at t_{30} and Symbioflor 1 at both time points. Interestingly, an *srtA* mutant showed a slightly attenuated virulence during UTI in mice [80]. However, among the genes encoding potential substrate proteins of SrtA, only EF2713 was up-regulated at t_5 in MMH594, whereas EF3314 showed an enhanced expression in Symbioflor 1 at both t_5 and t_{30}. This latter gene encodes a protein recently shown to be important for the pathogenicity of *E. faecalis* [81], and it is noteworthy that the only strain which showed an enhanced expression of this gene, was the probiotic strain.

Bacterial surface proteins are key players in host-pathogen interactions [80]. Therefore, the change of membrane bound proteins might alter the bacterium's potential of causing an infection. Regulation of several genes encoding proteins bound to the cell membrane or cell surface *i.e.* membrane proteins and lipoproteins was observed for all three strains (Table S1). Moreover, most microbial surface components recognizing adhesive matrix molecules (MSCRAMMs) and cell-wall anchor family proteins [82] including the endocarditis- and biofilm-associated pilus (*ebp*) [83,84] were either down-regulated, or not differential regulated (Table S1).

A gene encoding a chitin binding protein (EF0362) and one encoding a chitinase (EF0361) were up-regulated in all three strains at t_5. The direct function for these genes in response to urine is not clear, however a homologous protein GbpA in *Vibrio cholerae* was shown to facilitate binding to the chitin monomer N-acetylglucosamine [85], a sugar residue found on the surface of epithelial cells [86-88], which line the cavities and surfaces of structures including the urinary tract. Hence, it is possible that biological cues in urine trigger the up-regulation of these genes as an initial step of adherence to uroepithelial cells. Interestingly, growth of *E. faecalis* V583 in blood triggered an even more enhanced transcription of these two genes [71], but a functional study of these genes would be required to elucidate any function related to enterococcal virulence.

Mohamed *et al.* [89] demonstrated that a knockout mutant of the secreted antigen *salB* (EF0394) in OG1RF showed reduced biofilm formation in BHI, but enhanced biofilm production in the presence of serum or fibronectin. They also showed that the *salB* mutant was able to bind to the extra cellular matrix (ECM) proteins collagen type I and fibronectin, whereas wild type OG1RF did not bind these ECM proteins [89]. Furthermore they showed that a *salA* (EF3060; secreted lipase) mutant also produced slightly less biofilm than wild type OG1RF, while binding to ECM was unaffected. During growth in urine *salA* was down-regulated in all strains at both time points, while *salB* was down-regulated in all strains at t_5, and in MMH594 at t_{30}. Mohamed and co-workers [89] speculated that under certain conditions a down-regulation of *salB* would be sufficient to see similar effects as was seen for the *salB* mutant, thus it is possible that the expression of *salB* and possibly also *salA* is reduced in response to urine in order to promote colonization of the urinary tract.

At t_5, a gene encoding the major autolysin of *E. faecalis*, *atlA* (EF0799) was down-regulated in all three strains. An *atlA* deletion mutant of OG1RF showed delayed biofilm formation, reduced attachment on plastic surfaces and longer chains than the wild type OG1RF [78,90]. AtlA is also essential for DNA release and biofilm accumulation, which is needed for the development of a mature biofilm in *E. faecalis* [78,91]. MMH594 and Symbioflor 1 contain a second peptiodoglycan hydrolase encoding gene *atlB* (EF0355), which have been shown to compensate for the absence of AtlA in autolysis and cell separation [90]. *atlB* was down-regulated at t_{30} in MMH594, while not differentially expressed in Symbioflor 1. Two putative holin genes (EF0353-54) up-stream of *atlB* were also down-regulated in MMH594, however these two genes were absent in Symbioflor 1. The lowered expression of *atlA* and *atlB* may also be connected to reduced cell wall synthesis indicated by down regulation of several genes responsible for peptidoglycan biosynthesis (Table S1), which again is consistent with the significantly lower growth rate in urine compared to 2xYT.

Most of the genes within a cluster responsible for the production of a serotype-determining exopolysaccharide (EF2198-2177; *epa*) [92,93] were down-regulated both at t_5 and t_{30} in the three strains. An OG1RF Δ*epaB* mutant has previously been reported to show reduced virulence in mice [94], higher susceptibility to phagocytic killing [70], and decreased biofilm formation compared to the wild type [70,95]. Furthermore, Singh *et al.* recently showed that the *epaB* mutant was less competitive compared to the wild type in a model of UTI in mouse [96]. However, it is possible that the exopolysaccharide production is body-site dependent,

and could be more pronounced in *E. faecalis* that have reached the glomerular basement membrane in kidneys, which is a preferred site for *E. faecalis* colonization [96,97].

The serotype 2 capsular polysaccharide (*cps*) [98], which constitutes an important virulence factor that enables *E. faecalis* to evade phagocytic killing, by masking the lipoteichoic acids [69], is absent in both OG1RF and Symbioflor 1 (Fig. 3 and Table S1). Intriguingly, the *cps* gene cluster (EF2495-85) was down-regulated in MMH594 at t_{30}, which is similar to the response observed in V583 growing in blood [71]. It is tempting to speculate that a basal capsular polysaccharide production could be sufficient to protect *E. faecalis* from complement-mediated opsonophagocytosis, especially in infected tissues where micro-colonies or biofilm develop.

Glycosyl transferase family proteins are involved in formation of a number of cell surface structures including glycolipids, glycoproteins and polysaccharides [99]. Apart from the *epa* and *cps* loci, five genes encoding glycosyl transferases were also down-regulated in one or more strains in response to growth in urine. Neighboring the *epa* cluster, two glycosyl transferases (EF2170 and EF2167) proposed as potential virulence factors [100], together with the EF2172-66 genes, comprise a three operon locus possibly connected to lipopolysachharide production. This gene cluster is present in MMH594 only (Fig. 3 and Table S1), and most genes within this locus were down-regulated at both t_5 and t_{30}. The gene encoding the glycosyl transferase *bgsA* (EF2891), responsible for the biosynthesis of the major cell membrane glycolipid in *E. faecalis*, was down-regulated in OG1RF at t_{30}. A *bgsA* mutant showed a reduced ability to accumulate biofilm, reduced virulence in a mouse bacteremia model and reduced ability to adhere to colonic epithelial cells [101]. The *bgsA* mutant also displayed a reduced cell surface hydrophobicity compared to the wild type, an effect which may also contribute to the impaired biofilm production [101]. The neighboring gene, EF2890, also encodes a glycosyl transferase that was down-regulated in OG1RF and MMH594 at t_{30}. The function of EF2890 remains to be elucidated, but it could possibly be connected to that of *bgsA*. A putative n-acetlyglucosamine glycosyl transferase-encoding gene (EF0887) implicated in peptidoglycan-biosynthesis was up-regulated in all three strains at t_{30}, while down-regulated at t_5 in Symbioflor and OG1RF.

In sum, the human urine milieu appears to instigate a drastically altered composition of the cell envelope and cell surface structures, some of which might be advantageous or required for establishment of *E. faecalis* UTI.

Virulence traits and Regulatory genes

A number of genetic traits have been identified to contribute to virulence in *E. faecalis* [5,6,8,25,55,70,98,102,103]. The expression of selected virulence genes in MMH594 during growth in urine have previously been examined by real-time quantitative PCR (QPCR) [17]. More recently, a new QPCR study of the expression in several strains including MMH594 during growth in urine was published [104]. The two studies show some differences in gene expression in MMH594, *e.g.* of a gene encoding the enterococcal surface protein Esp (PAIef0056). Shepard and Gilmore found an enhanced expression of *esp*, while Carlos *et al.* found a reduced expression of the same gene. In the present study, we found that the *esp* gene was not significantly differentially expressed. Indeed, QPCR appear to be more sensitive and have a broader detection range than microarray, but the deviating results still seem to imply a problem when comparing these types of experiments. Shepard and Gilmore reported a growth-phase dependent difference in the expression of the virulence genes tested. Hence, the differences observed between these three similar experiments are most likely due to the different methods used for cultivation. Our aim was to investigate the immediate effect on actively growing *E. faecalis* cells upon the first encounter of urine. We revealed a significant impact on the transcription of a number of virulence related traits connected to stress, co-factor acquisition, and cell surface structures (described above), and a summary of these genes can be found in Table 2.

The *fsr* quorum sensing system has been shown to coordinate expression of the virulence factors *gelE* (encoding a gelatinase) and *sprE* (encoding a serine protease) during infection of *C. elegans* and in mouse preitonitis models [25,103], and several other genes were differentially expressed in wild type OG1RF compared to an *fsrB* mutant, indicating a more complex regulatory network [105]. Consistent with previous observations [17], we detected an up-regulation of the *fsrABC* genes (EF1822-20) in MMH594 at t_{30}. The *fsrA* gene was also up-regulated at t_5. Interestingly, we found no regulation of these genes in OG1RF (the genes are divergent in Symbioflor 1). In MMH594, the downstream *gelE* (EF1818) was down-regulated at t_5, but not at t_{30}. The *sprE* gene (EF1817) was not significantly regulated at either

time points. These results show that for MMH594, transfer to urine immediately triggers an elevated transcription of the *fsr*-quorum sensing system. Quorum sensing regulatory cascades are characteristically initiated by elevated expression of a regulatory unit, in this case *fsr*-operon, of which the most likely consequence would be the subsequent induction of the *fsr*-regulon.

The *fsr*-quorom sensing system is one of in total 18 two component systems in the V583 genome [106,107]. Of these two component systems, MMH594 contains 17, and OG1RF and Symbioflor contain 14. The histidine kinase -response regulator system 17 (hk-rr17; EF1633-32) has been suggested to be negatively regulated by *fsr* [105]. This could be consistent with modulation of *fsr* in MMH594. However, the absence of *fsr* in Symbioflor 1, and the observed down-regulation of hk-rr 17 system in this strain demonstrate that *fsr* can not be responsible for the repression of the hk-rr17 system in Symbioflor 1. Several of the other two-component systems were also affected by growth in urine such as hk-rr02 (EF3197-96) and hk-rr04 (EF1703-04), which were up-regulated in all strains at t_{30} and hk-rr10 (EF1050-51), which was down-regulated in all strains at both time points (although not significantly in all strains). The latter system encodes *etaRS*, which has been shown to be involved in stress response and virulence in *E. faecalis* [108].

The PAI is significantly more prevalent among infection-derived isolates compared to *E. faecalis* from other sources [22,28,109,110]. Moreover, the contribution of PAI-related genes to the pathogenicity of *E. faecalis* has been experimentally determined for certain traits (*araC*, cytolysin, *esp*)[5,102,111]. In the genome of the three strains used in this study only MMH594 contains the entire enterococcal PAI (129 genes), and 125 of the PAI genes are represented on the array. Fifteen genes including the *araC*-regulator (EF0524) were down-regulated, while twenty genes including manganese transporter (EF0575-77), *gls24* (EF0604) and a bile salt hydrolase (EF0521) were up-regulated at t_{30} in MMH594. The latter gene was also the only PAI gene which showed an enhanced expression in Symbioflor 1. These results demonstrate that potential virulence-, stress- and fitness-genes located in the PAI do in fact respond to an infection-relevant milieu like urine. However, the exact function of these genes in the pathogenicity of *E. faecalis* remains to be elucidated. Moreover, transcripts were detected for a substantial number of PAI genes, implying that their mere presence and basal expression might also be important during UTI.

Although the PAI is found in high frequency in infection derived isolates [22,28,109,110], the contribution of many PAI-genes to the pathogenicity of *E. faecalis* remains to be elucidated. Our experiment revealed that approximately one third of the PAI genes were differentially expressed in MMH594. In addition, transcripts were detected for a substantial number of PAI genes, implying that their mere presence and basal expression might be important also during UTI.

In conclusion, a significant proportion of the transcriptional responses seen during growth in urine were common for the three different strains examined, and the main differential regulation was observed among genes related to stress responses, energy metabolism, acquisition of trace metals, and a drastic modification of the cell envelope. One intriguing difference between the two pathogenic strains OG1RF and MMH594 was the regulation of the *fsr*-system, which could signify a difference in the virulence potential between these two strains.

Materials and methods

Bacterial strains and growth conditions: Bacterial strains used in this study are listed in Table 3. The growth capacity of six *Enterococcus faecalis* strains was examined. Three of these strains were selected for transcriptional profiling based on their origin. For all experiments *E. faecalis* strains were streaked on a 2xYT agar plate (1% (w/v) yeast extract, 1.6% (w/v) tryptone and 1% (w/v) NaCl) and incubated at 37°C over night (ON). Four individual colonies were then inoculated into the same tube of 5 ml 2xYT medium and grown ON without shaking at 37°C. For growth in urine, human urine was collected from four healthy men and women who had no history of UTI or antibiotic use in the last 6 months. The urine was pooled with equal amounts from each volunteer, centrifuged at 12000 x g and sterilized twice by filtration (0.22 µm-pore size). Since the composition of human urine may potentially be variable, samples were collected on three separate days for three replicate experiments and used within the next day.

Growth measurement: The six *E. faecalis* strains were pre-cultured as described above. ON cultures were diluted 1000x in either preheated urine (37ºC) or in preheated 2xYT medium and incubated ON. These cultures were then diluted 1000x in either preheated urine or 2xYT, and cell growth was measured spectrophotometrically with a Bioscreen instrument (Bioscreen

C) and by plating and colony forming units (cfu) counts. Growth experiments measured spectrophotometrically were performed in triplicates with a total volume of 300 µl of bacterial inoculum in fresh urine or 2xYT medium. Wells containing sterile urine / 2xYT were used as negative controls. Cultures were incubated at 37°C and optical density 600 nm (OD_{600}) was measured at 15-min intervals for 24 hours. To determine CFU/ml, viable cell counts were performed as follows: ON cultures were inoculated (1000x dilution) in preheated urine. Samples were collected immediately after inoculation, and after 2, 4, 6, 8, 10 and 24 hours for 2xYT, and also after 15 hours for urine. The number of CFU/ml was estimated by averaging the colony count values in two replicates per strain after ON incubation at 37 °C.

Cultivation and sampling prior to microarray analysis: The three selected *E. faecalis* strains, MMH594, OG1RF and Symbioflor 1 were pre-cultured as described above. The cultures were then diluted 1000x in 250 ml pre-warmed 2xYT medium and incubated further at 37°C. When the culture reached OD_{600} = 0.1 the cultures from each strain was split in two and centrifuged (10000 x *g* for 3 min at 37°C). For the control cultures the pellets were resuspended in 100 ml pre-warmed 2xYT (37°C) whereas for the test culture the pellet was resuspended in 100 ml pre-warmed urine (37°C). Samples (45 ml) of each culture were collected immediately after the resuspension in urine (t_5), and after 30 min (t_{30}) by centrifugation (8000 x *g* for 2 min at 37°C), and the pellets were immediately frozen in liquid nitrogen and kept at -80°C prior to RNA extraction.

RNA isolation, cDNA synthesis, fluorescent labeling and hybridization: Total RNA was isolated by FastPrep (Bio 101/Savant) and RNeasy Mini kit (QIAGEN) as previously described [71]. The concentrations of the RNA samples were measured by using the NanoDrop (NanoDrop Technologies), and the quality was assessed by using the RNA 600 Nano LabChip kit and the Bioanalyzer 2100 (Agilent Technologies). cDNA was synthesized and labeled with the Fairplay III Microarray labeling kit (Stratagene) according to the manufacturer's protocol, with the following modifications: For each labeling reaction, 10 µg of total RNA and 500 ng of random primers were initially preheated at 70°C for 10 min. A reverse transcription-PCR mixture (10x AffinityScript RT buffer, a 20x deoxynucleoside triphosphate mixture, 0.1 M dithiothreitol, 20 U RNase block, and AffinityScript HC RT) was added to the annealed primers and RNA, and the reaction mixture was further
incubated for 3 h at 42°C. After labeling, 1 µL of hydroxylamine (Sigma Aldrich) was added to quench the coupling reaction, and the reaction mixture was incubated 10 min. at room temperature. 70 µL RNase-free water was then added, and unincorporated dyes were removed

from the samples by using the QIAquick PCR purification kit (QIAGEN). Labeled samples were then dried, prior to resuspension in 140 µl hybridization solution (5x SSC, 0.1 % (w/v) SDS, 1.0 % (w/v) bovine serum albumin, 50 % (v/v) formamide and 0.01 % (w/v) single-stranded salmon sperm DNA) and hybridized for 16 h at 42 ºC to the array in a Tecan HS 400 pro hybridization station (Tecan). Arrays were washed twice at 42 ºC with 2x SSC + 0.2 % SDS, and twice at 23 ºC with 2x SSC, followed by more stringent washes at 23 ºC with 0.2x SSC and with filtrated H_2O. Three replicate hybridizations were performed with three separate batches of RNA. The three batches of RNA were obtained in three separate growth experiments. The Cy3 and Cy5 dyes (Amersham) used during cDNA synthesis were swapped in two of the three replicate hybridizations. All samples in the three experiments were co-hybridized with control samples collected at equal time points (*e.g.* t_5 was hybridized along with t_5). Hybridized arrays were scanned at wavelengths of 532 nm (Cy3) and 635 nm (Cy5) with a Tecan scanner LS (Tecan). Fluorescent intensities and spot morphologies were analyzed using GenePix Pro 6.0 (Molecular Devices), and spots were excluded based on slide or morphology abnormalities.

Microarrays: The microarray used in this work has been described previously [112]. The microarray designs have been deposited in the ArrayExpress database with the accession numbers A-MEXP-1688 and A-MEXP-1765.

Data analysis: Downstream analysis was done by the LIMMA package (www.bioconductor.org) in the R computing environment (www.r-project.org). Preprocessing and normalization followed a standard procedure using methods described by Smyth & Speed [113]. Testing for differential expressed gene was done by using a linear mixed model as described in Smyth [114]. A mixed-model approach was chosen to adequately describe between-array variation and still utilize probe-replicates (3 replicates of each probe in each array). An empirical Bayes smoothing of gene-wise variances was conducted according to Smyth *et al* [115]. For each gene, the p-value was adjusted to control the false discovery rate; hence, all p-values displayed are FDR-adjusted (and referred to as *q*-values). A gene was found to be significantly regulated if $q < 0.01$ and the $\log_2$-ratio was similar or above 0.5, or similar or below -0.5. A gene represented with less than 1 spot on one or more arrays was excluded from the final results and marked as NA.

Comparative genomic hybridization: Genomic DNA was isolated by using the FP120 FastPrep bead-beater (BIO101/Savent) and the QiaPrep MiniPrep kit (Qiagen), as previously

described [112], and then labeled and purified with the BioPrime Array CGH Genomic labeling System (Invitrogen) and Cyanine Smart Pack dUTP (PerkinElmer Life Sciences), according to the manufacturer's protocol. Standard methods in the LIMMA package [113] in R (http://www.r-project.org/), available from the Bioconductor (http://www.bioconductor.org) were employed for preprocessing and normalization. Within-array normalization was first conducted by subtracting the median from the log-ratios for each array. A standard loess-normalization was then performed, where smoothing was based only on spots with abs(log-ratio) < 2.0 to avoid biases due to extreme skewness in the log-ratio distribution. For the determination of present and divergent genes a method that predicts sequence identity based on array signals was used, as described by Snipen et al. [116]. A threshold of 0.75 was used in order to obtain a categorical response of presence or divergence, *i.e.* genes with *Sb*-value > 0.75 were classified as present, while genes with *Sb*-value < 0.75 were classified as divergent. Genes with *Sb*-value = 0.75 remained unclassified.

Microarray data accession number: The microarray data have been deposited in the ArrayExpress database with the series accession number E-TABM-885.

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Tables

Table 1: Differentially expressed genes with a proven or predicted function in various stress responses in *E. faecalis*.

ORF	Other names	Gene product	Log$_2$-ratio*						Reference
			MMH594		OG1RF		Symbioflor 1		
			t_5	t_{30}	t_5	t_{30}	t_5	t_{30}	
General stress response									
EF0453	Gsp65	OsmC/Ohr family protein	0.9	3.0	0.7	3.1	0.9	3.8	[52,56]
EF0770	Gsp62	Conserved hypothetical protein	1.1	4.0	0.9	2.0	0.9	3.1	[52,117]
EF1058		Universal stress protein family	-	-	-	-	2.2	2.3	[100]
EF1084		Universal stress protein family	-	-	-	-	-	0.7	[100]
EF1308	Gsp66	DnaK protein	0.8	-	-	- 1.1		- 0.6	[52,118]
EF1560	Gsp63	Hypothetical protein	1.2	3.1	-	-	-	1.3	[52,117]
EF1744		General stress protein, putative	0.6	1.8	-	-	0.8	1.8	[100]
EF1810		General stress protein A (*gspA-1*)	-	2.1	-	-	-	-	[100]
EF1811		General stress protein A (*gspA-2*)	1.1	4.1	1.3	-	-	2.7	[100]
EF1982	Gls33	Universal stress protein family	1.1	1.6	1.4	-	1.6	2.3	[100,117,119]
EF2633	Gsp67	Chaperonin, 60 kDa (*groEL*)	0.8	-	-	- 1.1	-	-	[52,118]
EF2797	Gsp64	Hypothetical protein	-	-	-	-	0.6	1.1	[52,117]
EF2894		General stress protein 13, putative	-	-	-	-	0.6	-	[100]
EF3035		Universal stress protein family	-	-	0.7	-	0.5	-	[100]
Oxidative stress									
EF0074		Transcriptional regulator, Crp/Fnr family (*ers*)	-	-	- 0.9	-	- 1.1	- 0.8	[60]
EF0463		Superoxide dismutase (*sodA*)	1.0	3.5	-	2.1	-	3.3	[100]
EF1211		NADH peroxidase (*npr*)	0.7	3.0	0.8	2.2	0.5	3.7	[100]
EF1338		Thioredoxine reductase (*trxB*)	-	1.2	-	1.4	-	1.1	[100]
EF1405		Thioredoxine (*trx*)	-	1.6	-		-	1.3	[58]
EF1525		Transcriptional regulator, Fur family (*fur*)	-	- 0.6	-	-	-	-	[58,59]
EF1585		Transcriptional regulator, Fur family (*perR*)		1.3	-	0.7	-	1.5	[58,59]
EF1586		NADH oxidase (*nox*)	- 1.2		- 1.2	0.9	- 0.8	0.7	[100]
EF1597		Catalase (*katA*)	- 0.8	2.0	- 1.2	- 1.0	-	1.1	[100]
EF1681		Peptide methionine-S-sulfoxide reductase (*msrA*)	-	3.2	-	-	-	1.7	[58]
EF2055		Oxidoreductase, pyridine nucleotide-disulfide family	- 0.7	1.4	- 0.8	1.5	-0.9	0.8	[100]
EF2417		Transcriptional regulator, Fur family (*zur*)	-	-	-	-	-	0.6	[58,59]
EF2958		Transcriptional regulator, LysR family (*hypR)*	-	-	-	-	0.5	0.9	[57,120]
EF3164		Peptide methionine-R-sulfoxide reductase (*msrB/ csrA*)	- 0.6	4.4	-	1.7	-	3.3	[57,121]
EF3233		Dps family protein (*dps)*	0.7	2.0	0.6	1.6	1.0	2.1	[100]
EF3257		Oxidoreductase, pyridine nucleotide-disulfide family	-	- 1.0	-	-	-	- 1.6	[100]
EF3270		Glutathione reductase (*gor*)	-	0.7	-	1.1	0.5	1.5	[100]
Osmotic stress									
EF0295		V-type ATPase, subunit J	-	- 0.7	-	-	- 0.5	- 1.0	[100]
EF0402		Na+/H+ antiporter	- 0.8	-	-	-	-	- 0.9	[100]
EF0636		Na+/H+ antiporter	1.0	- 4.5	1.2	- 5.3	-	- 3.8	[100]
Metal-ion resistance									
EF0298		Copper-translocating P-type ATPase		2.3	1.2	2.1	1.7	3.4	[100]
EF0299		Copper transport protein CopZ	-	2.3		2.7	-	4.1	[100]

EF0758		Cadmium-translocating P-type ATPase	-	-		-	-	1.0	[100]
EF0871		Cation-transporting ATPase, E1-E2 family	0.7	0.7	-	-	-	1.1	[100]
EF0875		Copper-translocating P-type ATPase	1.7	2.2	1.4	1.0	1.5	2.0	[100]
EF1268		Cation-transporting ATPase, E1-E2 family	-	1.2	-	-	-	0.6	[100]
EF1352		Magnesium-translocating P-type ATPase	-	-	1.3	- 0.7	1.5	-	[100]
EF1400		Cadmium-translocating P-type ATPase	-	- 0.8	-	-	-	-	[100]
EF1519		Cation-transporting ATPase, E1-E2 family	- 0.9	- 1.0	-	-	- 0.7	- 0.8	[100]
EF2623		Cadmium-translocating P-type ATPase	-	- 1.3	-	- 1.6	0.6	-	[100]
Heat shock									
EF1306		Heat-inducible transcription repressor HrcA (*hrcA*)	1.0	- 0.8	0.7	- 1.1	0.8	-	[100,118]
EF1307		Heat shock protein GrpE (*grpE*)	1.0	-	-	- 1.2	-	-	[100,118]
EF1646		Heat shock protein HslVU, ATPase subunit (*hslU*)	1.2	1.7	0.5		0.7	0.9	[100,118]
EF1647		Heat shock protein HslV (*hvlV*)	1.5	1.7	0.9		1.1	0.6	[100,118]
EF2634		Chaperonin, 10 kDa (*groES*)	0.9	-	0.7	-	-	- 0.7	[118]
Glucose starvation									
EF0079		Gls24 protein (*gls24*)	-	-	0.5	3.1	-	3.1	[119,122]
EF0080		Gls24 protein (*glsB*)	0.7	4.4	0.9	3.3	0.8	3.0	[119,122]
EF0099	Gls17	L-serine dehydratase, iron-sulfur-dependent	-	- 3.8	1.6	- 5.0	0.8	- 2.9	[117,119]
EF0106	Gls14	Carbamate kinase		- 2.2			-	- 2.9	[117,119]
EF1359	Gls40	Conserved hypothetical protein		1.0	0.6	-	0.6	- 0.6	[117,119]
EF1360	Gls10	Dihydroxyacetone kinase family protein		0.7	0.6		0.6	-	[117,119]
EF1361	Gls27	Dihydroxyacetone kinase family protein	0.7	2.0	0.9	1.3	0.9	-	[117,119]
EF1962	Gls23	Triosephosphate isomerase (*tpiA*)	-	- 1.3	-	-	-	-	[117,119]
EF2500	Gls37	GcvH family protein	-	- 1.0	- 0.8	-	- 0.6	- 1.0	[117,119]
PAIef0055[a]		Stress-induced protein Gls24	-	0.9	-	-	-	-	[22]

*Only significant log_2-ratios are listed.

[a] Present in MMH594 only.

Table 2: Differentially expressed genes with a proven or predicted virulence function in *E. faecalis*. Only significant log_2-ratios are listed.

ORF	Gene name	Gene product	Log₂-ratio*						Reference
			MMH594		OG1RF		Symbioflor 1		
			t5	t30	t5	t30	t5	t30	
EF0031		membrane protein, putative	-	0,6	-	-	-	1,0	[100]
EF0032		membrane protein, putative	-	-	-	0,9	-	0,7	[100]
EF0055		adhesion lipoprotein	-0,7	-0,7	-1,3	-	-	-0,8	[100]
EF0079	*gls24*	gls24 protein	-	-	0,5	3,1	-	3,1	[54,55]
EF0080	*glsB*	gls24 protein	0,7	4,4	0,9	3,3	0,8	3,0	[54,55]
EF0089		conserved domain protein	-0,8	-1,3	-1,4	-2,1	-1,0	-1,3	[100]
EF0123		conserved hypothetical protein	-	-0,5	-	-	-	-	[100]
EF0355	*atlB*	endolysin, putative	-	-1,0	-	-	-	-	[90,100]
EF0361		chitinase, family 2	0,9	-	0,6	-	0,7	-	[100]
EF0362		chitin binding protein, putative	1,1	-	0,8	-	0,7	-	[100]
EF0394	*salB*	secreted antigen, putative	-1,5	-0,7	-3,4	-	-1,1	-	[89,100]
EF0463	*sodA*	superoxide dismutase, Mn	1,0	3,5	-	2,1	0,4	3,3	[63]
EF0468		LemA family protein	4,0	-	5,7	-	3,8	1,4	[100]
EF0526	*cylL-S*	cylL-S protein	-	2,2	-	-	-	-	[100]
EF0527	*cylM*	cylM protein	-	-0,5	-	-	-	-	[100]
EF0577		adhesion lipoprotein	3,4	4,1	-	-	-	-	[100]
EF0645		exfoliative toxin A, putative	-0,6	-	-	-	-0,8	-	[100]
EF0680		penicillin-binding protein 2A	-	-	0,6	-	-	-	[100]
EF0700		hemolysin	-	-	-	-	-0,7	-	[100]
EF0746		penicillin-binding protein, putative	-	0,7	1,2	-	0,8	-	[100]
EF0799	*atlA*	autolysin	-1,7	-	-1,3	-	-1,9	-	[78,90,91,100]
EF0927		sensor histidine kinase	-	-0,4	0,6	-	-	-	[100]
EF0941		ABC transporter, ATP-binding	-	-	-	-	-0,6	-	[100]
EF0944		extracellular protein, putative	-1,7	-1,5	-1,6	-0,9	-2,1	-1,8	[100]
EF0955	*bopC*	aldose 1-epimerase, putative	-	-	1,2	-	-	-	[76]
EF0956	*bopB*	beta-phosphoglucomutase	-	-	1,2	-	-	-	[76]
EF0991	*pbpC*	penicillin-binding protein C	-0,6	-1,1	-1,1	-1,2	-1,0	-1,8	[100]
EF1032	*drrC*	daunorubicin resistance protein	-	1,4	1,1	1,2	0,5	1,7	[100]
EF1038		lipoprotein, putative	0,7	-	1,2	1,7	-	-	[100]
EF1050	*etaR*	DNA-binding response regulator	-	-	-1,0	-	-0,8	-1,0	[108]
EF1051	*etaS*	sensor histidine kinase	-	-0,9	-0,7	-	-0,8	-	[108]
EF1057		Mn2+/Fe2+ transporter	4,1	3,9	4,0	4,6	4,0	3,9	[100]
EF1148		penicillin-binding protein 1A	-	-0,4	-	-	-0,7	-0,9	[100]
EF1340		pheromone cAM373 prec.lipoprot.	-0,8	-1,5	-1,6	-0,9	-0,8	-1,1	[100]
EF1502		beta-lactamase, putative	-1,2	-3,0	-0,8	-1,6	-0,7	-1,7	[100]
EF1603	*scrB-1*	sucrose-6-phosphate dehydrogenase	2,0	3,8	2,3	-	3,2	4,4	[36,37]
EF1604	*scrR-1*	sucrose operon repressor ScrR	-	1,7	-	-	-	3,1	[36,37]
EF1740		penicillin-binding protein 1B, putative	-	-0,5	-	-	-	-	[100]
EF1818	*gelE*	coccolysin	-0,5	-	-	-	-	-	[25,100,103]
EF1820	*fsrC*	histidine kinase, putative	-	1,0	-	-	-	-	[25,103]
EF1821	*fsrB*	agrBfs protein	-	1,0	-	-	-	-	[25,103]
EF1822	*fsrA*	response regulator	0,7	0,8	-	-	-	-	[25,103]
EF2074	*efaC*	ABC transporter	2,8	3,0	3,1	3,1	3,7	3,4	[50]
EF2075	*efaB*	ABC transporter	2,7	3,5	3,0	3,7	3,6	3,4	[50]
EF2076	*efaA*	endocarditis specific antigen	2,3	2,9	2,8	3,4	3,0	3,2	[100] [50]
EF2093		endolysin domain protein	-	-0,6	-	-	-	-	[100]
EF2167		glycosyl transferase	-1,1	-2,6	-	-	-	-	[100]
EF2170		glycosyl transferase	-	-1,3	-	-	-	-	[100]
EF2174		conserved domain protein	-0,9	-	-	-	-1,0	-0,9	[100]
EF2176		glycosyl transferase	-0,8	-1,0	-1,7	-	-1,1	-0,5	[100]
EF2177	*epaR*	bacterial sugar transferase	-1,1	-	-	-	-0,8	-1,6	[70,95,96]
EF2178	*epaQ*	membrane protein, putative	-1,3	-1,9	-0,9	-1,2	-0,5	-2,1	[70,95,96]
EF2179	*epaP*	conserved hypothetical protein	-2,5	-3,6	-1,2	-0,9	-1,0	-2,7	[70,95,96]
EF2180	*epaO*	glycosyl transferase,	-1,4	-1,5	-0,8	-	-0,6	-1,6	[70,95,96]

EF2181	*epaN*	glycosyl transferase	-0,8	-2,1	-0,5	-0,7	-0,9	-1,7	[70,95,96]
EF2182	*epaM*	ABC transporter	-0,9	-1,5	-	-	-0,9	-2,1	[70,95,96]
EF2183	*epaL*	ABC transporter	-0,9	-1,9	-	-	-1,1	-2,3	[70,95,96]
EF2184	*epaK*	hypothetical protein	-0,7	-1,6	-1,2	-	-0,8	-1,8	[70,95,96]
EF2186		conserved domain protein	-1,2	-2,9	-	-	-	-	[70,95,96]
EF2188		racemase domain protein	-1,2	-1,8	-	-	-	-	[70,95,96]
EF2189	*epaJ*	conserved hypothetical protein	-1,2	-2,2	-1,1	-	-0,9	-1,4	[70,95,96]
EF2190	*epaI*	glycosyl transferase	-1,1	-2,0	-0,9	-	-0,6	-1,6	[70,95,96]
EF2191	*epaH*	dTDP-4-dehydrorhamnose reductase	-1,0	-1,5	-0,7	-	-0,8	-1,5	[70,95,96]
EF2192	*epaG*	dTDP-glucose 4,6-dehydratase	-0,7	-	-	-	-0,8	-	[70,95,96]
EF2193	*epaF*	dTDP-4-dehydrorhamnose	-0,7	-	-0,7	-	-0,6	-0,9	[70,95,96]
EF2194	*epaE*	glucose-1-ph thymidylyltransferase	-0,9	-1,1	-0,7	-0,6	-0,9	-1,8	[70,95,96]
EF2195	*epaD*	glycosyl transferase	-1,2	-1,7	-	-0,5	-0,9	-1,2	[70,95,96]
EF2196	*epaC*	glycosyl transferase	-1,0	-	-	-	-0,5	-0,5	[70,95,96]
EF2197	*epaB*	glycosyl transferase	-0,9	-	-	-	-0,5	-0,5	[70,95,96]
EF2198	*epaA*	glycosyl transferase	-0,8	-0,9	-	-	-0,5	-1,0	[70,95,96]
EF2202		tspO protein, putative	1,0	2,8	-	-	-	1,7	[100]
EF2439		undecaprenol kinase, putative	-1,4	-1,3	-1,5	-	-1,5	-1,8	[100]
EF2485	*cpsK*	ABC transporter	-	-3,1	-	-	-	-	[69,98]
EF2486	*cpsJ*	ABC transporter	-	-3,1	-	-	-	-	[69,98]
EF2487	*cpsI*	UDP-galactopyranose mutase	-	-2,7	-	-	-	-	[69,98]
EF2488	*cpsH*	lipoprotein, putative	-	-2,1	-	-	-	-	[69,98]
EF2489	*cpsG*	MurB family protein	-	-2,8	-	-	-	-	[69,98]
EF2490	*cpsF*	conserved hypothetical protein	-	-3,1	-	-	-	-	[69,98]
EF2491	*cpsE*	glycosyl transferase	-	-2,5	-	-	-	-	[69,98]
EF2492	*cpsD*	glycosyl transferase	-0,7	-2,3	-	-	-	-	[69,98]
EF2493	*cpsC*	teichoic acid biosynth. prot., putative	-	-1,0	-	-	-	-	[69,98]
EF2496		pheromone cOB1 precursor/lipoprot.	-	-	-	-	-0,9	-	[100]
EF2658		FemAB family protein	-	-	-0,8	-	-	-	[100]
EF2680		ABC transporter	-	0,7	-	-	-	-	[100]
EF2713		cell wall surface anchor family protein	2,2	-	-	-	-	-	[100]
EF2751		permease protein, putative	0,7	1,2	-	-	-	0,8	[100]
EF2802		endolysin	-	-	-	-	-	-0,6	[100]
EF2890		glycosyl transferase	-	-0,6	-	-1,2	-	-	[100]
EF2891	*bgsA*	glycosyl transferase	-	-	-	-1,1	-	-	[100,101]
EF2929		membrane protein, putative	-	0,8	-	-	-0,5	-	[100]
EF3023		polysaccharide lyase, family 8	-	-	-	-	-	-1,1	[100]
EF3056		sortase family protein	-	1,1	-	-	0,8	1,1	[78-80]
EF3060	*salA*	secreted lipase, putative	-3,5	-0,7	-3,6	-1,1	-3,1	-0,7	[89,100]
EF3076		cell wall surface anchor family protein	-	-0,5	-	-	-	-	[100]
EF3082		iron compound ABC transporter	-	2,3	-	3,4	-0,6	1,7	[100]
EF3083		iron compound ABC transporter	-	2,3	-	3,3	-	1,5	[100]
EF3084		iron compound ABC transporter	-0,7	2,7	-	4,0	-0,6	1,7	[100]
EF3085		iron compound ABC transporter	-	2,0	-	2,7	-	2,5	[100]
EF3106		peptide ABC transporter	0,6	5,1	0,8	3,4	-	-	[100]
EF3129		D-alanyl-D-alanine carboxypeptidase	-0,6	-0,8	-0,7	-0,7	-	-	[100]
EF3183		cell wall surface anchor family protein	-0,7	-1,1	-	-	-	-	[100]
EF3187		cell wall surface anchor family protein	-0,8	-0,9	-	-	-	-	[100]
EF3191		lipase, putative	-	0,6	-	-	-	0,8	[100]
EF3198		lipoprotein, YaeC family	-	0,7	-	0,7	-	1,5	[100]
EF3206		adhesion lipoprotein	-	-	-	1,1	-	-	[100]
EF3245		cell-envelope ass. acid phosphatase	-	-0,5	-	-	-	-	[100]
EF3256		pheromone cAD1 precursor lipoprot.	-0,6	-2,4	-	-	-	-0,6	[100]
EF3314		cell wall surface anchor family protein	-	-	-	-	0,9	3,5	[81,100]
EF3331		pheromone cCF10 percursor/lipoprot.	-	-1,5	-	-1,1	-	-1,4	[100]
PAIef0049[a]	*cyl I*	CylI protein	-	-0,9	-	-	-	-	[6,7,102]

*Only significant log_2-ratios are listed.

[a] Present in MMH594 only.

Table 3. Bacterial strains used in this study.

Strain	Country	Source	Isolation site	MLST CC	ST	Characteristics	Reference
Baby isolate 62	Norway	Non-hospitalized person < 1 year	Feces	S	66	Tet^R	[112]
MMH594	USA	Hospitalized patient	Blood	6	6	Ery^R, Gen^R, hospital outbreak	[21]
OG1RF	USA	Laboratory strain		21	1	Rif^R, Fus^R	[24]
Symbioflor 1	Germany	Non-hospitalized person	Feces	25	248	Probiotic	[20]
V583	USA	Hospitalized patient	Blood	6	6	Ery^R, Gen^R, Van^R	[123]
179Vet	Norway	Animal_dog	Urine	9	9	Multi-resistant*	[124]

* Tested against 16 different antibiotics, of which it was susceptible only to ampicillin.

Figure Legends

Figure. 1: Characterization of growth of *E. faecalis* MMH594 (black circle), OG1RF (red triangle), Symbioflor 1 (green square) Baby isolate 62 (yellow diamond), V583 (blue triangle) and 179Vet (pink hexagon) in urine. The growth curves are represented by colony forming units per millilitre (CFU/ml) on the Y-axis, and hours as indicated on the X-axis. The growth curves correspond to the mean ± STD of two parallels.

Figure 2. Venn diagram showing the distribution of genes classified as present in the three test strains. The percentages indicated for each strain specify how large part of total probe set represented on the array that was classified as present in the corresponding strain.

Figure 3. *E. faecalis* V583 genome-atlas [29] presentation of CGH analysis and transcriptional responses to growth (t_{30}) in urine compared to 2xYT. Mobile genetic elements [100,110] are indicated by brackets. From outer to inner lanes: 1) V583 annotated CDS, 2) CGH MMH594, 3) CGH Symbioflor1, 4) CGH OG1RF, 5) Urine transcriptome MMH594, 6) Urine transcriptome Symbioflor1, 7) Urine transcriptome OG1RF, 8) Intrinsic curvature, 9) Stacking energy, 10) Position Preference, 11) Global direct repeats, 12) Global inverted repeats, 13) GC skew, 14) AT percent. Interactive Genewiz atlases of CGH and transcriptome data are available at; http://ws.cbs.dtu.dk/cgi-bin/gwBrowser/edit.cgi?hexkey=603430a081eb5be3f306e744e94b151a, and http://ws.cbs.dtu.dk/cgi-bin/gwBrowser/edit.cgi?hexkey=3068b894fb6b9e44d9c135a210950f52, respectively.

Figure 4: Venn diagram showing the number of unique and common up- and down-regulated genes in MMH594, OG1RF and Symbioflor 1 when grown in urine compared to 2xYT after A: 5 minutes and B: 30 minutes.

Figure 5: Heat map visualizing the regulated genes in MMH594 (M), Symbioflor 1 (S) and OG1RF (O) when grown in urine compared to in 2xYT. The comparative genome hybridization (CGH) results for the respective regulated genes are shown in columns 1-3 (light blue: present gene, white: divergent gene). Genes found to be significantly regulated are indicated by either red (up-regulated), or blue (down-regulated). Genes regulated after growth for 5 minutes in urine compared to in 2xYT are listed in columns 4-6 and after 30 minutes in columns 7-9. The functional categories are sorted alphabetically (column 10). Significantly regulated hypothetical genes and genes encoding proteins with unknown function are not included in this heat map.

Figure 1

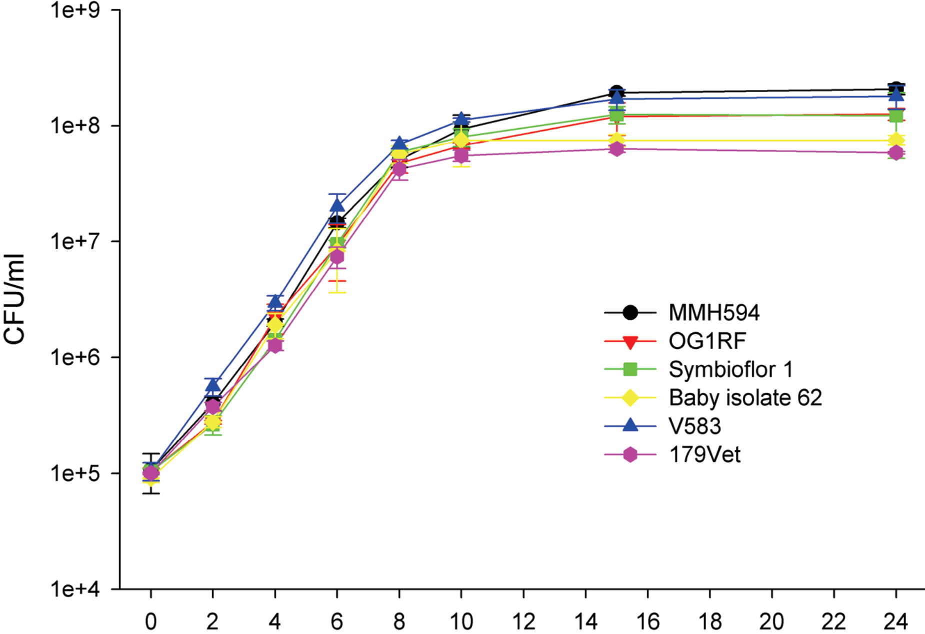


Figure 2

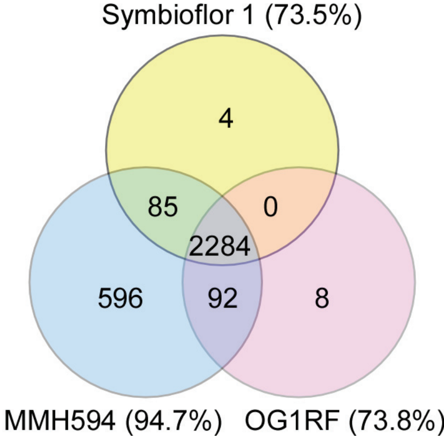


Figure 3

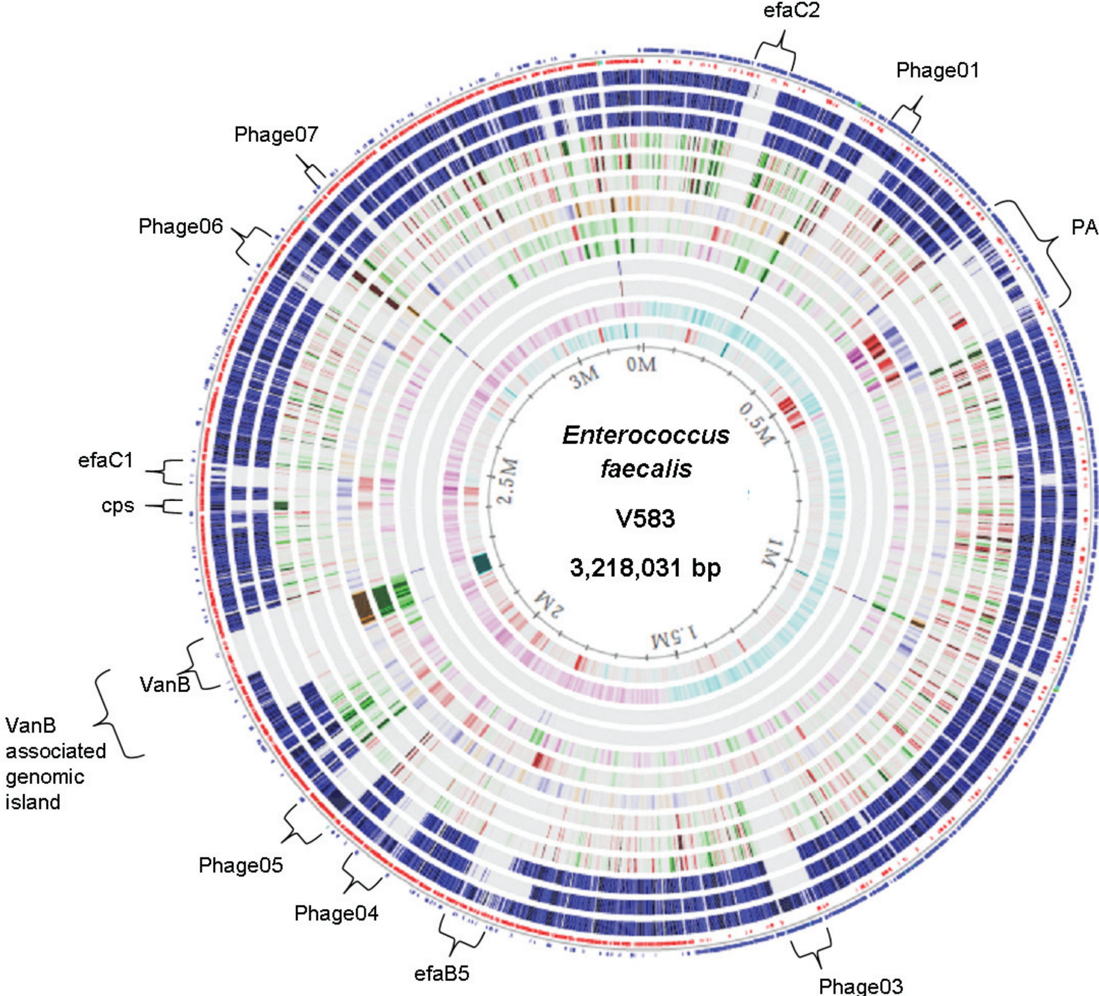


Figure 4

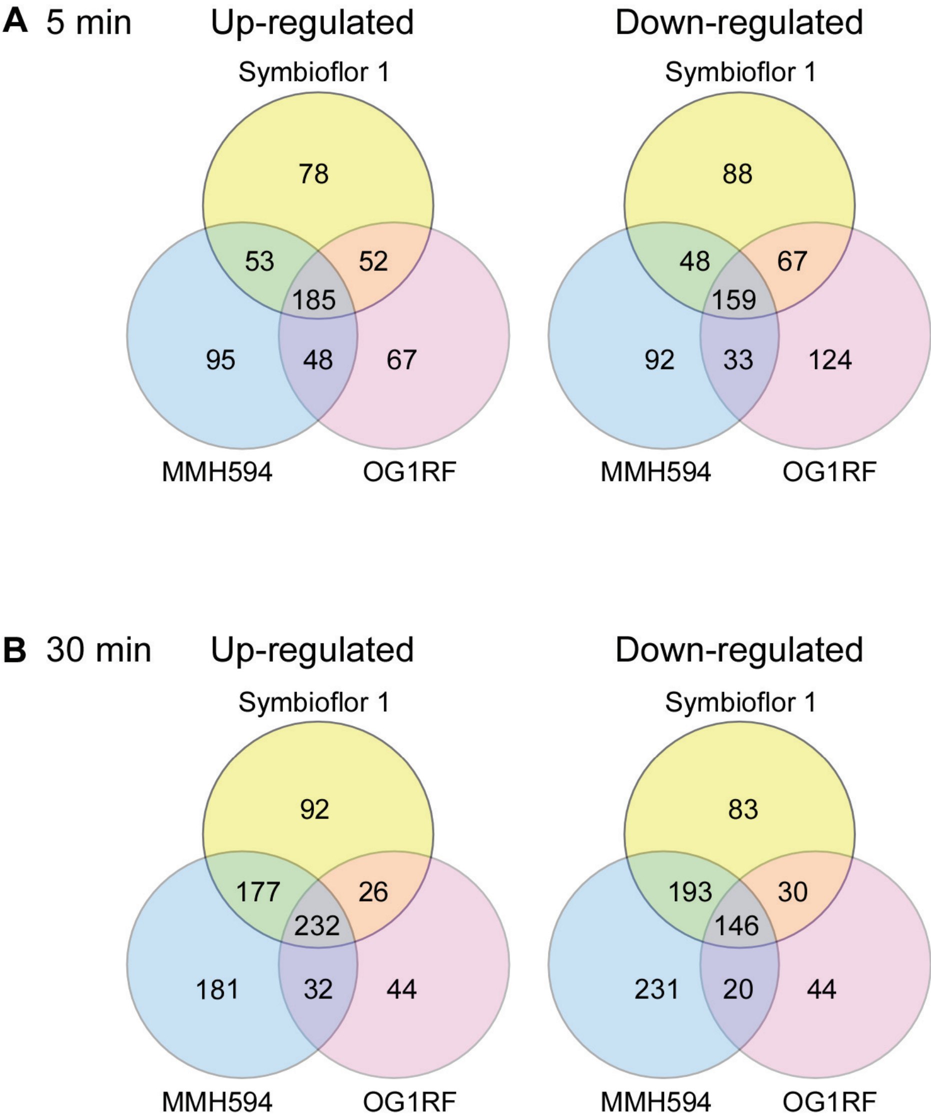
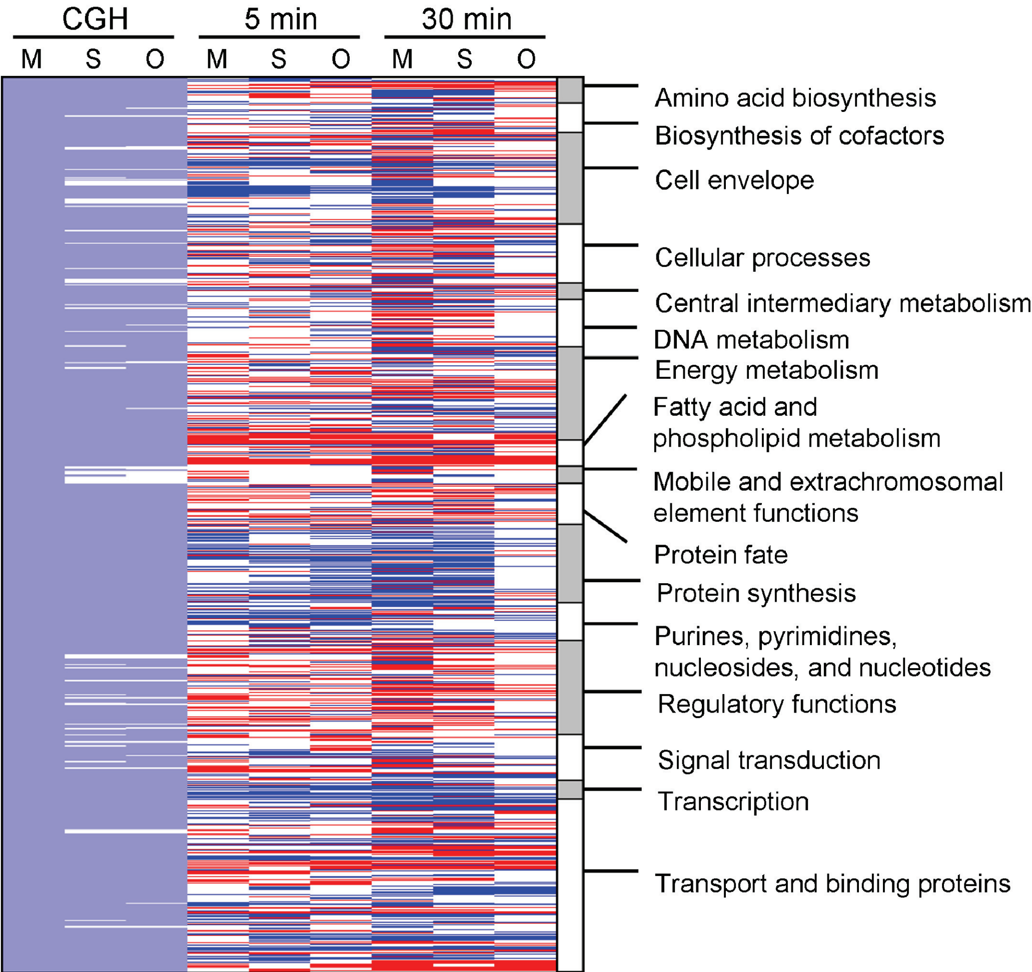


Figure 5



Supplementary material

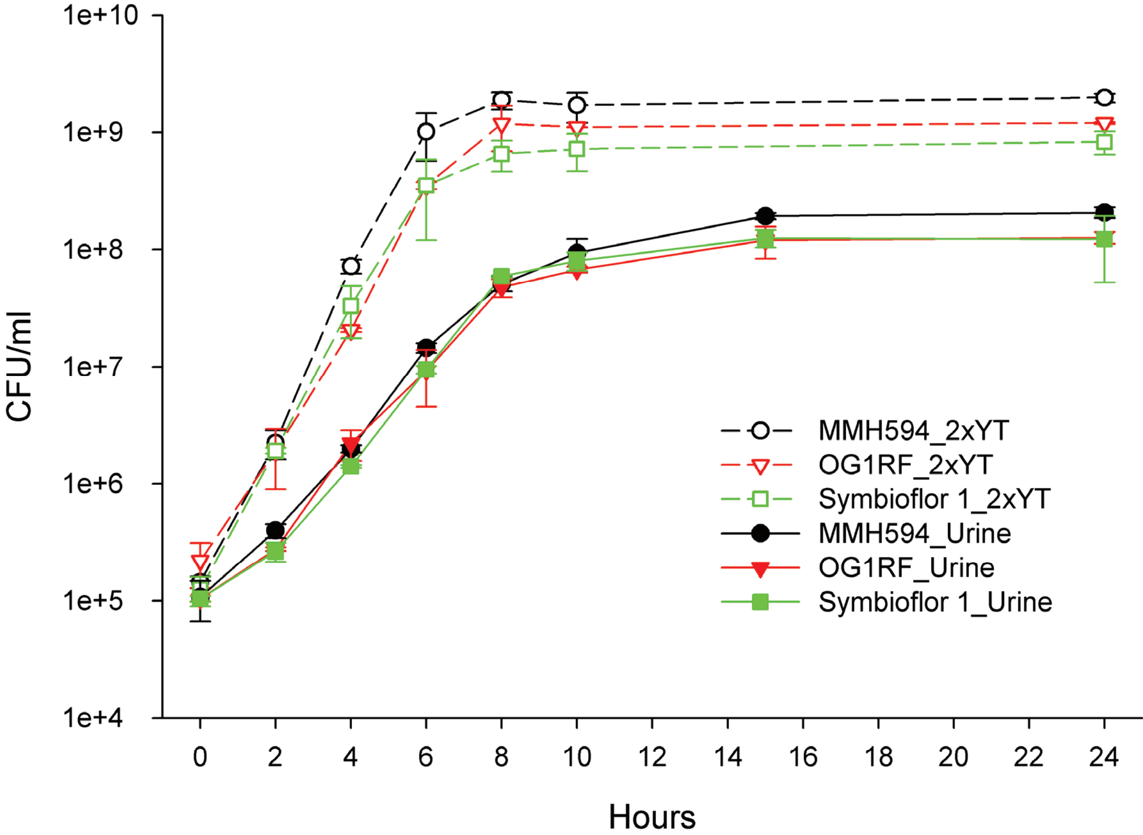


Figure S1: Characterization of growth of *E. faecalis* MMH594 (black circle), OG1RF (red triangle) and Symbioflor 1 (green square) in 2xYT (stippled lines) and urine (solid lines). The growth curves are represented by colony forming units per millilitre (CFU/ml) on the Y-axis, and hours as indicated on the X-axis. The growth curves correspond to the mean ± STD of two parallels

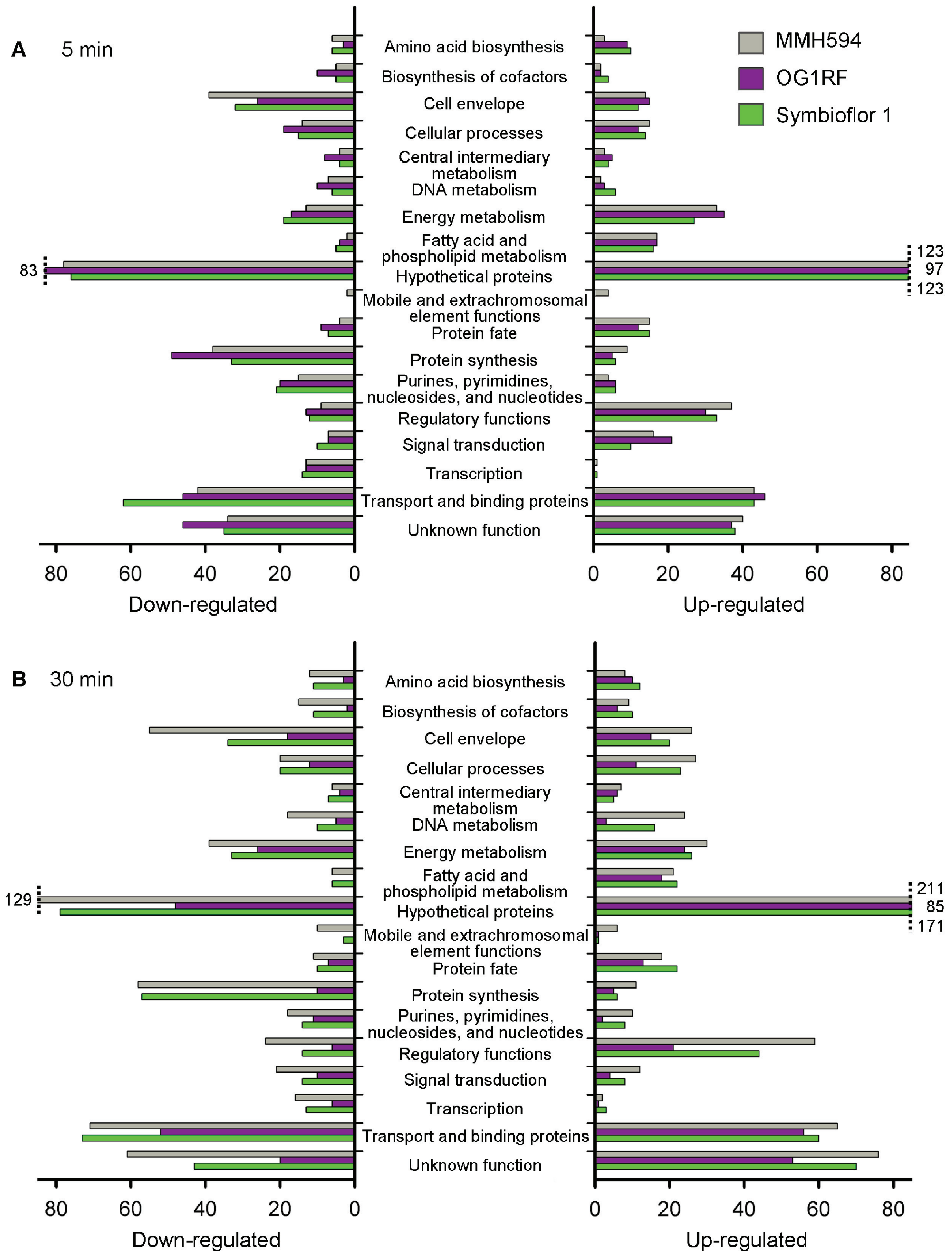


Figure S2: Overview of the number of up- and down-regulated genes in MMH594 (grey), OG1RF (purple) and Symbioflor 1 (green) at A) 5 minutes and B) 30 minutes. The functional categories are listed between the two bar-charts.

Table S1. Microarray expression data and comparative genome hybridization of *E. faecalis* strains MMH594 (M), OG1RF (O) and Symbioflor 1 (S). Differences in gene content were analyzed using comparative genomic hybridization (*): present (1), divergent (0), unclassified (U). Gene expression after 5 (t5) or 30 (t30) minutes of growth in urine is relative to 2xYT. Significantly regulated genes are $q < 0.01$ (bold), and log2-ratio > ±0.5). “NA” denotes non expressed or excluded genes.

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0001	*dnaA*	DNA metabolism	DNA replication, recombination, and repair	chromosomal replication initiator protein DnaA	1	1	1	0,3	0,22710	0,2	0,21220	0,3	0,05099	0,2	0,38730	0,2	0,10620	0,5	0,05128
EF0002	*dnaN*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, beta subunit	1	1	1	0,5	0,01377	0,5	**0,00025**	0,4	0,17140	0,3	0,46910	0,1	0,28960	0,5	**0,00893**
EF0003		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,40760	-1,0	**0,00005**	0,5	**0,00461**	-0,2	0,32310	0,6	**0,00031**	-0,7	**0,00132**
EF0004	*recF*	DNA metabolism	DNA replication, recombination, and repair	DNA replication and repair protein RecF	1	1	1	0,0	0,98580	-1,2	**0,00000**	0,6	0,06303	-0,5	0,07426	0,7	**0,00180**	-0,8	**0,00091**
EF0005	*gyrB*	DNA metabolism	DNA replication, recombination, and repair	DNA gyrase, B subunit	1	1	1	0,0	0,83580	-1,5	**0,00001**	0,4	0,02106	-0,5	0,01908	0,2	0,08812	-1,0	**0,00004**
EF0006	*gyrA*	DNA metabolism	DNA replication, recombination, and repair	DNA gyrase, A subunit	1	1	1	-0,1	0,59940	-1,5	**0,00000**	0,5	0,02146	-0,4	0,06577	-0,3	0,03101	-1,0	**0,00006**
EF0007	*rpsF*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S6	1	1	1	-0,7	**0,00403**	0,1	0,42060	-1,3	**0,00005**	-0,7	0,13780	-0,2	0,10650	-0,5	0,01382
EF0008	*ssb-1*	DNA metabolism	DNA replication, recombination, and repair	single-strand binding protein	1	1	1	-0,5	**0,00230**	-0,7	**0,00053**	-1,5	**0,00003**	-0,5	0,31520	-0,4	0,01168	-0,6	**0,00077**
EF0009	*rpsR*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S18	1	1	1	-0,7	**0,00085**	-0,1	0,70560	-1,5	**0,00002**	-0,4	0,41680	-0,2	0,11420	-0,3	0,23520
EF0011		Unknown function	Enzymes of unknown specificity	DHH family protein	1	1	1	0,4	0,13960	-0,7	**0,00004**	0,5	**0,00433**	0,0	0,98260	0,2	0,22280	-0,1	0,58820
EF0012	*rplI*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L9	1	1	1	0,5	**0,00792**	0,5	**0,00255**	0,8	**0,00159**	0,2	0,45550	0,2	0,05645	0,1	0,50500
EF0013	*dnaB*	DNA metabolism	DNA replication, recombination, and repair	replicative DNA helicase	1	1	1	-0,1	0,59630	0,7	**0,00190**	-0,2	0,41390	0,1	0,57160	-0,1	0,71020	0,5	0,04126
EF0014	*purA*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	adenylosuccinate synthetase	1	1	1	-0,3	0,09004	-3,9	**0,00000**	-0,4	0,02425	-1,0	0,06010	0,1	0,52020	-3,2	**0,00000**
EF0016		Unknown function	General	DegV family protein	1	1	1	0,6	**0,00719**	0,4	**0,00352**	0,8	**0,00300**	-0,3	0,32310	0,6	**0,00737**	0,8	**0,00022**
EF0017		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-1,3	**0,00002**	-1,5	**0,00000**	-1,6	**0,00001**	-0,8	**0,00055**	-1,0	**0,00003**	-1,3	**0,00002**
EF0018	*mptR*	Regulatory functions	Protein interactions	sigma-54 interaction domain protein	1	1	1	0,0	0,90000	-0,1	0,37100	0,4	0,03555	-0,4	0,05732	0,1	0,52480	0,0	0,92290
EF0019	*mptB*	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IIB component	1	1	1	0,1	0,54860	-0,5	0,11070	0,2	0,35390	-1,6	**0,00047**	0,1	0,79040	-1,6	**0,00033**
EF0020	*mptA*	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IIAB components	1	1	1	0,0	0,93350	-1,4	**0,00001**	0,3	0,18870	-1,8	**0,00221**	0,1	0,77890	-1,5	**0,00123**
EF0021	*mptC*	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IIC component	1	1	1	0,1	0,57910	-2,1	**0,00001**	0,5	**0,00456**	-2,0	**0,00045**	-0,7	**0,00017**	-1,8	**0,00013**
EF0022	*mptD*	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	PTS system, mannose-specific IID component	1	1	1	0,1	0,44140	-1,4	**0,00273**	0,4	0,06936	-2,1	**0,00026**	-1,1	**0,00000**	-1,5	**0,00066**
EF0024		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	**0,00774**	-0,3	**0,00308**	0,4	0,07507	-1,1	**0,00042**	0,5	0,01764	-1,1	**0,00036**
EF0025		Cell envelope	Other	membrane protein, putative	1	1	1	1,2	**0,00047**	0,8	0,02090	1,3	**0,00040**	1,4	**0,00036**	1,1	**0,00012**	3,0	**0,00000**
EF0026		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	2,3	**0,00000**	-0,2	0,16210	4,4	**0,00000**	-1,0	**0,00791**	1,8	**0,00000**	-0,1	0,57180
EF0027		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	1	1	NA	NA	NA	NA	1,6	**0,00209**	1,2	**0,00108**	1,4	**0,00000**	1,1	0,10380
EF0028		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	PTS system, IIBC components	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,7	0,02993
EF0029		Unknown function	Enzymes of unknown specificity	aminotransferase, class II	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0030		Transcription	Degradation of RNA	endoribonuclease L-PSP, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,2	0,38220	0,1	0,52840
EF0031		Cell envelope	Other	membrane protein, putative	1	1	1	0,2	0,18020	0,6	**0,00116**	0,2	0,31940	0,1	0,76660	-0,2	0,09122	1,0	**0,00006**
EF0032		Cell envelope	Other	membrane protein, putative	1	1	1	-0,2	0,12730	0,3	0,05302	0,2	0,27560	0,9	**0,00261**	0,3	0,12480	0,7	**0,00709**
EF0033		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0034		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,32790	0,3	0,24650	NA	NA	0,3	0,18990
EF0035		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,55880	0,2	0,33430	0,3	0,27780	0,7	**0,00440**	0,1	0,59840	0,5	0,03428
EF0036		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,41840	-0,2	0,05182	0,0	0,98310	0,2	0,54810	0,0	0,85810	0,1	0,57860
EF0037	*proA*	Amino acid biosynthesis	Glutamate family	gamma-glutamyl phosphate reductase	1	1	1	-0,8	0,01068	0,3	0,02533	-0,9	**0,00897**	-0,3	0,14470	-0,7	**0,00043**	0,5	0,03943
EF0038	*proB*	Amino acid biosynthesis	Glutamate family	glutamate 5-kinase	1	1	1	-1,0	**0,00121**	0,3	0,06675	-0,8	0,03710	-0,3	0,20400	-1,0	**0,00032**	0,1	0,60590
EF0039		Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	deoxyuridine 5`-triphosphate nucleotidohydrolase, putative	1	1	1	0,3	0,25730	-0,6	**0,00029**	0,3	0,06304	-0,2	0,33690	0,2	0,08819	-0,2	0,22930
EF0040	*radA*	DNA metabolism	DNA replication, recombination, and repair	DNA repair protein RadA	1	1	1	0,1	0,47790	-0,1	0,39430	0,5	0,01478	0,0	0,96280	0,3	0,08317	0,0	0,98310
EF0041		Unknown function	General	PIN domain protein	1	1	1	0,4	0,16560	-0,5	**0,00780**	0,3	0,25110	0,0	0,82340	0,3	0,07045	0,0	0,91200
EF0042	*ispF*	Biosynthesis of cofactors, prosthetic groups, carriers	Other	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1	1	1	0,1	0,69960	-0,1	0,21100	0,4	0,06185	-0,5	0,06591	0,1	0,68240	-0,1	0,54560
EF0043	*gltX*	Protein synthesis	tRNA aminoacylation	glutamyl-tRNA synthetase	1	1	1	0,0	0,81620	-0,3	0,01515	0,1	0,55950	0,4	0,03336	0,1	0,49920	0,1	0,59760
EF0044	*cysE*	Amino acid biosynthesis	Serine family	serine O-acetyltransferase	1	1	1	-0,2	0,40890	-1,6	**0,00000**	-0,6	0,01784	-0,4	0,10970	-0,8	**0,00008**	-0,9	**0,00004**
EF0045	*cysS*	Protein synthesis	tRNA aminoacylation	cysteinyl-tRNA synthetase	1	1	1	0,0	0,83510	-0,9	**0,00202**	-0,4	0,04270	-0,2	0,28070	-0,7	**0,00076**	-0,8	**0,00199**
EF0046		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,49130	-0,3	0,01382	-0,5	0,01715	0,0	0,96490	-0,4	0,01548	-0,4	0,13780
EF0047		Protein synthesis	tRNA and rRNA base modification	RNA methyltransferase, TrmH family	1	1	1	-0,1	0,58110	0,2	0,23840	-0,7	**0,00313**	0,0	0,94250	-0,3	0,05398	-0,1	0,66680
EF0048		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,16400	-0,2	0,13970	-0,8	0,01477	0,1	0,70250	-0,1	0,48180	0,1	0,74940
EF0049		Transcription	Transcription factors	sigma-70 factor family protien	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0050		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00074**	0,7	**0,00002**	0,9	**0,00259**	0,5	0,13540	0,4	**0,00833**	0,5	**0,00501**
EF0051	*ispE*	Biosynthesis of cofactors, prosthetic groups, carriers	Other	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	1	1	1	-0,6	0,20150	-0,8	**0,00003**	-0,2	0,42370	-0,2	0,53040	-0,6	**0,00147**	-0,8	**0,00164**
EF0052		Hypothetical proteins		hypothetical protein	1	0	U	-0,3	0,49480	-1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0053	*dnaQ*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, epsilon subunit	1	0	0	-0,7	**0,00041**	-2,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0054		Hypothetical proteins		hypothetical protein	1	0	0	-1,8	**0,00000**	-2,7	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0055		Cellular processes	Cell adhesion	adhesion lipoprotein	1	1	1	-0,7	**0,00225**	-0,7	**0,00016**	-1,3	**0,00002**	0,0	0,94440	-0,4	0,02107	-0,8	**0,00208**
EF0056		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,4	0,04519	-2,0	**0,00000**	-1,8	**0,00018**	0,0	0,90390	-0,4	0,03036	-1,2	**0,00002**
EF0057		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-0,3	0,10770	-1,7	**0,00000**	-1,5	**0,00002**	0,2	0,54310	-0,4	0,04783	-1,4	**0,00003**
EF0058	*purR*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	pur operon repressor PurR	1	1	1	-0,2	0,36970	-1,8	**0,00000**	-0,2	0,25110	-0,2	0,46130	-0,1	0,70960	-1,4	**0,00000**
EF0059	*glmU*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	UDP-N-acetylglucosamine pyrophosphorylase	1	1	1	-0,5	0,01087	-1,5	**0,00000**	-0,8	**0,00020**	-1,4	**0,00001**	-0,7	**0,00007**	-2,0	**0,00000**
EF0062		Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	5-nucleotidase family protein	1	1	1	0,1	0,86670	0,4	0,05158	0,5	0,08740	-0,1	0,81670	0,2	0,14570	0,3	0,10050
EF0063		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein, putative	1	1	1	2,0	**0,00073**	3,1	**0,00000**	4,7	**0,00001**	4,0	**0,00000**	NA	NA	2,5	**0,00003**
EF0064		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0065		Unknown function	General	bacterial luciferase family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0066	*ruvA*	DNA metabolism	DNA replication, recombination, and repair	Holliday junction DNA helicase RuvA	1	1	1	0,2	0,38260	0,1	0,52140	0,5	0,10620	0,5	0,13500	0,5	0,03016	1,0	**0,00004**
EF0067	*ruvB*	DNA metabolism	DNA replication, recombination, and repair	Holliday junction DNA helicase RuvB	1	1	1	0,0	0,85010	-0,6	0,04848	0,0	0,90920	0,2	0,45180	-0,1	0,75650	0,3	0,29100
EF0068		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0069		Central intermediary metabolism	Amino sugars	N-acetylmannosamine-6-phosphate epimerase, putative	1	1	1	0,1	0,79590	0,2	0,17290	0,5	0,02934	0,0	0,97310	0,2	0,28740	0,1	0,48650
EF0071		Cell envelope	Other	lipoprotein, putative	1	1	1	-1,3	**0,00030**	-2,8	**0,00000**	0,7	**0,00439**	-1,6	**0,00002**	-0,5	0,01405	-1,6	**0,00005**
EF0073		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,1	0,82460	0,3	0,09194
EF0074	*ers*	Regulatory functions	DNA interactions	transcriptional regulator, Crp/Fnr family	1	1	1	-0,3	0,07793	-0,2	0,45730	-0,9	**0,00035**	0,2	0,36680	-1,1	**0,00007**	-0,8	**0,00040**
EF0076		Unknown function	Enzymes of unknown specificity	oxidoreductase, short chain dehydrogenase/reductase family	1	1	1	0,5	0,01155	-0,1	0,70820	1,4	**0,00000**	2,2	**0,00001**	1,0	**0,00000**	3,8	**0,00000**
EF0077		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,33290	-0,1	0,85450	0,8	**0,00034**	2,8	**0,00000**	1,0	**0,00001**	2,1	**0,00000**
EF0078		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,63850	-0,5	0,02578	0,5	0,04270	3,1	**0,00000**	-0,1	0,60880	2,1	**0,00000**
EF0079	*gls24*	Cellular processes	Adaptations to atypical conditions	gls24 protein	1	1	1	0,1	0,61750	1,8	0,01130	0,5	**0,00220**	3,1	**0,00000**	0,3	0,01019	3,1	**0,00000**
EF0080	*glsB*	Cellular processes	Adaptations to atypical conditions	gls24 protein	1	1	1	0,7	**0,00020**	4,4	**0,00000**	0,9	**0,00042**	3,3	**0,00000**	0,8	**0,00002**	3,0	**0,00000**
EF0081		Cell envelope	Other	membrane protein, putative	1	1	1	1,0	**0,00072**	7,0	**0,00000**	1,0	**0,00391**	3,4	**0,00000**	0,6	**0,00118**	3,7	**0,00000**
EF0082		Transport and binding proteins	Unknown substrate	major facilitator family transporter	1	1	1	0,7	**0,00164**	1,8	**0,00000**	1,5	**0,00008**	3,4	**0,00000**	0,4	0,01666	1,0	**0,00089**
EF0083		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	1,9	**0,00010**	NA	NA	1,0	**0,00011**
EF0084		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0085		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	0,1	0,63540	0,4	0,08850	0,4	0,03991	NA	NA	0,2	0,30350
EF0086		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0089		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,8	**0,00132**	-1,3	**0,00156**	-1,4	**0,00005**	-2,1	**0,00000**	-1,0	**0,00026**	-1,3	**0,00029**
EF0090		Unknown function	General	diacylglycerol kinase catalytic domain protein	1	1	1	0,2	0,22380	1,3	**0,00000**	0,3	0,04804	0,9	**0,00279**	0,5	0,01116	1,0	**0,00029**
EF0091		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,91310	0,8	**0,00374**	0,7	**0,00163**	0,7	0,01234	0,5	**0,00653**	0,3	0,16720
EF0092		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0093		Cell envelope	Other	cell wall surface anchor family protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0094		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	formate/nitrite transporter family protein	1	1	1	-0,5	0,02483	-3,8	**0,00000**	-0,8	**0,00023**	-2,1	**0,00007**	-0,6	**0,00313**	-2,7	**0,00000**
EF0095		Cell envelope	Other	lipoprotein, putative	1	1	1	NA	NA	NA	NA	1,9	**0,00000**	-0,4	0,04455	1,5	**0,00009**	0,0	0,96540
EF0096		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00532**	0,1	0,29870	1,0	**0,00015**	0,4	0,07421	0,8	**0,00018**	0,4	0,01568
EF0097		Cellular processes	Pathogenesis	regulatory protein pfoR, putative	1	1	1	-0,7	**0,00730**	-5,3	**0,00000**	0,1	0,65030	-6,8	**0,00000**	-0,5	0,02661	-4,5	**0,00000**
EF0098	*sdhB-1*	Energy metabolism	Amino acids and amines	L-serine dehydratase, iron-sulfur-dependent, beta subunit	1	1	1	-0,2	0,35570	-4,4	**0,00000**	1,3	0,01228	-6,0	**0,00000**	0,4	0,23390	-3,5	**0,00000**
EF0099	*sdhA-1*	Energy metabolism	Amino acids and amines	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	1	1	1	0,1	0,51310	-3,8	**0,00000**	1,6	**0,00004**	-5,0	**0,00000**	0,8	**0,00565**	-2,9	**0,00000**
EF0100	*serS-1*	Protein synthesis	tRNA aminoacylation	seryl-tRNA synthetase	1	1	1	0,8	0,06782	-2,5	**0,00003**	1,8	**0,00008**	-4,7	**0,00000**	0,9	**0,00139**	-3,2	**0,00000**
EF0101		Unknown function	Enzymes of unknown specificity	hydrolase, alpha/beta hydrolase fold family	1	1	1	-0,1	0,85230	0,9	**0,00126**	0,0	0,93270	0,2	0,46570	-0,4	0,05500	0,2	0,32670
EF0102		Regulatory functions	DNA interactions	transcriptional regulator, ArgR family	1	1	1	0,0	0,89240	0,1	0,36910	0,7	**0,00389**	0,8	**0,00097**	0,3	0,06453	0,1	0,72840
EF0103		Regulatory functions	DNA interactions	transcriptional regulator, ArgR family	1	1	1	0,3	0,09442	1,5	**0,00000**	0,0	0,95680	1,6	**0,00002**	0,2	0,13130	1,7	**0,00001**
EF0104	*arcA*	Energy metabolism	Amino acids and amines	arginine deiminase	1	1	1	0,1	0,66220	-2,0	**0,00008**	0,2	0,33460	-2,3	**0,00001**	0,1	0,17090	-2,4	**0,00000**
EF0105	*argF-1*	Energy metabolism	Amino acids and amines	ornithine carbamoyltransferase	1	1	1	0,6	0,07145	-1,7	**0,00090**	0,2	0,37200	-1,5	**0,00247**	0,3	0,10390	-2,0	**0,00004**
EF0106	*arcC-1*	Energy metabolism	Amino acids and amines	carbamate kinase	1	1	1	0,7	0,17350	-2,2	**0,00015**	0,5	0,01144	-1,4	0,01148	0,2	0,24760	-2,9	**0,00003**
EF0107		Regulatory functions	DNA interactions	transcriptional regulator, Crp/Fnr family	1	1	1	0,4	0,07799	-4,4	**0,00000**	0,0	0,85520	-1,3	0,01034	0,1	0,49120	-3,5	**0,00000**
EF0108		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	C4-dicarboxylate transporter, putative	1	1	1	0,8	**0,00023**	-1,3	**0,00213**	0,6	0,01956	-1,1	**0,00846**	0,9	**0,00005**	-1,7	**0,00001**
EF0109		Unknown function	General	ThiJ/PfpI family protein	1	1	1	-0,6	**0,00524**	1,7	**0,00000**	-0,9	**0,00142**	-0,7	0,03169	-0,7	**0,00029**	1,1	**0,00002**
EF0110		Regulatory functions	DNA interactions	transcriptional regulator, ArsR family	1	1	1	-0,5	0,01251	1,1	**0,00000**	-0,7	**0,00779**	-0,6	0,01706	-0,7	**0,00123**	1,1	**0,00002**
EF0111		Unknown function	Enzymes of unknown specificity	oxidoreductase, zinc-binding	1	1	1	NA	NA	NA	NA	-0,2	0,16280	NA	NA	0,2	0,42580	NA	NA
EF0112		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,7	**0,00101**	1,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0113		Hypothetical proteins		hypothetical protein	1	0	0	0,7	**0,00228**	0,8	**0,00005**	NA	NA	NA	NA	NA	NA	NA	NA
EF0114		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl hydrolase, family 20	1	1	1	0,2	0,24220	-1,1	**0,00481**	0,6	0,01701	-1,8	**0,00004**	0,3	0,07248	-1,4	**0,00016**
EF0115		Transcription	Degradation of RNA	endoribonuclease L-PSP, putative	1	1	1	NA	NA	NA	NA	0,3	0,10900	-0,6	0,05732	-0,9	0,02152	-1,3	**0,00045**
EF0116		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,6	**0,00003**	1,8	**0,00000**	1,3	**0,00000**	1,2	**0,00025**	0,7	**0,00098**	1,3	**0,00002**
EF0117		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	1,2	**0,00061**	1,4	**0,00000**	1,5	**0,00000**	0,9	0,01793	0,9	**0,00018**	0,9	**0,00159**
EF0118		Energy metabolism	Amino acids and amines	ornithine cyclodeaminase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0119		Cellular processes	Toxin production and resistance	phenazine biosynthesis protein PhzF family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0120		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	-0,2	0,32690	-0,4	0,06316	-0,8	**0,00291**	0,0	0,88240	0,1	0,63690
EF0121		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,03060	-0,5	**0,00103**	-0,3	0,12550	-0,4	0,04051	0,1	0,66100	0,2	0,38740
EF0122		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,2	0,24030	-1,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0123		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,3	0,06194	-0,5	**0,00011**	NA	NA	NA	NA	NA	NA	NA	NA
EF0124		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,7	**0,00110**	0,2	0,56020	0,0	0,96630	0,3	0,09916
EF0125		Mobile and extrachromosomal element functions	Transposon functions	IS256, transposase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0126		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,72240	0,0	0,78010	NA	NA	NA	NA	NA	NA	NA	NA
EF0127		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0128		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0129		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0130		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0131		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0132		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0133		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0134		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0135		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0136		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0137		Unknown function	General	nucleotidyltransferase domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0138		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0139		Cellular processes	Cell division	FtsK/SpoIIIE family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0140		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0141		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0142		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0143		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0144		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0145		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0146		Cellular processes	Conjugation	surface exclusion protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0147		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0149	*asa*	Cellular processes	Conjugation	aggregation substance, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0150		Cell envelope	Other	membrane protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0151		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0152		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0153		Cell envelope	Other	cell wall surface anchor family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0154		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0155		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0156		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0158		Mobile and extrachromosomal element functions	Plasmid functions	conjugal transfer protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0159		Cell envelope	Other	membrane protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0160		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0161		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0162		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0163		Cell envelope	Other	lipoprotein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0164		Cell envelope	Other	lipoprotein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0165		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0166		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0167	*guaA*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	GMP synthase	1	1	1	-0,2	0,23860	0,3	0,04650	-0,4	0,04336	0,1	0,65700	-0,2	0,06105	-0,3	0,32100
EF0168		Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	pantothenate kinase, putative	1	1	1	-0,6	**0,00186**	-1,1	**0,00001**	-0,9	**0,00031**	-0,6	0,03052	-0,5	0,05367	-1,1	**0,00006**
EF0169		Fatty acid and phospholipid metabolism	Degradation	lipase/acylhydrolase	1	1	1	0,9	**0,00027**	2,3	**0,00000**	1,0	**0,00013**	1,6	**0,00204**	1,3	**0,00002**	2,4	**0,00000**
EF0170		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00073**	2,2	**0,00000**	0,9	**0,00370**	1,5	**0,00007**	1,0	**0,00012**	2,3	**0,00000**
EF0171	*adD*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	adenosine deaminase	1	1	1	-0,6	0,05883	0,3	0,07850	NA	NA	NA	NA	NA	NA	NA	NA
EF0172		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	-1,3	**0,00004**	-1,9	**0,00002**	-1,1	0,02273	-1,4	**0,00008**	-1,0	**0,00000**	-2,0	**0,00000**
EF0173	*pyn*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	pyrimidine-nucleoside phosphorylase	1	1	1	-1,0	**0,00005**	-2,1	**0,00000**	-0,6	0,01550	-2,3	**0,00000**	-0,9	**0,00003**	-2,5	**0,00000**
EF0174	*deoC*	Energy metabolism	Other	deoxyribose-phosphate aldolase	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0175	*cdd*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	cytidine deaminase	1	1	1	-0,9	**0,00037**	-2,5	**0,00000**	-0,5	0,01774	-2,5	**0,00000**	-0,7	**0,00017**	-2,7	**0,00000**
EF0176		Cell envelope	Other	basic membrane protein family	1	1	1	-0,7	**0,00051**	-2,0	**0,00000**	-0,9	**0,00016**	-2,4	**0,00000**	-0,4	**0,00333**	-2,1	**0,00000**
EF0177		Cell envelope	Other	basic membrane protein family	1	1	1	0,2	0,44250	-1,9	**0,00000**	0,0	0,81100	-2,4	**0,00000**	0,0	0,94560	-1,9	**0,00000**
EF0178		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,3	0,08377	-2,3	**0,00000**	-0,2	0,28530	-2,7	**0,00000**	-0,4	**0,00380**	-2,5	**0,00000**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0179		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-0,1	0,89630	-3,2	**0,00000**	0,0	0,97500	-2,8	**0,00000**	-0,1	0,64230	-2,8	**0,00000**
EF0180		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	0,3	0,04754	-1,4	**0,00000**	0,2	0,58180	-2,4	**0,00000**	0,3	0,15760	-1,6	**0,00002**
EF0183		Hypothetical proteins		hypothetical protein	1	0	1	-0,2	0,19090	0,1	0,47290	NA	NA	NA	NA	-0,5	**0,00239**	-1,1	**0,00013**
EF0184		Hypothetical proteins		hypothetical protein	1	0	1	0,1	0,64600	0,0	0,89810	NA	NA	NA	NA	-0,8	**0,00057**	-1,1	**0,00026**
EF0185	*deoB*	Purines, pyrimidines, nucleosides, and nucleotides	Other	phosphopentomutase	1	1	1	0,4	0,05425	0,2	0,19670	1,2	**0,00002**	0,4	0,04464	0,4	0,01207	0,5	**0,00223**
EF0186	*deoD-1*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	purine nucleoside phosphorylase	1	1	1	0,2	0,20430	0,0	0,73690	1,5	**0,00001**	0,5	0,03452	0,3	0,03547	0,7	**0,00842**
EF0187	*deoD-2*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	purine nucleoside phosphorylase	1	1	1	0,6	**0,00979**	1,2	0,01130	0,7	**0,00044**	0,6	**0,00344**	0,3	0,02019	0,6	**0,00111**
EF0188	*feuA*	Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, substrate-binding protein	1	1	1	-1,0	**0,00012**	0,8	**0,00017**	-0,9	**0,00080**	2,6	**0,00000**	-1,2	**0,00005**	0,5	0,06285
EF0191		Transport and binding proteins	Cations and iron carrying compounds	ferrichrome ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	-0,3	0,35210	1,4	**0,00044**	NA	NA	0,3	0,09565
EF0192		Transport and binding proteins	Cations and iron carrying compounds	ferrichrome ABC transporter, permease protein	1	1	1	-0,7	0,05588	0,3	0,03933	-0,8	**0,00911**	1,2	**0,00006**	-1,1	**0,00072**	0,2	0,26060
EF0193	*fhuG*	Transport and binding proteins	Cations and iron carrying compounds	ferrichrome ABC transporter, permease protein	1	1	1	-0,7	**0,00567**	0,3	0,04805	-0,8	**0,00429**	1,0	**0,00069**	-0,9	**0,00003**	0,4	0,04348
EF0194		Energy metabolism	Fermentation	NADH-dependent butanol dehydrogenase, putative	1	1	1	0,0	0,95830	2,9	**0,00000**	0,0	0,94040	1,3	**0,00044**	0,0	0,87130	2,4	**0,00000**
EF0195	*gpm*	Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate mutase 1	1	1	1	0,3	0,10960	0,0	0,98250	-0,2	0,23140	0,4	0,10980	0,3	0,03143	0,4	0,03709
EF0196		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, resolvase family	1	1	1	-0,6	0,05630	-1,7	**0,00000**	-0,7	**0,00920**	-1,0	**0,00042**	-0,3	0,06466	-0,9	**0,00019**
EF0197	*rpiA*	Energy metabolism	Pentose phosphate pathway	ribose 5-phosphate isomerase A	1	1	1	-0,8	**0,00140**	-2,0	**0,00000**	-0,9	**0,00174**	-0,8	**0,00205**	-0,4	0,02718	-0,9	**0,00065**
EF0198	*rpsL*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S12	1	1	1	-0,6	**0,00347**	-0,2	0,22200	-0,4	0,05881	-0,1	0,79210	-0,2	0,17190	-0,6	0,04612
EF0199	*rpsG*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S7	1	1	1	-1,1	**0,00014**	0,5	0,11830	-0,9	**0,00384**	0,1	0,50390	-0,7	**0,00080**	0,0	0,96060
EF0200	*fusA*	Protein synthesis	Translation factors	translation elongation factor G	1	1	1	-0,6	**0,00727**	-1,0	**0,00013**	-0,7	**0,00214**	-0,3	0,35750	-0,5	**0,00271**	-1,7	**0,00387**
EF0201	*tuf*	Protein synthesis	Translation factors	translation elongation factor Tu	1	1	1	0,7	**0,00034**	1,4	**0,00000**	0,1	0,63920	0,6	0,07681	0,0	0,82950	0,5	0,03363
EF0202		Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	phosphomethylpyrimidine kinase, putative	1	1	1	0,5	0,02708	0,2	0,21300	0,5	0,12220	0,9	**0,00112**	0,6	**0,00820**	2,2	**0,00000**
EF0203	*cfa*	Fatty acid and phospholipid metabolism	Biosynthesis	cyclopropane-fatty-acyl-phospholipid synthase	1	1	1	1,5	**0,00001**	1,3	**0,00000**	1,4	**0,00003**	1,5	**0,00030**	1,3	**0,00000**	1,9	**0,00000**
EF0205	*rpsJ*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S10	1	1	1	-0,5	0,05907	-0,9	**0,00117**	-1,0	**0,00012**	0,0	0,97590	-0,6	**0,00015**	-0,8	**0,00439**
EF0206	*rplC*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L3	1	1	1	-1,4	**0,00004**	-1,0	0,02138	-1,2	**0,00022**	-0,4	0,09205	-0,5	**0,00858**	-0,1	0,60130
EF0207	*rplD*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L4	1	1	1	-0,7	**0,00055**	-0,7	**0,00008**	-0,4	0,01413	-0,2	0,62100	-0,3	0,05961	-0,2	0,52140
EF0208	*rplW*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L23	1	1	1	-1,6	**0,00000**	-0,6	**0,00171**	-0,5	**0,00727**	-0,8	0,01502	-0,5	**0,00242**	-1,6	**0,00002**
EF0209	*rplB*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L2	1	1	1	-0,5	0,02369	-0,2	0,08710	-0,5	**0,00273**	0,0	0,90670	-0,4	**0,00467**	-0,3	0,15960
EF0210	*rpsS*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S19	1	1	1	-0,4	0,02224	-0,5	**0,00071**	-0,4	**0,00582**	0,0	0,96940	-0,3	0,01023	-0,4	0,09895
EF0211	*rplV*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L22	1	1	1	-0,4	0,07857	0,0	0,71060	-0,4	0,01167	0,0	0,88570	-0,2	0,06606	-0,2	0,44770
EF0212	*rpsC*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S3	1	1	1	-1,0	**0,00009**	-0,7	**0,00133**	-0,5	**0,00338**	-0,4	0,05469	-0,2	0,11750	-0,6	**0,00720**
EF0213	*rplP*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L16	1	1	1	-0,6	**0,00251**	-0,6	**0,00326**	-0,5	0,01349	0,0	0,94470	-0,2	0,07835	-0,6	0,01121
EF0214	*rpmC*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L29	1	1	1	-1,2	**0,00002**	-1,1	**0,00008**	-0,5	**0,00284**	-0,9	**0,00158**	-0,1	0,34560	-1,8	**0,00000**
EF0215	*rpsQ*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S17	1	1	1	-0,6	0,05378	-0,5	0,02207	-0,5	**0,00409**	-1,0	**0,00817**	-0,3	**0,00940**	-2,7	**0,00000**
EF0216	*rplN*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L14	1	1	1	0,0	0,86500	0,1	0,35720	0,0	0,75120	-0,2	0,23860	-0,1	0,35570	0,0	0,84680
EF0217	*rplX*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L24	1	1	1	-1,3	**0,00000**	-0,4	0,01111	0,0	0,97060	-0,2	0,23520	0,0	0,90530	0,0	0,93330
EF0218	*rplE*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L5	1	1	1	-0,8	**0,00023**	-0,3	0,16130	-0,1	0,36730	-0,4	0,05655	0,1	0,38630	-0,4	0,12990
EF0219	*rpsN-1*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S14	1	1	1	-0,1	0,77880	0,4	0,01700	0,0	0,90470	0,0	0,93160	-0,1	0,68650	-0,2	0,38290
EF0220	*rpsH*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S8	1	1	1	-0,3	0,23290	-0,1	0,69070	-0,1	0,68890	-0,8	0,04325	0,0	0,98320	-2,6	**0,00000**
EF0221	*rplF*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L6	1	1	1	-0,5	0,01103	-1,5	**0,00018**	-0,1	0,58220	-0,6	0,04124	0,2	0,08514	-0,6	**0,00293**
EF0223	*rplR*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L18	1	1	1	-0,1	0,38030	-0,3	0,05945	0,3	0,07712	-0,3	0,19950	0,3	0,02661	0,2	0,26780
EF0224	*rpsE*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S5	1	1	1	-0,6	0,01887	-1,4	**0,00010**	-0,3	0,13520	-1,1	**0,00471**	0,2	0,37460	-1,2	**0,00004**
EF0225	*rpmD*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L30	1	1	1	-0,8	**0,00014**	0,2	0,32790	0,3	0,10150	-0,1	0,68300	0,5	**0,00137**	0,3	0,17300
EF0226	*rplO*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L15	1	1	1	-0,3	0,16560	-0,4	0,04330	-0,1	0,49000	-0,7	0,03560	-0,1	0,38560	-1,2	**0,00001**
EF0227	*secY*	Protein fate	Protein and peptide secretion and trafficking	preprotein translocase, SecY subunit	1	1	1	-0,4	0,03832	-0,3	0,32930	-0,3	0,08917	-0,9	**0,00687**	-0,1	0,40790	-1,1	**0,00003**
EF0228	*adk*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	adenylate kinase	1	1	1	-1,4	**0,00027**	-4,0	**0,00000**	-0,1	0,60460	-0,6	0,01738	0,1	0,44040	-1,6	**0,00002**
EF0229	*infA*	Protein synthesis	Translation factors	translation initiation factor IF-1	1	1	1	-0,2	0,15970	-0,2	0,23450	0,1	0,60330	-0,2	0,56020	-0,3	0,04850	-0,4	0,08833
EF0230	*rpmJ*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L36	1	1	1	-1,2	**0,00001**	-3,7	**0,00000**	-1,1	**0,00013**	-1,0	**0,00356**	-0,7	**0,00011**	-2,8	**0,00000**
EF0231	*rpsM*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S13	1	1	1	-0,1	0,71790	-0,2	0,42030	-0,5	0,01349	-0,5	0,02754	-1,0	**0,00022**	-1,8	**0,00000**
EF0232	*rpsK*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S11	1	1	1	0,0	0,98530	0,1	0,64150	0,0	0,81360	-0,1	0,79180	-0,3	0,04565	-0,3	0,06269
EF0233	*rpoA*	Transcription	DNA-dependent RNA polymerase	DNA-directed RNA polymerase, alpha subunit	1	1	1	-0,8	**0,00012**	-1,3	**0,00002**	-0,5	0,03175	-0,1	0,62770	-0,2	0,16120	0,0	0,87610
EF0234	*rplQ*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L17	1	1	1	-1,1	**0,00011**	-1,8	**0,00001**	-0,7	**0,00209**	-0,2	0,47790	-0,3	0,03993	-0,1	0,73710
EF0235		Cell envelope	Other	membrane protein, putative	1	1	1	0,5	0,15690	0,5	**0,00386**	1,6	**0,00012**	1,2	**0,00057**	0,7	0,02722	1,2	**0,00005**
EF0236		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	0,4	0,27500	0,9	**0,00535**	1,2	**0,00276**	1,4	**0,00001**	0,9	**0,00201**	1,5	**0,00002**
EF0237		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,1	0,59870	0,1	0,41880	-0,2	0,26230	-0,3	0,14430	-0,1	0,48180	-0,8	**0,00050**
EF0238		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,4	0,01614	-0,7	**0,00007**	-0,4	0,01099	-0,4	0,03421	-0,5	**0,00258**	-0,9	**0,00017**
EF0239		Transport and binding proteins	Cations and iron carrying compounds	cobalt transport family protein	1	1	1	-0,3	0,18580	0,8	**0,00039**	-0,4	0,12600	0,0	0,93180	-0,8	**0,00148**	-0,3	0,08607
EF0241		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00146**	3,1	**0,00000**	0,0	0,83690	1,0	**0,00007**	0,5	**0,00056**	2,2	**0,00000**
EF0243	*brnQ*	Transport and binding proteins	Amino acids, peptides and amines	branched-chain amino acid transport system II carrier protein	1	1	1	0,3	0,50000	0,2	0,21590	0,5	0,17230	-0,3	0,26660	0,6	0,05673	0,8	**0,00389**
EF0244		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	1,6	**0,00125**	0,9	0,03422	2,7	**0,00002**	1,2	**0,00012**	1,8	**0,00186**	1,4	**0,00027**
EF0245		Unknown function	Enzymes of unknown specificity	decarboxylase family protein	1	1	1	-0,7	**0,00990**	-0,1	0,68750	-1,1	**0,00021**	0,5	0,03815	-0,7	**0,00437**	-0,3	0,10920
EF0246		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, ATP-binding protein	1	1	1	-1,4	**0,00000**	-1,5	**0,00000**	-0,4	0,08059	-0,2	0,38160	-1,0	**0,00003**	-0,5	**0,00893**
EF0247		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, amino acid-binding/permease protein	1	1	1	-1,3	**0,00001**	-2,3	**0,00000**	-0,5	**0,00810**	-0,5	0,05097	-0,9	**0,00006**	-1,7	**0,00000**
EF0248		Hypothetical proteins		hypothetical protein	1	1	1	0,4	0,17460	-0,6	**0,00948**	-0,1	0,60500	-0,3	0,64750	0,2	0,06471	0,4	0,01902
EF0249		Regulatory functions	Other	transcriptional regulator, Sir2 family	1	1	1	0,0	0,99410	1,0	**0,00001**	0,1	0,67550	0,2	0,28940	0,2	0,37460	0,6	0,02083
EF0250		Energy metabolism	Other	maltose O-acetyltransferase, putative	1	1	1	-0,3	0,06042	0,4	**0,00859**	0,0	0,79360	0,2	0,42980	-0,2	0,20780	-0,1	0,52470
EF0251		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	0,0	0,84880	0,5	**0,00180**	-0,3	0,06606	0,1	0,65180	-0,1	0,72420	0,3	0,11840
EF0252		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	N-acetylmuramoyl-L-alanine amidase, family 4	1	1	1	0,6	**0,00445**	0,2	0,56840	0,6	**0,00184**	0,8	0,01489	0,4	**0,00732**	0,5	0,05797
EF0253		Energy metabolism	Fermentation	aldehyde dehydrogenase	1	1	1	0,0	0,90000	-1,3	**0,00001**	0,0	0,96730	-1,7	**0,00001**	-0,2	0,23640	-2,1	**0,00001**
EF0255	*ldh-1*	Energy metabolism	Glycolysis/gluconeogenesis	L-lactate dehydrogenase	1	1	1	0,1	0,53600	-0,5	**0,00016**	0,8	**0,00348**	0,5	0,07024	0,0	0,89420	1,3	**0,00006**
EF0256	*pth*	Protein synthesis	Other	peptidyl-tRNA hydrolase	1	1	1	-0,9	**0,00581**	-1,9	**0,00000**	-0,2	0,34070	-0,1	0,70120	-0,9	**0,00007**	-1,0	**0,00023**
EF0257	*mfd*	DNA metabolism	DNA replication, recombination, and repair	transcription-repair coupling factor	1	1	1	-1,1	**0,00002**	-1,8	**0,00000**	-0,5	0,01227	-0,3	0,22160	-1,0	**0,00000**	-1,0	**0,00011**
EF0258		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	polysaccharide biosynthesis family protein	1	1	1	-0,7	**0,00269**	-0,5	0,01481	-0,2	0,48360	0,2	0,47170	-0,7	**0,00028**	-0,4	0,10620
EF0259		Unknown function	General	S4 RNA-binding domain protein	1	1	1	-0,6	0,03125	0,2	0,44450	-0,4	0,14460	0,6	0,04275	-0,2	0,15440	-0,1	0,85090
EF0260		Hypothetical proteins		hypothetical protein	1	1	1	-1,2	**0,00030**	-0,9	**0,00775**	-1,1	**0,00015**	-0,4	0,04058	-0,6	**0,00628**	-0,3	0,08834
EF0261		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,36750	-0,2	0,05119	-0,2	0,18110	0,1	0,81210	0,0	0,90900	0,1	0,41220
EF0262		Unknown function	General	S1 RNA-binding domain protein	1	1	1	-0,2	0,28980	0,4	0,04415	-0,3	0,07109	-0,1	0,67360	-0,1	0,45600	0,3	0,11840
EF0263	*tilS*	Hypothetical proteins	Domain	tRNA(Ile)-lysidine synthetase	1	1	1	0,0	0,83420	-0,3	0,03112	-0,4	0,03178	0,0	0,93180	-0,1	0,65150	0,1	0,67230
EF0264	*hpt*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	hypoxanthine-guanine phosphoribosyltransferase	1	1	1	-0,4	0,01993	0,2	0,13970	-0,9	**0,00803**	-0,1	0,64390	-0,9	**0,00020**	-0,5	0,06846
EF0265	*ftsH*	Cellular processes	Cell division	cell division protein FtsH	1	1	1	0,0	0,82480	0,2	0,12620	-0,1	0,49200	0,3	0,30400	0,0	0,87350	0,4	0,08500
EF0266		Protein fate	Protein folding and stabilization	chaperonin, 33 kDa	1	1	1	-0,6	0,01290	0,3	**0,00412**	-0,6	0,01036	0,1	0,79340	-0,9	**0,00024**	-0,3	0,18240
EF0267		Unknown function	General	zinc-binding TIM-barrel protein, nifR3 family, putative	1	1	1	-1,6	**0,00001**	-0,9	**0,00262**	-0,7	0,01636	0,0	0,99520	-1,4	**0,00008**	-0,7	**0,00600**
EF0268	*lysS*	Protein synthesis	tRNA aminoacylation	lysyl-tRNA synthetase	1	1	1	-1,0	**0,00223**	-1,0	**0,00008**	-1,2	**0,00002**	-0,4	0,06075	-1,0	**0,00003**	-1,1	**0,00001**
EF0270		Signal transduction	PTS	PTS system, beta-glucoside-specific IIABC component	1	1	0	0,7	**0,00513**	0,1	0,72770	-1,0	**0,00268**	-2,3	**0,00037**	NA	NA	NA	NA
EF0271		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	1,3	**0,00003**	0,3	0,03204	0,0	0,91690	-2,0	**0,00001**	-0,8	**0,00027**	-1,5	**0,00001**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0272		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	0,9	**0,00083**	0,2	0,07199	-0,3	0,18560	-1,1	**0,00716**	-0,4	0,06368	-1,0	**0,00192**
EF0273		Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate mutase family protein	1	1	1	0,9	**0,00140**	NA	NA	-0,2	0,32770	-0,9	**0,00059**	NA	NA	-0,7	0,04649
EF0274		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,63800	0,6	**0,00075**	-0,3	0,09291	0,3	0,19060	-0,2	0,24220	0,3	0,14340
EF0275		Regulatory functions	DNA interactions	ada regulatory protein, putative	1	1	1	0,9	**0,00042**	2,5	**0,00000**	0,8	**0,00341**	1,4	**0,00051**	0,8	**0,00010**	1,9	**0,00000**
EF0277	*ogt*	DNA metabolism	DNA replication, recombination, and repair	methylated-DNA--protein-cysteine S-methyltransferase	1	1	1	NA	NA	NA	NA	0,2	0,18560	-0,2	0,30400	0,4	0,02378	0,1	0,48550
EF0278	*tag-1*	DNA metabolism	DNA replication, recombination, and repair	DNA-3-methyladenine glycosylase I	1	1	1	0,2	0,61910	-0,1	0,27870	0,2	0,54410	-0,2	0,46130	0,4	0,04202	0,3	0,10820
EF0279		Unknown function	General	HD domain protein	1	1	1	0,1	0,81280	-0,1	0,77420	-0,1	0,79900	-0,2	0,48400	0,4	0,01232	0,4	0,15910
EF0280		Transport and binding proteins	Cations and iron carrying compounds	cation efflux family protein	1	1	1	0,7	0,07214	-0,6	**0,00989**	-0,1	0,82700	-0,8	**0,00801**	0,3	0,02094	-0,8	**0,00142**
EF0281		Hypothetical proteins		hypothetical protein	1	1	1	0,6	0,02891	0,2	0,08181	0,1	0,79080	-0,2	0,56640	0,3	0,11530	0,0	0,96800
EF0282	*fabI*	Fatty acid and phospholipid metabolism	Biosynthesis	enoyl-(acyl-carrier-protein) reductase	1	1	1	4,4	**0,00000**	5,2	**0,00000**	4,1	**0,00000**	5,4	**0,00000**	3,8	**0,00000**	4,3	**0,00000**
EF0283	*fabF-1*	Fatty acid and phospholipid metabolism	Biosynthesis	3-oxoacyl-(acyl-carrier-protein) synthase II	1	1	1	4,0	**0,00000**	3,9	**0,00000**	3,9	**0,00000**	5,4	**0,00000**	3,2	**0,00000**	3,0	**0,00001**
EF0284	*fabZ-1*	Fatty acid and phospholipid metabolism	Biosynthesis	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase	1	1	1	3,9	**0,00000**	3,7	**0,00000**	3,5	**0,00000**	5,4	**0,00000**	2,3	**0,00003**	2,3	**0,00000**
EF0285	*pyrD-1*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	dihydroorotate dehydrogenase	1	1	1	-0,1	0,66290	1,0	**0,00000**	-0,1	0,53750	1,8	**0,00001**	-0,3	0,09061	0,3	0,10140
EF0286		Transport and binding proteins	Other	fibronectin-binding protein, putative	1	1	1	-0,1	0,82220	0,3	0,10340	-0,9	**0,00076**	0,0	0,97440	-0,1	0,65940	0,1	0,63530
EF0287	*efp*	Protein synthesis	Translation factors	translation elongation factor P	1	1	1	0,0	0,95830	-0,2	0,06286	-0,7	**0,00137**	-0,2	0,37410	0,0	0,90010	-0,5	0,02710
EF0288		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,08674	-1,1	**0,00004**	0,0	0,85390	-1,0	**0,00558**	-0,8	**0,00002**	-1,1	**0,00046**
EF0289		Amino acid biosynthesis	Serine family	cysteine synthase B, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0290	*metC*	Amino acid biosynthesis	Aspartate family	cystathionine beta-lyase	1	1	1	-2,0	**0,00000**	-3,1	**0,00000**	-1,0	**0,00432**	-2,5	**0,00011**	-2,1	**0,00000**	-2,1	**0,00000**
EF0291		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	1,5	**0,00137**	NA	NA	0,6	0,01685	NA	NA	0,4	0,03449	NA	NA
EF0292		Signal transduction	PTS	PTS system, IIC component	1	1	1	1,2	**0,00163**	-0,5	0,01186	0,5	**0,00727**	NA	NA	0,2	0,17260	-0,3	0,33230
EF0293		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	1	1	0,1	0,67870	0,1	0,41810	0,4	0,03524	0,4	0,05041	0,0	0,90900	0,1	0,51100
EF0294		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,17110	0,5	**0,00483**	0,3	0,29470	0,1	0,51130	0,5	0,01039	0,5	**0,00501**
EF0295		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit J	1	1	1	-0,4	0,08602	-0,7	**0,00103**	-0,2	0,42540	-0,2	0,27400	-0,5	**0,00901**	-1,0	**0,00002**
EF0296	*napA*	Transport and binding proteins	Cations and iron carrying compounds	Na+/H+ antiporter	1	1	1	-0,1	0,77930	-0,5	**0,00855**	0,3	0,23590	0,2	0,49620	-0,2	0,38220	-0,3	0,11600
EF0297	*copY*	Regulatory functions	DNA interactions	transcriptional repressor CopY	1	1	1	1,4	**0,00004**	2,6	**0,00060**	1,7	**0,00000**	2,2	**0,00000**	2,5	**0,00000**	2,9	**0,00000**
EF0298		Cellular processes	Detoxification	copper-translocating P-type ATPase	1	1	1	0,7	0,01267	2,3	**0,00290**	1,2	**0,00020**	2,1	**0,00001**	1,7	**0,00003**	3,4	**0,00000**
EF0299	*copZ*	Transport and binding proteins	Cations and iron carrying compounds	copper transport protein CopZ	1	1	1	0,3	0,06418	2,3	**0,00100**	0,8	0,02901	1,7	**0,00004**	0,3	0,27790	4,1	**0,00000**
EF0300		Cell envelope	Other	membrane protein, putative	1	1	1	1,2	**0,00006**	0,7	**0,00022**	1,3	**0,00024**	-0,4	0,14130	0,9	**0,00013**	0,6	**0,00487**
EF0301		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,9	**0,00071**	NA	NA	1,2	**0,00013**	-0,4	0,25460	1,1	**0,00050**	0,8	0,01118
EF0302	*pepC*	Protein fate	Degradation of proteins, peptides, and glycopeptides	aminopeptidase C	1	1	1	1,5	**0,00000**	2,7	**0,00000**	1,5	**0,00000**	1,4	**0,00001**	1,1	**0,00003**	2,0	**0,00000**
EF0303		Mobile and extrachromosomal element functions	Prophage functions	phage integrase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0304		Cell envelope	Other	lipoprotein, putative	1	0	0	0,5	**0,00811**	-0,2	0,16270	NA	NA	NA	NA	NA	NA	NA	NA
EF0305		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,4	0,09442	-0,2	0,27810	NA	NA	NA	NA	NA	NA	NA	NA
EF0306		Mobile and extrachromosomal element functions	Prophage functions	transcriptional regulator, Cro/CI family	1	0	0	0,2	0,13510	-0,4	0,01311	NA	NA	NA	NA	NA	NA	NA	NA
EF0307		Mobile and extrachromosomal element functions	Prophage functions	transcriptional regulator, Cro/CI family	1	0	0	0,3	0,17490	0,2	0,22150	NA	NA	NA	NA	NA	NA	NA	NA
EF0308		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,0	0,88900	0,2	0,16180	NA	NA	NA	NA	NA	NA	NA	NA
EF0309		Mobile and extrachromosomal element functions	Prophage functions	excisionase, putative	1	0	0	0,2	0,27500	0,2	0,09366	NA	NA	NA	NA	NA	NA	NA	NA
EF0310		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,07751	0,8	**0,00457**	NA	NA	NA	NA	NA	NA	NA	NA
EF0311		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,55980	0,5	**0,00087**	NA	NA	NA	NA	NA	NA	NA	NA
EF0312		Unknown function	General	aspartate 1-decarboxylase domain protein	1	0	0	0,2	0,19240	0,1	0,40900	NA	NA	NA	NA	NA	NA	NA	NA
EF0313		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,68630	0,3	0,05549	NA	NA	NA	NA	NA	NA	NA	NA
EF0314		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,69710	0,2	0,22660	NA	NA	NA	NA	NA	NA	NA	NA
EF0315		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,2	0,33900	-0,3	0,04424	NA	NA	NA	NA	NA	NA	NA	NA
EF0316		Hypothetical proteins		hypothetical protein	1	0	0	0,2	0,43010	0,0	0,84080	NA	NA	NA	NA	NA	NA	NA	NA
EF0317		Mobile and extrachromosomal element functions	Prophage functions	transcriptional regulator, Cro/CI family	1	0	0	0,3	0,14030	-0,1	0,79050	NA	NA	NA	NA	NA	NA	NA	NA
EF0318		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,0	0,92720	-0,1	0,43050	NA	NA	NA	NA	NA	NA	NA	NA
EF0319		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,73000	0,0	0,69560	NA	NA	NA	NA	NA	NA	NA	NA
EF0320		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,95690	-0,3	0,01402	NA	NA	NA	NA	NA	NA	NA	NA
EF0321		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,68200	0,1	0,64280	NA	NA	NA	NA	NA	NA	NA	NA
EF0322		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,71690	0,3	0,05781	NA	NA	NA	NA	NA	NA	NA	NA
EF0323		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,99870	-0,3	0,06823	NA	NA	NA	NA	NA	NA	NA	NA
EF0324		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,97920	0,2	0,20260	NA	NA	NA	NA	NA	NA	NA	NA
EF0325		DNA metabolism	DNA replication, recombination, and repair	DNA polymerase, putative	1	0	0	-0,3	0,26120	0,4	0,01606	NA	NA	NA	NA	NA	NA	NA	NA
EF0326		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,4	0,05275	-1,3	**0,00059**	NA	NA	NA	NA	NA	NA	NA	NA
EF0327		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,11610	-0,9	**0,00005**	NA	NA	NA	NA	NA	NA	NA	NA
EF0328		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,2	0,48870	0,1	0,29730	NA	NA	NA	NA	NA	NA	NA	NA
EF0329		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,1	0,68200	-0,1	0,47390	NA	NA	NA	NA	NA	NA	NA	NA
EF0330		Unknown function	General	SNF2 domain protein	1	0	0	-0,3	0,37230	-0,6	**0,00250**	NA	NA	NA	NA	NA	NA	NA	NA
EF0331		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0332		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,3	0,27700	-1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0333		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01630	1	0	0	-0,1	0,60900	-0,7	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF0334		Mobile and extrachromosomal element functions	Prophage functions	portal protein	1	0	0	0,1	0,76320	0,0	0,96690	NA	NA	NA	NA	NA	NA	NA	NA
EF0335		Mobile and extrachromosomal element functions	Prophage functions	minor head protein	1	0	0	-0,2	0,30560	-0,3	0,05251	NA	NA	NA	NA	NA	NA	NA	NA
EF0336		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,02279	0,5	**0,00024**	NA	NA	NA	NA	NA	NA	NA	NA
EF0337		Hypothetical proteins		hypothetical protein	1	0	0	-0,4	0,01910	-0,5	**0,00117**	NA	NA	NA	NA	NA	NA	NA	NA
EF0338		Mobile and extrachromosomal element functions	Prophage functions	scaffold protein	1	0	0	-0,3	0,21960	-1,0	**0,00014**	NA	NA	NA	NA	NA	NA	NA	NA
EF0339		Mobile and extrachromosomal element functions	Prophage functions	major capsid protein, putative	1	0	0	-0,3	0,34400	-0,1	0,77670	NA	NA	NA	NA	NA	NA	NA	NA
EF0340		Hypothetical proteins		hypothetical protein	1	0	0	-0,7	**0,00119**	-1,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0341		Hypothetical proteins		hypothetical protein	1	0	0	-0,5	**0,00720**	-0,8	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF0342		Hypothetical proteins		hypothetical protein	1	0	0	-0,6	**0,00990**	-0,9	**0,00008**	NA	NA	NA	NA	NA	NA	NA	NA
EF0343		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01725	1	0	0	-0,5	**0,00772**	-0,9	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF0344		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,15520	-0,6	**0,00221**	NA	NA	NA	NA	NA	NA	NA	NA
EF0345		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,3	0,33200	0,2	0,44400	NA	NA	NA	NA	NA	NA	NA	NA
EF0346		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,86760	0,2	0,36940	NA	NA	NA	NA	NA	NA	NA	NA
EF0347		Unknown function	General	peptide methionine sulfoxide reductase domain protein	1	0	0	-0,2	0,23290	-0,6	0,02744	NA	NA	NA	NA	NA	NA	NA	NA
EF0348		Mobile and extrachromosomal element functions	Prophage functions	tail protein	1	0	0	-0,2	0,20280	-0,3	0,01826	NA	NA	NA	NA	NA	NA	NA	NA
EF0349		Mobile and extrachromosomal element functions	Prophage functions	tail protein, putative	1	0	0	-0,4	0,06252	-0,4	0,08161	NA	NA	NA	NA	NA	NA	NA	NA
EF0350		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,3	0,24080	-0,2	0,19980	NA	NA	NA	NA	NA	NA	NA	NA
EF0351		Mobile and extrachromosomal element functions	Prophage functions	structural protein, putative	1	0	0	-0,2	0,46140	-0,2	0,22420	NA	NA	NA	NA	NA	NA	NA	NA
EF0352		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,32140	0,0	0,93130	NA	NA	NA	NA	NA	NA	NA	NA
EF0353		Mobile and extrachromosomal element functions	Prophage functions	holin, putative	1	0	0	-0,2	0,33260	-0,8	**0,00004**	NA	NA	NA	NA	NA	NA	NA	NA
EF0354		Mobile and extrachromosomal element functions	Prophage functions	holin, putative	1	0	0	-0,4	0,04002	-1,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0355	*atlB*	Mobile and extrachromosomal element functions	Prophage functions	endolysin, putative	1	0	1	-0,2	0,25540	-1,0	**0,00006**	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0356		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,3	0,02158	1,3	**0,00019**
EF0357		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	0,01357	2,4	**0,00000**	0,3	0,13520	1,1	**0,00028**	0,4	0,02182	1,9	**0,00000**
EF0358		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,7	**0,00367**	2,4	**0,00000**	0,4	0,05922	1,2	**0,00645**	0,5	**0,00371**	2,1	**0,00000**
EF0359	*sugE-1*	Protein fate	Protein folding and stabilization	sugE protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0360	*sugE-2*	Protein fate	Protein folding and stabilization	sugE protein	1	1	1	-0,4	0,11410	NA	NA	-0,7	**0,00510**	-1,5	**0,00045**	-0,9	**0,00015**	NA	NA
EF0361		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	chitinase, family 2	1	1	1	0,9	**0,00036**	0,3	0,22650	0,6	**0,00068**	NA	NA	0,7	**0,00046**	0,0	0,88510
EF0362		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	chitin binding protein, putative	1	1	1	1,1	**0,00028**	0,2	0,24200	0,8	**0,00040**	-0,3	0,21950	0,7	**0,00105**	-0,3	0,11080
EF0365		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,18370	0,0	0,89860	-0,2	0,20650	-0,3	0,07316	-0,1	0,67490	-0,1	0,51330
EF0366		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,04315	-0,4	0,06466	-0,2	0,16890	-0,2	0,24380	-0,2	0,37620	-0,1	0,51000
EF0367		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,29250	-0,8	**0,00001**	-0,7	**0,00276**	-0,4	0,21630	-0,3	0,03135	-0,5	**0,00415**
EF0368		Amino acid biosynthesis	Aspartate family	aspartate kinase	1	1	1	0,1	0,82140	1,4	**0,00001**	1,2	**0,00065**	1,3	**0,00022**	0,2	0,43300	1,8	**0,00002**
EF0369		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-0,5	0,02384	NA	NA	-0,5	0,02188	-0,7	**0,00849**	-0,5	**0,00341**	-0,8	**0,00048**
EF0370		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,68550	-0,5	**0,00487**	-0,8	**0,00020**	-0,6	**0,00271**	-0,1	0,48580	-0,7	**0,00091**
EF0371		Unknown function	Enzymes of unknown specificity	aminotransferase, class V	1	1	1	0,1	0,52640	-0,3	0,06083	-0,5	**0,00283**	-0,5	0,03452	0,0	0,78410	-0,7	**0,00033**
EF0372		Signal transduction	Two-component systems	DNA-binding response regulator	1	1	1	0,6	**0,00738**	0,5	**0,00449**	0,8	**0,00434**	0,3	0,33050	-0,1	0,80350	0,3	0,21250
EF0373		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	0,7	**0,00193**	1,1	**0,00000**	1,3	**0,00002**	0,9	**0,00072**	0,6	**0,00090**	1,1	**0,00081**
EF0374		Cell envelope	Other	lipoprotein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0375		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0376		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0377		Unknown function	General	ankyrin repeat family protein	1	1	1	-0,3	0,15220	1,8	**0,00000**	-0,1	0,60460	2,1	**0,00001**	-0,2	0,06684	1,3	**0,00004**
EF0379		Unknown function	General	death-on-curing family protein	1	1	0	0,6	**0,00465**	1,8	**0,00000**	0,4	0,07303	0,7	**0,00424**	NA	NA	NA	NA
EF0380		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	0,6	0,01671	1,4	**0,00002**	0,2	0,33900	0,5	0,01432	NA	NA	NA	NA
EF0381		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,43740	0,7	**0,00045**	-0,1	0,47540	0,7	0,01727	-0,4	0,02423	0,7	0,01505
EF0382		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,62680	1,0	**0,00000**	0,2	0,26770	1,1	**0,00945**	-0,3	**0,00554**	1,0	**0,00003**
EF0383		Hypothetical proteins	Conserved	protein FdrA/conserved hypothetical protein	1	1	1	0,3	0,13190	NA	NA	0,3	0,17470	NA	NA	0,2	0,35480	-0,4	0,21910
EF0384		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,15570	NA	NA	0,3	0,08357	NA	NA	0,4	0,01750	-0,4	0,45130
EF0385		Transport and binding proteins	Unknown substrate	major facilitator family transporter	1	1	1	0,2	0,49520	NA	NA	0,0	0,76010	NA	NA	-0,2	0,09446	-0,4	0,08473
EF0386	*arcC-2*	Energy metabolism	Amino acids and amines	carbamate kinase	1	1	1	0,0	0,96040	1,7	**0,00223**	-0,3	0,21660	NA	NA	NA	NA	NA	NA
EF0387		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sodium/dicarboxylate symporter family protein	1	1	1	0,0	0,99260	2,6	**0,00000**	0,0	0,85840	1,3	**0,00876**	NA	NA	NA	NA
EF0388	*allD*	Energy metabolism	Other	ureidoglycolate dehydrogenase	1	1	1	-0,2	0,44410	1,9	**0,00038**	-0,2	0,52850	0,6	0,11280	-0,2	0,22440	0,6	**0,00562**
EF0389		Cell envelope	Other	membrane protein, putative	1	1	1	-0,5	0,03841	2,5	**0,00000**	0,0	0,90880	0,9	0,01252	-0,6	**0,00352**	0,8	0,03903
EF0390		Unknown function	Enzymes of unknown specificity	N-acyl-D-amino-acid deacylase family protein	1	1	1	-0,2	0,43610	2,5	**0,00000**	-0,6	**0,00355**	0,4	0,21890	-0,1	0,59420	1,1	**0,00112**
EF0392		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,1	0,75320
EF0393		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0394	*salB*	Protein fate	Other	secreted antigen, putative	1	1	1	-1,5	**0,00685**	-0,7	**0,00183**	-3,4	**0,00002**	0,0	0,94430	-1,1	**0,00055**	-0,3	0,15020
EF0395		Amino acid biosynthesis	Aspartate family	methionine synthase, putative	1	1	1	1,1	0,01030	1,3	**0,00000**	0,9	**0,00008**	1,2	**0,00037**	0,2	0,13020	1,6	**0,00000**
EF0396		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,80490	0,8	**0,00010**	0,5	0,04114	0,4	0,14270	0,1	0,57910	0,3	0,12480
EF0397		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,85900	0,6	**0,00042**	0,3	0,31410	0,1	0,64570	0,2	0,30970	0,5	**0,00514**
EF0398		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0399		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,81280	-0,8	**0,00287**	0,4	0,05982	0,5	0,05539	0,1	0,69060	-0,1	0,61170
EF0400		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,59340	-2,2	**0,00054**	0,0	0,92250	0,3	0,48810	-0,2	0,20930	-0,6	0,01464
EF0401	*pcp*	Protein fate	Degradation of proteins, peptides, and glycopeptides	pyrrolidone-carboxylate peptidase	1	1	1	0,2	0,54380	0,0	0,84340	0,4	0,02065	0,7	**0,00362**	0,2	0,18250	-0,2	0,57120
EF0402	*nhaC-1*	Transport and binding proteins	Cations and iron carrying compounds	Na+/H+ antiporter	1	1	1	-0,8	**0,00015**	-0,2	0,22110	0,3	0,20720	-0,2	0,58250	-0,4	**0,00384**	-0,9	**0,00056**
EF0403		Cellular processes	Toxin production and resistance	transcriptional regulator, MarR family	1	1	1	NA	NA	NA	NA	-0,4	0,26700	0,1	0,59930	-0,1	0,73340	-0,1	0,53330
EF0404		Unknown function	Enzymes of unknown specificity	nitroreductase family protein	1	1	1	0,1	0,69830	-0,4	**0,00987**	-0,4	0,05881	0,1	0,62180	0,1	0,63010	-0,2	0,27850
EF0405		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,6	**0,00319**	0,0	0,89990	0,2	0,54500	0,2	0,57240	0,2	0,13030	0,2	0,30690
EF0406		Signal transduction	PTS	PTS system, IIBC component	1	1	1	-0,3	0,40720	NA	NA	-0,4	0,10140	-0,4	0,08977	-0,3	0,21260	-0,2	0,27540
EF0407		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	-0,5	0,14540	-0,7	**0,00286**	-0,2	0,29770	-0,5	0,09737	-0,4	0,04953	-0,4	0,12300
EF0408		Signal transduction	PTS	PTS system, IIA component	1	1	1	-0,6	0,02360	-0,6	**0,00046**	-0,1	0,72310	-0,5	0,08551	-0,2	0,40170	-0,6	0,02369
EF0409		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,07895	0,9	**0,00009**
EF0411		Signal transduction	PTS	PTS system, mannitol-specfic IIBC components	1	1	1	0,4	0,14090	-1,1	**0,00065**	1,3	**0,00003**	0,3	0,57130	-0,1	0,74150	0,0	0,93140
EF0412	*mltF*	Signal transduction	PTS	PTS system, mannitol-specific IIA component	1	1	1	NA	NA	NA	NA	0,9	**0,00087**	NA	NA	0,7	0,01229	-0,1	0,69790
EF0413	*mtlD*	Energy metabolism	Sugars	mannitol-1-phosphate 5-dehydrogenase	1	1	1	1,1	**0,00633**	-0,8	**0,00145**	1,0	**0,00213**	-1,0	0,01287	1,1	**0,00148**	-0,3	0,35620
EF0414		Unknown function	Enzymes of unknown specificity	oxidoreductase, DadA family	1	1	1	NA	NA	NA	NA	0,2	0,47450	0,3	0,29310	0,0	0,90080	0,1	0,67290
EF0415		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,4	**0,00002**	3,7	**0,00000**	1,1	**0,00021**	1,4	**0,00057**	1,3	**0,00000**	2,3	**0,00000**
EF0417		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,4	**0,00008**	-0,6	**0,00083**	2,7	**0,00000**	-1,3	**0,00002**	0,9	**0,00007**	-0,4	0,05128
EF0419		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	3,2	**0,00000**	2,2	**0,00001**	2,9	**0,00000**	2,4	**0,00004**	2,6	**0,00000**	2,5	**0,00000**
EF0420		Transport and binding proteins	Cellular processes	drug resistance transporter, EmrB/QacA family protein	1	1	1	3,3	**0,00000**	2,3	**0,00000**	3,1	**0,00000**	2,3	**0,00004**	2,8	**0,00000**	1,8	**0,00001**
EF0421		Regulatory functions	DNA interactions	transcriptional regulator, MerR family	1	1	1	3,7	**0,00000**	2,2	**0,00000**	3,4	**0,00000**	1,4	**0,00044**	3,3	**0,00000**	2,7	**0,00000**
EF0422		Regulatory functions	DNA interactions	transcriptional regulator, IclR family	1	1	1	0,7	**0,00100**	0,6	**0,00040**	1,0	**0,00006**	0,5	0,05507	0,4	**0,00538**	0,8	**0,00022**
EF0423	*eda-1*	Energy metabolism	Entner-Doudoroff	2-dehydro-3-deoxyphosphogluconate aldolase	1	1	1	NA	NA	-0,6	0,02128	NA	NA	NA	NA	NA	NA	-0,1	0,88860
EF0424		Energy metabolism	Entner-Doudoroff	2-dehydro-3-deoxygluconokinase, putative	1	1	1	NA	NA	-1,3	**0,00013**	0,1	0,77150	-0,6	0,06173	0,0	0,96080	-0,4	0,14810
EF0425	*kdul-1*	Energy metabolism	Biosynthesis and degradation of polysaccharides	4-deoxy-l-threo-5-hexosulose-uronate ketol-isomerase	1	1	1	NA	NA	-0,6	0,03336	0,0	0,95600	-0,2	0,75650	0,0	0,95710	-0,1	0,59670
EF0426		Central intermediary metabolism	Other	gluconate 5-dehydrogenase, putative	1	1	1	NA	NA	-0,2	0,56660	0,3	0,24350	-0,1	0,76670	0,1	0,61720	-0,1	0,63530
EF0428		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0429		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	TRAP dicarboxylate transporter, DctP subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0430		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	TRAP dicarboxylate transporter, DctQ subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0431		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	TRAP dicarboxylate transporter, DctM subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,7	**0,00163**
EF0432		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0433		Energy metabolism	Sugars	rhamnulokinase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0434	*rhaA*	Energy metabolism	Sugars	L-rhamnose isomerase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0435	*rhaD*	Energy metabolism	Sugars	rhamnulose-1-phosphate aldolase	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0436		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0437		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0438		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0439		Cellular processes	Toxin production and resistance	immunity protein PlnM, putative	1	1	1	-0,4	0,02068	-1,4	**0,00000**	0,0	0,89430	-0,5	0,16030	-0,5	**0,00167**	-0,5	0,02060
EF0440		Transport and binding proteins	Amino acids, peptides and amines	di-/tripeptide transporter	1	1	1	0,3	0,10010	0,8	0,03303	-0,2	0,42930	0,1	0,68920	0,3	0,11310	1,4	**0,00001**
EF0441		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0442		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0443		Unknown function	General	LysM domain protein	1	1	1	-4,1	**0,00000**	-2,2	**0,00000**	-4,3	**0,00000**	-2,5	**0,00004**	-4,1	**0,00000**	-3,0	**0,00000**
EF0445	*menB*	Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	naphthoate synthase	1	1	1	0,4	0,02502	-0,3	**0,00753**	0,4	0,01664	0,5	0,10050	-0,1	0,29810	-0,8	**0,00069**
EF0446		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	O-succinylbenzoic acid--CoA ligase, putative	1	1	1	0,4	0,04038	-0,6	0,01427	0,3	0,10290	0,7	**0,00687**	0,1	0,45310	-0,3	0,31730
EF0447		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	menaquinone-specific isochorismate synthase, putative	1	1	1	0,2	0,37430	-0,4	0,02141	-0,1	0,54940	0,6	0,01167	-0,3	0,07609	-0,5	0,05203

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0448	*menD*	Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase	1	1	1	-0,3	0,31870	-0,6	**0,00068**	-0,3	0,29930	0,6	0,01538	-0,4	0,01110	-0,3	0,34900
EF0449		Unknown function	Enzymes of unknown specificity	hydrolase, alpha/beta hydrolase fold family	1	1	1	-0,5	0,06047	-0,6	**0,00231**	-0,4	0,26600	0,9	0,01374	-0,8	**0,00005**	-0,6	0,06488
EF0450		Energy metabolism	Other	mandelate racemase/muconate lactonizing enzyme family protein	1	1	1	-0,6	0,01412	-0,6	0,01278	-0,6	**0,00395**	1,2	**0,00033**	-0,6	**0,00019**	-0,8	0,01450
EF0451		Central intermediary metabolism	Amino sugars	glucosamine-6-phosphate isomerase, putative	1	1	1	NA	NA	-0,6	**0,00761**	0,0	0,90840	-0,3	0,30200	0,0	0,95790	0,1	0,82300
EF0452		Unknown function	General	AMP-binding family protein	1	1	1	-0,1	0,76520	-1,5	**0,00027**	-0,1	0,57470	-0,8	**0,00193**	-0,5	**0,00150**	-1,1	**0,00011**
EF0453	*ohr*	Unknown function	General	OsmC/Ohr family protein	1	1	1	0,9	**0,00323**	3,0	**0,00002**	0,7	**0,00142**	3,1	**0,00000**	0,9	**0,00053**	3,8	**0,00000**
EF0454		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,43720	0,0	0,99520	-0,1	0,57720	-0,1	0,56570
EF0455		Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	0,6	0,07767	NA	NA	NA	NA	-0,2	0,71590
EF0456		Signal transduction	PTS	PTS system, IID component	1	1	1	NA	NA	NA	NA	0,6	0,06028	NA	NA	0,1	0,78990	-0,3	0,24700
EF0457		Signal transduction	PTS	PTS system, IIB component	1	1	1	0,0	0,90000	-0,2	0,18180	0,7	**0,00353**	0,0	0,93610	0,3	0,10670	-0,3	0,20790
EF0458		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	1	1	-0,1	0,77950	0,4	**0,00607**	0,4	0,06759	-0,1	0,80930	0,4	0,12010	0,0	0,90180
EF0459		Unknown function	General	glucokinase regulator-related protein	1	1	1	0,2	0,22670	0,4	0,01697	0,4	0,08571	0,0	0,92420	0,3	0,07369	0,0	0,82820
EF0460		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,90120	0,1	0,46620	0,5	0,07968	-0,1	0,85780	0,1	0,55100	-0,3	0,41550
EF0461		Signal transduction	PTS	PTS system, IIA component	1	1	1	NA	NA	NA	NA	0,3	0,12530	0,0	0,85370	-0,1	0,53230	-0,3	0,13060
EF0462		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,4	0,06376	-0,1	0,60980	-0,5	**0,00630**	0,0	0,88540	0,0	0,74700	0,0	0,96640
EF0463	*sodA*	Cellular processes	Detoxification	superoxide dismutase, Mn	1	1	1	1,0	**0,00008**	3,5	**0,00000**	-0,1	0,47700	2,1	**0,00000**	0,4	**0,00208**	3,3	**0,00000**
EF0464	*dapF*	Amino acid biosynthesis	Aspartate family	diaminopimelate epimerase	1	1	1	0,3	0,04853	0,2	0,26590	-0,2	0,27560	0,7	**0,00310**	-0,2	0,27510	0,1	0,71840
EF0465		Regulatory functions	Other	transcriptional regulator	1	1	1	-0,8	**0,00023**	-0,8	**0,00007**	-0,7	**0,00091**	0,0	0,85370	-0,9	**0,00012**	-0,9	**0,00035**
EF0466	*nagB*	Central intermediary metabolism	Amino sugars	glucosamine-6-phosphate isomerase	1	1	1	2,2	**0,00000**	1,8	**0,00000**	2,1	**0,00000**	1,2	**0,00148**	2,5	**0,00000**	2,1	**0,00000**
EF0467		Transport and binding proteins	Cations and iron carrying compounds	MgtC family protein	1	1	1	0,4	0,07385	0,1	0,43400	0,3	0,13910	0,1	0,78680	0,3	0,18900	0,6	**0,00532**
EF0468		Unknown function	General	LemA family protein	1	1	1	4,0	**0,00001**	-0,1	0,80110	5,7	**0,00000**	0,2	0,50360	3,8	**0,00000**	1,4	**0,00004**
EF0469		Hypothetical proteins	Domain	conserved domain protein	1	1	1	3,5	**0,00000**	0,7	**0,00071**	5,7	**0,00000**	0,4	0,04497	3,6	**0,00000**	1,8	**0,00000**
EF0470	*nrdF*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	ribonucleoside-diphosphate reductase 2, beta subunit	1	1	1	-1,1	**0,00137**	0,4	0,02539	-1,7	**0,00000**	-0,5	**0,00959**	-1,6	**0,00000**	-0,3	0,22420
EF0471	*nrdE*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	ribonucleoside-diphosphate reductase 2, alpha subunit	1	1	1	-0,9	**0,00243**	2,1	**0,00001**	-0,8	**0,00176**	-0,4	0,09132	-1,3	**0,00017**	0,4	0,06493
EF0472	*nrdI*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	nrdI protein	1	1	1	-0,3	0,48300	2,8	**0,00124**	-0,8	0,02454	-0,4	0,07045	-1,2	**0,00008**	0,5	0,01626
EF0473	*nrdH*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	ribonucleoside-diphosphate reductase 2, NrdH-redoxin	1	1	1	0,0	0,98500	1,7	**0,00001**	-0,6	**0,00767**	-0,3	0,15450	-0,2	0,11810	1,5	**0,00033**
EF0475	*feoA*	Transport and binding proteins	Cations and iron carrying compounds	ferrous iron transport protein A	1	1	1	0,3	0,04481	1,5	**0,00008**	0,3	0,06894	2,0	**0,00000**	1,2	**0,00004**	1,1	**0,00022**
EF0476	*feoB*	Transport and binding proteins	Cations and iron carrying compounds	ferrous iron transport protein B	1	1	1	-0,3	0,11450	2,1	**0,00000**	0,0	0,99900	3,0	**0,00000**	0,5	**0,00690**	1,7	**0,00001**
EF0477		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00209**	1,9	**0,00000**	0,6	0,02206	2,5	**0,00001**	0,7	**0,00055**	1,7	**0,00000**
EF0478		Hypothetical proteins		hypothetical protein	1	0	1	0,4	0,02054	0,1	0,42290	NA	NA	NA	NA	0,4	**0,00206**	0,4	0,06882
EF0479		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	1	0	1	0,2	0,36950	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0480		Mobile and extrachromosomal element functions	Prophage functions	excisionase, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0481		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0482		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0485		Cellular processes	Conjugation	aggregation substance	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0486		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0487		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0488		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0489		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0490		Cell envelope	Other	cell wall surface anchor family protein	1	0	0	0,1	0,50200	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0491		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0492		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0494		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0498		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0499	*ssb-2*	DNA metabolism	DNA replication, recombination, and repair	single-strand binding protein	1	0	0	0,0	0,86630	1,1	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF0500		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0501		Cell envelope	Other	lipoprotein, putative	1	0	0	0,1	0,61130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0502		Cell envelope	Other	membrane protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0503		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0504		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0505		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0506		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0507		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0508		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0509		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0510	*ssb-3*	DNA metabolism	DNA replication, recombination, and repair	single-strand binding protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0511	*nuc-1*	DNA metabolism	DNA replication, recombination, and repair	thermonuclease precursor	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0512		Unknown function	General	DNA-damage-inducible protein J, putative	1	0	0	0,2	0,28160	0,3	0,21980	NA	NA	NA	NA	NA	NA	NA	NA
EF0513		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00053	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0516		Cell envelope	Other	membrane protein, putative	1	0	1	0,3	0,20320	-0,9	**0,00104**	NA	NA	NA	NA	0,1	0,44810	-0,8	**0,00012**
EF0517		Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	2-dehydropantoate 2-reductase, putative	1	0	1	0,4	0,08948	-1,9	**0,00038**	NA	NA	NA	NA	0,0	0,95710	-1,5	**0,00003**
EF0518		Cell envelope	Other	cell wall surface anchor family protein	1	0	0	0,3	0,28980	0,0	0,81330	NA	NA	NA	NA	NA	NA	NA	NA
EF0519		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,79470	1,2	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0521		Energy metabolism	Other	bile salt hydrolase	1	0	1	1,6	**0,00000**	4,7	**0,00000**	NA	NA	NA	NA	1,2	**0,00000**	2,8	**0,00000**
EF0524	*araC*	Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	-0,3	0,07943	-0,6	**0,00043**	NA	NA	NA	NA	NA	NA	NA	NA
EF0525		Unknown function	General	cylL-L protein	1	0	0	-0,1	0,80390	0,1	0,68470	NA	NA	NA	NA	NA	NA	NA	NA
EF0526		Unknown function	General	cylL-S protein	1	0	0	0,3	0,12750	2,2	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0527	*cylM*	Cellular processes	Toxin production and resistance	cylM protein	1	0	0	0,1	0,82950	-0,5	**0,00689**	NA	NA	NA	NA	NA	NA	NA	NA
EF0530		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0531		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0532		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,38300	-0,3	0,23600	NA	NA	NA	NA	NA	NA	NA	NA
EF0533		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0534		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, resolvase family	1	0	0	0,7	**0,00169**	0,1	0,70390	NA	NA	NA	NA	NA	NA	NA	NA
EF0539		Regulatory functions	DNA interactions	phosphosugar-binding transcriptional regulator, RpiR family	1	0	1	-0,2	0,35570	0,4	**0,00320**	NA	NA	NA	NA	NA	NA	NA	NA
EF0540		Central intermediary metabolism	Amino sugars	N-acetylmannosamine-6-phosphate epimerase, putative	1	0	0	0,8	**0,00023**	0,0	0,89380	NA	NA	NA	NA	NA	NA	NA	NA
EF0542		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,9	**0,00027**	-0,9	**0,00286**	NA	NA	NA	NA	NA	NA	NA	NA
EF0543		Cell envelope	Other	membrane protein, putative	1	0	0	-0,7	**0,00072**	-1,0	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF0544	*rpmF-1*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L32	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0545		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,5	0,04994	-0,8	**0,00046**	NA	NA	NA	NA	NA	NA	NA	NA
EF0546		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,5	0,14060	-0,4	0,06572	NA	NA	NA	NA	NA	NA	NA	NA
EF0547		Transport and binding proteins	Cations and iron carrying compounds	ammonium transporter family protein	1	0	0	-0,5	0,02449	-0,6	0,01617	NA	NA	NA	NA	NA	NA	NA	NA
EF0548		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,72840	0,3	0,03715	NA	NA	NA	NA	NA	NA	NA	NA
EF0550		Regulatory functions	DNA interactions	xylose repressor, putative	1	0	0	0,5	**0,00272**	0,6	0,01039	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0551		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 31	1	0	0	0,5	0,04400	-0,1	0,53500	NA	NA	NA	NA	NA	NA	NA	NA
EF0552		Signal transduction	PTS	PTS system, IIC component	1	0	0	-0,1	0,63550	-0,3	0,06573	NA	NA	NA	NA	NA	NA	NA	NA
EF0553		Signal transduction	PTS	PTS system, IID component	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0554		Signal transduction	PTS	PTS system, IIB component	1	0	0	0,5	0,01412	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0555		Signal transduction	PTS	PTS system, IIA component	1	0	0	0,6	0,01297	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0556	*xylA*	Energy metabolism	Sugars	xylose isomerase	1	0	0	0,4	0,04665	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0557	*xylB*	Energy metabolism	Sugars	D-xylulose kinase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0559		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	polysaccharide biosynthesis family protein	1	0	0	-0,6	0,05469	0,4	0,03907	NA	NA	NA	NA	NA	NA	NA	NA
EF0562		Hypothetical proteins		hypothetical protein	1	0	0	0,5	0,02875	-0,1	0,30740	NA	NA	NA	NA	NA	NA	NA	NA
EF0563		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,13540	0,2	0,15280	NA	NA	NA	NA	NA	NA	NA	NA
EF0564		Hypothetical proteins		hypothetical protein	1	0	0	0,2	0,50800	-0,1	0,42290	NA	NA	NA	NA	NA	NA	NA	NA
EF0566	*kdpF*	Transport and binding proteins	Cations and iron carrying compounds	potassium transporter stabilization peptide KdpF	1	0	0	0,4	0,07214	0,3	0,05726	NA	NA	NA	NA	NA	NA	NA	NA
EF0567	*kdpA*	Transport and binding proteins	Cations and iron carrying compounds	potassium-transporting ATPase, subunit A	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0568	*kdpB*	Transport and binding proteins	Cations and iron carrying compounds	potassium-transporting ATPase, subunit B	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0569	*kdpC*	Transport and binding proteins	Cations and iron carrying compounds	potassium-transporting ATPase, subunit C	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0570	*kdpD*	Signal transduction	Two-component systems	sensor histidine kinase KdpD	1	0	0	-0,1	0,82100	1,2	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0571		Signal transduction	Two-component systems	DNA-binding response regulator	1	0	0	-0,3	0,04557	0,8	**0,00022**	NA	NA	NA	NA	NA	NA	NA	NA
EF0573		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0574		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0575		Transport and binding proteins	Cations and iron carrying compounds	cationic ABC transporter, ATP-binding protein	1	0	0	2,8	**0,00006**	3,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0576		Transport and binding proteins	Cations and iron carrying compounds	cation ABC transporter, permease protein	1	0	0	3,0	**0,00003**	3,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0577		Cellular processes	Cell adhesion	adhesion lipoprotein	1	0	0	3,4	**0,00001**	4,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0578		Regulatory functions	DNA interactions	helix-turn-helix protein, iron-dependent repressor family	1	0	0	2,5	**0,00056**	2,3	**0,00386**	NA	NA	NA	NA	NA	NA	NA	NA
EF0579		Regulatory functions	Other	transcriptional regulator, putative	1	0	0	2,6	**0,00012**	3,4	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0580		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	1,3	**0,00051**	2,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0581		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	0	0,6	0,01136	1,4	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0582		Cell envelope	Other	membrane protein, putative	1	0	0	0,7	**0,00435**	2,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0583		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein/permease protein	1	0	0	0,3	0,35730	1,8	**0,00103**	NA	NA	NA	NA	NA	NA	NA	NA
EF0584		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	0	0	-0,4	0,11490	1,7	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF0585	*rpsN-2*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S14	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0586	*rpmF-2*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L32	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0587		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0588	*rpmG-1*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L33	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0589		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0590		Energy metabolism	Biosynthesis and degradation of polysaccharides	polysaccharide deacetylase family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0594		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0599		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0600		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	0	0	-0,1	0,68300	-0,5	**0,00114**	NA	NA	NA	NA	NA	NA	NA	NA
EF0601		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	0	0	0,1	0,84310	0,3	0,06168	NA	NA	NA	NA	NA	NA	NA	NA
EF0603		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	0,0	0,93940	NA	NA	NA	NA	NA	NA	NA	NA
EF0604		Cellular processes	Adaptations to atypical conditions	gls24 protein	1	0	0	-0,5	0,01233	1,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0605		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,8	**0,00292**	0,8	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF0606	*dps*	Cellular processes	Adaptations to atypical conditions	Dps family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0607		Unknown function	General	ParB-like nuclease domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0608		Hypothetical proteins		hypothetical protein	1	1	0	-0,1	0,68530	-0,5	**0,00073**	NA	NA	NA	NA	NA	NA	NA	NA
EF0609		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,0	0,91270	-0,4	**0,00556**	NA	NA	NA	NA	NA	NA	NA	NA
EF0610		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,24080	-0,8	**0,00027**	NA	NA	NA	NA	NA	NA	NA	NA
EF0611		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0612		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0613		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0615		Mobile and extrachromosomal element functions	Transposon functions	transposase, IS200 family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,4	0,02397	0,0	0,97300
EF0616		Energy metabolism	Amino acids and amines	ornithine cyclodeaminase, putative	1	0	0	0,0	0,87670	-1,5	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0617		Cell envelope	Other	membrane protein, putative	1	0	0	0,0	0,84430	-1,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF0618		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,2	0,57910	-1,2	**0,00005**	NA	NA	NA	NA	NA	NA	NA	NA
EF0619		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0621		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0622		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0624		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0625		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0626		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0627		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0628		Signal transduction	PTS	PTS system, IIA component, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0629		Unknown function	Enzymes of unknown specificity	oxidoreductase, aldo/keto reductase family	1	1	1	-0,2	0,17400	NA	NA	-0,7	**0,00971**	-0,6	0,01163	-0,8	**0,00011**	-0,7	0,01006
EF0630		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,0	0,96250	-0,7	**0,00007**	-0,3	0,04665	-0,9	**0,00026**	-0,2	0,05864	-0,6	**0,00330**
EF0631		Fatty acid and phospholipid metabolism	Biosynthesis	cardiolipin synthetase, putative	1	1	1	-0,8	**0,00624**	-1,1	**0,00000**	-1,3	**0,00006**	-0,7	0,01025	-0,7	**0,00019**	-0,7	**0,00018**
EF0633	*tryS-1*	Protein synthesis	tRNA aminoacylation	tyrosyl-tRNA synthetase	1	1	1	1,8	**0,00001**	3,7	**0,00000**	0,4	**0,00819**	2,9	**0,00000**	0,2	0,34560	0,5	**0,00850**
EF0634		Unknown function	Enzymes of unknown specificity	decarboxylase, putative	1	1	1	0,8	**0,00951**	-4,4	**0,00000**	-0,1	0,60310	-5,2	**0,00000**	0,4	**0,00887**	-4,1	**0,00000**
EF0635		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	0,9	**0,00480**	-5,4	**0,00000**	0,5	0,16300	-5,8	**0,00000**	0,4	0,02447	-4,3	**0,00000**
EF0636	*nhaC-2*	Transport and binding proteins	Cations and iron carrying compounds	Na+/H+ antiporter	1	1	1	1,0	**0,00167**	-4,5	**0,00000**	1,2	**0,00168**	-5,3	**0,00000**	0,0	0,79040	-3,8	**0,00000**
EF0637		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,08398	1,1	**0,00000**	0,5	**0,00716**	0,9	**0,00136**	0,6	**0,00089**	1,2	**0,00002**
EF0638		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,98500	2,6	**0,00000**	0,0	0,89130	NA	NA	0,6	**0,00020**	1,6	**0,00002**
EF0639		Cellular processes	Adaptations to atypical conditions	low temperature requirement C protein, putative	1	1	1	-0,1	0,40260	0,2	0,05085	-0,4	0,01678	0,0	0,87150	-0,5	**0,00228**	0,1	0,55990
EF0640		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,28780	NA	NA	NA	NA	NA	NA
EF0641	*ldh-2*	Energy metabolism	Glycolysis/gluconeogenesis	L-lactate dehydrogenase	1	1	1	NA	NA	-2,1	**0,00000**	-0,6	**0,00281**	-1,8	**0,00004**	-0,8	**0,00084**	-0,5	0,03964
EF0642		Hypothetical proteins		hypothetical protein	1	0	1	-0,2	0,47620	-0,3	0,05973	0,2	0,46670	0,1	0,69540	NA	NA	0,0	0,99110
EF0643		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	-0,3	0,04611	-0,1	0,56670	0,3	0,35640	0,1	0,38090	-0,1	0,54560
EF0644		Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	0,0	0,97030	1,7	**0,00000**	-0,4	**0,00712**	0,0	0,92710	-0,1	0,41010	0,8	**0,00026**
EF0645		Cellular processes	Pathogenesis	exfoliative toxin A, putative	1	1	1	-0,6	**0,00569**	-0,3	0,10410	-0,3	0,18040	-0,7	0,01244	-0,8	**0,00036**	-0,4	0,03949
EF0646		Energy metabolism	Sugars	NAD-dependent epimerase/dehydratase family protein	1	1	1	-0,7	**0,00178**	-0,5	**0,00858**	-0,3	0,32970	-0,4	0,14730	-0,8	**0,00008**	-0,4	0,02887
EF0647		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,70690	1,7	**0,00000**	0,2	0,32160	0,8	**0,00123**	0,4	0,07154	1,5	**0,00004**
EF0648		Unknown function	Enzymes of unknown specificity	nitroreductase family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0650	*lplA-1*	Protein fate	Protein modification and repair	lipoate-protein ligase A	1	1	1	1,6	**0,00000**	2,4	**0,00000**	2,0	**0,00003**	1,6	**0,00254**	2,2	**0,00000**	2,4	**0,00000**
EF0652		Hypothetical proteins		hypothetical protein	1	1	1	0,6	**0,00394**	1,2	**0,00001**	0,6	0,02217	1,0	**0,00325**	0,7	**0,00073**	1,3	**0,00001**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0653		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,11490	1,0	**0,00003**	0,4	0,01258	0,8	0,01166	0,4	0,01477	0,8	**0,00026**
EF0654		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	0,0	0,80390	1,1	**0,00009**	0,2	0,14060	0,8	0,04391	0,5	**0,00313**	0,9	**0,00253**
EF0655		Unknown function	Enzymes of unknown specificity	nitroreductase family protein, putative	1	1	1	0,5	**0,00581**	1,2	**0,00000**	0,3	0,08020	1,3	**0,00379**	1,0	**0,00034**	1,5	**0,00001**
EF0656		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,6	**0,00448**	1,3	**0,00000**	0,5	**0,00604**	1,4	**0,00010**	1,0	**0,00001**	1,6	**0,00001**
EF0657		Regulatory functions	DNA interactions	transcriptional regulator, DeoR family	1	1	1	1,5	**0,00000**	1,3	**0,00000**	1,1	**0,00001**	0,3	0,19980	1,5	**0,00000**	2,6	**0,00002**
EF0658		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,4	**0,00000**	1,7	**0,00000**	0,8	**0,00020**	0,5	0,02271	1,3	**0,00000**	2,7	**0,00000**
EF0659		Unknown function	General	phage SPO1 DNA polymerase-related protein, putative	1	1	1	0,6	**0,00346**	1,1	**0,00004**	0,0	0,83680	0,3	0,14090	0,4	**0,00583**	1,8	**0,00004**
EF0660		Transport and binding proteins	Other	MATE efflux family protein	1	1	1	-0,3	0,04344	0,0	0,75810	-0,5	0,01971	-0,6	0,04481	-0,8	**0,00010**	0,0	0,91260
EF0661		Protein fate	Degradation of proteins, peptides, and glycopeptides	oligoendopeptidase F, putative	1	1	1	0,3	0,29560	2,1	**0,00000**	0,1	0,77130	1,0	**0,00847**	0,2	0,27190	1,8	**0,00000**
EF0662		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00480**	-0,2	0,04280	-1,2	**0,00011**	-0,1	0,74690	-0,6	**0,00124**	-0,6	0,02801
EF0663		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01033	1	1	1	0,6	**0,00717**	0,2	0,15490	0,7	**0,00469**	0,0	0,98020	0,7	**0,00238**	0,4	0,06253
EF0664		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,66010	-0,3	0,14860	0,1	0,53370	-0,6	0,01297	0,1	0,56050	-0,6	0,01252
EF0665		Hypothetical proteins		hypothetical protein	1	1	1	1,1	**0,00014**	3,0	**0,00000**	0,4	**0,00975**	2,0	**0,00001**	0,7	**0,00653**	2,5	**0,00000**
EF0666		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,1	0,57270	1,3	**0,00000**	0,3	0,27010	1,7	**0,00027**	0,4	**0,00380**	2,0	**0,00002**
EF0667		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,98420	2,1	**0,00000**	-0,4	0,04757	1,5	**0,00004**	0,0	0,92580	1,9	**0,00000**
EF0668		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylmuramoylalanyl-D-glutamate diaminopimelate ligase	1	1	1	0,1	0,76320	0,0	0,92740	0,0	0,90810	0,3	0,20430	-0,2	0,23780	-0,4	0,20360
EF0669		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	polysaccharide biosynthesis family protein	1	1	1	-0,5	0,02010	0,1	0,52570	-0,7	**0,00375**	0,2	0,45110	-0,8	**0,00018**	-0,3	0,27040
EF0671		Protein fate	Degradation of proteins, peptides, and glycopeptides	xaa-his dipeptidase	1	1	1	0,3	0,08059	2,0	**0,00000**	0,1	0,43250	0,6	0,03288	0,3	0,16380	0,5	0,17620
EF0672		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,19320	1,1	**0,00046**
EF0673		Cell envelope	Other	membrane protein, putative	1	1	1	-0,6	0,03237	3,9	**0,00000**	-1,0	**0,00028**	1,8	**0,00013**	-0,6	0,05679	2,4	**0,00000**
EF0674		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline ABC trans, ATP-binding protein	1	1	1	0,5	0,01301	1,3	**0,00000**	0,4	0,01689	1,8	**0,00001**	0,7	**0,00011**	2,3	**0,00000**
EF0675		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline ABC trans/binding protein	1	1	1	0,3	0,16930	1,6	**0,00000**	0,2	0,14170	1,8	**0,00003**	0,5	0,01002	2,2	**0,00000**
EF0676	*argR*	Regulatory functions	DNA interactions	arginine repressor	1	1	1	-0,3	0,08027	-0,9	**0,00001**	-0,3	0,13920	-0,6	0,02535	-0,1	0,34560	-0,4	0,12100
EF0677		Energy metabolism	Sugars	phosphoglucomutase/phosphomannomutase family protein	1	1	1	-0,5	0,11600	-0,9	**0,00260**	-0,3	0,19650	-1,0	**0,00236**	-0,6	**0,00675**	-0,7	0,06530
EF0678		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,3	0,07321	-1,0	**0,00005**	0,0	0,90280	-1,4	**0,00055**	0,0	0,98630	-0,9	**0,00143**
EF0680		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein 2A	1	1	1	-0,2	0,48900	0,1	0,51350	0,6	**0,00342**	-0,3	0,22460	-0,2	0,34150	-0,1	0,60020
EF0681		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,32860	0,4	**0,00508**	0,0	0,99280	-0,3	0,15270	0,1	0,28550	0,6	**0,00208**
EF0682		DNA metabolism	DNA replication, recombination, and repair	DNA repair exonuclease family protein	1	1	1	0,1	0,70780	0,1	0,63060	0,1	0,43410	-0,1	0,58680	0,2	0,07742	0,1	0,56280
EF0683		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,55950	-0,2	0,34540	0,2	0,14950	-0,4	0,16590	0,3	0,02718	0,1	0,46940
EF0684		Unknown function	General	cmp-binding protein, putative	1	1	1	0,0	0,94830	0,9	**0,00001**	0,0	0,98190	0,3	0,31010	0,1	0,79040	0,5	**0,00579**
EF0685		Protein fate	Protein folding and stabilization	rotamase family protein	1	1	1	0,1	0,43830	-0,4	0,08577	-0,1	0,41200	0,1	0,73400	0,0	0,74720	0,0	0,96390
EF0686		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00574**	1,3	**0,00000**	0,8	**0,00129**	0,3	0,26930	0,8	**0,00009**	1,6	**0,00000**
EF0687		Unknown function	General	HIT family protein	1	1	1	0,3	0,11930	0,6	**0,00006**	0,5	**0,00932**	0,2	0,43420	0,4	**0,00310**	1,1	**0,00004**
EF0688		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,2	0,48690	-0,1	0,65770	-0,1	0,40130	-0,1	0,65610	-0,1	0,74260	-0,1	0,56950
EF0689		Cell envelope	Other	membrane protein, putative	1	1	1	-0,2	0,75820	-0,3	0,46280	-0,1	0,75510	-0,3	0,24470	-0,3	0,27620	-0,4	0,13010
EF0690		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,31870	-1,2	**0,00000**	-0,5	**0,00564**	-0,2	0,46790	-0,4	0,01691	-0,7	**0,00493**
EF0691		Unknown function	Enzymes of unknown specificity	methyltransferase, putative	1	1	1	-1,0	**0,00020**	-1,5	**0,00000**	-1,2	**0,00001**	-0,3	0,15660	-1,1	**0,00001**	-1,0	**0,00003**
EF0692		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, RpiR family, putative	1	1	1	NA	NA	NA	NA	-0,1	0,58000	NA	NA	0,1	0,39250	0,0	0,88660
EF0693	*fruK-1*	Energy metabolism	Glycolysis/gluconeogenesis	1-phosphofructokinase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,8	**0,00015**	-1,5	**0,00001**
EF0694		Signal transduction	PTS	PTS system, fructose-specific family, IIBC components	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,6	0,05329	-1,5	**0,00000**
EF0695		Signal transduction	PTS	PTS system, IIA component	1	1	1	NA	NA	NA	NA	0,4	0,20800	NA	NA	-0,1	0,47220	-1,2	**0,00009**
EF0696	*lacD-1*	Energy metabolism	Biosynthesis and degradation of polysaccharides	tagatose 1,6-diphosphate aldolase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0697		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,53590	0,4	**0,00654**	-0,3	0,32480	0,5	0,11840	0,4	**0,00639**	1,2	**0,00004**
EF0698		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	0,3	0,14630	1,0	**0,00000**	0,4	0,10500	0,5	0,05670	0,7	**0,00059**	1,0	**0,00184**
EF0699		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,70930	1,7	**0,00420**	-0,1	0,64560	1,0	**0,00057**	-0,2	0,38670	1,5	**0,00007**
EF0700		Cellular processes	Pathogenesis	hemolysin	1	1	1	-0,4	0,01746	0,0	0,92320	-0,5	0,12500	0,2	0,58660	-0,7	**0,00007**	-0,1	0,52200
EF0701	*prfC*	Protein synthesis	Translation factors	peptide chain release factor 3	1	1	1	-1,0	**0,00025**	-1,1	**0,00001**	-1,5	**0,00001**	-0,3	0,29830	-1,5	**0,00001**	-1,4	**0,00000**
EF0702		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,45120	-0,1	0,41830	-1,0	**0,00040**	-0,6	0,01226	-0,5	0,02991	-0,6	0,01254
EF0703		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,69390	-0,1	0,20420	-1,1	**0,00213**	-1,0	**0,00063**	-0,7	**0,00129**	-0,9	**0,00022**
EF0704		Cell envelope	Other	lipoprotein, putative	1	1	1	0,5	0,01600	0,9	**0,00002**	-0,2	0,34070	0,1	0,55400	-0,2	0,17930	0,0	0,93330
EF0705		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,2	**0,00003**	1,6	**0,00000**	0,7	0,02163	0,2	0,40440	1,3	**0,00000**	1,9	**0,00000**
EF0706	*clpE*	Protein fate	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, ATP-binding subunit ClpE	1	1	1	1,0	**0,00022**	2,4	**0,00000**	1,3	**0,00012**	0,8	**0,00846**	0,8	**0,00009**	2,4	**0,00000**
EF0707		Hypothetical proteins		hypothetical protein	1	1	1	0,6	0,07589	NA	NA	0,3	0,03636	NA	NA	0,4	**0,00618**	0,9	**0,00078**
EF0708		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,76730	0,1	0,37720	0,5	**0,00739**	0,3	0,20520	0,0	0,85240	-0,6	0,01333
EF0709	*ptsH*	Signal transduction	PTS	phosphocarrier protein HPr	1	1	1	0,1	0,70910	0,4	0,02250	0,1	0,64720	0,0	0,96350	0,1	0,43970	0,1	0,53570
EF0710	*ptsI*	Signal transduction	PTS	phosphoenolpyruvate-protein phosphotransferase enzyme I	1	1	1	-0,2	0,38920	-0,2	0,19320	0,2	0,32940	-0,1	0,85360	-0,1	0,68900	0,0	0,79390
EF0711		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,4	0,12550	NA	NA	1,1	**0,00023**	NA	NA
EF0713		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,6	0,10150	NA	NA	1,1	**0,00018**	1,1	**0,00051**
EF0714		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,6	**0,00180**	1,3	**0,00005**
EF0715	*tig*	Protein fate	Protein and peptide secretion and trafficking	trigger factor	1	1	1	-0,1	0,85360	-0,6	0,04629	-0,8	**0,00244**	0,0	0,87250	-0,3	0,06287	-0,8	**0,00089**
EF0716		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,2	**0,00175**	-2,2	**0,00000**	-0,6	**0,00604**	-0,9	**0,00387**	-0,6	**0,00177**	-1,0	**0,00003**
EF0717		Signal transduction	PTS	PTS system, fructose-specific family, IIABC components	1	1	1	-0,9	**0,00024**	-2,9	**0,00002**	-0,4	0,17350	0,4	0,45350	-0,5	**0,00540**	-0,2	0,57360
EF0718	*fruK-2*	Energy metabolism	Glycolysis/gluconeogenesis	1-phosphofructokinase	1	1	1	-0,4	0,07656	-1,7	**0,00649**	0,0	0,95530	1,1	0,05317	-0,2	0,22270	0,3	0,31410
EF0719		Regulatory functions	DNA interactions	transcriptional regulator, DeoR family	1	1	1	-0,5	0,04955	-1,0	0,04902	0,3	0,25720	1,6	0,01122	-0,3	0,05913	0,4	0,23090
EF0720		Transport and binding proteins	Anions	voltage-gated chloride channel family protein	1	1	1	0,3	0,05050	0,4	**0,00450**	0,5	**0,00724**	0,9	**0,00183**	0,8	**0,00009**	0,9	**0,00018**
EF0721	*pcrA*	DNA metabolism	DNA replication, recombination, and repair	ATP-dependent DNA helicase PcrA	1	1	1	-0,2	0,37980	-1,4	**0,00000**	-0,3	0,07264	-0,7	**0,00410**	-0,3	0,03316	-1,1	**0,00002**
EF0722	*ligA*	DNA metabolism	DNA replication, recombination, and repair	DNA ligase, NAD-dependent	1	1	1	-0,2	0,30770	-0,3	0,22660	-0,2	0,34300	-0,3	0,14330	-0,6	**0,00141**	-0,5	0,02569
EF0723		Hypothetical proteins		hypothetical protein	1	1	1	-1,0	**0,00255**	-0,4	**0,00389**	-0,5	0,03225	-0,5	0,01272	-0,9	**0,00004**	-0,4	0,02595
EF0724	*gatC*	Protein synthesis	tRNA aminoacylation	glutamyl-tRNA(Gln) amidotransferase, C subunit	1	1	1	0,2	0,54080	-0,2	0,13700	0,0	0,90800	-0,2	0,45170	0,1	0,45450	-0,2	0,28780
EF0725	*gatA*	Protein synthesis	tRNA aminoacylation	glutamyl-tRNA(Gln) amidotransferase, A subunit	1	1	1	-0,4	0,20350	-1,1	**0,00214**	-0,4	0,04869	-0,5	0,06249	0,0	0,78840	-0,8	**0,00435**
EF0726	*gatB*	Protein synthesis	tRNA aminoacylation	glutamyl-tRNA(Gln) amidotransferase, B subunit	1	1	1	-0,9	**0,00054**	-2,5	**0,00000**	-0,4	0,03377	-0,6	0,05396	-0,2	0,19510	-0,9	**0,00089**
EF0727		Unknown function	General	diacylglycerol kinase catalytic domain protein	1	1	1	0,0	0,92290	-0,1	0,52900	-0,2	0,18030	0,1	0,52290	0,0	0,93010	0,6	**0,00284**
EF0728		Protein synthesis	tRNA and rRNA base modification	RNA methyltransferase, TrmA family	1	1	1	-1,1	**0,00020**	-0,9	0,02687	-0,9	**0,00093**	-0,2	0,43150	-1,0	**0,00005**	-0,4	0,10290
EF0730		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	**0,00255**	NA	NA	0,9	**0,00064**	NA	NA	NA	NA	NA	NA
EF0731		Regulatory functions	DNA interactions	transcriptional regulator, luxR family	1	1	1	-0,5	0,04348	-0,9	**0,00003**	-0,6	**0,00940**	-0,7	0,06371	-0,4	0,06287	-0,5	0,01034
EF0732	*argF-2*	Energy metabolism	Amino acids and amines	ornithine carbamoyltransferase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0733		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0734		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0735	*arcC-3*	Energy metabolism	Amino acids and amines	carbamate kinase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0737		Unknown function	Enzymes of unknown specificity	amidase, putative	1	1	1	-1,0	**0,00123**	-0,3	0,14850	-0,8	**0,00085**	-0,6	0,01252	-0,9	**0,00008**	-0,6	**0,00345**
EF0738		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0739		Transport and binding proteins	Other	nicotinamide mononucleotide transporter PnuC, putative	1	1	1	-0,9	**0,00017**	-0,6	**0,00009**	-1,5	**0,00000**	-0,8	**0,00080**	-1,3	**0,00010**	-0,4	0,04888
EF0740		Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	deoxynucleoside kinase	1	1	1	-1,3	**0,00038**	-1,6	**0,00000**	-1,7	**0,00000**	-1,3	**0,00017**	-1,6	**0,00000**	-1,5	**0,00000**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0741		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,7	**0,00175**	-0,4	0,01832	-1,3	**0,00001**	-1,3	**0,00039**	-1,5	**0,00000**	-0,8	0,02233
EF0742		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00169**	0,7	**0,00028**	0,0	0,86410	-0,4	0,20180	0,5	**0,00528**	0,7	**0,00376**
EF0743		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,02730	0,8	**0,00004**	0,3	0,16330	0,5	0,06747	0,4	0,10760	0,8	**0,00022**
EF0744		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sodium/dicarboxylate symporter family protein	1	1	1	-0,2	0,39160	0,2	0,21350	-0,3	0,21890	0,3	0,24900	-0,3	0,27600	0,2	0,46940
EF0745		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,2	0,44460	1,1	**0,00000**	-0,2	0,39700	0,7	**0,00579**	0,0	0,98250	0,5	0,03054
EF0746		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein, putative	1	1	1	0,0	0,92980	0,7	**0,00449**	1,2	**0,00046**	0,8	0,01967	0,8	**0,00015**	0,6	0,03453
EF0747		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,89630	0,9	**0,00012**	0,8	**0,00041**	0,9	**0,00999**	0,6	**0,00380**	1,2	**0,00010**
EF0748		Cellular processes	Detoxification	rhodanese family protein	1	1	1	-0,4	0,03042	0,9	**0,00001**	-0,5	**0,00134**	1,7	**0,00001**	-0,2	0,17640	1,1	**0,00011**
EF0750		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	-0,4	0,08094	-0,5	0,08551	NA	NA	NA	NA
EF0751		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,75750	NA	NA	NA	NA	NA	NA
EF0752		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,5	0,04247	-0,9	**0,00157**	-0,4	0,03006	-0,5	0,05203
EF0753		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,5	0,16900	-0,5	0,07343	NA	NA	-0,3	0,25010
EF0754		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,3	0,20990	-0,4	0,05317	NA	NA	-0,3	0,19940
EF0755		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0756		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,8	**0,00440**	-0,3	0,39620	NA	NA	NA	NA
EF0757		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,6	0,01567	NA	NA	NA	NA	NA	NA
EF0758		Transport and binding proteins	Cations and iron carrying compounds	cadmium-translocating P-type ATPase	1	1	1	0,0	0,92270	0,3	0,08277	0,8	0,01925	0,4	0,13750	0,0	0,99270	1,0	**0,00004**
EF0759		Unknown function	General	sapB protein, putative	1	1	1	0,1	0,59640	0,3	0,06846	0,7	**0,00216**	NA	NA	-0,1	0,52880	0,2	0,51620
EF0760		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, ATP-binding protein	1	1	1	-0,3	0,06033	-1,2	**0,00012**	-0,5	**0,00574**	-2,5	**0,00000**	-0,7	**0,00011**	-1,9	**0,00000**
EF0761		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, amino acid-binding/permease protein	1	1	1	-0,4	0,02363	-2,1	**0,00000**	0,2	0,26640	-2,4	**0,00000**	-0,3	0,03539	-1,8	**0,00000**
EF0762	*uvrB*	DNA metabolism	DNA replication, recombination, and repair	excinuclease ABC, subunit B	1	1	1	0,2	0,31560	0,6	**0,00012**	0,5	**0,00992**	0,3	0,23370	0,8	**0,00008**	0,6	**0,00676**
EF0763	*uvrA*	DNA metabolism	DNA replication, recombination, and repair	excinuclease ABC, subunit A	1	1	1	0,0	0,94670	1,3	**0,00000**	-0,2	0,32780	0,6	**0,00965**	0,0	0,84620	1,1	**0,00005**
EF0764		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,9	0,01421	NA	NA	NA	NA	NA	NA
EF0765		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0766		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,92510	0,2	0,26070	0,4	0,06042	-0,8	**0,00386**	0,7	**0,00202**	0,6	**0,00228**
EF0767		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	-0,1	0,67180	0,5	**0,00029**	0,4	0,03122	-0,3	0,21150	0,5	**0,00617**	0,4	0,06973
EF0768		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,84000	1,1	**0,00007**	0,4	0,02880	-0,1	0,59310	0,5	**0,00872**	1,1	**0,00002**
EF0769		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00876**	-0,1	0,31040	0,1	0,53010	-0,5	0,16150	-0,2	0,18690	0,1	0,67610
EF0770		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,1	**0,00007**	4,0	**0,00000**	0,9	**0,00037**	2,0	**0,00004**	0,9	**0,00001**	3,1	**0,00000**
EF0771	*clpP*	Protein fate	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, proteolytic subunit ClpP	1	1	1	0,2	0,47470	0,0	0,95010	0,4	0,01001	0,6	**0,00410**	0,4	**0,00814**	0,7	**0,00049**
EF0773		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	**0,00836**	0,4	**0,00539**	0,0	0,90290	0,2	0,31830	0,6	**0,00025**	0,2	0,23530
EF0774		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00359**	1,3	**0,00011**	0,3	0,06101	0,6	0,04553	0,6	**0,00124**	0,7	**0,00433**
EF0775		Cell envelope	Other	gram positive anchor protein, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0776		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0778		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,09949	0,2	0,04492	1,0	**0,00396**	0,0	0,90990	0,2	0,28550	0,9	**0,00021**
EF0779		Fatty acid and phospholipid metabolism	Degradation	glycerophosphoryl diester phosphodiesterase family protein	1	1	1	0,2	0,22720	0,5	**0,00192**	0,4	0,03543	-0,3	0,26370	-0,2	0,14780	0,5	**0,00502**
EF0780		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	0,1	0,55790	-0,2	0,22610	0,3	0,49200	-0,3	0,11620	-0,5	**0,00070**	0,1	0,69950
EF0781		Cellular processes	Adaptations to atypical conditions	cold shock domain family protein	1	1	1	-0,1	0,59020	0,0	0,94460	-0,4	0,04944	0,0	0,91270	-0,1	0,65160	0,0	0,87610
EF0782	*rpoN*	Transcription	Transcription factors	RNA polymerase sigma-54 factor	1	1	1	0,0	0,84750	-0,9	**0,00001**	-0,1	0,53080	-0,2	0,17310	0,3	0,03835	-0,5	0,01549
EF0783		Unknown function	Enzymes of unknown specificity	acyltransferase, putative	1	1	1	-0,7	**0,00239**	0,1	0,32530	0,4	0,14730	0,8	**0,00910**	-0,4	0,09339	0,4	0,01673
EF0784	*metK*	Central intermediary metabolism	Other	S-adenosylmethionine synthetase	1	1	1	-0,2	0,21580	-1,0	**0,00001**	-1,0	**0,00004**	-1,8	**0,00000**	-0,1	0,54470	-1,1	**0,00017**
EF0785		Transport and binding proteins	Other	drug resistance transporter, EmrB/QacA family protein	1	1	1	0,0	0,92980	-0,7	**0,00020**	-0,6	0,01894	0,4	0,05329	0,0	0,76020	-0,8	**0,00345**
EF0786		Fatty acid and phospholipid metabolism	Degradation	tributyrin esterase, putative	1	1	1	0,0	0,94840	-0,5	**0,00101**	-0,8	**0,00049**	0,5	0,02879	0,3	0,06806	0,2	0,32110
EF0787		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	-0,3	0,18760	-0,6	**0,00145**	-0,4	0,10960	0,4	0,03205	-0,1	0,75400	0,2	0,41480
EF0789		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,6	0,05527	-0,5	0,05306	-1,2	**0,00046**	0,2	0,28940	-0,6	0,01979	-0,1	0,74540
EF0790		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-1,2	**0,00002**	-0,9	**0,00001**	-1,6	**0,00003**	0,3	0,29740	-0,9	**0,00005**	-0,5	0,01016
EF0791		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	-0,5	0,02105	-1,1	**0,00005**	-0,3	0,03514	-0,3	0,29740	-0,4	0,01466	-0,5	0,04119
EF0792		Transport and binding proteins	Unknown substrate	permease domain protein	1	1	1	-0,2	0,38240	-0,2	0,27700	0,1	0,72450	-0,5	0,03676	0,0	0,99310	-0,1	0,59770
EF0793	*hrtB*	Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0794		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00045**	-1,7	**0,00000**	-0,3	0,13650	0,4	0,20390	-0,8	**0,00068**	-1,1	**0,00009**
EF0795		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01212	1	1	1	-1,3	**0,00025**	-1,7	**0,00000**	-0,2	0,23060	0,0	0,93610	-1,1	**0,00006**	-1,1	**0,00002**
EF0796		Unknown function	Enzymes of unknown specificity	type 2 phosphatidic acid phosphatase family protein	1	1	1	-1,1	**0,00452**	-2,1	**0,00000**	-0,2	0,16880	0,0	0,92900	-1,5	**0,00010**	-1,7	**0,00001**
EF0797		Hypothetical proteins	Domain	conserved domain protein	1	0	1	2,4	**0,00000**	0,0	0,85730	4,2	**0,00000**	0,0	0,96350	1,3	**0,00002**	0,0	0,82530
EF0798		Hypothetical proteins		hypothetical protein	1	1	1	2,4	**0,00000**	0,0	0,74390	4,2	**0,00000**	0,0	0,92420	1,6	**0,00000**	-0,3	0,30160
EF0799	*atlA*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	autolysin	1	1	1	-1,7	**0,00048**	-0,4	0,01868	-1,3	**0,00002**	-0,5	0,21450	-1,9	**0,00000**	-0,8	0,02068
EF0801	*leuS*	Protein synthesis	tRNA aminoacylation	leucyl-tRNA synthetase	1	1	1	0,0	0,94150	-0,3	0,04098	-0,1	0,60060	0,2	0,46160	0,0	0,86670	0,1	0,79110
EF0802		Hypothetical proteins		hypothetical protein	1	1	1	-1,2	**0,00027**	0,0	0,68190	-1,0	**0,00017**	-1,4	**0,00081**	-0,7	**0,00181**	-0,7	**0,00200**
EF0803		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,9	**0,00319**	-1,6	**0,00000**	-0,8	**0,00414**	-1,4	**0,00031**	-0,8	**0,00098**	-1,2	**0,00003**
EF0804		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, amino acid-binding protein	1	1	1	0,5	**0,00699**	NA	NA	0,2	0,31960	-0,1	0,81210	0,2	0,20460	0,1	0,72500
EF0805		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, ATP-binding protein	1	1	1	0,4	0,05935	-0,4	0,02341	0,3	0,12660	-0,2	0,42210	0,1	0,34730	-0,1	0,61160
EF0806		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, permease protein	1	1	1	0,4	0,32020	-0,2	0,46850	0,3	0,11390	-0,1	0,86740	0,0	0,84270	-0,2	0,37060
EF0807		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein, putative	1	1	1	0,9	**0,00092**	2,3	**0,00000**	0,9	**0,00823**	1,1	0,01816	0,8	**0,00009**	2,2	**0,00000**
EF0808		Hypothetical proteins		hypothetical protein	1	1	1	0,6	0,10170	2,4	**0,00000**	0,8	**0,00023**	1,3	0,01780	0,9	**0,00002**	2,7	**0,00000**
EF0809		Cell envelope	Other	membrane protein, putative	1	1	1	0,7	0,01136	4,6	**0,00000**	-0,1	0,58000	2,9	**0,00000**	0,3	0,05172	4,2	**0,00000**
EF0810		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	0,0	0,96050	2,3	**0,00000**	-0,1	0,59610	-0,1	0,93440	NA	NA	NA	NA
EF0811		Hypothetical proteins		hypothetical protein	1	1	0	-0,2	0,46100	1,6	**0,00043**	-0,4	0,31940	NA	NA	NA	NA	NA	NA
EF0812		Energy metabolism	Biosynthesis and degradation of polysaccharides	glucuronyl hydrolase, putative	1	1	0	0,8	**0,00471**	0,4	0,04954	1,1	**0,00008**	-0,2	0,49620	NA	NA	NA	NA
EF0813		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 35	1	1	0	0,6	**0,00677**	0,4	0,04507	0,7	**0,00036**	0,0	0,93440	NA	NA	NA	NA
EF0814		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	0	1,1	**0,00008**	2,0	**0,00001**	1,6	**0,00001**	0,6	0,01280	NA	NA	NA	NA
EF0815		Signal transduction	PTS	PTS system, IIAB components	1	1	0	NA	NA	NA	NA	0,6	0,01627	NA	NA	NA	NA	NA	NA
EF0816		Signal transduction	PTS	PTS system, IIC component	1	1	0	0,5	0,10810	-0,8	**0,00095**	1,1	**0,00068**	-0,6	0,01914	NA	NA	NA	NA
EF0817		Signal transduction	PTS	PTS system, IID component	1	1	0	NA	NA	NA	NA	0,8	**0,00051**	NA	NA	NA	NA	NA	NA
EF0818		Cellular processes	Pathogenesis	polysaccharide lyase, family 8	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0819		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00032**	2,6	**0,00000**	0,6	**0,00607**	1,0	0,07537	1,1	**0,00001**	1,6	**0,00000**
EF0820	*rplY*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L25	1	1	1	0,7	**0,00116**	1,6	**0,00000**	1,1	**0,00012**	2,4	**0,00000**	2,0	**0,00000**	3,1	**0,00000**
EF0822		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,3	0,20880	0,1	0,47570	-0,4	0,01108	1,1	**0,00032**	0,2	0,27900	0,1	0,82560
EF0823		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,26590	NA	NA	-0,1	0,65530	NA	NA	NA	NA	NA	NA
EF0824		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	0,3	0,11180	0,8	**0,00005**	0,7	**0,00149**	1,1	**0,00008**	0,1	0,23970	0,9	**0,00021**
EF0825	*udk*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	uridine kinase	1	1	1	-0,7	**0,00061**	-1,3	**0,00000**	-1,9	**0,00001**	-0,2	0,42030	-1,2	**0,00000**	-1,5	**0,00004**
EF0826		Regulatory functions	DNA interactions	transcriptional regulator, PemK family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0827		Unknown function	Enzymes of unknown specificity	oxidoreductase, Gfo/Idh/MocA family	1	1	1	0,3	0,03354	0,1	0,63840	0,5	0,02912	0,2	0,40380	0,3	0,04964	0,2	0,48990
EF0828		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	-0,2	0,13660	0,1	0,77270	NA	NA	0,0	0,78330	-0,3	0,17660
EF0829		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,74010	NA	NA	0,2	0,11960	-0,2	0,51100

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0830		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,3	0,31940	-0,4	0,16170	0,3	0,16370	-0,9	**0,00130**
EF0831		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,71350	NA	NA	0,3	0,08007	-0,4	0,05103
EF0832		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,3	0,14060	NA	NA	0,2	0,23730	-0,8	**0,00374**
EF0833		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,56870	NA	NA	-0,1	0,51820	-0,5	0,02181
EF0834		Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	0,1	0,53420	NA	NA	-0,2	0,20120	-0,8	**0,00169**
EF0835		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,63920	-0,4	0,14330	-0,1	0,63010	-0,4	0,07399
EF0836		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,42670	-0,2	0,69740	0,2	0,16210	-0,3	0,18390
EF0837		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,35220	NA	NA	0,3	0,07264	0,0	0,99590	0,3	0,21480	-0,3	0,18370
EF0838		Unknown function	Enzymes of unknown specificity	pyridoxal phosphate-dependent enzyme, putative	1	1	1	0,1	0,45650	NA	NA	0,4	0,06303	0,0	0,95830	0,3	0,15600	-0,4	0,08611
EF0839		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,58880	NA	NA	0,4	0,02661	NA	NA	0,0	0,92830	-0,2	0,28040
EF0840		Energy metabolism	Sugars	carbohydrate kinase, pfkB family	1	1	1	-0,1	0,75980	-0,1	0,71880	0,4	0,09676	0,1	0,62750	0,1	0,70250	-0,4	0,08061
EF0841		Hypothetical proteins	Domain	conserved domain protein	1	1	1	1,0	**0,00004**	1,2	**0,00013**	1,0	**0,00163**	0,9	**0,00471**	0,4	0,01543	1,3	**0,00003**
EF0842		Unknown function	General	YaiI/YqxD family protein	1	1	1	0,3	0,33290	0,5	**0,00337**	0,5	0,04448	0,7	0,03888	-0,1	0,37860	0,3	0,18720
EF0843		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	D-alanine--D-alanine ligase	1	1	1	0,0	0,90920	-0,2	0,33160	0,2	0,56800	0,2	0,60320	-0,3	0,02685	-1,1	**0,00004**
EF0844		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,31080	0,1	0,38200	0,6	0,09936	0,4	0,36270	-0,8	**0,00199**	-0,3	0,04527
EF0845	*murF*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylmuramoylalanyl-D-glutamyl-diaminopimelate- ligase	1	1	1	-0,1	0,68080	-0,9	**0,00060**	-0,3	0,33460	-0,1	0,67890	0,0	0,78330	-0,4	0,08423
EF0846		Transcription	Other	ATP-dependent RNA helicase, DEAD/DEAH box family	1	1	1	-0,8	**0,00025**	-1,3	**0,00000**	-1,3	**0,00006**	-0,2	0,46070	-1,3	**0,00000**	-1,4	**0,00002**
EF0847		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0848	*acpS*	Fatty acid and phospholipid metabolism	Biosynthesis	holo-(acyl-carrier-protein) synthase	1	1	1	1,3	**0,00004**	2,8	**0,00000**	0,6	**0,00459**	1,0	**0,00093**	1,1	**0,00001**	1,4	**0,00002**
EF0849	*alr*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	alanine racemase	1	1	1	0,7	**0,00028**	1,7	**0,00000**	0,5	0,02206	0,9	**0,00082**	0,9	**0,00006**	1,5	**0,00000**
EF0850		Regulatory functions	DNA interactions	transcriptional regulator, PemK family	1	1	1	1,0	**0,00012**	1,6	**0,00000**	0,5	0,05199	1,1	**0,00024**	1,3	**0,00000**	1,5	**0,00000**
EF0851		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0852		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0853		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0854		Protein fate	Protein and peptide secretion and trafficking	signal peptidase I	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0855		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,2	0,64980	0,3	0,07978	0,4	0,08775	0,5	0,05871	0,6	**0,00449**	0,8	**0,00218**
EF0856		Unknown function	General	aldo/keto reductase family protein	1	1	1	0,7	**0,00374**	1,0	**0,00000**	1,0	**0,00007**	0,3	0,26720	0,9	**0,00005**	1,4	**0,00005**
EF0857		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,12920	0,0	0,84420	0,3	0,14940	-0,1	0,62580	0,3	0,03203	0,4	0,06607
EF0858	*pip*	Unknown function	General	phage infection protein	1	1	1	-1,8	**0,00000**	-1,5	**0,00000**	-2,4	**0,00000**	-1,4	**0,00003**	-1,7	**0,00000**	-1,2	**0,00059**
EF0859		Transport and binding proteins	Cations and iron carrying compounds	cation efflux family protein	1	1	1	-1,3	**0,00487**	-0,6	**0,00180**	-1,4	**0,00002**	-1,4	**0,00062**	-1,8	**0,00000**	-1,8	**0,00006**
EF0860		Cell envelope	Other	membrane protein, putative	1	1	1	-0,2	0,12110	-1,1	**0,00000**	-0,3	0,26700	-1,4	**0,00001**	-1,0	**0,00036**	-1,5	**0,00001**
EF0861		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,2	0,38420	0,4	0,16270	0,3	0,09291	0,8	0,05589	0,0	0,88980	0,6	0,24980
EF0862		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline ABC transporter, permease protein	1	1	1	0,0	0,84240	2,5	**0,00001**	-0,2	0,29670	1,2	**0,00133**	0,0	0,85810	1,6	**0,00000**
EF0863		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline ABC transporter/binding protein	1	1	1	0,0	0,90000	1,2	**0,00022**	0,0	0,99420	1,3	**0,00013**	-0,3	0,16030	2,1	**0,00000**
EF0864		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline ABC transporter, permease protein	1	1	1	-0,1	0,61080	1,5	**0,00000**	-0,1	0,70330	1,1	**0,00019**	0,1	0,38580	2,1	**0,00000**
EF0865		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/carnitine/choline transporter, ATP-binding protein	1	1	1	0,3	0,02550	0,7	**0,00007**	0,4	0,05577	1,0	**0,00094**	0,4	0,01011	1,3	**0,00000**
EF0867		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	1,3	**0,00014**	NA	NA	1,1	**0,00004**	NA	NA	1,5	**0,00000**	NA	NA
EF0868	*queA*	Protein synthesis	tRNA and rRNA base modification	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1	1	1	0,6	**0,00648**	0,1	0,20540	-0,1	0,53920	0,2	0,29860	0,2	0,05709	0,4	0,06465
EF0869		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	0,9	**0,00117**	1,4	**0,00000**	0,2	0,20770	0,0	0,88710	1,2	**0,00001**	1,5	**0,00000**
EF0871		Transport and binding proteins	Cations and iron carrying compounds	cation-transporting ATPase, E1-E2 family	1	1	1	0,7	**0,00056**	0,7	**0,00001**	0,1	0,49510	0,3	0,19810	0,1	0,58020	1,1	**0,00018**
EF0872		Transport and binding proteins	Cations and iron carrying compounds	potassium uptake protein	1	1	1	-1,4	**0,00004**	0,0	0,79770	-1,3	**0,00049**	-0,2	0,48900	-1,2	**0,00000**	-0,8	**0,00062**
EF0873		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0875		Cellular processes	Detoxification	copper-translocating P-type ATPase	1	1	1	1,7	**0,00007**	2,2	**0,00000**	1,4	**0,00018**	1,0	**0,00583**	1,5	**0,00000**	2,0	**0,00000**
EF0876		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,5	0,03225	NA	NA	NA	NA	NA	NA
EF0877		Unknown function	Enzymes of unknown specificity	oxidoreductase, aldo/keto reductase 2 family	1	1	1	0,9	**0,00326**	0,9	**0,00091**	0,5	0,01814	0,7	**0,00589**	0,5	**0,00435**	0,7	**0,00052**
EF0878	*polA*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase I	1	1	1	0,4	0,19350	1,1	**0,00015**	0,6	0,02063	0,5	0,21550	0,5	**0,00351**	0,8	**0,00032**
EF0879	*fpg*	DNA metabolism	DNA replication, recombination, and repair	formamidopyrimidine-DNA glycosylase	1	1	1	-0,2	0,47010	1,2	**0,00000**	0,3	0,07446	0,4	0,10500	0,0	0,76240	1,1	**0,00018**
EF0880		Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	dephospho-CoA kinase, putative	1	1	1	-0,1	0,80910	1,2	**0,00001**	0,2	0,46070	0,4	0,14470	-0,2	0,36600	1,1	**0,00007**
EF0881		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00244	1	1	1	0,9	**0,00023**	2,1	**0,00000**	0,7	**0,00042**	0,6	0,01780	0,8	**0,00005**	1,7	**0,00000**
EF0882		DNA metabolism	DNA replication, recombination, and repair	replication initiation and membrane attachment protein DnaB, putative	1	1	1	0,3	0,10880	1,0	**0,00000**	0,7	0,03278	0,6	0,09536	0,5	**0,00053**	1,4	**0,00000**
EF0883	*dnaI*	DNA metabolism	DNA replication, recombination, and repair	primosomal protein DnaI	1	1	1	0,2	0,44920	1,7	**0,00001**	0,2	0,23530	0,1	0,43420	0,5	**0,00186**	1,0	**0,00007**
EF0884		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,61050	0,7	**0,00004**	-0,1	0,66780	0,1	0,65190	-0,1	0,51350	0,4	0,11350
EF0885		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00752**	0,4	**0,00226**	-0,3	0,16970	0,4	0,34880	-0,3	0,02629	0,2	0,27360
EF0886		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,06999	0,6	0,01655	-0,4	0,02755	0,7	0,01297	-0,3	0,03513	0,7	**0,00807**
EF0887		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-0,2	0,21750	0,9	**0,00016**	-0,8	**0,00074**	0,8	**0,00203**	-0,7	**0,00037**	0,9	**0,00035**
EF0888		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00235**	0,1	0,46620	-0,8	**0,00053**	0,6	0,01929	-0,8	**0,00012**	0,6	0,01399
EF0889		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,9	**0,00030**	0,5	**0,00091**	-1,3	**0,00001**	1,2	**0,00846**	-1,2	**0,00002**	0,1	0,64870
EF0890		Hypothetical proteins		hypothetical protein	1	1	1	-0,8	**0,00040**	0,4	**0,00578**	-1,1	**0,00073**	1,0	**0,00014**	-0,2	0,32820	0,6	0,02136
EF0891		Amino acid biosynthesis	Aspartate family	aspartate aminotransferase, putative	1	1	1	0,2	0,51740	5,6	**0,00000**	3,4	**0,00000**	1,0	**0,00007**	1,0	**0,00002**	4,9	**0,00000**
EF0892		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, ATP-binding protein	1	1	1	0,2	0,50780	5,4	**0,00000**	3,9	**0,00000**	1,2	**0,00003**	1,2	**0,00000**	4,9	**0,00000**
EF0893		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, amino acid-binding/permease protein	1	1	1	0,7	0,01819	3,5	**0,00000**	3,6	**0,00000**	0,8	**0,00040**	1,3	**0,00015**	3,1	**0,00000**
EF0895		Central intermediary metabolism	Other	glycerol dehydrogenase, putative	1	1	1	0,5	0,02190	2,7	**0,00000**	2,9	**0,00001**	1,8	**0,00004**	1,3	**0,00001**	3,5	**0,00000**
EF0896	*tgt*	Protein synthesis	tRNA and rRNA base modification	queuine tRNA-ribosyltransferase	1	1	1	-0,8	**0,00027**	-0,8	**0,00033**	-1,2	**0,00012**	-1,0	**0,00016**	-0,7	**0,00005**	-0,7	**0,00068**
EF0897		Protein fate	Protein and peptide secretion and trafficking	preprotein translocase, YajC subunit, putative	1	1	1	0,0	0,96320	0,6	0,03899	-0,6	**0,00109**	0,2	0,37190	0,0	0,89780	0,5	0,01078
EF0898		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,03725	0,3	**0,00852**	0,4	0,13710	0,4	0,45800	-0,2	0,14000	0,1	0,52200
EF0899		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,03059	-1,1	**0,00000**	-0,6	**0,00076**	-0,2	0,34880	-0,5	**0,00395**	-1,0	**0,00025**
EF0900	*adhE*	Energy metabolism	Fermentation	aldehyde-alcohol dehydrogenase	1	1	1	-0,5	**0,00394**	-0,3	0,06772	-0,4	0,07636	-1,2	**0,00678**	-0,6	**0,00025**	-0,4	0,03017
EF0901		Biosynthesis of cofactors, prosthetic groups, carriers	Other	isopentenyl diphosphate delta isomerase, putative	1	1	1	-1,2	**0,00024**	-1,1	**0,00000**	-2,2	**0,00003**	-0,5	0,04218	-1,6	**0,00000**	-1,3	**0,00002**
EF0902		Central intermediary metabolism	Other	phosphomevalonate kinase	1	1	1	-1,2	**0,00002**	-1,1	**0,00000**	-1,7	**0,00007**	-0,7	**0,00168**	-1,5	**0,00000**	-1,6	**0,00001**
EF0903	*mvaD*	Central intermediary metabolism	Other	mevalonate diphosphate decarboxylase	1	1	1	-0,8	**0,00036**	-0,2	0,15440	-1,0	**0,00046**	-0,9	**0,00108**	-1,0	**0,00005**	-1,3	**0,00032**
EF0904	*mvk*	Central intermediary metabolism	Other	mevalonate kinase	1	1	1	-0,5	**0,00540**	-0,3	0,01718	-0,1	0,49500	-0,5	0,04391	-0,6	0,01030	-0,9	**0,00436**
EF0905		Unknown function	General	pentapeptide repeat family protein	1	1	1	0,5	0,01223	2,2	**0,00000**	1,0	**0,00033**	1,9	**0,00052**	0,0	0,82950	1,1	**0,00005**
EF0906		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	2,1	**0,00000**	3,1	**0,00000**	3,0	**0,00001**	2,7	**0,00001**	1,4	**0,00011**	1,2	**0,00113**
EF0907		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, peptide-binding protein	1	1	1	1,4	**0,00032**	2,1	**0,00000**	3,4	**0,00000**	2,4	**0,00000**	2,0	**0,00001**	3,9	**0,00000**
EF0908		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,13150	1,4	**0,00000**	0,9	0,07792	1,3	**0,00298**	0,2	0,10650	2,6	**0,00000**
EF0909		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, permease protein	1	1	1	-0,3	0,30540	0,1	0,51560	0,4	0,27480	0,9	**0,00099**	-0,2	0,34840	1,0	**0,00002**
EF0910		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, permease protein	1	1	1	0,0	0,95830	2,5	**0,00000**	0,2	0,59890	1,1	**0,00090**	-0,5	**0,00859**	2,0	**0,00000**
EF0911		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, ATP-binding protein	1	1	1	-0,5	0,02240	0,3	0,01179	-0,2	0,61460	1,3	**0,00028**	-0,4	**0,00870**	2,0	**0,00000**
EF0912		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, ATP-binding protein	1	1	1	-0,7	**0,00575**	0,3	**0,00547**	0,1	0,82370	0,5	0,12010	-0,6	**0,00327**	1,4	**0,00000**
EF0913		Mobile and extrachromosomal element functions	Transposon functions	transposase, putative	1	1	1	-0,3	0,25270	2,8	**0,00000**	0,4	0,31940	2,6	**0,00001**	-0,4	0,02471	3,2	**0,00000**
EF0914	*infC*	Protein synthesis	Translation factors	translation initiation factor IF-3	1	1	1	-2,7	**0,00000**	-4,6	**0,00000**	-3,4	**0,00000**	-0,4	0,23980	-2,1	**0,00000**	-3,3	**0,00000**
EF0915	*rpmI*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L35	1	1	1	-1,5	**0,00004**	-2,3	**0,00001**	-2,8	**0,00000**	-0,1	0,84970	-1,7	**0,00000**	-2,1	**0,00000**
EF0916	*rplT*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L20	1	1	1	-1,8	**0,00002**	-2,4	**0,00001**	-3,0	**0,00000**	-0,1	0,73820	-1,6	**0,00000**	-2,1	**0,00000**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF0917		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	0,01290	1,1	**0,00001**	0,8	**0,00317**	0,7	0,02321	0,5	**0,00574**	0,7	**0,00122**
EF0918		Cell envelope	Other	membrane protein, putative	1	1	1	-0,7	**0,00042**	1,5	**0,00000**	-1,8	**0,00000**	0,6	0,01304	-0,9	**0,00014**	-0,2	0,35380
EF0919		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,8	**0,00028**	0,5	**0,00020**	-0,8	**0,00138**	0,1	0,63600	-0,3	0,03949	0,4	0,03972
EF0920		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00413**	0,5	**0,00038**	-1,0	**0,00007**	0,1	0,57010	-0,3	0,10060	0,4	0,02514
EF0921		Transport and binding proteins	Anions	sulfate transporter family protein	1	1	1	-0,8	**0,00153**	0,0	0,81670	-1,4	**0,00002**	0,4	0,06862	-0,8	**0,00108**	-0,3	0,26640
EF0922		Cell envelope	Other	membrane protein, putative	1	1	1	0,0	0,88720	0,9	**0,00001**	0,3	0,18230	0,8	0,02070	-0,1	0,43730	0,4	0,24810
EF0923		Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	0,5	0,02077	1,6	**0,00000**	1,0	**0,00027**	1,0	**0,00828**	1,0	**0,00007**	1,7	**0,00002**
EF0924		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,15220	3,2	**0,00000**	0,6	0,05291	1,3	**0,00094**	0,7	**0,00121**	2,3	**0,00004**
EF0925		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,81490	0,9	**0,00001**	0,3	0,30670	0,4	0,28020	-0,1	0,37810	0,3	0,11170
EF0926		Signal transduction	Two-component systems	DNA-binding response regulator	1	1	1	0,4	0,07623	0,3	0,07397	1,1	**0,00009**	0,0	0,88570	0,4	0,08405	0,1	0,67230
EF0927		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	-0,1	0,84430	-0,4	**0,00258**	0,6	**0,00042**	-0,1	0,66660	0,3	0,12750	-0,2	0,36660
EF0928		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	glucose uptake protein	1	1	1	-1,1	**0,00027**	-0,8	**0,00015**	-1,3	**0,00013**	-1,4	**0,00105**	-1,6	**0,00000**	-1,4	**0,00020**
EF0929		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	-1,3	**0,00005**	-1,9	**0,00000**	-1,6	**0,00003**	-1,6	**0,00130**	-1,5	**0,00001**	-2,1	**0,00000**
EF0930	*metG*	Protein synthesis	tRNA aminoacylation	methionyl-tRNA synthetase	1	1	1	-0,1	0,73500	-1,2	**0,00004**	-0,6	**0,00611**	-0,4	0,12230	-0,3	0,06569	-1,1	**0,00359**
EF0931		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,70350	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0932		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00161**	0,2	0,17300	3,0	**0,00000**	-0,2	0,47060	1,2	**0,00003**	0,0	0,96800
EF0933		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,2	**0,00001**	-0,9	**0,00055**	-1,2	**0,00001**	-1,0	0,01599	-0,7	**0,00020**	-0,4	0,05981
EF0934		Unknown function	Enzymes of unknown specificity	hydrolase, TatD family	1	1	1	0,4	0,05378	-0,4	**0,00597**	0,1	0,80620	-0,2	0,56160	0,4	0,03146	0,4	0,12040
EF0935		Unknown function	General	primase-related protein	1	1	1	0,5	0,04623	-0,1	0,42930	0,2	0,31880	-0,2	0,32080	0,3	0,02686	0,3	0,26640
EF0936	*ksgA*	Protein synthesis	tRNA and rRNA base modification	dimethyladenosine transferase	1	1	1	0,2	0,39560	0,3	0,03920	0,0	0,88660	0,0	0,92460	-0,1	0,54620	0,3	0,20890
EF0937		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00411**	1,9	**0,00000**	-0,1	0,75370	-0,2	0,47130	0,4	0,01405	1,5	**0,00000**
EF0938		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/TOBE domain protein	1	1	1	-1,4	**0,00246**	-3,2	**0,00000**	-1,5	**0,00002**	-1,7	**0,00279**	-1,0	**0,00001**	-1,2	**0,00059**
EF0939	*mgsA*	Energy metabolism	Other	methylglyoxal synthase	1	1	1	0,4	0,05075	1,4	**0,00000**	0,1	0,26760	0,6	**0,00884**	0,5	**0,00466**	1,3	**0,00002**
EF0940		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,09425	-1,0	**0,00001**	-0,3	0,08827	-1,0	**0,00542**	0,0	0,85240	-1,0	**0,00499**
EF0941		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,4	0,15830	-0,3	0,30330	-0,2	0,31090	0,1	0,79160	-0,6	**0,00275**	-0,1	0,64030
EF0942		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,2	0,38970	0,0	0,85950	0,0	0,93040	0,5	0,10910	0,1	0,74010	0,1	0,53130
EF0943		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,02257	-0,4	**0,00074**	0,5	0,01712	0,0	0,95480	0,0	0,78670	0,1	0,49170
EF0944		Cell envelope	Other	extracellular protein, putative	1	1	1	-1,7	**0,00000**	-1,5	**0,00000**	-1,6	**0,00002**	-0,9	**0,00247**	-2,1	**0,00000**	-1,8	**0,00001**
EF0945		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-1,1	**0,00003**	-1,6	**0,00003**	-1,7	**0,00013**	-1,4	**0,00407**	-1,6	**0,00001**	-1,5	**0,00557**
EF0946		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,35850	-0,1	0,29020	0,3	0,05199	-0,3	0,16170	0,2	0,12630	0,1	0,73120
EF0947		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,0	0,98530	-0,5	0,12670	0,1	0,59890	-0,2	0,50250	-0,1	0,59220	-0,1	0,79160
EF0948	*ung*	DNA metabolism	DNA replication, recombination, and repair	uracil-DNA glycosylase	1	1	1	-0,3	0,33200	-0,2	0,02848	-0,3	0,31280	0,2	0,25360	0,0	0,89000	0,2	0,44400
EF0949	*eutD*	Energy metabolism	Fermentation	phosphotransacetylase	1	1	1	-0,2	0,24430	-1,0	**0,00001**	-1,4	**0,00070**	0,0	0,96940	-1,0	**0,00003**	-0,3	0,06675
EF0950		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00150	1	1	1	-0,6	0,08744	0,0	0,82680	-0,8	**0,00634**	-0,8	**0,00536**	-0,4	0,02588	-0,1	0,83740
EF0951		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,4	0,10850	-0,2	0,33330	-0,8	**0,00387**	-0,8	**0,00033**	-0,4	0,03750	-0,2	0,37870
EF0953		Hypothetical proteins		hypothetical protein	1	1	1	0,6	0,02868	0,7	**0,00011**	0,5	**0,00800**	0,2	0,46480	0,5	**0,00842**	0,6	0,01263
EF0954	*malR/bop*	Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	0,4	0,20880	0,4	**0,00848**	0,6	0,04294	0,1	0,74570	0,0	0,98630	0,2	0,40380
EF0955	*malM/bop*	Energy metabolism	Sugars	aldose 1-epimerase, putative	1	1	1	NA	NA	NA	NA	1,2	**0,00185**	-0,4	0,09481	NA	NA	NA	NA
EF0956	*malB/bop*	Energy metabolism	Sugars	beta-phosphoglucomutase	1	1	1	1,0	0,05291	0,0	0,84860	1,2	**0,00166**	-0,4	0,20150	0,4	0,25440	0,3	0,32110
EF0957	*malP/bop*	Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 65	1	1	1	NA	NA	NA	NA	0,7	0,02548	NA	NA	NA	NA	NA	NA
EF0958	*malT*	Signal transduction	PTS	PTS system, IIABC components	1	1	1	NA	NA	-0,7	**0,00305**	1,3	**0,00389**	-0,7	0,20150	-0,5	**0,00420**	0,1	0,73790
EF0959		Hypothetical proteins		hypothetical protein	1	0	1	0,5	0,08059	0,0	0,92350	NA	NA	NA	NA	0,6	0,01004	0,5	0,05585
EF0960		Unknown function	Enzymes of unknown specificity	endonuclease/exonuclease/phosphatase family protein	1	1	1	0,6	0,02512	0,3	0,18850	0,6	0,01788	0,7	0,18530	0,6	0,01801	0,6	0,01203
EF0961		Amino acid biosynthesis	Glutamate family	pyrroline-5-carboxylate reductase, putative	1	1	1	0,2	0,54180	-0,3	0,16790	0,2	0,18470	-0,2	0,59520	-0,5	**0,00306**	-0,6	0,01714
EF0962		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	0,1	0,59430	0,2	0,06422	-0,1	0,73570	0,2	0,52360	0,4	0,01075	0,3	0,14750
EF0963		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,03265	1,1	**0,00001**	0,1	0,43060	0,2	0,29590	0,3	0,21180	0,4	0,02174
EF0964		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,20790	0,8	**0,00001**	0,0	0,89720	0,2	0,69110	0,2	0,10060	0,5	0,10110
EF0965		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	0,7	0,01061	NA	NA	NA	NA	NA	NA	NA	NA
EF0966		Regulatory functions	DNA interactions	transcriptional regulator, MerR family	1	0	0	0,4	0,02295	1,3	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF0967		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF0968	*rplU*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L21	1	1	1	-0,4	0,26580	0,2	0,32750	-1,7	**0,00000**	0,0	0,99590	-0,8	**0,00039**	-0,6	**0,00774**
EF0969		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,17540	-0,1	0,60110	-2,2	**0,00002**	0,0	0,94440	-1,3	**0,00008**	0,1	0,83740
EF0970	*rpmA*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L27	1	1	1	-0,4	0,15530	-0,5	0,02071	-2,2	**0,00000**	-1,0	0,01385	-0,8	**0,00003**	-2,5	**0,00000**
EF0971		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	**0,00538**	1,3	**0,00001**	0,6	0,08792	0,4	0,09652	0,9	**0,00055**	1,6	**0,00000**
EF0972		DNA metabolism	DNA replication, recombination, and repair	DNA repair exonuclease family protein	1	1	1	-1,3	**0,00022**	0,0	0,93510	0,1	0,79040	0,1	0,58680	-0,7	**0,00022**	0,3	0,25010
EF0973	*pepQ-1*	Protein fate	Degradation of proteins, peptides, and glycopeptides	proline dipeptidase	1	1	1	0,7	**0,00066**	1,4	**0,00000**	0,8	0,05645	0,4	0,06020	0,6	**0,00121**	1,6	**0,00000**
EF0974		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00027**	1,7	**0,00000**	0,9	**0,00180**	0,5	0,04134	0,4	0,06497	1,5	**0,00000**
EF0976		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	**0,00087**	1,1	**0,00000**	0,3	0,21660	0,0	0,89240	0,4	0,01325	0,5	**0,00200**
EF0977	*nusB*	Transcription	Transcription factors	N utilization substance protein B	1	1	1	0,1	0,55980	1,0	**0,00771**	0,2	0,46490	0,1	0,71730	0,2	0,19870	1,4	**0,00000**
EF0978	*folD*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	methylenetetrahydrofolate dehydrogenase	1	1	1	-0,2	0,40360	0,4	**0,00318**	0,2	0,48590	-0,2	0,42210	0,0	0,82390	0,4	0,06857
EF0979	*xseA*	DNA metabolism	Degradation of DNA	exodeoxyribonuclease VII, large subunit	1	1	1	-0,4	0,16480	0,0	0,69120	0,1	0,73080	-0,2	0,48140	-0,2	0,15630	0,2	0,23140
EF0980	*xseB*	DNA metabolism	Degradation of DNA	exodeoxyribonuclease VII, small subunit	1	1	1	-0,1	0,83420	0,0	0,75810	0,0	0,95600	-0,2	0,33640	-0,5	**0,00202**	-0,1	0,70170
EF0981	*ispA*	Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	geranyltranstransferase	1	1	1	0,0	0,90000	0,0	0,75260	0,1	0,68480	-0,1	0,81060	-0,1	0,47040	0,1	0,44610
EF0982	*tlyA*	Cellular processes	Pathogenesis	hemolysin A	1	1	1	0,0	0,90000	0,6	**0,00583**	-0,2	0,29800	0,1	0,76320	-0,2	0,11480	0,0	0,91330
EF0983		Regulatory functions	DNA interactions	transcriptional regulator, ArgR family	1	1	1	-0,3	0,21690	0,1	0,74900	-0,2	0,33240	-0,4	0,05292	0,5	**0,00098**	0,3	0,12680
EF0984	*recN*	DNA metabolism	DNA replication, recombination, and repair	DNA repair protein RecN	1	1	1	-0,3	0,15530	0,3	0,04245	-0,2	0,22300	-0,5	0,07441	0,3	0,03513	0,5	0,08104
EF0985		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00420**	1,4	**0,00000**	0,7	**0,00115**	0,5	0,08962	0,0	0,93350	0,7	**0,00432**
EF0986		Transport and binding proteins	Cations and iron carrying compounds	cation transporter	1	1	1	0,7	**0,00208**	2,4	**0,00000**	0,9	**0,00361**	1,3	**0,00117**	1,4	**0,00000**	2,2	**0,00001**
EF0987		Cell envelope	Other	lipoprotein, putative	1	1	1	-1,3	**0,00012**	0,5	**0,00651**	-1,5	**0,00002**	0,0	0,94340	-1,7	**0,00001**	-0,5	**0,00814**
EF0988		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00242	1	1	1	-0,4	0,03882	0,5	**0,00196**	-0,6	**0,00142**	0,0	0,99600	-0,3	0,01157	-0,2	0,28780
EF0989		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00006	1	1	1	-0,5	0,01545	0,1	0,39780	-0,9	**0,00050**	-0,6	**0,00486**	-0,6	**0,00058**	-0,5	**0,00875**
EF0990		Cellular processes	Cell division	cell division protein	1	1	1	-0,5	0,01021	-0,8	0,05063	-0,9	**0,00032**	-1,0	**0,00110**	-0,5	**0,00074**	-0,9	**0,00057**
EF0991	*pbpC*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein C	1	1	1	-0,6	**0,00213**	-1,1	**0,00010**	-1,1	**0,00043**	-1,2	**0,00106**	-1,0	**0,00003**	-1,8	**0,00000**
EF0992	*mraY*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	phospho-N-acetylmuramoyl-pentapeptide-transferase	1	1	1	-1,0	**0,00056**	-1,5	**0,00000**	-1,3	**0,00041**	-0,9	0,01739	-1,4	**0,00002**	-1,3	**0,00001**
EF0993	*murD*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1	1	1	-1,3	**0,00071**	-2,0	**0,00000**	-1,6	**0,00004**	-1,3	**0,00006**	-1,0	**0,00002**	-1,6	**0,00001**
EF0994	*murG*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylglucosamine-N-acetylmuramyl pyrophosphoryl transf	1	1	1	-0,7	**0,00135**	-0,8	**0,00007**	-0,6	**0,00136**	-0,9	**0,00093**	-0,5	**0,00089**	-1,1	**0,00004**
EF0995	*ftsQ*	Cellular processes	Cell division	cell division protein FtsQ	1	1	1	-0,9	**0,00012**	-0,7	**0,00004**	-0,7	**0,00094**	-0,9	**0,00026**	-0,6	**0,00069**	-1,2	**0,00005**
EF0996	*ftsA*	Cellular processes	Cell division	cell division protein FtsA	1	1	1	0,1	0,45450	0,7	0,01102	-0,1	0,70370	0,1	0,52640	0,0	0,84620	0,3	0,06589
EF0997	*ftsZ*	Cellular processes	Cell division	cell division protein FtsZ	1	1	1	0,2	0,26360	0,1	0,75200	0,0	0,95530	0,0	0,98020	-0,1	0,54230	0,4	0,03524
EF0998		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00044	1	1	1	-0,5	**0,00677**	-0,8	**0,00006**	0,0	0,99560	0,5	0,04392	-0,2	0,12240	0,5	**0,00570**
EF0999		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,92100	-0,2	0,19420	-0,1	0,53080	0,0	0,90490	-0,1	0,59350	-0,3	0,07320
EF1000		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,33480	-0,6	**0,00849**	0,2	0,42670	0,2	0,36700	-0,2	0,13510	-1,2	**0,00001**
EF1001		Unknown function	General	S4 domain protein	1	1	1	0,6	**0,00383**	2,0	**0,00000**	0,3	0,26770	0,5	0,09135	0,1	0,71420	0,8	**0,00135**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1002	*divIVA*	Cellular processes	Cell division	cell division protein DivIVA	1	1	1	0,3	0,30220	2,4	**0,00000**	0,1	0,77500	0,6	**0,00928**	0,2	0,25550	1,0	**0,00009**
EF1003	*ileS*	Protein synthesis	tRNA aminoacylation	isoleucyl-tRNA synthetase	1	1	1	0,4	0,06194	0,5	**0,00044**	-0,1	0,55850	0,4	0,02115	-0,3	0,13540	-0,1	0,76840
EF1004	*zwf*	Energy metabolism	Pentose phosphate pathway	glucose-6-phosphate 1-dehydrogenase	1	1	1	0,4	0,03686	0,3	0,02811	0,6	**0,00345**	0,7	0,04020	0,1	0,34260	0,1	0,53790
EF1005		Regulatory functions	DNA interactions	iron-dependent repressor	1	1	1	-0,2	0,23700	-0,5	**0,00148**	0,4	**0,00820**	0,5	0,04713	-0,1	0,67060	-0,2	0,22280
EF1006		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,24430	1,8	**0,00000**	0,9	**0,00052**	1,0	**0,00030**	0,8	**0,00119**	1,7	**0,00000**
EF1008		Unknown function	Enzymes of unknown specificity	oxidoreductase, Gfo/Idh/MocA family	1	1	1	0,9	**0,00807**	2,3	**0,00000**	0,9	**0,00071**	1,6	**0,00164**	0,8	**0,00003**	2,0	**0,00000**
EF1009		Transcription	Other	ATP-dependent RNA helicase, DEAD/DEAH box family	1	1	1	0,7	**0,00121**	2,3	**0,00000**	0,4	0,01774	1,7	**0,00010**	0,7	**0,00011**	1,8	**0,00007**
EF1010		Regulatory functions	Protein interactions	sigma-54 interaction domain protein	1	1	1	0,4	0,03738	2,0	**0,00000**	0,3	0,08743	1,5	**0,00039**	0,1	0,47870	1,4	**0,00000**
EF1013		Signal transduction	PTS	PTS system, IIC component	1	1	1	0,4	0,07563	-2,3	**0,00000**	0,7	**0,00065**	-1,3	0,04314	0,3	0,15610	-0,2	0,44400
EF1014		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,01430	-0,8	**0,00122**	0,8	**0,00009**	-0,4	0,29580	0,5	0,05854	0,2	0,23830
EF1015		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00055**	-0,8	**0,00005**	0,7	**0,00042**	-0,5	0,16740	0,4	0,10880	0,1	0,75430
EF1016		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00071**	-0,2	0,53580	0,7	**0,00236**	NA	NA	NA	NA	0,2	0,60130
EF1017		Signal transduction	PTS	PTS system, IIB component	1	1	1	-0,5	0,01108	0,0	0,89240	-0,1	0,61790	0,3	0,52260	-0,6	**0,00097**	0,5	0,04639
EF1018		Signal transduction	PTS	PTS system, IIA component	1	1	1	-1,0	**0,00014**	-1,3	**0,00066**	-0,1	0,71830	-0,1	0,85780	-0,8	**0,00005**	0,2	0,56520
EF1019		Signal transduction	PTS	PTS system, IIC component	1	1	1	-1,4	**0,00011**	-2,8	**0,00000**	0,3	0,19330	-0,4	0,52630	-0,7	**0,00030**	0,1	0,81400
EF1020		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	-0,2	0,31570	-1,9	**0,00000**	0,9	**0,00176**	-1,3	0,05871	0,2	0,40150	0,4	0,17460
EF1021		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,01535	-0,2	0,26050	1,0	**0,00013**	-0,2	0,34400	0,4	0,09157	0,8	0,01292
EF1022		Hypothetical proteins		hypothetical protein	1	1	1	1,0	**0,00011**	2,5	**0,00000**	0,7	**0,00432**	1,7	**0,00006**	1,2	**0,00001**	2,5	**0,00000**
EF1023		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,81280	-0,2	0,18690	-0,4	0,04648	-0,4	0,09674	0,5	**0,00103**	1,1	**0,00001**
EF1024	*ppdK*	Energy metabolism	Other	pyruvate phosphate dikinase	1	1	1	0,6	**0,00717**	0,9	**0,00002**	0,6	0,01234	0,4	0,08584	0,0	0,96250	0,5	0,05949
EF1025		Unknown function	General	CBS domain protein	1	1	1	0,7	**0,00220**	-0,5	**0,00023**	0,9	**0,00029**	0,0	0,97280	-0,4	0,01050	-0,3	0,28200
EF1026		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,02071	-0,6	**0,00042**	0,3	0,05932	-0,2	0,68350	-0,4	0,01142	-0,5	0,01026
EF1028		Unknown function	Enzymes of unknown specificity	hydrolase, alpha/beta hydrolase fold family	1	1	1	0,5	0,08108	0,1	0,61670	-0,1	0,72810	0,0	0,91990	0,2	0,23730	-0,1	0,80420
EF1029		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	**0,00045**	2,5	**0,00000**	0,3	0,12920	0,4	0,20630	0,5	0,01029	1,6	**0,00000**
EF1030		Unknown function	Enzymes of unknown specificity	endonuclease/exonuclease/phosphatase family protein	1	1	1	0,6	**0,00863**	2,1	**0,00000**	0,0	0,95760	0,6	0,04520	0,4	0,04121	1,4	**0,00004**
EF1031		Unknown function	Enzymes of unknown specificity	phosphorylase family protein	1	1	1	0,0	0,90000	1,5	**0,00000**	-0,2	0,26320	0,6	**0,00360**	-0,1	0,42020	1,0	**0,00005**
EF1032	*drrC*	Transport and binding proteins	Other	daunorubicin resistance protein	1	1	1	0,6	0,02896	1,4	**0,00000**	1,1	**0,00002**	1,2	**0,00133**	0,5	**0,00294**	1,7	**0,00001**
EF1033		Central intermediary metabolism	Other	6-aminohexanoate-cyclic-dimer hydrolase, putative	1	1	1	-1,2	**0,00004**	NA	NA	-0,8	**0,00039**	0,3	0,29300	-1,0	**0,00003**	0,3	0,28450
EF1034		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,1	0,70830	-0,5	0,01473	0,0	0,94650	-0,1	0,78610	0,0	0,84000	0,0	0,90320
EF1035		Cell envelope	Other	lipoprotein, putative	1	1	1	-0,5	**0,00827**	-0,8	**0,00013**	-0,3	0,09659	-0,3	0,19560	-0,4	**0,00216**	-0,2	0,35300
EF1036		Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	nucleoside diphosphate kinase	1	1	1	-0,7	**0,00139**	-0,2	0,09427	-0,7	**0,00903**	0,3	0,41740	-0,7	**0,00053**	0,1	0,65730
EF1037		Amino acid biosynthesis	Aspartate family	L-aspartate beta-decarboxylase, putative	1	1	1	1,9	**0,00000**	2,8	**0,00000**	2,3	**0,00000**	2,3	**0,00000**	2,5	**0,00000**	2,3	**0,00000**
EF1038		Cell envelope	Other	lipoprotein, putative	1	1	1	0,7	**0,00448**	NA	NA	1,2	**0,00053**	1,7	**0,00028**	NA	NA	NA	NA
EF1039		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-0,4	0,01302	1,0	**0,00001**	0,2	0,44760	0,5	0,01498	-0,3	0,01009	0,1	0,61510
EF1040		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1041		Transport and binding proteins	Nucleosides, purines and pyrimidines	xanthine/uracil permeases family protein	1	1	1	1,8	**0,00000**	NA	NA	2,1	**0,00007**	0,8	**0,00438**	2,3	**0,00000**	NA	NA
EF1042		Transport and binding proteins	Other	multidrug resistance protein, putative	1	1	1	0,4	0,04171	1,6	**0,00000**	0,7	**0,00815**	1,8	**0,00001**	0,7	**0,00009**	1,6	**0,00000**
EF1043		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,13030	0,9	**0,00095**	-0,4	0,04263	0,7	**0,00471**	0,0	0,95710	0,0	0,83860
EF1044	*dnaE*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, alpha subunit	1	1	1	0,0	0,89220	0,7	**0,00020**	0,2	0,26820	0,2	0,52630	0,2	0,16920	0,4	0,13530
EF1045	*pfk*	Energy metabolism	Glycolysis/gluconeogenesis	6-phosphofructokinase	1	1	1	-0,6	**0,00157**	-0,6	**0,00015**	-0,5	0,02430	-0,1	0,58100	-0,2	0,18900	-1,0	**0,00011**
EF1046	*pyk*	Energy metabolism	Glycolysis/gluconeogenesis	pyruvate kinase	1	1	1	0,0	0,93720	-0,2	0,16570	-0,5	**0,00286**	0,0	0,86830	0,0	0,90330	0,3	0,12040
EF1047		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00672**	-0,5	**0,00665**	-1,2	**0,00001**	-0,9	**0,00072**	-0,9	**0,00019**	-1,0	**0,00001**
EF1048	*rpmF-3*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L32	1	1	1	-0,6	0,02309	0,1	0,68270	-1,1	**0,00019**	-0,3	0,26230	-0,6	**0,00756**	-0,6	**0,00607**
EF1049	*gnd*	Energy metabolism	Pentose phosphate pathway	6-phosphogluconate dehydrogenase, decarboxylating	1	1	1	0,4	0,15750	0,4	0,06181	-0,5	0,03153	-0,1	0,62520	0,0	0,96100	0,3	0,34090
EF1050	*etaR*	Signal transduction	Two-component systems	DNA-binding response regulator	1	1	1	-0,4	0,04593	-0,6	0,04704	-1,0	**0,00040**	-0,8	0,02031	-0,8	**0,00025**	-1,0	**0,00074**
EF1051	*etaS*	Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	-0,7	0,04018	-0,9	**0,00052**	-0,7	**0,00114**	-0,8	0,06447	-0,8	**0,00693**	-0,6	0,16010
EF1052		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,13310	-0,9	**0,00016**	-0,9	0,01630	-0,2	0,76290	-1,1	**0,00007**	-1,8	**0,00033**
EF1053		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1054		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1055	*efaR*	Cellular processes	Toxin production and resistance	tunicamycin resistance protein, putative	1	1	1	NA	NA	NA	NA	-0,2	0,35660	NA	NA	NA	NA	NA	NA
EF1056		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1057		Transport and binding proteins	Cations and iron carrying compounds	Mn2+/Fe2+ transporter, NRAMP family	1	1	1	4,1	**0,00000**	3,9	**0,00000**	4,0	**0,00001**	4,6	**0,00000**	4,0	**0,00000**	3,9	**0,00000**
EF1058		Cellular processes	Adaptations to atypical conditions	universal stress protein family	1	1	1	NA	NA	NA	NA	NA	NA	2,0	0,01190	2,2	**0,00009**	2,3	**0,00533**
EF1059		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	**0,00188**	1,8	**0,00000**	1,2	**0,00035**	0,8	0,02960	1,0	**0,00044**	1,6	**0,00000**
EF1060		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1061		Unknown function	Enzymes of unknown specificity	N-acyl-D-amino-acid deacylase family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1062		Unknown function	Enzymes of unknown specificity	N-acyl-D-amino-acid deacylase family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1063		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,30220	1,4	0,04924	0,3	0,20650	1,3	**0,00060**	0,2	0,33320	1,6	**0,00002**
EF1065		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1066		Unknown function	Enzymes of unknown specificity	hexapeptide-repeat containing-acetyltransferase	1	1	1	-0,4	0,07146	0,8	**0,00002**	-0,4	0,01622	-0,1	0,61660	-0,3	0,05647	0,6	**0,00381**
EF1067		Hypothetical proteins		hypothetical protein	1	1	1	1,2	**0,00020**	4,7	**0,00000**	1,2	**0,00001**	0,6	0,05655	1,1	**0,00003**	3,7	**0,00000**
EF1068	*galM*	Energy metabolism	Sugars	aldose 1-epimerase	1	1	1	-0,1	0,86760	NA	NA	0,5	0,01494	-0,5	0,12490	0,2	0,35340	0,3	0,10670
EF1069	*galK*	Energy metabolism	Sugars	galactokinase	1	1	1	0,3	0,23120	NA	NA	0,6	0,03700	0,0	0,92080	0,8	**0,00011**	1,5	**0,00875**
EF1071	*galT*	Energy metabolism	Sugars	galactose-1-phosphate uridylyltransferase	1	1	1	NA	NA	NA	NA	0,5	0,01162	NA	NA	0,5	0,01029	1,0	**0,00703**
EF1072	*galR*	Regulatory functions	DNA interactions	galactose operon repressor galR	1	1	1	0,1	0,80490	NA	NA	-0,2	0,32530	0,6	0,11590	0,4	**0,00398**	1,3	**0,00002**
EF1073		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,6	**0,00302**	0,3	0,32930	-0,1	0,53940	0,4	0,04628
EF1074		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,72370	-0,3	0,01184	0,0	0,96880	0,1	0,70050	0,3	0,09716	1,0	**0,00008**
EF1075		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	0,0	0,93720	0,3	0,05607	0,1	0,49200	-0,1	0,61660	0,2	0,13720	0,4	0,02766
EF1076		Cellular processes	Toxin production and resistance	streptomycin 3-adenylyltransferase, putative	1	1	1	-0,2	0,56010	0,1	0,78490	-0,3	0,36200	-0,9	0,05256	-0,3	0,09334	-0,2	0,55730
EF1077		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,1	0,62170	NA	NA	-0,3	0,16920	-0,1	0,48330	0,2	0,44540	0,4	0,03714
EF1078		Transport and binding proteins	Other	multidrug resistance protein, putative	1	1	1	-0,3	0,14360	-1,2	**0,00000**	-0,5	0,09976	-0,3	0,32000	-0,4	**0,00524**	-1,3	**0,00264**
EF1080		DNA metabolism	DNA replication, recombination, and repair	ImpB/MucB/SamB family protein	1	1	1	0,2	0,27170	0,3	**0,00799**	0,0	0,96420	-0,2	0,31550	0,1	0,47910	0,1	0,70460
EF1081		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,40760	0,8	**0,00018**	0,0	0,96420	0,0	0,89620	0,0	0,80350	0,4	0,04494
EF1082		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,0	0,87830	0,0	0,92420	NA	NA	0,5	0,06007
EF1083		Hypothetical proteins		hypothetical protein	1	1	1	0,5	**0,00851**	0,8	**0,00004**	0,3	0,03995	0,1	0,73820	0,3	0,05249	0,8	**0,00094**
EF1084		Cellular processes	Adaptations to atypical conditions	universal stress protein family	1	1	1	0,1	0,74410	0,4	**0,00888**	-0,1	0,63450	-0,2	0,29770	0,3	0,05343	0,7	**0,00546**
EF1085		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,4	0,05247	0,7	**0,00004**	0,2	0,62790	0,0	0,89320	0,0	0,87930	0,8	**0,00078**
EF1086		Energy metabolism	Amino acids and amines	spermine/spermidine acetyltransferase, putative	1	1	1	-0,1	0,70780	-0,1	0,47420	-0,3	0,10500	-0,6	0,05535	0,1	0,72170	0,0	0,99110
EF1088		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,06816	0,2	0,23850	0,0	0,92030	0,2	0,47780	-0,1	0,49870	0,0	0,99020
EF1089		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,64710	1,9	**0,00010**	-0,6	**0,00269**	1,2	**0,00069**	0,4	0,01944	2,1	**0,00000**
EF1090		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,7	**0,00220**	-0,1	0,74750	NA	NA	NA	NA
EF1091	*ebpA*	Unknown function	General	von Willebrand factor type A domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,1	0,67140
EF1092	*ebpB*	Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	NA	NA	-0,3	0,43180	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1093	*ebpC*	Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	-1,1	0,03660	-0,1	0,79230	-0,7	0,18960	-0,1	0,70770	-0,2	0,35540
EF1094	*srtC*	Cell envelope	Surface structures	sortase family protein	1	1	1	NA	NA	NA	NA	NA	NA	-0,2	0,40380	NA	NA	NA	NA
EF1095		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,60560	0,5	0,01659	0,2	0,55650	0,3	0,20210	0,4	0,05144	0,4	0,05208
EF1096		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,14620	3,5	**0,00000**	0,7	0,01728	1,1	**0,00088**	0,9	**0,00006**	3,7	**0,00000**
EF1097		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,2	0,39730	NA	NA	NA	NA	NA	NA
EF1098		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	**0,00685**	0,2	0,37880	-0,4	0,04648	0,4	0,14060	-0,8	**0,00104**	0,1	0,76820
EF1099	*ace*	Cell envelope	Other	collagen adhesin protein	1	1	1	0,1	0,78950	NA	NA	-0,7	0,05743	NA	NA	0,3	0,02727	-0,6	0,29490
EF1100		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	NA	NA	NA	NA	-0,3	0,24410	-0,4	0,37410	0,0	0,89990	-0,2	0,37980
EF1101		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,0	0,98630	-0,2	0,38380	0,6	**0,00165**	0,7	**0,00170**
EF1102		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01655	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1103		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	3,0	**0,00000**	2,0	**0,00000**	3,4	**0,00000**	3,5	**0,00000**	3,1	**0,00000**	2,3	**0,00000**
EF1104		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,2	0,52710	0,1	0,29790	0,3	0,29960	0,7	0,16110	-0,2	0,32070	0,0	0,83010
EF1105		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,94670	0,5	**0,00054**	-0,2	0,35140	0,2	0,54460	0,1	0,70920	0,7	0,01272
EF1106		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1107		Hypothetical proteins		hypothetical protein	1	1	1	1,3	**0,00001**	0,4	**0,00448**	0,9	**0,00020**	1,0	**0,00033**	0,7	**0,00055**	0,9	**0,00011**
EF1108	*lutA*	Unknown function	Enzymes of unknown specificity	oxidoreductase, putative	1	1	1	1,2	**0,00046**	0,0	0,87150	1,1	**0,00003**	0,7	**0,00620**	0,5	**0,00100**	0,2	0,37420
EF1109	*lutB*	Energy metabolism	Electron transport	iron-sulfur cluster binding protein	1	1	1	1,2	**0,00006**	0,1	0,36540	0,9	**0,00173**	0,7	0,01285	0,6	**0,00148**	0,3	0,13470
EF1110	*lutC*	Unknown function	General	YkgG family protein	1	1	1	1,1	**0,00006**	0,9	**0,00002**	0,8	**0,00035**	1,2	**0,00009**	0,6	**0,00155**	1,0	**0,00025**
EF1111		Protein fate	Protein and peptide secretion and trafficking	signal peptidase I	1	1	1	0,4	0,11940	1,0	0,02747	0,1	0,40270	0,3	0,30780	0,4	**0,00360**	0,6	0,01584
EF1112	*rexB*	DNA metabolism	DNA replication, recombination, and repair	exonuclease RexB	1	1	1	0,1	0,57270	-0,5	**0,00071**	0,4	0,03926	-0,2	0,36700	0,0	0,87720	-0,2	0,32630
EF1113	*rexA*	DNA metabolism	DNA replication, recombination, and repair	exonuclease RexA	1	1	1	-0,1	0,77340	0,2	0,65710	0,4	0,17950	-0,2	0,58830	-0,3	0,06466	0,3	0,19690
EF1114		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00023**	1,6	**0,00000**	-0,1	0,51660	0,0	0,97690	0,4	**0,00476**	0,4	0,01741
EF1115	*pheS*	Protein synthesis	tRNA aminoacylation	phenylalanyl-tRNA synthetase, alpha subunit	1	1	1	0,4	0,06518	-1,0	**0,00000**	-0,4	0,03555	-0,5	0,01599	-0,1	0,34510	-0,6	**0,00144**
EF1116	*pheT*	Protein synthesis	tRNA aminoacylation	phenylalanyl-tRNA synthetase, beta subunit	1	1	1	0,2	0,33630	-1,2	**0,00039**	-0,6	**0,00709**	-0,5	0,02953	-0,2	0,17030	-0,5	**0,00507**
EF1117		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, permease protein	1	1	1	0,4	0,28100	1,8	**0,00000**	1,7	**0,00165**	2,7	**0,00000**	NA	NA	1,8	**0,00001**
EF1118		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, permease protein	1	1	1	0,9	**0,00545**	2,6	**0,00001**	2,8	**0,00000**	2,5	**0,00061**	0,2	0,59460	2,1	**0,00001**
EF1119		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, amino acid-binding protein	1	1	1	1,0	**0,00036**	2,3	**0,00000**	2,9	**0,00001**	2,4	**0,00000**	NA	NA	2,1	**0,00000**
EF1120		Transport and binding proteins	Amino acids, peptides and amines	amino acid ABC transporter, ATP-binding protein	1	1	1	1,1	0,01424	2,6	**0,00000**	3,5	**0,00000**	2,2	**0,00000**	0,6	0,05028	1,9	**0,00001**
EF1121	*murI*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	glutamate racemase	1	1	1	0,2	0,32610	NA	NA	0,1	0,55340	0,2	0,40440	0,4	0,08070	0,3	0,14560
EF1122	*rph*	Transcription	RNA processing	ribonuclease PH/Ham1 protein	1	1	1	0,4	0,08459	0,3	0,18800	0,3	0,04878	0,3	0,31570	0,2	0,27830	0,2	0,58620
EF1123		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,49480	0,4	0,40250	0,3	0,06784	0,1	0,62180	0,2	0,19620	0,2	0,39730
EF1124		Regulatory functions	DNA interactions	transcriptional regulator, DeoR family	1	1	1	NA	NA	NA	NA	-0,1	0,80560	NA	NA	NA	NA	0,4	0,19700
EF1125		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1126		Signal transduction	PTS	PTS system, IIA component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1127	*sgaT*	Transport and binding proteins	Unknown substrate	putative transport protein SgaT protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1128	*sgaB*	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	phosphotransferase enzyme II, B compnent SgaB	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1129		Energy metabolism	Sugars	hexulose-6-phosphate synthase, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1130		Energy metabolism	Sugars	hexulose-6-phosphate isomerase SgbU, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1131	*araD*	Energy metabolism	Sugars	L-ribulose-5-phosphate 4-epimerase	1	1	1	0,1	0,50780	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1132		Unknown function	General	CBS domain protein	1	1	1	0,2	0,48950	-0,1	0,49500	-0,7	**0,00254**	0,3	0,16740	-0,1	0,40890	-0,2	0,29230
EF1133	*dapD*	Amino acid biosynthesis	Aspartate family	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	1	1	1	-0,1	0,74410	1,4	**0,00000**	-0,6	**0,00775**	0,4	0,21450	0,0	0,78720	1,6	**0,00001**
EF1134		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	0,1	0,75820	2,2	**0,00000**	-0,6	0,02973	0,9	0,02385	0,0	0,85260	2,2	**0,00001**
EF1135		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,04081	-0,1	0,74390	-0,5	0,09186	-0,2	0,39620	0,0	0,79040	-0,3	0,09897
EF1136		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1137		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,57560	-0,4	0,07432	0,3	0,13340	0,1	0,77880	0,2	0,09920	0,8	**0,00380**
EF1138		Unknown function	Enzymes of unknown specificity	oxidoreductase, aldo/keto reductase family	1	1	1	0,6	0,03289	1,7	**0,00002**	0,8	**0,00149**	2,0	**0,00000**	0,8	**0,00002**	1,6	**0,00000**
EF1139		Unknown function	Enzymes of unknown specificity	glutamine amidotransferase, class I	1	1	1	0,2	0,32610	1,2	**0,00000**	0,3	0,04270	1,1	**0,00036**	0,4	**0,00694**	1,4	**0,00001**
EF1140	*gloA*	Energy metabolism	Other	lactoylglutathione lyase	1	1	1	0,4	0,08503	4,7	**0,00000**	-0,4	0,03164	2,4	**0,00000**	0,1	0,74260	3,1	**0,00000**
EF1141		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	0,1	0,68960	1,2	**0,00001**	0,3	0,18590	0,1	0,68230	0,3	0,01681	1,1	**0,00069**
EF1142		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,1	0,43040	0,3	0,07164	0,2	0,62440	0,4	0,48900	0,2	0,14050	0,0	0,88370
EF1143		Unknown function	General	HD domain protein	1	1	1	0,5	0,01974	0,4	0,01882	0,6	0,11380	0,2	0,48160	0,6	**0,00104**	0,9	**0,00193**
EF1144		Protein fate	Protein modification and repair	lipoate-protein ligase A family protein, putative	1	1	1	0,7	**0,00216**	1,0	**0,00000**	0,6	0,04041	0,2	0,48110	0,5	**0,00216**	0,6	**0,00280**
EF1145		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,03649	0,1	0,27900	-1,1	**0,00146**	0,1	0,73400	-0,4	0,01410	-0,3	0,29480
EF1146		Transcription	DNA-dependent RNA polymerase	DNA-directed RNA polymerase, delta subunit, putative	1	1	1	-0,9	**0,00156**	-1,0	**0,00000**	-0,9	**0,00295**	-0,3	0,27510	-0,7	**0,00058**	-1,7	**0,00099**
EF1147	*pyrG*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	CTP synthase	1	1	1	-0,6	**0,00576**	-4,0	**0,00000**	-1,9	**0,00000**	-2,2	**0,00002**	-1,2	**0,00000**	-3,6	**0,00000**
EF1148		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein 1A	1	1	1	-0,3	0,08470	-0,4	**0,00167**	-0,5	0,01516	-0,3	0,23100	-0,7	**0,00017**	-0,9	**0,00110**
EF1149	*recU*	DNA metabolism	DNA replication, recombination, and repair	recombination protein U	1	1	1	-0,1	0,73000	-0,2	0,02862	-0,2	0,35030	-0,1	0,66370	-0,3	0,02207	-0,7	**0,00425**
EF1150		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,16370	0,7	**0,00075**	0,3	0,24460	0,7	**0,00693**	0,2	0,20650	0,8	**0,00034**
EF1151		Cellular processes	Cell division	cell division protein DivIVA, putative	1	1	1	0,2	0,60560	-0,2	0,35030	-0,1	0,49920	-0,2	0,33590	0,4	0,01530	-0,2	0,28580
EF1152		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,68630	NA	NA	-0,5	0,07238	-0,2	0,47780	NA	NA	NA	NA
EF1153		Protein fate	Degradation of proteins, peptides, and glycopeptides	thermostable carboxypeptidase 1	1	1	1	-0,6	0,05000	0,2	0,58290	-0,7	**0,00062**	-0,4	0,16760	-0,6	0,02691	-0,1	0,72050
EF1154		DNA metabolism	DNA replication, recombination, and repair	DNA replication protein DnaD, putative	1	1	1	-0,8	**0,00685**	0,4	0,14110	-1,0	**0,00011**	-0,4	0,05871	-0,8	**0,00005**	-0,1	0,67140
EF1155	*nth*	DNA metabolism	DNA replication, recombination, and repair	endonuclease III	1	1	1	-0,5	0,04994	0,9	**0,00007**	-0,8	**0,00305**	-0,1	0,79030	-0,4	0,06609	0,5	0,01823
EF1156		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	NA	NA	NA	NA	0,7	**0,00414**	0,0	0,89460	0,8	0,02282	0,6	0,03794
EF1157		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	NA	NA	NA	NA	0,6	0,03618	0,1	0,85330	0,8	**0,00005**	0,7	**0,00360**
EF1158		Energy metabolism	Biosynthesis and degradation of polysaccharides	N4-(beta-N-acetylglucosaminyl)-L-asparaginase, putative	1	1	1	NA	NA	NA	NA	0,0	0,95600	NA	NA	NA	NA	-0,1	0,75430
EF1159		Signal transduction	PTS	PTS system, cellobiose-specific IIB component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1160		Signal transduction	PTS	PTS system, cellobiose-specific IIC component	1	1	1	NA	NA	NA	NA	0,5	0,02136	NA	NA	-0,1	0,53380	-0,5	0,13150
EF1161		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1162		Unknown function	Enzymes of unknown specificity	helicase, putative	1	1	1	0,5	**0,00757**	1,6	**0,00000**	0,5	0,10030	1,1	**0,00201**	0,8	**0,00010**	1,4	**0,00073**
EF1163		Energy metabolism	Amino acids and amines	L-asparaginase, putative	1	1	1	0,2	0,15840	0,1	0,46750	-0,4	0,13330	0,2	0,40670	-0,1	0,32060	-0,1	0,83700
EF1164		Unknown function	General	HD domain protein	1	1	1	-0,1	0,82070	0,1	0,80520	-0,4	0,23450	0,4	0,15490	-0,4	**0,00402**	-0,3	0,25280
EF1165		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00381**	0,8	**0,00001**	0,6	**0,00147**	0,0	0,96650	0,5	**0,00131**	1,2	**0,00002**
EF1166		Unknown function	General	YitT family protein	1	1	1	-1,0	**0,00011**	-1,2	**0,00000**	-0,6	**0,00446**	-0,3	0,31560	-0,3	0,12990	-0,7	**0,00432**
EF1167	*fba*	Energy metabolism	Glycolysis/gluconeogenesis	fructose-bisphosphate aldolase class-II	1	1	1	0,6	0,02092	0,0	0,84460	-0,3	0,21290	0,0	0,89510	0,0	0,77990	-0,3	0,20140
EF1168		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,72330	-0,3	0,02047	0,0	0,90400	-0,1	0,81060	0,4	0,17260	0,5	0,04386
EF1169	*murAB*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	1	1	1	-0,8	**0,00070**	-1,1	**0,00002**	-0,8	0,01840	-0,7	0,01396	-0,6	**0,00304**	-1,4	**0,00001**
EF1170	*rho*	Transcription	Transcription factors	transcription termination factor Rho	1	1	1	-0,9	0,04445	-1,9	**0,00009**	-1,2	**0,00095**	-0,8	0,03151	-0,7	**0,00085**	-1,0	0,01016
EF1171	*rpmE*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L31	1	1	1	-0,6	0,03903	-1,2	**0,00111**	-0,2	0,52850	0,0	0,94440	-0,1	0,76760	-0,8	**0,00491**
EF1172		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	teichoic acid biosynthesis protein B, putative	1	0	0	-0,5	0,07168	-0,6	**0,00598**	NA	NA	NA	NA	NA	NA	NA	NA
EF1173		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, WecB/TagA/CpsF family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1174		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1175	*gct*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	glycerol-3-phosphate cytidylyltransferase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1176		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1177		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1179	*cscK*	Energy metabolism	Sugars	fructokinase	1	1	1	-0,4	0,09151	-0,8	0,01297	-0,6	0,03161	-0,6	0,03205	-0,1	0,59220	0,1	0,72040
EF1180		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,5	**0,00001**	4,9	**0,00000**	0,6	**0,00727**	1,6	**0,00001**	1,2	**0,00000**	3,4	**0,00000**
EF1181		Unknown function	Enzymes of unknown specificity	nitroreductase family protein	1	1	1	0,1	0,52420	0,3	0,10800	0,0	0,97350	0,7	**0,00471**	0,0	0,93710	0,5	0,03645
EF1182	*luxS*	Cellular processes	Other	autoinducer-2 production protein LuxS	1	1	1	0,1	0,76150	0,2	0,21960	0,0	0,97550	0,3	0,07785	-0,2	0,08456	0,0	0,90320
EF1183	*asd*	Amino acid biosynthesis	Aspartate family	aspartate-semialdehyde dehydrogenase	1	1	1	-0,4	0,18270	0,1	0,69600	-0,1	0,59890	-0,1	0,53460	-0,2	0,16340	0,3	0,33330
EF1184	*dapA*	Amino acid biosynthesis	Aspartate family	dihydrodipicolinate synthase	1	1	1	-0,3	0,32290	0,3	0,03543	-0,2	0,29730	0,1	0,82370	-0,5	**0,00138**	0,3	0,17010
EF1185		Unknown function	Enzymes of unknown specificity	metallo-beta-lactamase superfamily protein	1	1	1	0,1	0,67870	0,3	0,17250	0,1	0,80030	0,2	0,46280	-0,2	0,18230	-0,2	0,66760
EF1186		Unknown function	Enzymes of unknown specificity	Ser/Thr protein phosphatase family protein	1	1	1	0,7	**0,00626**	0,1	0,63140	0,4	0,01943	0,1	0,78720	0,4	0,01608	0,0	0,95470
EF1187		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,06628	0,0	0,89670	0,0	0,89720	0,0	0,99960	0,0	0,85820	-0,3	0,19200
EF1188		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase family	1	1	1	0,1	0,86920	-0,4	0,39250	-0,2	0,32110	0,1	0,84160	-0,1	0,45930	-0,4	0,14800
EF1189		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,96320	-0,1	0,64730	-0,3	0,21970	-0,1	0,72900	-0,3	0,13050	-0,1	0,74370
EF1190		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,2	**0,00030**	1,2	**0,00000**	2,2	**0,00000**	1,6	**0,00003**	2,3	**0,00000**	1,4	**0,00012**
EF1191		Unknown function	General	DegV family protein	1	1	1	1,2	**0,00007**	1,2	**0,00000**	1,9	**0,00000**	1,2	**0,00359**	1,9	**0,00000**	0,7	**0,00405**
EF1192		Transport and binding proteins	Porins	aquaporin Z	1	1	1	-0,7	**0,00235**	0,3	0,06327	-1,1	**0,00035**	-1,8	**0,00016**	-0,4	0,03545	-0,3	0,10390
EF1193	*vicR*	Regulatory functions	DNA interactions	DNA-binding response regulator VicR	1	1	1	-0,2	0,39320	0,1	0,38360	-0,3	0,08370	-0,1	0,56960	0,0	0,78390	-0,1	0,56610
EF1194	*vicK*	Signal transduction	Two-component systems	sensory box histidine kinase VicK	1	1	1	-0,6	0,05852	-0,4	**0,00106**	-0,1	0,73650	-0,1	0,83350	-0,1	0,40800	0,1	0,67290
EF1195		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,13860	0,1	0,38200	-0,1	0,72500	-0,1	0,74630	-0,3	0,06446	0,2	0,39310
EF1196		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00177**	0,3	0,11090	-0,5	**0,00478**	0,0	0,87250	-0,4	0,02818	0,2	0,15080
EF1197		Unknown function	Enzymes of unknown specificity	metallo-beta-lactamase YycJ	1	1	1	-0,6	0,26660	-0,2	0,11720	-0,7	**0,00342**	-0,1	0,79180	-0,4	0,07594	-0,2	0,18730
EF1198		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,08392	0,4	**0,00973**	0,5	0,01258	0,7	**0,00665**	0,5	**0,00208**	0,0	0,83860
EF1199		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,45920	0,1	0,47530	0,4	0,07801	0,6	0,02773	0,3	0,03828	-0,1	0,64070
EF1200		Cell envelope	Other	membrane protein, putative	1	1	1	0,5	0,03334	0,6	**0,00066**	0,5	**0,00420**	0,6	**0,00818**	0,3	0,01131	1,0	**0,00005**
EF1201		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,02429	0,6	**0,00183**	0,5	**0,00232**	0,3	0,25470	0,7	**0,00005**	0,9	**0,00015**
EF1202		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00467**	2,4	**0,00002**	0,9	**0,00279**	0,3	0,26930	0,8	**0,00005**	1,6	**0,00001**
EF1203		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00250	1	1	1	0,7	**0,00184**	2,6	**0,00000**	0,8	**0,00793**	0,3	0,22070	0,7	**0,00044**	1,3	**0,00003**
EF1204		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,31840	1,4	**0,00054**	0,5	0,01626	0,1	0,74680	0,5	**0,00443**	1,0	0,03275
EF1206		Energy metabolism	Other	malate dehydrogenase, decarboxylating	1	1	1	1,4	**0,00028**	NA	NA	0,7	**0,00246**	NA	NA	1,5	**0,00005**	-1,4	**0,00003**
EF1207		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	citrate carrier protein, CCS family	1	1	1	1,0	**0,00699**	-1,1	**0,00602**	0,4	0,08135	-1,5	0,03754	1,1	**0,00063**	-2,3	**0,00000**
EF1209		Signal transduction	Two-component systems	sensory box histidine kinase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,93680
EF1210		Signal transduction	Two-component systems	response regulator	1	1	1	NA	NA	NA	NA	0,0	0,87410	NA	NA	0,2	0,23480	-0,2	0,47730
EF1211	*npr*	Energy metabolism	Electron transport	NADH peroxidase	1	1	1	0,7	**0,00767**	3,0	**0,00000**	0,8	**0,00143**	2,2	**0,00003**	0,9	**0,00008**	3,7	**0,00000**
EF1212		Regulatory functions	Other	transcriptional regulator	1	1	1	-0,3	0,16770	0,1	0,38670	-0,6	0,02324	-0,3	0,08208	-0,2	0,20850	-0,3	0,06636
EF1213	*alsS*	Amino acid biosynthesis	Pyruvate family	acetolactate synthase, catabolic	1	1	1	0,5	0,06600	1,2	**0,00001**	0,6	**0,00506**	1,6	**0,00002**	-0,3	0,04278	1,7	**0,00000**
EF1214	*budA*	Energy metabolism	Fermentation	alpha-acetolactate decarboxylase	1	1	1	-0,2	0,21540	1,4	**0,00000**	-0,3	0,16450	1,8	**0,00004**	-0,5	**0,00041**	1,4	**0,00011**
EF1215		Hypothetical proteins		hypothetical protein	1	1	1	0,4	0,03103	2,1	**0,00000**	0,3	0,07565	1,1	**0,00379**	0,5	**0,00378**	2,1	**0,00001**
EF1216		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1217		Cell envelope	Other	lipoprotein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1218		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, permease protein	1	1	1	1,7	**0,00020**	0,4	**0,00431**	1,2	**0,00075**	0,5	0,07345	2,5	**0,00000**	0,6	0,01766
EF1219		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, permease protein	1	1	1	1,3	**0,00101**	0,1	0,58160	0,9	0,02934	0,0	0,91680	2,0	**0,00000**	0,3	0,08743
EF1220		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, ATP-binding protein	1	1	1	1,2	**0,00112**	NA	NA	0,6	0,11650	-0,5	0,28190	1,8	**0,00000**	0,3	0,25770
EF1221		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter/-binding protein	1	1	1	1,2	**0,00025**	NA	NA	0,2	0,53080	-0,2	0,71450	1,2	**0,00044**	0,1	0,70170
EF1222	*ade*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	adenine deaminase	1	1	1	NA	NA	NA	NA	0,2	0,75200	0,0	0,94760	NA	NA	0,0	0,85190
EF1223		Unknown function	Enzymes of unknown specificity	chlorohydrolase family protein	1	1	1	0,1	0,69650	NA	NA	-0,6	0,11800	-0,4	0,23280	-0,2	0,53660	-0,4	0,51670
EF1224		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	-0,1	0,61570	NA	NA	-0,2	0,40270	0,0	0,98390	0,1	0,48810	-0,1	0,76060
EF1225		Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	thiamin biosynthesis ApbE, putative	1	1	1	0,3	0,11030	-1,6	**0,00019**	0,0	0,81510	0,0	0,88710	0,6	**0,00103**	-0,1	0,81760
EF1226		Unknown function	Enzymes of unknown specificity	oxidoreductase, putative	1	1	1	0,2	0,41760	-2,5	**0,00000**	0,2	0,34070	0,2	0,39330	0,5	**0,00506**	-0,1	0,76880
EF1227		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,02310	-2,3	**0,00001**	0,4	0,02764	-0,1	0,77540	0,5	**0,00719**	0,0	0,97630
EF1228		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,43040	-1,5	**0,00000**	-0,4	0,14670	0,3	0,15680	-0,1	0,46670	-0,7	**0,00160**
EF1229		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,68380	-1,4	**0,00000**	-0,3	0,09003	0,0	0,87330	0,1	0,76070	-0,6	0,03746
EF1230		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,53590	-1,8	**0,00000**	-0,4	0,02160	0,4	0,30800	0,1	0,71420	-0,5	**0,00717**
EF1231		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,8	**0,00808**	NA	NA	-0,2	0,46690	NA	NA	-0,2	0,55910	-0,6	0,05507
EF1232		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	NA	NA	-0,8	0,03023	-0,4	0,11320	-1,3	0,03731	-0,1	0,60110	-1,3	**0,00056**
EF1233		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	NA	NA	-1,5	**0,00011**	0,2	0,36060	-1,1	0,01780	0,2	0,50250	-1,2	**0,00119**
EF1234		Transport and binding proteins	Unknown substrate	ABC transporter, substrate-binding protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,5	0,01405	NA	NA
EF1235		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	1,1	**0,00081**	NA	NA	0,9	**0,00108**	-0,5	0,07024
EF1236		Energy metabolism	Biosynthesis and degradation of polysaccharides	acetyl xylan esterase, putative	1	1	1	NA	NA	NA	NA	1,3	**0,00004**	NA	NA	0,7	0,01242	-0,8	**0,00071**
EF1237		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,7	0,09659	NA	NA	0,6	0,01998	-0,4	0,14300
EF1238		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 3	1	1	1	NA	NA	NA	NA	0,5	0,13880	NA	NA	0,7	0,03033	-0,3	0,19690
EF1239		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,3	0,30690	NA	NA	0,4	0,05896	NA	NA
EF1240		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	-0,1	0,79110	-0,6	0,02250	-0,1	0,73650	-0,1	0,70550	0,2	0,17480	-0,8	**0,00117**
EF1241		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,18240	0,2	0,06545	0,1	0,62490	0,5	0,01820	-0,1	0,75620	0,1	0,53460
EF1242		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,3	0,14030	0,3	0,16220	0,4	0,14490	0,0	0,96300	0,7	**0,00025**	1,2	**0,00041**
EF1243		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	-0,7	**0,00516**	0,4	0,04370	-0,8	**0,00295**	-0,4	0,12650	-0,1	0,66860	0,6	0,02238
EF1244		Unknown function	Enzymes of unknown specificity	oxidoreductase, Gfo/Idh/MocA family	1	1	1	-0,5	0,02502	0,4	0,14220	-1,0	**0,00070**	-0,3	0,39790	0,0	0,98630	0,7	0,01029
EF1246		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,09897	0,0	0,84890	-0,2	0,36890	0,2	0,57160	-0,1	0,71420	0,3	0,20760
EF1247		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00319**	1,0	**0,00000**	-0,1	0,70380	0,9	**0,00395**	0,8	**0,00027**	1,1	**0,00059**
EF1248		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,15300	1,5	**0,00000**	-0,5	**0,00549**	1,4	**0,00094**	0,1	0,43130	1,3	**0,00000**
EF1249		Transport and binding proteins	Other	fibronectin/fibrinogen-binding protein, putative	1	1	1	0,3	0,04018	0,4	0,01476	0,2	0,18510	0,2	0,45800	-0,1	0,72840	0,1	0,46940
EF1250		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,84000	0,4	**0,00288**	-0,5	0,04111	0,1	0,80930	0,1	0,56020	0,2	0,27310
EF1251		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00354**	1,5	**0,00000**	0,2	0,39740	0,2	0,30160	0,7	**0,00012**	1,1	**0,00001**
EF1253		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,2	**0,00348**	NA	NA	-0,6	**0,00962**	-0,2	0,45690	0,9	0,02480	0,0	0,99110
EF1254		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	1,0	**0,00089**	-0,8	0,02080	-1,0	**0,00067**	-0,6	0,03852	0,9	0,04734	-0,2	0,38210
EF1255		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,6	0,04557	-0,2	0,21230	-0,8	**0,00119**	-0,4	0,16230	0,4	0,31660	0,0	0,97010
EF1258		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	**0,00657**	0,3	0,04029	-1,5	**0,00000**	-1,4	**0,00009**	-0,8	**0,00027**	-0,9	**0,00051**
EF1259		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-0,1	0,55950	-0,8	**0,00004**	-0,8	**0,00012**	-0,3	0,08846	-0,1	0,61400	-0,7	**0,00102**
EF1260		Regulatory functions	DNA interactions	DNA-binding response regulator	1	1	1	0,3	0,09864	0,2	0,25200	0,2	0,28370	-0,1	0,49050	0,3	0,16100	0,4	0,02451
EF1261		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	0,0	0,95830	0,4	0,01507	0,1	0,64120	-0,3	0,48860	-0,2	0,28150	0,6	0,11060
EF1262		Hypothetical proteins		hypothetical protein	1	1	1	1,1	**0,00137**	0,6	**0,00011**	NA	NA	2,0	**0,00033**	0,7	**0,00491**	1,1	**0,00077**
EF1263		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00447**	0,0	0,92490	0,8	0,02815	2,5	**0,00025**	0,5	0,01429	1,4	**0,00001**
EF1264		Unknown function	General	sulfatase domain protein	1	1	1	-0,5	**0,00442**	0,2	0,16780	0,0	0,88950	0,8	**0,00293**	-0,5	0,04376	-0,5	0,02336
EF1265		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00304**	-1,2	**0,00000**	-1,0	**0,00037**	-0,6	0,02523	-0,7	**0,00201**	-1,2	**0,00006**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1266		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	0,0	0,97590	NA	NA	NA	NA
EF1267	*rnhC*	Transcription	Degradation of RNA	ribonuclease HIII	1	1	1	-0,3	0,04975	0,3	**0,00510**	-0,2	0,17970	0,1	0,75140	0,1	0,44470	-0,2	0,34110
EF1268		Transport and binding proteins	Cations and iron carrying compounds	cation-transporting ATPase, E1-E2 family	1	1	1	0,4	0,25310	1,2	**0,00005**	0,4	0,01713	-0,1	0,65550	0,5	**0,00265**	0,6	**0,00807**
EF1269		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1270		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,0	**0,00395**	-2,2	**0,00000**	-1,2	**0,00008**	-1,1	**0,00010**	-1,5	**0,00002**	-1,6	**0,00000**
EF1271	*nusA*	Transcription	Transcription factors	N utilization substance protein A	1	1	1	-1,4	**0,00005**	-2,0	**0,00000**	-1,3	**0,00004**	-0,8	**0,00056**	-1,7	**0,00001**	-1,5	**0,00335**
EF1272		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,3	**0,00028**	-1,7	**0,00000**	-1,3	**0,00020**	-0,9	**0,00022**	-1,6	**0,00000**	-1,5	**0,00059**
EF1273		Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L7A family	1	1	1	-1,5	**0,00016**	-2,2	**0,00000**	-1,2	**0,00002**	-0,8	**0,00045**	-1,4	**0,00000**	-1,6	**0,00058**
EF1274	*infB*	Protein synthesis	Translation factors	translation initiation factor IF-2	1	1	1	-1,6	**0,00001**	-2,1	**0,00001**	-1,3	**0,00021**	-0,6	0,14420	-1,0	**0,00031**	-1,3	**0,00161**
EF1275	*rbfA*	Transcription	RNA processing	ribosome-binding factor A	1	1	1	-1,7	**0,00000**	-1,7	**0,00000**	-1,3	**0,00005**	-0,5	0,15770	-0,8	**0,00006**	-1,1	**0,00012**
EF1276		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,90320	0,2	0,06877	0,3	0,19590	-0,1	0,63680	0,2	0,35440	0,7	**0,00561**
EF1277		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	0,0	0,86630	0,1	0,38510	0,3	0,06189	0,0	0,88870	0,1	0,72170	0,5	0,02324
EF1278		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,56680	-0,2	0,48350	NA	NA	NA	NA
EF1279		Mobile and extrachromosomal element functions	Prophage functions	DNA replication protein, putative	1	1	1	NA	NA	0,0	0,75930	0,2	0,42230	0,1	0,66170	NA	NA	-0,2	0,36240
EF1280		Mobile and extrachromosomal element functions	Prophage functions	DNA replication protein, putative	1	1	1	0,0	0,91450	0,2	0,39250	0,4	0,03848	-0,3	0,13910	-0,1	0,26180	0,2	0,41250
EF1281		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,94670	0,2	0,13480	0,2	0,52210	-0,3	0,17250	NA	NA	NA	NA
EF1282		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,84130	0,0	0,91180	0,1	0,50670	-0,2	0,15510	0,0	0,94210	0,1	0,48180
EF1283		Regulatory functions	DNA interactions	transcriptional regulator, RinA family	1	1	1	0,1	0,76010	0,3	0,07716	-0,2	0,14770	-0,3	0,18030	NA	NA	NA	NA
EF1284		Mobile and extrachromosomal element functions	Prophage functions	structural protein, putative	1	1	1	0,1	0,84000	0,6	**0,00048**	0,1	0,59720	0,0	0,98260	NA	NA	0,3	0,38190
EF1285		Mobile and extrachromosomal element functions	Prophage functions	major tail protein	1	1	1	NA	NA	NA	NA	0,0	0,97060	-0,3	0,31760	NA	NA	0,1	0,66680
EF1286		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,0	0,88980	-0,5	0,11090	NA	NA	NA	NA
EF1287		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,0	0,98630	-0,6	0,08397	NA	NA	NA	NA
EF1288		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,76630	-0,5	0,05859	NA	NA	NA	NA
EF1289		Mobile and extrachromosomal element functions	Prophage functions	tail protein, putative	1	1	1	NA	NA	NA	NA	-0,1	0,63850	-0,9	0,01167	NA	NA	NA	NA
EF1290		Mobile and extrachromosomal element functions	Prophage functions	structural protein, putative	1	1	1	NA	NA	NA	NA	-0,2	0,27250	-0,9	0,01139	NA	NA	NA	NA
EF1291		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,0	0,99860	-0,7	0,01427	NA	NA	NA	NA
EF1292		Mobile and extrachromosomal element functions	Prophage functions	holin, putative	1	1	1	NA	NA	NA	NA	0,0	0,92290	-0,8	0,05567	NA	NA	NA	NA
EF1293	*ply-1*	Mobile and extrachromosomal element functions	Prophage functions	endolysin	1	1	1	NA	NA	NA	NA	-0,1	0,48450	-0,6	0,03039	NA	NA	NA	NA
EF1295	*ribF*	Biosynthesis of cofactors, prosthetic groups, carriers	Riboflavin, FMN, and FAD	riboflavin biosynthesis protein RibF	1	1	1	-0,6	**0,00581**	-1,0	**0,00003**	-1,0	**0,00004**	-0,2	0,35090	-0,5	**0,00419**	-0,4	0,15590
EF1296		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,4	0,11140	-0,8	**0,00043**	-0,8	**0,00051**	0,1	0,67180	-0,6	**0,00063**	-0,4	0,22100
EF1297		Regulatory functions	DNA interactions	transcriptional regulator, PadR family	1	1	1	0,3	0,19680	0,0	0,97300	-0,9	**0,00143**	-0,3	0,26330	0,3	0,01782	0,2	0,39480
EF1298		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,88320	-0,1	0,69590	-1,0	**0,00104**	-0,1	0,76530	0,1	0,35040	0,4	0,05305
EF1299		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,93740	-0,1	0,51930	-1,1	**0,00007**	-0,3	0,26650	0,4	0,02629	0,2	0,22570
EF1300		Cellular processes	Cell division	cell division protein, FtsW/RodA/SpoVE family	1	1	1	-0,5	0,01005	-1,5	**0,00002**	-0,7	**0,00767**	NA	NA	NA	NA	NA	NA
EF1301		Cellular processes	Cell division	cell division protein, FtsW/RodA/SpoVE family	1	1	1	-0,2	0,25060	-0,3	0,07534	-1,2	**0,00712**	-0,7	**0,00236**	0,3	0,25370	0,3	0,07519
EF1302		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	-0,4	0,04990	0,1	0,33210	0,5	0,02725	0,0	0,92710	0,1	0,49380	0,7	**0,00535**
EF1303		Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	-0,4	0,15520	0,0	0,95010	0,4	0,20790	-0,1	0,61680	0,3	0,06793	0,3	0,15080
EF1304		Transport and binding proteins	Cations and iron carrying compounds	magnesium-translocating P-type ATPase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1305		Biosynthesis of cofactors, prosthetic groups, carriers	Heme, porphyrin, and cobalamin	oxygen-independent coproporphyrinogen III oxidase, putative	1	1	1	-0,7	0,01301	NA	NA	-0,4	0,04016	0,2	0,54260	-0,3	0,21490	NA	NA
EF1306	*hrcA*	Regulatory functions	DNA interactions	heat-inducible transcription repressor HrcA	1	1	1	1,0	**0,00061**	-0,8	**0,00018**	0,7	**0,00180**	-1,1	**0,00012**	0,8	**0,00014**	0,2	0,34390
EF1307	*grpE*	Protein fate	Protein folding and stabilization	heat shock protein GrpE	1	1	1	1,0	**0,00079**	-0,2	0,23870	0,5	0,02543	-1,2	**0,00002**	0,5	**0,00158**	-0,2	0,40940
EF1308	*dnaK*	Protein fate	Protein folding and stabilization	dnak protein	1	1	1	0,8	**0,00037**	0,1	0,46120	0,5	0,01349	-1,1	**0,00005**	0,3	0,02378	-0,6	**0,00289**
EF1309		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,89300	-1,4	**0,00012**	0,0	0,93760	-1,3	**0,00001**	-0,1	0,34720	-0,9	0,01272
EF1310	*dnaJ*	Protein fate	Protein folding and stabilization	dnaJ protein	1	1	1	0,1	0,44140	-1,3	**0,00002**	-0,1	0,65540	-1,1	**0,00007**	0,0	0,80350	-0,9	**0,00212**
EF1311		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	**0,00015**	3,3	**0,00000**	1,1	**0,00171**	0,8	0,03957	1,0	**0,00002**	2,3	**0,00000**
EF1312		Unknown function	General	S1 RNA binding domain protein	1	1	1	0,5	0,02370	1,1	**0,00001**	0,2	0,23130	0,3	0,18940	0,1	0,45430	0,7	**0,00600**
EF1313		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,47430	1,0	**0,00004**	0,0	0,99160	0,6	0,01105	0,1	0,59220	0,9	**0,00168**
EF1314		Amino acid biosynthesis	Aspartate family	aspartate aminotransferase, putative	1	1	1	0,0	0,86920	-0,1	0,40680	0,8	**0,00049**	0,6	0,04021	0,6	**0,00069**	0,6	**0,00386**
EF1315		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,31350	0,5	0,01009	-0,6	**0,00289**	-0,5	0,01142	-0,9	**0,00012**	-0,5	0,01208
EF1316		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	-0,9	**0,00101**	-1,3	**0,00000**	-0,7	**0,00293**	-0,5	0,02164	-1,5	**0,00002**	-1,0	**0,00014**
EF1317	*nagA-1*	Central intermediary metabolism	Amino sugars	N-acetylglucosamine-6-phosphate deacetylase	1	1	1	1,1	**0,00045**	0,2	0,71180	0,9	**0,00012**	0,9	**0,00556**	1,0	**0,00002**	1,0	**0,00053**
EF1318		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,91090	-1,3	**0,00000**	-0,3	0,33240	0,7	0,01129	-0,7	**0,00283**	-1,1	**0,00018**
EF1319		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-1,1	**0,00146**	-1,2	**0,00001**	-1,2	**0,00016**	0,0	0,99520	-1,4	**0,00000**	-0,7	**0,00101**
EF1320		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,8	0,06592	0,7	0,02184	0,5	0,01345	0,4	0,06523	0,5	0,05854	0,8	**0,00768**
EF1321		Transport and binding proteins	Unknown substrate	permease domain protein	1	1	1	0,8	**0,00475**	1,2	**0,00000**	0,7	**0,00817**	0,6	0,11060	0,6	**0,00019**	1,4	**0,00001**
EF1322		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,7	**0,00090**	0,6	0,01053	2,6	**0,00000**	-1,2	**0,00036**	0,8	**0,00056**	-0,6	0,03721
EF1324		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,57340	NA	NA	NA	NA	NA	NA
EF1325		Hypothetical proteins		hypothetical protein	1	1	1	0,4	0,04909	2,3	**0,00000**	-0,4	0,05033	-0,2	0,50960	0,6	**0,00176**	2,0	**0,00000**
EF1326		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	-0,6	**0,00665**	-0,4	0,02688	-0,4	0,02912	0,1	0,70050	-0,6	**0,00173**	0,1	0,70120
EF1327		Unknown function	General	BadF/BadG/BcrA/BcrD ATPase family protein	1	1	1	0,6	**0,00514**	0,8	**0,00406**	0,7	**0,00080**	1,0	**0,00048**	0,6	**0,00124**	0,6	**0,00190**
EF1328		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,3	0,06570	-0,3	0,04698	0,2	0,38600	0,1	0,51960	0,4	0,01894	0,5	0,01811
EF1329		Unknown function	General	HesA/MoeB/ThiF family protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1330		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1331		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1332		Cell envelope	Other	membrane protein, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1333		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1334		Unknown function	General	AgrC domain protein	1	0	1	-0,1	0,81230	NA	NA	0,1	0,54090	0,4	0,13750	0,1	0,55880	0,1	0,55900
EF1335		Signal transduction	Two-component systems	sensor histidine kinase, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1336		Signal transduction	Two-component systems	response regulator	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,4	**0,00605**	0,6	**0,00720**
EF1337		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	0,1	0,79050	NA	NA	-0,1	0,52900	NA	NA	0,5	0,02685	0,1	0,67030
EF1338	*trxB*	Energy metabolism	Electron transport	thioredoxin reductase	1	1	1	-0,4	0,03954	1,2	**0,00000**	-0,4	0,01905	1,4	**0,00055**	0,2	0,23890	1,1	**0,00007**
EF1339		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,21120	1,0	**0,00000**	-0,2	0,24660	0,6	0,03452	0,2	0,06118	1,8	**0,00000**
EF1340		Cellular processes	Other	pheromone cAM373 precursor lipoprotein	1	1	1	-0,8	**0,00183**	-1,5	**0,00000**	-1,6	**0,00000**	-0,9	**0,00305**	-0,8	**0,00018**	-1,1	**0,00053**
EF1341		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	0,8	**0,00058**	1,3	**0,00000**	0,4	0,14550	0,0	0,92990	0,2	0,05291	1,4	**0,00001**
EF1342		Regulatory functions	DNA interactions	transcriptional regulator, Mar family	1	1	1	0,9	**0,00034**	0,8	**0,00004**	0,4	0,04688	0,1	0,75570	0,7	**0,00025**	0,5	0,03732
EF1343		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sugar ABC transporter, permease protein	1	1	1	0,7	**0,00615**	0,2	0,22910	1,0	**0,00304**	NA	NA	0,2	0,42080	-0,3	0,41280
EF1344		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sugar ABC transporter, permease protein	1	1	1	0,9	0,02078	-0,3	0,20240	1,1	**0,00025**	-1,0	**0,00867**	0,3	0,17160	-0,1	0,68100
EF1345		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sugar ABC transporter, sugar-binding protein	1	1	1	0,9	**0,00420**	-0,1	0,84080	1,0	**0,00005**	-0,8	0,09084	0,3	0,14520	-0,2	0,61910
EF1346		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1347		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 13	1	1	1	NA	NA	-0,8	0,06499	0,2	0,64370	NA	NA	0,1	0,78020	-0,4	0,16700
EF1348		Energy metabolism	Biosynthesis and degradation of polysaccharides	glucan 1,6-alpha-glucosidase, putative	1	1	1	0,5	0,14560	-0,5	0,01289	1,1	**0,00284**	-0,5	0,29590	0,2	0,36250	-0,9	**0,00339**
EF1349		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 13	1	1	1	1,2	0,01123	-0,9	**0,00014**	1,1	**0,00375**	-0,9	**0,00132**	0,9	**0,00842**	-1,1	**0,00028**
EF1350		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00398**	0,1	0,51480	1,0	**0,00012**	0,9	**0,00096**	0,9	**0,00008**	0,3	0,05576

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1351		Hypothetical proteins		hypothetical protein	1	1	1	0,2	0,37750	-0,7	**0,00097**	0,7	0,05227	-0,5	0,10690	1,1	**0,00053**	-0,1	0,80740
EF1352		Transport and binding proteins	Cations and iron carrying compounds	magnesium-translocating P-type ATPase	1	1	1	0,4	0,19390	-0,2	0,14570	1,3	**0,00416**	-0,7	**0,00554**	1,5	**0,00002**	-0,5	0,06681
EF1353	*pdhA*	Energy metabolism	Pyruvate dehydrogenase	pyruvate dehydrogenase complex E1 component, alpha subunit	1	1	1	0,2	0,11750	0,6	**0,00040**	0,4	0,03245	1,7	**0,00000**	0,4	**0,00244**	2,1	**0,00000**
EF1354	*pdhB*	Energy metabolism	Pyruvate dehydrogenase	pyruvate dehydrogenase complex, E1 component, beta subunit	1	1	1	0,2	0,23290	0,6	**0,00021**	0,4	0,03003	1,8	**0,00005**	0,4	**0,00540**	2,3	**0,00000**
EF1355	*aceF*	Energy metabolism	Pyruvate dehydrogenase	pyruvate dehydrogenase E2, dihydrolipoamide acetyltransferase	1	1	1	-0,3	0,29860	0,8	**0,00138**	-0,2	0,21280	1,7	**0,00001**	-0,1	0,43660	0,0	0,86810
EF1356	*lpdA*	Energy metabolism	Pyruvate dehydrogenase	pyruvate dehydrogenase E3, dihydrolipoamide dehydrogenase	1	1	1	-0,3	0,33480	-0,3	0,30340	0,0	0,96730	2,0	**0,00000**	-0,1	0,52100	-0,1	0,66670
EF1357		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	-0,3	0,17070	-1,5	**0,00000**	-0,3	0,08080	-0,5	0,04275	-0,2	0,28290	-0,5	0,01415
EF1358		Central intermediary metabolism	Other	glycerol dehydrogenase, putative	1	1	1	0,5	0,01126	0,0	0,95280	0,8	**0,00100**	0,0	0,89620	0,4	0,02216	-1,1	**0,00861**
EF1359		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,02929	1,0	**0,00010**	0,6	**0,00527**	0,5	0,09540	0,6	**0,00356**	-0,6	0,06102
EF1360		Unknown function	Enzymes of unknown specificity	dihydroxyacetone kinase family protein	1	1	1	0,5	0,02074	0,7	**0,00021**	0,6	**0,00109**	0,7	0,02013	0,6	**0,00431**	0,1	0,87500
EF1361		Unknown function	Enzymes of unknown specificity	dihydroxyacetone kinase family protein	1	1	1	0,7	**0,00163**	2,0	**0,00000**	0,9	**0,00007**	1,3	**0,00005**	0,9	**0,00004**	0,0	0,85900
EF1362		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,6	**0,00300**	1,4	**0,00001**	0,7	**0,00192**	0,3	0,31950	0,4	0,01002	0,6	**0,00619**
EF1363		Central intermediary metabolism	Other	hydroxymethylglutaryl-CoA synthase	1	1	1	-0,4	0,01932	0,6	**0,00008**	0,1	0,70910	0,9	**0,00084**	0,1	0,46800	0,1	0,54200
EF1364		Central intermediary metabolism	Other	acetyl-CoA acetyltransferase/hydroxymethylglutaryl-CoA reductase	1	1	1	-0,2	0,13660	-0,8	**0,00025**	-0,5	**0,00149**	-0,6	0,01399	-0,2	0,13120	-1,3	**0,00000**
EF1365		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,31810	0,0	0,80840	-0,5	0,01258	0,7	0,05897	-0,3	0,08317	0,2	0,21970
EF1366		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,75120	0,6	**0,00015**	0,0	0,97730	0,4	0,15150	-0,1	0,33370	0,2	0,39600
EF1367		Cellular processes	Adaptations to atypical conditions	cold-shock domain family protein	1	1	1	-0,2	0,25440	-0,3	0,02569	-1,4	**0,00001**	-1,6	**0,00037**	-0,3	0,01715	-1,3	**0,00014**
EF1368		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,2	**0,00002**	5,8	**0,00000**	1,2	**0,00027**	1,8	**0,00054**	0,9	**0,00002**	4,5	**0,00000**
EF1369		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	0,9	**0,00045**	0,6	**0,00013**	1,2	**0,00001**	0,2	0,35450	0,8	**0,00003**	0,6	**0,00409**
EF1370		Transport and binding proteins	Other	drug resistance transporter, EmrB/QacA family protein	1	1	1	0,1	0,60690	-0,5	**0,00422**	-0,4	0,12560	-0,4	0,13930	0,4	0,03137	0,0	0,90320
EF1371		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,01799	0,3	0,02141	0,6	**0,00524**	0,1	0,69340	0,5	**0,00743**	0,8	0,01769
EF1372		Unknown function	General	CBS domain protein	1	1	1	0,4	0,04575	0,0	0,97920	0,4	0,01111	-0,1	0,73520	0,2	0,07037	0,3	0,12270
EF1373		Unknown function	Enzymes of unknown specificity	DHH family protein	1	1	1	0,5	0,03137	0,8	**0,00171**	0,1	0,39400	0,2	0,29770	0,1	0,49830	0,6	**0,00574**
EF1374	*phnA*	Unknown function	General	phnA protein	1	1	1	0,0	0,86670	0,1	0,21300	-0,3	0,06989	-0,1	0,71480	-0,5	**0,00488**	-0,3	0,10820
EF1375		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00093**	2,1	**0,00000**	0,9	**0,00032**	1,5	**0,00003**	0,9	**0,00001**	1,7	**0,00000**
EF1376		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,24300	-0,1	0,57120	-0,5	**0,00439**	-0,6	**0,00905**	-0,3	**0,00878**	-0,3	0,15330
EF1377		Transcription	Other	ATP-dependent RNA helicase, DEAD/DEAH box family	1	1	1	-0,3	0,11490	-1,3	**0,00001**	-0,8	**0,00109**	-0,8	**0,00321**	-0,6	0,02385	-0,9	**0,00033**
EF1378		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	0,2	0,50490	NA	NA	0,0	0,99900	-0,4	0,21420	0,4	0,04188	0,3	0,24980
EF1379	*alaS*	Protein synthesis	tRNA aminoacylation	alanyl-tRNA synthetase	1	1	1	0,3	0,25730	-1,0	**0,00014**	0,0	0,92980	0,4	0,14500	0,1	0,73340	-0,6	0,02828
EF1380		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,46040	-1,0	**0,00004**	0,1	0,65730	0,0	0,92660	-0,3	0,14910	-0,7	0,04696
EF1381		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00486	1	1	1	-0,2	0,25310	-1,1	**0,00000**	-0,3	0,13080	0,0	0,94460	-0,3	0,01777	-0,6	**0,00393**
EF1382	*pepT-1*	Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase T	1	1	1	0,0	0,86630	-1,4	**0,00000**	-0,3	0,11850	0,0	0,90270	-0,1	0,75620	-0,6	0,01557
EF1383		Cell envelope	Other	membrane protein, putative	1	1	1	-1,0	0,01136	-0,9	**0,00026**	-1,0	**0,00008**	-0,8	**0,00130**	-0,1	0,71250	-0,2	0,57860
EF1384		Cell envelope	Other	membrane protein, putative	1	1	1	-1,1	**0,00008**	-1,3	**0,00007**	-1,5	**0,00002**	-0,9	0,04394	-0,4	0,08586	-0,4	0,23640
EF1385		Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdopterin-guanine dinucleotide biosynthesis protein A, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1386		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	formate/nitrite transporter family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1387		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1388		Energy metabolism	Electron transport	NAD-dependent formate dehydrogenase, gamma subunit, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1389		Energy metabolism	Electron transport	NAD-dependent formate dehydrogenase, beta subunit, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1390	*fdhA*	Energy metabolism	Electron transport	NAD-dependent formate dehydrogenase, alpha subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1391		Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdenum cofactor biosynthesis family protein	1	1	1	NA	NA	NA	NA	0,6	**0,00898**	NA	NA	NA	NA	NA	NA
EF1392	*moaC*	Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdenum cofactor biosynthesis protein MoaC	1	1	1	NA	NA	NA	NA	NA	NA	-0,5	0,04569	NA	NA	-0,5	0,08951
EF1393		Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdopterin cofactor biosynthesis protein A, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,4	**0,00829**	-1,3	**0,00025**
EF1394		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	-0,6	0,03002	0,0	0,86830	-0,5	0,27540	-0,2	0,11690	-1,3	**0,00055**
EF1395		Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdenum cofactor biosynthesis family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,1	**0,00084**
EF1396		Biosynthesis of cofactors, prosthetic groups, carriers	Molybdopterin	molybdenum cofactor biosynthesis family protein, putative	1	1	1	NA	NA	NA	NA	0,4	0,27710	NA	NA	0,7	0,03152	-0,8	0,02039
EF1397		Transport and binding proteins	Cations and iron carrying compounds	molybdenum ABC transporter, molybdenum-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,4	0,31730
EF1398		Transport and binding proteins	Cations and iron carrying compounds	molybdenum ABC transporter, permease protein	1	1	1	NA	NA	NA	NA	0,9	**0,00046**	NA	NA	0,7	**0,00336**	-1,0	**0,00387**
EF1399		Transport and binding proteins	Cations and iron carrying compounds	molybdenum ABC transporter, ATP-binding protein, putative	1	1	1	NA	NA	NA	NA	0,5	0,22460	NA	NA	0,8	**0,00449**	-1,0	0,01551
EF1400		Transport and binding proteins	Cations and iron carrying compounds	cadmium-translocating P-type ATPase	1	1	1	0,1	0,75240	-0,8	**0,00003**	0,5	0,02063	-0,2	0,54810	0,1	0,75620	-0,5	0,05919
EF1401		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1402		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,1	0,61010	-0,2	0,19420	0,1	0,73000	0,2	0,28920	0,3	0,11460	-0,2	0,39190
EF1403		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,74000	-0,3	0,01675	0,0	0,94650	0,2	0,62740	0,0	0,89210	-0,3	0,22410
EF1404		DNA metabolism	Other	MutS2 family protein	1	1	1	-0,3	0,21780	-0,2	0,21700	-0,3	0,11880	0,0	0,97360	-0,4	0,02589	0,0	0,98180
EF1405	*trx*	Energy metabolism	Electron transport	thioredoxin	1	1	1	0,3	0,16500	1,6	**0,00000**	-0,4	0,08652	0,6	0,01738	0,2	0,09665	1,3	**0,00001**
EF1406	*uvrC*	DNA metabolism	DNA replication, recombination, and repair	excinuclease ABC, subunit C	1	1	1	0,2	0,43010	0,7	**0,00057**	-0,4	0,11980	0,2	0,60430	0,4	0,02841	0,7	**0,00286**
EF1407		Hypothetical proteins		hypothetical protein	1	1	1	0,6	0,03324	0,0	0,85430	0,5	0,06267	NA	NA	-0,1	0,66240	0,1	0,71210
EF1408		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,2	0,38380	0,2	0,22200	0,4	0,23470	0,0	0,97750	0,0	0,77890	0,4	0,18660
EF1409		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,92980	0,4	**0,00177**	0,2	0,45060	-0,2	0,49250	0,1	0,68100	0,3	0,28440
EF1410		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	0,3	0,24880	0,1	0,68600	0,8	**0,00049**	0,2	0,54260	0,2	0,22830	0,5	0,03943
EF1411		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 4	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,52650
EF1412		Hypothetical proteins	Domain	conserved domain protein	1	1	1	1,8	**0,00000**	0,3	0,02850	3,7	**0,00000**	-0,3	0,22560	2,1	**0,00000**	0,0	0,88380
EF1413		Cellular processes	Toxin production and resistance	msrC protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1414		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,05484	-0,4	**0,00120**	-0,8	**0,00018**	-0,4	0,07045	-0,4	**0,00187**	-0,8	**0,00047**
EF1415	*gdhA*	Amino acid biosynthesis	Glutamate family	glutamate dehydrogenase	1	1	1	1,0	**0,00399**	2,5	**0,00001**	0,6	0,02703	1,1	**0,00274**	0,7	**0,00021**	0,8	0,03017
EF1416	*pgi*	Energy metabolism	Glycolysis/gluconeogenesis	glucose-6-phosphate isomerase	1	1	1	1,1	**0,00044**	1,5	**0,00000**	0,3	0,04424	0,5	0,01597	0,5	**0,00476**	0,4	0,13150
EF1417		Mobile and extrachromosomal element functions	Prophage functions	site-specific recombinase, phage integrase family	1	0	0	0,5	**0,00335**	0,8	**0,00002**	NA	NA	NA	NA	NA	NA	NA	NA
EF1418		Hypothetical proteins		hypothetical protein	1	0	0	0,7	**0,00066**	1,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1419		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,4	0,04994	0,8	**0,00005**	NA	NA	NA	NA	NA	NA	NA	NA
EF1420		Hypothetical proteins		hypothetical protein	0	0	0	0,6	0,01612	0,4	**0,00505**	NA	NA	NA	NA	NA	NA	NA	NA
EF1421		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,8	**0,00076**	0,9	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF1422		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	1,0	**0,00047**	1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1423		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	0,5	0,01290	0,8	**0,00005**	NA	NA	NA	NA	NA	NA	NA	NA
EF1424		Hypothetical proteins		hypothetical protein	1	0	0	0,6	**0,00321**	0,5	**0,00151**	NA	NA	NA	NA	NA	NA	NA	NA
EF1425		Hypothetical proteins		hypothetical protein	1	0	0	0,6	0,05378	0,5	**0,00033**	NA	NA	NA	NA	NA	NA	NA	NA
EF1426		Cellular processes	Pathogenesis	vrlI protein, putative	1	0	0	0,5	**0,00590**	0,3	0,07920	NA	NA	NA	NA	NA	NA	NA	NA
EF1427		Hypothetical proteins		hypothetical protein	1	0	0	0,5	0,08580	0,5	0,03558	NA	NA	NA	NA	NA	NA	NA	NA
EF1428		Hypothetical proteins		hypothetical protein	1	0	0	0,8	**0,00338**	0,5	**0,00388**	NA	NA	NA	NA	NA	NA	NA	NA
EF1429		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,02912	0,4	0,01944	NA	NA	NA	NA	NA	NA	NA	NA
EF1430		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,6	0,01002	0,6	**0,00014**	NA	NA	NA	NA	NA	NA	NA	NA
EF1431		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1432		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1433		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,0	0,87670	0,5	0,11920	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1434		Unknown function	General	DnaD domain protein	1	0	0	0,1	0,79080	0,0	0,75820	NA	NA	NA	NA	NA	NA	NA	NA
EF1435		Mobile and extrachromosomal element functions	Prophage functions	recombination protein U, putative	1	0	0	NA	NA	0,3	0,06642	NA	NA	NA	NA	NA	NA	NA	NA
EF1436		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,93950	0,3	0,19980	NA	NA	NA	NA	NA	NA	NA	NA
EF1437		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,66710	0,3	0,06999	NA	NA	NA	NA	NA	NA	NA	NA
EF1438		Hypothetical proteins		hypothetical protein	0	0	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,2	0,29270	0,1	0,81410
EF1439		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1440		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01671	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1441		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,91180	0,0	0,84080	NA	NA	NA	NA	NA	NA	NA	NA
EF1442		Unknown function	General	DNA topoisomerase domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1443		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,0	0,98470	0,1	0,15870	NA	NA	NA	NA	NA	NA	NA	NA
EF1444		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,91550	0,1	0,71590
EF1445		Unknown function	General	replicase domain protein	1	0	0	-0,1	0,36200	-0,2	0,27200	NA	NA	NA	NA	NA	NA	NA	NA
EF1446		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,08513	-0,2	0,08579	NA	NA	NA	NA	NA	NA	NA	NA
EF1447		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,1	0,84750	0,0	0,92120	NA	NA	NA	NA	NA	NA	NA	NA
EF1448		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,34380	-0,2	0,16270	NA	NA	NA	NA	NA	NA	NA	NA
EF1449		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,2	0,34550	0,2	0,20090	NA	NA	NA	NA	NA	NA	NA	NA
EF1450		Regulatory functions	DNA interactions	positive control factor, putative	1	0	0	NA	NA	0,1	0,46970	NA	NA	NA	NA	NA	NA	NA	NA
EF1451		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1452		DNA metabolism	Restriction/modification	adenine methyltransferase, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1453		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1454		Disrupted reading frame		terminase, small subunit, internal deletion	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1455		Mobile and extrachromosomal element functions	Prophage functions	terminase, large subunit, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1456		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01555	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1457		Mobile and extrachromosomal element functions	Prophage functions	minor head protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1458		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1459		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1460		Unknown function	General	LysM domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1461		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1462		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1463		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1464		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1465		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1466		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1467		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1468		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1469		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1470		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1471		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1472		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1473		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1474		Unknown function	General	LysM domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1475		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1476		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1477		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1478		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1479		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1480		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1481		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1482		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1483		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1484		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1485		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1486	*ply-2*	Mobile and extrachromosomal element functions	Prophage functions	endolysin	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1487		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1488		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1489		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1490		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,60760	1,4	**0,00000**	-0,2	0,16890	0,5	0,01612	0,0	0,85810	1,4	**0,00000**
EF1491		Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	nrdI family protein	1	1	1	0,9	**0,00056**	0,9	**0,00011**	0,8	**0,00389**	0,0	0,94760	0,6	**0,00228**	1,2	**0,00091**
EF1492		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit F	1	1	1	-0,1	0,47010	-0,2	0,07227	0,0	0,82720	-0,9	**0,00432**	-0,7	**0,00065**	-0,6	**0,00654**
EF1493		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit I	1	1	1	-0,4	0,05905	-0,1	0,70640	-0,2	0,21970	-1,0	**0,00062**	-1,0	**0,00002**	-0,9	**0,00039**
EF1494		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit K	1	1	1	-0,3	0,05394	-0,3	0,13630	-0,1	0,59090	-1,2	**0,00003**	-0,6	**0,00068**	-0,9	**0,00054**
EF1495		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit E	1	1	1	-0,5	0,02307	-0,5	**0,00018**	-0,4	0,02857	-1,3	**0,00001**	-1,0	**0,00000**	-1,3	**0,00001**
EF1496		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit C	1	1	1	-0,1	0,76010	-0,3	0,05555	-0,1	0,67740	-1,1	**0,00006**	-0,4	0,01206	-0,5	**0,00841**
EF1497		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit G	1	1	1	-0,2	0,31330	-0,4	0,01422	-0,1	0,70950	-1,1	**0,00029**	-0,2	0,09681	-1,0	**0,00003**
EF1498		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit A	1	1	1	-0,4	0,06966	-0,9	**0,00020**	-0,1	0,60330	-1,3	**0,00183**	-0,1	0,67320	-0,8	**0,00273**
EF1499		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit B	1	1	1	-0,1	0,73700	-0,8	**0,00009**	0,0	0,89050	-1,2	**0,00010**	0,0	0,94210	-0,9	**0,00052**
EF1500		Transport and binding proteins	Cations and iron carrying compounds	V-type ATPase, subunit D	1	1	1	0,2	0,35040	-0,3	0,01190	-0,1	0,58300	-1,2	**0,00028**	0,0	0,81240	-0,8	**0,00025**
EF1501		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,05398	-0,5	0,13540	-0,4	0,03848	-1,1	**0,00220**	-0,1	0,81500	-0,6	**0,00563**
EF1502		Cellular processes	Toxin production and resistance	beta-lactamase, putative	1	1	1	-1,2	**0,00018**	-3,0	**0,00000**	-0,8	**0,00138**	-1,6	**0,00059**	-0,7	**0,00046**	-1,7	**0,00005**
EF1503		Energy metabolism	Glycolysis/gluconeogenesis	fructose-1,6-bisphosphatase, putative	1	1	1	-1,5	0,01628	-3,5	**0,00000**	-1,0	**0,00388**	-2,3	**0,00003**	-1,3	**0,00005**	-2,0	**0,00000**
EF1504	*lysA*	Amino acid biosynthesis	Aspartate family	diaminopimelate decarboxylase	1	1	1	0,0	0,95430	1,0	0,01033	-0,1	0,72310	0,6	**0,00380**	0,2	0,19490	1,0	**0,00059**
EF1505		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00056**	2,1	**0,00000**	0,8	**0,00724**	1,0	**0,00101**	1,1	**0,00008**	1,8	**0,00001**
EF1506		Hypothetical proteins		hypothetical protein	1	1	1	-2,6	**0,00000**	-1,0	**0,00008**	-2,6	**0,00000**	-1,1	**0,00040**	-2,1	**0,00000**	-0,6	0,01505
EF1507		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,70830	NA	NA	0,1	0,74760	NA	NA
EF1508		Hypothetical proteins		hypothetical protein	1	1	1	-0,1	0,86970	NA	NA	0,1	0,49150	0,2	0,43540	-0,1	0,70600	0,1	0,84800
EF1509		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,01991	NA	NA	-0,4	0,03136	0,1	0,84970	0,0	0,94800	NA	NA
EF1510		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,86670	0,4	0,01632	-0,5	**0,00448**	0,0	0,91680	0,0	0,97370	0,2	0,43290
EF1511		Energy metabolism	Other	mandelate racemase/muconate lactonizing enzyme family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	2,1	**0,00008**
EF1512		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	1,9	**0,00032**	NA	NA	NA	NA	NA	NA	2,2	**0,00001**
EF1513		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1,0	0,01108
EF1515		Regulatory functions	RNA interactions	transcription antiterminator, bglG family	1	1	1	-0,6	**0,00466**	-1,9	**0,00000**	-0,8	0,02063	-1,0	0,01136	-1,1	**0,00010**	-1,8	**0,00000**
EF1516		Signal transduction	PTS	PTS system, IIABC components	1	1	1	-1,0	**0,00235**	-2,4	**0,00000**	-1,1	**0,00185**	-1,3	**0,00433**	-1,0	**0,00143**	-2,0	**0,00001**
EF1517		Hypothetical proteins		hypothetical protein	1	1	1	-0,6	0,19520	0,8	0,04846	0,0	0,81800	NA	NA	-0,2	0,24250	0,5	0,04641

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1518		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,14390	1,3	**0,00049**	-0,2	0,33220	0,2	0,45180	-0,3	0,07046	0,5	0,07299
EF1519		Transport and binding proteins	Cations and iron carrying compounds	cation-transporting ATPase, E1-E2 family	1	1	1	-0,9	**0,00021**	-1,0	**0,00000**	-0,4	0,02661	-0,1	0,67520	-0,7	**0,00028**	-0,8	**0,00461**
EF1521	*dnaG*	DNA metabolism	DNA replication, recombination, and repair	DNA primase	1	1	1	-0,4	0,10490	0,8	**0,00004**	-0,3	0,44040	0,3	0,09596	-0,2	0,17840	0,4	**0,00864**
EF1522	*sigA*	Transcription	Transcription factors	RNA polymerase sigma-43 factor	1	1	1	-0,7	**0,00109**	0,3	0,01993	-0,9	**0,00091**	-0,4	0,08846	-0,7	**0,00026**	0,0	0,84760
EF1523		Hypothetical proteins	Domain	conserved domainl protein	1	1	1	-0,5	0,03073	-0,4	0,08439	0,0	0,94090	0,0	0,90990	-0,1	0,56830	-0,3	0,44630
EF1524		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,02322	-1,4	**0,00000**	-0,3	0,05287	0,2	0,28940	-0,3	0,01961	-1,2	**0,00001**
EF1525	*fur*	Regulatory functions	DNA interactions	transcriptional regulator, Fur family	1	1	1	-0,1	0,75820	-0,6	**0,00068**	-0,2	0,31610	0,0	0,86880	-0,3	0,01666	0,0	0,94230
EF1526	*gap-1*	Energy metabolism	Glycolysis/gluconeogenesis	glyceraldehyde 3-phosphate dehydrogenase	1	1	1	0,8	**0,00027**	2,7	**0,00001**	1,8	**0,00000**	3,2	**0,00000**	1,6	**0,00000**	3,8	**0,00000**
EF1527		Unknown function	General	GTP-binding protein	1	1	1	0,2	0,37980	-0,5	**0,00567**	-0,5	0,01549	-0,2	0,44170	-0,1	0,24950	-0,1	0,45360
EF1528		Hypothetical proteins		hypothetical protein	1	1	1	0,8	**0,00145**	-0,3	0,04571	0,7	**0,00475**	-0,1	0,76560	0,4	0,01273	0,1	0,67160
EF1529		Signal transduction	PTS	PTS system, IIC component, putative	1	1	1	0,5	0,02332	NA	NA	0,1	0,33410	-0,3	0,33720	0,5	**0,00236**	-0,1	0,76880
EF1531		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	NA	NA	NA	NA	0,2	0,42480	NA	NA	NA	NA	NA	NA
EF1532		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,53920	NA	NA	NA	NA	NA	NA
EF1533		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	**0,00095**	NA	NA	3,4	**0,00000**	NA	NA	NA	NA	NA	NA
EF1534		Protein fate	Protein folding and stabilization	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1	1	1	-0,4	0,09781	-0,5	0,02688	0,0	0,98890	0,0	0,87270	-0,3	0,14520	0,1	0,85930
EF1535		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00876**	0,5	**0,00121**	0,9	**0,00123**	-0,2	0,53440	1,0	**0,00000**	0,8	0,03996
EF1536		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,8	**0,00119**	-0,5	**0,00163**	-0,5	0,01306	0,0	0,86760	-0,4	**0,00397**	-0,3	0,19690
EF1537		DNA metabolism	DNA replication, recombination, and repair	integrase/recombinase XerD, putative	1	1	1	0,3	0,30340	0,2	0,04172	0,0	0,94630	0,1	0,75130	0,3	0,08943	0,3	0,17960
EF1538	*scpA*	Segregation and condensation protein A	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,06567	-0,8	**0,00002**	-0,3	0,14490	-0,4	0,20180	-0,2	0,28860	-0,6	0,03558
EF1539	*scpB*	Segregation and condensation protein B	Conserved	conserved hypothetical protein TIGR00281	1	1	1	-0,5	0,01929	-0,7	**0,00078**	-0,4	0,03521	-0,4	0,02373	-0,2	0,11430	-0,7	**0,00837**
EF1541		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,12910	1,4	**0,00002**	-0,3	0,14490	2,4	**0,00000**	-0,2	0,44120	1,6	**0,00020**
EF1542		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00489**	0,8	**0,00001**	-0,7	**0,00049**	0,7	0,01231	-0,6	**0,00610**	0,6	**0,00364**
EF1543	*fer*	Energy metabolism	Electron transport	ferredoxin	1	1	1	0,1	0,59120	1,5	**0,00000**	-0,3	0,11100	1,4	**0,00000**	0,2	0,18360	1,2	**0,00004**
EF1544		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00556**	0,9	**0,00283**	-0,7	**0,00209**	0,4	0,09980	-0,7	**0,00137**	1,1	**0,00012**
EF1545	*recQ-1*	DNA metabolism	DNA replication, recombination, and repair	ATP-dependent DNA helicase RecQ	1	0	1	-0,9	0,15400	0,3	0,25670	-1,1	**0,00282**	0,2	0,69540	-0,3	0,24250	0,3	0,23090
EF1546		Unknown function	General	LysM domain protein	1	1	1	0,0	0,80490	0,0	0,82850	-0,1	0,44760	0,5	0,05221	0,0	0,71420	-0,2	0,38100
EF1547	*cmk*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	cytidylate kinase	1	1	1	-0,1	0,64830	0,3	0,14630	-0,7	**0,00420**	0,3	0,15270	-0,1	0,39960	-0,1	0,58320
EF1548		Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S1	1	1	1	0,2	0,47080	1,6	**0,00000**	0,0	0,96570	0,4	0,08871	0,1	0,69850	0,8	**0,00461**
EF1549		Unknown function	General	GTPase, putative	1	1	1	-1,4	**0,00023**	-2,1	**0,00000**	-1,3	**0,00068**	-1,1	**0,00065**	-1,4	**0,00001**	-2,2	**0,00000**
EF1550	*hup*	DNA metabolism	Chromosome-associated proteins	DNA-binding protein HU	1	1	1	-0,1	0,64150	-0,2	0,14690	-0,2	0,14530	-0,8	0,08977	0,0	0,70960	-0,5	0,05784
EF1551		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	0,2	0,26680	NA	NA	NA	NA
EF1552		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00065**	1,0	**0,00002**	0,9	**0,00401**	0,8	**0,00317**	1,1	**0,00010**	1,4	**0,00000**
EF1553		Unknown function	General	TPR domain protein	1	1	1	0,3	0,12600	0,8	**0,00001**	0,4	0,06606	-0,3	0,18850	0,3	0,03539	0,4	0,01567
EF1554		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,29250	1,0	**0,00007**	0,3	0,03172	-0,1	0,63530	-0,1	0,71010	0,3	0,17150
EF1555		Unknown function	General	YitT family protein	1	1	1	1,0	**0,00003**	1,2	**0,00000**	0,6	**0,00362**	0,8	**0,00095**	0,9	**0,00002**	1,0	**0,00013**
EF1556		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,12730	-1,0	**0,00001**	-0,3	0,17990	-0,2	0,30910	-0,3	0,25370	-0,8	**0,00185**
EF1557	*dapB*	Amino acid biosynthesis	Aspartate family	dihydrodipicolinate reductase	1	1	1	-0,3	0,21400	-1,3	**0,00001**	-0,3	0,06470	-0,2	0,36700	0,1	0,52930	-0,8	**0,00006**
EF1558	*papS*	Transcription	RNA processing	poly A polymerase	1	1	1	-0,4	0,02520	-1,3	**0,00000**	-0,2	0,28910	-0,3	0,14090	-0,1	0,33870	-1,0	**0,00013**
EF1559		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,06262	-1,4	**0,00000**	-0,4	0,01647	-0,2	0,38820	-0,2	0,09061	-1,0	**0,00002**
EF1560		Hypothetical proteins		hypothetical protein	1	1	1	1,2	**0,00012**	3,1	**0,00000**	0,1	0,64340	0,5	0,01139	0,4	**0,00505**	1,3	**0,00000**
EF1561	*aroE*	Amino acid biosynthesis	Aromatic amino acid family	shikimate 5-dehydrogenase	1	1	1	-1,1	**0,00002**	-0,6	**0,00166**	-0,3	0,10130	1,0	**0,00055**	-1,1	**0,00001**	-1,1	**0,00002**
EF1562		Amino acid biosynthesis	Aromatic amino acid family	phospho-2-dehydro-3-deoxyheptonate aldolase, putative	1	1	1	-1,3	**0,00019**	-1,7	**0,00000**	-0,3	0,06705	0,5	0,06982	-1,0	**0,00001**	-2,0	**0,00000**
EF1563	*aroB*	Amino acid biosynthesis	Aromatic amino acid family	3-dehydroquinate synthase	1	1	1	-1,0	**0,00021**	-2,4	**0,00000**	0,0	0,95530	0,2	0,34640	0,0	0,98630	-1,3	**0,00001**
EF1564	*aroC*	Amino acid biosynthesis	Aromatic amino acid family	chorismate synthase	1	1	1	-0,3	0,15130	-2,0	**0,00000**	0,4	0,02737	0,0	0,88570	0,7	**0,00208**	-1,2	**0,00001**
EF1565		Amino acid biosynthesis	Aromatic amino acid family	prephenate dehydrogenase	1	1	1	0,1	0,55450	-1,9	**0,00000**	0,7	**0,00034**	-0,1	0,58390	0,7	**0,00113**	-1,0	**0,00008**
EF1566	*aroA*	Amino acid biosynthesis	Aromatic amino acid family	3-phosphoshikimate 1-carboxyvinyltransferase	1	1	1	0,7	**0,00581**	-1,5	**0,00000**	0,7	0,01137	0,1	0,75130	1,0	**0,00053**	-0,7	**0,00565**
EF1567	*aroK*	Amino acid biosynthesis	Aromatic amino acid family	shikimate kinase	1	1	1	0,8	0,04565	-1,1	**0,00047**	0,5	0,01308	-0,1	0,59680	0,9	**0,00015**	-0,6	0,02820
EF1568		Amino acid biosynthesis	Aromatic amino acid family	prephenate dehydratase	1	1	1	0,7	0,02268	-0,5	**0,00572**	0,0	0,87240	0,1	0,63020	0,8	**0,00024**	-0,2	0,30860
EF1569	*psr*	Regulatory functions	Other	transcriptional regulator, PSR protein	1	1	1	-0,5	0,02040	-0,7	**0,00913**	-0,3	0,27070	-0,7	0,01168	0,0	0,89420	-1,0	**0,00284**
EF1570		Unknown function	General	DegV family protein	1	1	1	-0,9	**0,00717**	-1,3	**0,00004**	-0,7	**0,00648**	0,0	0,96410	-0,8	**0,00012**	-1,3	**0,00013**
EF1571		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,02878	0,3	0,02215	0,2	0,24250	-0,2	0,37940	0,5	**0,00419**	0,3	0,09762
EF1572		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,27050	0,1	0,32260	0,4	0,09092	0,2	0,45690	0,4	**0,00969**	0,2	0,21040
EF1573		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,14610	-0,3	0,03660	-0,8	**0,00055**	-0,3	0,22230	0,0	0,86310	-0,3	0,19850
EF1574		Transport and binding proteins	Cations and iron carrying compounds	Na+/H+ antiporter, putaive	1	1	1	-0,2	0,65600	-0,6	0,01241	-1,0	**0,00582**	-0,5	0,05603	-0,3	0,44770	-0,6	0,10320
EF1575		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,2	0,35520	-0,7	**0,00006**	-0,4	0,07643	-0,6	**0,00695**	0,0	0,97460	-0,3	0,29840
EF1576	*thyA*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	thymidylate synthase	1	1	1	-0,5	0,10410	-0,3	0,07642	-0,6	**0,00925**	-0,8	**0,00236**	-0,6	**0,00155**	-0,5	0,03375
EF1577	*folA*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	dihydrofolate reductase	1	1	1	-0,7	**0,00399**	-0,8	**0,00026**	-0,8	**0,00296**	-0,7	0,01521	-0,6	**0,00049**	-0,6	0,01673
EF1578		Energy metabolism	Electron transport	iron-sulfur cluster-binding protein, putative	1	1	1	-0,4	0,06385	-0,8	**0,00007**	-0,9	**0,00047**	-0,7	0,03694	-0,6	**0,00413**	-0,5	0,03940
EF1579	*lexA*	Regulatory functions	DNA interactions	transcriptional repressor LexA	1	1	1	0,4	0,01440	0,6	**0,00010**	0,5	**0,00230**	0,3	0,27930	0,6	**0,00594**	0,7	**0,00029**
EF1580		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,03728	0,2	0,04850	-0,1	0,50830	-0,1	0,56490	0,1	0,62770	0,2	0,23900
EF1582		Transport and binding proteins	Unknown substrate	major facilitator family transporter	1	1	1	0,1	0,43570	-0,3	0,05649	0,5	0,01626	0,7	0,04539	0,7	**0,00052**	0,3	0,09710
EF1583		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	N-acetylmuramoyl-L-alanine amidase, family 4	1	1	1	-0,2	0,36270	0,0	0,88600	-0,7	**0,00023**	-0,4	0,05138	-0,2	0,10740	-0,6	**0,00357**
EF1584	*cysK*	Amino acid biosynthesis	Serine family	cysteine synthase A	1	1	1	0,8	0,02293	3,1	**0,00000**	0,7	**0,00164**	2,0	**0,00000**	1,0	**0,00002**	2,9	**0,00000**
EF1585	*perR*	Regulatory functions	DNA interactions	transcriptional regulator, Fur family	1	1	1	0,7	0,04994	1,3	**0,00000**	0,3	0,05703	0,7	**0,00353**	0,4	**0,00554**	1,5	**0,00013**
EF1586	*nox*	Energy metabolism	Electron transport	NADH oxidase	1	1	1	-1,2	**0,00018**	0,5	0,05474	-1,2	**0,00001**	0,9	**0,00298**	-0,8	**0,00113**	0,7	**0,00248**
EF1587		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	-0,1	0,48160	0,7	**0,00006**	0,6	**0,00219**	0,3	0,21400	0,1	0,31210	0,6	**0,00086**
EF1589		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	0,0	0,82970	1,1	**0,00001**	-0,4	0,09006	1,1	**0,00017**	0,2	0,25790	1,5	**0,00004**
EF1590		Regulatory functions	Other	protease synthase and sporulation negative regulatory protein pai 1	1	1	1	-1,8	**0,00001**	0,0	0,90580	-2,0	**0,00000**	0,3	0,32030	-1,0	**0,00003**	0,9	**0,00249**
EF1591		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	0,3	0,16890	NA	NA	0,1	0,66290	-0,7	0,01492	0,2	0,27640	-0,1	0,47280
EF1592		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	NA	NA	NA	NA	-1,2	**0,00360**	-0,4	0,29740	NA	NA	NA	NA
EF1593		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	NA	NA	NA	NA	-1,0	**0,00127**	-0,3	0,28140	NA	NA	NA	NA
EF1594		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,5	0,01728	-0,3	0,57160	-0,2	0,58680	0,2	0,33230
EF1595		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,1	0,63750	0,3	0,17360
EF1596		Cell envelope	Other	lipoprotein, putative	1	1	1	-0,5	0,01420	-0,7	**0,00033**	-0,1	0,80620	-0,8	0,01383	0,0	0,94720	-0,3	0,41480
EF1597	*katA*	Cellular processes	Detoxification	catalase/peroxidase	1	1	1	-0,8	**0,00193**	2,0	**0,00014**	-1,2	**0,00200**	-1,0	**0,00116**	-0,5	0,02324	1,1	**0,00056**
EF1598	*phrB*	DNA metabolism	DNA replication, recombination, and repair	deoxyribodipyrimidine photolyase	1	1	1	0,5	0,02071	1,8	**0,00000**	0,2	0,14440	0,6	0,03949	0,5	**0,00248**	0,8	**0,00086**
EF1599		Regulatory functions	DNA interactions	TPR domain transcriptional regulator, Cro/CI family	1	1	1	-0,1	0,82220	0,8	**0,00034**	-0,3	0,12550	0,0	0,98130	-0,1	0,53230	0,1	0,48450
EF1601		Signal transduction	PTS	PTS system, IIABC components	1	1	1	0,7	**0,00218**	NA	NA	1,0	**0,00021**	0,8	0,03300	1,7	**0,00000**	2,3	**0,00002**
EF1602		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 13	1	1	1	2,0	**0,00000**	1,6	**0,00004**	2,4	**0,00000**	2,1	**0,00007**	2,9	**0,00000**	2,7	**0,00001**
EF1603	*scrB-1*	Energy metabolism	Biosynthesis and degradation of polysaccharides	sucrose-6-phosphate dehydrogenase	1	1	1	2,0	**0,00001**	3,8	**0,00000**	2,3	**0,00000**	2,0	0,09526	3,2	**0,00000**	4,4	**0,00000**
EF1604	*scrR-1*	Regulatory functions	DNA interactions	sucrose operon repressor ScrR	1	1	1	0,5	0,01173	1,7	**0,00000**	0,0	0,98890	0,5	0,05865	0,5	0,01221	3,1	**0,00000**
EF1605		Hypothetical proteins		hypothetical protein	1	1	1	0,6	**0,00269**	2,8	**0,00000**	0,5	0,03144	0,8	**0,00325**	1,0	**0,00003**	2,8	**0,00000**
EF1606		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	-1,5	**0,00001**	-0,5	**0,00111**	-1,7	**0,00004**	-0,1	0,86990	-1,6	**0,00001**	-0,3	0,24770

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1608		Fatty acid and phospholipid metabolism	Biosynthesis	cardiolipin synthetase, putative	1	1	1	0,7	0,05110	1,4	**0,00000**	1,1	**0,00276**	0,4	0,17610	0,8	**0,00009**	1,4	**0,00000**
EF1609		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,74200	0,3	0,03396	-0,6	**0,00407**	0,3	0,18030	0,1	0,80540	-0,2	0,48350
EF1610		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,6	**0,00698**	-1,3	**0,00000**	-0,1	0,64010	-0,6	0,03452	-0,2	0,22270	-0,4	0,02756
EF1611	*ppaC*	Central intermediary metabolism	Phosphorus compounds	inorganic pyrophosphatase, manganese-dependent	1	1	1	-0,3	0,19040	-0,9	**0,00021**	-0,4	0,03947	-0,4	0,03287	-0,2	0,18690	-0,4	0,05459
EF1612	*pflA*	Energy metabolism	Fermentation	pyruvate formate-lyase activating enzyme	1	1	1	0,1	0,68750	-2,7	**0,00000**	0,2	0,22200	-0,7	0,01521	-0,2	0,12660	-0,7	**0,00064**
EF1613	*pflB*	Energy metabolism	Fermentation	formate acetyltransferase	1	1	1	0,2	0,33810	-2,1	**0,00000**	0,4	0,02059	-0,4	0,12240	0,2	0,07672	-0,6	**0,00580**
EF1614	*parC*	DNA metabolism	DNA replication, recombination, and repair	DNA topoisomerase IV, A subunit	1	1	1	-0,7	**0,00225**	-1,7	**0,00000**	-0,3	0,33910	-0,1	0,87010	-0,3	0,05851	-0,9	**0,00507**
EF1615	*parE*	DNA metabolism	DNA replication, recombination, and repair	DNA topoisomerase IV, B subunit	1	1	1	-0,4	0,11750	-0,7	**0,00059**	-0,4	0,16370	0,0	0,92900	-0,2	0,21650	-0,5	0,01238
EF1616		Unknown function	General	CoA-binding domain protein	1	1	1	0,7	**0,00734**	1,5	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1617		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1618	*eutH*	Energy metabolism	Amino acids and amines	ethanolamine utilization protein EutH	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1619		Cellular processes	Other	carbon dioxide concentrating mechanism protein CcmL, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1620		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1621		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,54980	NA	NA	NA	NA	NA	NA
EF1622		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1623		Central intermediary metabolism	Other	microcompartment protein	1	1	1	NA	NA	NA	NA	-0,2	0,43320	NA	NA	NA	NA	NA	NA
EF1624		Energy metabolism	Fermentation	aldehyde dehydrogenase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1625		Unknown function	General	microcompartment protein family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1626	*eutL*	Energy metabolism	Amino acids and amines	ethanolamine utilization protein EutL	1	1	1	NA	NA	NA	NA	0,2	0,52160	NA	NA	NA	NA	NA	NA
EF1627	*eutC*	Energy metabolism	Amino acids and amines	ethanolamine ammonia-lyase small subunit	1	1	1	NA	NA	NA	NA	0,5	0,05044	NA	NA	NA	NA	NA	NA
EF1629	*eutB*	Energy metabolism	Amino acids and amines	ethanolamine ammonia-lyase large subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1632		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	NA	NA	-1,1	**0,00389**	-0,7	**0,00562**	-1,4	**0,00017**	-0,6	**0,00267**	-1,1	**0,00254**
EF1633		Signal transduction	Two-component systems	response regulator	1	1	1	-0,7	**0,00226**	-1,1	**0,00000**	-0,5	0,03298	-1,1	**0,00172**	-0,2	0,24240	-0,4	0,05577
EF1634		Unknown function	General	propanediol utilization protein PduU	1	1	1	-0,5	0,05218	-1,1	**0,00001**	-0,5	0,09343	-0,7	**0,00868**	-0,4	0,05460	-0,5	0,33260
EF1635		Energy metabolism	Fermentation	propanol dehydrogenase PduQ, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1637		Energy metabolism	Other	ATP:cob(I)alamin adenosyltransferase, putative	1	1	1	NA	NA	NA	NA	0,0	0,94090	NA	NA	NA	NA	NA	NA
EF1638	*eutP*	Unknown function	General	ethanolamine utilization protein, EutP	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1639		Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, ATP-binding protein	1	1	1	-0,2	0,33480	-0,4	0,06620	NA	NA	NA	NA	NA	NA	NA	NA
EF1640		Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, permease protein	1	1	1	NA	NA	-0,8	**0,00032**	0,0	0,88470	NA	NA	NA	NA	NA	NA
EF1641		Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, iron compound-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1643		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00023	1	1	1	-1,4	**0,00012**	-1,7	**0,00000**	-1,7	**0,00005**	-0,5	0,06518	-1,4	**0,00001**	-1,5	**0,00000**
EF1644		Unknown function	General	lacX protein, putative	1	1	1	0,4	0,12570	2,2	**0,00000**	0,1	0,43020	1,0	**0,00934**	0,1	0,46670	0,7	0,06224
EF1645	*codY*	Regulatory functions	DNA interactions	transcriptional regulator CodY	1	1	1	0,8	**0,00126**	1,3	**0,00008**	0,5	**0,00512**	0,7	**0,00599**	0,5	**0,00466**	1,0	**0,00031**
EF1646	*hslU*	Cellular processes	Adaptations to atypical conditions	heat shock protein HslVU, ATPase subunit HslU	1	1	1	1,2	**0,00004**	1,7	**0,00000**	0,5	**0,00526**	0,6	0,01105	0,7	**0,00045**	0,9	**0,00501**
EF1647	*hslV*	Protein fate	Protein folding and stabilization	heat shock protein HslV	1	1	1	1,5	**0,00011**	1,7	**0,00000**	0,9	**0,00006**	0,6	0,05979	1,1	**0,00003**	0,6	**0,00639**
EF1648		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1649	*gid*	Unknown function	General	glucose-inhibited division protein	1	1	1	-0,6	**0,00709**	-0,3	0,08903	NA	NA	NA	NA	NA	NA	NA	NA
EF1650	*topA*	DNA metabolism	DNA replication, recombination, and repair	DNA topoisomerase I	1	1	1	-0,6	0,01377	-0,4	0,02783	-0,5	0,01358	0,0	0,98390	-0,2	0,44540	-0,1	0,63610
EF1651		Unknown function	General	abortive infection protein	1	1	1	0,0	0,95830	0,7	**0,00011**	0,5	0,17390	1,1	**0,00215**	0,1	0,75620	0,8	0,02193
EF1652		Cellular processes	DNA transformation	DNA processing protein DprA, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1653	*rnhB*	Transcription	Degradation of RNA	ribonuclease HII	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1654		Unknown function	General	GTPase of unknown function	1	1	1	-0,4	0,05850	-0,8	**0,00748**	NA	NA	NA	NA	NA	NA	-0,6	0,01219
EF1655		Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	2-dehydropantoate 2-reductase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1656		Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	-0,8	0,04429	-1,1	**0,00665**	-0,7	0,04154	-0,6	0,19560	-0,9	**0,00010**	-1,1	**0,00011**
EF1657		Cell envelope	Other	membrane protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1658	*bkdC*	Energy metabolism	Amino acids and amines	branched-chain alpha-keto acid, E2, dihydrolipoamide acetyltransferase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1659	*bkdB*	Energy metabolism	Amino acids and amines	branched-chain alpha-keto acid dehydrogenase, E1 beta subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1660	*bkdA*	Energy metabolism	Amino acids and amines	branched-chain alpha-keto acid dehydrogenase, E1 alpha subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1661	*bkdD*	Energy metabolism	Amino acids and amines	branched-chain alpha-keto acid dehydrogenase, E3	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,4	0,22400	-1,4	**0,00354**
EF1662	*buk*	Energy metabolism	Other	butyrate kinase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1663	*ptb*	Fatty acid and phospholipid metabolism	Degradation	branched-chain phosphotransacylase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,2	**0,00027**
EF1664		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,01535	0,9	**0,00004**	-0,7	**0,00435**	0,4	0,36850	-0,7	**0,00413**	0,3	0,09860
EF1665		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,03698	NA	NA	-0,4	0,07073	-0,6	0,07665	NA	NA	NA	NA
EF1666		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1667		Unknown function	Enzymes of unknown specificity	short chain dehydrogenase family protein	1	1	1	1,1	**0,00023**	3,6	**0,00000**	0,3	0,04448	2,2	**0,00001**	0,8	**0,00006**	2,9	**0,00000**
EF1668		Regulatory functions	DNA interactions	transcriptional regulator, MarR family	1	1	1	0,3	0,04853	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1669		Unknown function	Enzymes of unknown specificity	glyoxylase family protein	1	1	1	0,1	0,83610	NA	NA	-0,1	0,85690	0,5	0,13370	0,6	0,01039	NA	NA
EF1670		Unknown function	Enzymes of unknown specificity	phospholipase/carboxylesterase family protein	1	0	1	0,1	0,68300	1,3	**0,00001**	-0,2	0,55850	NA	NA	0,5	**0,00717**	NA	NA
EF1671		Unknown function	Enzymes of unknown specificity	oxidoreductase, zinc-binding	1	1	1	1,7	**0,00000**	3,4	**0,00000**	0,9	**0,00084**	1,6	**0,00102**	1,3	**0,00000**	NA	NA
EF1672		Transport and binding proteins	Unknown substrate	permease protein, putative	1	1	1	NA	NA	NA	NA	1,1	**0,00110**	NA	NA	NA	NA	NA	NA
EF1673		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1674		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,22230	0,6	**0,00027**	0,0	0,88490	NA	NA	0,2	0,59110	0,6	0,09767
EF1675		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,0	0,92660	0,4	0,02915	NA	NA	NA	NA	NA	NA	NA	NA
EF1676		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,2	0,41020	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1677		Cell envelope	Other	lipoprotein, putative	1	1	1	0,9	**0,00055**	2,7	**0,00000**	0,5	0,03719	NA	NA	NA	NA	NA	NA
EF1678		Protein fate	Protein and peptide secretion and trafficking	signal peptidase I	1	1	1	-0,1	0,76740	0,6	**0,00311**	NA	NA	NA	NA	NA	NA	NA	NA
EF1679		Protein fate	Degradation of proteins, peptides, and glycopeptides	carboxyl-terminal protease	1	1	1	-0,2	0,50750	0,4	0,01121	NA	NA	NA	NA	NA	NA	NA	NA
EF1680		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,90530	2,9	**0,00000**	0,1	0,72310	0,3	0,30430	0,2	0,22400	1,9	**0,00000**
EF1681	*msrA*	Protein fate	Protein modification and repair	peptide methionine sulfoxide reductase	1	1	1	0,2	0,42990	3,2	**0,00000**	0,1	0,57510	0,4	0,11150	0,1	0,55210	1,7	**0,00000**
EF1682		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,64920	1,1	**0,00002**	0,3	0,15360	0,2	0,31940	0,1	0,67060	1,2	**0,00002**
EF1683		Unknown function	Enzymes of unknown specificity	Lipase/Acylhydrolase, putative	1	1	1	-0,1	0,50150	0,4	**0,00469**	0,2	0,35550	0,1	0,63490	0,2	0,11870	0,8	**0,00179**
EF1684		Unknown function	General	DegV family protein, putative	1	1	1	0,4	0,02875	0,2	0,03567	-0,1	0,48410	NA	NA	0,4	**0,00484**	0,3	0,17250
EF1685	*hlyIII*	Cellular processes	Pathogenesis	hemolysin III	1	1	1	0,4	0,11450	1,0	**0,00021**	0,2	0,50450	0,5	0,25030	0,3	0,01540	1,0	**0,00006**
EF1686		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,77360	1,2	**0,00001**	0,4	0,06170	0,3	0,26520	0,4	0,01635	2,1	**0,00000**
EF1687	*apt*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	adenine phosphoribosyltransferase	1	1	1	-0,7	**0,00807**	-1,4	**0,00000**	NA	NA	NA	NA	-0,2	0,34560	-0,6	0,08358
EF1688	*recJ*	DNA metabolism	DNA replication, recombination, and repair	single-stranded-DNA-specific exonuclease RecJ	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1689		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,06439	0,2	0,13460	-0,2	0,25540	0,0	0,91800	0,3	0,15900	0,3	0,17960
EF1690		Unknown function	Enzymes of unknown specificity	oxidoreductase, short-chain dehydrogenase/reductase family	1	1	1	0,2	0,30760	-0,1	0,45380	-0,2	0,29440	-0,1	0,70690	0,1	0,42200	0,0	0,98640
EF1691		Unknown function	Enzymes of unknown specificity	metallo-beta-lactamase, AtsA/ElaC family	1	1	1	0,3	0,04567	0,0	0,80650	0,1	0,65630	-0,1	0,65700	0,4	0,02207	0,0	0,84680
EF1692		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00012**	0,3	0,25070	0,4	0,01199	-0,3	0,06871	0,5	**0,00174**	1,2	**0,00018**
EF1693		Unknown function	General	KH domain protein	1	1	1	-0,3	0,08003	-0,8	**0,00002**	-0,5	**0,00856**	-0,9	0,14060	0,2	0,28290	-0,6	**0,00483**
EF1694	*rpsP*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S16	1	1	1	-0,5	**0,00297**	-1,2	**0,00000**	-0,5	**0,00426**	-0,6	0,31010	0,0	0,83840	-1,2	**0,00013**
EF1695		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,2	0,51290	0,2	0,29090	-0,1	0,65860	0,1	0,70700	-0,1	0,67880	0,3	0,12160

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1698		Unknown function	General	NADPH-dependent FMN reductase domain protein	1	1	1	1,6	**0,00002**	4,3	**0,00000**	1,0	**0,00036**	2,2	**0,00000**	1,5	**0,00000**	3,5	**0,00000**
EF1699		Regulatory functions	DNA interactions	transcriptional regulator, MerR family	1	1	1	NA	NA	0,8	**0,00545**	0,4	0,04944	1,0	0,04443	0,7	**0,00104**	2,0	**0,00000**
EF1700	*ffh*	Protein fate	Protein and peptide secretion and trafficking	signal recognition particle protein	1	1	1	0,0	0,84130	-0,8	**0,00002**	-0,5	0,01812	-0,4	0,09032	-0,1	0,54200	-0,6	**0,00063**
EF1701		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,01828	-0,8	**0,00002**	-0,4	0,05182	-0,3	0,24040	-0,2	0,11430	-0,3	0,35180
EF1702		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,01982	-0,2	0,07846	-0,4	0,07789	-0,2	0,47450	-0,2	0,27920	0,0	0,90960
EF1703	*phoP*	Regulatory functions	DNA interactions	alkaline phosphatase synthesis transcr regulatory protein PhoP	1	1	1	0,1	0,80140	0,9	**0,00006**	0,4	0,02659	0,8	**0,00121**	0,3	0,14780	0,7	**0,00398**
EF1704		Regulatory functions	Small molecule interactions	sensory box histidine kinase	1	1	1	0,0	0,90480	1,1	**0,00134**	0,2	0,18870	0,8	**0,00095**	0,2	0,18720	1,0	**0,00162**
EF1705		Transport and binding proteins	Anions	phosphate-binding protein	1	1	1	-0,1	0,77170	0,7	**0,00207**	NA	NA	0,0	0,92420	NA	NA	0,5	0,04323
EF1706		Unknown function	Enzymes of unknown specificity	aminotransferase, class I	1	1	1	0,2	0,54090	0,5	**0,00374**	0,3	0,28940	0,1	0,79160	0,1	0,63670	0,8	**0,00399**
EF1707		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 38	1	1	1	0,1	0,84210	-0,5	**0,00388**	0,7	0,01061	-0,5	0,12360	0,7	**0,00690**	0,4	0,23140
EF1708		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,30160	-0,4	0,01117	0,3	0,18470	NA	NA	NA	NA	0,3	0,26340
EF1709		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, GntR family	1	1	1	0,3	0,16010	-0,1	0,70220	1,0	**0,00171**	0,0	0,88720	0,7	**0,00027**	0,3	0,18920
EF1710		Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	-0,3	0,13860	2,3	**0,00000**	-0,7	**0,00177**	1,0	**0,00971**	0,2	0,32700	1,4	**0,00010**
EF1711		Central intermediary metabolism	Other	carbonic anhydrase, putative	1	1	1	-0,2	0,52630	1,2	**0,00001**	-0,6	**0,00496**	1,2	**0,00209**	0,1	0,64920	1,0	**0,00567**
EF1712	*pyrE*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	orotate phosphoribosyltransferase	1	1	1	-1,2	**0,00050**	0,5	0,04910	-1,5	**0,00006**	NA	NA	NA	NA	NA	NA
EF1713	*pyrF*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	orotidine 5`-phosphate decarboxylase	1	1	1	-1,4	**0,00012**	-0,1	0,51650	-1,8	**0,00001**	-0,2	0,41100	-0,3	0,11410	0,3	0,15120
EF1714	*pyrD-2*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	dihydroorotate dehydrogenase	1	1	1	-2,1	**0,00015**	-1,1	**0,00007**	-2,8	**0,00001**	-0,1	0,70750	-1,4	**0,00002**	-0,3	0,15970
EF1715	*pyrDII*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	dihydroorotate dehydrogenase electron transfer subunit	1	1	1	-2,0	**0,00009**	-0,6	**0,00875**	-2,6	**0,00007**	-0,3	0,40380	-1,4	**0,00015**	-0,4	0,33120
EF1716	*pyraB*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	carbamoyl-phosphate synthase, large subunit	1	1	1	-0,6	0,10410	-0,3	0,03913	-1,3	**0,00489**	-0,2	0,52240	-1,2	**0,00072**	0,1	0,72600
EF1717	*pyraA*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	carbamoyl-phosphate synthase, small subunit	1	1	1	-0,4	0,13070	-0,1	0,49510	-0,8	0,05169	0,2	0,60880	-1,0	**0,00007**	0,2	0,44400
EF1718	*pyrC*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	dihydroorotase	1	1	1	-0,3	0,24810	-0,6	0,01068	-0,8	0,04146	0,1	0,91190	-0,9	**0,00175**	-0,1	0,68470
EF1719	*pyrB*	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	aspartate carbamoyltransferase	1	1	1	-0,2	0,61050	0,0	0,97890	-0,3	0,55850	NA	NA	-0,4	0,18670	NA	NA
EF1720		Transport and binding proteins	Nucleosides, purines and pyrimidines	uracil permease	1	1	1	-0,3	0,23390	-0,4	0,01053	-0,6	0,20100	0,1	0,90390	-0,9	**0,00091**	0,3	0,46940
EF1721	*pyrR*	Transcription	Transcription factors	pyrimidine operon regulatory protein PyrR	1	1	1	0,0	0,91090	0,1	0,59260	-0,8	0,02856	0,1	0,79500	-0,6	**0,00177**	0,2	0,61710
EF1723	*lspA*	Protein fate	Protein and peptide secretion and trafficking	signal peptidase II	1	1	1	-0,2	0,42320	-0,2	0,08409	-0,4	0,06777	0,3	0,28260	-0,1	0,66360	0,0	0,84630
EF1724		Unknown function	General	CBS domain protein	1	1	1	0,0	0,86280	0,2	0,24580	-0,2	0,30100	0,3	0,30110	0,1	0,28860	0,5	0,02379
EF1725	*fhs*	Central intermediary metabolism	One-carbon metabolism	formate--tetrahydrofolate ligase	1	1	1	0,4	0,21860	1,0	**0,00004**	0,1	0,78650	0,1	0,75990	0,3	0,13050	NA	NA
EF1726		Cellular processes	Adaptations to atypical conditions	cold-shock domain family protein	1	1	1	0,1	0,63620	0,4	0,01171	-0,3	0,11990	-0,1	0,69400	0,4	0,01974	0,7	**0,00392**
EF1727	*ebsa*	Cellular processes	Conjugation	ebsA protein	1	1	1	-0,1	0,35930	0,9	**0,00001**	-0,4	0,03946	0,1	0,80980	-0,2	0,15120	0,3	0,08636
EF1728	*ebsB*	Cellular processes	Conjugation	EbsB protein	1	1	1	0,1	0,59880	0,5	**0,00105**	0,1	0,41630	0,4	0,03452	0,0	0,95070	0,6	**0,00247**
EF1730		Cellular processes	Conjugation	EbsC protein	1	1	1	0,0	0,92170	0,7	**0,00036**	-0,2	0,26770	0,2	0,54810	NA	NA	NA	NA
EF1731	*aroD*	Amino acid biosynthesis	Aromatic amino acid family	3-dehydroquinate dehydratase, type I	1	1	1	-0,2	0,40660	0,4	0,02027	NA	NA	NA	NA	NA	NA	NA	NA
EF1732		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein, MDR family	1	0	1	-0,1	0,76450	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1733		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein, MDR family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1734		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00626**	-1,3	**0,00000**	-1,4	**0,00000**	-0,7	0,01093	-0,2	0,29090	-0,6	0,01326
EF1735		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,01775	0,2	0,23800	NA	NA	NA	NA	NA	NA	NA	NA
EF1736	*nfo*	DNA metabolism	DNA replication, recombination, and repair	endonuclease IV	1	1	1	-0,4	0,05850	0,2	0,07539	-0,9	**0,00091**	0,5	0,04901	-0,1	0,59280	0,4	0,17060
EF1737		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,38740	0,7	**0,00114**	-1,0	**0,00330**	0,6	0,01124	-0,2	0,07905	1,0	**0,00060**
EF1738		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,12490	0,5	**0,00152**	-0,7	**0,00295**	NA	NA	NA	NA	NA	NA
EF1739	*tryS-2*	Protein synthesis	tRNA aminoacylation	tyrosyl-tRNA synthetase	1	1	1	-0,4	0,02256	-1,3	**0,00005**	-0,9	**0,00217**	-0,4	0,15680	-0,3	0,08232	-0,6	**0,00438**
EF1740		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein 1B, putative	1	1	1	-0,1	0,60430	-0,5	**0,00286**	0,2	0,49860	0,2	0,52290	-0,2	0,35330	-0,1	0,73850
EF1741	*ccpA*	Regulatory functions	DNA interactions	catabolite control protein A	1	1	1	0,5	**0,00682**	0,9	**0,00014**	-0,3	0,27580	0,3	0,30080	0,5	**0,00499**	0,2	0,23990
EF1743	*pepQ-2*	Protein fate	Degradation of proteins, peptides, and glycopeptides	proline dipeptidase	1	1	1	0,4	0,03139	0,5	0,04287	0,2	0,27150	0,6	0,04274	0,3	0,07856	0,9	**0,00774**
EF1744		Cellular processes	Adaptations to atypical conditions	general stress protein, putative	1	1	1	0,6	**0,00142**	1,8	**0,00000**	0,0	0,96570	0,5	0,04275	0,8	**0,00003**	1,8	**0,00002**
EF1745		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00009**	2,0	**0,00000**	0,2	0,53610	0,4	0,21370	0,8	**0,00005**	1,6	**0,00002**
EF1746	*galU*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	UTP-glucose-1-phosphate uridylyltransferase	1	1	1	0,0	0,99960	0,1	0,51530	-0,4	0,20690	-0,2	0,61680	0,1	0,71430	-0,1	0,84860
EF1747	*gpsA*	Energy metabolism	Other	glycerol-3-phosphate dehydrogenase (NAD(P)+)	1	1	1	-0,1	0,36590	-0,3	0,05732	-0,4	0,10270	-0,3	0,14480	-0,3	0,06468	0,0	0,91560
EF1748	*lgt*	Protein fate	Protein modification and repair	prolipoprotein diacylglyceryl transferase	1	1	1	-0,2	0,40070	-0,2	0,09764	NA	NA	-0,1	0,84010	-0,1	0,79440	0,0	0,86950
EF1749	*hprK*	Regulatory functions	Protein interactions	HPr(Ser) serine kinase/phosphatase	1	1	1	0,0	0,95660	-0,1	0,55630	-0,2	0,57160	-0,3	0,34730	-0,1	0,56280	-0,3	0,15020
EF1750		Unknown function	General	endo/excinuclease amino terminal domain protein	1	1	1	-0,6	**0,00411**	NA	NA	-1,1	**0,00025**	0,3	0,15640	-0,4	0,02938	-0,1	0,79090
EF1751		Cell envelope	Other	membrane protein, putative	1	1	1	1,5	**0,00002**	1,6	**0,00000**	1,8	**0,00000**	0,4	0,12020	1,2	**0,00018**	1,2	**0,00001**
EF1752		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,4	**0,00001**	1,0	**0,00002**	2,2	**0,00000**	0,2	0,41100	1,0	**0,00008**	1,0	**0,00031**
EF1753		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	2,6	**0,00000**	0,5	**0,00278**	4,0	**0,00000**	-0,3	0,29590	2,2	**0,00000**	0,7	**0,00638**
EF1754		Unknown function	General	PhoU family protein	1	1	1	-0,5	0,01875	-0,3	0,02516	-0,6	**0,00202**	-0,4	0,26530	0,0	0,92930	NA	NA
EF1755		Transport and binding proteins	Anions	phosphate ABC transporter, ATP-binding protein	1	1	1	-0,8	**0,00061**	-1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1756		Transport and binding proteins	Anions	phosphate ABC transporter, ATP-binding protein	1	0	1	-0,6	**0,00178**	-1,3	**0,00000**	-0,7	0,01994	-0,4	0,03191	-0,6	**0,00104**	-1,1	**0,00029**
EF1757		Transport and binding proteins	Anions	phosphate ABC transporter, permease protein	1	1	1	-0,7	**0,00055**	-1,6	**0,00001**	-0,8	**0,00065**	-0,6	**0,00999**	-0,5	**0,00271**	-0,8	**0,00710**
EF1758		Transport and binding proteins	Anions	phosphate ABC transporter, permease protein	1	1	1	-0,7	**0,00536**	-1,7	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF1759		Transport and binding proteins	Anions	phosphate ABC transporter, phosphate-binding protein	1	1	1	-0,7	**0,00063**	-0,8	**0,00010**	-0,6	0,01304	-0,4	0,08104	-0,6	0,02295	-0,5	0,10050
EF1760		Cellular processes	Cell division	cell division ABC transporter, permease protein FtsX, putative	1	1	1	-1,5	**0,00004**	-1,0	**0,00008**	NA	NA	-0,6	0,19860	-1,0	**0,00022**	-0,7	0,04753
EF1761	*ftsE*	Cellular processes	Cell division	cell division ATP-binding protein FtsE	1	1	1	-1,5	**0,00001**	-0,8	0,06321	-1,1	**0,00002**	-0,8	**0,00176**	-1,4	**0,00000**	-1,7	**0,00000**
EF1763	*secA*	Protein fate	Protein and peptide secretion and trafficking	preprotein translocase, SecA subunit	1	1	1	0,1	0,45790	-0,6	**0,00105**	-0,2	0,16920	-0,3	0,07659	0,0	0,75360	-0,5	0,01460
EF1764	*yfiA*	Protein synthesis	Translation factors	ribosomal subunit interface protein	1	1	1	0,8	**0,00349**	1,1	**0,00001**	-0,1	0,71820	0,2	0,44430	0,6	**0,00033**	0,3	0,06620
EF1765	*comFC*	Cellular processes	DNA transformation	competence protein F	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1767	*comFA*	Cellular processes	DNA transformation	competence protein F	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1768		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,0	0,94830	-0,1	0,29050	0,3	0,06101	0,2	0,39620	NA	NA	-0,1	0,50950
EF1769		Signal transduction	PTS	PTS system, IIB component, putative	1	1	1	0,3	0,19420	0,9	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF1770		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	0,4	**0,00518**	NA	NA	NA	NA	NA	NA	NA	NA
EF1771		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00257	1	1	1	-0,4	0,03954	0,3	0,02419	-0,3	0,09006	0,4	0,11780	-0,4	0,03304	0,1	0,48180
EF1772		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,07589	0,3	**0,00634**	-0,3	0,13520	0,5	0,02846	-0,3	0,07045	0,2	0,28290
EF1773		Fatty acid and phospholipid metabolism	Biosynthesis	short chain dehydrogenase	1	1	1	-0,5	0,01002	-0,3	0,01945	-0,4	**0,00617**	-0,1	0,68000	-0,7	**0,00031**	0,1	0,64230
EF1774		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,3	**0,00000**	-1,9	**0,00000**	-1,7	**0,00001**	-0,5	0,15520	-1,5	**0,00003**	-0,9	**0,00033**
EF1775		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1776		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,5	**0,00304**	1,3	**0,00000**	0,3	0,20650	0,5	0,01729	0,7	**0,00077**	1,2	**0,00001**
EF1777	*purD*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylamine--glycine ligase	1	1	1	NA	NA	NA	NA	NA	NA	0,5	0,35490	NA	NA	NA	NA
EF1778	*purH*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazolecarboxamide formyltransferase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1779	*purN*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylglycinamide formyltransferase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1780	*purM*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylformylglycinamidine cyclo-ligase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1781	*purF*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	amidophosphoribosyltransferase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1782	*purL*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylformylglycinamidine synthase II	1	1	1	NA	NA	NA	NA	0,8	0,01245	NA	NA	NA	NA	NA	NA
EF1783	*purQ*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylformylglycinamidine synthetase I	1	1	1	NA	NA	NA	NA	0,6	0,04396	NA	NA	1,6	**0,00012**	NA	NA
EF1784	*purS*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylformylglycinamidine synthase, PurS protein	1	1	1	NA	NA	NA	NA	0,2	0,52850	NA	NA	NA	NA	NA	NA
EF1785	*purC*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole-succinocarboxamide synthase	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1786	*purK-1*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole carboxylase, ATPase subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1787	*purE*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole carboxylase, catalytic subunit	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1789		Unknown function	General	SPFH domain/Band 7 family protein	1	1	1	1,5	**0,00012**	2,1	**0,00000**	0,8	**0,00194**	0,6	0,09652	1,1	**0,00005**	2,1	**0,00000**
EF1790		Unknown function	General	YjeF-related protein	1	1	1	0,6	**0,00985**	0,5	**0,00821**	0,7	**0,00177**	0,1	0,67360	0,6	**0,00276**	1,0	**0,00052**
EF1791		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	0,4	0,30290	0,6	**0,00190**	NA	NA	NA	NA	NA	NA	NA	NA
EF1792		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,73890	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1793	*ilvE*	Amino acid biosynthesis	Pyruvate family	branched-chain amino acid aminotransferase	1	1	1	-0,3	0,18830	-0,1	0,22110	-0,1	0,54820	-0,2	0,49250	-0,1	0,73340	0,1	0,62400
EF1794		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,2	**0,00040**	2,8	**0,00000**	0,5	0,12920	0,7	0,03425	NA	NA	NA	NA
EF1796		Cell envelope	Other	lipoprotein, putative	1	1	1	0,5	**0,00653**	3,6	**0,00000**	0,2	0,43230	2,5	**0,00000**	0,5	**0,00927**	3,4	**0,00000**
EF1797		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,06840	-0,2	0,06276	-0,4	0,08370	0,1	0,64310	0,0	0,99310	0,2	0,40940
EF1798		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,35270	0,0	0,85000	-0,2	0,50310	0,5	0,03363	0,0	0,94560	0,0	0,90620
EF1800		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1801		Signal transduction	PTS	PTS system, IIA component	1	1	1	0,7	**0,00717**	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1802		Signal transduction	PTS	PTS system, IID component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1803		Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1804		Signal transduction	PTS	PTS system, IIB component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1805		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 35	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1806	*lacC*	Energy metabolism	Biosynthesis and degradation of polysaccharides	tagatose-6-phosphate kinase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1807	*lacD-2*	Energy metabolism	Biosynthesis and degradation of polysaccharides	tagatose 1,6-diphosphate aldolase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1808		Unknown function	Enzymes of unknown specificity	agaS protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1809		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1810	*gspA-1*	Cellular processes	Adaptations to atypical conditions	general stress protein A	1	1	1	0,6	0,04494	2,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1811	*gspA-2*	Cellular processes	Adaptations to atypical conditions	general stress protein A	1	1	1	1,1	**0,00023**	4,1	**0,00000**	1,3	**0,00001**	NA	NA	NA	NA	2,7	**0,00002**
EF1812		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1813		Unknown function	General	sulfatase domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1814		Transport and binding proteins	Other	drug resistance transporter, EmrB/QacA family protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1815		Regulatory functions	DNA interactions	transcriptional regulator, LysR family, putative	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1816		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	-0,1	0,46100	-0,1	0,56920	0,2	0,42790	0,2	0,32080	NA	NA	NA	NA
EF1817	*sprE*	Protein fate	Degradation of proteins, peptides, and glycopeptides	serine proteinase, V8 family	1	1	0	-0,5	0,02068	0,2	0,15500	NA	NA	NA	NA	NA	NA	NA	NA
EF1818	*gelE*	Cell envelope	Other	coccolysin	1	1	0	-0,5	**0,00633**	-0,2	0,21200	-0,4	0,03869	NA	NA	NA	NA	NA	NA
EF1820	*fsrC*	Signal transduction	Two-component systems	histidine kinase, putative	1	1	0	0,2	0,52410	1,0	**0,00007**	NA	NA	NA	NA	NA	NA	NA	NA
EF1821	*fsrB*	Unknown function	General	agrBfs protein	1	1	0	0,2	0,20280	1,0	**0,00001**	0,3	0,16920	0,2	0,34960	NA	NA	NA	NA
EF1822	*fsrA*	Signal transduction	Two-component systems	response regulator	1	1	0	0,7	**0,00179**	0,8	**0,00002**	0,4	0,13650	0,4	0,23300	NA	NA	NA	NA
EF1823		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	N-acetylmuramoyl-L-alanine amidase, family 4	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1824		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl hydrolase, family 31/fibronectin type III domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1825		Hypothetical proteins	Domain	conserved domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1826		Energy metabolism	Fermentation	alcohol dehydrogenase, zinc-containing	1	1	0	0,6	0,01791	0,1	0,56000	0,1	0,67370	NA	NA	NA	NA	NA	NA
EF1827		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1828		Transport and binding proteins	Other	glycerol uptake facilitator protein, putative	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1829		Signal transduction	PTS	PTS system, IID component	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1830		Signal transduction	PTS	PTS system, IIC component	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1833		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1834	*lacB*	Energy metabolism	Biosynthesis and degradation of polysaccharides	galactose-6-phosphate isomerase, LacB subunit	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1835	*lacA*	Energy metabolism	Biosynthesis and degradation of polysaccharides	galactose-6-phosphate isomerase, LacA subunit	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1836		Signal transduction	PTS	PTS system, IIA component, putative	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1837		Signal transduction	PTS	PTS system, IIB component, putative	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1838		Signal transduction	PTS	PTS system, IIC component	1	1	0	0,5	0,12390	NA	NA	0,3	0,09006	NA	NA	NA	NA	NA	NA
EF1839	*lacR*	Regulatory functions	DNA interactions	lactose phosphotransferase system repressor LacR	1	1	0	0,3	0,28740	0,6	**0,00665**	0,1	0,78660	NA	NA	NA	NA	NA	NA
EF1841		Unknown function	General	HD domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1843		Energy metabolism	Biosynthesis and degradation of polysaccharides	polysaccharide deacetylase family protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1844		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1846		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1847		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	1	0	0	0,2	0,36640	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1848		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1849		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1850		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1851		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 35	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1853		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,15380	0,0	0,96190	NA	NA	NA	NA	NA	NA	NA	NA
EF1855		Mobile and extrachromosomal element functions	Transposon functions	transposase, IS256 family	1	0	0	0,1	0,79610	0,2	0,16200	NA	NA	NA	NA	NA	NA	NA	NA
EF1858	*panD*	Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	aspartate 1-decarboxylase	1	0	0	0,4	0,13910	-1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF1859	*panC*	Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	pantoate--beta-alanine ligase	1	0	0	0,3	0,23890	-0,9	**0,00002**	NA	NA	NA	NA	NA	NA	NA	NA
EF1860	*panB*	Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	3-methyl-2-oxobutanoate hydroxymethyltransferase	1	0	0	0,4	0,03017	-0,4	0,01840	NA	NA	NA	NA	NA	NA	NA	NA
EF1861		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,2	0,41750	-0,6	**0,00070**	NA	NA	NA	NA	NA	NA	NA	NA
EF1863		Signal transduction	Two-component systems	sensor histidine kinase	1	0	0	-0,2	0,63800	-0,3	0,02307	NA	NA	NA	NA	NA	NA	NA	NA
EF1864		Regulatory functions	DNA interactions	DNA-binding response regulator	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1867		Transport and binding proteins	Unknown substrate	permease, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1868		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1869		Transport and binding proteins	Unknown substrate	permease, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1871		Energy metabolism	Electron transport	thioredoxin family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1872		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1874		Mobile and extrachromosomal element functions	Transposon functions	transposase, IS256 family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1875		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1876		Cell envelope	Other	lipoprotein, NLP/P60 family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1877		Cell envelope	Other	membrane protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1878		Unknown function	General	ATP/GTP-binding protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1879		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1880		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1881		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1882		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1883		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1884		Mobile and extrachromosomal element functions	Transposon functions	transposase, IS116/IS110/IS902 family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1885		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1886		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1887		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1888		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1889		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,2	0,39500	0,5	0,01350	NA	NA	NA	NA	NA	NA	NA	NA
EF1890		Hypothetical proteins	Domain	conserved domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1892		Cellular processes	Cell division	FtsK/SpoIIIE family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1893		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1894		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1895		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1896		Cell envelope	Other	cell wall surface anchor family protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1897		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1898	*rplS*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L19	1	1	1	-0,3	0,16770	-0,8	**0,00047**	-1,3	**0,00002**	-0,6	0,18720	-0,4	**0,00414**	-1,9	**0,00000**
EF1899	*trmD*	Protein synthesis	tRNA and rRNA base modification	tRNA (guanine-N1)-methyltransferase	1	1	1	0,0	0,91310	-0,5	**0,00088**	-0,2	0,12650	0,1	0,59310	-0,3	0,03326	-0,2	0,33450
EF1900	*rimM*	Transcription	RNA processing	16S rRNA processing protein RimM	1	1	1	-0,4	0,03544	0,0	0,89100	NA	NA	NA	NA	NA	NA	NA	NA
EF1901		Transport and binding proteins	Cations and iron carrying compounds	Mn2+/Fe2+ transporter, NRAMP family	1	1	1	1,4	**0,00051**	2,5	**0,00000**	1,3	**0,00030**	0,7	**0,00165**	1,8	**0,00005**	1,6	**0,00006**
EF1902		Unknown function	Enzymes of unknown specificity	glyoxylase family protein	1	1	1	0,6	0,02110	1,4	**0,00000**	0,3	0,02946	0,6	**0,00846**	0,7	**0,00121**	1,5	**0,00000**
EF1903		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	0,02526	0,5	0,02374	1,3	**0,00171**	0,0	0,88540	1,0	**0,00026**	0,2	0,44770
EF1904		Fatty acid and phospholipid metabolism	Degradation	glycerophosphoryl diester phosphodiesterase family protein	1	1	1	0,1	0,75230	-0,9	**0,00058**	1,0	**0,00426**	-0,6	0,03767	0,4	0,08858	-0,6	**0,00985**
EF1906		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,11830	0,1	0,48870	-0,8	**0,00168**	-0,1	0,83940	-0,3	0,07486	0,0	0,92290
EF1907		Unknown function	General	maoC family protein	1	1	1	-0,3	0,04904	0,1	0,44800	-0,6	**0,00317**	0,1	0,61860	-0,3	0,02378	-0,3	0,12040
EF1908	*murC*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylmuramate--alanine ligase	1	1	1	-0,1	0,52290	-0,7	**0,00013**	NA	NA	NA	NA	NA	NA	NA	NA
EF1909		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1910		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,34670	0,8	**0,00002**	NA	NA	NA	NA	NA	NA	NA	NA
EF1911		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,38920	0,4	0,02158	0,2	0,44550	0,7	0,09135	0,2	0,44870	1,0	0,02578
EF1912		Unknown function	General	ROK family protein	1	1	1	-0,3	0,23890	-0,6	**0,00311**	-0,1	0,55970	-0,3	0,28030	-0,3	0,06230	-0,2	0,29780
EF1913		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00278	1	1	1	0,2	0,27580	0,0	0,99160	0,1	0,52160	0,1	0,78800	0,0	0,91550	0,1	0,54700
EF1914		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1915		Hypothetical proteins		hypothetical protein	1	1	1	0,8	**0,00125**	1,1	**0,00001**	0,3	0,14120	0,5	0,01772	0,6	**0,00065**	1,5	**0,00000**
EF1916		Unknown function	General	GTP-binding protein	1	1	1	-0,2	0,23980	-0,9	**0,00008**	NA	NA	NA	NA	-0,2	0,60430	NA	NA
EF1917	*clpX*	Protein fate	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, ATP-binding subunit ClpX	1	1	1	-0,4	0,16360	-0,2	0,09392	-0,6	**0,00917**	-0,1	0,66400	-0,4	0,02711	-0,1	0,76840
EF1918		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,22660	-0,1	0,28760	0,1	0,39230	-0,4	0,07876	0,3	0,04376	0,1	0,48020
EF1919		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	1,0	**0,00424**	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1920		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	C4-dicarboxylate anaerobic carrier	1	1	1	0,2	0,22840	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1921		Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	inosine-uridine preferring nucleoside hydrolase	1	1	1	0,4	0,04481	-0,8	**0,00264**	0,4	0,03934	-0,1	0,77110	0,9	**0,00076**	0,7	0,02066
EF1922		Regulatory functions	DNA interactions	transcriptional regulator, LacI/carbohydrate kinase, PfkB	1	1	1	0,0	0,98020	0,1	0,36430	-0,1	0,41220	0,2	0,60220	0,4	0,04672	0,2	0,35470
EF1923		Hypothetical proteins		hypothetical protein	1	1	1	0,4	0,14720	0,4	0,02688	0,4	0,01684	-0,1	0,60880	0,6	0,03089	0,6	0,02912
EF1925		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,06229	0,0	0,76590	-0,3	0,07993	-0,1	0,90290	NA	NA	NA	NA
EF1926		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	-0,1	0,81690	0,4	**0,00710**	NA	NA	NA	NA	NA	NA	NA	NA
EF1927	*glpF*	Transport and binding proteins	Other	glycerol uptake facilitator protein	1	1	1	1,4	**0,00001**	NA	NA	0,9	**0,00012**	NA	NA	1,3	**0,00011**	0,0	0,90110
EF1928		Energy metabolism	Other	alpha-glycerophosphate oxidase	1	1	1	1,3	**0,00001**	NA	NA	1,0	**0,00109**	NA	NA	NA	NA	NA	NA
EF1929	*glpK*	Energy metabolism	Other	glycerol kinase	1	1	1	0,9	**0,00073**	NA	NA	0,5	0,01971	-1,8	**0,00010**	0,6	**0,00150**	NA	NA
EF1931		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,08832	0,4	0,01293	0,1	0,70680	0,2	0,44650	0,4	**0,00893**	0,9	**0,00070**
EF1932		Unknown function	Enzymes of unknown specificity	oxidoreductase, pyridine nucleotide-disulfide family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1933		Hypothetical proteins		hypothetical protein	1	1	1	-0,6	0,02526	2,8	**0,00000**	-1,1	**0,00023**	1,9	**0,00005**	-0,6	0,04091	3,2	**0,00000**
EF1934		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,6	0,06350	1,8	**0,00000**	-1,0	**0,00168**	1,0	**0,00017**	-0,5	**0,00527**	2,0	**0,00000**
EF1935		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1936		Hypothetical proteins		hypothetical protein	1	1	1	0,2	0,38750	0,5	**0,00694**	NA	NA	NA	NA	NA	NA	0,2	0,39320
EF1937		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1938		Transport and binding proteins	Cations and iron carrying compounds	cation-transporting ATPase, E1-E2 family	1	1	1	0,0	0,93950	0,2	0,07829	-0,6	**0,00042**	-0,1	0,72280	0,1	0,75340	NA	NA
EF1939		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,9	**0,00135**	-0,4	0,01517	NA	NA	NA	NA	NA	NA	NA	NA
EF1940		Regulatory functions	Other	cyclic AMP receptor protein, putative	1	1	1	0,8	**0,00066**	1,7	**0,00000**	0,9	**0,00078**	1,4	**0,00054**	0,6	**0,00635**	1,4	**0,00002**
EF1941		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,78010	1,0	**0,00060**	0,3	0,08600	0,9	**0,00277**	0,2	0,38930	1,1	**0,00013**
EF1943		Transport and binding proteins	Other	drug resistance transporter, Bcr/CflA family protein	1	1	1	-0,2	0,30400	0,9	**0,00456**	-0,3	0,49580	0,8	0,01006	0,0	0,84000	0,9	**0,00005**
EF1944		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,13030	-0,2	0,35850	-0,4	0,03064	0,2	0,41370	-0,6	**0,00155**	-0,7	**0,00402**
EF1945		Cell envelope	Other	membrane protein, putative	1	1	1	-0,3	0,12920	0,4	**0,00510**	0,0	0,98450	NA	NA	NA	NA	NA	NA
EF1946		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,03137	-0,3	0,42060	-0,3	0,37980	-0,2	0,37410	0,6	**0,00229**	0,1	0,88070
EF1947		Hypothetical proteins		hypothetical protein	1	1	1	-0,1	0,52390	0,3	0,01075	0,0	0,99560	-0,2	0,21640	0,9	**0,00027**	0,3	0,22010
EF1948		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,97950	1,1	**0,00009**	0,5	0,03724	0,9	**0,00735**	NA	NA	NA	NA
EF1949		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	0,02081	1,6	**0,00000**	0,3	0,23570	NA	NA	0,6	**0,00128**	NA	NA
EF1950	*mphD*	Unknown function	General	mocD family protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1951	*mphC*	Unknown function	General	phosphosugar-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1952	*mphB*	Signal transduction	PTS	PTS system, IID component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1953	*mphA*	Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1955	*mphR*	Regulatory functions	Protein interactions	sigma-54 dependent DNA-binding response regulator	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,4	0,02722	0,6	0,04432
EF1956		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1958		Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	deoxyguanosinetriphosphate triphosphohydrolase, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1959		Hypothetical proteins	Domain	conserved domain protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,8	**0,00402**
EF1961	*eno*	Energy metabolism	Glycolysis/gluconeogenesis	enolase	1	1	1	0,2	0,28880	0,5	**0,00060**	0,0	0,91170	-0,2	0,39740	0,1	0,62560	0,2	0,27790
EF1962	*tpiA*	Energy metabolism	Glycolysis/gluconeogenesis	triosephosphate isomerase	1	1	1	0,0	0,95940	-1,3	**0,00000**	0,1	0,69670	-0,3	0,39590	-0,2	0,31160	-0,1	0,62430
EF1963	*pgk*	Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate kinase	1	1	1	-0,2	0,38600	-0,9	**0,00001**	0,1	0,73260	0,0	0,99520	-0,1	0,63480	-0,3	0,11920
EF1964	*gap-2*	Energy metabolism	Glycolysis/gluconeogenesis	glyceraldehyde 3-phosphate dehydrogenases	1	1	1	0,2	0,21350	-0,1	0,32260	0,1	0,60950	0,2	0,47130	0,2	0,11550	0,6	0,14010
EF1965		Regulatory functions	Other	transcriptional regulator, SorC family	1	1	1	0,7	**0,00243**	0,6	0,01098	0,7	0,06303	0,3	0,30370	0,4	0,04051	0,6	0,20470
EF1966		Unknown function	General	YitT family protein	1	1	1	-0,5	0,03103	-0,3	0,02181	-0,4	0,02391	0,0	0,90960	-0,1	0,44300	-0,3	0,08839
EF1967		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,05175	-0,4	0,01441	NA	NA	NA	NA	NA	NA	NA	NA
EF1968		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	-0,5	**0,00117**	NA	NA	NA	NA	NA	NA	NA	NA
EF1969		Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	phosphomethylpyrimidine kinase, putative	1	1	1	NA	NA	-0,4	0,06779	NA	NA	NA	NA	NA	NA	NA	NA
EF1970	*aspS*	Protein synthesis	tRNA aminoacylation	aspartyl-tRNA synthetase	1	1	1	0,0	0,92350	-1,4	**0,00000**	-0,3	0,28570	-0,3	0,17730	-0,1	0,77140	-0,5	0,04266
EF1971	*hisS*	Protein synthesis	tRNA aminoacylation	histidyl-tRNA synthetase	1	1	1	0,1	0,59940	-0,6	**0,00026**	-0,1	0,77010	-0,2	0,59310	0,1	0,59230	-0,2	0,52530
EF1972		Hypothetical proteins		hypothetical protein	1	1	1	-0,6	0,02784	0,2	0,15230	-0,2	0,16190	-0,3	0,15370	-0,5	**0,00842**	0,0	0,93140
EF1973		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00256	1	1	1	-0,8	**0,00053**	0,0	0,98030	-0,2	0,12620	-0,5	0,07426	-0,4	0,01098	-0,1	0,81270
EF1974	*relA*	Cellular processes	Adaptations to atypical conditions	GTP pyrophosphokinase	1	1	1	-0,1	0,79610	0,0	0,93150	-0,1	0,81800	NA	NA	NA	NA	NA	NA
EF1975		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00046	1	1	1	-0,3	0,24080	-0,6	**0,00606**	-0,1	0,68850	NA	NA	NA	NA	NA	NA
EF1976	*prmA*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L11 methyltransferase	1	1	1	-0,2	0,22590	-1,2	**0,00001**	-0,2	0,35420	-0,2	0,51690	-0,2	0,21070	-0,4	0,12630
EF1977		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,81490	-0,9	**0,00002**	-0,2	0,20830	-0,3	0,23370	-0,2	0,35440	-0,7	**0,00746**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF1978		DNA metabolism	DNA replication, recombination, and repair	DNA-3-methyladenine glycosylase	1	1	1	0,0	0,90210	-0,8	**0,00007**	-0,2	0,39270	-0,3	0,40830	-0,1	0,73050	-0,4	0,25990
EF1979		Unknown function	General	ATPase, AAA family	1	1	1	0,5	0,02008	0,4	**0,00259**	0,5	**0,00915**	0,4	0,12840	0,3	0,07161	1,5	**0,00000**
EF1980		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	**0,00346**	-0,8	**0,00010**	0,0	0,99420	0,1	0,65970	0,0	0,96600	-0,3	0,20360
EF1981		Hypothetical proteins		hypothetical protein	1	1	1	1,0	**0,00043**	1,5	**0,00000**	1,0	**0,00165**	0,6	0,06255	1,5	**0,00001**	1,7	**0,00006**
EF1982		Cellular processes	Adaptations to atypical conditions	universal stress protein family	1	1	1	1,1	**0,00023**	1,6	**0,00000**	1,4	**0,00004**	0,5	0,16930	1,6	**0,00000**	2,3	**0,00000**
EF1983	*ackA*	Energy metabolism	Fermentation	acetate kinase	1	1	1	-0,8	**0,00043**	-1,8	**0,00000**	-1,4	**0,00000**	-0,7	0,02773	-0,7	**0,00073**	-1,0	**0,00431**
EF1985		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1986	*comG6*	Cellular processes	DNA transformation	competence protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1987		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1988		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1989	*hemH*	Biosynthesis of cofactors, prosthetic groups, carriers	Heme, porphyrin, and cobalamin	ferrochelatase	1	0	0	-0,2	0,47290	-0,4	**0,00437**	NA	NA	NA	NA	NA	NA	NA	NA
EF1990		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1991	*cspC*	Cellular processes	Adaptations to atypical conditions	cold shock protein CspC	1	1	0	0,0	0,96860	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1992		Mobile and extrachromosomal element functions	Prophage functions	endolysin	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1993		Mobile and extrachromosomal element functions	Prophage functions	holin	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1994		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF1995		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2001		Mobile and extrachromosomal element functions	Prophage functions	minor structural protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2002		Mobile and extrachromosomal element functions	Prophage functions	tail protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2003		Mobile and extrachromosomal element functions	Prophage functions	tape measure protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2004		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2005		Mobile and extrachromosomal element functions	Prophage functions	major tail protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2006		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2007		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2008		Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L23, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2010		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2011		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2012		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2013		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2014		Unknown function	General	coenzyme F420 hydrogenase domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2015		Mobile and extrachromosomal element functions	Prophage functions	minor head protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2016		Mobile and extrachromosomal element functions	Prophage functions	portal protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2017		Mobile and extrachromosomal element functions	Prophage functions	terminase, large subunit, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2018		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2019		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,39320	0,1	0,32430	NA	NA	NA	NA	NA	NA	NA	NA
EF2020		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	0,5	0,02596	NA	NA	NA	NA	NA	NA	NA	NA
EF2021		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2022		Hypothetical proteins	Domain	conserved domain protein	1	1	0	0,6	**0,00580**	-0,3	**0,00526**	NA	NA	NA	NA	NA	NA	NA	NA
EF2023		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2024		Regulatory functions	DNA interactions	transcriptional regulator, ArpU family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2025		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2027		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2028		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2031		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2032		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2033		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2034		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2036		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2037		Regulatory functions	Other	antirepressor, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2038		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2039		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2040		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	0,6	**0,00786**	0,3	0,07524	NA	NA	NA	NA	NA	NA	NA	NA
EF2041		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,19670	-0,2	0,22610	NA	NA	NA	NA	NA	NA	NA	NA
EF2042		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,5	0,06764	0,0	0,78840	NA	NA	NA	NA	NA	NA	NA	NA
EF2043		Mobile and extrachromosomal element functions	Prophage functions	site-specific recombinase, phage integrase family	1	0	0	0,2	0,31010	0,0	0,95920	NA	NA	NA	NA	NA	NA	NA	NA
EF2044	*comG3*	Cellular processes	DNA transformation	competence protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2045	*comG2*	Cellular processes	DNA transformation	competence protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2046	*comG1*	Cellular processes	DNA transformation	competence protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2047		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	-0,6	**0,00138**	0,3	0,02256	-1,0	**0,00210**	-0,2	0,32030	-0,4	0,01881	0,0	0,90110
EF2048		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00048	1	1	1	-0,3	0,14560	-0,5	0,06286	NA	NA	NA	NA	NA	NA	NA	NA
EF2049		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein, putative	1	1	1	0,3	0,05075	-0,2	0,20850	NA	NA	NA	NA	NA	NA	NA	NA
EF2050		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2051		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,2	0,23740	-0,2	0,13480	NA	NA	NA	NA	NA	NA	NA	NA
EF2052		Cellular processes	Cell division	cell division protein, FtsK/SpoIIIE family	1	1	1	-0,7	**0,00163**	-0,4	**0,00111**	-0,5	0,01716	0,3	0,23800	-0,3	0,06210	-0,6	**0,00247**
EF2055		Unknown function	Enzymes of unknown specificity	oxidoreductase, pyridine nucleotide-disulfide family	1	1	1	-0,7	**0,00135**	1,4	**0,00000**	-0,8	**0,00004**	1,5	**0,00000**	-0,9	**0,00018**	0,8	**0,00461**
EF2056		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative	1	1	1	-0,3	0,08778	0,3	0,02050	-0,6	**0,00284**	0,0	0,96720	-0,1	0,47320	0,4	0,18540
EF2057		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	heptaprenyl diphosphate synthase, component II, putative	1	1	1	0,1	0,61080	0,0	0,90040	-0,6	**0,00621**	0,7	**0,00387**	-0,1	0,54920	0,3	0,10090
EF2058		Energy metabolism	Electron transport	transport ATP-binding protein CydD, putative	1	1	1	-0,6	0,05216	0,0	0,97940	-0,4	0,17390	0,0	0,89240	-0,5	0,05168	0,1	0,56570
EF2059		Energy metabolism	Electron transport	transport ATP-binding protein CydC, putative	1	1	1	-0,4	0,02279	-0,4	0,04389	0,0	0,95600	0,1	0,85360	-0,3	0,05864	0,0	0,90320
EF2060	*cydB*	Energy metabolism	Electron transport	cytochrome d ubiquinol oxidase, subunit II	1	1	1	-0,1	0,54120	0,8	**0,00039**	0,1	0,58840	0,3	0,11930	0,1	0,77460	0,4	0,02919
EF2061	*cydA*	Energy metabolism	Electron transport	cytochrome d ubiquinol oxidase, subunit I	1	1	1	-0,1	0,60530	0,3	0,15380	0,4	0,05606	0,1	0,57950	0,1	0,43550	-0,2	0,26680
EF2062		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2063		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	-0,5	0,01231	0,0	0,98710	-0,5	0,12150	NA	NA	NA	NA	NA	NA
EF2064	*topB-1*	DNA metabolism	DNA replication, recombination, and repair	DNA topoisomerase III	1	1	1	-0,5	0,01614	0,3	0,04053	-0,7	**0,00062**	0,0	0,91880	-0,5	0,03124	0,0	0,88370
EF2065		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,24830	1,1	**0,00000**	-0,5	0,02812	0,6	0,01821	0,5	0,02207	1,3	**0,00289**
EF2066		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	NA	NA	0,4	**0,00678**	0,1	0,76010	0,2	0,22230	0,4	0,05228	0,4	0,19760
EF2067		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00481	1	1	1	2,4	**0,00000**	3,7	**0,00000**	3,2	**0,00000**	2,8	**0,00000**	2,2	**0,00000**	2,8	**0,00000**
EF2068		Transport and binding proteins	Other	multidrug resistance protein, putative	1	1	1	1,9	**0,00000**	3,5	**0,00000**	2,8	**0,00000**	2,4	**0,00000**	2,2	**0,00000**	2,8	**0,00000**
EF2069		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2070	*trmU*	Protein synthesis	tRNA and rRNA base modification	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1	1	1	-0,5	0,02686	0,3	0,08771	-0,3	0,03991	NA	NA	-0,1	0,68920	0,3	0,17700
EF2071		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,84880	0,3	0,02123	-0,3	0,16720	0,1	0,53450	0,3	0,14450	0,4	0,12360
EF2072		Unknown function	Enzymes of unknown specificity	aminotransferase, class V	1	1	1	0,2	0,23330	1,1	**0,00000**	-0,1	0,42540	0,5	0,02416	0,4	0,01131	0,9	**0,00044**
EF2073	*prsA-1*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	ribose-phosphate pyrophosphokinase	1	1	1	0,3	0,16210	0,2	0,08837	0,1	0,64460	0,3	0,08846	0,2	0,10460	0,5	0,01308

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2074	*efaC*	Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	2,8	**0,00000**	3,0	**0,00000**	3,1	**0,00000**	3,1	**0,00000**	3,7	**0,00000**	3,4	**0,00000**
EF2075	*efaB*	Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	2,7	**0,00000**	3,5	**0,00000**	3,0	**0,00000**	3,7	**0,00000**	3,6	**0,00000**	3,4	**0,00000**
EF2076	*efaA*	Cellular processes	Cell adhesion	endocarditis specific antigen	1	1	1	2,3	**0,00004**	2,9	**0,00000**	2,8	**0,00001**	3,4	**0,00000**	3,0	**0,00000**	3,2	**0,00000**
EF2077		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,3	0,22680	NA	NA	-0,1	0,74670	NA	NA	NA	NA	NA	NA
EF2078		Hypothetical proteins		hypothetical protein	1	1	1	0,2	0,26770	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2079		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2080		Cell envelope	Other	lipoprotein, YaeC family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2081		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2082		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2083		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,04413	0,0	0,68480	NA	NA	NA	NA	NA	NA	NA	NA
EF2084		Hypothetical proteins		hypothetical protein	1	0	1	0,0	0,99960	NA	NA	-0,4	0,03882	NA	NA	NA	NA	NA	NA
EF2085		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-1,3	**0,00007**	-0,9	**0,00040**	NA	NA	NA	NA	NA	NA	NA	NA
EF2086		Mobile and extrachromosomal element functions	Prophage functions	endolysin	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2087		Mobile and extrachromosomal element functions	Prophage functions	holin	1	0	0	-0,4	0,14360	0,0	0,74230	NA	NA	NA	NA	NA	NA	NA	NA
EF2088		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,1	0,66670	NA	NA	NA	NA	NA	NA	NA	NA
EF2089		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2090		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,73320	-0,2	0,14210	NA	NA	NA	NA	NA	NA	NA	NA
EF2091		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,18830	-0,6	**0,00272**	NA	NA	NA	NA	NA	NA	NA	NA
EF2092		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,3	0,01600	NA	NA	NA	NA	NA	NA	NA	NA
EF2093		Unknown function	General	endolysin domain protein	1	0	0	-0,2	0,27710	-0,6	**0,00323**	NA	NA	NA	NA	NA	NA	NA	NA
EF2094		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,2	0,29650	NA	NA	NA	NA	NA	NA	NA	NA
EF2095		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2096		Mobile and extrachromosomal element functions	Prophage functions	tail protein	1	0	0	NA	NA	-0,7	**0,00013**	NA	NA	NA	NA	NA	NA	NA	NA
EF2097		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,3	0,09914	NA	NA	NA	NA	NA	NA	NA	NA
EF2098		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,2	0,50510	NA	NA	NA	NA	NA	NA	NA	NA
EF2099		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,5	**0,00105**	NA	NA	NA	NA	NA	NA	NA	NA
EF2100		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2101		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,16500	-0,6	**0,00018**	NA	NA	NA	NA	NA	NA	NA	NA
EF2102		Hypothetical proteins		hypothetical protein	1	0	0	-0,3	0,20880	-0,7	**0,00013**	NA	NA	NA	NA	NA	NA	NA	NA
EF2103		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,3	0,08264	NA	NA	NA	NA	NA	NA	NA	NA
EF2104		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,76950	-0,7	**0,00675**	NA	NA	NA	NA	NA	NA	NA	NA
EF2105		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,96860	-0,8	**0,00156**	NA	NA	NA	NA	NA	NA	NA	NA
EF2106		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	-0,5	**0,00710**	NA	NA	NA	NA	NA	NA	NA	NA
EF2107		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,97030	-0,6	**0,00079**	NA	NA	NA	NA	NA	NA	NA	NA
EF2108		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,82580	-0,4	**0,00679**	NA	NA	NA	NA	NA	NA	NA	NA
EF2109		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,1	0,67170	-0,5	0,01507	NA	NA	NA	NA	NA	NA	NA	NA
EF2110		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,34900	-0,5	**0,00104**	NA	NA	NA	NA	NA	NA	NA	NA
EF2111		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,95750	-0,1	0,44800	NA	NA	NA	NA	NA	NA	NA	NA
EF2112		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2113		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2114		Mobile and extrachromosomal element functions	Prophage functions	adenine methyltransferase, putative	1	0	0	NA	NA	-0,1	0,62710	NA	NA	NA	NA	NA	NA	NA	NA
EF2115		Regulatory functions	DNA interactions	transcriptional regulator, ArpU family	1	0	0	-0,1	0,73000	0,2	0,16640	NA	NA	NA	NA	NA	NA	NA	NA
EF2116		Hypothetical proteins		hypothetical protein	1	0	1	0,1	0,90200	0,2	0,18420	NA	NA	NA	NA	NA	NA	NA	NA
EF2117		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,82120	-0,6	**0,00442**	NA	NA	NA	NA	NA	NA	NA	NA
EF2118		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,0	0,96790	-0,4	**0,00688**	NA	NA	NA	NA	NA	NA	NA	NA
EF2119		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,86970	0,1	0,46620	NA	NA	NA	NA	NA	NA	NA	NA
EF2120		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,79050	0,2	0,27990	NA	NA	NA	NA	NA	NA	NA	NA
EF2121		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,98500	-0,2	0,15810	NA	NA	NA	NA	NA	NA	NA	NA
EF2122		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,94280	-0,5	0,01618	NA	NA	NA	NA	NA	NA	NA	NA
EF2123		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,49960	-0,7	**0,00011**	NA	NA	NA	NA	NA	NA	NA	NA
EF2124		Mobile and extrachromosomal element functions	Prophage functions	methyltransferase, putative	1	0	0	0,1	0,75690	0,0	0,87650	NA	NA	NA	NA	NA	NA	NA	NA
EF2125		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,75920	0,2	0,06500	NA	NA	NA	NA	NA	NA	NA	NA
EF2126		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,64720	0,1	0,35970	NA	NA	NA	NA	NA	NA	NA	NA
EF2127		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,38750	0,1	0,74790	NA	NA	NA	NA	NA	NA	NA	NA
EF2128		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,1	0,59430	0,2	0,20510	NA	NA	NA	NA	NA	NA	NA	NA
EF2129		Mobile and extrachromosomal element functions	Prophage functions	DNA replication protein, putative	1	0	0	0,1	0,58800	0,1	0,42420	NA	NA	NA	NA	NA	NA	NA	NA
EF2130		Unknown function	General	DnaD domain protein	1	0	0	0,4	0,06204	0,3	0,04584	NA	NA	NA	NA	NA	NA	NA	NA
EF2131		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	1,3	**0,00002**	1,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2132		Mobile and extrachromosomal element functions	Prophage functions	recT protein, putative	1	0	1	0,4	0,09791	0,7	0,01744	NA	NA	NA	NA	NA	NA	NA	NA
EF2133		Hypothetical proteins		hypothetical protein	1	0	0	0,6	**0,00096**	0,7	**0,00012**	NA	NA	NA	NA	NA	NA	NA	NA
EF2134		Hypothetical proteins		hypothetical protein	1	0	0	0,6	**0,00226**	0,9	**0,00004**	NA	NA	NA	NA	NA	NA	NA	NA
EF2135		Hypothetical proteins		hypothetical protein	1	0	0	0,6	**0,00626**	0,5	**0,00077**	NA	NA	NA	NA	NA	NA	NA	NA
EF2136		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,05769	-0,1	0,29050	NA	NA	NA	NA	NA	NA	NA	NA
EF2137		Hypothetical proteins		hypothetical protein	1	0	0	0,5	0,02325	0,5	**0,00096**	NA	NA	NA	NA	NA	NA	NA	NA
EF2138		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	0,4	0,05555	0,5	**0,00303**	NA	NA	NA	NA	NA	NA	NA	NA
EF2139		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,14360	0,6	**0,00093**	NA	NA	NA	NA	NA	NA	NA	NA
EF2140		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,4	0,12250	0,5	**0,00734**	NA	NA	NA	NA	NA	NA	NA	NA
EF2141		Mobile and extrachromosomal element functions	Prophage functions	transcriptional regulator, Cro/CI family	1	0	0	0,8	0,01531	0,8	**0,00410**	NA	NA	NA	NA	NA	NA	NA	NA
EF2142		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	1,3	**0,00001**	1,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2143		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,9	**0,00021**	0,9	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF2144		Cell envelope	Other	lipoprotein, putative	1	0	0	0,9	**0,00009**	1,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2145		Mobile and extrachromosomal element functions	Prophage functions	site-specific recombinase, phage integrase family	1	0	0	1,0	**0,00119**	1,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2146		Cell envelope	Other	membrane protein, putative	1	1	1	-0,4	0,17400	-1,2	**0,00000**	0,1	0,65530	-0,1	0,73260	-0,1	0,42760	-0,3	0,07484
EF2147		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,48300	0,6	**0,00088**	-0,1	0,54630	0,1	0,85360	0,0	0,96520	-0,3	0,27790
EF2148		Hypothetical proteins		hypothetical protein	1	1	1	-1,4	**0,00043**	-0,9	**0,00013**	-1,3	**0,00004**	-2,1	**0,00007**	-0,8	**0,00118**	-1,2	**0,00001**
EF2149		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,11410	-0,6	**0,00708**	-0,9	**0,00273**	-1,8	**0,00004**	-0,4	**0,00953**	-0,9	**0,00032**
EF2150		Cellular processes	Toxin production and resistance	FemAB family protein	1	1	1	-0,2	0,18380	-0,5	**0,00604**	-1,0	**0,00110**	-2,0	**0,00001**	-0,5	**0,00699**	-1,1	**0,00003**
EF2151	*glmS*	Central intermediary metabolism	Amino sugars	glucosamine--fructose-6-phosphate aminotransferase, isomerizing	1	1	1	-2,7	**0,00000**	-5,5	**0,00000**	-2,1	**0,00000**	-4,0	**0,00000**	-2,5	**0,00000**	-3,0	**0,00000**
EF2152		Transport and binding proteins	Cations and iron carrying compounds	cobalt transport family protein	1	1	1	-0,8	**0,00109**	-2,6	**0,00000**	-1,2	**0,00068**	-1,0	**0,00183**	-1,1	**0,00011**	-2,1	**0,00000**
EF2153		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,8	0,02299	-2,3	**0,00000**	-1,2	**0,00004**	-1,2	**0,00033**	-0,7	**0,00012**	-2,0	**0,00000**
EF2154		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	0,02387	-0,9	**0,00483**	-1,0	**0,00209**	-0,6	0,01700	-0,4	0,08218	-1,6	**0,00000**
EF2156		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,19040	0,4	0,01119	0,1	0,61580	-0,2	0,28190	0,1	0,48980	0,0	0,88240
EF2157		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00159	1	1	1	0,1	0,57540	0,6	**0,00060**	0,3	0,12900	0,3	0,32630	0,2	0,13400	0,5	**0,00357**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2158		Energy metabolism	Electron transport	pyruvate ferredoxin/flavodoxin oxidoreductase family protein	1	1	1	0,2	0,24330	-0,7	**0,00023**	-0,3	0,05898	-0,7	**0,00445**	-0,2	0,09414	-0,3	0,12380
EF2159	*glnA*	Amino acid biosynthesis	Glutamate family	glutamine synthetase, type I	1	1	1	0,4	0,04543	-1,1	**0,00001**	0,6	0,03724	-2,6	**0,00000**	0,2	0,10950	-0,8	**0,00020**
EF2160	*glnR*	Regulatory functions	DNA interactions	regulatory protein GlnR	1	1	1	0,8	**0,00091**	-1,4	**0,00000**	0,7	**0,00108**	-2,5	**0,00000**	0,6	**0,00069**	-0,6	**0,00485**
EF2161		Unknown function	General	GTP-binding protein	1	1	1	-0,9	**0,00072**	-0,7	**0,00002**	-0,8	0,02207	-0,7	0,02652	-0,9	**0,00005**	-1,4	**0,00001**
EF2162	*miaA*	Protein synthesis	tRNA and rRNA base modification	tRNA delta(2)-isopentenylpyrophosphate transferase	1	1	1	-0,4	0,01311	-0,3	0,07755	-0,6	**0,00175**	-0,5	0,03310	-0,6	**0,00354**	-1,0	**0,00335**
EF2163		Fatty acid and phospholipid metabolism	Degradation	glycerophosphoryl diester phosphodiesterase, putative	1	1	1	-0,5	0,02092	0,0	0,91770	-0,2	0,19160	-0,4	0,08397	-0,4	0,01635	-0,8	**0,00036**
EF2164		Cell envelope	Other	membrane protein, putative	1	0	0	-0,4	0,17810	-0,9	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2165		Energy metabolism	Sugars	NAD-dependent epimerase/dehydratase family protein	1	0	1	-0,6	0,01370	-0,8	**0,00001**	-0,6	**0,00848**	-0,8	**0,00065**	-0,8	**0,00058**	-1,4	**0,00000**
EF2166		Cell envelope	Other	membrane protein, putative	1	0	0	-1,3	**0,00009**	-1,7	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2167		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	0	0	-1,1	**0,00119**	-2,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2168		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	licD1 protein, putative	1	0	0	-1,1	**0,00025**	-1,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2169		Cell envelope	Other	membrane protein, putative	1	0	0	-1,0	**0,00577**	-1,0	**0,00100**	NA	NA	NA	NA	NA	NA	NA	NA
EF2170		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	0	0	-0,6	0,02299	-1,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2171		Unknown function	Enzymes of unknown specificity	epimerase/dehydratase, putative	1	0	0	-0,9	**0,00026**	-1,7	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2172	*ispD*	Hypothetical proteins	Conserved	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	1	0	1	-0,8	**0,00108**	-1,8	**0,00000**	NA	NA	NA	NA	-0,8	**0,00598**	-1,3	**0,00021**
EF2173		Mobile and extrachromosomal element functions	Transposon functions	ISEf1, transposase	1	0	0	-0,1	0,49130	0,0	0,87110	NA	NA	NA	NA	NA	NA	NA	NA
EF2174		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,9	**0,00088**	-0,4	0,03776	-0,5	0,02439	-0,3	0,27490	-1,0	**0,00141**	-0,9	**0,00051**
EF2175		Unknown function	General	licD-related protein	1	0	1	-0,8	**0,00127**	-0,9	**0,00007**	NA	NA	NA	NA	-1,0	**0,00010**	-0,5	**0,00707**
EF2176		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-0,8	**0,00050**	-1,0	**0,00067**	-1,7	**0,00000**	-0,3	0,19810	-1,1	**0,00043**	-0,5	**0,00937**
EF2177	*epaR*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	bacterial sugar transferase	1	1	1	-1,1	**0,00033**	-0,6	0,02374	-0,6	0,05140	-0,3	0,27540	-0,8	**0,00413**	-1,6	**0,00001**
EF2178	*epaQ*	Cell envelope	Other	membrane protein, putative	1	1	1	-1,3	**0,00003**	-1,9	**0,00000**	-0,9	**0,00012**	-1,2	**0,00004**	-0,5	**0,00701**	-2,1	**0,00000**
EF2179	*epaP*	Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-2,5	**0,00000**	-3,6	**0,00000**	-1,2	**0,00053**	-0,9	**0,00032**	-1,0	**0,00001**	-2,7	**0,00000**
EF2180	*epaO*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-1,4	**0,00019**	-1,5	**0,00000**	-0,8	**0,00086**	-0,5	0,01093	-0,6	**0,00085**	-1,6	**0,00000**
EF2181	*epaN*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-0,8	**0,00473**	-2,1	**0,00000**	-0,5	**0,00574**	-0,7	**0,00261**	-0,9	**0,00002**	-1,7	**0,00001**
EF2182	*epaM*	Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,9	**0,00047**	-1,5	**0,00000**	-0,2	0,10190	-0,5	0,01920	-0,9	**0,00002**	-2,1	**0,00000**
EF2183	*epaL*	Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-0,9	**0,00028**	-1,9	**0,00000**	-0,5	0,03882	-0,4	0,11020	-1,1	**0,00106**	-2,3	**0,00000**
EF2184	*epaK*	Hypothetical proteins		hypothetical protein	1	1	1	-0,7	**0,00214**	-1,6	**0,00000**	-1,2	**0,00011**	-0,5	0,10110	-0,8	**0,00077**	-1,8	**0,00002**
EF2186		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-1,2	**0,00005**	-2,9	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2188		Unknown function	General	racemase domain protein	1	0	0	-1,2	**0,00004**	-1,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2189	*epaJ*	Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,2	**0,00135**	-2,2	**0,00000**	-1,1	**0,00002**	-0,3	0,26560	-0,9	**0,00014**	-1,4	**0,00004**
EF2190	*epaI*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-1,1	**0,00019**	-2,0	**0,00000**	-0,9	**0,00066**	-0,4	0,01427	-0,6	**0,00042**	-1,6	**0,00001**
EF2191	*epaH*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	dTDP-4-dehydrorhamnose reductase	1	1	1	-1,0	**0,00089**	-1,5	**0,00002**	-0,7	**0,00058**	-0,4	0,02885	-0,8	**0,00015**	-1,5	**0,00000**
EF2192	*epaG*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	dTDP-glucose 4,6-dehydratase	1	1	1	-0,7	**0,00311**	-0,2	0,14210	-0,5	0,01835	0,1	0,81160	-0,8	**0,00007**	-0,2	0,42280
EF2193	*epaF*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	dTDP-4-dehydrorhamnose 3,5-epimerase	1	1	1	-0,7	**0,00060**	-0,3	0,07620	-0,7	**0,00046**	-0,3	0,08355	-0,6	**0,00029**	-0,9	**0,00006**
EF2194	*epaE*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glucose-1-phosphate thymidylyltransferase	1	1	1	-0,9	**0,00862**	-1,1	**0,00004**	-0,7	**0,00020**	-0,6	**0,00746**	-0,9	**0,00002**	-1,8	**0,00000**
EF2195	*epaD*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-1,2	**0,00002**	-1,7	**0,00000**	-0,5	0,01822	-0,5	**0,00757**	-0,9	**0,00001**	-1,2	**0,00001**
EF2196	*epaC*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-1,0	**0,00022**	-0,3	0,12900	-0,4	0,03358	-0,6	0,03462	-0,5	**0,00165**	-0,5	**0,00836**
EF2197	*epaB*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	-0,9	**0,00050**	-0,3	0,01175	-0,4	0,03259	-0,2	0,16230	-0,5	**0,00040**	-0,5	**0,00596**
EF2198	*epaA*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 4 family protein	1	1	1	-0,8	**0,00036**	-0,9	**0,00004**	-0,5	0,05471	-0,7	0,02963	-0,5	**0,00128**	-1,0	**0,00002**
EF2199	*yihY*	Transcription	RNA processing	YihY family protein	1	1	1	-0,5	**0,00698**	-0,1	0,48840	-0,4	0,03860	-0,4	0,12040	-0,5	**0,00030**	-0,4	0,05023
EF2200	*map*	Protein fate	Protein modification and repair	methionine aminopeptidase, type I	1	1	1	0,5	**0,00703**	0,4	**0,00412**	0,1	0,57500	0,0	0,95780	0,3	0,03411	0,6	**0,00322**
EF2201		Energy metabolism	Electron transport	flavodoxin	1	1	1	-0,4	0,02162	-0,8	**0,00006**	-0,6	**0,00260**	-0,7	**0,00106**	-0,5	**0,00112**	-0,8	**0,00212**
EF2202		Regulatory functions	Other	tspO protein, putative	1	1	1	1,0	**0,00029**	2,8	**0,00000**	0,7	0,01256	0,9	0,01432	0,6	0,01090	1,7	**0,00001**
EF2203		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	0,3	0,06439	1,8	**0,00000**	0,5	**0,00232**	0,6	**0,00265**	0,7	**0,00068**	1,8	**0,00001**
EF2205		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,8	**0,00025**	-0,2	0,58680	-0,5	0,01191	-0,5	0,03972
EF2206		Unknown function	Enzymes of unknown specificity	cytidine/deoxycytidylate deaminase family protein	1	1	1	-0,3	0,08392	0,1	0,37720	-0,4	0,02548	0,2	0,32620	-0,2	0,28860	-0,1	0,76840
EF2207		Regulatory functions	DNA interactions	DNA-binding protein, Fis family	1	1	1	-0,6	**0,00733**	-1,7	**0,00000**	-0,3	0,07448	-0,5	0,02407	-0,5	**0,00639**	-1,3	**0,00003**
EF2208		Cellular processes	Toxin production and resistance	phenazine biosynthesis protein PhzF family	1	1	1	-0,7	**0,00745**	-1,8	**0,00000**	-0,4	0,07944	-0,5	0,10290	-0,4	**0,00946**	-0,8	**0,00030**
EF2209		Hypothetical proteins		hypothetical protein	1	1	1	1,1	**0,00013**	3,1	**0,00000**	0,2	0,23130	0,4	0,20180	0,9	**0,00108**	2,2	**0,00000**
EF2210		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,20030	0,2	0,30090	0,0	0,89940	0,0	0,89240	0,2	0,33120	0,1	0,68070
EF2211		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01655	1	1	1	0,1	0,68840	0,0	0,99920	-0,2	0,22290	-0,8	0,01231	0,1	0,57070	0,2	0,26870
EF2212		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	0,02927	-1,7	**0,00000**	-0,4	0,13080	-0,9	0,02299	-0,6	**0,00329**	-1,4	0,03903
EF2213		Signal transduction	PTS	PTS system, IIBC components	1	1	1	-0,5	0,13820	-2,3	**0,00000**	-0,5	0,01800	-1,5	0,01046	-0,5	0,16680	-2,3	**0,00002**
EF2214		Unknown function	Enzymes of unknown specificity	glyoxylase family protein	1	1	1	-0,2	0,33110	-0,1	0,60320	-0,5	0,02110	0,3	0,40750	-0,5	**0,00544**	-0,7	0,01231
EF2215		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,24100	0,4	**0,00340**	-0,4	**0,00957**	0,7	**0,00273**	-0,2	0,34560	-0,3	0,08636
EF2216		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,1	0,63630	-0,6	0,02961	-0,4	0,43000	0,0	0,98390	-0,5	0,03443	-0,9	**0,00836**
EF2217		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	alpha-1,2-mannosidase, putative	1	1	1	0,1	0,66090	-1,1	**0,00001**	-0,1	0,59080	-0,4	0,10430	0,1	0,64370	-0,9	**0,00119**
EF2218		Regulatory functions	DNA interactions	DNA-binding response regulator, AraC family	1	1	1	-0,5	0,01635	-0,6	**0,00004**	-0,1	0,58980	0,1	0,84180	0,0	0,95770	-0,7	**0,00487**
EF2219		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	-0,6	0,01261	-0,6	**0,00020**	0,0	0,85270	0,0	0,99590	-0,1	0,47240	-0,5	0,05500
EF2220		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,39740	NA	NA	-0,2	0,56400	NA	NA	0,2	0,49240	-0,2	0,65990
EF2221		Transport and binding proteins	Unknown substrate	ABC transporter, substrate-binding protein	1	1	1	0,2	0,46320	0,5	0,01743	0,0	0,83250	0,5	0,01937	0,5	0,01887	0,2	0,68590
EF2222		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	0,6	0,01519	-0,5	0,08252	0,1	0,41550	-0,2	0,64310	0,9	**0,00041**	0,0	0,95740
EF2223		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	0,4	0,06950	NA	NA	0,2	0,30130	NA	NA	0,7	**0,00617**	0,0	0,97300
EF2224		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	-0,6	0,04270	NA	NA	NA	NA	NA	NA
EF2225		Regulatory functions	DNA interactions	transcriptional regulator, MerR family	1	1	1	0,1	0,84120	-0,4	**0,00655**	-0,4	0,03514	0,1	0,68230	0,2	0,10380	-0,3	0,13050
EF2226		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-1,2	**0,00017**	-0,5	**0,00317**	NA	NA	NA	NA	NA	NA	-0,7	**0,00360**
EF2227		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,7	**0,00861**	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2228		Protein synthesis	tRNA aminoacylation	tryptophanyl-tRNA synthetase	1	1	1	-0,1	0,55900	-0,5	**0,00507**	0,0	0,75700	-0,3	0,09942	-0,8	**0,00015**	-0,1	0,58920
EF2229		Hypothetical proteins	Domain	conserved domain protein	1	1	0	NA	NA	NA	NA	0,0	0,96550	NA	NA	NA	NA	NA	NA
EF2230		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	0,1	0,70330	NA	NA	NA	NA	NA	NA
EF2231		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	0,3	0,12580	NA	NA	NA	NA	NA	NA
EF2232		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	0	NA	NA	NA	NA	0,8	**0,00984**	NA	NA	NA	NA	NA	NA
EF2233		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	0	NA	NA	NA	NA	0,6	0,02709	NA	NA	NA	NA	NA	NA
EF2234		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	sugar ABC transporter, sugar-binding protein, putative	1	1	0	NA	NA	NA	NA	0,6	0,10500	NA	NA	NA	NA	NA	NA
EF2235		Energy metabolism	Biosynthesis and degradation of polysaccharides	glucuronyl hydrolase, putative	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2236		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2237		Cell envelope	Other	lipoprotein, putative	1	1	0	NA	NA	NA	NA	0,0	0,92290	NA	NA	NA	NA	NA	NA
EF2238		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	0	0,7	**0,00094**	0,8	**0,00005**	0,5	**0,00555**	0,5	0,04277	NA	NA	NA	NA
EF2239		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	0,4	0,10040	NA	NA	NA	NA	NA	NA
EF2240		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	1	0	0	0,3	0,41510	0,8	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF2241		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,3	0,11750	1,3	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF2243		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2244		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2245		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,2	0,39780	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2247		Regulatory functions	Other	transcriptional regulator	1	0	0	0,3	0,18520	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2248		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2249		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2250		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2251		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2252		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2253		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2254		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2255		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2257		Signal transduction	PTS	PTS system, IIC component, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2258		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2259		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	0	0	0,0	0,88500	0,1	0,36260	NA	NA	NA	NA	NA	NA	NA	NA
EF2260		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,1	0,73310	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2261		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2262		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2263		Central intermediary metabolism	Other	gluconate 5-dehydrogenase, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2264	*kdul-2*	Energy metabolism	Biosynthesis and degradation of polysaccharides	4-deoxy-l-threo-5-hexosulose-uronate ketol-isomerase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2265		Energy metabolism	Sugars	carbohydrate kinase, pfkB family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2266		Energy metabolism	Entner-Doudoroff	2-dehydro-3-deoxyphosphogluconate aldolase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2267		Signal transduction	PTS	PTS system, IIA component	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2268		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2269		Signal transduction	PTS	PTS system, IID component	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2270		Signal transduction	PTS	PTS system, IIC component	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2271		Signal transduction	PTS	PTS system, IIB component	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2272		Energy metabolism	Biosynthesis and degradation of polysaccharides	glucuronyl hydrolase, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2273		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	0	0	0,1	0,83420	0,6	**0,00473**	NA	NA	NA	NA	NA	NA	NA	NA
EF2275		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,19580	0,3	0,06369	NA	NA	NA	NA	NA	NA	NA	NA
EF2276		Hypothetical proteins		hypothetical protein	1	0	0	0,5	0,01424	0,8	**0,00008**	NA	NA	NA	NA	NA	NA	NA	NA
EF2277		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2278		Cell envelope	Other	lipoprotein, NLP/P60 family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2279		Cell envelope	Other	membrane protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2280		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2281		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2282		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,1	0,75820	-0,3	0,04856	NA	NA	NA	NA	NA	NA	NA	NA
EF2283		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, resolvase family, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2284		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2285		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2286		Unknown function	General	ParB-like nuclease domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2287		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2288		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2289		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2290		Transcription	Transcription factors	RNA polymerase sigma-70 factor, ECF subfamily	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2291		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2292		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2293	*vanX*	Protein fate	Degradation of proteins, peptides, and glycopeptides	D-alanyl-D-alanine dipeptidase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2294	*vanB*	Cellular processes	Toxin production and resistance	D-alanine--D-lactate ligase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2295		Cellular processes	Toxin production and resistance	D-specific alpha-keto acid dehydrogenase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2296	*vanW*	Signal transduction	Two-component systems	vancomycin B-type resistance protein VanW	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2297	*vanYB*	Cellular processes	Toxin production and resistance	D-alanyl-D-alanine carboxypeptidase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2298	*vanSB*	Signal transduction	Two-component systems	sensor histidine kinase VanSB	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2299	*vanRB*	Signal transduction	Two-component systems	DNA-binding response regulator VanRB	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2300		Cellular processes	Toxin production and resistance	streptomycin resistance protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2302		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2303		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2304		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2305		DNA metabolism	Other	toprim domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2306		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	U	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2307		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2308		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2309		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2310		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2311		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2312	*topB-2*	DNA metabolism	DNA replication, recombination, and repair	DNA topoisomerase III	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2313		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2314		Cellular processes	Toxin production and resistance	bacteriocin, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2315		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2316		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2317		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2318		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M23/M37 family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2319		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2320		Mobile and extrachromosomal element functions	Plasmid functions	traE protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2321		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2322		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2324		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2325		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2326		Mobile and extrachromosomal element functions	Transposon functions	group II intron reverse transcriptase maturase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2327		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2328		Mobile and extrachromosomal element functions	Plasmid functions	TraG family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2329		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2330		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2331		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2332		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2333		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2334		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2335		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2336		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2337		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2338		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2339		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2340		DNA metabolism	Restriction/modification	C-5 cytosine-specific DNA methylase	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2341		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,32840	-0,9	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF2342		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,61780	-0,4	**0,00376**	NA	NA	NA	NA	NA	NA	NA	NA
EF2343		Cellular processes	Cell division	FtsK/SpoIIIE family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2344		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2345		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2346		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2347		Cell envelope	Other	cell wall surface anchor family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2348		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,99260	0,0	0,80050	NA	NA	NA	NA	NA	NA	NA	NA
EF2349		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,43780	0,5	**0,00220**	NA	NA	NA	NA	NA	NA	NA	NA
EF2350		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	0,3	0,19230	1,0	**0,00002**	NA	NA	NA	NA	NA	NA	NA	NA
EF2351		Hypothetical proteins		hypothetical protein	1	0	0	-0,7	**0,00235**	-1,2	**0,00100**	NA	NA	NA	NA	NA	NA	NA	NA
EF2352	*lepA*	Unknown function	General	GTP-binding protein LepA	1	1	1	-0,1	0,63630	-0,6	0,01160	-0,7	**0,00067**	-0,2	0,30800	-0,1	0,59220	-0,5	0,01639
EF2353		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,2	0,31350	-0,3	0,01411	-0,2	0,26830	0,1	0,62170	-0,2	0,34600	-0,2	0,56320
EF2354		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,21830	0,2	0,04382	0,2	0,33410	0,5	0,01839	0,0	0,96600	0,1	0,59020
EF2355	*clpB*	Protein fate	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, ATP-binding subunit ClpB	1	1	1	1,5	**0,00000**	2,1	**0,00000**	2,1	**0,00004**	0,8	**0,00928**	1,3	**0,00010**	1,9	**0,00001**
EF2357		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,03312	NA	NA	-0,3	0,29430	0,3	0,43550	-0,3	0,10760	0,2	0,24910
EF2360		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2361	*purB*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	adenylosuccinate lyase	1	1	1	-0,5	0,01875	-0,8	**0,00003**	-0,3	0,26520	-0,1	0,73440	-0,3	0,09924	-0,2	0,41950
EF2362	*purK-2*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole carboxylase, ATPase subunit	1	1	1	-0,2	0,23550	0,0	0,81690	-0,1	0,40590	0,2	0,32030	-0,3	0,06090	-0,2	0,14090
EF2363		Hypothetical proteins		hypothetical protein	1	1	1	0,0	0,88090	0,4	0,01342	-0,1	0,44540	0,2	0,34060	-0,2	0,18590	0,0	0,86030
EF2364		Transport and binding proteins	Nucleosides, purines and pyrimidines	xanthine permease	1	1	1	-0,2	0,44920	-0,1	0,53920	-1,1	0,01508	0,1	0,74150	-0,6	0,01203	-0,6	**0,00643**
EF2365	*xpt*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	xanthine phosphoribosyltransferase	1	1	1	0,0	0,91380	0,4	0,02664	-0,5	0,05645	0,3	0,14190	0,1	0,55060	0,2	0,21850
EF2366		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	0,01105	0,8	**0,00005**	0,4	0,14810	0,1	0,72590	0,6	**0,00395**	0,4	0,08423
EF2367		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	N-acetylmuramoyl-L-alanine amidase, family 4	1	1	1	0,8	**0,00056**	0,5	**0,00389**	0,6	0,01835	0,1	0,78710	0,9	**0,00011**	0,6	0,02182
EF2368		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00175**	0,8	**0,00042**	0,7	0,04624	0,3	0,29090	1,0	**0,00005**	0,6	0,01255
EF2369		Hypothetical proteins		hypothetical protein	1	1	1	1,0	**0,00032**	1,3	**0,00000**	0,6	**0,00567**	0,3	0,27290	0,9	**0,00011**	0,6	0,03916
EF2370		Unknown function	Enzymes of unknown specificity	oxidoreductase, Gfo/Idh/MocA family	1	1	1	0,3	0,19740	0,2	0,19480	0,2	0,16090	1,0	**0,00070**	0,4	**0,00740**	1,0	**0,00022**
EF2371	*asnS*	Protein synthesis	tRNA aminoacylation	asparaginyl-tRNA synthetase	1	1	1	-0,1	0,76730	0,6	0,05085	0,0	0,96420	-0,1	0,90270	-0,3	0,09700	0,3	0,18600
EF2372	*aspB*	Amino acid biosynthesis	Aspartate family	aspartate aminotransferase	1	1	1	-0,3	0,29100	0,1	0,64160	-0,1	0,66810	0,1	0,78800	-0,4	0,06371	0,1	0,45590
EF2373		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,06223	0,3	0,02475	0,0	0,94810	0,2	0,40590	-0,2	0,22040	0,6	**0,00434**
EF2374		DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG	1	1	1	-0,3	0,08425	-0,6	**0,00119**	0,0	0,86590	0,0	0,90960	-0,2	0,23380	-0,7	0,01478
EF2376		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2377		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	-0,6	**0,00180**	-3,3	**0,00000**	-0,8	**0,00123**	-2,3	**0,00000**	-0,5	**0,00521**	-2,5	**0,00000**
EF2378		DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, alpha subunit, Gram-positive type	1	1	1	-0,3	0,13040	-0,6	**0,00056**	-0,1	0,81490	-0,3	0,15200	0,1	0,70900	-0,5	0,01028
EF2379	*proS*	Protein synthesis	tRNA aminoacylation	prolyl-tRNA synthetase	1	1	1	0,1	0,58430	0,3	0,02699	-0,4	0,20290	-0,1	0,73870	-0,5	**0,00424**	-0,6	0,01076
EF2380		Protein fate	Degradation of proteins, peptides, and glycopeptides	membrane-associated zinc metalloprotease, putative	1	1	1	0,4	0,04814	0,2	0,15110	0,2	0,45860	0,1	0,82980	0,1	0,41890	-0,1	0,71730
EF2381		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2382	*gdh*	Energy metabolism	Other	glucose 1-dehydrogenase	1	1	0	NA	NA	NA	NA	0,1	0,83600	NA	NA	NA	NA	NA	NA
EF2383		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2384		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2385		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,82380	-0,2	0,02850	NA	NA	NA	NA	NA	NA	NA	NA
EF2386		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,04481	0,3	0,06573	NA	NA	NA	NA	NA	NA	NA	NA
EF2387		Cellular processes	Cell division	chromosome partitioning ATPase, ParA family	1	0	0	0,3	0,06284	0,0	0,93370	NA	NA	NA	NA	NA	NA	NA	NA
EF2388		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	0,1	0,67370	NA	NA	NA	NA	NA	NA
EF2389		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	-0,1	0,67200	NA	NA	NA	NA	NA	NA
EF2390		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,80400	1,0	**0,00003**	-0,1	0,33720	1,0	**0,00018**	-0,2	0,19690	0,9	**0,00018**
EF2391		Unknown function	General	NifU family protein	1	1	1	-0,3	0,20320	0,9	**0,00019**	0,0	0,92450	1,0	**0,00144**	-0,3	0,01618	0,3	0,05816
EF2392		Unknown function	Enzymes of unknown specificity	aminotransferase, class V	1	1	1	-0,3	0,47540	0,2	0,41240	0,1	0,81360	0,7	**0,00134**	-0,4	**0,00434**	0,2	0,19940
EF2393		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,31870	0,4	0,01119	-0,1	0,70950	0,9	**0,00095**	-0,1	0,55100	0,5	0,03655
EF2394		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,0	0,96520	0,1	0,64520	0,3	0,04648	1,2	**0,00139**	0,1	0,52760	0,9	**0,00055**
EF2395	*frr*	Protein synthesis	Translation factors	ribosome recycling factor	1	1	1	-0,2	0,19280	-2,5	**0,00000**	-0,9	**0,00009**	-0,6	0,05979	-0,4	0,02464	-1,2	**0,00000**
EF2396	*pyrH*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	uridylate kinase	1	1	1	0,0	0,83330	-2,6	**0,00000**	-1,1	**0,00002**	-0,4	0,09536	-0,5	**0,00351**	-1,6	**0,00000**
EF2397	*tsf*	Protein synthesis	Translation factors	translation elongation factor Ts	1	1	1	-0,2	0,13730	-3,0	**0,00000**	-1,2	**0,00004**	-0,2	0,54460	-0,3	0,05052	-1,7	**0,00000**
EF2398	*rpsB*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S2	1	1	1	0,1	0,69650	-2,1	**0,00000**	-0,8	**0,00052**	-0,6	0,05821	0,0	0,78600	-1,2	**0,00007**
EF2399		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	0,4	0,08774	0,0	0,89140	-0,2	0,25110	0,0	0,86080	0,2	0,10730	0,0	0,96800
EF2400		Protein synthesis	tRNA and rRNA base modification	RNA methyltransferase, TrmH family	1	1	1	0,3	0,23120	-0,1	0,66650	-0,1	0,75370	0,0	0,97690	0,4	0,01945	0,1	0,71430
EF2401	*acyP*	Fatty acid and phospholipid metabolism	Other	acylphosphatase	1	1	1	1,1	**0,00013**	2,5	**0,00000**	1,0	**0,00110**	0,7	**0,00846**	1,1	**0,00001**	2,1	**0,00000**
EF2404		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,01382	0,1	0,25200	-0,6	0,01500	0,0	0,92990	-0,2	0,07551	0,0	0,78850
EF2405		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,07472	-1,5	**0,00000**	-0,1	0,57340	0,1	0,66400	-0,3	0,03768	-0,4	0,04519
EF2406	*glyS*	Protein synthesis	tRNA aminoacylation	glycyl-tRNA synthetase, beta subunit	1	1	1	0,1	0,56630	-1,4	**0,00000**	-0,3	0,11280	-0,2	0,45750	-0,1	0,57230	-1,0	**0,00031**
EF2407	*glyQ*	Protein synthesis	tRNA aminoacylation	glycyl-tRNA synthetase, alpha subunit	1	1	1	0,0	0,94380	-1,5	**0,00001**	-0,2	0,20750	-0,4	0,19410	0,0	0,85710	-0,8	**0,00187**
EF2408		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,07838	-1,0	**0,00002**	-0,3	0,04897	0,0	0,94440	-0,1	0,73400	-0,9	0,02603
EF2409		DNA metabolism	DNA replication, recombination, and repair	DNA repair protein RecO, putative	1	1	1	0,1	0,59200	-0,8	**0,00001**	0,1	0,60430	-0,6	0,02689	-0,4	0,01242	-0,5	0,02296
EF2410	*era*	Regulatory functions	Small molecule interactions	GTP-binding protein Era	1	1	1	-0,1	0,60450	-0,1	0,63940	-0,7	**0,00094**	0,4	0,04371	-0,4	**0,00327**	0,0	0,87130
EF2411	*dgkA*	Fatty acid and phospholipid metabolism	Biosynthesis	diacylglycerol kinase	1	1	1	-0,3	0,05057	-0,7	**0,00035**	-0,4	0,06037	0,2	0,64310	-0,8	**0,00065**	-0,3	0,12280
EF2412		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00043	1	1	1	-0,1	0,50800	0,2	0,03151	-0,2	0,20060	0,3	0,20180	-0,7	**0,00009**	-0,6	0,01320
EF2413		Unknown function	General	HD domain protein	1	1	1	-0,2	0,23350	-0,3	0,03315	-0,1	0,65600	0,1	0,63600	-0,3	0,04294	-0,4	0,02379
EF2414	*phoH*	Unknown function	General	phoH-like protein	1	1	1	-0,2	0,18010	-0,3	0,02509	-0,1	0,71360	0,1	0,43310	0,1	0,57280	-0,4	0,06314
EF2415		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	**0,00445**	1,4	**0,00001**	-0,9	**0,00008**	0,2	0,39740	-0,2	0,07324	0,5	**0,00520**
EF2416	*rpsU*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S21	1	1	1	0,0	0,83420	0,9	**0,00004**	-0,7	**0,00033**	0,2	0,46970	0,0	0,99150	0,8	**0,00235**
EF2417	*zur*	Regulatory functions	DNA interactions	transcriptional regulator, Fur family	1	1	1	0,4	0,01875	0,4	0,01702	-0,2	0,22760	0,4	0,06278	0,3	0,02303	0,6	**0,00741**
EF2419		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,99410	-0,2	0,34250	-0,1	0,40270	-0,1	0,67130	0,1	0,39990	0,1	0,69930
EF2420	*thrB*	Amino acid biosynthesis	Aspartate family	homoserine kinase	1	1	1	0,1	0,59020	0,2	0,28160	0,4	0,03848	0,3	0,16870	0,2	0,07299	1,1	**0,00002**
EF2421	*thrC*	Amino acid biosynthesis	Aspartate family	threonine synthase	1	1	1	0,1	0,77930	0,3	0,16560	0,3	0,03454	0,4	0,10470	0,2	0,15480	0,5	**0,00846**
EF2422	*hom*	Amino acid biosynthesis	Aspartate family	homoserine dehydrogenase	1	1	1	0,3	0,08790	0,4	0,03109	0,5	0,01840	0,3	0,14470	0,3	0,03391	0,6	**0,00285**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2423		Regulatory functions	DNA interactions	transcriptional regulator, ArsR family	1	1	1	0,7	**0,00126**	0,9	**0,00022**	0,3	0,07198	0,3	0,23100	0,6	**0,00126**	1,1	**0,00001**
EF2424		Amino acid biosynthesis	Glutamate family	pyrroline-5-carboxylate reductase, putative	1	1	1	-0,6	**0,00186**	0,2	0,07024	-0,1	0,72590	-0,3	0,20180	-0,3	0,20930	0,1	0,78770
EF2425		Energy metabolism	Sugars	phosphoglucomutase/phosphomannomutase family protein	1	1	1	-0,3	0,31130	-0,3	0,02517	0,0	0,96080	-0,3	0,12230	-0,1	0,41800	-0,6	**0,00179**
EF2426		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	-0,2	0,27660	-0,4	**0,00469**	-0,2	0,58450	-0,2	0,41750	-0,1	0,42210	0,0	0,91330
EF2427		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00477**	0,2	0,02699	0,8	**0,00025**	-0,4	0,24820	1,0	**0,00003**	0,9	**0,00005**
EF2428		Regulatory functions	DNA interactions	transcriptional regulator, PadR family	1	1	1	0,9	**0,00009**	1,0	**0,00001**	1,3	**0,00003**	-0,4	0,07112	1,0	**0,00005**	1,2	**0,00000**
EF2429	*guaC*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	GMP reductase	1	1	1	1,5	**0,00006**	0,1	0,54060	1,3	**0,00018**	0,1	0,81250	2,2	**0,00000**	0,2	0,22570
EF2430		Transport and binding proteins	Nucleosides, purines and pyrimidines	xanthine/uracil permease family protein	1	1	1	1,1	**0,00011**	-0,3	0,04798	1,1	**0,00153**	-0,6	0,16370	1,3	**0,00007**	-0,1	0,72130
EF2431		Unknown function	Enzymes of unknown specificity	chlorohydrolase family protein	1	1	1	1,2	**0,00009**	NA	NA	1,3	**0,00020**	-0,1	0,78240	2,1	**0,00000**	0,3	0,27850
EF2432		Unknown function	Enzymes of unknown specificity	metallo-beta-lactamase superfamily protein	1	1	1	0,2	0,30090	0,9	**0,00036**	0,4	0,09471	0,7	0,01412	0,3	0,03684	0,8	**0,00032**
EF2433		Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate mutase family protein	1	1	1	0,2	0,23310	1,1	**0,00000**	0,3	0,44370	0,5	0,23370	0,5	0,01867	0,9	**0,00703**
EF2434		Regulatory functions	DNA interactions	phosphosugar-binding transcriptional regulator, RpiR family	1	1	1	0,3	0,18370	0,1	0,49180	0,2	0,47310	0,0	0,84820	0,3	0,03036	0,2	0,29640
EF2435		Signal transduction	PTS	PTS system, IIBC components	1	1	1	NA	NA	NA	NA	0,0	0,85160	NA	NA	0,2	0,33040	-0,3	0,21590
EF2436		Unknown function	General	glucokinase regulator-related protein	1	1	1	NA	NA	NA	NA	-0,2	0,29600	-0,4	0,13780	-0,1	0,36640	-0,3	0,04696
EF2437		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,94960	-0,3	0,16790
EF2438		Signal transduction	PTS	PTS system, IIA component	1	1	1	-0,1	0,58370	2,8	**0,00000**	-0,3	0,09712	1,1	**0,00025**	-0,4	0,01500	1,3	**0,00008**
EF2439		Cellular processes	Toxin production and resistance	undecaprenol kinase, putative	1	1	1	-1,4	**0,00030**	-1,3	**0,00000**	-1,5	**0,00009**	-0,3	0,28260	-1,5	**0,00002**	-1,8	**0,00001**
EF2440		Unknown function	General	celC-related protein	1	1	1	-0,6	**0,00822**	-2,4	**0,00000**	-0,2	0,24350	-1,6	**0,00080**	-0,3	0,11590	-1,4	**0,00011**
EF2441		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	0,01123	-2,0	**0,00000**	-0,4	0,05158	-1,3	**0,00084**	-0,8	**0,00015**	-1,5	**0,00003**
EF2442		Transport and binding proteins	Anions	phosphate transporter family protein	1	1	1	-0,8	**0,00019**	-1,7	**0,00000**	-0,4	0,01258	-0,8	0,01199	-1,1	**0,00002**	-1,2	**0,00045**
EF2443	*rpsT*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S20	1	1	1	-0,6	0,02078	-0,8	**0,00056**	-1,3	**0,00001**	-0,2	0,40880	-0,6	**0,00470**	-1,4	**0,00000**
EF2444		Fatty acid and phospholipid metabolism	Other	acyl-CoA thioester hydrolase	1	1	1	-0,6	**0,00480**	-1,9	**0,00000**	-1,4	**0,00001**	-0,2	0,49650	-0,8	**0,00008**	-1,6	**0,00000**
EF2445		Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	2-dehydropantoate 2-reductase, putative	1	1	1	0,9	**0,00440**	1,6	**0,00005**	0,1	0,63920	1,1	**0,00278**	0,3	0,23380	0,6	0,01763
EF2446		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	0,07799	-0,4	**0,00146**	-0,5	0,03692	-0,4	0,06712	-0,6	**0,00498**	-0,9	**0,00231**
EF2447		Cellular processes	DNA transformation	DNA internalization-related competence protein ComEC/Rec2	1	1	1	NA	NA	0,6	**0,00111**	NA	NA	0,3	0,34460	NA	NA	NA	NA
EF2448		Cellular processes	DNA transformation	comE operon protein 2, putative	1	1	1	-0,7	0,02193	0,4	0,04170	-0,5	0,02217	-0,1	0,60410	-0,7	**0,00232**	0,2	0,41100
EF2449	*comEA*	Cellular processes	DNA transformation	competence protein comEA	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2450		Unknown function	General	PDZ domain protein	1	1	1	-0,4	0,16400	-1,1	**0,00016**	-0,1	0,50560	-0,2	0,47510	-0,2	0,24200	-0,3	0,06493
EF2451	*coaD*	Biosynthesis of cofactors, prosthetic groups, carriers	Pantothenate and coenzyme A	pantetheine-phosphate adenylyltransferase	1	1	1	-0,3	0,23700	-0,8	**0,00003**	-0,2	0,26900	-0,3	0,12630	-0,1	0,47040	0,0	0,96720
EF2452		Unknown function	Enzymes of unknown specificity	methylase, putative	1	1	1	-0,5	0,02081	-0,7	**0,00019**	-0,1	0,75200	0,0	0,96650	-0,3	0,02594	0,1	0,72130
EF2453		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,17450	-0,2	0,06155	-0,4	0,05267	0,0	0,94760	-0,4	**0,00761**	0,1	0,48970
EF2454		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,52750	-0,3	0,14990	-0,4	0,01701	-0,2	0,45800	-0,3	0,05902	0,0	0,85340
EF2455		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,03404	-0,6	0,01718	-0,1	0,72310	-0,2	0,62090	-0,5	**0,00219**	-0,4	0,07519
EF2456	*pycA*	Energy metabolism	Glycolysis/gluconeogenesis	pyruvate carboxylase	1	1	1	-0,5	0,04310	-1,0	**0,00548**	0,0	0,95600	-0,2	0,49650	-0,4	0,06354	-0,4	0,15700
EF2457		Cellular processes	Cell division	cell division protein, FtsW/RodA/SpoVE family	1	1	1	-0,2	0,17900	-0,6	**0,00588**	-0,2	0,55030	-0,5	0,07768	-0,3	0,05864	-0,5	0,12040
EF2458		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,26430	-0,5	**0,00449**	-0,3	0,08036	-0,5	0,07408	-0,1	0,65410	-0,1	0,65100
EF2459	*recQ-2*	DNA metabolism	DNA replication, recombination, and repair	ATP-dependent DNA helicase RecQ	1	1	1	-0,5	0,09093	-0,5	**0,00258**	-0,6	**0,00313**	-0,2	0,47620	-0,1	0,41670	-0,2	0,21080
EF2460		Unknown function	General	GTP-binding protein TypA	1	1	1	-0,8	**0,00219**	-1,5	**0,00001**	-1,4	**0,00033**	-0,9	0,01754	-1,1	**0,00001**	-1,9	**0,00001**
EF2461		Unknown function	General	inositol monophosphatase protein family	1	1	1	0,7	**0,00034**	0,1	0,49570	0,6	**0,00629**	0,7	**0,00589**	0,4	**0,00358**	0,1	0,74680
EF2462		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,25660	-0,3	0,05390	0,4	0,02708	0,5	0,13930	0,1	0,53230	-0,3	0,20410
EF2463		Transport and binding proteins	Anions	voltage-gated chloride channel family protein	1	1	1	-0,2	0,37820	-0,3	0,03618	-0,3	0,32970	0,1	0,62430	-0,6	**0,00571**	-0,3	0,13780
EF2464		Hypothetical proteins	Domain	conserved domain protein	1	1	0	NA	NA	NA	NA	-0,1	0,79230	0,4	0,06020	NA	NA	NA	NA
EF2465		Hypothetical proteins		hypothetical protein	1	1	0	0,1	0,52220	0,2	0,22790	0,0	0,93710	0,9	**0,00101**	NA	NA	NA	NA
EF2466		Hypothetical proteins	Domain	conserved domain protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2467		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2469		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	0,5	0,01601	1,0	**0,00007**	0,1	0,56940	0,2	0,41140	0,4	0,03513	0,7	**0,00143**
EF2470		Unknown function	General	HD domain protein	1	1	1	0,0	0,83710	-0,3	0,35940	0,2	0,27320	0,5	0,16260	0,1	0,43970	0,7	**0,00674**
EF2471	*argS*	Protein synthesis	tRNA aminoacylation	arginyl-tRNA synthetase	1	1	1	0,0	0,94690	0,0	0,96190	0,5	0,03598	0,2	0,46070	0,2	0,15440	0,9	**0,00140**
EF2472	*gcp*	Protein fate	Degradation of proteins, peptides, and glycopeptides	O-sialoglycoprotein endopeptidase	1	1	1	-0,7	**0,00099**	-0,9	**0,00000**	-1,1	**0,00013**	-0,2	0,38510	-1,1	**0,00000**	-0,9	**0,00253**
EF2473		Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal-protein-alanine acetyltransferase, putative	1	1	1	-1,0	**0,00007**	-1,3	**0,00000**	-1,0	**0,00052**	-0,3	0,30080	-0,9	**0,00001**	-1,2	**0,00001**
EF2474		Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal-protein-alanine acetyltransferase, putative	1	1	1	-0,8	**0,00035**	-1,2	**0,00000**	-0,5	**0,00304**	-0,2	0,47450	-0,8	**0,00002**	-1,0	**0,00010**
EF2475		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,3	**0,00002**	-1,8	**0,00000**	-0,9	**0,00355**	-0,7	**0,00838**	-1,0	**0,00012**	-0,9	**0,00012**
EF2476		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein 4	1	1	1	-0,3	0,05057	0,2	0,14380	0,3	0,14130	0,2	0,43950	0,1	0,49920	0,4	0,05622
EF2477		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00023**	1,1	**0,00002**	1,2	**0,00006**	0,3	0,16870	0,8	**0,00002**	1,4	**0,00001**
EF2478		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	**0,00005**	1,5	**0,00000**	1,5	**0,00007**	0,6	0,04149	0,6	**0,00068**	1,7	**0,00001**
EF2479		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,1	**0,00030**	2,3	**0,00000**	1,1	**0,00007**	0,7	0,03310	0,3	0,02401	1,9	**0,00000**
EF2480		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,5	**0,00530**	-1,6	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2481		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	NA	NA	NA	NA	0,0	0,85520	0,3	0,34130	-0,4	0,02398	-0,1	0,68310
EF2483		Hypothetical proteins		hypothetical protein	1	1	1	1,8	**0,00000**	1,2	**0,00000**	0,8	0,01906	0,4	0,06712	1,2	**0,00000**	1,5	**0,00000**
EF2484		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,08987	-1,3	**0,00001**	-0,3	0,15650	-0,1	0,74450	0,2	0,15800	0,1	0,75040
EF2485	*cpsK*	Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	0	0	-0,2	0,41920	-3,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2486	*cpsJ*	Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	0	-0,4	0,04216	-3,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2487	*cpsI*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	UDP-galactopyranose mutase	1	0	0	-0,3	0,21090	-2,7	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2488	*cpsH*	Cell envelope	Other	lipoprotein, putative	1	0	0	-0,3	0,27350	-2,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2489	*cpsG*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	MurB family protein	1	0	0	-0,5	0,03541	-2,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2490	*cpsF*	Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,4	0,08920	-3,1	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2491	*cpsE*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	0	0	-0,2	0,18520	-2,5	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2492	*cpsD*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	0	0	-0,7	**0,00675**	-2,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2493	*cpsC*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	teichoic acid biosynthesis protein, putative	1	0	0	-0,4	0,06439	-1,0	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF2494	*cdsA*	Fatty acid and phospholipid metabolism	Biosynthesis	phosphatidate cytidylyltransferase	1	1	1	-0,4	0,10110	-0,1	0,56320	0,2	0,25730	-0,2	0,48230	0,0	0,80350	-0,1	0,40660
EF2495	*uppS*	Biosynthesis of cofactors, prosthetic groups, carriers	Other	undecaprenyl diphosphate synthase	1	1	1	-0,3	0,03578	-0,4	**0,00848**	0,1	0,68810	-0,3	0,18260	0,0	0,93890	-0,3	0,10550
EF2496		Cellular processes	Other	pheromone cOB1 precursor/lipoprotein, YaeC family	1	1	1	0,1	0,84250	-0,1	0,52910	-0,4	0,06470	0,1	0,74450	-0,9	**0,00003**	0,3	0,17960
EF2497		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-0,2	0,48020	0,0	0,73460	-0,5	0,07921	-0,3	0,32310	-1,3	**0,00005**	-0,3	0,08053
EF2498		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,3	0,10600	-0,2	0,07219	-0,2	0,24580	0,0	0,96940	-0,8	**0,00026**	0,0	0,81270
EF2499		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,07283	0,1	0,46600	-0,5	0,02457	0,1	0,74680	-0,4	0,03950	0,1	0,62640
EF2500		Unknown function	General	GcvH family protein	1	1	1	-0,5	0,03353	-1,0	**0,00000**	-0,8	**0,00283**	-0,4	0,23680	-0,6	**0,00091**	-1,0	**0,00025**
EF2501		Cellular processes	Detoxification	arsenate reductase, putative	1	1	1	-0,3	0,12300	-0,6	**0,00016**	-0,7	**0,00556**	-0,4	0,31010	-0,7	**0,00008**	-1,2	**0,00016**
EF2502		Cellular processes	Cell division	cell division protein, FtsW/RodA/SpoVE family	1	1	1	-0,6	0,09174	-0,1	0,40960	-0,7	**0,00629**	-0,1	0,78010	-0,9	**0,00007**	-1,3	**0,00003**
EF2503		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	-0,9	**0,00012**	-0,6	**0,00344**	NA	NA	NA	NA
EF2504		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	-0,7	**0,00562**	-0,6	**0,00542**	NA	NA	NA	NA
EF2505		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	-0,2	0,27320	-0,4	0,08927	NA	NA	0,1	0,80670
EF2507		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,56070	1,0	**0,00018**	-0,4	0,11740	-0,1	0,79110	0,0	0,84730	0,1	0,53560
EF2508		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	0,1	0,67000	1,0	**0,00013**	-0,5	**0,00431**	-0,4	0,01780	0,2	0,21050	0,7	**0,00112**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	q-value	M_t30	q-value	O_t5	q-value	O_t30	q-value	S_t5	q-value	S_t30	q-value
EF2509		Unknown function	General	AzlC family protein	1	1	1	-0,4	0,03096	0,8	0,02269	-0,6	**0,00469**	-0,1	0,70120	0,0	0,99150	0,8	0,01902
EF2512		Cell envelope	Other	lipoprotein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2513		Cell envelope	Other	lipoprotein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2514		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2515		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2516		Cell envelope	Other	membrane protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2517		Mobile and extrachromosomal element functions	Plasmid functions	conjugal transfer protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2518		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2519		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2520		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2521		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2522		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2523		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2524	*srtB*	Cell envelope	Surface structures	sortase family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2525		Cell envelope	Other	cell wall surface anchor family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2526		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2527		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2528		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2529		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2530		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2531		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2532		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2533		Cellular processes	Cell division	FtsK/SpoIIIE family protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2534		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,3	0,29250	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2535		Unknown function	General	nucleotidyltransferase domain protein	1	0	0	1,4	**0,00001**	2,4	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2536		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	0,7	**0,00624**	NA	NA	NA	NA	NA	NA	NA	NA
EF2537		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	0,4	0,08671	NA	NA	NA	NA	NA	NA	NA	NA
EF2538		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2539		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2540		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2541		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	0,5	0,02440	NA	NA	NA	NA	NA	NA	NA	NA
EF2542		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2543		Regulatory functions	Other	transcriptional regulator, putative	0	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2544		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2545		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2546		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, phage integrase family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2547		Hypothetical proteins		hypothetical protein	1	1	1	1,6	**0,00001**	3,4	**0,00000**	1,6	**0,00046**	2,2	**0,00000**	2,0	**0,00000**	3,4	**0,00000**
EF2548		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00071**	1,2	**0,00000**	0,4	0,08486	0,5	0,02167	1,1	**0,00000**	1,6	**0,00001**
EF2549	*upp*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	uracil phosphoribosyltransferase	1	1	1	0,2	0,18190	0,7	**0,00001**	-0,3	0,09586	-0,1	0,57950	0,2	0,03149	0,2	0,24980
EF2550	*glyA*	Amino acid biosynthesis	Serine family	serine hydroxymethyltransferase	1	1	1	0,0	0,83510	0,2	0,05692	-0,6	0,01516	-0,1	0,69540	-0,3	0,02410	-0,3	0,12180
EF2552		Unknown function	General	Sua5/YciO/YrdC/YwlC family protein	1	1	1	-0,4	0,08832	-0,9	**0,00005**	-0,8	**0,00180**	-0,3	0,05349	-0,8	**0,00027**	-0,6	**0,00369**
EF2553	*hemK*	Biosynthesis of cofactors, prosthetic groups, carriers	Heme, porphyrin, and cobalamin	hemK protein	1	1	1	-0,1	0,57910	-0,9	**0,00000**	-0,7	**0,00063**	-0,2	0,34550	-0,5	**0,00253**	-0,9	**0,00072**
EF2554	*prfA*	Protein synthesis	Translation factors	peptide chain release factor 1	1	1	1	-0,3	0,04860	-1,2	**0,00000**	-0,6	**0,00124**	-0,5	0,01515	-0,4	**0,00475**	-1,2	**0,00001**
EF2555	*tdK*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	thymidine kinase	1	1	1	-0,3	0,08584	-0,7	**0,00009**	-0,7	**0,00121**	-0,4	0,03642	-0,2	0,07458	-1,2	**0,00001**
EF2556		Energy metabolism	Anaerobic	fumarate reductase flavoprotein subunit precursor, putative	1	1	1	-1,3	**0,00001**	-5,0	**0,00000**	-1,7	**0,00000**	-2,9	**0,00000**	-1,6	**0,00000**	-3,3	**0,00000**
EF2558		Transport and binding proteins	Cations and iron carrying compounds	cation transporter	1	1	1	0,3	0,19520	0,0	0,86260	0,2	0,17250	-0,4	0,28940	-0,2	0,17080	-0,3	0,13940
EF2559		Energy metabolism	Electron transport	pyruvate flavodoxin/ferredoxin oxidoreductase family protein	1	1	1	NA	NA	NA	NA	1,1	**0,00057**	NA	NA	0,7	**0,00622**	-0,7	**0,00579**
EF2560	*gltA*	Amino acid biosynthesis	Glutamate family	glutamate synthase (NADPH), homotetrameric	1	1	1	0,4	0,07068	-0,3	0,14380	0,7	**0,00867**	-1,2	**0,00074**	-0,1	0,76020	-1,3	**0,00012**
EF2561		Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis	dihydroorotate dehydrogenase electron transfer subunit, putative	1	1	1	0,2	0,34100	-0,4	0,12620	0,4	0,08171	-1,7	**0,00028**	-0,2	0,34720	-1,2	**0,00007**
EF2562		Energy metabolism	Electron transport	flavodoxin	1	1	1	0,2	0,34810	-0,6	0,04665	0,0	0,97730	-1,6	**0,00014**	-0,4	0,03236	-1,2	**0,00008**
EF2563		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,6	0,03926	NA	NA	NA	NA	NA	NA
EF2564		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2565		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	1,0	**0,00018**	NA	NA	0,9	**0,00439**	-0,4	0,51000
EF2566		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,10290	NA	NA	1,1	**0,00900**	NA	NA	0,8	0,01238	-0,5	0,19940
EF2567	*selD*	Protein synthesis	tRNA aminoacylation	selenide, water dikinase	1	1	1	0,2	0,44380	0,0	0,93780	0,9	0,01209	NA	NA	0,5	0,10460	-0,7	0,02543
EF2568		Unknown function	Enzymes of unknown specificity	aminotransferase, class V	1	1	1	0,1	0,74430	-0,2	0,19130	0,6	0,04336	NA	NA	0,3	0,15450	-0,9	0,01208
EF2569		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,58280	-0,9	**0,00001**	0,4	0,02188	-1,0	**0,00132**	0,4	0,22100	-1,1	**0,00338**
EF2570		Unknown function	Enzymes of unknown specificity	aldehyde oxidoreductase, putative	1	1	1	0,0	0,97590	-0,6	0,02020	-0,3	0,06770	-0,5	0,30830	0,1	0,82730	-0,7	0,02525
EF2571		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,1	0,54890	0,0	0,99160	0,2	0,27360	-0,1	0,74570	0,4	0,08560	-0,2	0,52200
EF2572		Unknown function	General	molybdenum transport domain protein	1	1	1	0,3	0,26800	-0,6	**0,00013**	0,4	0,04146	-0,1	0,85490	0,4	0,10500	-0,4	0,02287
EF2573		Transport and binding proteins	Nucleosides, purines and pyrimidines	xanthine/uracil permease family protein	1	1	1	0,1	0,62170	0,1	0,43130	0,3	0,12840	0,1	0,64890	0,1	0,53850	-0,7	**0,00335**
EF2574		Transcription	Degradation of RNA	endoribonuclease L-PSP, putative	1	1	1	NA	NA	NA	NA	0,2	0,31570	NA	NA	0,4	0,09854	NA	NA
EF2575	*arcC-4*	Energy metabolism	Amino acids and amines	carbamate kinase	1	1	1	NA	NA	NA	NA	0,2	0,25730	NA	NA	0,4	0,03514	NA	NA
EF2576		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,55990	NA	NA	0,5	0,03908	NA	NA
EF2577		Unknown function	Enzymes of unknown specificity	aspartate/ornithine carbamoyltransferase family protein	1	1	1	NA	NA	NA	NA	0,2	0,34420	NA	NA	0,3	0,09793	NA	NA
EF2578		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	NA	NA	NA	NA	0,4	0,01213	NA	NA	0,1	0,37640	NA	NA
EF2579		Energy metabolism	Other	diaminopropionate ammonia-lyase, putative	1	1	1	NA	NA	NA	NA	0,6	0,02949	NA	NA	0,4	0,05982	NA	NA
EF2580		Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	D-hydantoinase	1	1	1	NA	NA	NA	NA	0,8	0,02703	NA	NA	0,5	0,21480	-0,3	0,39780
EF2581		Unknown function	Enzymes of unknown specificity	oxidoreductase, pyridine nucleotide-disulfide family	1	1	1	NA	NA	NA	NA	0,6	0,08154	NA	NA	NA	NA	-0,5	0,11000
EF2582		Unknown function	Enzymes of unknown specificity	chlorohydrolase family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,92290
EF2583		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,96520	1,7	**0,00000**	-0,5	0,01870	1,0	**0,00224**	0,1	0,64670	1,0	**0,00119**
EF2584		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,81090	0,5	**0,00177**	0,3	0,26560	0,5	0,06485	0,1	0,65410	0,3	0,26420
EF2585		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	mur ligase family protein	1	1	1	-0,4	0,03302	-0,1	0,55030	-0,4	0,03358	-0,1	0,62740	-0,1	0,35150	-0,1	0,72900
EF2586		Biosynthesis of cofactors, prosthetic groups, carriers	Heme, porphyrin, and cobalamin	cobyric acid synthase, putative	1	1	1	-0,1	0,49400	0,3	0,06999	-0,6	**0,00629**	-0,1	0,54810	-0,4	0,03949	-0,2	0,21100
EF2587		Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	inosine-uridine preferring nucleoside hydrolase	1	1	1	-1,5	**0,00000**	-3,4	**0,00000**	-2,0	**0,00000**	-2,9	**0,00000**	-1,0	**0,00006**	-2,1	**0,00000**
EF2588		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,7	**0,00004**	-3,5	**0,00000**	-1,9	**0,00000**	-3,0	**0,00000**	-1,2	**0,00002**	-2,5	**0,00000**
EF2589	*manA*	Energy metabolism	Sugars	mannose-6-phosphate isomerase, class I	1	1	1	0,0	0,82540	-0,5	**0,00040**	-0,1	0,65530	-0,1	0,60760	0,1	0,65980	-0,2	0,23460
EF2590		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00816**	-0,2	0,26410	-0,6	**0,00712**	-0,5	0,14660	-0,6	**0,00227**	0,0	0,99570
EF2591		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	-0,1	0,48160	-0,1	0,23140	-0,4	0,06041	-0,2	0,49810	0,0	0,78330	-0,4	0,09231
EF2592		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	2,4	**0,00000**	-0,5	0,07192	1,0	**0,00149**	0,4	0,17830	1,9	**0,00000**	0,7	0,03392
EF2593		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	2,7	**0,00000**	-0,8	**0,00032**	1,3	**0,00040**	0,1	0,76670	2,1	**0,00000**	0,1	0,61960
EF2594		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	2,2	**0,00000**	-1,0	**0,00002**	1,1	**0,00012**	-0,1	0,74410	1,7	**0,00001**	0,0	0,95900
EF2595	*gmk-1*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	guanylate kinase	1	1	1	0,2	0,30030	0,4	**0,00356**	0,0	0,84510	0,1	0,65220	0,2	0,08258	0,3	0,17700

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2597		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 1	1	1	1	0,6	**0,00526**	NA	NA	-0,7	0,06969	-2,0	**0,00001**	-0,8	**0,00024**	-0,7	0,01644
EF2598		Signal transduction	PTS	PTS system, beta-glucoside-specific IIABC component	1	1	1	0,4	0,06439	1,1	**0,00004**	-2,6	**0,00000**	-2,8	**0,00228**	-2,2	**0,00000**	-1,0	**0,00040**
EF2599		Regulatory functions	RNA interactions	transcriptional antiterminator, bglG family	1	1	1	-0,5	0,02245	0,0	0,75930	-1,5	**0,00001**	-0,8	0,12230	-0,7	**0,00171**	-0,3	0,31370
EF2601		Fatty acid and phospholipid metabolism	Biosynthesis	acyl carrier protein, putative	1	1	1	-0,2	0,26910	-1,6	**0,00000**	-0,4	0,03219	0,3	0,16740	-0,4	0,04194	-1,7	**0,00000**
EF2602		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,23470	0,3	0,36370	1,0	**0,00540**	0,2	0,37770	0,7	**0,00147**	1,9	**0,00000**
EF2603		Signal transduction	PTS	PTS system, IIA component	1	1	1	0,9	**0,00085**	1,3	**0,00000**	0,6	**0,00150**	0,0	0,97310	0,4	0,05022	1,0	**0,00030**
EF2604		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,86920	0,3	0,06606	-0,4	0,03586	0,0	0,99600	-0,3	0,05864	0,1	0,51920
EF2605	*murAA*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	1	1	1	0,0	0,84350	0,8	**0,00003**	-0,6	0,01118	0,2	0,25510	0,1	0,79330	-0,1	0,72140
EF2606		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,01752	1,4	**0,00001**	0,4	**0,00783**	1,0	**0,00589**	0,6	**0,00521**	1,3	**0,00010**
EF2607	*atpC*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F1, epsilon subunit	1	1	1	-0,1	0,58080	0,7	**0,00032**	-0,3	0,25440	1,2	**0,00009**	0,3	0,01093	1,0	**0,00004**
EF2608	*atpD*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F1, beta subunit	1	1	1	-0,3	0,12000	0,1	0,42440	0,2	0,56810	1,5	**0,00008**	-0,1	0,33140	0,2	0,28590
EF2609	*atpG*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F1, gamma subunit	1	1	1	-0,3	0,06881	0,0	0,93850	-0,1	0,59720	0,4	0,02932	-0,3	0,04853	-0,3	0,13320
EF2610	*atpA*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F1, alpha subunit	1	1	1	-0,2	0,20260	-0,2	0,10630	0,0	0,80800	0,1	0,69740	-0,1	0,38820	-0,3	0,08418
EF2611	*atpH*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F1, delta subunit	1	1	1	0,0	0,96920	0,1	0,55930	0,1	0,31930	0,3	0,13780	-0,1	0,54750	-0,2	0,24980
EF2612	*atpF*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F0, B subunit	1	1	1	0,0	0,96040	-0,2	0,07549	0,1	0,59320	0,0	0,96650	0,0	0,78870	-0,1	0,35540
EF2613	*atpE*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F0, C subunit	1	1	1	0,1	0,51110	0,1	0,67010	0,4	0,15700	0,2	0,46580	-0,2	0,23660	0,2	0,32860
EF2614	*atpB*	Energy metabolism	ATP-proton motive force interconversion	ATP synthase F0, A subunit	1	1	1	0,2	0,27860	0,0	0,78230	0,2	0,46240	0,0	0,94760	0,1	0,71420	-0,1	0,74410
EF2615		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,03055	0,0	0,95010	0,2	0,16340	0,1	0,67310	-0,1	0,58860	-0,9	**0,00007**
EF2616	*smpB*	Protein synthesis	Other	SsrA-binding protein	1	1	1	0,3	0,07638	0,5	**0,00057**	0,1	0,51550	0,4	0,05317	0,1	0,34720	0,5	**0,00448**
EF2617	*vacB*	Transcription	Degradation of RNA	ribonuclease R	1	1	1	0,3	0,14580	-0,1	0,30810	0,3	0,10930	0,1	0,79180	0,2	0,11530	0,5	0,01491
EF2618		Fatty acid and phospholipid metabolism	Degradation	carboxylesterase precursor, putative	1	1	1	0,7	**0,00999**	0,5	**0,00121**	0,7	**0,00365**	0,3	0,36380	0,9	**0,00078**	0,6	**0,00711**
EF2619		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,65540	0,0	0,96000	0,0	0,85140	NA	NA
EF2620	*secG*	Protein fate	Protein and peptide secretion and trafficking	preprotein translocase, SecG subunit	1	1	1	-0,1	0,60830	-0,4	**0,00384**	-0,3	0,18870	0,0	0,91850	-0,1	0,23550	-0,3	0,21390
EF2621		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,02942	0,2	0,07467	0,1	0,73260	-0,7	**0,00461**	0,3	0,02002	0,5	**0,00867**
EF2622		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00103**	0,2	0,07471	0,2	0,21280	-0,8	**0,00146**	0,5	**0,00260**	0,6	**0,00509**
EF2623	*cadA*	Transport and binding proteins	Cations and iron carrying compounds	cadmium-translocating P-type ATPase	1	1	1	0,6	0,01933	-1,3	**0,00000**	0,4	0,02116	-1,6	**0,00076**	0,6	**0,00738**	-0,4	0,17300
EF2624		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2625	*nadE*	Biosynthesis of cofactors, prosthetic groups, carriers	Pyridine nucleotides	NH(3)-dependent NAD+ synthetase	1	1	1	0,2	0,47750	2,2	**0,00000**	-0,1	0,59890	0,9	**0,00260**	0,0	0,71420	1,8	**0,00000**
EF2626		Biosynthesis of cofactors, prosthetic groups, carriers	Pyridine nucleotides	nicotinate phosphoribosyltransferase, putative	1	1	1	0,4	0,08076	2,6	**0,00000**	0,3	0,24460	0,7	0,01982	0,5	0,03530	1,1	**0,00055**
EF2627		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	teichoic acid glycosylation protein, putative	1	1	1	0,0	0,89630	-0,5	**0,00278**	0,0	0,94940	-0,3	0,11590	-0,1	0,73340	-0,6	0,01514
EF2628		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	N-acetylmuramoyl-L-alanine amidase, family 4	1	1	1	NA	NA	NA	NA	0,5	0,02385	NA	NA	0,4	0,05883	0,7	0,01101
EF2629		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2630		Regulatory functions	Other	transcriptional regulator	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	0,5	0,02859	0,5	0,05585
EF2631		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,3	0,04785	NA	NA	NA	NA	0,5	0,01193
EF2633	*groEL*	Protein fate	Protein folding and stabilization	chaperonin, 60 kDa	1	1	1	0,8	**0,00061**	-0,4	**0,00254**	0,3	0,05407	-1,1	**0,00020**	0,1	0,63750	-0,4	0,06206
EF2634	*groES*	Protein fate	Protein folding and stabilization	chaperonin, 10 kDa	1	1	1	0,9	**0,00100**	0,0	0,87320	0,7	**0,00183**	-0,4	0,10740	0,1	0,33990	-0,7	**0,00027**
EF2636		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,16830	0,8	0,01053	0,1	0,67370	-0,1	0,62680	0,4	0,11030	0,3	0,13190
EF2637		Unknown function	General	abortive infection protein	1	1	1	0,0	0,95160	0,6	**0,00221**	-0,1	0,68400	-0,1	0,69890	0,1	0,67490	1,0	**0,00032**
EF2638		Unknown function	General	DNA-binding protein, putative	1	1	1	0,5	0,01136	2,2	**0,00000**	-0,2	0,46510	2,1	**0,00001**	0,4	0,01523	0,9	**0,00264**
EF2639		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,1	0,75850	0,5	**0,00016**	0,1	0,57360	0,3	0,16740	0,0	0,85290	0,2	0,25490
EF2640		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	0,1	0,59960	0,6	**0,00063**	-0,1	0,53260	0,5	0,03118	-0,3	0,01431	0,3	0,13300
EF2641		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/L-proline ABC transporter, ATP-binding subunit	1	1	1	-1,4	**0,00037**	-0,5	**0,00352**	-1,7	**0,00003**	-1,0	**0,00471**	-1,1	**0,00140**	-0,6	0,07226
EF2642		Transport and binding proteins	Amino acids, peptides and amines	glycine betaine/L-proline ABC transporter/-binding/permease	1	1	1	-2,1	**0,00008**	-0,6	**0,00073**	-2,7	**0,00001**	-1,5	**0,00006**	-1,8	**0,00003**	-0,9	**0,00376**
EF2643		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,1	**0,00023**	3,2	**0,00000**	1,1	**0,00001**	0,9	**0,00086**	1,4	**0,00000**	2,2	**0,00000**
EF2644		Unknown function	General	diacylglycerol kinase catalytic domain protein	1	1	1	0,8	**0,00015**	2,5	**0,00000**	0,7	**0,00063**	1,2	**0,00136**	1,0	**0,00001**	2,3	**0,00000**
EF2645		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,3	0,13600	0,9	**0,00002**	1,0	**0,00025**	-0,2	0,43570	0,4	0,04388	0,4	0,06224
EF2646		Energy metabolism	Glycolysis/gluconeogenesis	glycerate kinase, putative	1	1	1	1,0	**0,00099**	NA	NA	1,0	**0,00029**	-0,6	**0,00932**	0,6	0,01116	-0,2	0,39480
EF2647		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	permease, GntP family	1	1	1	1,1	**0,00061**	NA	NA	0,9	0,01306	NA	NA	0,1	0,43550	-0,5	0,08757
EF2648		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,2	0,30810	0,0	0,84640	NA	NA	NA	NA	NA	NA	NA	NA
EF2649		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter/-binding protein	1	1	1	-0,4	**0,00695**	-1,9	**0,00000**	-1,1	**0,00096**	-1,6	**0,00001**	-1,2	**0,00003**	-2,0	**0,00000**
EF2650		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, permease protein	1	1	1	-0,3	0,19010	-1,9	**0,00000**	-0,8	0,02152	-1,8	**0,00002**	-1,2	**0,00008**	-2,0	**0,00000**
EF2651		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, permease protein	1	1	1	-0,3	0,41730	-1,4	**0,00020**	-0,8	**0,00086**	-1,7	**0,00000**	-1,0	**0,00001**	-2,1	**0,00000**
EF2652		Transport and binding proteins	Amino acids, peptides and amines	spermidine/putrescine ABC transporter, ATP-binding subunit	1	1	1	-0,4	0,03567	-1,2	**0,00002**	-0,6	**0,00943**	-1,6	**0,00005**	-0,7	**0,00051**	-1,3	**0,00003**
EF2653		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	1	1	-0,2	0,59120	-1,0	**0,00006**	-0,4	0,11760	-1,0	**0,00395**	-0,1	0,56610	-0,8	**0,00132**
EF2654		Energy metabolism	Fermentation	alcohol dehydrogenase, zinc-containing	1	1	1	1,2	**0,00009**	0,4	**0,00979**	1,1	**0,00019**	0,0	0,85060	1,0	**0,00070**	0,5	0,01955
EF2655		Unknown function	General	flavoprotein-related protein	1	1	1	0,7	**0,00564**	0,4	0,01045	0,7	**0,00474**	0,3	0,12120	0,6	**0,00304**	0,9	**0,00018**
EF2656		Unknown function	Enzymes of unknown specificity	flavoprotein family protein	1	1	1	0,4	0,07331	0,3	0,02564	0,3	0,02063	0,3	0,22770	0,2	0,05902	0,4	0,02020
EF2657		Cell envelope	Other	membrane protein, putative	1	1	1	0,1	0,35220	0,5	**0,00030**	0,2	0,44650	0,6	**0,00651**	0,0	0,75620	0,3	0,14750
EF2658		Cellular processes	Toxin production and resistance	FemAB family protein	1	1	1	-0,8	0,01841	0,1	0,72560	-0,8	**0,00176**	-0,5	0,10160	-0,1	0,57000	-0,1	0,50660
EF2659		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-3,2	**0,00000**	-3,7	**0,00000**	-3,7	**0,00000**	-2,7	**0,00000**	-3,3	**0,00000**	-3,8	**0,00000**
EF2661		Unknown function	General	diacylglycerol kinase catalytic domain protein	1	1	1	-0,2	0,29820	-0,1	0,49220	-0,9	**0,00141**	0,1	0,69910	-0,4	0,01395	-0,4	0,04163
EF2662		Cell envelope	Other	choline binding protein	1	0	0	-0,2	0,27300	-0,4	**0,00133**	NA	NA	NA	NA	NA	NA	NA	NA
EF2663		DNA metabolism	DNA replication, recombination, and repair	helicase, putative, RecD/TraA family	1	1	1	-0,3	0,07258	0,4	**0,00258**	-0,7	**0,00943**	-0,1	0,75260	-0,2	0,35890	1,0	**0,00029**
EF2664		Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate mutase family protein	1	1	1	-0,5	0,02449	0,3	**0,00996**	-0,9	**0,00241**	-0,1	0,63680	-0,1	0,50720	0,8	**0,00284**
EF2665		Protein synthesis	tRNA and rRNA base modification	RNA methyltransferase, TrmH family	1	1	1	0,1	0,47000	-0,6	**0,00041**	-0,4	0,11350	0,1	0,76670	-0,2	0,09700	-0,6	0,02060
EF2666		Protein synthesis	tRNA and rRNA base modification	ribosomal RNA large subunit methyltransferase A, putative	1	1	1	-0,8	**0,00012**	-0,9	**0,00001**	-1,5	**0,00062**	-0,1	0,65550	-0,8	**0,00027**	-0,7	**0,00430**
EF2667		Transport and binding proteins	Cations and iron carrying compounds	copper homeostasis protein, putative	1	1	1	-0,3	0,04295	-0,8	**0,00016**	-0,5	**0,00389**	-0,7	**0,00934**	-0,3	0,01764	-0,7	**0,00018**
EF2668	*mgtE*	Transport and binding proteins	Cations and iron carrying compounds	magnesium transporter	1	1	1	-0,4	0,03209	-1,1	**0,00000**	-0,4	0,02357	0,3	0,20120	-0,6	**0,00121**	-1,2	**0,00007**
EF2670		Biosynthesis of cofactors, prosthetic groups, carriers	Pyridine nucleotides	inorganic polyphosphate/ATP-NAD kinase, putative	1	1	1	0,6	0,01841	0,1	0,21460	0,3	0,16900	0,1	0,79210	0,0	0,98250	-0,3	0,09686
EF2671		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	0,02343	-0,1	0,60380	0,5	**0,00777**	-0,2	0,36380	0,4	0,01157	-0,2	0,25320
EF2672		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00165**	2,6	**0,00000**	0,8	**0,00350**	1,2	**0,00782**	1,0	**0,00001**	1,4	**0,00004**
EF2673		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,7	**0,00225**	3,0	**0,00000**	0,4	0,03416	1,8	**0,00001**	1,2	**0,00001**	1,6	**0,00033**
EF2674	*pepF*	Protein fate	Degradation of proteins, peptides, and glycopeptides	oligoendopeptidase F,plasmid	1	1	1	0,1	0,59340	1,5	**0,00005**	0,5	0,11830	1,1	**0,00610**	0,1	0,64900	2,2	**0,00000**
EF2675		Cellular processes	DNA transformation	competence protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2677		Regulatory functions	Other	negative regulator of genetic competence MecA, putative	1	1	1	0,5	0,01169	1,8	**0,00000**	0,5	**0,00904**	0,5	0,08301	1,0	**0,00001**	1,5	**0,00000**
EF2678		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,60350	0,4	**0,00798**	-0,1	0,75110	-0,4	0,24380	0,1	0,35450	-0,6	**0,00674**
EF2679	*trpS*	Protein synthesis	tRNA aminoacylation	tryptophanyl-tRNA synthetase	1	1	1	-0,2	0,20060	0,8	**0,00003**	-0,1	0,63920	0,2	0,29610	-0,2	0,23550	0,5	0,01993
EF2680		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	0,1	0,47540	0,7	**0,00202**	-0,1	0,35510	0,4	0,01967	-0,2	0,19710	-0,1	0,59690
EF2681		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-1,2	**0,00013**	-0,9	**0,00619**	-1,2	**0,00013**	-1,5	**0,00034**	-0,9	**0,00014**	-1,0	**0,00039**
EF2682		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2683		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,2	0,46520	NA	NA	-0,1	0,64610	0,3	0,13110
EF2684		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,73650	-0,2	0,63520	-0,2	0,47240	0,1	0,60780
EF2686	*inl*	Cellular processes	Pathogenesis	internalin protein family, authentic point mutation	1	1	1	NA	NA	NA	NA	-0,1	0,61050	NA	NA	-0,1	0,49640	0,3	0,16870

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2687		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,9	**0,00066**	0,3	0,24340	-0,5	0,14880	-0,3	0,07737	-0,4	0,02711	0,0	0,93140
EF2688		Unknown function	General	Snf2 family protein	1	1	1	-0,5	0,01894	-0,5	**0,00151**	-0,4	0,08730	-0,6	**0,00309**	-0,5	0,01302	-0,2	0,23170
EF2689	*sbcC*	DNA metabolism	DNA replication, recombination, and repair	exonuclease SbcC	1	1	1	-0,1	0,40930	-0,1	0,39590	0,2	0,27560	-0,9	**0,00189**	0,0	0,82950	-0,2	0,38430
EF2690	*sbcD*	DNA metabolism	DNA replication, recombination, and repair	exonuclease SbcD	1	1	1	-0,5	0,01040	-0,4	**0,00326**	0,2	0,09663	-1,2	**0,00421**	-0,1	0,33310	-0,4	0,04124
EF2691		Fatty acid and phospholipid metabolism	Biosynthesis	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	1	1	1	0,2	0,36760	0,3	0,06182	0,0	0,89860	0,1	0,47320	0,3	0,01085	0,4	0,02181
EF2692		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,73000	1,2	**0,00005**	0,4	0,07741	0,8	**0,00360**	0,0	0,84970	1,3	**0,00001**
EF2693		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,50190	0,7	**0,00003**	0,3	0,06969	0,9	0,01045	0,0	0,97620	1,0	**0,00013**
EF2694	*pfs*	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	MTA/SAH nucleosidase	1	1	1	0,6	**0,00369**	1,1	**0,00000**	0,4	0,02617	0,2	0,36030	0,5	**0,00181**	0,8	**0,00034**
EF2695		Hypothetical proteins		hypothetical protein	1	1	1	0,5	0,02363	1,0	**0,00002**	0,4	0,01901	0,2	0,23650	0,7	**0,00043**	0,5	**0,00627**
EF2696		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	0,4	0,02071	0,8	**0,00001**	0,7	**0,00209**	0,4	0,04275	0,7	**0,00037**	0,4	0,01014
EF2697		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,9	**0,00004**	0,3	0,06031	3,2	**0,00000**	0,0	0,88110	0,8	**0,00041**	0,0	0,88070
EF2698		Cellular processes	Toxin production and resistance	tellurite resistance protein, putative	1	1	1	0,9	**0,00018**	0,3	**0,00760**	2,5	**0,00000**	0,0	0,98340	1,0	**0,00067**	0,4	0,03080
EF2699		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,7	**0,00721**	NA	NA	NA	NA	NA	NA
EF2700		DNA metabolism	DNA replication, recombination, and repair	MutT/nudix family protein	1	1	1	0,2	0,30160	0,3	0,03062	0,0	0,84440	0,2	0,23380	0,3	0,01863	0,4	0,04047
EF2701		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,3	0,06252	-0,3	0,04634	0,0	0,79920	0,1	0,63960	-0,1	0,67060	-0,1	0,74680
EF2702		Hypothetical proteins		hypothetical protein	1	1	1	2,2	**0,00000**	3,8	**0,00000**	1,5	**0,00000**	0,9	**0,00379**	2,7	**0,00000**	4,0	**0,00000**
EF2703		Regulatory functions	Other	transcriptional regulator	1	1	1	0,2	0,14060	0,4	**0,00288**	-0,9	**0,00035**	-0,1	0,70280	0,1	0,69860	NA	NA
EF2704	*mutY*	DNA metabolism	DNA replication, recombination, and repair	A/G-specific adenine glycosylase	1	1	1	-0,3	0,16240	1,2	**0,00000**	0,1	0,67740	0,3	0,26070	-0,5	**0,00412**	0,9	**0,00011**
EF2705		Regulatory functions	Other	regulatory protein RecX, putative	1	1	1	-0,1	0,70780	0,7	**0,00072**	-0,1	0,61900	0,1	0,48160	-0,3	0,09853	0,8	**0,00127**
EF2706		Protein synthesis	tRNA and rRNA base modification	RNA methyltransferase, TrmA family	1	1	1	-0,5	**0,00672**	-0,9	**0,00000**	-0,7	**0,00577**	-0,8	**0,00025**	-0,5	**0,00738**	-0,4	0,05670
EF2707		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,32480	-0,3	0,08775	-0,2	0,36510	NA	NA	-0,7	**0,00618**	-0,1	0,55980
EF2708		Cell envelope	Other	membran protein, putative	1	1	1	-0,1	0,57270	3,1	**0,00000**	-0,9	**0,00209**	0,3	0,29380	0,0	0,78990	2,9	**0,00000**
EF2709		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 2	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2710		Transport and binding proteins	Amino acids, peptides and amines	amino acid permease family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2711		Regulatory functions	DNA interactions	transcriptional regulator, AraC family	1	1	1	-0,4	0,02299	-0,4	**0,00185**	-0,3	0,07618	-1,1	**0,00022**	-0,6	**0,00352**	-0,7	**0,00975**
EF2712		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2713		Cell envelope	Other	cell wall surface anchor family protein	1	0	0	2,2	**0,00000**	0,0	0,84190	NA	NA	NA	NA	NA	NA	NA	NA
EF2715	*rplL*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L7/L12	1	1	1	-0,5	0,04853	-2,2	**0,00000**	-1,6	**0,00000**	-1,1	0,03300	-0,7	**0,00031**	-1,8	**0,00000**
EF2716	*rplJ*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L10	1	1	1	-1,0	**0,00035**	-2,0	**0,00000**	-0,7	0,04348	-0,6	0,14730	-0,1	0,33640	-1,6	**0,00019**
EF2718	*rplA*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L1	1	1	1	-1,4	**0,00154**	-3,1	**0,00000**	-1,5	**0,00004**	-1,5	**0,00196**	-1,1	**0,00000**	-2,0	**0,00000**
EF2719	*rplK*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L11	1	1	1	-1,0	0,01819	-4,2	**0,00000**	-1,1	**0,00005**	-0,8	0,02606	-0,6	**0,00107**	-1,6	**0,00000**
EF2720		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,1	0,73900	1,1	**0,00035**	0,7	**0,00396**	0,9	0,01883	-0,6	**0,00548**	1,1	**0,00056**
EF2721	*sdhB-2*	Energy metabolism	Amino acids and amines	L-serine dehydratase, iron-sulfur-dependent, beta subunit	1	1	1	-0,4	0,02852	0,5	0,02699	-0,3	0,27370	0,2	0,31610	0,0	0,81920	-0,2	0,32110
EF2722	*sdhA-2*	Energy metabolism	Amino acids and amines	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	1	1	1	-0,1	0,69680	0,4	0,04704	-0,4	0,01464	0,1	0,55700	0,1	0,69860	0,0	0,96800
EF2723		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2724		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M42 family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,4	0,27360
EF2725		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2727		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	1	1	1,2	**0,00020**	1,6	**0,00000**	1,9	**0,00000**	2,4	**0,00000**	1,6	**0,00000**	2,1	**0,00000**
EF2728		Cell envelope	Other	lipoprotein, putative	1	1	1	-0,2	0,37620	-1,2	**0,00003**	-0,5	0,02228	-0,2	0,25930	-0,5	**0,00081**	-0,5	0,06314
EF2729	*nusG*	Transcription	Transcription factors	transcription antitermination protein NusG	1	1	1	-0,8	**0,00457**	-1,0	**0,00005**	-1,2	**0,00001**	-0,2	0,26800	-1,1	**0,00000**	-1,3	**0,00001**
EF2730	*secE*	Protein fate	Protein and peptide secretion and trafficking	preprotein translocase, SecE subunit	1	1	1	0,1	0,55250	-0,2	0,08640	-0,1	0,53140	0,0	0,90990	0,5	0,01164	-0,2	0,27850
EF2731	*rpmG-2*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L33	1	1	1	0,2	0,34700	0,2	0,13700	0,1	0,58230	0,6	**0,00318**	0,5	**0,00413**	0,2	0,34310
EF2732		Unknown function	General	CBS domain protein	1	1	1	0,6	0,02478	2,1	**0,00000**	0,9	**0,00046**	0,9	**0,00999**	0,6	**0,00413**	2,7	**0,00000**
EF2733	*murB*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	UDP-N-acetylenolpyruvoylglucosamine reductase	1	1	1	-0,2	0,49170	0,1	0,32010	0,2	0,45030	-0,3	0,08116	-0,3	0,02382	-0,5	0,01079
EF2734		Unknown function	Enzymes of unknown specificity	oxidoreductase, Gfo/Idh/MocA family	1	1	1	0,6	0,18320	1,0	**0,00091**	0,6	**0,00214**	0,3	0,15720	0,3	0,17080	0,3	0,06864
EF2735	*exoA*	DNA metabolism	DNA replication, recombination, and repair	exodeoxyribonuclease	1	1	1	0,1	0,51380	0,1	0,74790	0,2	0,54410	0,4	0,13660	0,4	0,06138	0,6	0,01259
EF2736		DNA metabolism	Degradation of DNA	exonuclease	1	1	1	0,1	0,74720	0,2	0,18460	0,2	0,57500	0,5	0,21430	0,3	0,29710	0,7	0,01897
EF2738	*ahpF*	Unknown function	Enzymes of unknown specificity	thioredoxin reductase/glutathione-related protein	1	1	1	0,7	**0,00202**	0,5	**0,00056**	1,2	**0,00008**	0,6	0,07093	0,5	**0,00204**	3,2	**0,00000**
EF2739	*ahpC*	Cellular processes	Detoxification	alkyl hydroperoxide reductase, C subunit	1	1	1	1,6	**0,00006**	2,2	**0,00000**	0,7	**0,00224**	0,9	0,02922	0,2	0,08645	2,5	**0,00000**
EF2740		Unknown function	Enzymes of unknown specificity	O-methyltransferase family protein	1	1	1	-0,3	0,11140	-0,6	0,01886	-0,8	**0,00046**	0,0	0,96940	-0,7	**0,00098**	-0,6	**0,00272**
EF2741	*lplA-2*	Protein fate	Protein modification and repair	lipoate-protein ligase A	1	1	1	-0,2	0,32960	-0,2	0,44490	-0,2	0,20830	0,8	**0,00358**	-0,1	0,34560	0,6	**0,00119**
EF2742		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,57580	0,6	0,17240	0,0	0,88840	0,8	**0,00970**	-0,2	0,29640	1,2	**0,00031**
EF2743		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,1	0,76740	0,1	0,43720	0,1	0,49500	-0,3	0,16740	0,3	0,08825	0,6	0,02635
EF2744		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M42 family	1	1	1	0,3	0,07741	0,0	0,88420	0,2	0,36830	-0,2	0,38240	0,7	**0,00009**	1,3	**0,00013**
EF2746	*dltD*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	dltD protein	1	1	1	-0,3	0,19230	-0,3	0,15630	-0,4	0,13750	-0,5	0,11970	-0,9	**0,00233**	-0,6	0,01091
EF2747	*dltC*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	D-alanyl carrier protein	1	1	1	-0,4	0,02751	-1,1	**0,00001**	-0,7	**0,00347**	-0,5	0,01816	-0,9	**0,00003**	-0,9	**0,00007**
EF2748	*dltB*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	basic membrane protein DltB	1	1	1	0,0	0,97950	-0,4	**0,00515**	0,1	0,58220	-0,4	0,29770	-0,4	0,05647	-0,4	0,02375
EF2749	*dltA*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	D-alanine-activating enzyme, putative	1	1	1	0,0	0,81710	-0,2	0,05302	0,3	0,33460	-0,1	0,79340	0,1	0,58410	-0,2	0,45360
EF2750		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00272**	-0,3	0,14910	0,4	0,38360	-0,5	0,16870	0,1	0,61400	-0,2	0,17960
EF2751		Transport and binding proteins	Unknown substrate	permease protein, putative	1	1	1	0,7	**0,00119**	1,2	**0,00003**	0,7	0,02041	0,7	0,06789	0,4	0,03353	0,8	**0,00129**
EF2752		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,9	0,01155	1,0	**0,00009**	0,8	**0,00207**	0,7	**0,00678**	0,7	**0,00330**	0,9	**0,00123**
EF2754	*nrdD*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	anaerobic ribonucleoside-triphosphate reductase	1	1	1	0,0	0,98500	0,0	0,89230	-0,2	0,19050	-0,8	**0,00719**	-1,0	**0,00032**	0,6	0,06286
EF2755	*nrdG*	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	anaerobic ribonucleoside-triphosphate reductase activating protein	1	1	1	-0,1	0,57830	0,7	**0,00034**	-0,1	0,54270	-0,8	**0,00828**	-0,7	**0,00037**	0,9	**0,00089**
EF2756	*dinP*	Unknown function	General	DNA-damage-inducible protein P	1	1	1	0,4	0,16110	0,9	**0,00001**	0,4	0,08929	0,0	0,83250	0,2	0,11410	0,8	**0,00026**
EF2757		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00245	1	1	1	-0,6	**0,00592**	-0,9	**0,00000**	-0,4	0,05048	-0,7	0,10980	-0,6	**0,00135**	-0,6	**0,00364**
EF2758		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,4	0,16560	-0,4	**0,00507**	-0,7	**0,00056**	-0,5	0,07246	-0,3	0,06709	-0,5	0,03247
EF2759		Unknown function	Enzymes of unknown specificity	tetrapyrrole methylase family protein	1	1	1	-0,3	0,23120	-1,1	**0,00010**	-0,5	0,07379	-0,7	**0,00541**	-0,3	0,28700	-0,4	0,12260
EF2760		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,09503	-0,4	**0,00848**	-0,5	**0,00732**	-0,2	0,45180	-0,1	0,33640	-0,1	0,71990
EF2761		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00513**	-0,4	**0,00347**	-0,4	0,14760	0,1	0,65490	-0,5	0,02207	-0,3	0,14260
EF2762	*holB*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, delta prime subunit	1	1	1	-0,5	0,01528	-1,1	**0,00011**	-0,1	0,75390	0,1	0,70210	-0,4	**0,00972**	-0,1	0,54700
EF2763		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,27380	0,4	0,02564	0,3	0,06267	0,5	0,06010	0,1	0,26830	0,9	**0,00019**
EF2764	*tmk*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	thymidylate kinase	1	1	1	0,1	0,75920	0,2	0,30160	0,5	**0,00209**	0,4	0,17630	0,5	**0,00054**	1,3	**0,00001**
EF2765		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,01816	-1,0	**0,00001**	-1,1	**0,00066**	-0,3	0,14470	-1,2	**0,00001**	-0,9	**0,00005**
EF2766	*recR*	DNA metabolism	DNA replication, recombination, and repair	recombination protein RecR	1	1	1	-0,1	0,68380	-0,3	0,03571	-0,9	**0,00052**	0,0	0,86700	-0,4	0,01778	-0,4	0,06603
EF2767		Regulatory functions	Other	transcriptional regulator	1	1	1	-0,4	0,19390	NA	NA	-0,4	0,31710	0,7	**0,00571**	NA	NA	NA	NA
EF2768		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,0	**0,00189**	-0,2	0,31520	-0,4	0,13470	0,9	**0,00240**	-0,9	**0,00102**	0,0	0,92340
EF2769		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,6	**0,00328**	0,3	0,09868	-0,3	0,29440	0,7	**0,00773**	-0,2	0,11920	0,3	0,23460
EF2770		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,8	**0,00314**	-0,2	0,16650	-0,2	0,59870	0,7	0,01142	-0,5	0,02109	0,2	0,48650
EF2771		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,5	**0,00009**	0,4	0,02631	-2,1	**0,00002**	-1,1	0,01175	-1,5	**0,00002**	0,0	0,81430
EF2773		Transport and binding proteins	Unknown substrate	major facilitator family transporter	1	1	1	NA	NA	NA	NA	NA	NA	-0,1	0,44650	-0,6	**0,00543**	-0,8	**0,00212**
EF2774		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,03029	0,2	0,06923	0,2	0,41220	0,3	0,14580	0,5	**0,00145**	0,1	0,63530
EF2775	*thiD*	Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	phosphomethylpyrimidine kinase	1	1	1	NA	NA	NA	NA	NA	NA	0,2	0,40250	NA	NA	0,1	0,78740
EF2776	*thiE*	Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	thiamine-phosphate pyrophosphorylase	1	1	1	NA	NA	NA	NA	-0,2	0,57310	0,2	0,46070	NA	NA	-0,3	0,35540

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2777		Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	hydroxyethylthiazole kinase, putative	1	1	1	NA	NA	NA	NA	-0,4	0,19780	0,2	0,52430	NA	NA	-0,1	0,70640
EF2778		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,7	0,02879	0,2	0,31860	NA	NA	-0,1	0,55460
EF2780		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00103	1	1	1	-0,2	0,28300	-0,3	0,02489	-0,2	0,14170	-0,1	0,77610	0,0	0,97500	-0,2	0,33440
EF2781	*dnaX*	DNA metabolism	DNA replication, recombination, and repair	DNA polymerase III, gamma and tau subunits	1	1	1	-0,1	0,43410	-0,3	0,01153	-0,1	0,66290	-0,2	0,20430	-0,1	0,51000	-0,4	0,03871
EF2782		Energy metabolism	Sugars	galactose-1-phosphate uridylyltransferase, putative	1	1	1	-0,6	**0,00334**	-1,4	**0,00000**	-0,5	0,01177	-0,5	0,03608	-0,3	0,03036	-0,7	**0,00248**
EF2783	*galE-2*	Energy metabolism	Sugars	UDP-glucose 4-epimerase	1	1	1	0,0	0,96420	-0,8	**0,00004**	-0,1	0,58980	-0,5	0,04210	0,1	0,68840	-0,2	0,29480
EF2784		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,07623	0,7	**0,00101**	0,5	**0,00787**	0,2	0,40530	0,6	**0,00169**	1,4	**0,00001**
EF2785		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00174**	2,2	**0,00000**	1,2	**0,00003**	2,2	**0,00000**	0,9	**0,00027**	2,3	**0,00000**
EF2786		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	**0,00007**	2,5	**0,00000**	1,1	**0,00003**	2,0	**0,00000**	0,8	**0,00008**	2,1	**0,00000**
EF2787		Cellular processes	Detoxification	rhodanese family protein	1	1	1	0,3	0,12420	-1,0	**0,00000**	-0,2	0,28110	0,1	0,49250	-0,4	0,02328	-0,5	**0,00907**
EF2788	*glcK*	Energy metabolism	Glycolysis/gluconeogenesis	glucokinase	1	1	1	-0,1	0,68380	-0,5	0,02188	-0,4	0,20790	0,1	0,62270	-0,9	**0,00049**	-1,1	**0,00001**
EF2789		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,54860	-0,5	**0,00237**	-0,4	0,01346	0,0	0,94440	-0,5	**0,00159**	-1,1	**0,00001**
EF2790		Transport and binding proteins	Unknown substrate	small hydrophobic molecule transporter protein, putative	1	1	1	-0,2	0,54380	-0,4	0,05649	-0,2	0,23230	0,1	0,80860	-0,4	0,02125	-0,4	0,01014
EF2791		Unknown function	Enzymes of unknown specificity	5-formyltetrahydrofolate cyclo-ligase family protein	1	1	1	0,1	0,71210	-0,2	0,08498	-0,1	0,71780	0,0	0,96580	-0,2	0,27530	-0,1	0,52710
EF2792		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,01126	1,1	**0,00001**	0,4	0,02812	0,9	**0,00999**	0,5	**0,00229**	1,0	**0,00239**
EF2793		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,4	**0,00038**	-0,7	0,05462	-0,5	**0,00409**	-1,6	**0,00006**	-0,4	0,05982	-0,5	0,01245
EF2794		Cell envelope	Other	membrane protein, putative	1	1	1	0,0	0,89240	0,3	0,03365	0,2	0,19800	-0,7	0,08432	-0,4	0,07493	0,0	0,90320
EF2795		Cell envelope	Other	LysM domain lipoprotein	1	1	1	0,0	0,89300	0,1	0,35570	0,0	0,86310	-0,5	0,10980	-0,1	0,69230	-0,2	0,39520
EF2796		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,04776	2,7	**0,00000**	-0,5	0,04648	0,6	0,07426	-1,0	**0,00138**	2,1	**0,00000**
EF2797		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,3	0,08177	0,2	0,27960	0,6	**0,00058**	1,1	**0,00002**
EF2798		Hypothetical proteins		hypothetical protein	1	0	0	-1,3	**0,00006**	-2,5	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2801		Hypothetical proteins		hypothetical protein	1	0	0	-1,5	**0,00004**	-2,7	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2802		Mobile and extrachromosomal element functions	Prophage functions	endolysin	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,82600	-0,6	**0,00247**
EF2803		Mobile and extrachromosomal element functions	Prophage functions	holin	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,1	0,42080	-0,4	0,01902
EF2804		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,86520	-0,6	**0,00213**
EF2805		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2806		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2807		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2810		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2811		Mobile and extrachromosomal element functions	Prophage functions	minor structural protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2812		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2813		Mobile and extrachromosomal element functions	Prophage functions	tail tape measure protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2814		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2815		Mobile and extrachromosomal element functions	Prophage functions	major tail protein, phi13 family	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,92090	-0,3	0,06544
EF2816		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01725	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2817		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2818		Mobile and extrachromosomal element functions	Prophage functions	minor structural protein, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2819		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2820		Mobile and extrachromosomal element functions	Prophage functions	major capsid protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,98630	-0,1	0,79780
EF2821		Protein fate	Other	prohead protease	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,2	0,14210	0,0	0,90530
EF2822		Mobile and extrachromosomal element functions	Prophage functions	portal protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2823		Mobile and extrachromosomal element functions	Prophage functions	terminase, large subunit, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,1	0,45150	-0,3	0,17290
EF2824		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2825		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2826		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2828		Regulatory functions	DNA interactions	transcriptional regulator, ArpU family	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2829		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2830		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,59780	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2831		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2832		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2833		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,2	0,33260	-0,1	0,41450	NA	NA	NA	NA	NA	NA	NA	NA
EF2834		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,1	0,73870	-0,9	**0,00047**
EF2835		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,96090	-0,6	0,03217
EF2836		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2837		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2838		Mobile and extrachromosomal element functions	Prophage functions	DNA replication protein DnaC, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,87480	-0,7	**0,00386**
EF2839		Unknown function	General	DnaD domain protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,0	0,87500	-0,9	**0,00697**
EF2840		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	1	0,2	0,44410	NA	NA	NA	NA	NA	NA	0,1	0,50960	-0,9	**0,00182**
EF2841		Mobile and extrachromosomal element functions	Prophage functions	recT protein, putative	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,33970	-0,8	**0,00135**
EF2842		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,1	0,40160	-0,6	0,05505
EF2843		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,35970	-0,7	0,01219
EF2844		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	0,3	0,06210	-0,7	0,01590
EF2845		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2846		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2847		Hypothetical proteins	Domain	conserved domain protein	1	0	0	0,3	0,06679	0,6	**0,00924**	NA	NA	NA	NA	NA	NA	NA	NA
EF2848		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2849		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2850		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,2	0,41730	0,2	0,28100	NA	NA	NA	NA	NA	NA	NA	NA
EF2851		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	0,4	0,01461	NA	NA	NA	NA	NA	NA	NA	NA
EF2852		Mobile and extrachromosomal element functions	Prophage functions	transcriptional regulator, Cro/CI family	1	0	0	0,7	**0,00250**	-0,4	0,01049	NA	NA	NA	NA	NA	NA	NA	NA
EF2853		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,6	**0,00388**	-0,3	0,13700	NA	NA	NA	NA	NA	NA	NA	NA
EF2854		Transport and binding proteins	Cations and iron carrying compounds	ion transporter, putative	1	0	0	0,6	0,01695	-0,2	0,19660	NA	NA	NA	NA	NA	NA	NA	NA
EF2855		Mobile and extrachromosomal element functions	Prophage functions	site-specific recombinase, phage integrase family	1	0	0	0,8	**0,00061**	-0,5	0,06817	NA	NA	NA	NA	NA	NA	NA	NA
EF2856	*rpmG-3*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L33	1	1	1	-0,8	**0,00105**	-1,1	**0,00003**	-1,0	**0,00123**	-0,4	0,20180	-0,3	0,02279	-0,6	0,03417
EF2857		Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	penicillin-binding protein 2B	1	1	1	0,1	0,81650	0,6	0,04520	0,3	0,35820	0,1	0,89980	0,3	0,08686	0,2	0,29630
EF2858	*thrS*	Protein synthesis	tRNA aminoacylation	threonyl-tRNA synthetase	1	1	1	1,2	**0,00009**	-0,3	0,26700	1,7	**0,00011**	0,3	0,39570	2,2	**0,00000**	0,0	0,88460
EF2859		Energy metabolism	Other	4-oxalocrotonate tautomerase, putative	1	1	1	-0,7	**0,00252**	-0,9	**0,00009**	0,0	0,96400	-0,4	0,05317	0,3	0,06055	-0,2	0,37110
EF2860		Unknown function	General	ErfK/YbiS/YcfS/YnhG family protein, putative	1	1	1	-0,1	0,63800	1,8	**0,00000**	0,2	0,18510	0,5	0,19420	-0,5	0,04257	0,5	0,02552
EF2861	*aadK*	Cellular processes	Toxin production and resistance	aminoglycoside 6-adenylyltransferase	1	1	1	0,2	0,23890	0,0	0,82370	0,0	0,94090	0,2	0,63490	NA	NA	NA	NA
EF2862		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,45210	0,8	**0,00002**	0,4	0,04008	0,8	**0,00132**	0,2	0,32500	0,8	**0,00085**
EF2863		Energy metabolism	Biosynthesis and degradation of polysaccharides	endo-beta-N-acetylglucosaminidase	1	1	1	1,3	**0,00009**	-0,9	**0,00004**	0,3	0,30540	-0,8	**0,00424**	0,4	0,11200	-1,9	**0,00000**
EF2864		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,3	0,13540	-0,5	0,01080	-0,1	0,67200	0,0	0,91090	0,5	**0,00076**	0,3	0,13630
EF2866		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR01033	1	1	1	-0,1	0,62030	-0,8	**0,00003**	-0,5	0,01270	-0,3	0,20180	-0,3	0,02397	-1,0	**0,00006**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2867		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,8	**0,00035**	-0,7	**0,00007**	-0,8	**0,00100**	0,0	0,93540	-0,9	**0,00007**	-0,2	0,49510
EF2868		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,50710	-0,2	0,27790	-0,6	**0,00176**	0,5	0,01738	-0,6	**0,00101**	-0,3	0,18780
EF2870		Unknown function	General	HD domain protein	1	1	1	-0,6	**0,00066**	-0,2	0,17240	-0,5	0,02949	0,3	0,18530	-0,4	**0,00807**	0,1	0,81270
EF2871	*nadD*	Biosynthesis of cofactors, prosthetic groups, carriers	Pyridine nucleotides	nicotinate-nucleotide adenylyltransferase	1	1	1	-0,6	**0,00183**	-1,0	**0,00002**	-0,4	0,05737	0,2	0,42670	-1,0	**0,00002**	-0,7	**0,00793**
EF2872		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00253	1	1	1	-0,7	0,01031	-0,6	**0,00171**	-0,5	**0,00872**	0,0	0,95410	-0,9	**0,00001**	-0,9	**0,00091**
EF2873		Unknown function	General	GTPase of unknown function	1	1	1	-0,4	0,11700	-0,7	**0,00027**	-0,9	**0,00209**	-0,1	0,74570	-1,2	**0,00000**	-1,0	**0,00004**
EF2874		Unknown function	Enzymes of unknown specificity	hydrolase, HAD subfamily IIIA	1	1	1	0,2	0,31840	0,0	0,87350	0,0	0,80560	0,3	0,31610	0,0	0,99460	-0,2	0,39500
EF2875	*accA*	Fatty acid and phospholipid metabolism	Biosynthesis	acetyl-CoA carboxylase, carboxyl transferase alpha subunit	1	1	1	0,3	0,41920	4,4	**0,00000**	-0,6	0,13740	4,9	**0,00000**	-0,5	0,03443	2,0	**0,00017**
EF2876	*accD*	Fatty acid and phospholipid metabolism	Biosynthesis	acetyl-CoA carboxylase, carboxyl transferase beta subunit	1	1	1	0,7	0,06133	4,9	**0,00000**	-0,8	0,07028	5,3	**0,00000**	-0,7	**0,00011**	2,3	**0,00000**
EF2877	*accC*	Fatty acid and phospholipid metabolism	Biosynthesis	acetyl-CoA carboxylase, biotin carboxylase	1	1	1	1,3	**0,00052**	4,8	**0,00000**	0,0	0,99420	5,1	**0,00000**	-0,4	0,02973	2,3	**0,00000**
EF2878	*fabZ-2*	Fatty acid and phospholipid metabolism	Biosynthesis	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase	1	1	1	1,7	**0,00001**	3,5	**0,00000**	0,5	0,19550	4,9	**0,00000**	-0,1	0,52850	1,4	**0,00001**
EF2879	*accB*	Fatty acid and phospholipid metabolism	Biosynthesis	acetyl-CoA carboxylase, biotin carboxyl carrier protein	1	1	1	2,0	**0,00000**	3,6	**0,00000**	0,9	**0,00223**	4,4	**0,00000**	0,5	**0,00128**	2,0	**0,00000**
EF2880	*fabF-2*	Fatty acid and phospholipid metabolism	Biosynthesis	3-oxoacyl-(acyl-carrier-protein) synthase II	1	1	1	1,9	**0,00000**	4,0	**0,00000**	1,4	**0,00036**	5,0	**0,00000**	0,7	**0,00006**	3,1	**0,00000**
EF2881	*fabG*	Fatty acid and phospholipid metabolism	Biosynthesis	3-oxoacyl-(acyl-carrier-protein) reductase	1	1	1	2,3	**0,00000**	3,5	**0,00000**	1,7	**0,00000**	4,6	**0,00000**	1,5	**0,00000**	2,9	**0,00000**
EF2882	*fabD*	Fatty acid and phospholipid metabolism	Biosynthesis	malonyl CoA-acyl carrier protein transacylase	1	1	1	3,2	**0,00000**	4,6	**0,00000**	2,3	**0,00000**	4,9	**0,00000**	2,4	**0,00000**	2,2	**0,00003**
EF2883	*fabK*	Fatty acid and phospholipid metabolism	Biosynthesis	enoyl-(acyl-carrier-protein) reductase II	1	1	1	3,4	**0,00000**	5,1	**0,00000**	3,0	**0,00000**	5,0	**0,00000**	3,1	**0,00000**	2,8	**0,00000**
EF2884		Fatty acid and phospholipid metabolism	Biosynthesis	acyl carrier protein, putative	1	1	1	3,4	**0,00000**	4,2	**0,00000**	2,6	**0,00001**	4,3	**0,00000**	3,2	**0,00000**	3,1	**0,00000**
EF2885	*fabH*	Fatty acid and phospholipid metabolism	Biosynthesis	3-oxoacyl-(acyl-carrier-protein) synthase III	1	1	1	3,5	**0,00000**	4,9	**0,00000**	2,9	**0,00000**	4,5	**0,00000**	3,6	**0,00000**	3,2	**0,00000**
EF2886		Regulatory functions	DNA interactions	transcriptional regulator, MarR family	1	1	1	3,7	**0,00000**	4,7	**0,00000**	3,1	**0,00000**	4,6	**0,00000**	3,8	**0,00000**	3,5	**0,00000**
EF2888		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,21420	0,0	0,84140	-0,4	0,01659	-0,3	0,30340	0,3	0,01320	0,6	**0,00748**
EF2889	*glxR*	Energy metabolism	Other	2-hydroxy-3-oxopropionate reductase	1	1	1	0,5	0,01033	0,3	0,01523	0,6	**0,00185**	0,0	0,85640	0,5	**0,00738**	0,3	0,17660
EF2890		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 1 family protein	1	1	1	-0,1	0,46730	-0,6	**0,00029**	-0,1	0,69810	-1,2	**0,00006**	-0,1	0,72420	-0,2	0,18780
EF2891	*bgsA*	Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 1 family protein	1	1	1	0,0	0,99250	-0,1	0,56040	0,3	0,14700	-1,1	**0,00016**	0,1	0,44870	-0,3	0,28280
EF2892		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2893		Hypothetical proteins		hypothetical protein	1	1	1	0,2	0,27710	0,1	0,25250	0,3	0,03641	0,4	0,15770	-0,1	0,59100	0,1	0,63330
EF2894		Cellular processes	Adaptations to atypical conditions	general stress protein 13, putative	1	1	1	0,4	0,14320	0,1	0,46080	0,6	0,01229	0,4	0,14570	0,6	**0,00277**	0,0	0,79720
EF2895		Unknown function	Enzymes of unknown specificity	aminotransferase, class II	1	1	1	0,5	0,05057	0,3	0,03662	0,4	0,07273	0,3	0,09980	0,3	0,09372	0,3	0,08375
EF2896		Hypothetical proteins		hypothetical protein	1	1	1	-0,5	0,04398	1,4	**0,00000**	0,0	0,95550	0,0	0,90960	-0,6	**0,00057**	0,4	0,13850
EF2898		Protein fate	Protein folding and stabilization	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1	1	1	0,1	0,76520	0,2	0,08146	-0,6	**0,00648**	0,2	0,24860	0,1	0,50790	-0,3	0,03334
EF2899		Unknown function	Enzymes of unknown specificity	oxidoreductase, pyridine nucleotide-disulfide family	1	1	1	-0,9	**0,00055**	-1,1	**0,00001**	-1,6	**0,00005**	0,3	0,48810	-1,8	**0,00000**	-1,4	**0,00001**
EF2900		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2901		Unknown function	Enzymes of unknown specificity	D-isomer specific 2-hydroxyacid dehydrogenase family protein	1	1	1	0,8	**0,00573**	1,8	**0,00000**	0,8	**0,00507**	1,3	**0,00014**	0,8	**0,00137**	2,3	**0,00000**
EF2902		Purines, pyrimidines, nucleosides, and nucleotides	Other	2,3-cyclic-nucleotide 2-phosphodiesterase, putative	1	1	1	-0,5	0,01625	-2,1	**0,00000**	-0,8	**0,00040**	-1,6	**0,00003**	0,1	0,65980	-1,5	**0,00000**
EF2903		Transport and binding proteins	Unknown substrate	ABC transporter, substrate-binding protein	1	1	1	-0,3	0,03686	-2,2	**0,00000**	-1,2	**0,00005**	-1,2	**0,00008**	0,2	0,34400	-1,4	**0,00001**
EF2904		Hypothetical proteins		hypothetical protein	1	0	1	-0,9	**0,00015**	-2,3	**0,00000**	-1,4	**0,00000**	-0,9	**0,00121**	-0,4	0,03148	-1,5	**0,00001**
EF2905		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-1,4	**0,00002**	-2,3	**0,00000**	-1,3	**0,00010**	-1,0	**0,00087**	-1,1	**0,00014**	-1,8	**0,00000**
EF2906		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	-0,6	**0,00876**	-1,6	**0,00000**	-1,4	**0,00022**	-0,9	**0,00022**	-1,1	**0,00086**	-1,9	**0,00000**
EF2907		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	-0,7	**0,00131**	-1,3	**0,00000**	-1,2	**0,00000**	-0,7	**0,00071**	-0,7	**0,00011**	-1,2	**0,00001**
EF2908		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	1	1	1	0,0	0,90000	0,0	0,99750	-0,4	0,01711	0,1	0,66670	-0,1	0,23580	-0,1	0,37780
EF2909		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,02578	1,5	**0,00000**	0,0	0,96420	0,3	0,16870	0,2	0,14700	0,8	**0,00014**
EF2910		Transport and binding proteins	Cations and iron carrying compounds	potassium uptake protein	1	1	1	-0,1	0,44860	0,0	0,69920	0,3	0,19780	0,1	0,63900	-0,1	0,33930	0,0	0,99950
EF2911		Regulatory functions	DNA interactions	DNA-binding response regulator, LuxR family	1	1	1	0,8	**0,00039**	0,1	0,24970	1,5	**0,00016**	-0,4	0,19130	0,8	**0,00040**	-0,1	0,74980
EF2912		Signal transduction	Two-component systems	sensor histidine kinase, putative	1	1	1	1,1	**0,00007**	1,0	**0,00000**	1,8	**0,00002**	-0,4	0,05476	1,0	**0,00018**	0,7	**0,00184**
EF2913		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,9	**0,00087**	0,3	0,02139	1,6	**0,00051**	-0,6	0,10300	0,3	0,06294	-0,3	0,13820
EF2914	*greA*	Transcription	Transcription factors	transcription elongation factor GreA	1	1	1	-1,0	**0,00030**	-1,9	**0,00000**	-1,4	**0,00000**	-1,1	**0,00011**	-0,8	**0,00003**	-1,4	**0,00000**
EF2915		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00247	1	1	1	-1,2	**0,00012**	-0,6	**0,00004**	-0,8	**0,00036**	0,0	0,88790	-0,7	**0,00029**	-0,8	**0,00296**
EF2916		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,1	0,58880	0,9	**0,00046**	0,0	0,85770	0,5	0,05112	-0,1	0,56060	0,8	**0,00035**
EF2917		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	UDP-N-acetylglucosamine 2-epimerase	1	1	1	0,5	0,01382	0,8	**0,00002**	0,1	0,45300	0,4	0,05110	0,4	**0,00487**	0,9	**0,00051**
EF2918		Unknown function	Enzymes of unknown specificity	bacterial transferase, putative	1	1	1	0,3	0,04398	0,9	**0,00000**	0,3	0,07282	0,3	0,29550	0,2	0,09920	0,8	**0,00011**
EF2919		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,7	**0,00556**	0,6	**0,00018**	-0,5	**0,00853**	0,8	**0,00059**	-0,5	**0,00231**	0,7	**0,00619**
EF2920		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding/permease protein	1	1	1	-0,6	0,01136	0,1	0,69950	-0,1	0,62930	0,8	**0,00171**	-0,4	0,04790	0,4	0,06577
EF2921		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2922		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,9	0,01080	-0,5	0,02419	-0,9	**0,00287**	-0,5	0,06422	-0,9	**0,00008**	-0,6	0,02246
EF2923		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	0,01005	-1,1	**0,00003**	-0,9	**0,00076**	0,1	0,70050	-0,9	**0,00006**	-1,3	**0,00001**
EF2924		Unknown function	Enzymes of unknown specificity	metallo-beta-lactamase superfamily protein	1	1	1	-0,9	**0,00442**	-1,5	**0,00060**	-0,7	**0,00057**	0,1	0,48650	-0,8	**0,00027**	-1,1	**0,00001**
EF2925		Cellular processes	Adaptations to atypical conditions	cold-shock domain family protein	1	1	1	-0,2	0,19520	0,4	**0,00369**	-0,1	0,60790	0,5	0,01252	-0,1	0,48980	-0,2	0,19240
EF2926	*radC*	DNA metabolism	DNA replication, recombination, and repair	DNA repair protein RadC	1	1	1	0,3	0,06570	NA	NA	0,0	0,81980	-0,2	0,29830	0,1	0,35300	0,0	0,94830
EF2927		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,2	0,33260	1,2	**0,00000**	0,3	0,04224	0,7	**0,00351**	0,2	0,08858	0,8	**0,00083**
EF2928		Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	FolC family protein	1	1	1	0,7	**0,00130**	1,0	**0,00000**	0,9	**0,00084**	0,3	0,28780	0,7	**0,00014**	0,7	**0,00141**
EF2929		Cell envelope	Other	membrane protein, putative	1	1	1	-0,3	0,24430	0,8	**0,00014**	-0,3	0,04765	0,3	0,33400	-0,5	**0,00511**	0,2	0,19760
EF2930		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	0,04400	0,4	0,02344	-0,9	**0,00053**	0,2	0,40440	-0,7	**0,00205**	0,1	0,37030
EF2931	*valS*	Protein synthesis	tRNA aminoacylation	valyl-tRNA synthetase	1	1	1	0,2	0,24850	0,0	0,86950	0,1	0,60700	0,1	0,43580	0,1	0,53750	-0,3	0,18620
EF2932		Unknown function	Enzymes of unknown specificity	AhpC/TSA family protein	1	1	1	-0,2	0,30340	0,2	0,08014	-0,3	0,03769	-0,3	0,30210	0,3	0,03513	0,3	0,15080
EF2933		Unknown function	General	DNA-binding protein,putative	1	1	1	-0,2	0,49170	-2,7	**0,00000**	0,3	0,12020	-0,4	0,13680	0,0	0,83310	-0,7	**0,00399**
EF2934	*thiI*	Biosynthesis of cofactors, prosthetic groups, carriers	Thiamine	thiazole biosynthesis protein ThiI	1	1	1	-0,4	0,04880	0,3	0,17970	-0,9	**0,00273**	-0,1	0,65860	-0,4	**0,00498**	-0,7	**0,00564**
EF2935		Transport and binding proteins	Nucleosides, purines and pyrimidines	xanthine/uracil permeases family protein	1	1	1	-0,7	**0,00099**	-0,2	0,02802	0,5	0,04082	-1,0	**0,00868**	0,2	0,25440	-1,6	**0,00000**
EF2936		Hypothetical proteins		hypothetical protein	1	0	0	0,3	0,07799	-0,1	0,63580	NA	NA	NA	NA	NA	NA	NA	NA
EF2937		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,02128	0,5	**0,00156**	NA	NA	NA	NA	NA	NA	NA	NA
EF2938		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,5	0,01437	0,7	**0,00008**	NA	NA	NA	NA	NA	NA	NA	NA
EF2939		Cellular processes	Adaptations to atypical conditions	cold-shock domain family protein	1	0	0	0,1	0,43120	0,8	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EF2940		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,03042	1,2	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EF2941		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,01833	0,7	**0,00073**	NA	NA	NA	NA	NA	NA	NA	NA
EF2942		Hypothetical proteins		hypothetical protein	1	0	0	0,5	0,01477	0,6	**0,00017**	NA	NA	NA	NA	NA	NA	NA	NA
EF2943		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,02011	0,4	**0,00335**	NA	NA	NA	NA	NA	NA	NA	NA
EF2944		Hypothetical proteins		hypothetical protein	1	0	0	0,1	0,59430	0,0	0,94510	NA	NA	NA	NA	NA	NA	NA	NA
EF2945		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,49530	-0,1	0,46750	NA	NA	NA	NA	NA	NA	NA	NA
EF2946		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,51320	0,2	0,11870	NA	NA	NA	NA	NA	NA	NA	NA
EF2947		Hypothetical proteins	Domain	conserved domain protein	1	0	0	-0,2	0,33260	0,4	0,01233	NA	NA	NA	NA	NA	NA	NA	NA
EF2948		Unknown function	General	DNA primase domain protein	1	0	0	-0,3	0,37310	-0,1	0,41210	NA	NA	NA	NA	NA	NA	NA	NA
EF2949		Hypothetical proteins		hypothetical protein	1	0	0	-0,2	0,16470	-0,1	0,36200	NA	NA	NA	NA	NA	NA	NA	NA
EF2950		Hypothetical proteins		hypothetical protein	1	0	0	-0,5	0,15190	-0,4	0,01944	NA	NA	NA	NA	0,2	0,39100	-0,1	0,55590
EF2951		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	0,2	0,31130	-0,1	0,61000	NA	NA	NA	NA	NA	NA	NA	NA
EF2952		Hypothetical proteins		hypothetical protein	1	0	0	0,0	0,86760	0,4	**0,00328**	-0,1	0,63320	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF2953		Hypothetical proteins		hypothetical protein	1	0	0	0,4	0,12750	0,9	**0,00019**	NA	NA	NA	NA	NA	NA	NA	NA
EF2954		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	0,1	0,72370	0,0	0,81330	NA	NA	NA	NA	NA	NA	NA	NA
EF2955		Mobile and extrachromosomal element functions	Prophage functions	site-specific recombinase, phage integrase family	1	0	0	-0,4	0,06223	-0,7	**0,00011**	NA	NA	NA	NA	NA	NA	NA	NA
EF2956		Unknown function	Enzymes of unknown specificity	oxidoreductase, short-chain dehydrogenase/reductase family	1	1	1	NA	NA	NA	NA	-0,2	0,46420	NA	NA	NA	NA	NA	NA
EF2957		Unknown function	Enzymes of unknown specificity	hexapeptide-repeat containing-acetyltransferase	1	1	1	0,0	0,88010	0,0	0,87620	0,0	0,86830	0,0	0,90730	-0,1	0,40930	0,2	0,29350
EF2958	*hypR*	Regulatory functions	DNA interactions	transcriptional regulator, LysR family	1	1	1	0,1	0,73000	NA	NA	0,1	0,63140	NA	NA	0,5	**0,00117**	0,9	**0,00026**
EF2959		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	ribose uptake protein, putative	1	1	1	1,8	**0,00000**	1,1	**0,00000**	1,9	**0,00003**	0,7	0,02873	1,1	**0,00010**	1,5	**0,00004**
EF2960		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	ribose transporter protein RbsD	1	1	1	1,5	**0,00000**	0,5	**0,00210**	1,9	**0,00000**	0,4	0,07327	1,3	**0,00004**	1,2	**0,00036**
EF2961	*rbsK*	Energy metabolism	Sugars	ribokinase	1	1	1	1,7	**0,00000**	0,4	0,02310	1,8	**0,00000**	0,2	0,21550	1,7	**0,00000**	1,3	**0,00007**
EF2962		Regulatory functions	DNA interactions	sugar-binding transcriptional regulator, LacI family	1	1	1	-0,4	0,03686	-0,4	0,01223	-0,7	**0,00900**	-0,7	0,01105	0,0	0,99860	-0,4	0,07519
EF2963		Unknown function	Enzymes of unknown specificity	esterase, putative	1	1	1	0,4	0,02355	-0,2	0,06145	0,7	**0,00420**	0,7	0,01890	0,4	**0,00878**	0,8	**0,00126**
EF2964		Transport and binding proteins	Unknown substrate	putative transport protein, SgaT family	1	1	1	0,6	0,01041	-1,4	**0,00000**	0,5	0,02247	-0,8	**0,00556**	0,8	**0,00077**	0,1	0,76880
EF2965		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,5	0,02087	-1,2	**0,00006**	0,4	0,06894	-1,2	**0,00022**	1,0	**0,00148**	0,1	0,66760
EF2966		Regulatory functions	RNA interactions	transcriptional antiterminator, bglG family	1	1	1	0,8	**0,00109**	-0,3	0,01079	-0,3	0,04260	-1,9	**0,00007**	0,9	**0,00038**	0,3	0,20380
EF2967		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,5	0,02266
EF2968		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2969		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2970		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,2	0,38370
EF2972		Cellular processes	Toxin production and resistance	amidinotransferase family protein	1	1	1	0,3	0,13020	0,0	0,85530	-0,3	0,08912	0,4	0,06444	0,3	0,02403	0,8	**0,00190**
EF2973	*phoZ*	Central intermediary metabolism	Phosphorus compounds	alkaline phosphatase	1	1	1	NA	NA	NA	NA	-0,7	**0,00217**	-0,4	0,07426	NA	NA	NA	NA
EF2974		DNA metabolism	Other	MutS2 family protein	1	1	1	NA	NA	NA	NA	-0,7	0,01135	-0,2	0,32080	NA	NA	NA	NA
EF2977	*mpoD*	Signal transduction	PTS	PTS system, IID component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2978	*mpoC*	Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	0,2	0,15650	NA	NA	-0,3	0,15630	-0,5	0,10410
EF2979	*mpoB*	Signal transduction	PTS	PTS system, IIB component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2980	*mpoA*	Signal transduction	PTS	PTS system, IIA component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2981	*mpoR*	Transcription	Transcription factors	sigma-54 dependent DNA-binding response regulator	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2982	*pgm*	Energy metabolism	Glycolysis/gluconeogenesis	phosphoglycerate mutase family protein	1	1	1	0,6	0,01136	1,7	**0,00000**	0,3	0,03096	0,7	0,01231	0,6	**0,00126**	1,7	**0,00000**
EF2983		Protein synthesis	tRNA aminoacylation	glutamyl-tRNA(Gln) amidotransferase, A subunit, putative	1	1	1	0,9	**0,00094**	2,7	**0,00000**	0,7	**0,00328**	1,5	**0,00031**	1,1	**0,00002**	2,4	**0,00000**
EF2984		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2985		Transport and binding proteins	Unknown substrate	permease, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2986		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	NA	NA	-1,1	**0,00013**	-0,6	0,01643	-1,0	0,04159	-0,9	**0,00147**	NA	NA
EF2987		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2988		Cellular processes	Detoxification	rhodanese family protein	1	1	1	-0,5	0,01855	NA	NA	-0,8	**0,00134**	NA	NA	-0,3	0,06399	NA	NA
EF2989		Central intermediary metabolism	Other	coenzyme A disulfide reductase	1	1	1	-0,1	0,68630	0,6	**0,00373**	-0,5	0,03682	0,6	0,02209	0,0	0,77640	0,4	0,12100
EF2990		Cellular processes	Detoxification	rhodanese family protein	1	1	1	0,3	0,17400	NA	NA	-0,3	0,26640	0,3	0,60320	0,1	0,49240	NA	NA
EF2991		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2992		Transport and binding proteins	Unknown substrate	major facilitator family transporter	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2994		Unknown function	Enzymes of unknown specificity	aminotransferase, class V	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2995		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00848**	2,8	**0,00000**	1,1	**0,00004**	1,4	**0,00034**	1,1	**0,00004**	2,6	**0,00000**
EF2996		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	1,0	**0,00383**	0,9	0,01885	NA	NA	NA	NA
EF2997		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF2999		Purines, pyrimidines, nucleosides, and nucleotides	Other	allantoinase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3000		Transport and binding proteins	Nucleosides, purines and pyrimidines	cytosine/purines, uracil, thiamine, allantoin permease family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3001		Regulatory functions	Other	protease synthase and sporulation negative regulatory protein pai 1	1	1	1	0,0	0,85510	1,3	**0,00000**	0,1	0,63450	-0,3	0,30370	-0,1	0,61180	1,3	**0,00017**
EF3002		Regulatory functions	DNA interactions	transcriptional regulator, MarR family	1	1	1	-0,3	0,25440	1,3	**0,00001**	0,2	0,21870	-0,4	0,24380	-0,1	0,69370	1,3	**0,00004**
EF3003		Cell envelope	Other	lipoprotein, putative	1	0	1	0,1	0,58610	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3004		Transport and binding proteins	Anions	sulfate transporter family/STAS domain protein	1	1	1	-0,2	0,44860	-1,8	**0,00000**	-0,5	**0,00920**	-0,1	0,69880	-0,5	**0,00234**	-1,7	**0,00000**
EF3005		Energy metabolism	Other	choloylglycine hydrolase family protein	1	1	1	-0,6	**0,00321**	-0,3	0,26380	0,3	0,30760	-1,1	**0,00009**	0,1	0,70970	-0,3	0,18730
EF3006		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,35570	0,4	0,02244	0,3	0,07166	0,8	**0,00059**	NA	NA	NA	NA
EF3007		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,97590	0,6	**0,00345**	0,3	0,20810	0,8	0,03189	-0,1	0,58000	0,8	**0,00086**
EF3008		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,90200	NA	NA	0,0	0,84500	NA	NA	-0,3	0,07124	0,0	0,98280
EF3009		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,7	**0,00962**	NA	NA
EF3010		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3011		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,1	0,68810	NA	NA	NA	NA	NA	NA
EF3012		Cell envelope	Other	membrane protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3013		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,4	0,11870	1,6	**0,00000**	0,6	0,01566	0,7	0,01004	0,3	0,02464	1,1	**0,00004**
EF3014		Transport and binding proteins	Cations and iron carrying compounds	cation-transporting ATPase, E1-E2 family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3015		Transport and binding proteins	Unknown substrate	sodium:dicarboxylate symporter family protein	1	1	1	-0,8	**0,00807**	0,6	**0,00039**	0,3	0,24480	-0,3	0,33050	-0,4	0,01038	0,6	0,05488
EF3016		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,35570	-0,1	0,49180	-0,1	0,54770	-0,1	0,69610	0,1	0,48810	-0,4	0,03532
EF3018		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,1	0,74000	-0,9	**0,00002**	1,4	**0,00001**	-1,0	**0,00020**	-0,5	**0,00101**	-0,7	**0,00149**
EF3019		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,5	**0,00580**	NA	NA	-0,2	0,46690	0,0	0,96370	-0,3	0,03326	-0,4	0,02851
EF3020		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,11140	NA	NA	-0,3	0,24460	NA	NA	-0,4	0,05417	-0,3	0,27890
EF3021		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,7	**0,00002**	2,6	**0,00000**	1,6	**0,00007**	0,8	**0,00136**	1,6	**0,00000**	2,4	**0,00000**
EF3022		Transport and binding proteins	Unknown substrate	sodium:dicarboxylate symporter family protein	1	1	1	-0,4	0,14010	-0,8	**0,00005**	-1,7	**0,00011**	-0,4	0,29830	-1,2	**0,00012**	-1,2	**0,00001**
EF3023		Cellular processes	Pathogenesis	polysaccharide lyase, family 8	1	1	1	NA	NA	NA	NA	-0,3	0,21860	NA	NA	-0,3	0,02795	-1,1	**0,00017**
EF3024		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3025		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00246	1	1	1	0,0	0,88010	-0,1	0,72770	0,1	0,41390	-0,1	0,54810	0,5	0,01488	0,3	0,21010
EF3027	*htrA*	Protein fate	Degradation of proteins, peptides, and glycopeptides	serine protease DO	1	1	1	0,6	**0,00326**	2,9	**0,00000**	0,6	**0,00133**	1,9	**0,00002**	1,0	**0,00002**	2,4	**0,00000**
EF3028		Unknown function	General	putative tRNA-binding domain protein	1	1	1	-0,1	0,52750	-1,3	**0,00000**	-0,3	0,03423	-0,6	0,01375	-0,4	**0,00375**	-0,6	**0,00191**
EF3029		Signal transduction	PTS	PTS system, IID component	1	0	0	0,4	0,29560	-0,4	0,03780	NA	NA	NA	NA	NA	NA	NA	NA
EF3030		Signal transduction	PTS	PTS system, IIC component	1	0	0	0,4	0,05588	-0,5	**0,00790**	NA	NA	NA	NA	NA	NA	NA	NA
EF3031		Signal transduction	PTS	PTS system, IIB component	1	0	0	0,6	0,01851	-0,4	**0,00773**	NA	NA	NA	NA	NA	NA	NA	NA
EF3032		Signal transduction	PTS	conserved hypothetical protein	1	0	0	0,8	**0,00247**	-0,5	**0,00324**	NA	NA	NA	NA	NA	NA	NA	NA
EF3033		Signal transduction	PTS	PTS system, IIA component	1	0	0	1,2	**0,00035**	-0,6	**0,00194**	NA	NA	NA	NA	NA	NA	NA	NA
EF3034		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	0	0	1,2	**0,00033**	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3035		Cellular processes	Adaptations to atypical conditions	universal stress protein family	1	1	1	0,4	0,06439	0,1	0,48400	0,7	**0,00031**	0,1	0,58110	0,5	**0,00091**	0,0	0,98180
EF3036		Energy metabolism	Electron transport	thioredoxin family protein	1	1	1	0,3	0,09602	-0,3	0,07511	0,1	0,62700	0,3	0,09294	0,2	0,22990	-0,2	0,34400
EF3037	*pepA*	Protein fate	Degradation of proteins, peptides, and glycopeptides	glutamyl-aminopeptidase	1	1	1	0,7	**0,00143**	0,0	0,72950	0,6	**0,00858**	0,1	0,68180	0,5	**0,00229**	0,2	0,30900
EF3039		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,07339	1,4	**0,00000**	0,5	0,05638	0,5	0,05200	0,6	**0,00015**	0,9	**0,00013**
EF3040		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3041		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	-1,6	**0,00000**	-3,3	**0,00000**	-1,7	**0,00000**	-3,0	**0,00000**	-1,2	**0,00001**	-1,9	**0,00000**
EF3042		Signal transduction	PTS	PTS system, IID component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3043		Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	q-value	M_t30	q-value	O_t5	q-value	O_t30	q-value	S_t5	q-value	S_t30	q-value
EF3044	*nagA-2*	Central intermediary metabolism	Amino sugars	N-acetylglucosamine-6-phosphate deacetylase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3045		Signal transduction	PTS	PTS system, IIB component	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3046		Signal transduction	PTS	PTS system, IIA component	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3047		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	0,2	0,56360	0,3	0,81250	-0,1	0,82340	0,1	0,85860
EF3048		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3049		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, RpiR family	1	1	1	0,8	**0,00061**	1,1	**0,00000**	0,4	**0,00985**	0,3	0,16930	0,9	**0,00008**	1,4	**0,00001**
EF3050	*tag-2*	DNA metabolism	DNA replication, recombination, and repair	DNA-3-methyladenine glycosylase I	1	1	1	-0,1	0,49170	0,9	**0,00004**	-0,3	0,06070	-0,6	0,03077	-0,2	0,14280	0,4	0,03291
EF3051		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,1	0,51740	0,5	**0,00054**	-0,2	0,32900	-0,5	0,12090	-0,2	0,10590	0,3	0,08049
EF3052		Hypothetical proteins		hypothetical protein	1	1	1	1,4	**0,00002**	2,8	**0,00000**	0,9	**0,00029**	1,1	**0,00022**	1,3	**0,00001**	2,0	**0,00000**
EF3053		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,33260	0,9	**0,00000**	0,0	0,91610	0,9	**0,00086**	0,0	0,86530	0,4	0,02216
EF3054		Cell envelope	Other	lipoprotein, putative	1	1	1	0,3	0,06134	0,4	**0,00606**	0,5	0,01108	0,5	0,01228	0,3	0,02973	1,0	**0,00017**
EF3055		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,3	0,13120	1,2	**0,00015**	0,2	0,16970	-0,3	0,33640	0,4	0,06210	0,4	0,01250
EF3056	*srtA*	Cell envelope	Surface structures	sortase family protein	1	1	1	0,5	0,01382	1,1	**0,00649**	0,4	0,02281	0,2	0,44800	0,8	**0,00004**	1,1	**0,00008**
EF3057		Hypothetical proteins		hypothetical protein	1	1	1	0,7	**0,00100**	0,3	0,02047	1,4	**0,00005**	-0,5	0,10430	0,9	**0,00005**	0,4	0,07070
EF3058		Regulatory functions	Protein interactions	phosphotyrosine protein phosphatase	1	1	1	-0,1	0,40190	0,2	0,16370	0,1	0,77010	-0,3	0,29590	0,3	0,08611	0,1	0,59660
EF3059		Regulatory functions	DNA interactions	transcriptional regulator, TetR family	1	1	1	-0,1	0,59830	0,2	0,07503	0,5	0,01500	-0,1	0,72100	0,3	0,06032	0,0	0,82920
EF3060	*salA*	Unknown function	Enzymes of unknown specificity	secreted lipase, putative	1	1	1	-3,5	**0,00002**	-0,7	**0,00179**	-3,6	**0,00000**	-1,1	**0,00006**	-3,1	**0,00000**	-0,7	**0,00086**
EF3061	*mreD*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	rod shape-determining protein MreD	1	1	1	-1,0	**0,00458**	-0,1	0,26970	-0,6	0,11280	0,2	0,75990	-0,2	0,29390	-0,3	0,32640
EF3062	*mreC*	Cell envelope	Biosynthesis/degradation of murein sacculus/peptidoglycan	rod shape-determining protein MreC	1	1	1	-0,5	0,01180	0,1	0,19710	-0,3	0,11800	0,1	0,81030	-0,2	0,38080	0,0	0,85090
EF3063		Cellular processes	Toxin production and resistance	immunity protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3064	*pnpA*	Transcription	Degradation of RNA	polyribonucleotide nucleotidyltransferase	1	1	1	-1,0	**0,00005**	-0,9	**0,00059**	-1,6	**0,00000**	-0,9	**0,00059**	-1,2	**0,00002**	-2,0	**0,00000**
EF3065	*rpsO*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S15	1	1	1	-0,7	0,01231	-0,9	0,01821	-2,1	**0,00000**	-0,7	0,04256	-0,8	**0,00476**	-2,1	**0,00001**
EF3066	*def-1*	Protein fate	Protein modification and repair	polypeptide deformylase	1	1	1	0,7	0,02687	0,0	0,89670	0,2	0,34160	0,1	0,57750	0,6	**0,00349**	-0,4	0,04964
EF3067		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-0,7	**0,00123**	-1,2	**0,00000**	-1,2	**0,00005**	-0,2	0,38380	-1,1	**0,00005**	-1,1	**0,00009**
EF3068		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,3	0,09567	-0,8	**0,00001**	-0,6	**0,00775**	-0,4	0,11930	-0,5	**0,00458**	-0,8	**0,00151**
EF3069		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	formate/nitrite transporter family protein	1	1	1	-1,2	**0,00003**	-2,9	**0,00000**	-1,7	**0,00003**	-0,5	0,27030	-1,4	**0,00001**	-2,3	**0,00000**
EF3070	*rpsD*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S4	1	1	1	-1,4	**0,00009**	-2,6	**0,00000**	-2,5	**0,00000**	-0,2	0,46490	-1,4	**0,00001**	-1,7	**0,00006**
EF3071		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3072		Biosynthesis of cofactors, prosthetic groups, carriers	Biotin	BioY family protein	1	1	1	-0,3	0,13570	-0,4	0,02141	0,0	0,86150	2,5	**0,00000**	-0,2	0,12280	0,2	0,20360
EF3073		Protein fate	Protein and peptide secretion and trafficking	signal peptidase I	1	1	1	0,4	0,04853	1,3	**0,00000**	0,6	**0,00213**	2,0	**0,00000**	0,1	0,35840	1,0	**0,00011**
EF3074		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3075		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3076		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	-0,5	**0,00296**	NA	NA	-0,2	0,68920	-0,2	0,51350	0,0	0,91890
EF3078		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,2	**0,00020**	-0,2	0,43280	-1,1	**0,00174**	-0,9	**0,00053**	-1,1	**0,00012**	-0,1	0,71830
EF3079		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	1	-0,9	0,01764	0,1	0,32790	-0,9	**0,00082**	-0,8	**0,00316**	-0,6	0,01715	0,1	0,75040
EF3080	*pepT-2*	Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase T	1	1	1	-0,8	**0,00492**	-1,0	**0,00015**	-0,2	0,28110	0,5	0,01365	-0,5	**0,00691**	-0,1	0,80040
EF3081		Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,7	**0,00137**	-0,2	0,60590
EF3082	*fatB*	Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, substrate-binding protein	1	1	1	-0,2	0,33200	2,3	**0,00000**	-0,1	0,62930	3,4	**0,00000**	-0,6	**0,00609**	1,7	**0,00000**
EF3083	*ceuD*	Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, ATP-binding protein	1	1	1	-0,3	0,21400	2,3	**0,00000**	0,0	0,78980	3,3	**0,00000**	-0,4	0,01937	1,5	**0,00001**
EF3084	*ceuC*	Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, permease protein	1	1	1	-0,7	**0,00617**	2,7	**0,00000**	-0,2	0,13540	4,0	**0,00000**	-0,6	**0,00210**	1,7	**0,00000**
EF3085	*ceuB*	Transport and binding proteins	Cations and iron carrying compounds	iron compound ABC transporter, permease protein	1	1	1	-0,4	0,01907	2,0	**0,00000**	-0,2	0,26680	2,7	**0,00011**	-0,1	0,27120	2,5	**0,00000**
EF3086		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,49960	1,0	**0,00001**	-0,3	0,17490	0,5	**0,00922**	0,0	0,98630	1,3	**0,00000**
EF3087		Hypothetical proteins		hypothetical protein	1	1	1	0,1	0,74720	-0,2	0,22770	0,1	0,55270	0,5	0,27380	-0,6	**0,00217**	-0,3	0,04790
EF3088		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,59390	-0,2	0,06263	-0,3	0,14490	0,1	0,89320	-0,1	0,40230	0,1	0,53160
EF3089		Biosynthesis of cofactors, prosthetic groups, carriers	Glutathione and analogs	glutamate--cysteine ligase, putative/amino acid ligase, putative	1	1	1	0,6	0,19810	0,8	**0,00001**	0,4	0,07461	0,7	0,01772	0,6	**0,00052**	1,4	**0,00000**
EF3090		Unknown function	Enzymes of unknown specificity	isochorismatase family protein	1	1	1	0,4	0,03096	1,0	**0,00000**	NA	NA	0,2	0,29610	NA	NA	NA	NA
EF3091		Unknown function	General	YitT family protein	1	1	1	-0,9	**0,00025**	-1,5	**0,00000**	-0,6	**0,00383**	-0,7	**0,00334**	-1,0	**0,00012**	-1,5	**0,00001**
EF3092		Unknown function	Enzymes of unknown specificity	glyoxalase family protein	1	1	1	0,0	0,96250	2,0	**0,00000**	-0,3	0,09729	-0,3	0,20430	0,2	0,09924	1,0	**0,00003**
EF3093		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-1,5	**0,00002**	-1,8	**0,00001**	-1,5	**0,00005**	-1,0	**0,00570**	-0,8	**0,00152**	-1,5	**0,00000**
EF3094	*ftsY*	Protein fate	Protein and peptide secretion and trafficking	signal recognition particle-docking protein FtsY	1	1	1	-0,8	**0,00204**	-1,9	**0,00000**	-1,1	**0,00014**	-0,7	**0,00928**	-0,8	**0,00017**	-1,4	**0,00003**
EF3095		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	-0,9	**0,00071**	-2,1	**0,00000**	-0,9	**0,00031**	-0,5	0,01498	-0,8	**0,00052**	-1,3	**0,00039**
EF3096		Cellular processes	Cell division	chromosome partition protein SMC	1	1	1	0,0	0,86280	-0,4	**0,00221**	-0,5	0,01304	-0,3	0,07398	0,0	0,86410	-0,7	**0,00836**
EF3097	*rnc*	Transcription	RNA processing	ribonuclease III	1	1	1	0,1	0,74720	-0,6	**0,00041**	-0,2	0,35140	-0,4	0,21020	-0,2	0,23930	-1,0	**0,00058**
EF3099		Transport and binding proteins	Unknown substrate	transporter accessory protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3101		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	-0,3	0,23890	NA	NA	NA	NA	NA	NA	NA	NA
EF3102		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	-0,9	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EF3103		Cell envelope	Other	membrane protein, putative	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3104		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	0	0	NA	NA	-0,2	0,14420	NA	NA	NA	NA	NA	NA	NA	NA
EF3105		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,75570	0,0	0,77860	NA	NA	NA	NA	NA	NA	NA	NA
EF3106		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, peptide-binding protein	1	1	1	0,6	**0,00672**	5,1	**0,00000**	0,8	**0,00407**	3,4	**0,00000**	-0,2	0,10600	0,4	0,14480
EF3107		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, permease protein	1	1	1	0,7	0,01341	4,5	**0,00000**	1,8	**0,00005**	3,2	**0,00000**	-0,1	0,55710	0,5	0,02313
EF3108		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, permease protein	1	1	1	1,2	**0,00223**	4,7	**0,00000**	2,9	**0,00001**	3,3	**0,00001**	-0,1	0,52280	0,4	0,06023
EF3109		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, ATP-binding protein	1	1	1	1,4	**0,00399**	4,7	**0,00000**	3,1	**0,00000**	2,8	**0,00003**	0,2	0,19620	0,6	0,02769
EF3110		Transport and binding proteins	Amino acids, peptides and amines	peptide ABC transporter, ATP-binding protein	1	1	1	1,7	**0,00087**	4,3	**0,00000**	3,1	**0,00000**	3,0	**0,00000**	0,4	0,02736	0,6	**0,00836**
EF3111	*acpP*	Fatty acid and phospholipid metabolism	Biosynthesis	acyl carrier protein	1	1	1	0,2	0,54190	0,0	0,84830	-0,7	**0,00388**	-0,1	0,74150	0,0	0,99860	-0,2	0,29350
EF3112	*plsX*	Fatty acid and phospholipid metabolism	Biosynthesis	fatty acid/phospholipid synthesis protein PlsX	1	1	1	0,1	0,75820	-0,2	0,43690	-0,4	0,01205	-0,1	0,55760	0,0	0,85190	-0,3	0,20930
EF3113	*recG*	DNA metabolism	DNA replication, recombination, and repair	ATP-dependent DNA helicase RecG	1	1	1	-0,3	0,06220	-1,4	**0,00000**	-0,5	0,10340	-0,9	**0,00910**	-0,5	0,02685	-0,8	**0,00160**
EF3114		Unknown function	General	DAK2 domain protein	1	1	1	-0,1	0,84130	-0,7	**0,00006**	-0,1	0,52850	-0,5	0,03788	0,2	0,19170	-0,1	0,73870
EF3115		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,44730	-0,3	0,04955	0,0	0,81060	-0,5	0,05421	0,4	0,01723	-0,1	0,58380
EF3116	*rpmB*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L28	1	1	1	-0,5	0,01535	-1,3	**0,00002**	-0,7	**0,00127**	-0,6	0,20180	-0,5	**0,00120**	-1,2	**0,00014**
EF3117		Unknown function	Enzymes of unknown specificity	thiamin pyrophosphokinase family protein	1	1	1	-0,3	0,07655	-0,1	0,77440	-0,2	0,21870	-0,3	0,22070	-0,3	0,06944	0,1	0,59020
EF3118	*rpe*	Energy metabolism	Pentose phosphate pathway	ribulose-phosphate 3-epimerase	1	1	1	-0,8	**0,00066**	-0,8	**0,00301**	-0,7	**0,00102**	-0,4	0,03779	-0,5	**0,00571**	-0,2	0,39520
EF3119		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00157	1	1	1	-0,2	0,36610	0,0	0,77630	-0,1	0,49240	0,0	0,98940	-0,1	0,76020	0,3	0,11170
EF3120		Regulatory functions	Protein interactions	serine/threonine protein kinase	1	1	1	-0,5	**0,00577**	-0,6	**0,00066**	-0,8	0,02161	-0,4	0,16090	-0,6	**0,00033**	-0,1	0,61170
EF3121		Unknown function	Enzymes of unknown specificity	protein phosphatase 2C, putative	1	1	1	-0,4	0,04724	-0,2	0,21310	-1,0	**0,00180**	-0,6	0,01596	-0,8	**0,00002**	-0,4	0,15720
EF3122	*sun*	Protein synthesis	tRNA and rRNA base modification	Sun protein	1	1	1	-0,6	**0,00299**	-0,8	**0,00001**	-1,2	**0,00116**	-0,8	**0,00193**	-1,7	**0,00000**	-1,2	**0,00002**
EF3123	*fmt*	Protein synthesis	tRNA aminoacylation	methionyl-tRNA formyltransferase	1	1	1	0,1	0,68440	-0,2	0,18430	-0,5	0,03064	-0,4	0,03901	-0,5	**0,00137**	-0,1	0,37970
EF3125	*priA*	DNA metabolism	DNA replication, recombination, and repair	primosomal protein n	1	1	1	0,3	0,14710	0,2	0,29070	0,1	0,66760	-0,2	0,55560	0,3	0,12390	-0,1	0,53640
EF3126	*rpoZ*	Transcription	DNA-dependent RNA polymerase	DNA-directed RNA polymerase, omega subunit	1	1	1	-0,7	**0,00485**	0,0	0,76050	-0,7	**0,00055**	-0,1	0,74380	-0,6	**0,00468**	0,5	**0,00497**
EF3127	*gmk-2*	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	guanylate kinase	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3129		Cellular processes	Toxin production and resistance	D-alanyl-D-alanine carboxypeptidase	1	1	1	-0,6	**0,00504**	-0,8	**0,00029**	-0,7	**0,00104**	-0,7	**0,00430**	-0,2	0,06363	-0,4	0,06470
EF3130		Hypothetical proteins		hypothetical protein	1	1	1	0,9	**0,00079**	1,5	**0,00000**	0,2	0,28110	0,3	0,17410	0,6	**0,00039**	0,8	**0,00032**
EF3131		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00255	1	1	1	0,7	**0,00057**	0,1	0,50480	0,2	0,24440	0,1	0,68920	0,3	0,03633	0,4	0,02525

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF3132		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,8	**0,00420**	0,4	**0,00597**	0,3	0,12090	0,0	0,92420	0,4	0,02629	0,6	**0,00399**
EF3133		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,2	0,46210	-0,4	0,03827	-0,5	**0,00272**	-0,2	0,26290
EF3134	*eda-2*	Energy metabolism	Entner-Doudoroff	2-dehydro-3-deoxyphosphogluconate aldolase	1	1	1	1,9	**0,00001**	NA	NA	1,0	**0,00013**	NA	NA	0,6	**0,00156**	-0,9	**0,00532**
EF3135		Energy metabolism	Sugars	mannonate dehydratase, putative	1	1	1	2,1	**0,00003**	NA	NA	1,6	**0,00000**	NA	NA	1,0	**0,00010**	-0,8	**0,00306**
EF3136		Signal transduction	PTS	PTS system, IIA component	1	1	1	1,8	**0,00004**	NA	NA	1,4	**0,00001**	NA	NA	0,9	**0,00010**	-0,7	0,01194
EF3137		Signal transduction	PTS	PTS system, IIB component	1	1	1	1,7	**0,00006**	NA	NA	1,3	**0,00000**	NA	NA	1,0	**0,00021**	-0,8	0,01002
EF3138		Signal transduction	PTS	PTS system, IID component	1	1	1	1,8	**0,00069**	NA	NA	1,1	**0,00002**	NA	NA	1,1	**0,00052**	-0,5	0,07500
EF3139		Signal transduction	PTS	PTS system, IIC component	1	1	1	1,6	**0,00018**	NA	NA	1,1	**0,00114**	NA	NA	1,1	**0,00217**	-1,0	**0,00325**
EF3140		Energy metabolism	Fermentation	alcohol dehydrogenase, iron-containing	1	1	1	1,2	**0,00061**	-0,5	0,01182	1,4	**0,00001**	NA	NA	0,7	0,01618	-0,8	0,01744
EF3141		Unknown function	Enzymes of unknown specificity	D-isomer specific 2-hydroxyacid dehydrogenase family protein	1	1	1	0,3	0,23120	-1,8	**0,00000**	1,3	**0,00001**	-1,5	**0,00006**	0,5	0,02315	-1,1	**0,00043**
EF3142		Energy metabolism	Sugars	6-phosphogluconate dehydrogenase family protein	1	1	1	0,0	0,89110	-1,7	**0,00001**	1,0	**0,00018**	-1,9	**0,00004**	0,1	0,76760	-1,1	**0,00020**
EF3144		Regulatory functions	DNA interactions	phosphosugar-binding transcriptional regulator, RpiR family	1	1	1	0,0	0,96370	-0,6	0,01470	0,3	0,21220	-0,2	0,38700	-0,5	**0,00195**	-0,2	0,31070
EF3145		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	0,1	0,38080	0,0	0,97590	NA	NA	NA	NA
EF3146		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	0,5	**0,00621**	0,2	0,29770	NA	NA	NA	NA
EF3148	*pgsA*	Fatty acid and phospholipid metabolism	Biosynthesis	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	1	1	1	-0,5	0,02045	-0,4	0,02339	-0,4	0,05364	0,2	0,71600	-0,2	0,40940	-0,3	0,09809
EF3149		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,3	0,21900	-0,3	0,35700	-0,2	0,33760	-0,2	0,34910	-0,6	**0,00320**	-0,6	0,03418
EF3150		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M16 family	1	1	1	-0,4	0,10310	-0,5	**0,00189**	0,3	0,22290	0,2	0,40750	-0,3	0,05677	-0,1	0,58830
EF3151		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,95210	0,0	0,72560	0,4	0,03161	-0,2	0,39590	-0,1	0,55750	-0,4	0,04186
EF3152	*mscL*	Cellular processes	Adaptations to atypical conditions	large conductance mechanosensitive channel protein	1	1	1	0,6	**0,00117**	3,9	**0,00000**	0,2	0,32070	1,7	**0,00004**	0,5	**0,00182**	3,2	**0,00000**
EF3153		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3154		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3155		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3156		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	-0,3	0,05986	-0,8	**0,00001**	-0,1	0,55810	-0,2	0,35550	-0,1	0,39990	0,0	0,99700
EF3157		Energy metabolism	Biosynthesis and degradation of polysaccharides	glycosyl hydrolase, family 65	1	1	1	-1,0	**0,00004**	-2,5	**0,00000**	-0,8	**0,00034**	-1,1	**0,00124**	-1,0	**0,00001**	-2,0	**0,00001**
EF3158		Unknown function	Enzymes of unknown specificity	hydrolase, haloacid dehalogenase-like family	1	1	1	0,3	0,10740	-1,5	**0,00000**	0,4	0,01167	-0,5	0,06831	0,6	**0,00307**	-2,0	**0,00006**
EF3160		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	0,1	0,48430	-0,1	0,52040	0,1	0,40160	0,0	0,96920
EF3161		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3163	*prsA-2*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	ribose-phosphate pyrophosphokinase	1	1	1	-0,3	0,12000	0,5	**0,00163**	-0,6	**0,00437**	-0,1	0,52240	-0,2	0,24110	0,1	0,53460
EF3164	*msrB*	Unknown function	General	PilB family protein	1	1	1	-0,6	**0,00795**	4,4	**0,00000**	0,3	0,22430	1,7	**0,00005**	0,0	0,88760	3,3	**0,00000**
EF3165	*maf*	Cellular processes	Cell division	maf protein	1	1	1	-0,5	**0,00530**	-0,3	0,04687	0,0	0,91570	0,2	0,42030	-0,1	0,45400	-0,1	0,49550
EF3166	*hexB*	DNA metabolism	DNA replication, recombination, and repair	DNA mismatch repair protein HexB	1	1	1	-0,6	**0,00374**	-0,8	**0,00002**	0,1	0,76420	0,1	0,74150	0,0	0,73340	-0,1	0,45610
EF3167	*hexA*	DNA metabolism	DNA replication, recombination, and repair	DNA mismatch repair protein HexA	1	1	1	-0,2	0,40130	-0,2	0,34230	0,0	0,92980	0,1	0,76660	0,1	0,61530	0,2	0,15910
EF3168		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,1	0,58430	-0,3	0,04614	0,0	0,88980	-0,2	0,25350	0,1	0,23860	0,1	0,33930
EF3169		Hypothetical proteins	Conserved	conserved hypothetical protein TIGR00282	1	1	1	-0,1	0,78370	-0,1	0,63840	0,1	0,81100	0,1	0,70120	0,2	0,14920	-0,3	0,05645
EF3170		Unknown function	General	HD/KH domain protein	1	1	1	0,0	0,99240	-0,6	**0,00013**	-0,8	0,08726	0,3	0,29970	-0,1	0,78840	-0,2	0,21080
EF3171	*recA*	DNA metabolism	DNA replication, recombination, and repair	recA protein	1	1	1	-0,2	0,16710	0,9	**0,00000**	-0,1	0,78540	1,0	**0,00010**	0,0	0,78500	1,0	**0,00006**
EF3172	*cinA*	DNA metabolism	DNA replication, recombination, and repair	competence/damage-inducible protein CinA	1	1	1	0,6	**0,00780**	1,4	**0,00000**	0,4	0,03732	1,0	**0,00165**	0,7	**0,00041**	1,0	**0,00058**
EF3173		Hypothetical proteins		hypothetical protein	1	1	1	-0,3	0,21540	-1,7	**0,00000**	-0,1	0,53580	-1,9	**0,00017**	0,2	0,10860	-1,0	**0,00194**
EF3174		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,19750	1,2	**0,00000**	0,3	0,04665	0,7	**0,00251**	0,2	0,27900	0,7	**0,00402**
EF3175		Unknown function	General	rrf2 family protein	1	1	1	0,1	0,60830	0,6	**0,00060**	0,2	0,14210	0,0	0,84240	0,2	0,08317	0,6	**0,00892**
EF3176		Cell envelope	Other	membrane protein, putative	1	1	1	-0,1	0,61590	-0,1	0,53550	0,0	0,87040	-0,6	0,03584	-0,5	**0,00193**	-0,3	0,13020
EF3177		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,2	0,55450	1,2	**0,00000**	0,3	0,08640	0,6	0,01114	-0,1	0,44170	1,0	**0,00005**
EF3178		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, M20/M25/M40 family	1	1	1	1,4	**0,00004**	2,9	**0,00000**	1,3	**0,00008**	1,1	**0,00153**	1,4	**0,00000**	2,5	**0,00000**
EF3179		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,1	0,68210	0,3	**0,00644**	-0,3	0,08743	0,4	0,15270	-0,2	0,11840	0,5	0,01954
EF3180	*sigV*	Transcription	Transcription factors	RNA polymerase sigma-70 factor, ECF subfamily	1	1	1	NA	NA	NA	NA	-0,1	0,40270	0,2	0,34830	NA	NA	0,3	0,19360
EF3181		Hypothetical proteins		hypothetical protein	1	1	1	0,3	0,12990	1,1	**0,00000**	-0,2	0,41550	0,3	0,21450	0,2	0,09954	1,1	**0,00103**
EF3182		Hypothetical proteins		hypothetical protein	1	1	1	0,2	0,35570	0,7	**0,00054**	0,1	0,36240	0,2	0,22280	0,2	0,24950	1,0	**0,00001**
EF3183		Cell envelope	Other	cell wall surface anchor family protein, putative	1	1	1	-0,7	**0,00440**	-1,1	**0,00060**	-0,4	0,02083	-0,4	0,07663	NA	NA	-0,1	0,60130
EF3184		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	**0,00736**	-0,5	**0,00049**	-0,2	0,18870	-0,1	0,69290	0,0	0,86310	0,0	0,88000
EF3185		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00179**	-1,5	**0,00001**	-0,2	0,53940	-0,2	0,48970	-0,2	0,29140	-0,1	0,71930
EF3186		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	**0,00198**	-1,0	**0,00001**	0,0	0,96000	-0,1	0,51300	NA	NA	-0,1	0,83360
EF3187		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	-0,8	**0,00139**	-0,9	**0,00001**	0,4	0,04266	-0,1	0,66380	-0,3	0,18850	-0,2	0,49170
EF3188		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,7	**0,00221**	-0,2	0,05726	0,3	0,04266	0,2	0,22460	-0,3	0,05896	0,1	0,70010
EF3189		Hypothetical proteins		hypothetical protein	1	1	1	-0,4	0,02491	-0,2	0,26690	0,2	0,19540	0,1	0,49830	-0,5	0,01344	-0,3	0,10410
EF3191		Fatty acid and phospholipid metabolism	Degradation	lipase, putative	1	1	1	0,1	0,64720	0,6	**0,00061**	0,3	0,06230	0,5	0,01428	0,1	0,73340	0,8	**0,00025**
EF3192		Unknown function	Enzymes of unknown specificity	isochorismatase family protein	1	1	1	0,4	0,18040	0,9	**0,00026**	0,4	0,04270	0,8	**0,00201**	0,5	**0,00597**	1,2	**0,00001**
EF3193	*lrgB*	Unknown function	General	LrgB family protein	1	1	1	NA	NA	NA	NA	-0,2	0,41060	0,1	0,78260	-0,8	0,01131	NA	NA
EF3194	*lrgA*	Unknown function	General	LrgA family protein	1	1	1	-1,0	0,13150	NA	NA	-1,3	**0,00883**	NA	NA	NA	NA	-0,3	0,14050
EF3196		Signal transduction	Two-component systems	response regulator	1	1	1	0,0	0,87390	1,7	**0,00000**	0,3	0,03064	1,4	**0,00010**	0,2	0,44460	1,4	**0,00000**
EF3197		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	0,0	0,97740	1,5	**0,00000**	-0,1	0,66760	1,0	**0,00133**	0,2	0,08398	1,0	**0,00006**
EF3198		Cell envelope	Other	lipoprotein, YaeC family	1	1	1	-0,1	0,65880	0,7	**0,00237**	-0,6	0,01712	0,7	**0,00317**	-0,2	0,05854	1,5	**0,00000**
EF3199		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	0,2	0,63800	0,7	**0,00016**	-0,4	0,12550	1,5	**0,00009**	0,0	0,84620	1,5	**0,00009**
EF3200		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,0	0,95630	NA	NA	0,3	0,19920	1,3	**0,00007**	0,8	**0,00027**	2,1	**0,00000**
EF3201		Unknown function	General	OsmC/Ohr family protein	1	1	1	0,7	**0,00682**	1,9	**0,00000**	0,3	0,07855	1,0	**0,00054**	1,2	**0,00091**	1,8	**0,00001**
EF3202	*rpsN-3*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S14	1	1	1	NA	NA	0,2	0,19660	-0,4	0,03494	1,1	**0,00121**	NA	NA	0,3	0,15730
EF3203	*rpmG-4*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L33	1	1	1	NA	NA	NA	NA	NA	NA	0,4	0,10170	NA	NA	NA	NA
EF3204		Unknown function	General	cobalamin synthesis protein/P47K family protein	1	1	1	-0,1	0,83320	-0,4	0,03113	-0,2	0,53080	1,6	**0,00046**	NA	NA	0,4	0,27790
EF3205		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	-0,2	0,50830	1,2	**0,00051**	NA	NA	0,1	0,87040
EF3206		Cell envelope	Other	adhesion lipoprotein	1	1	1	NA	NA	NA	NA	-0,2	0,70910	1,1	**0,00095**	NA	NA	0,3	0,41490
EF3207		Unknown function	Enzymes of unknown specificity	dihydrouridine synthase family protein	1	0	1	-1,0	0,01092	-0,3	0,05758	-1,2	**0,00001**	0,2	0,23150	-0,9	**0,00041**	-0,3	0,28180
EF3208		Transport and binding proteins	Unknown substrate	ABC transporter, permease protein	1	1	1	0,3	0,16810	0,4	0,07667	-0,2	0,34240	0,7	0,02219	0,1	0,63480	0,2	0,19840
EF3209		Transport and binding proteins	Unknown substrate	ABC transporter, ATP-binding protein	1	1	1	0,6	0,02169	0,9	**0,00007**	0,4	0,14350	1,0	**0,00261**	0,6	**0,00626**	0,9	**0,00208**
EF3210		Signal transduction	PTS	PTS system, IIA component, putative	1	1	1	-0,7	**0,00183**	-2,4	**0,00000**	-0,6	0,04067	-3,1	**0,00000**	0,1	0,61720	-1,6	**0,00005**
EF3211		Signal transduction	PTS	PTS system, IIB component	1	1	1	-0,3	0,20260	-2,3	**0,00001**	-0,5	0,09419	-3,0	**0,00000**	0,1	0,70210	-1,1	**0,00086**
EF3212		Signal transduction	PTS	PTS system, IIC component	1	1	1	-0,8	**0,00175**	-2,5	**0,00000**	-0,3	0,19630	-3,3	**0,00000**	0,0	0,91870	-1,6	**0,00001**
EF3213		Signal transduction	PTS	PTS system, IID component	1	1	1	-0,2	0,17250	-1,6	**0,00001**	0,4	0,14350	-2,1	**0,00013**	0,4	0,15730	-0,7	**0,00435**
EF3214		Transcription	Other	ATP-dependent helicase, DEAH-box family, putative	1	1	1	NA	NA	NA	NA	0,3	0,06133	-0,4	0,03169	NA	NA	-0,3	0,07500
EF3216		Regulatory functions	Other	transcriptional regulator, putative	1	1	1	-0,1	0,72370	-0,2	0,28080	0,4	0,07632	-0,2	0,39460	0,2	0,27620	-0,2	0,48840
EF3217		Unknown function	Enzymes of unknown specificity	helicase, putative	1	0	0	0,2	0,34740	0,2	0,33560	NA	NA	NA	NA	NA	NA	NA	NA
EF3218		DNA metabolism	DNA replication, recombination, and repair	mutator MutT protein, putative	1	0	0	0,5	0,05277	0,3	0,02914	NA	NA	NA	NA	NA	NA	NA	NA
EF3220		Hypothetical proteins		hypothetical protein	1	0	0	-0,1	0,71210	-0,3	0,09771	NA	NA	NA	NA	NA	NA	NA	NA
EF3221		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	1	0	0	-0,1	0,67170	-0,1	0,54770	NA	NA	NA	NA	NA	NA	NA	NA
EF3222		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	q-value	M_t30	q-value	O_t5	q-value	O_t30	q-value	S_t5	q-value	S_t30	q-value
EF3223		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3224		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3225		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3226		DNA metabolism	DNA replication, recombination, and repair	Rep protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3227		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3230	*rpsI*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein S9	1	1	1	-1,4	**0,00045**	-4,3	**0,00000**	-1,9	**0,00002**	-0,7	0,26540	-0,3	0,03547	-2,7	**0,00000**
EF3232		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3233		Cellular processes	Adaptations to atypical conditions	Dps family protein	1	1	1	0,7	**0,00066**	2,0	**0,00000**	0,6	**0,00701**	1,6	**0,00012**	1,0	**0,00001**	2,1	**0,00000**
EF3234		Cell envelope	Other	lipoprotein, putative	1	1	1	0,5	0,12490	1,1	**0,00000**	0,6	**0,00180**	0,6	**0,00634**	0,4	0,02257	1,1	**0,00010**
EF3235		Energy metabolism	Sugars	gluconate kinase, putative	1	1	1	0,3	0,18520	1,4	**0,00000**	0,7	**0,00375**	1,1	**0,00059**	0,6	**0,00104**	1,3	**0,00002**
EF3236		Protein fate	Protein and peptide secretion and trafficking	type III leader peptidase family	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3237	*rpoC*	Transcription	DNA-dependent RNA polymerase	DNA-directed RNA polymerase, beta-prime subunit	1	1	1	-1,3	**0,00272**	-3,4	**0,00001**	-1,2	**0,00002**	-1,1	**0,00085**	-0,9	**0,00044**	-1,1	**0,00006**
EF3238	*rpoB*	Transcription	DNA-dependent RNA polymerase	DNA-directed RNA polymerase, beta subunit	1	1	1	-1,4	**0,00120**	-3,1	**0,00000**	-1,9	**0,00004**	-1,2	**0,00026**	-1,2	**0,00002**	-1,7	**0,00005**
EF3239		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,3	**0,00003**	0,2	0,16230	2,1	**0,00001**	0,1	0,77610	1,3	**0,00011**	0,6	**0,00190**
EF3240	*birA*	Regulatory functions	DNA interactions	BirA bifunctional protein	1	1	1	-0,3	0,07994	0,1	0,30020	-0,4	0,01925	0,0	0,87980	0,1	0,55880	0,3	0,14560
EF3241		Cellular processes	Other	abortive phage resistance protein, putative	1	0	0	0,1	0,62160	0,0	0,99340	NA	NA	NA	NA	NA	NA	NA	NA
EF3242		Cellular processes	Other	abortive phage resistance protein, putative	1	0	0	0,1	0,72420	-0,2	0,05077	NA	NA	NA	NA	NA	NA	NA	NA
EF3243		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3244		Hypothetical proteins		hypothetical protein	1	1	1	-0,9	**0,00304**	-0,3	**0,00947**	0,8	0,01026	0,3	0,38420	-0,4	0,02133	-0,5	0,01599
EF3245		Unknown function	Enzymes of unknown specificity	cell-envelope associated acid phosphatase	1	1	1	-0,9	0,01002	-0,5	**0,00103**	0,8	0,03521	0,3	0,39620	-0,4	0,04494	-0,4	0,08559
EF3247		Hypothetical proteins		hypothetical protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,6	0,01751	-0,3	0,31330
EF3248		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3249		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,09174	0,2	0,05188	0,5	0,02142	0,6	0,01883	0,2	0,43300	0,7	**0,00697**
EF3250		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3251		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3252		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3253		Cell envelope	Other	cell wall surface anchor family protein	1	0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3254		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative	1	1	1	-0,4	0,04928	-2,3	**0,00000**	0,0	0,95680	-1,2	**0,00537**	-0,2	0,26850	-0,8	**0,00060**
EF3255		Cell envelope	Other	thiamin biosynthesis lipoprotein ApbE, putative	1	1	1	-0,4	0,09053	-1,8	**0,00000**	-0,1	0,67370	-1,1	0,01405	0,0	0,89000	-0,9	**0,00113**
EF3256		Cell envelope	Other	pheromone cAD1 precursor lipoprotein	1	1	1	-0,6	**0,00152**	-2,4	**0,00006**	0,0	0,93590	-0,6	0,02738	-0,2	0,09658	-0,6	**0,00194**
EF3257		Unknown function	Enzymes of unknown specificity	oxidoreductase, pyridine nucleotide-disulfide family	1	1	1	-0,1	0,82120	-1,0	**0,00419**	-0,4	0,11650	0,3	0,29590	-0,3	0,08317	-1,6	**0,00000**
EF3258		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,0	0,80390	-0,6	**0,00092**	0,0	0,99420	-0,7	**0,00155**	-0,1	0,41710	-0,6	**0,00184**
EF3259		Hypothetical proteins	Domain	conserved domain protein	1	1	1	-0,3	0,16960	-0,5	**0,00069**	-0,5	0,01242	-0,9	**0,00041**	-0,3	0,04294	-0,4	0,03871
EF3260		Biosynthesis of cofactors, prosthetic groups, carriers	Menaquinone and ubiquinone	heptaprenyl diphosphate synthase, component II, putative	1	1	1	-0,4	0,01957	-1,0	**0,00016**	-0,7	**0,00347**	-1,0	**0,00076**	-0,4	0,01791	-0,9	0,11840
EF3261		Regulatory functions	DNA interactions	transcriptional regulator, AbrB family	1	0	1	0,0	0,96600	1,0	**0,00006**	NA	NA	NA	NA	NA	NA	NA	NA
EF3262		Regulatory functions	DNA interactions	transcriptional regulator, PemK family	1	0	0	0,1	0,73180	1,0	**0,00010**	NA	NA	NA	NA	NA	NA	NA	NA
EF3263		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,2	0,45690	NA	NA	NA	NA	NA	NA	-0,3	0,04746	-0,8	**0,00522**
EF3264		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EF3265	*folP*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	dihydropteroate synthase	1	1	1	-0,2	0,34700	0,4	0,01783	-0,1	0,78000	0,2	0,35870	-0,3	0,03006	0,7	**0,00145**
EF3266		Unknown function	General	Ham1 family protein, putative	1	1	1	-0,2	0,19970	0,3	0,02894	-0,1	0,66040	0,0	0,91960	-0,3	0,07641	0,7	**0,00363**
EF3267	*folE*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	GTP cyclohydrolase I	1	1	1	0,1	0,49290	0,8	**0,00001**	0,3	0,06931	0,1	0,77610	0,1	0,32880	1,0	**0,00002**
EF3268	*folK*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	hydroxymethyldihydropteridine pyrophosphokinase	1	1	1	0,0	0,96250	0,8	**0,00001**	0,4	0,10270	0,1	0,85360	0,1	0,36510	0,9	**0,00167**
EF3269	*folB*	Biosynthesis of cofactors, prosthetic groups, carriers	Folic acid	dihydroneopterin aldolase	1	1	1	0,3	0,11600	1,0	**0,00004**	0,3	0,12490	0,1	0,70980	0,3	0,01128	1,0	**0,00212**
EF3270	*gor*	Cellular processes	Detoxification	glutathione reductase	1	1	1	0,1	0,84750	0,7	**0,00158**	0,3	0,07633	1,1	**0,00043**	0,5	**0,00043**	1,5	**0,00000**
EF3271		Hypothetical proteins		hypothetical protein	1	1	1	-0,1	0,86270	0,5	**0,00185**	0,1	0,68850	0,9	0,01966	1,3	**0,00003**	2,7	**0,00000**
EF3272		Regulatory functions	DNA interactions	zinc-binding transcriptional regulator, Cro/CI family	1	1	0	0,0	0,90330	0,7	**0,00010**	0,2	0,26390	1,1	**0,00702**	NA	NA	NA	NA
EF3273		Hypothetical proteins		hypothetical protein	1	1	0	0,1	0,77170	0,2	0,22520	0,4	0,06556	0,9	0,01209	NA	NA	NA	NA
EF3274		Hypothetical proteins		hypothetical protein	1	1	0	0,1	0,73450	0,3	0,02076	0,3	0,24410	0,9	0,01475	NA	NA	NA	NA
EF3275		Central intermediary metabolism	Other	hydantoinase/oxoprolinase	1	1	1	0,7	0,13150	1,5	**0,00414**	2,0	**0,00328**	4,1	**0,00000**	1,6	**0,00051**	4,0	**0,00000**
EF3276		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	0,22150	1,2	**0,00410**	1,6	0,01664	3,4	**0,00000**	1,7	**0,00061**	3,7	**0,00000**
EF3277		Transport and binding proteins	Nucleosides, purines and pyrimidines	cytosine permease, putative	1	1	1	1,5	0,01784	2,5	**0,00000**	3,6	**0,00003**	4,5	**0,00000**	2,7	**0,00002**	4,9	**0,00000**
EF3278		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,4	0,07844	-0,5	0,01314	0,4	0,03981	-0,2	0,64830	0,2	0,22400	-0,1	0,74300
EF3279		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, U32 family	1	1	1	-0,2	0,33290	-1,0	**0,00001**	-0,2	0,09295	-0,3	0,10590	-0,5	**0,00088**	-0,9	**0,00021**
EF3280		Protein fate	Degradation of proteins, peptides, and glycopeptides	peptidase, U32 family, putative	1	1	1	0,4	0,19750	-0,9	**0,00060**	-0,1	0,46690	-0,2	0,30360	-0,5	**0,00380**	-0,7	**0,00077**
EF3281		Hypothetical proteins	Domain	conserved domain protein	1	1	1	0,9	**0,00073**	0,1	0,57480	0,8	**0,00012**	0,9	**0,00592**	0,3	0,05084	0,4	0,05124
EF3282	*clpC*	Protein fate	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, ATP-binding subunit ClpC	1	1	1	0,7	**0,00120**	3,0	**0,00000**	0,5	**0,00347**	0,9	0,02554	0,7	**0,00022**	2,7	**0,00000**
EF3283	*ctsR*	Regulatory functions	DNA interactions	transcriptional regulator CtsR	1	1	1	0,9	**0,00089**	3,3	**0,00000**	0,9	**0,00009**	1,2	**0,00279**	0,9	**0,00002**	2,9	**0,00000**
EF3284		Amino acid biosynthesis	Aspartate family	cystathionine gamma-synthase, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	-0,6	0,01559	-0,4	0,16740
EF3285		Signal transduction	PTS	PTS system, IIC component	1	1	1	NA	NA	NA	NA	-1,0	**0,00540**	-0,6	**0,00475**	-0,7	**0,00096**	-0,7	**0,00247**
EF3286		Regulatory functions	Other	phosphosugar-binding transcriptional regulator, putative	1	1	1	0,8	**0,00056**	0,4	**0,00713**	0,7	**0,00057**	0,2	0,22460	0,5	**0,00485**	0,3	0,06719
EF3287		Hypothetical proteins		hypothetical protein	1	1	1	-1,6	**0,00001**	-1,7	**0,00001**	-1,5	**0,00149**	0,1	0,39330	-0,9	**0,00010**	-2,1	**0,00000**
EF3289		Regulatory functions	DNA interactions	DNA-binding response regulator	1	1	1	-0,1	0,41210	0,7	**0,00005**	0,3	0,07789	0,0	0,97710	0,1	0,49920	0,2	0,25490
EF3290		Signal transduction	Two-component systems	sensor histidine kinase	1	1	1	-0,1	0,76990	0,0	0,87620	0,4	0,03041	0,1	0,79180	0,2	0,05770	0,1	0,70420
EF3292	*serS-2*	Protein synthesis	tRNA aminoacylation	seryl-tRNA synthetase	1	1	1	0,7	**0,00032**	-1,1	**0,00001**	0,5	0,01307	0,0	0,83570	0,1	0,50450	-1,1	**0,00003**
EF3293	*guaB*	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	inosine-5`-monophosphate dehydrogenase	1	1	1	-0,4	0,17490	1,7	**0,00001**	-0,3	0,40270	-0,6	0,04226	-0,6	**0,00414**	-0,7	**0,00030**
EF3294		Cell envelope	Other	membrane protein, putative	1	1	1	-1,2	**0,00163**	-1,3	**0,00002**	-1,5	**0,00000**	-0,5	0,01451	-1,2	**0,00050**	-1,1	**0,00002**
EF3295		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,6	0,19740	-1,1	**0,00000**	-1,1	**0,00020**	-0,3	0,26800	-0,8	**0,00002**	-1,3	**0,00001**
EF3296		Unknown function	General	GTP-binding protein, GTP1/OBG family	1	1	1	-0,4	0,08096	-1,4	**0,00008**	-0,9	**0,00046**	-0,5	0,06379	-0,8	**0,00028**	-1,4	**0,00000**
EF3297		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	-0,4	0,18420	-1,5	**0,00000**	-0,7	0,02423	-0,4	0,11370	-0,5	**0,00075**	-1,3	**0,00001**
EF3298		Cellular processes	Cell division	chromosome partitioning protein ParB family	1	1	1	-0,5	0,03404	-1,1	**0,00001**	-0,5	0,02499	-0,3	0,15350	-0,6	**0,00100**	-1,0	**0,00007**
EF3299		Cellular processes	Cell division	ATPase, ParA family	1	1	1	-0,5	**0,00851**	-1,4	**0,00002**	-0,5	0,02848	0,0	0,89200	-0,6	**0,00128**	-0,7	**0,00371**
EF3300	*gidB*	Unknown function	General	glucose-inhibited division protein B	1	1	1	-0,7	**0,00316**	-1,6	**0,00000**	-0,7	**0,00775**	0,0	0,98260	-0,8	**0,00081**	-0,8	**0,00176**
EF3301		Hypothetical proteins		hypothetical protein	1	1	1	1,2	**0,00030**	0,7	**0,00003**	1,4	**0,00006**	0,5	**0,00828**	1,3	**0,00011**	0,9	**0,00157**
EF3302		Hypothetical proteins		hypothetical protein	1	1	1	-0,2	0,40790	-0,2	0,11070	0,2	0,42610	-0,2	0,56020	-0,4	0,07160	0,1	0,62460
EF3303		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,7	**0,00480**	1,9	**0,00000**	0,8	**0,00200**	-0,3	0,53510	0,5	0,04091	2,5	**0,00000**
EF3304	*mipB*	Energy metabolism	Pentose phosphate pathway	transaldolase-like protein MIPB	1	1	1	0,7	**0,00789**	NA	NA	0,2	0,23470	NA	NA	0,9	**0,00027**	-0,4	0,11840
EF3305		Signal transduction	PTS	PTS system, sorbitol-specific IIA component	1	1	1	0,7	0,04610	NA	NA	0,1	0,64560	NA	NA	0,8	**0,00183**	-0,4	0,16740
EF3306		Signal transduction	PTS	PTS system, sorbitol-specific IIBC components	1	1	1	0,9	**0,00248**	-0,8	**0,00055**	0,6	**0,00171**	-0,1	0,85370	1,0	**0,00017**	-0,5	0,06185
EF3307		Signal transduction	PTS	PTS system, sorbitol-specific IIC component	1	1	1	0,5	0,10100	NA	NA	0,7	**0,00044**	NA	NA	1,0	**0,00060**	-0,6	0,03112
EF3308	*srlR*	Regulatory functions	DNA interactions	transcriptional regulator SrlR	1	1	1	0,5	0,03042	NA	NA	0,9	**0,00006**	NA	NA	NA	NA	-0,3	0,11110
EF3309	*srlM*	Regulatory functions	DNA interactions	putative transcriptional activator SrlM	1	1	1	0,3	0,24500	NA	NA	0,5	0,01766	-0,1	0,69580	0,5	0,02397	-0,4	0,12120
EF3310		Unknown function	Enzymes of unknown specificity	oxidoreductase, short chain dehydrogenase/reductase family	1	1	1	0,5	0,01972	NA	NA	0,4	0,01157	0,0	0,93540	0,6	0,01952	-0,1	0,79150
EF3311	*gidA*	Unknown function	General	glucose-inhibited division protein A	1	1	1	-1,2	**0,00001**	-2,3	**0,00000**	-0,7	**0,00981**	-1,0	**0,00028**	-0,5	**0,00653**	-1,4	**0,00001**

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EF3312	*trmE*	Cellular processes	Detoxification	tRNA modification GTPase TrmE	1	1	1	-1,0	**0,00032**	-2,7	**0,00000**	-0,6	**0,00929**	-1,2	**0,00003**	-0,4	0,05084	-1,7	**0,00001**
EF3313		Hypothetical proteins		hypothetical protein	1	1	1	-1,1	**0,00004**	-2,9	**0,00000**	-0,9	**0,00008**	-1,3	**0,00003**	-0,6	**0,00039**	-1,8	**0,00000**
EF3314		Cell envelope	Other	cell wall surface anchor family protein	1	1	1	NA	NA	NA	NA	0,0	0,92400	NA	NA	0,9	**0,00001**	3,5	**0,00000**
EF3315		Unknown function	General	CitG family protein	1	1	1	0,3	0,06592	2,0	**0,00000**	0,3	0,07166	1,3	**0,00013**	0,3	0,09503	1,1	**0,00007**
EF3316		Unknown function	Enzymes of unknown specificity	malic enzyme family protein	1	1	1	0,2	0,26080	0,9	**0,00008**	0,0	0,89340	1,0	**0,00078**	0,3	0,10010	0,2	0,30520
EF3317		Unknown function	Enzymes of unknown specificity	carboxylase, putative	1	1	1	0,7	**0,00612**	0,9	**0,00001**	0,5	**0,00295**	0,9	**0,00013**	0,7	**0,00056**	0,0	0,88120
EF3318	*citX*	Energy metabolism	Fermentation	apo-citrate lyase pyrophosphoribosyl-dephosph-CoA transferase	1	1	1	0,7	0,01910	0,9	**0,00023**	0,6	**0,00604**	0,7	**0,00917**	0,9	**0,00004**	0,4	0,12040
EF3319	*citF*	Energy metabolism	Fermentation	citrate lyase, alpha subunit	1	1	1	0,9	**0,00119**	1,1	**0,00002**	0,6	**0,00043**	0,9	**0,00024**	0,8	**0,00008**	0,4	0,10230
EF3320	*citE*	Energy metabolism	Fermentation	citrate lyase, beta subunit	1	1	1	0,9	**0,00015**	1,1	**0,00002**	0,9	**0,00004**	0,9	**0,00063**	0,8	**0,00003**	0,3	0,21400
EF3321	*citD*	Energy metabolism	Fermentation	citrate lyase, gamma subunit	1	1	1	0,9	**0,00122**	0,5	**0,00122**	0,8	**0,00019**	0,9	**0,00053**	0,9	**0,00002**	0,3	0,25320
EF3322	*citC*	Energy metabolism	Fermentation	citrate lyase ligase	1	1	1	0,8	**0,00707**	0,9	**0,00002**	0,7	**0,00092**	0,9	**0,00146**	0,9	**0,00052**	0,6	0,03054
EF3323		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	1,0	0,01855	1,2	**0,00018**	0,5	0,01150	1,1	**0,00008**	0,6	**0,00199**	0,0	0,90470
EF3324		Energy metabolism	Other	sodium ion-translocating decarboxylase, beta subunit	1	1	1	1,0	**0,00062**	1,3	**0,00003**	0,8	**0,00053**	1,1	**0,00132**	0,6	0,01082	0,4	0,26200
EF3325		Energy metabolism	Other	sodium ion-translocating decarboxylase/biotin carboxyl carrier protein	1	1	1	0,7	**0,00786**	0,0	0,82800	0,3	0,11850	0,7	0,12250	0,7	0,02839	0,4	0,35540
EF3326		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	0,6	**0,00928**	-0,3	0,10130	0,1	0,70320	1,1	**0,00436**	0,8	**0,00128**	0,6	0,13190
EF3327		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	citrate transporter	1	1	1	NA	NA	NA	NA	0,2	0,41280	0,3	0,48860	0,6	**0,00662**	-0,3	0,34360
EF3328		Regulatory functions	DNA interactions	transcriptional regulator, GntR family	1	1	1	-0,5	**0,00416**	0,3	0,01718	-0,4	0,09959	-0,5	0,01982	0,1	0,68650	0,4	0,03036
EF3329		Regulatory functions	DNA interactions	DNA-binding response regulator	1	1	1	-0,2	0,47190	NA	NA	-0,8	**0,00487**	-0,6	0,01231	0,0	0,89210	-0,5	0,04998
EF3330		Unknown function	General	jag protein, putative	1	1	1	-0,1	0,33260	-1,1	**0,00001**	-0,1	0,54940	-0,6	0,01392	-0,1	0,52720	-0,9	**0,00036**
EF3331		Cell envelope	Other	pheromone cCF10 percursor/lipoprotein, 60 kDa	1	1	1	-0,3	0,24080	-1,5	**0,00000**	-0,3	0,06169	-1,1	**0,00025**	-0,2	0,07070	-1,4	**0,00000**
EF3332	*rnpA*	Transcription	RNA processing	ribonuclease P protein component	1	1	1	-0,2	0,29820	-1,0	**0,00002**	-0,3	0,28530	-0,6	0,04415	-0,2	0,21490	-0,2	0,24350
EF3333	*rpmH*	Protein synthesis	Ribosomal proteins: synthesis and modification	ribosomal protein L34	1	1	1	-0,8	**0,00430**	-2,4	**0,00000**	-1,7	**0,00000**	-0,6	0,19600	-0,8	**0,00070**	-2,0	**0,00000**
EFA0001	*repA-1*	Mobile and extrachromosomal element functions	Plasmid functions	replication-associated protein RepA	1	0	0	-0,9	**0,00163**	-0,9	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0002	*traB-1*	Mobile and extrachromosomal element functions	Plasmid functions	pheromone shutdown protein TraB	1	0	0	-0,5	0,31890	-1,2	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0003	*traC-1*	Mobile and extrachromosomal element functions	Plasmid functions	traC protein	1	0	0	0,0	0,96520	-0,3	0,19700	NA	NA	NA	NA	NA	NA	NA	NA
EFA0004	*traA*	Mobile and extrachromosomal element functions	Plasmid functions	traA protein	1	0	0	-1,1	**0,00013**	-1,4	**0,00002**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0007		Cellular processes	Toxin production and resistance	ribosomal RNA adenine dimethylase family protein	1	0	0	0,2	0,40360	1,4	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0010		Transport and binding proteins	Other	multidrug resistance protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0012		Mobile and extrachromosomal element functions	Plasmid functions	replication protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0014		Transport and binding proteins	Other	drug resistance transporter, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0015		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0016		Mobile and extrachromosomal element functions	Transposon functions	transposase, IS6 family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0017		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0019	*ssb-4*	DNA metabolism	DNA replication, recombination, and repair	single-strand binding protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0021		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0022		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0024		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0025		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0026		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0028		Hypothetical proteins	Domain	conserved domain protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0029		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0030		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0031		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0032		Cell envelope	Other	lipoprotein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0035		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0036		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0037		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0039		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0042		Cellular processes	Conjugation	cell wall surface anchor signal protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0047	*asa1*	Cellular processes	Conjugation	aggregation substance Asa1	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0048		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0050		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0051		Hypothetical proteins		hypothetical protein	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0052	*sea1*	Cellular processes	Conjugation	surface exclusion protein Sea1	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0054	*traE1*	Regulatory functions	Other	regulatory protein TraE1	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0057	*copS*	Mobile and extrachromosomal element functions	Plasmid functions	copS protein	1	0	0	0,3	0,21300	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0058	*repE*	Mobile and extrachromosomal element functions	Plasmid functions	repE protein	1	0	0	-0,5	0,08611	-0,9	**0,00235**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0060		Unknown function	Enzymes of unknown specificity	acetyltransferase, GNAT family	1	1	0	-0,3	0,21400	-1,0	**0,00004**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0061		Cellular processes	Toxin production and resistance	6-aminoglycoside N-acetyltransferase	1	0	0	-0,4	0,03353	-0,7	**0,00055**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0065		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0066		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0067		Signal transduction	PTS	PTS system, IIABC components	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0069	*scrB-2*	Energy metabolism	Biosynthesis and degradation of polysaccharides	sucrose-6-phosphate hydrolase	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0070	*scrR-2*	Regulatory functions	DNA interactions	sucrose operon repressor ScrR	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0071		Regulatory functions	DNA interactions	PemK family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0072		Unknown function	General	PemI family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0074		Hypothetical proteins	Domain	conserved domain protein	1	1	0	0,2	0,34720	0,9	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0075		Hypothetical proteins		hypothetical protein	1	1	0	0,2	0,18580	1,5	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0076		Hypothetical proteins		hypothetical protein	1	1	0	-0,1	0,73320	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0078		DNA metabolism	DNA replication, recombination, and repair	ImpB/MucB/SamB family protein	1	1	0	0,5	0,01019	1,1	**0,00003**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0079		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	0	0,4	0,01972	0,7	**0,00918**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0080		Regulatory functions	Other	transcriptional regulator, UvrC family	1	1	0	0,4	0,09141	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFA0081		Hypothetical proteins	Conserved	conserved hypothetical protein	1	0	0	-0,1	0,67870	-0,7	**0,00108**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0082	*repC*	Mobile and extrachromosomal element functions	Plasmid functions	replication-associated protein RepC	1	0	0	0,1	0,58610	0,9	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
EFA0083	*repB-1*	Mobile and extrachromosomal element functions	Plasmid functions	replication-associated protein RepB	1	0	0	-0,2	0,57430	-0,1	0,73300	NA	NA	NA	NA	NA	NA	NA	NA
EFB0001	*repA-2*	Mobile and extrachromosomal element functions	Plasmid functions	replication-associated protein RepA	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0003	*traB-2*	Mobile and extrachromosomal element functions	Plasmid functions	pheromone shutdown protein TraB	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0004	*traC-2*	Mobile and extrachromosomal element functions	Plasmid functions	TraC protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0005		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0005.1		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0007		Mobile and extrachromosomal element functions	Plasmid functions	probable pheromone-responsive regulatory protein R	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0010	*prgA*	Cellular processes	Conjugation	surface exclusion protein PrgA	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0012	*prgC*	Cellular processes	Conjugation	surface protein PrgC	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Locus	Gene	Functional category	Subcategory	Putative function	M*	O*	S*	M_t5	*q*-value	M_t30	*q*-value	O_t5	*q*-value	O_t30	*q*-value	S_t5	*q*-value	S_t30	*q*-value
EFB0013		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0014		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0015		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0016		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0017		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0018		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0019		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0020		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0021		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0022		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0023		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0024		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0025		Mobile and extrachromosomal element functions	Plasmid functions	TraG family protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0026		Hypothetical proteins	Domain	conserved domain protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0027		Unknown function	General	LtrD-related protein, putative	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0029		Hypothetical proteins	Conserved	conserved hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0030		Mobile and extrachromosomal element functions	Plasmid functions	relaxase	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0031		Hypothetical proteins		hypothetical protein	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0032		Hypothetical proteins		hypothetical protein	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0033		Hypothetical proteins	Conserved	conserved hypothetical protein	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0034		Hypothetical proteins	Domain	conserved domain protein	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0035		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0036		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0037		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0038		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0040		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0041		Hypothetical proteins		hypothetical protein	1	1	0	0,9	**0,00183**	0,5	0,21200	NA	NA	NA	NA	NA	NA	NA	NA
EFB0042		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0043	*ssb-6*	DNA metabolism	DNA replication, recombination, and repair	single-strand binding protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0044		Hypothetical proteins		hypothetical protein	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0045	*nuc-2*	DNA metabolism	DNA replication, recombination, and repair	thermonuclease precursor	1	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0046		Hypothetical proteins		hypothetical protein	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0047		Cell envelope	Other	membrane protein, putative	0	1	0	-0,1	0,68490	0,0	0,74790	NA	NA	NA	NA	NA	NA	NA	NA
EFB0048		Regulatory functions	DNA interactions	transcriptional regulator, Cro/CI family	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0049		Cell envelope	Biosynthesis and degradation of surface poly/liposaccharides	glycosyl transferase, group 2 family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0050		Transport and binding proteins	Other	toxin ABC transporter, ATP-binding/permease protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0051		Cell envelope	Other	membrane protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0053		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0054		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0055		Cell envelope	Other	lipoprotein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0056		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0057		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0058		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, resolvase family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0059		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0060		DNA metabolism	DNA replication, recombination, and repair	ImpB/MucB/SamB family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0061		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0062		Regulatory functions	Other	transcriptional regulator, UvrC family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0063	*prgN*	Mobile and extrachromosomal element functions	Plasmid functions	replication control protein PrgN	1	1	0	-0,3	0,30140	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0064		Cellular processes	Cell division	ParA family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFB0065		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0001	*prgZ*	Transport and binding proteins	Amino acids, peptides and amines	pheromone binding protein	0	1	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0002		Hypothetical proteins	Conserved	conserved hypothetical protein, degenerate	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0005		Unknown function	General	restriction endonuclease related protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0006		DNA metabolism	DNA replication, recombination, and repair	ImpB/MucB/SamB family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0008		Hypothetical proteins	Domain	conserved domain protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0009		DNA metabolism	DNA replication, recombination, and repair	site-specific recombinase, resolvase family	1	1	0	0,3	0,06479	1,5	**0,00001**	NA	NA	NA	NA	NA	NA	NA	NA
EFC0011		Regulatory functions	Other	transcriptional regulator, UvrC family	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0012		Hypothetical proteins	Conserved	conserved hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0013		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0014		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0015		DNA metabolism	DNA replication, recombination, and repair	ImpB/MucB/SamB family protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0016		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0017		Hypothetical proteins		hypothetical protein	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0018	*repB-2*	Mobile and extrachromosomal element functions	Plasmid functions	replication-associated protein RepB	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EFC0019		Mobile and extrachromosomal element functions	Plasmid functions	repS protein, putative	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0047	*cylB*	Cellular processes	Toxin production and resistance	CylB protein	1	0	0	0,0	0,98530	0,1	0,48760	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0048	*cylA*	Cellular processes	Toxin production and resistance	CylA protein	1	0	0	0,1	0,58630	-0,2	0,27310	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0049	*cylI*	Cellular processes	Toxin production and resistance	CylI protein	1	0	0	-0,2	0,55040	-0,9	**0,00021**	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0050		Hypothetical proteins		Hypothetical	1	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0051		Hypothetical proteins		Hypothetical	1	0	0	1,1	**0,00307**	-0,7	**0,00240**	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0052	*nsr*	Cellular processes	Toxin production and resistance	Nisin-resistance protein	1	0	0	0,8	**0,00480**	-0,6	**0,00148**	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0053		Hypothetical proteins		Hypothetical	1	0	0	0,0	0,96520	0,7	0,01160	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0054		Hypothetical proteins		Putative 6-kDa protein	1	0	0	0,2	0,41310	2,3	**0,00000**	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0055	*gls24*	Cellular processes	Adaptations to atypical conditions	Stress-induced protein Gls24	1	0	0	-0,3	0,20560	0,9	**0,00020**	NA	NA	NA	NA	NA	NA	NA	NA
PAIef0056	*esp*	Cell envelope	Other	Surface protein	1	0	0	-0,2	0,56850	-0,3	0,09925	NA	NA	NA	NA	NA	NA	NA	NA