Genetic analysis of DMSP metabolism in the marine Roseobacter clade

Mark Kirkwood

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Declaration

I declare that the work in this thesis has not been previously submitted for a degree at the University of East Anglia or any other university, and all research has been carried out by myself, unless otherwise stated.

Signed

Mark Kirkwood

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Abstract

Genetic, biochemical, bioinformatic and molecular approaches were used to analyse microbial catabolism of dimethylsulfoniopropionate (DMSP), an abundant anti-stress compound made by marine phytoplankton.

Members of the Roseobacter clade of marine α-proteobacteria may catabolise DMSP by two different routes; demethylation to form methylmercaptopropionate (MMPA), and cleavage by DMSP-lyases, yielding volatile dimethylsulfide (DMS) plus acrylate.

The DMSP-lyase, DddP, was purified from *Roseovarius nubinhibens* ISM and characterised *in vitro*. Nuclear magnetic resonance spectroscopy and gas chromatography confirmed *bona fide* DMSP lyase activity and mutation of predicted active-site residues abolished DMS production.

DddP was also detected in the fungal coral pathogen *Aspergillus sydowii,* likely acquired from bacteria by inter-Domain horizontal-gene-transfer.

A new DMSP-lyase, DddW, was identified in another Roseobacter species, *Ruegeria pomeroyi* DSS-3, initially by microarray-based demonstrations that transcription of *dddW* was induced in cells grown with DMSP. An adjacent gene encoded the cognate transcriptional regulator. *Escherichia coli* cells that over-expressed DddW cleaved DMSP into DMS plus acrylate. Thus, *Ruegeria pomeroyi* has three DMSP-lyases, with DddP and DddQ being known already; mutational analyses showed that all three contributed to its DMSP-dependent DMS (Ddd$^+$) phenotype.

Moran’s laboratory had shown that the DMSP demethylase was encoded by *R. pomeroyi dmdA.* I unveiled intimate links between the demethylation and the cleavage pathway(s). A key player is *acuI*, which is co-transcribed with *dmdA*, both genes being induced by DMSP and, more markedly, the DMSP-catabolite, acrylate. Furthermore, AcuI$^-$ mutants failed to grow on acrylate as sole carbon source and were more sensitive to its toxic effects. AcuI$^-$ mutants failed to grow on DMSP so, surprisingly, *Ruegeria* likely uses lyase pathway(s) to grow on this compound. A potential regulatory gene, transcribed divergently from *dmdA*, was also identified.

The microarray also, wholly unexpectedly, revealed a suite of *cox* genes involved in carbon monoxide oxidation that was up-regulated in response to DMS.

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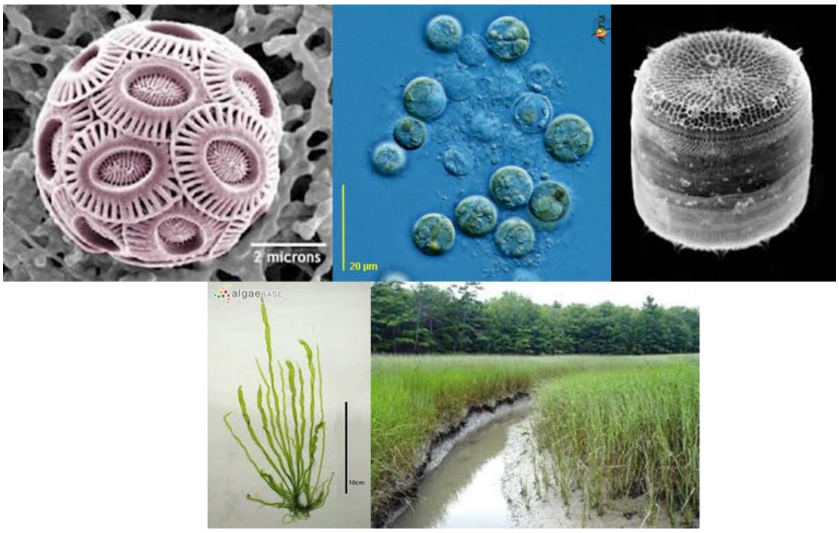
Chapter 1

General Introduction

1.1 Dimethylsulfoniopropionate

Dimethylsulfoniopropionate (DMSP) is a zwitterionic sulfonium compound that is synthesised globally in huge amounts, as much as ~10^9 tons annually (Kettle *et al.*, 1999; Stefels, 2000; Stefels *et al.*, 2007). This biosynthetic ability occurs sporadically throughout a wide range of organisms, including species of the Phyla Haptophyta (e.g. the coccolithophore *Emiliania huxleyi* and *Phaeocystis* sp.), Dinoflagellata (e.g. *Symbiodinium* sp. and *Crypthecodinium cohnii)* and Heterokontophyta (e.g. the diatoms *Melosira nummuloides*, *Thalassiosira pseudonana* and *Fragilariopsis cylindrus*) in the Kingdom Chromoalveolata, as well as widely dispersed members of the Plantae Kingdom, from single-celled Prasinophycae (e.g. *Tetraselmis* sp.) to seaweed macroalgae such as *Ulva intestinalis* (green alga), *Polysiphonia* (red alga) and the angiosperms *Spartina* (salt marsh cord grass) and the beach sunflower *Wollastonia biflora* in the *Compositae* (Stefels, 2000; Otte *et al*., 2004; Broadbent *et al.*, 2002).

Figure 1.1 Organisms that synthesise DMSP



Clockwise from top left: *Emiliania huxleyi*, *Symbiodinium* sp., *Thalassiosira pseudonana*, *Spartina alterniflora* and *Ulva intestinalis*.

Soluble DMSP is present at concentrations of less than ~1-2 nM in the open oceans but can reach several µM in phytoplankton blooms (Van Duyl *et al.*, 1998). For example, diatom-dominated sea-ice communities have DMSP concentrations 2-3 orders of magnitude greater than the average ocean concentration (Kirst *et al.,* 1991; Trevena and Jones, 2006). The intracellular concentrations of DMSP that may accumulate in such organisms are astonishing, ranging from 0.1 to as high as 1 M (Stefels, 2000; Yoch, 2002). The DMSP may comprise 1-16% of the total cellular carbon in some phytoplankton, accounting for the fate of ~11% of the total carbon that is fixed, and between 26% and 44% of the sulfur demand in blooms of these organisms (Matrai and Keller, 1994; Archer *et al*., 2001). Diatoms alone contribute to ~45% of the total oceanic primary production, and this represents ~25% of global carbon fixation (Nelson *et al.,* 1995). Organisms that do not synthesise DMSP may still exhibit high concentrations of the compound within them. Thus, many cnidarians contain high levels of DMSP, due to symbiotic dinoflagellates, known as zooxanthellae, which associate with these invertebrates in corals (Van Alstyne *et al.,* 2006, 2009; Raina *et al*., 2009).

1.2 DMSP synthetic pathways

DMSP biosynthetic pathways are not identical throughout the above taxonomic types, and the sporadic distribution of DMSP production is indicative of several independent evolutionary events. However, all of the known pathways begin with *L*-methionine. There are three general mechanisms for DMSP synthesis, differing between the higher plants, algae and diatoms (Hanson *et al*., 1994a; James *et al*., 1995; Kitaguchi *et al.*, 1999).

1.2.1 DMSP synthesis in angiosperms

In the angiosperm, *Wollastonia biflora*, *L*-methionine is first methylated to form *S*-methyl-methionine (SMM), followed by successive decarboxylation and deamination to DMSP-aldehyde, and finally, an oxidation step to form DMSP (Hanson *et al.,* 1994a). In the saltmarsh cordgrass, *Spartina alterniflora*, the reaction is thought to proceed in a similar way, but with an additional, putative DMSP amine intermediate between SMM and DMSP aldehyde as shown in figure 1.2 (Kocsis *et al.,* 1998; Kocsis and Hanson, 2000).

1.2.2 DMSP synthesis in algae and phytoplankton

Despite the abundance of DMSP in plankton communities, no gene, expressed sequence tag or enzyme responsible for its synthesis had been identified. Recently, however, progress has been made in investigating the molecular basis of DMSP synthesis in the algal diatoms *Fragilariopsis cylindrus* CCMP1102 and *Thalassiosira pseudonana* (Lyon *et al.*, 2011; J D Todd, personal communication).

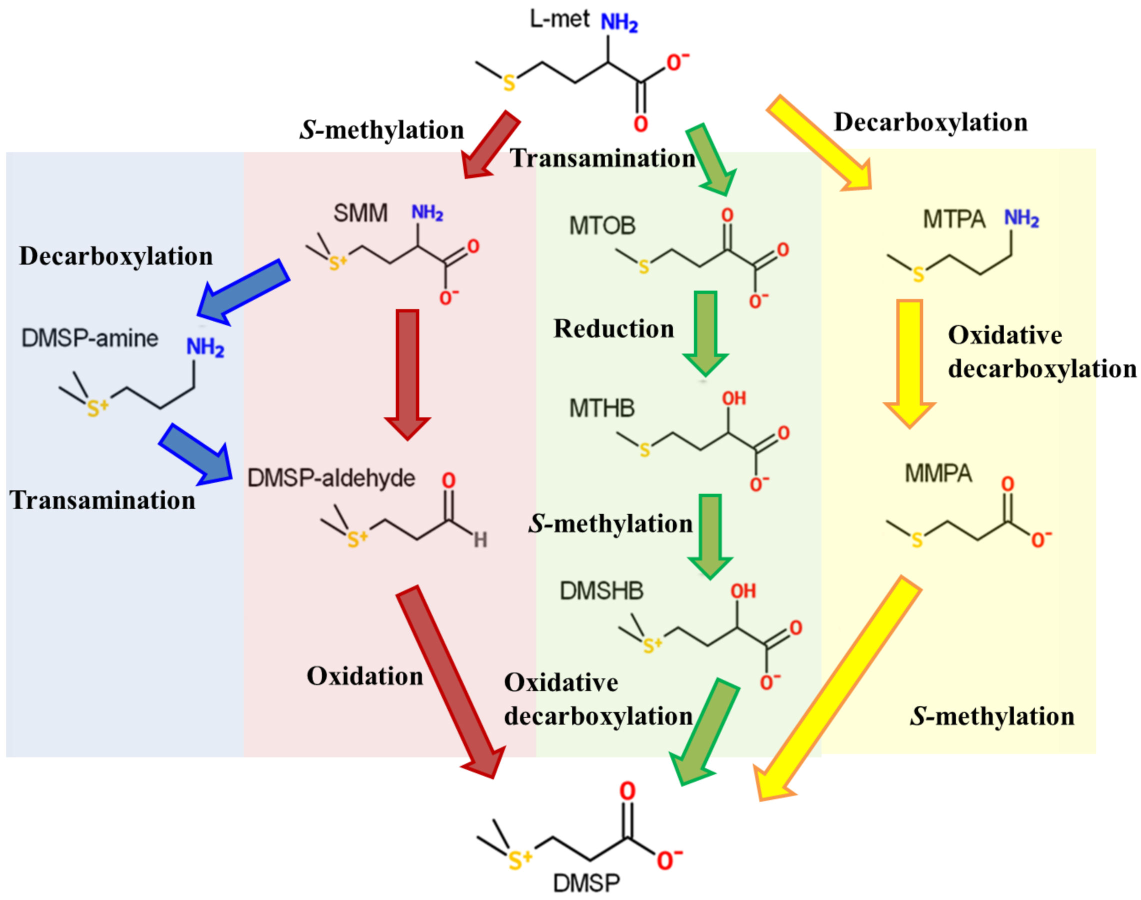
Diatoms had been shown to have a very different method of making DMSP, via the so-called transamination pathway (Figure 1.2).There is evidence that this pathway also operates in coccolithophores and the green alga *Ulva* (Gage *et al.*, 1997; Summers *et al.*, 1998). The first step is catalysed by a methionine aminotransferase, transferring the amino group to 2-oxoglutarate, yielding glutamate plus 4-methylthio-2-oxobutyrate (MTOB), which is then reduced to *D*-4-methylthio-2-hydroxybutyrate (MTHB) by MTOB reductase. An MTHB *S*-methyltransferase then catalyses the *S*-adenosyl-*L*-methionine (SAM)-dependent *S*-methylation of MTHB, yielding *D*-4-dimethylsulfonio-2-hydroxybutyrate (DMSHB). Finally, DMSHB is decarboxylated to form DMSP by a DMSHB decarboxylase.

Importantly, the activity of the *S*-methyltransferase only occurs at significant levels within DMSP-producing organisms and is predicted to be specific for DMSP biosynthesis. In the sea-ice diatom *Fragilariopsis cylindrus*, a proteomics approach identified a number of proteins that were increased in their expression in the presence of DMSP, whose intracellular concentration itself increased following raised salinity; under such conditions, one third of the proteins were related to amino acid pathways, and members from all four of the enzyme classes involved in the algal DMSP transaminase biosynthesis pathway were elevated (Lyon *et al.*, 2011). Additionally, a number of specific enzymes have now been ratified, with the genes for both the MTOB reductase and MTHB *S*-methyltransferase from diatoms having been cloned and expressed successfully in the γ-proteobacterium, *Escherichia coli* (J D Todd, personal communication).

1.2.3 DMSP synthesis in dinoflagellates

The biosynthesis of DMSP in dinoflagellates differs quite significantly from those described in the angiosperms and algae (Figure 1.2). The dinophyceae, *Crypthecodinium cohnii,* uses *L*-methionine as a starting point, as in the other organisms, but this is decarboxylated to form methanethiolpropanamine and then converted to methylmercaptopropionate (MMPA) through oxidative decarboxylation. A final *S*-methylation step yields the DMSP product (Kitaguchi *et al.,* 1999).

Figure 1.2 The DMSP biosynthesis pathway in angiosperms, phytoplankton and dinoflagellates



Chemical reactions are labelled, with the predicted enzymes illustrated. Panels indicate systems identified in different organisms.

Blue panel: *Spartina alterniflora*; Pink panel: *Wollastonia biflora*; Green panel: coccolithophores (*Emiliania huxleyi*), diatoms (*Thalassiosira pseudonana* and *Fragilariopsis cylindrus*) and green algae (*Ulva*); Yellow panel: dinoflagellates (*Crypthecodinium cohnii*).

***L*-met, methionine; SMM, *S*-methylmethionine; DMSP, dimethylsulfoniopropionate; MTOB, 4-methyl-2-oxobutyrate; MTHB, 4-methyl-2-hydroxybutyrate; DMSHB, 4-dimethylsulfonio-2-hydroxybutyrate; MTPA, methanethiolpropanamine; MMPA, methylmercaptopropionate; DMSP, dimethylsulfoniopropionate.**

Adapted from Trossat *et al*., 1998; Hanson *et al.*, 1994a; Gage *et al.*, 1997; Kocsis *et al.*, 1998.

1.2.4 Cellular localisation of DMSP synthetic enzymes

DMSP synthesis in plants may occur in the chloroplast, with DMSP and the enzyme reportedly being concentrated in this organelle in *W. biflora* (Trossat *et al.,* 1998). Tentatively, the localisation of the relevant enzymes in the diatoms matches this, since the methionine aminotransferase, MTHB *S*-methyltransferase and DMSHB decarboxylase polypeptides of *F. cylindrus* and *T. pseudonana* contain N-terminal leader sequences that are predicted to target them to the chloroplast (Gruber *et al.,* 2007; Lyon *et al.,* 2011; J D Todd, personal communication).

1.3 Physiological uses of DMSP

DMSP has been implicated in a number of important physiological processes, and is primarily thought to act as compatible solute that protects the cells that accumulate it from osmotic stress in the saline marine environment (Otte and Morris, 1994; Edwards, *et al*., 1988). However, direct evidence for this is scarce and not wholly consistent. For example, phytoplankton species such as *Ulothrix* spp. (Chlorophyta) and *Enteromorpha bulbosa* (Now *Ulva*, Chlorophyta) exhibit a clear, positive DMSP-accumulation response to salinity (Karsten *et al.,* 1992), as do diatoms, but *Spartina* spp. display no such response (Otte *et al*., 2004). Studies using a heterologous host, *E. coli,* have shown that DMSP bestows halo-tolerance under artificial, laboratory conditions (Cosquer *et al.,* 1999). Interestingly, β-alanine betaine, a structural analogue of DMSP, is used by members of the Plumbaginaceae as a salt stress response molecule (Hanson *et al*., 1994b). Likewise, DMSP resembles glycine betaine, a widely utilised osmo-protectant in terrestrial organisms. It has been suggested that DMSP is favoured in marine environments due to the abundance of sulfur and scarcity of nitrogen in the seas; on land, the reverse is true, favouring the use of the amino acid osmoticum (Kiene *et al.* 2000; Galinski *et al*., 1995).

Other biological functions for DMSP have also been proposed. One such use is as an anti-stress compound, for protection from UV light and/or amelioration of oxidative damage (Otte *et al.,* 2004; Sunda *et al.,* 2002). Known oxidative stressors such as carbon and iron limitation in *E. huxleyi* and *Thalassiosira pseudonana* also increase production of DMSP (Sunda *et al.,* 2002). It has also been suggested that DMSP acts as an herbivore deterrent via the release of one its catabolic products, acrylate (Van Alstyne *et al*., 2003a). This might explain why species that readily synthesise DMSP are less likely to be targeted by zooplankton predators than those that accumulate lower concentrations (Wolfe, 1997). DMSP may also act as a biological sulfur sink in the form of reduced sulfur (Kiene *et al*., 1999; see below), as an overflow mechanism during nitrogen limitation (Stefels, 2000), or as a cryoprotectant (Karsten *et al.,* 1996).

Of course, these proposed functions are not mutually exclusive. These may be resolved (at last!) if and when a mutant that is defective in DMSP production becomes available for at least one organism.

1.4 DMSP utilisation

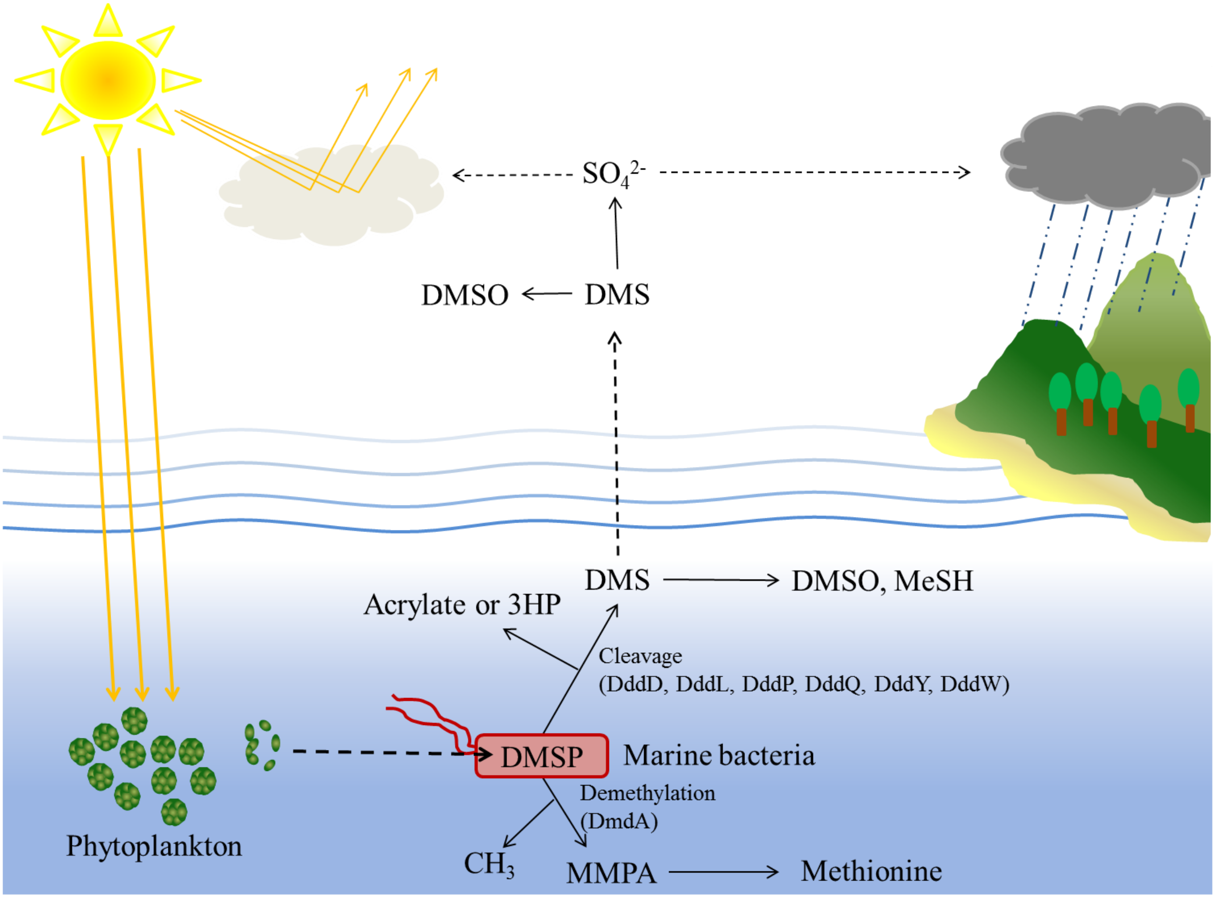
The release of DMSP from the producing plankton cells may occur through viral lysis, senescence or predation (Malmstrom *et al*., 2004a). Several marine bacteria can import DMSP from the environment, including members of the cyanobacteria (*Synechococcus* and *Prochlorococcus*) and many heterotrophic species (Malmstrom *et al*., 2004b; Vila-Costa *et al*., 2006, Sun *et al.,* 2011). These include the SAR11 clade of the α-proteobacteria, which are prodigiously abundant in the oceans (see later) and which favour the use of reduced forms of sulfur, even ahead of such abundant S sources as sulfate which are bio-energetically more expensive to assimilate (Tripp *et al*., 2008).

In addition, a few of the algae and phytoplankton that synthesise DMSP may catabolise it. Indeed, one of the first DMSP catabolic reactions to be described was in the red seaweed *Polysiphonia lanosa,* and involves the cleavage of DMSP into acrylate plus the volatile, dimethyl sulfide (DMS) (Cantoni and Anderson, 1956; Steinke *et al.,* 1998). However, the cultures were never reliably confirmed to be axenic, and although DMSP biotransformation has since been reported in some species of single-celled phytoplankton, such as the haptophyte *E. huxleyi*, this criticism also applies to many of these studies on Eukaryotic algae (Franklin *et al.,* 2010; S Newton-Payne, personal communication). What is indisputable, though, is that many marine bacteria, and a few fungi, can catabolise DMSP, with acrylate and DMS being the products in some examples of this phenomenon.

In total, it has been estimated that of the *ca.* one billion tons of DMSP catabolised annually, around one third is subjected to this form of cleavage; the remainder being degraded by demethylation, which does not liberate any DMS – see below. Much of the resultant DMS appears to be retained in these microbial communities, but roughly 10% escapes into the atmosphere. Here, it may be spontaneously oxidised into sulfates, sulfur dioxide, methanesulfonic acid, and other products that act as cloud condensation nuclei (Hatakeyama *et al.*, 1982). This involves major movement of S from sea to air thence back to land, via precipitation, making DMSP a significant player in the global sulfur cycle (Andreae, 1990). The increase in albedo created by DMS oxidation products has been predicted to affect the climate via a positive feedback loop, termed the CLAW hypothesis, shown in Figure 1.3 (Charlson *et al.,* 1987). However, recent counterclaims have suggested DMS has little to no effect as cloud condensation nuclei, other than at a local level in regions of high primary productivity, such as coral reefs (Quinn and Bates, 2011). These are the richest source of DMSP, and hence of DMS, because of the dinoflagellate *Symbiodinium* and the many bacteria in these ecosystems (Jones and Trevena, 2005; Raina *et al.,* 2009; 2010).

Atmospheric or dissolved DMS can also act as a potent chemo-attractant for marine animals, including shearwaters, seals, penguins and crustaceans (Steinke *et al.,* 2002; 2006; Nevitt, 2008; 2011; Cunningham *et al*., 2008).This was even found to act through more than one trophic level. For example, bacterial production of DMS from the DMSP released by phytoplankton encourages grazing by crustaceans and acts as a spatial foraging cue for procellariiform birds, such as petrels (Nevitt and Bonadonna, 2005).

Figure 1.3 Formation and catabolic fate of DMSP



Once released by phytoplanktonic producers, through grazing, senescence or viral lysis, dimethylsulfoniopropionate (DMSP) is subjected to bacterial degradation by two general pathways. The demethylation pathway leads to the production of methylmercaptopropionate (MMPA), whereas the cleavage pathway yields dimethyl sulfide (DMS) and either acrylate or 3-hydroxypropionate (3HP). The DMS can be further transformed by bacteria into dimethyl sulfoxide (DMSO) and other products. Some of the DMS escapes to the atmosphere, where it is oxidised, forming cloud condensation nuclei, perhaps leading to increased albedo. The transfer of these compounds to the Earth's surface, via rain or snow, is an important step in the global sulfur (S) cycle, creating a flow of S from sea, to air thence to land. MeSH, methanethiol. Adapted from Curson *et al.*, 2011a.

1.5 α-proteobacteria, Rhodobacterales, Roseobacters and *Ruegeria pomeroyi* DSS-3

There is one group of organisms that is consistently the dominant player in DMSP utilisation. These are members of the sub-phylum of α-proteobacteria, and particularly one or two taxa within this group. The α-proteobacteria form one of the largest and most diverse groups within the Eubacteria, with diverse metabolic profiles, and with examples of phototrophs, chemolithotrophs, chemoorganotrophs and aerobic photoheterotrophs (Venter *et al*., 2004; Kersters *et al*., 2006). Among this sub-phylum, two groups, the SAR11 clade and the Roseobacters are especially abundant in the oceans and play a pivotal role in global turnover of DMSP.

1.5.1 General introduction to the Roseobacters

DMSP is a major component of the lifestyle for a group collectively as the Roseobacters, as exemplified initially by physiological, and then by genetic studies. The first description of members of the Roseobacter clade occurred with the culturing from Japanese coastal waters of a high density population of pink, aerobic, anoxygenic phototrophs (AAoP) that contained bacteriochlorophyll-α (Shiba *et al.*, 1979). The genus *Roseobacter* and the species *Roseobacter denitrificans* (previously *Erythrobacter* sp.) and *R. litoralis*, were created for AAoP that contained bacteriochlorophyll-α and which were isolated from marine algae (Shiba *et al*., 1991). Later, examinations of estuarine and coastal seawater samples using 16S rRNA PCR showed that these species, along with other Roseobacters such as *Sulfitobacter* EE-36 and members of the α-proteobacteria, were a numerically dominant group in marine bacterioplankton communities (González and Moran, 1997). Although the term Roseobacter is not an officially recognised taxonomic term, it is widely used as informal shorthand for a group of some 17 taxonomically coherent genera, within the Rhodobacteraceae family (Buchan *et al.*, 2005; Tang *et al.*, 2010). Apart from their taxonomic relatedness, members of the Roseobacters share one other pivotal feature – they are all marine-living, unlike other genera in the Rhodobacteraceae, such as *Paracoccus*. Indeed, the Roseobacters are now thought of as one of the ten main taxa found in coastal and open waters, comprising up to 30% of the total number of cells in these environments. They can represent ~3% of all cells in open ocean waters and also occur in hypersaline lagoons, coastal waters, marine sediments, and sea ice (Labrenz *et al*., 1998; Eilers *et al*., 2000; Brinkmeyer *et al*., 2003; Buchan *et al.,* 2005; Biers *et al*., 2009). During algal bloom events in coastal waters large amounts of DMSP are released into the milieu and Roseobacters are the dominant taxon in these environments (González *et al*., 2000).

Over 40 members of the Roseobacter lineage have had their genomes sequenced, yet only recently has a robust phylogenetic analysis occurred (Newton *et al*., 2010; Tang *et al.*, 2010). Different Roseobacter genera display at least 89% identity in their 16S rRNA sequences, and share a similar G + C content (*ca.* 50-60%). However, there is considerable variation in their genomes, with genome sizes that range from 3.5 Mbp (Mega base pairs) to 5.3 Mbp - corresponding to 3500 to 5500 genes (Buchan *et al*., 2005; Tang *et al.*, 2010). In addition to a conserved set of core genes retained through vertical evolution, there exists a significant subset of accessory genes, which have undergone extensive lateral gene transfer during the evolution of the Roseobacters (Tang *et al.,* 2010; see chapters 4, 5, 6). Included in this portfolio of accessory genes are those involved in DMSP catabolism (see below).

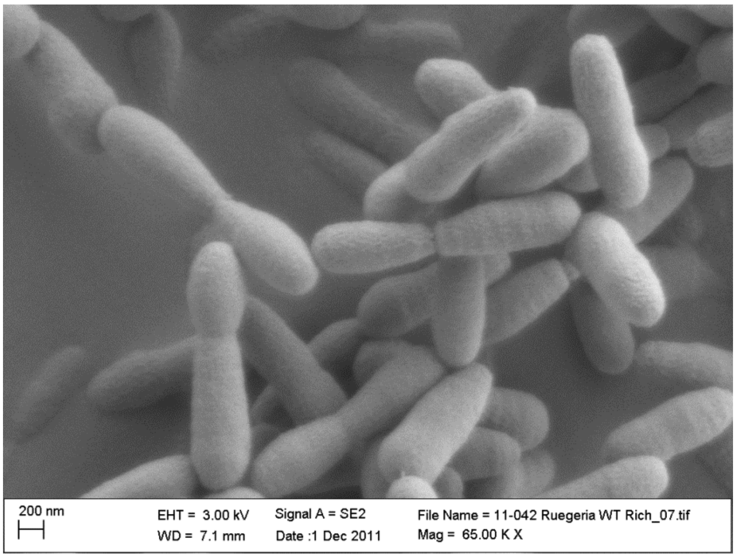
Some characteristic physiologies of the Roseobacters include:

- the ability to carry out organic and inorganic sulfur metabolism, contributing significantly to the biogeochemical cycling of this element (Moran *et al*., 2003; see below);
- the oxidation of carbon monoxide, a potentially significant response to the photolysis of dissolved organic matter (Zuo and Jones, 1995; King, 2003);
- symbiotic relationships with eukaryotic marine organisms such as the dinoflagellate, *Pfiesteria* (Alavi *et al*., 2001), and including pathogenic effects on scleractinian corals (Cooney *et al*., 2002).

1.5.2 *Ruegeria pomeroyi* DSS-3

The model Roseobacter, *Ruegeria pomeroyi* DSS-3 (originally named *Silicibacter pomeroyi* but subsequently re-classified [Yi *et al*., 2007]), was isolated from the Coastal Atlantic, off the shores of Georgia. It forms short, rod-shaped cells with a complex, polar flagellum that confers motility (Figure 1.4). It was clear, soon after its isolation, that this strain can catabolise DMSP by both of the general pathways that had been partially described earlier, but which had been seen in different organisms. *Ruegeria pomeroyi* is rather a glutton for DMSP, as it can catabolise this compound by two different mechanisms, known as demethylation and cleavage (González *et al*., 1999; 2003; see below).

Figure 1.4 Microscopic analysis of *Ruegeria pomeroyi* DSS-3



Scanning electron micrograph of *R. pomeroyi* DSS-3 cells grown in rich ½ YTSS medium. Scale bar given. (R T Green, personal communication).

R. pomeroyi DSS-3 is easily cultured compared to many of its relatives (González and Moran, 1997), and was the first Roseobacter to be genome-sequenced (Moran *et al*., 2004). It has 4,283 genes in a total genome that is 4.1 Mbp in size, and includes a 491 kilo base pair (kbp) megaplasmid (www.roseobase.org). The original sequencing study identified a number of genes related to its metabolic profile, as discussed in following chapters.

1.5.3 The SAR11 Clade

The second of the two groups of α-proteobacteria that are known to metabolise DMSP is the SAR11 clade, or “Pelagibacteraceae”, belonging to the Order Rickettsiales. These were first identified by culture-independent approaches, using environmental 16S rRNA sequences obtained from the Sargasso Sea (Giovannoni *et al.*, 1990). A member of the SAR11 clade was cultured, with some difficulty, in free-living form (the doubling time of a cell is *ca.* 29 hours). This species, *Candidatus* Pelagibacter ubique, has a rod shape with one of the smallest lengths of any self-replicating cell, at 0.4-0.9 μm and a diameter of only 0.1-0.2 μm. It also has the smallest genome of any free living organism at 1,308,759 bp, and yet these bacteria are massive in terms of their global population and distribution. There are *ca*. 10^{28} cells of Pelagibacter in the seas, comprising around 50% of cells in the temperate oceans during summer (Morris *et al*. 2002; Giovannoni *et al.*, 2005; Thrash *et al.*, 2011). It is a scavenger, whose ability to recycle dissolved organic carbon means that it plays a major role in the Earth’s carbon cycle. Pelagibacter spp. are only known to harbour the genes for DMSP demethylation at present (see below).

Both of these groups of organisms are important to global DMSP utilisation. However, whilst the SAR11 clade only demethylates DMSP, many Roseobacters harbour the enzymes necessary for both forms of DMSP degradation. The pathway that occurs in both Roseobacters and the SAR11 clade, DMSP demethylation, is a good starting point to examine these systems in more detail.

1.6 DMSP demethylation

The predominant pathway of DMSP catabolism, which accounts for approximately 70% of the globally consumed DMSP, occurs through the “demethylase pathway” (Figure 1.5; Kiene, 1996; Kiene *et al.*, 1999; 2000). The discovery of DMSP demethylation began with the observation by Mopper and Taylor (1986) that methane thiol (MeSH) and methyl mercaptopropionate (MMPA) were the dominant thiols present in anoxic marine intertidal sediments, and that these sediments specifically produced MMPA and MeSH when amended with DMSP (Kiene *et al.,* 1988; Taylor and Visscher, 1996; González *et al*., 1999).

Tracer experiments on the catabolic fate of ^{35}S labelled DMSP, showed that 15-40% of DMSP in natural populations of bacterioplankton from subtropical and temperate marine waters was incorporated into macromolecules, via conversion of MeSH to methionine, and it was inferred that this was via the demethylation route (Kiene and Service, 1991).

Although there had been several suggestions for the pathway(s) of DMSP demethylation, it is only recently that a combination of biochemistry and genetics has generated what appears to be the definitive pathway, at least in one strain, namely the model Roseobacter, *Ruegeria pomeroyi* DSS-3.

1.6.1 DmdA

The first gene found to have a role in the demethylation pathway was *dmdA*, encoding a DMSP demethylase enzyme, DmdA (Howard *et al*., 2006). A *Ruegeria pomeroyi* DSS-3 Tn5 transposon mutagenesis library was screened for mutants that were unable to produce MeSH, but could still release DMS. The DNA from one such mutant was sequenced out from the transposon site and the gene identified as *SPO1913*. Complementation assays confirmed that the gene product was responsible for the DMSP to MeSH phenotype, and cell extract assays narrowed this down to the first step in the reaction, that of DMSP demethylation to MMPA.

Bioinformatic analysis of DmdA placed it within a family of glycine cleavage proteins (EC 2.1.2.10), exemplified by the GcvT of *E. coli* (Stauffer *et al.,* 1993; Moran *et al*., 2004). DmdA also shares domains with dimethylglycine oxidase and sarcosine oxidase, but exhibits greatest homology with the glycine cleavage system (Schuller *et al.,* 2012). There is a ~25% identity between homologues of DmdA and other members of the GcvT family (e.g. *E. coli*) and phylogenetically, the DMSP demethylases form a distinct out-group (Reisch *et al.,* 2008).

A common characteristic among these enzymes is the requirement for a tetrahydrofolate (THF) co-factor. In the case of DmdA, this involves the transfer of the *S*-methyl group from DMSP to THF, to form 5-methyl THF and MMPA, as noted in *Candidatus* Pelagibacter ubique and *Ruegeria pomeroyi* (Reisch *et al.,* 2008). Interestingly, this co-factor differs from other enzymes in the GcvT family, whose reactions involve the production of 5,10-methylene-THF (Schübert *et al.,* 2003). The use of THF as a cofactor is discussed in more detail in chapter 6.

1.6.2 DMSP demethiolation

It had been thought that two mechanisms may exist for the subsequent catabolism of the MMPA produced from DMSP demethylation. The first is via a second demethylation, which converts MMPA to 3-mercaptopropionate (MPA), as noted in anoxic marine sediment (Kiene and Taylor, 1988; Visscher *et al*., 1992; Visscher and Taylor, 1994). However, there is limited evidence for the physiological significance of this pathway in aerobic marine surface waters.

The second proposed, but non-ratified, pathway is known as demethiolation and, crucially, allows the siphoning of DMSP into central metabolism, and as a precursor to amino acids via conversion of MeSH (Kiene *et al.* 1999, 2000). The pathway involves a fatty acid β-oxidation-like reaction, in order to produce MeSH, acetaldehyde, CO_2 and CoA (Figure 1.5; Reisch *et al*., 2011a; 2011b; see chapters 5 and 6). These products can then be easily shuttled into systems such as amino acid synthesis (methionine) and central metabolism (the citric acid cycle). These successive steps are carried out by the DmdB, DmdC and DmdD enzymes, recently characterised in *Ruegeria pomeroyi* DSS-3 (Reisch *et al*., 2008; 2011a; 2011b).

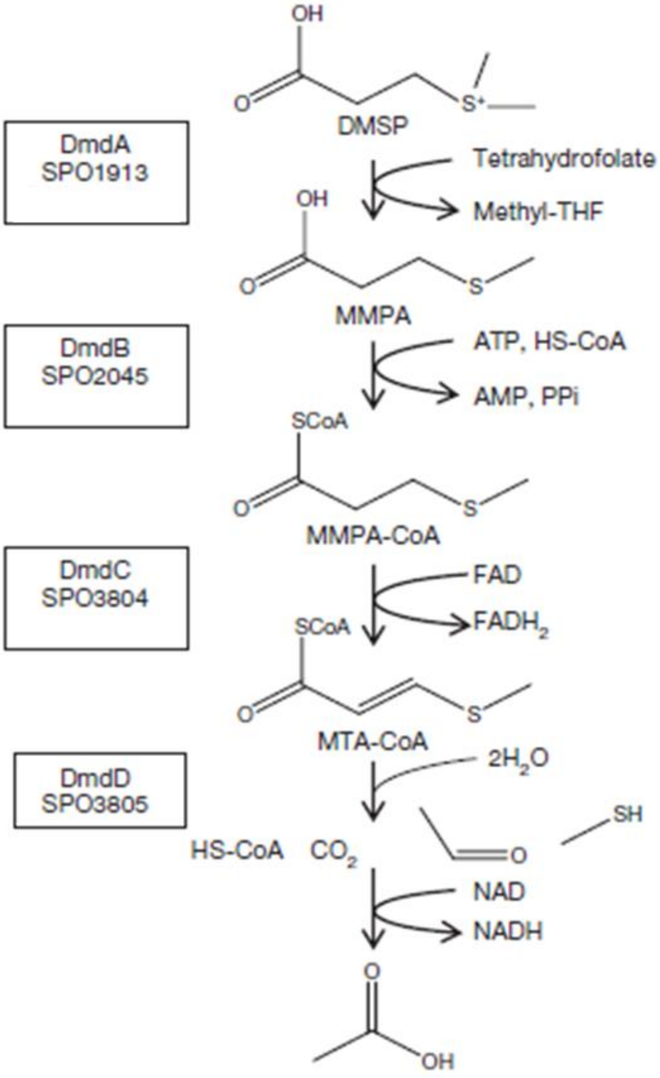
1.6.3 DmdB/DmdC/DmdD

DmdB (the product of *R. pomeroyi* gene, *SPO2045*) is an ATP dependent enzyme, originally labelled as a fatty acid CoA ligase, which forms an MMPA-CoA thioester from MMPA. The FAD-dependent enzyme DmdC (*SPO3804* in *R. pomeroyi*) converts this to methylthioacryloyl-CoA (MTA-CoA). Finally, the crotonase-like DmdD (encoded by

SPO3805) completes the reaction by demethiolating MTA-CoA to CoA, CO_2 and MeSH (Figure 1.5).

The transcript levels responsible for the three enzymes were seen to increase in response to DMSP or MMPA, and mutations in *dmdA, dmdB, dmdC* or *dmdD* of *R. pomeroyi* abolished DMSP-dependent production of MeSH (Howard *et al.,* 2006; Reisch *et al.,* 2011a; 2011b). Interestingly, the *dmdC*$^-$ mutant was able to grow well on DMSP as a sole C source, and a *dmdD*$^-$ mutant was inhibited for growth on the same substrate. Thus, it is likely that products of DMSP cleavage are sufficient for growth of *R. pomeroyi* in the absence of MMPA, and it seems that the MTA-CoA intermediate may be toxic, given its accumulation in the *dmdD*$^-$ mutant. Excitingly, this also implies that MMPA may be used for growth in a pathway independent of DMSP demethylation, and this will be explored further in chapters 5 and 7.

Figure 1.5 DMSP demethiolation pathway in *Ruegeria pomeroyi* DSS-3



Enzymes given with relevant "SPO" gene number. DMSP is first demethylated to MMPA by DmdA, using tetrahydrofolate as a cofactor. An MMPA-CoA thioester is then formed, with the concomitant consumption of ATP and production of AMP. The MMPA-CoA is then dehydrogenated to an enoyl-CoA intermediate, MTA-CoA. This is then hydrated, releasing MeSH, CoA, CO_2 and acetaldehyde, which is then oxidized to acetic acid by acetaldehyde dehydrogenase. From Reisch *et al.,* 2011b.

1.6.4 Distribution of the *dmd* genes

DmdA is almost exclusively found in the SAR11 bacteria and in the Roseobacters, with a high level of conservation at the amino acid level among most of these homologues, with weaker matches in the γ-proteobacterium, HTCC2080 and a newly discovered member of the SAR116 clade (Howard *et al.,* 2006; 2008; Reisch *et al.,* 2008, Varaljay *et al*., 2010).

The distribution of the secondary *dmd* genes is curious, with *dmdB* and *dmdC* being present in all 36 *dmdA*-possessing organisms in the genomic database, but also in several species that lack DmdA, including many β- and γ-proteobacteria; representatives of these bacteria produced MeSH from MMPA (Reisch *et al.,* 2011b), implying that there are alternative sources of MMPA that do not originate from DMSP catabolism.

The DmdD enzyme appears to be significantly less abundant than the other enzymes. A BLASTp interrogation of the Global Ocean Sampling (GOS) database, which is a metagenomic database of environmental DNA samples taken from the world's oceans (Rusch *et al.,* 2007), only retrieved 16 weak homologues. DmdD may be replaced by non-orthologous iso-functional enzymes in other organisms, given the activity of this pathway in *R. lacuscaerulensis*, which possesses DmdB and DmdC, but not DmdD (Reisch *et al.,* 2011b).

1.7 The DMSP lyases

Although the DMSP demethylation pathway may account for the majority of the degradation of DMSP in the natural marine environments, and the *dmdA* gene is very widespread in marine metagenomic data bases, this pathway does not release the environmentally influential gas, DMS. For many years, it was thought that this volatile was formed by a cleavage of the DMSP by an enzyme known generically as DMSP lyase, which would form acrylate as the other, C3 catabolite.

However, it is only thanks to recent genetic work that has extended earlier physiological and biochemical work that we have a clear idea of the mechanisms and the pathways that are involved. As seen below, these newer studies have ratified previous thinking in some cases, but in others, there have been some unexpected outcomes. To a large extent, this is because there has been a wholly unexpected degree of diversity, with different microbes (some of which were wholly unanticipated) using a range of different enzymes and generating a collection of different intermediate catabolites.

The overall phenotype that describes the breakdown of DMSP with the concomitant liberation of DMS has been termed Ddd$^+$ (DMSP-dependent DMS). Thanks to work in the UEA lab, no fewer than six different “primary” Ddd enzymes have been shown to mediate the cleavage of DMSP, and many other polypeptides and the corresponding genes have been shown to be involved in such ancillary functions as the transport of the DMSP substrate into the cells, the regulation of the expression of the *ddd* genes, in the catalysis of subsequent, downstream catabolic steps and even in the protection of the cell against damage inflicted by one of the intermediate catabolites.

The isolation and characterisation of these six different *ddd* genes, namely *dddD, dddL, dddP, dddQ, dddW* and *dddY* followed a standard approach, as follows. First, either novel strains of DMSP-catabolising bacteria were isolated, or known strains with this ability were obtained from other labs or culture collections. Next, genomic libraries of such strains were made in a wide host-range cosmid vector. These cosmids in this library were then introduced into an appropriate bacterial host strain that does not catabolise DMSP and screened for transconjugants that either cleaved DMSP to release DMS (Ddd$^+$ phenotype) and/or which grew on DMSP as sole carbon source. These genes would then be localised by sub-cloning and/or mutagenesis. The availability of genomic sequences of bacteria that are known to catabolise DMSP was exploited to search for the presence or absence of the various *ddd* genes. Once identified, the selected microbes were examined for those that contain homologues of the *ddd* genes already identified as above and confirmed that these can cleave DMSP even if they had hitherto not been suspected of having this ability. This cycle was then repeated for those cases where it was known that a given strain had a Ddd$^+$ phenotype, but its genome lacked any of the previously identified *ddd* genes.

The features of these six primary genes and their products are now presented, with the exception of DddW, which is a result of the work described in chapter 4.

1.7.1 DddD

The first *ddd* gene was discovered in the γ-proteobacterium, *Marinomonas* sp. MWYL1, isolated from the rhizosphere of the salt marsh grass *Spartina anglica*, on the basis of its ability to grow well on DMSP as sole carbon (C) source (Todd *et al.*, 2007). A fosmid library of this strain was introduced into *E. coli* and screened for a Ddd$^+$ phenotype using gas chromatography. This identified two transcriptional units that were responsible for DMS release in *Marinomonas* (see below; Figure 1.6). It was shown that both *dddD* and the divergently transcribed *dddTBCR* were required for a Ddd$^+$ phenotype in *Marinomonas* itself, but that, *dddD* alone conferred a Ddd$^+$ phenotype to *E. coli* if the cloned gene was expressed from an active ectopic promoter (Todd *et al.*, 2007).

The DddD polypeptide belongs to the Class III CoA-transferases and shares homology with CaiB of *E. coli*. CaiB is involved in an anaerobic respiratory pathway, transferring CoA to the amino acid carnitine, which is used as an electron acceptor (Eichler *et al.*, 1994; Elssner *et al*., 2001). CaiB is a homodimer whose individual polypeptides are approximately half the size of the DddD polypeptide. Interestingly, DddD comprises two repeated CaiB-like domains with a short linker region (Rangarajan *et al*., 2005; Todd *et al.*, 2007) suggesting that DddD acts as a form of "intra-molecular dimer". This would allow it to transfer CoA to DMSP from an acyl-CoA donor before the release of DMS, and would result in an acyl-CoA intermediate prior to the DMS releasing step (Todd *et al*., 2007). Unfortunately, no *in vitro* study of DddD has confirmed this mechanism.

1.7.1.1 Distribution of DddD

Following the discovery of DddD in *Marinomonas* sp. strain MWYL1, further Ddd$^+$ strains were identified by growth on DMSP as a sole C source. Thus, Curson *et al.* (2010) isolated two species of γ-proteobacteria from the gut of the Atlantic herring, *Clupea harengus* which possessed the *dddD* gene. These species, *Pseudomonas* strain J465 and *Psychrobacter* strain J466, were found to possess homologues of closely linked *ddd* genes that resembled those in *Marinomonas* sp. strain MWYL1 (Figure 1.6 and see below).

Using bioinformatics as a form of gene mining, close homologues of DddD were found *in silico* using BLAST analysis. In addition to matches to other species of *Marinomonas* (>90% identity at peptide level) and another γ-proteobacterium, *Oceanimonas doudoroffii,* there were also homologues of DddD in certain members of the α-proteobacteria, namely the Roseobacters, *Sagittula stellata* E37, *Hoeflea phototrophica* DFL-43, *Dinoroseobacter shibae* DFL 12, *Rhodobacterales* sp. KLH11 and *Ruegeria pomeroyi* DSS-3 (Johnston *et al*., 2008; Todd *et al.,* 2010; Curson *et al.,* 2011a). Interestingly, DddD also appeared in other "terrestrial" strains. These included the α-proteobacterium *Rhizobium* NGR234, which is a particularly unusual strain, in that it nodulates a wide range of hosts, including *Parasponium,* which is a non-legume plant (Trinick, 1973). Another homologue was found in the β-proteobacterium, *Burkholderia cepacia* AMMD, which is present in the rhizosphere of many angiosperms (Ramette *et al*., 2005). The two latter examples were shown not to be able to grow on DMSP as a sole C source, but were confirmed to exhibit Ddd$^+$ phenotypes when provided with DMSP and an alternative C source. The DddD-like polypeptides from *D. shibae*, *Rhodobacterales* sp. KLH11 and *R. pomeroyi* DSS-3 form a distinct out-group from the other Roseobacter DddD enzymes, being >72% identical to each other, yet only sharing 40% identity with the original *Marinomonas* peptide. Additionally, mutations into the gene responsible for this "*dddD"* gene in *R. pomeroyi* (*SPO1703*) had no discernible effect on DMSP dependent DMS production and quantitative real time PCR (qRT-PCR) analysis of *dddD* illustrated low (if any) expression of its messenger RNA (Todd *et al.,* 2011).

The presence of DddD in these organisms almost certainly arose via Horizontal Gene Transfer (HGT) between the lineages (Todd *et al.,* 2007). Indeed, an inter-Domain HGT event may even have occurred between bacteria and the coccolithophore, *Emiliania huxleyi*, which has a deduced polypeptide with ~30% identity to *Marinomonas* DddD (Curson *et al.,* 2011a).

1.7.1.2 DddD in *Halomonas* HTNK1

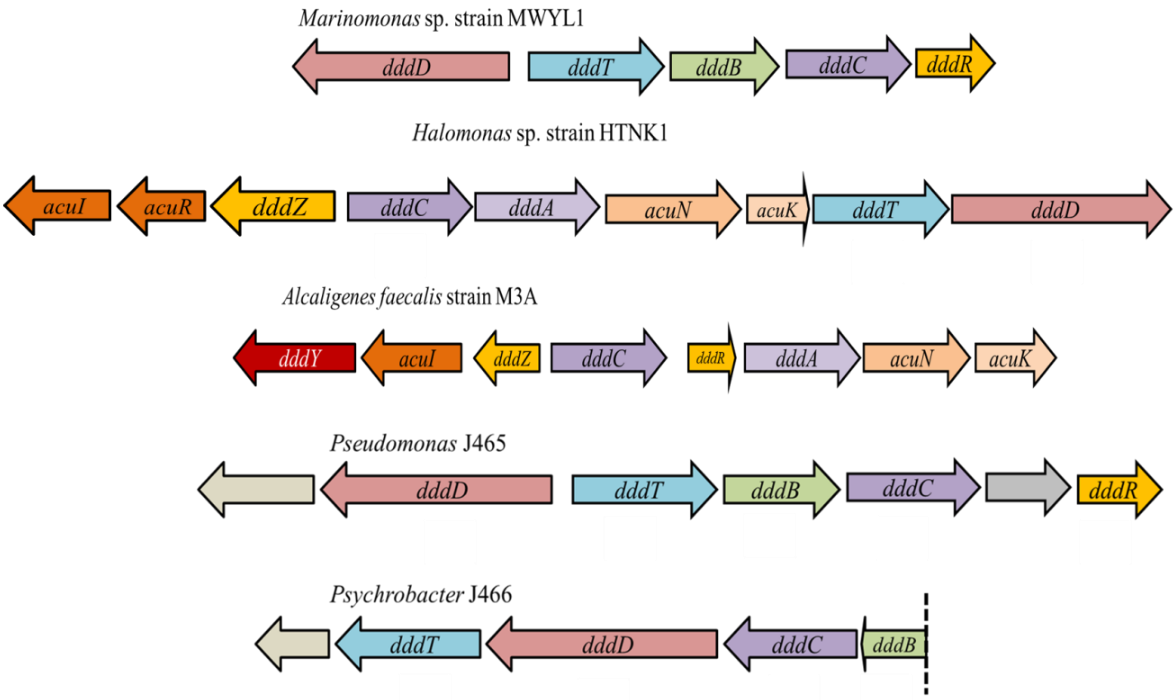
Although many of the DddD-containing bacteria, (notably the γ-proteobacteria) grew well on DMSP, they did not grow on acrylate as sole C source. Initially, this was surprising because the generally accepted view was that DMSP lyase generated acrylate as the initial, C3 catabolite. It was therefore surprising that none of the DddD-containing organisms (above) could grow on acrylate as a sole C source. Therefore, a search was made to find a strain that could grow on both acrylate and DMSP. This led to the isolation from the surface of the DMSP-producing macroalga *Ulva lactuca* (sea lettuce), of the γ-proteobacterium, *Halomonas* strain HTNK1 (Todd *et al.*, 2010) which, like *Marinomonas,* is in the *Oceanospiralleles*.

The gene cluster responsible for the growth phenotype in *Halomonas* was then discovered using similar methods to *Marinomonas*, as above. It contains *dddD, dddT* and *dddC* homologues (see below), plus several other genes that had not been seen in the *ddd* gene clusters described above (Figure 1.6). Therefore, *Halomonas* HTNK1 was chosen to undertake a biochemical study of the fate of DMSP (Todd *et al.*, 2010).

1.7.1.3 The Ddd and Acu enzymes – a mechanism for DMSP or acrylate dependent 3HP production

As noted, DddD mediates the initial transfer of CoA onto DMSP, and when *Halomonas* DddD was expressed in *E. coli*, it was found that cell-free extracts of the engineered strain converted DMSP to 3-hydroxypropionate (3HP) plus DMS. Consistent with this, *Halomonas* itself could grow on 3HP, the subsequent catabolic steps being mediated by the DddA and DddC enzymes which, respectively, catalyse the conversion of 3HP to malonate semialdehyde (MalSA) and the latter to acetyl-CoA (Todd *et al.*, 2007; 2010; Curson *et al.* 2008; Figure 1.7). Note that *Marinomonas* MWYL1 does not have a *dddA* gene but that the *ddd* cluster includes *dddB,* which is conversely absent from that of *Halomonas.* Both genes encode an alcohol dehydrogenase enzyme, but belong to different families; DddA and DddB are thought to bind flavin and Fe, respectively. However, it is thought that they achieve similar physiological goals.

Figure 1.6 The *dddD/TBCR, dddZ, acuR, acuI* and *dddY* genes in strains of *Marinomonas, Halomonas, Alcaligenes faecalis, Pseudomonas* and *Psychrobacter*



Gene names given inside arrows. Not to scale. Dashed line indicates break point in cosmid library.

***dddD*: DMSP lyase; *dddY*: DMSP lyase;**

***dddT*: Betaine carnitine choline transport (BCCT) family, DMSP transporter;**

***dddB, dddA*: Flavin containing alcohol dehydrogenase; *dddC*: methyl-malonate semialdehyde dehydrogenase;**

***dddR*: LysR-like regulator; *dddZ*: DddR-like regulator;**

***acuI*: acryloyl-CoA reductase (see chapter 5); *acuR*: TetR-like regulator;**

***acuN*: CaiB-like gene product, crotonobetainyl-CoA / carnitine CoA transferase; *acuK*: CaiD-like gene product, crotonobetainyl-CoA hydratase;**

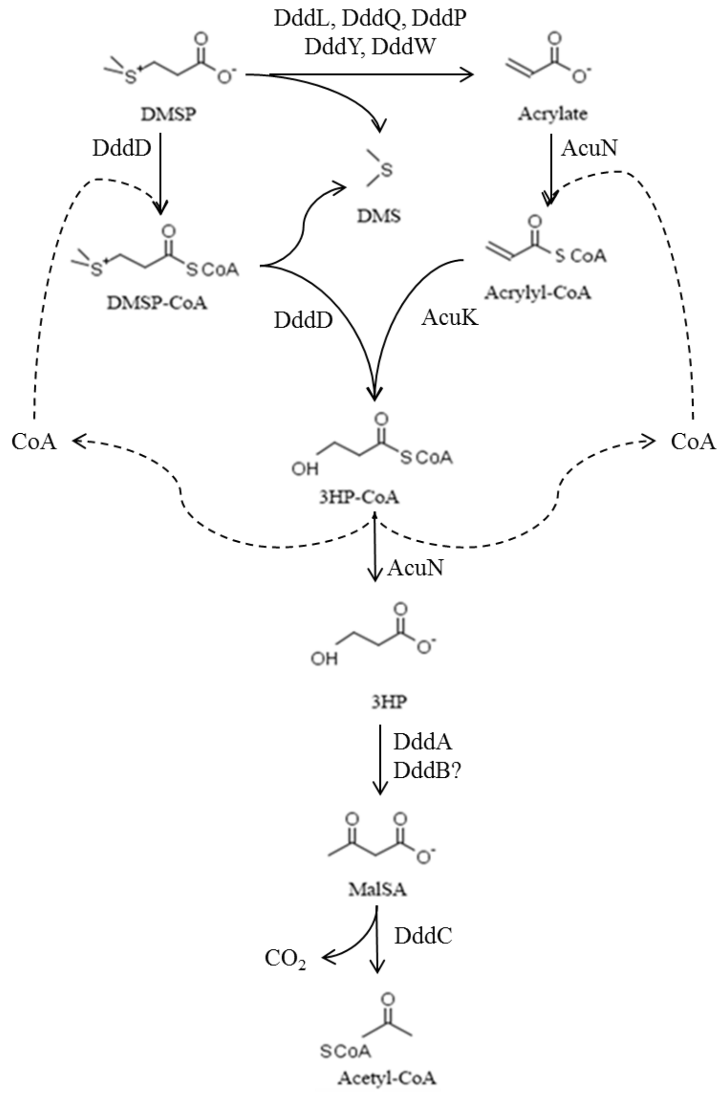
***ddd*: DMSP dependent DMS production; *acu*: Acrylate utilisation.**

Adapted from Todd *et al.*, 2007; Curson *et al.*, 2011b; 2011c.

Although this explained the pathway for DMSP catabolism, it did not account for the growth of *Halomonas* on acrylate. For that ability, two other genes in the *ddd* cluster are needed. These *acuN* and *acuK* (Acu = acrylate utilisation) genes respectively encode gene products that resemble the CaiB and CaiD enzymes of *E. coli*. CaiB forms a homodimeric crotonobetainyl-CoA / carnitine-CoA transferase, while CaiD is a crotonobetainyl-CoA hydratase (Elssner *et al.*, 2001). It is hypothesised that 3HP is produced from DMSP or acrylate via one or more CoA intermediates, through the actions of DddD or AcuN/K, respectively. Thus, DddD produces DMSP-CoA, and AcuNK produce acryloyl-CoA, 3HP-CoA and 3HP (Figure 1.7). Importantly, mutations in AcuN or AcuK abolish growth on acrylate, as found in *Alcaligenes faecalis* M3A (see below; Curson *et al.*, 2011c).

To recap, DddD shares homology with the CaiB enzyme and this is reflected in the similar activities of the two systems. DddD may in fact act as several enzymes at once, carrying out the initial addition of CoA to DMSP, followed by a hydration, with concomitant DMS release. An exquisite suggestion is that the 3HP-CoA formed by the actions of AcuNK enzymes may act as the acyl-CoA donor in the first step of the reaction, creating a self-perpetuating system (Figure 1.7; Todd *et al*., 2010). Alternatively, an as yet unknown CoA donor may be utilised.

Figure 1.7 Predicted mechanism of DMSP and acrylate-dependent 3HP production



The suggested convergence of the DddD, DMSP lyase and the AcuN/K pathways at a shared intermediate, 3HP-CoA, before conversion to 3HP is shown. The 3HP-CoA may act as the acyl CoA donor for the initial addition of CoA to DMSP or acrylate by DddD or AcuN, respectively, as shown by dashed arrows. From 3HP, there is a conversion to malonate semi-aldehyde (MalSA), catalysed by very different types of alcohol dehydrogenases – DddA in the case of (e.g.) *Halomonas* and DddB in (e.g.) *Marinomonas.* The MalSA is then converted to acetyl CoA and CO_2 via DddC. In organisms that do not contain AcuNK enzymes, such as *Ruegeria pomeroyi*, a different catabolic pathway for acrylate is predicted (see chapters 5 and 7). Adapted from Elssner *et al.*, 2001; Todd *et al.*, 2007; 2010.

Thus, the ability to grow on DMSP and on acrylate is not due to the conversion of the former to the latter, but to the independent catabolism of each, converging at 3HP.

Interestingly, some *Archaea*, such as *Metallosphaera sedula* contain a pathway known as the 3HP/4-hydroxybutyrate pathway. In this pathway, CO_2 and acetyl CoA are combined to produce malonyl-CoA, with this being reduced to MalSA by a NADPH-dependent malonate semialdehyde dehydrogenase. It is then converted through via 3HP, 3HP CoA and acryloyl-CoA (Berg *et al.*, 2007; Stines-Chaumeil *et al.*, 2006; Hügler *et al.*, 2003). This is the reverse reaction that is predicted to occur in *Halomonas* HTNK1 (Figure 1.7; Todd *et al.*, 2010).

1.7.1.4 DddD and DMSP Transporters

It was noted that the *dddD*-containing gene clusters of several γ-proteobacteria included one or more genes that were strongly predicted to encode polypeptides that would import the DMSP substrate. Strikingly, these were of two very different types, namely BCCT-type and ABC-type, both of which had been shown in other bacteria to import molecules that closely resemble DMSP.

Thus, the *dddD*-containing clusters of *Halomonas* HTNK1, *Oceanimonas doudoroffii, Psychrobacter* J465 and *Pseudomonas* J466 include *dddT*, whose product is a strongly predicted betaine importer of the BCCT (Betaine, Carnitine Choline Transporter) family. These are defined by the Transporter Classification Database (2.A.15) as proteins that transport molecules with quaternary ammonium groups (Saier *et al.*, 2009). They vary in their mode of transport, but nearly all of them depend on Na^+ or H^+ for maintenance of a motive force. Many also contain osmoregulatory or osmosensory properties (Saier *et al*, 2009). BCCT proteins transport DMSP, in addition to its canonical substrates, likely due to the structural similarity of these compounds (Todd *et al.* 2010; Sun *et al.*, 2011). DddT expressed in an *E. coli* mutant defective in betaine transport conferred the ability to import DMSP. The flexibility of DddT, as with other BCCTs, was also illustrated by the recovery of growth when provided with glycine betaine (Todd *et al.*, 2010; Sun *et al.*, 2011).

In contrast to the examples above, the *dddD* genes of *Burkholderia ambifaria* AMMD, and the α-proteobacteria, *Rhizobium* sp. NGR234, *Rhodobacterales* KLH11 and *Hoeflea phototrophica* DFL-43, are all clustered with genes that encode ATP-binding cassette (ABC) transporters, belonging to sub-families involved in proline/glycine betaine transport (COG2113) and spermidine/putrescine binding transport systems (COG0687). The ABC transporters are massively widespread, and comprise a periplasmic binding substrate binding protein, a membrane-bound transporter and an energy-providing ATP-ase domain (Eitinger *et al.,* 2011). *E. coli* and other enteric bacteria were also able to import DMSP and glycine betaine in response to increased salinity, via a ProU-mediated system (Cosquer *et al.,* 1999). The ProU transport system, originally discovered in *Salmonella typhimurium,* imports betaines such as proline in response to osmotic stress (Cairney *et al*., 1985; Haardt *et al.,* 1995).

1.7.1.5 The DddR, DddZ and DddH regulators

In addition to the genes that encode the enzymes for DMSP and acrylate transport and for the import of DMSP, some regulatory *ddd* genes have been identified.

Firstly, it was noted that a mutation in *dddR* of *Marinomonas* MWYL1 abolished the Ddd$^+$ phenotype. Furthermore, a *dddD-lacZ* transcriptional fusion was not expressed in the *dddR*$^-$ mutant strain, whereas in the wild-type background, it was transcribed at high levels, but only in DMSP-grown cells (Johnston *et al.,* 2008). Consistent with this, the DddR protein resembles a LysR-type transcriptional activator, a huge family of regulators that activate expression of their target genes and which, usually, are negatively auto-regulatory (Maddocks and Oyston, 2008). The DddR protein in *Marinomonas* is unusual in that it is positively auto-regulatory, the opposite of most LysR-type regulators (Curson *et al.,* 2011a). This may induce a positive feedback loop that results in rapid consumption of DMSP upon activation.

The *dddR* gene is also found in other species, including *Pseudomonas* J465, which has a highly similar *ddd* gene arrangement to that of *Marinomonas* and also to others, but these are less similar in sequence (Figure 1.6). A cloned DddR-like gene product in *Burkholderia cepacia* AMMD could activate expression of the *Marinomonas dddD* when expressed heterologously (Todd *et al.,* 2007). A less similar homologue of DddR also exists in *Rhizobium* NGR234, with an identity of only 25% at the peptide level. Indeed, it was termed DddZ and predicted to be involved in the regulation of the divergently transcribed *dddA-dddC* genes in that strain (Johnston *et al.,* 2008). The *dddZ* gene became of more interest when a homologue of DddZ was found in *Halomonas* HTNK1, and the gene encoding it was found to be divergently transcribed from the *dddCA-acuNK-dddT* operon, along with another gene, *dddH* (Todd *et al.,* 2010). The DddH protein is very different from the other two regulators, belonging to the TetR family of transcriptional regulators. A role for either of these proteins has yet to be demonstrated directly.

The significant level of HGT that has occurred during the evolution of *dddD* has resulted in copies of this gene being present in many different genera of bacteria. The *dddD* gene appears to be closely linked to growth on DMSP, being prevalent in bacteria isolated on the basis of their ability to use DMSP as a sole C source. Many of these organisms are located in areas of high DMSP concentration, such as corals, seaweeds, marine sediments and the gut of plankton-eating fish (Curson *et al.,* 2010; 2011a).

The appearance of a non-functional *dddD* gene in *R. pomeroyi* suggests a different physiological role for this enzyme from DMSP-dependent DMS production. *R. pomeroyi* DSS-3 already has several DMSP lyases (see later; chapters 4 and 5) and perhaps this form of DddD is responsible for a reaction involving a substrate similar, but not identical to, DMSP; for example, the addition of a CoA moiety to a molecule similar to DMSP (Todd *et al.,* 2011).

Interestingly, some bacterial strains known to cleave DMSP and release DMS were found to lack any detectable homologues of *dddD,* so must have possessed an alternative enzyme (Johnston *et al., 2*008).

1.7.2 DddL

As mentioned previously, DMSP can be cleaved to release equimolar amounts of DMS and acrylate. Following the discovery of the “a-typical” lyase, DddD, I shall now discuss those enzymes that are involved in the more common and direct, DMSP cleavage reaction, starting with DddL.

1.7.2.1 Identification of *dddL* in *Sulfitobacter* EE-36

One of the bacterial strains that was known to release DMS from DMSP but whose genome was seen to lack *dddD,* was *Sulfitobacter* EE-36, which is a member of the Roseobacter clade. A cosmid library of this strain was made in the wide host-range cosmid pLAFR3 (Staskawicz *et al*., 1987) and one cosmid was obtained that conferred a Ddd$^+$ phenotype to a strain of *Rhizobium leguminosarum*. This was chosen as the heterologous host for two reasons; like *Sulfitobacter* it is an α-proteobacterium and, secondly, it has many σ-factors, and so may favour the expression of heterologous genes from other bacteria (Young *et al.,* 2006). A single gene, *dddL,* sub-cloned form the original cosmid, was sufficient to bestow a Ddd$^+$ phenotype in *E. coli.* Importantly, high pressure liquid chromatography (HPLC) analysis identified acrylate as the C3 compound released from DMSP, in addition to DMS (Curson *et al.,* 2008). This made DddL the first *bona fide* DMSP lyase, in the generally accepted definition of this enzymatic activity. DddL had previously been described as a DUF (domain of unknown function), but has a C-terminal domain with similarity to cupins (Curson *et al.,* 2008; Todd *et al.,* 2011; see later). However, *Sulfitobacter* is unable to grow on DMSP as a sole C source, a clear distinction from the previously mentioned *Marinomonas* strain.

1.7.2.2 Distribution of DddL homologues

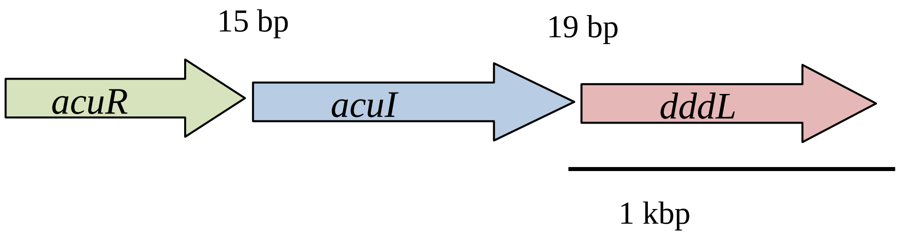
By using DddL as a probe *in silico,* homologues (~50-65% amino acid identity) were found in other genome-sequenced strains of *Rhodobactereceae,* namely *Rhodobacter sphaeroides* 2.4.1, *Loktanella vestfoldensis, Oceanicola batsensis* HTCC2597, *Stappia aggregata,* and also in *Fulvimarina pelagi* HTCC2506, in the closely related *Aurantimonadaceae* family. It was confirmed that all these strains had a Ddd$^+$ phenotype (Curson *et al.*, 2008).

Rhodobacter sphaeroides is a metabolically diverse, purple, non-sulfur bacterium that can respire through fermentation, anaerobic or aerobic respiration, and can fix molecular N_2 (Ferguson *et al*., 1987). Also, for decades, it has been a model organism for the study of bacterial photosynthesis (Oh and Kaplan, 2001), but it had never been implicated in DMSP catabolism

1.7.2.3 The *acuR-acuI-dddL* operon

In most of these strains *dddL* was in a one-gene operon, but there was one striking exception, in some strains of *R. sphaeroides,* in which it was the third gene in a three gene operon (Figure 1.8). Two strains (2.4.1. and ATCC17029) of *Rhodobacter sphaeroides* possessed DddL homologues, which were near-identical to each other and 46% identical to DddL of *Sulfitobacter* and both these strains have a Ddd$^+$ phenotype. In contrast, a third strain of *Rhodobacter sphaeroides* (17025) lacked a *dddL* gene and, reassuringly, did not cleave DMSP (Curson *et al*., 2008). The *dddL* and neighbouring genes of *R. sphaeroides* 2.4.1 were examined in more detail (Choudhary *et al.*, 2007; Curson *et al.*, 2008; Sullivan *et al.*, 2011).

Figure 1.8 *Rhodobacter sphaeroides* 2.4.1 *acuR-acuI-dddL* genes



Approximate scale provided. Gene names shown in arrows. Intergenic gaps given in base pairs (bp). Adapted from Sullivan *et al.* (2011).

The promoter-distal gene *dddL*, the central gene, *acuI* and a promoter proximal gene, *acuR* are in a single transcriptional unit (Figure 1.8). The *acuR* gene encodes a TetR-like transcriptional regulator that represses expression of the operon, unless relieved by its co-inducer molecule acrylate. Although growth of the *R. sphaeroides* cells in DMSP also increased the expression of *acuRI-dddL,* this required its conversion to the authentic inducer, acrylate, by the DMSP lyase, DddL. However, neither substrate was sufficient for growth of *R. sphaeroides* as a sole C source (Curson *et al.,* 2008; Sullivan *et al.,* 2011).

From a regulatory point of view, this operon is of particular interest because its mRNA lacks a leader sequence; the 5' end of the transcript coincides with the ATG of *acuR* and therefore lacks a ribosomal binding site. This is highly unusual in bacteria, but may account for the low expression of *acuR* relative to *acuI* and *dddL* as measured by their translational but not transcriptional efficiencies (Sullivan *et al.,* 2011).

Another significant finding from this work was the discovery of the novel gene, *acuI.* AcuI had been (and still is) labelled in the NCBI database as a zinc-dependent alcohol dehydrogenase, in the medium chain dehydrogenase/reductase (MDR) super-family, which has >15,000 members, spread over ~500 peptide families (Persson *et al.,* 2008). This label is a misnomer, as explained further in chapter 5 and chapter 7. Suffice to say here that AcuI has a role in the processing of acrylate in the organisms that harbour it. This was first indicated by Sullivan *et al.* (2011), who observed that AcuI$^-$ mutants of *R. sphaeroides* 2.4.1 were (a) more sensitive to the toxic effects of acrylate in the growth medium and (b) reduced in their ability to undertake partial catabolism of radio-labelled acrylate.

Other genome-sequenced bacteria were known to make DMS from DMSP, and yet these contained neither *dddD* nor *dddL.* Thus, there were yet other versions of DMSP lyase to be found. One such enzyme was DddP, first identified in a strain of the Roseobacter clade, as follows.

1.7.3 DddP

DddP was discovered in the α-proteobacterium Roseobacter, *Roseovarius nubinhibens* ISM, which had been shown to have a Ddd^+ phenotype (Todd *et al.,* 2009) but whose genome lacked *dddL* or *dddD* (Todd *et al.,* 2007; 2009). To identify the gene for the novel lyase in this strain, a cosmid from a newly constructed genomic library was identified that conferred a Ddd^+ phenotype to the heterologous host, *Rhizobium leguminosarum* strain J391, just as was done to identify *dddL* (above). The gene responsible for the phenotype was localised by sub-cloning and sequencing and was termed *dddP*.

1.7.3.1 Notable features of DddP

The DddP enzyme was shown to be a "classical" DMSP lyase, since *E. coli* strains containing *dddP* cloned in an expression plasmid cleaved DMSP into DMS plus acrylate (Todd *et al.,* 2009).Expression of *dddP* is enhanced, *ca*. 4-fold in cells of *Roseovarius nubinhibens* ISM that were grown in DMSP-supplemented medium, but, unlike *dddL* of *Rhodobacter sphaeroides*, its expression was not induced by acrylate (Todd *et al.*, 2009; chapter 2). DddP is a member of the M24B family (COG0006) of peptidases, as shown in the MEROPS database (Rawlings *et al.*, 2010). These enzymes are often metallopeptidases, although work described in chapter 2 will investigate this label (or rather, misnomer!) in further detail.

1.7.3.2 Distribution of DddP

Homologues of DddP were found in several, but not all Roseobacters – including the "model strain" *Ruegeria pomeroyi* DSS-3. Other α-proteobacteria include *Mesorhizobium* spp. and >55% identity was found to homologues in the genomes of the γ-proteobacteria, *Oceanimonas doudoroffii, Vibrio orientalis* and *Pseudomonas putida*. Thus, DddP appears to be present in both terrestrial and marine organisms. Interestingly, *O. doudoroffii* possesses two very different orthologues of DddP, both of which are active and confer a Ddd^+ phenotype when cloned, individually into *E. coli* (Todd *et al.,* 2009; Curson *et al.,* 2011b). Incidentally, this species also has a functional DddD enzyme.

An exciting discovery was that the *dddP* gene also occurred in some species of fungi and in several cases, these were confirmed as having DMSP lyase activity (Todd *et al*., 2009). Homologues (~53% identity at peptide level) included members of the Sordariomycetes, *Fusarium graminearum*, *F. culmorum* and *F.oxysporum* f.sp. *lycopersici*. These species are well known as the causative agents of a number of crop diseases, such as head blight of cereals and tomato wilt (Sutton, 1982; Snijders *et al.*, 1990; Cooper *et al.*, 1978). Other homologues (also ~53% identity at peptide level) were found in some Euritiomycetes, such as *Aspergillus oryzae* RIB40 and *A. flavus*. These two *Aspergillus* strains are very similar in their genomic structure, differing in only a few instances, such as the presence of a suite of aflotoxin (*aflR*) production genes in *A. flavus* (Watson *et al.,* 1999). There is a very close similarity between the DddP sequences from *Aspergillus* and *Fusarium* species (~90% identity). The bacterial (i.e. *Roseovarius nubinhibens*) and fungal proteins are also similar in their peptide sequence, with ~54% identity to one another, despite their last common ancestor being ~2.7 billion years ago (Nei *et al*., 2001). The *Aspergillus* and *Fusarium* copies of the gene lack introns, pointing to a relatively recent acquisition of *dddP* (Nielsen *et al.,* 2004).

In fact, the presence of a fungal ‘lyase’ was inferred several years earlier from the DMS released by fungi, predominantly Ascomycetes, associated with the rhizosphere of the DMSP synthesising angiosperm, *Spartina alterniflora,* and other salt marsh grasses (Otte, 2004; Bacic *et al.,* 1998). One of these, expressed by *Fusarium lateritium*, was later characterised as a DMSP lyase, and shown to be induced by DMSP (Bacic and Yoch, 1998).

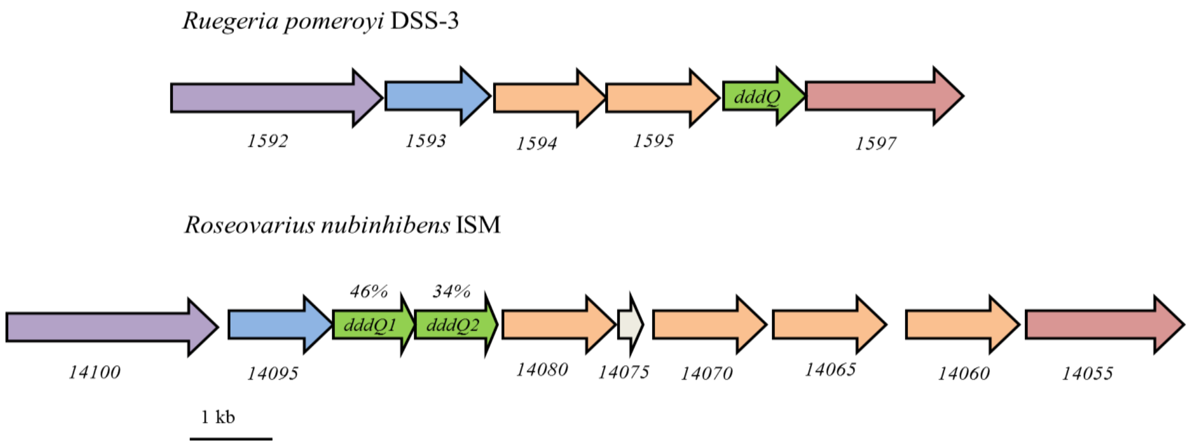
A GOS metagenome database interrogation using DddP from *R. nubinhibens* (Todd *et al.*, 2009) resulted in 92 matches ($< e^{-80}$). The majority (83) of these matches clustered into a single group, which represented proteins in many of the marine α-proteobacteria, and the fungal representatives clustered together in another subgroup. Interestingly, *dddP* was also found in viral metagenomes isolated from environments as diverse as the Arctic Ocean and a coral reef on the equatorial Pacific Ocean island Kiritimati (Raina *et al.*, 2010).

1.7.4 DddQ

A DddP$^-$ mutant strain of *Roseovarius nubinhibens* ISM, created for the work mentioned above, still had a Ddd$^+$ phenotype, albeit at much reduced (~10%) of the wild type level (Todd *et al.*, 2011), suggesting that it had at least one other DMSP lyase. To identify this putative gene, a similar approach to the one used to identify *dddP* was used. Thus, the *Roseovarius nubinhibens* ISM pLAFR3 cosmid library was mobilized into *Rhizobium leguminosarum* strain J391, and the resulting transconjugants were individually assayed for DMS production when provided with DMSP (Todd *et al.*, 2011).

Sequencing of a cloned cosmid that conferred a Ddd$^+$ phenotype to *Rhizobium,* revealed the presence of two adjacent genes, termed *dddQ1* and *dddQ2,* which were predicted to be in a large, 10 gene transcriptional unit (Figure 1.9). The DddQ1 and dddQ2 gene products were 39% identical to each other and were of interest because, like DddL (above), they had a cupin motif. Indeed, when each of these genes was cloned, alone, in *E. coli,* they conferred the ability to catabolise DMSP, forming DMS and acrylate as the products.The functions of the other genes in the operon are not known but it was noted that there was a similar gene arrangement in *Ruegeria pomeroyi.* However, in this strain there was only one copy of *dddQ* and only two copies of the enolase superfamily genes, compared to the four in *Roseovarius nubinhibens* (Figure 1.9).

Figure 1.9 Location of *dddQ* genes in *Roseovarius nubinhibens* ISM and *Ruegeria pomeroyi* DSS-3



Genes in *Roseovarius nubinhibens* ISM and *Ruegeria pomeroyi* DSS-3 are shown as arrows, with their gene tags, but lacking the prefixes 'SPO' and 'ISM_' respectively. The *R. pomeroyi dddQ* (*SPO1596*) and the *R. nubinhibens dddQ1* (*ISM_14090*) and *dddQ2* (*ISM_14085*) genes are coloured green. The %age identities between DddQ and either DddQ1 or DddQ2 are shown above the *R. nubinhibens* genes.

Genes for:

- **aminomethyl transferase family protein (*SPO1592* and *ISM_14100*) are purple**
- **Zn alcohol dehydrogenase family (*SPO1593* and *ISM_14095*) are blue,**
- **acetyl ornithine aminotransferase family (*SPO1597* and *ISM_14055*) are red**
- ***ISM_14075* of *R. nubinhibens* (absent from *R. pomeroyi*) encodes a Cupin-2-like protein and is grey.**
- **enolase super-family are orange, the two versions in *R. pomeroyi* (*SPO1594* and *SPO1595*) being most similar, respectively, to *ISM_14080* and *ISM_14065* of *R. nubinhibens*.**

Adapted from Todd *et al*., 2011.

Given the close phylogenetic relationship between the two species, and the level of synteny between the two genome regions, the *dddQ* genes are surprisingly dissimilar from one another; the *dddQ* gene product from *Ruegeria pomeroyi* shares only 46% and 34% identity with the products of *dddQ1* and *dddQ2* from *Roseovarius nubinhibens*, respectively, and much of this identity relates to the cupin domain present in both homologues.

1.7.4.1 DddL and DddQ Cupin domains

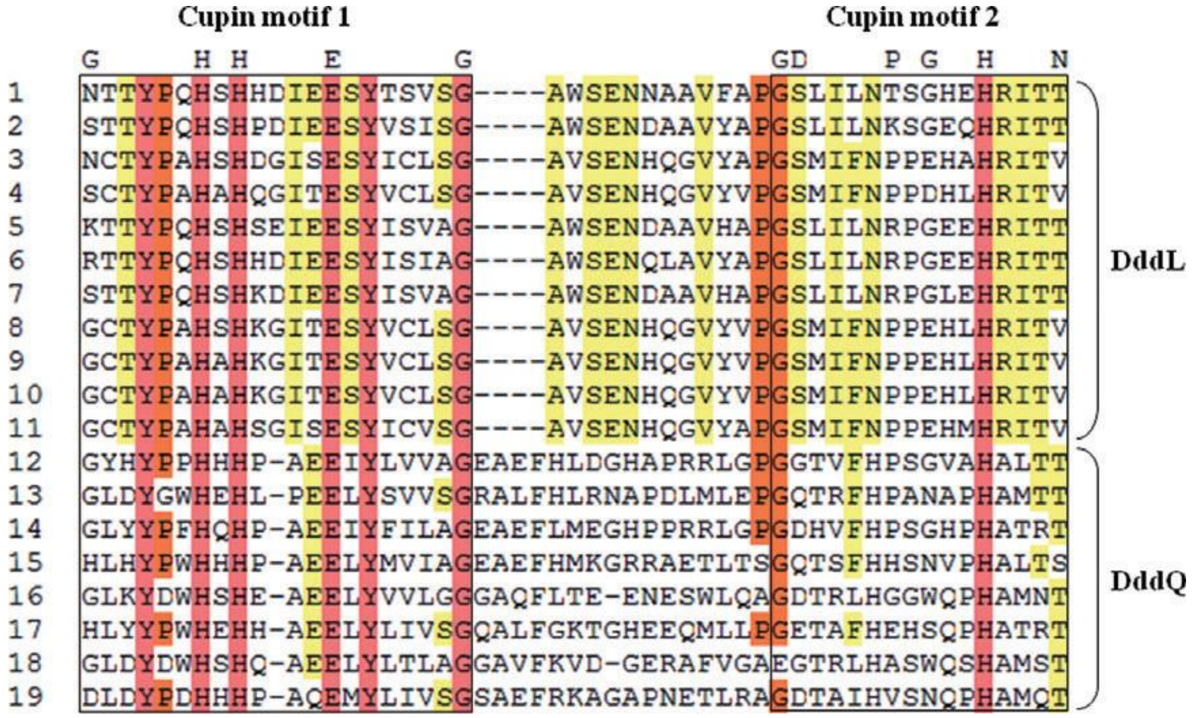
Cupins (Latin “cupa” means “small barrel”), are a super-family of domains with a β-barrel structure (Dunwell, 1998; Dunwell and Gane, 1998). They are functionally diverse, with many examples in all three Domains of life, being initially discovered as germin-like proteins from wheat. Typically, a cupin domain has two conserved motifs, 1 and 2, as shown below:

Motif 1: $(\mathrm{X})_5\mathbf{H}\mathrm{X}\mathbf{H}(\mathrm{X})_{3,4}\mathrm{E}(\mathrm{X})_6\mathbf{G}$

Motif 2: $\mathrm{G}(\mathrm{X})_5\mathrm{PXG}(\mathrm{X})_2\mathbf{H}(\mathrm{X})_3\mathrm{N}$

These motifs are separated by an inter-motif region, between 11 and 100 amino acids in length, depending on the organism and function (Dunwell *et al*., 2000; 2001; 2004). Cupins are generally metal-binding proteins, with the predicted metal-binding residues being two histidine and one glutamine residues within motif 1, and a single histidine in motif 2 (shown in bold in the above sequences), acting as ligands to bind a variety of metals, including manganese, nickel, zinc, iron and copper (Woo *et al*., 2000). Different proteins may contain one or more cupin domains, known as mono-, bi- or even multi- cupin proteins. Chapter 4 has further discussion of cupins in other proteins, particularly the novel DMSP lyases.

Figure 1.10 Alignment of cupin regions of selected DddL and DddQ polypeptides



```
1   NTTYPQHSHHDIEESYTSVSG----AWSENNAAVFAPGSLILNTSGHEHRITT
2   STTYPQHSHPDIEESYVSISG----AWSENDAAVYAPGSLILNKSGEQHRITT
3   NCTYPAHSHDGISESYICLSG----AVSENHQGVYAPGSMIFNPPEHAHRITV
4   SCTYPAHAHQGITESYVCLSG----AVSENHQGVYVPGSMIFNPPDHLHRITV
5   KTTYPQHSHSEIEESYISVAG----AWSENDAAVHAPGSLILNRPGEEHRITT
6   RTTYPQHSHHDIEESYISIAG----AWSENQLAVYAPGSLILNRPGEEHRITT
7   STTYPQHSHKDIEESYISVAG----AWSENDAAVHAPGSLILNRPGLEHRITT
8   GCTYPAHSHKGITESYVCLSG----AVSENHQGVYVPGSMIFNPPEHLHRITV
9   GCTYPAHAHKGITESYVCLSG----AVSENHQGVYVPGSMIFNPPEHLHRITV
10  GCTYPAHAHKGITESYVCLSG----AVSENHQGVYVPGSMIFNPPEHLHRITV
11  GCTYPAHAHSGISESYICVSG----AVSENHQGVYAPGSMIFNPPEHMHRITV
12  GYHYPPHHHP-AEEIYLVVAGEAEFHLDGHAPRRLGPGGTVFHPSGVAHALTT
13  GLDYGWHEHL-PEELYSVVSGRALFHLRNAPDLMLEPGQTRFHPANAPHAMTT
14  GLYYPFHQHP-AEEIYFILAGEAEFLMEGHPPRRLGPGDHVFHPSGHPHATRT
15  HLHYPWHHHP-AEELYMVIAGEAEFHMKGRRAETLTSGQTSFHHSNVPHALTS
16  GLKYDWHSHE-AEELYVVLGGGAQFLTE-ENESWLQAGDTRLHGGWQPHAMNT
17  HLYYPWHEHH-AEELYLIVSGQALFGKTGHEEQMLLPGETAFHEHSQPHATRT
18  GLDYDWHSHQ-AEELYLTLAGGAVFKVD-GERAFVGAEGTRLHASWQSHAMST
19  DLDYPDHHHP-AQEMYLIVSGSAEFRKAGAPNETLRAGDTAIHVSNQPHAMQT
```

The region spanning the conserved cupin motifs 1 and 2 (boxed) is shown, with residues conserved in the cupin superfamily (Dunwell *et al.*, 2004) shown above the sequence. Residues marked in red, orange and yellow are, respectively, 100%, >80% and >60% identical in all the sequences. Sequences are from: 1 = *Dinoroseobacter shibae* DFL 12, DshiDRAFT_1825; 2 = *Fulvimarina pelagi* HTCC2506, FP2506_12684; 3 = *Labrenzia alexandrii* DFL-11, SADFL11_5101; 4 = *Loktanella vestfoldensis* SKA53, SKA53_01756; 5 = *Oceanicola batsensis* HTCC2597, OB2597_08014; 6 = Rhodobacterales HTCC2654, HTCC2654_RB2654; 7 = *Rhodobacter sphaeroides* 2.4.1, Rsp_1433; 8 = Roseobacter GAI101, RGAI101_3508; 9 = *Sulfitobacter* sp. EE-36, EE36_11918; 10 = *Sulfitobacter* sp. NAS-14.1, NAS141_17149; 11 = *Stappia aggregata* IAM 12614, SIAM614_20126; 12 = *Roseovarius nubinhibens* ISM, ISM_14090; 13 = *R. nubinhibens* ISM, ISM_14085; 14 = *Ruegeria pomeroyi* DSS-3, SPO1596; 15 = Rhodobacterales bacterium HTCC2150, RB2150_06543; 16 = Rhodobacterales bacterium Y4I, RBY4I_2503; 17 = *Roseobacter* sp. SK209-2-6, RSK20926_17292; 18 = *Silicibacter lacuscaerulensis* ITI_1157, SL1157_0332; 19 = *Thalassiobium* sp. R2A62, TR2A62_3487.

From Todd *et al.* (2011).

The DddL and DddQ homologues share many of the conserved residues of cupin domain proteins (Figure 1.10) (Dunwell *et al.,* 2004; Todd *et al.,* 2011). It is not known how the separate proteins evolved, either through convergent or divergent evolution. However, it is clear that the cupin domain is important for cleavage of DMSP.

1.7.4.2 Distribution of DddQ

An NCBI BLASTp found DddQ homologues in a few other Roseobacters, including *Silicibacter lacuscaerulensis*, and also in a SAR116 Clade α-proteobacterium, HIMB100. Due to the diversity between the groups of these enzymes, a relatively low cut-off value of NCBI bit score >109 was used to interrogate the GOS with DddQ. This retrieved >200 matches and these primarily clustered into 3 main groups (Todd *et al.,* 2011). Given the diversity of DddQ, even ratified ones, it is not clear which of these GOS sequences are *bona fide* DMSP lyases. However, one gene from each group was chosen and synthesised *in vitro*, before being cloned into pBluescript and transformed into *E. coli*. All 3 conferred a Ddd$^+$ phenotype (Todd *et al.,* 2011).

1.7.5 DddY

Following the discovery of DddQ, the gene for another DMSP lyase, DddY, was identified, but this time, it was one that had been encountered before, from a biochemical approach. DddY was initially found in the β-proteobacterium *Alcaligenes faecalis* M3A, isolated from intertidal sediment containing the DMSP-producing cordgrass, *Spartina* (de Souza and Yoch, 1995a). Prior work had shown that this bacterium could convert DMSP to acrylate, and could also use both of these compounds as carbon sources (Ansede *et al*., 1999). In a demanding series of experiments, Yoch *et al.* purified the DMSP lyase from *A. faecalis* M3A and even obtained its N-terminal sequence, but they did not extend the work to identify the corresponding gene (de Souza and Yoch, 1995a; 1995b; 1996; Yoch *et al*.,1997). This approach was only undertaken some 14 years later, by Curson *et al*. (2011c), and has led to some intriguing outcomes on what is another, very different system for DMSP catabolism.

1.7.5.1 DddY, a membrane-bound lyase

As before, the isolation of *dddY* involved the construction of a library in a wide host-range cosmid, followed by the screening for function in a heterologous host. In this case, the host was *Pseudomonas putida* and transconjugants containing the library of cosmids were selected for growth on DMSP as sole C source. Following the sub-cloning from a cosmid that conferred this property, a fragment, and then a single gene, termed *dddY*, could confer a Ddd$^+$ phenotype to *E. coli*, converting DMSP into DMS plus acrylate. Further, a mutation in *dddY* in *A. faecalis* M3A itself abolished its ability to make DMS from this substrate (Curson *et al*., 2011c). Reassuringly, the deduced *dddY* gene product contains an N-terminal sequence which is strongly predicted to include an N-terminal leader that would guide it to the bacterial periplasm. This is in keeping with the earlier suggestion by Ansede *et al.* (1999) that the lyase in *A. faecalis* M3A was associated with the cell surface and this was further substantiated by Curson *et al.,* (2011c) who showed by sub-cellular fractionation that the lyase was associated with the periplasm. And, most satisfying of all, when the N-terminal sequence was cleaved *in silico* at the predicted cleavage site (21 amino acids from the N-terminus) this generated a polypeptide whose deduced sequence matched the one that had been described by de Souza and Yoch (1996) for the mature, functional enzyme. Other than that, there were no sequence-based clues on the enzymatic function of DddY, as demonstrated by the fact that, hitherto, it had been annotated as a Domain of Unknown Function (DUF), with no similarity to any other polypeptide of defined enzymatic activity

1.7.5.2 Distribution of DddY

Following a search of the NCBI database, the DddY polypeptide was not seen in any other species of *Alcaligenes*, but homologues with identities of ~35% were found in certain members of the γ-proteobacteria, *Shewanella* spp. (Curson *et al*., 2011c). A DddY homologue was also found in the ε-proteobacterium *Arcobacter nitrofigilis* DSM7299 (Pati *et al.,* 2010). The sequences of the *Shewanella* and *Arcobacter* strains were ~75% identical to each other and, like that of *A. faecalis,* were strongly predicted to be periplasmic. All of these strains exhibited Ddd$^+$ phenotypes, meaning that *Arcobacter nitrofigilis* is the first demonstrated ε-proteobacterium with this ability (Curson *et al.,* 2011c). Unsurprisingly, *A.*

nitrofigilis was isolated from the roots of the DMSP synthesising salt marsh plant, *Spartina alterniflora* (McClung *et al.,* 1983).

Just as they had done with *A. faecalis,* deSouza and Yoch (1996) purified a DMSP lyase from the γ-proteobacterium, *Oceanimonas doudoroffii,* and found that its N-terminus was very similar to that of the *A. faecalis* DddY. However, the near-complete genome of this strain lacks a *dddY* gene (Curson *et al.,* 2011c), although it does contain *dddD* and two versions of *dddP* (see above). The reason for this discrepancy is not known.

There were no detectable DddY homologues in the GOS, or any other, metagenomic database.

1.7.5.3 DddY and acrylate metabolism

Examination of the region close to *dddY* of *A. faecalis* M3A revealed several other genes that corresponded to those in the *ddd* gene clusters of other bacteria, notably *Halomonas* HTNK1 (Figure 1.6). Thus, both these strains contained *dddA, dddC, acuN* and *acuK,* all of whose corresponding products are ~70% identical in the two species. However, there were two obvious and explicable differences. First, the two strains differed in the nature of the genes that encoded the initial DMSP lyase – *dddY* for *Alcaligenes* and *dddD* for *Halomonas.* Second, the *ddd* cluster of *Halomonas* includes the transporter gene *dddT* but *Alcaligenes* does not. This, of course, is fully consistent with the fact that DddY is located in the periplasm, so there is no need for a dedicated import system for the substrate.

It is striking that both gene clusters include the *acuNK* genes, which are involved in the conversion of acrylate to 3HP (see above). Whereas the AcuNK enzymes of *Halomonas* need only act on exogenously supplied acrylate (DddD does not generate this product from DMSP), in the case of *Alcaligenes* can also be generated via the action of DddY on DMSP. Whatever the source, the resultant 3HP can then be used as the substrate for further catabolism, via DddC and DddA, as described above for *Halomonas,* Interestingly, an intermediate in AcuNK mediated acrylate catabolism is acryloyl-CoA, and this happens to be the cognate molecule for the AcuI enzyme, encoded by the nearby *acuI* gene in *Halomonas* (see above; chapter 5).

Alcaligenes contains homologues of the previously mentioned *dddZ* and *acuR* genes from *Halomonas* HTNK1 (Curson *et al*., 2011c) and indeed, an *acuI* gene whose product is 60% and 65% identical to the *Rhodobacter sphaeroides* 2.4.1. and *Halomonas* HTNK1 proteins, respectively. AcuR appears to act as a repressor in *A. faecalis* also, with an AcuR$^-$ mutant exhibiting a ~11 fold increase in DMS production. Growth experiments illustrated that the DddZ protein may be responsible for acrylate catabolism, via regulation of AcuN, AcuK, or perhaps downstream acrylate catabolic enzymes. Transcriptional *lacZ* fusions showed that the *dddY* operon was up-regulated in response to acrylate, and its precursor, DMSP, but no induction of *dddZ* was noted.

Interestingly, *A. faecalis* may also have an alternative method of catabolising DMSP, since DddY$^-$ strains could still use DMSP as a sole C source, despite producing significantly less DMS from DMSP.

1.8 Current knowledge

These recent genetic studies have provided something of a sea-change in our understanding of bacterial DMSP catabolism, and there are a number of key points to remember, going forward.

1. Diversity – The genes and enzymes responsible for DMSP degradation are varied and often unique, with at least 6 classified DMSP lyases that display several different characteristics.
2. Distribution – The DMSP lyases can be found in a wide range of bacteria, particularly the marine Roseobacters. Additionally, the presence of these genes in species of fungi and phytoplankton implies an important role for this pathway throughout the Kingdoms.
3. Horizontal Gene Transfer – These genes have likely undergone considerable levels of HGT between bacterial species, and even between the Domains.
4. Multiple systems in single strains – The possession of multiple DMSP degradation systems in certain species (e.g. *Ruegeria pomeroyi* which harbours at least *dddP, dddQ, dddW* and *dmdA* – see chapters 4, 5 and 7) implies a high level of adaptation to the DMSP molecule and has much potential for studies into the portioning of these systems *in vivo.*
5. Odd regulation – The unusual regulation observed in some of these systems, such as the acrylate mediated induction of *dddL* in *Rhodobacter sphaeroides* 2.4.1. point to more complicated control of these genes than first thought.

1.9 Aims and objectives

In 2008, when this project started, the full extent of the diversity and complexity of the DMSP catabolic pathways was only beginning to emerge. It was clear, though, that the initial genetic studies had formed the platform for a set of new studies, aimed at clarifying and extending what was known in terms of the biochemistry, physiology, genetics, genomics, ecology and even the evolution of these processes.

My project therefore was to gain more information on the mechanism and regulation of DMSP in bacteria, in particular in the Roseobacter clade, for which DMSP catabolism is an important part of their nutritional lifestyle. The experimental programme was to include genetics, bioinformatics, transcriptomics and bacterial physiology.

There exists a significant pool of knowledge concerning the enzymes involved in the degradation of the osmolyte DMSP. The demethylase and lyases have been examined in closer detail, illustrating the remarkable leaps in understanding that have occurred in a relatively short period of time. Despite attempts to investigate the regulation of genes in response to DMSP in bacterial communities and in particular species, such as *R. pomeroyi* DSS-3, there are still areas that would benefit from further research. Until now, the effects of the DMSP degradation products at a global transcriptomics level have been neglected, discounting the cells response to compounds such as acrylate and DMS, which may provide greater insight into the intricacies of the metabolic regulation that occurs in *Ruegeria pomeroyi* DSS-3, a model organism that utilizes both mechanisms of DMSP degradation and multiple DMSP lyase pathways.

The work in this thesis will address the following:

- To over-express, purify and further characterise, biochemically, the DddP DMSP lyase from the Roseobacter, *Roseovarius nubinhibens* ISM, and to investigate the presence of homologous enzymes in novel fungal species.
- To use transcriptomics to investigate the response of *Ruegeria pomeroyi* DSS-3 to the osmolyte DMSP, and two of its degradation products, acrylate and DMS.
- To identify and ratify novel genes and enzymes involved in DMSP metabolism through bioinformatics and molecular genetic approaches, including the use of transcriptional fusions, RT-PCR and mutations.
- To begin an investigation of the regulatory mechanisms that effect transcriptional responses to DMSP and/or its catabolites.
- To begin to understand the complex interactions between several apparently autonomous metabolic pathways in response to DMSP, and to come to conclusions as to the evolution of such systems in *Ruegeria pomeroyi* DSS-3, and other DMSP utilising marine bacteria.

Chapter 2

The DMSP lyase, DddP

2.1 Introduction

Prior to the studies into the genome-wide response of *Ruegeria pomeroyi* to DMSP, DMS and acrylate, I was involved in some much more specific work regarding one particular DMSP lyase, DddP. As discussed in the introduction, work by Todd *et al.* (2009) had identified a DMSP lyase in *Roseovarius nubinhibens* ISM and shown that it conferred a Ddd^+ phenotype when the corresponding gene, *dddP*, was expressed heterologously in other bacteria. Following on from this discovery I wished to ratify the function of DddP as a *bona fide* DMSP lyase that cleaved DMSP into acrylate plus DMS *in vitro.*

2.2 Results

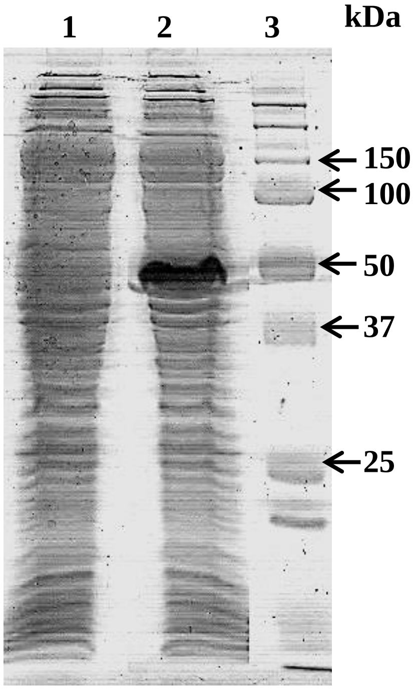
2.2.1 Over-expression of the *Roseovarius nuibinhibens* ISM DddP protein

To characterise the DddP polypeptide and confirm its function as a DMSP lyase, I set out to purify it to an acceptable level of homogeneity. This was done for the *Roseovarius nubinhibens* version of the enzyme, since this strain had (at the time) become something of a model for the Roseobacter clade in the UEA laboratory, as well as elsewhere. A purification protocol was developed as follows.

A 1392 bp fragment containing the intact *dddP* gene was amplified from *R. nubinhibens,* using primers DddPF and DddPR, and cloned into the pET21a plasmid expression vector (Novagen), to form the recombinant plasmid pBIO1658, which was transformed into *E. coli* strain BL21 pLysS (Miroux and Walker, 1996). The pET21a plasmid contains a *lacI* repressor gene, a viral T7 promoter, a polylinker site and Amp^R. Thus, when isopropyl β-D-1-thiogalactopyranoside (IPTG) is added to cells containing this plasmid, rapid and significant transcription of the inserted DNA occurs, making it a useful tool for heterologous gene expression. This initial cloning was done by J. D. Todd (see Todd *et al.,* 2009).

To obtain significant amounts of the DddP polypeptide, a 100ml culture of the *E. coli:*: pBIO1658 strain was grown at 37°C in LB containing ampicillin to an OD_{600nm} of 0.4-0.6. Then, 10 µM IPTG was added to induce expression of the cloned *dddP* gene and the culture was further incubated at 25°C until stationary phase. The cells were was pelleted by centrifugation and re-suspended in TRIS buffer, before being lysed by sonication. This initial extract was run on an SDS-PAGE gel and a ~50 kDa band was observed to be significantly more abundant than any other. This corresponded to the predicted molecular weight of DddP, at 49,972 kDa, and the band was not seen in empty vector (see Figure 2.1).

Figure 2.1 Cell lysate from *E. coli* cultures expressing empty pET21a vector and vector containing *Roseovarius nubinhibens* ISM DddP, separated by SDS-PAGE



Polypeptides were separated by SDS-PAGE on 12% acrylamide gels and stained with Coomassie Blue. Lanes: 1, crude cell extract from *E. coli* cells containing empty pET21a vector; 2, crude cell extract from *E. coli* cells induced for expression of *R. nubinhibens* DddP (pBIO1658) 3, broad-range protein marker (Bio-Rad).

2.2.2 Purification of DddP from *E. coli* expressing pBIO1658

The cell lysate was then partially precipitated using $(NH_4)_2SO_4$. Increasing the salt concentration, and thus ionic strength, causes proteins to become insoluble and precipitate. An iterative process was initially used to determine at which concentration the $(NH_4)_2SO_4$ would pull out as much protein from the lysate as possible, without precipitating DddP. And so, addition of 25% (w/v) $(NH_4)_2SO_4$ precipitated a proportion (*ca.* 40%) of the proteins without removing DddP itself (Figure 2.2, lane 3). The resulting lysate was centrifuged and the supernatant subjected to three separate column chromatograph steps. At each stage of purification, an absorbance trace was used to determine which fractions contained protein, and these were checked using SDS-PAGE for the presence of an appropriate band. DMS assays were also carried out on the pooled fractions to confirm that DddP retained activity.

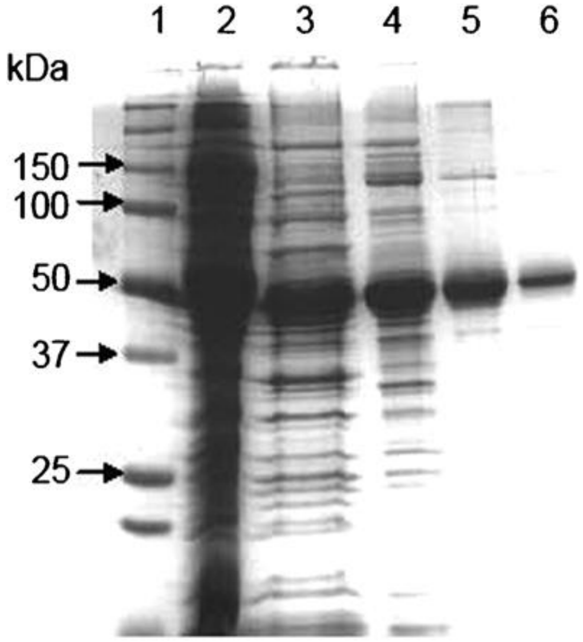
First, the supernatant was run through a phenyl-sepharose high performance column, which utilises the hydrophobic chromatography principle (Hofstee, 1973). The hydrophobic ligand (phenyl-sepharose) reversibly binds the hydrophobic surface residues on proteins in high salt concentrations. As the salt concentration decreases, proteins disassociate and are eluted. Therefore, the column was equilibrated with 20 mM Tris containing 25% $(NH_4)_2SO_4$. DddP was then eluted by applying a 25% – 0% $(NH_4)_2SO_4$ gradient (flow rate 3 ml min^{-1}).

There were three DddP-containing fractions, each of 3 ml (Figure 2.2, lane 4). These were pooled and applied to a DEAE anion exchange column equilibrated with 20 mM Tris, pH8. This separated the proteins on the basis of their charge. DddP has a predicted isoelectric point (pI) of ~5.1 (ExPASy Compute - Bjellqvist *et al.*, 1993), and so at pH8 has a net negative charge, making it ideal for binding to a positively charged solid phase, as used in anion exchange chromatography (Williams and Frasca, 2001). A 0 – 1M NaCl gradient was applied (flow rate 5 ml min^{-1}), increasing the ionic strength and causing proteins to elute.

Again, three DddP-containing fractions, each of 2 ml, were retrieved and pooled (Figure 2.2, lane 5), then applied to the final, gel filtration column, to separate the remaining proteins on the basis of molecular weight (Lathe and Ruthven, 1955). To do this, the pooled fractions were concentrated using an Amicon Ultra centrifugal filter (Millipore), loaded onto a Superdex 200 column equilibrated with 50 mM MES buffer, and run through at a flow volume of 1 ml min^{-1}. Two DddP-containing fractions, of 5 ml each, were pooled and stored at 4°C for further use, with no detectable loss in activity, even after several weeks.

As shown in Figure 2.2, lane 6, the final step yielded a single visible band on Coomassie Blue with an approximate purity of >95%, and yielded ~ 50 mg DddP L^{-1} of initial *E. coli* culture, as estimated from A_{280} measurements, using the protein extinction coefficient, 76,860 M^{-1} cm^{-1}, calculated from the tyrosine, tryptophan and cysteine residues in the amino acid sequence (Gill and von Hippel, 1989).

Figure 2.2 Purified *Roseovarius nubinhibens* ISM DddP protein from *E. coli* cultures, separated by SDS-PAGE



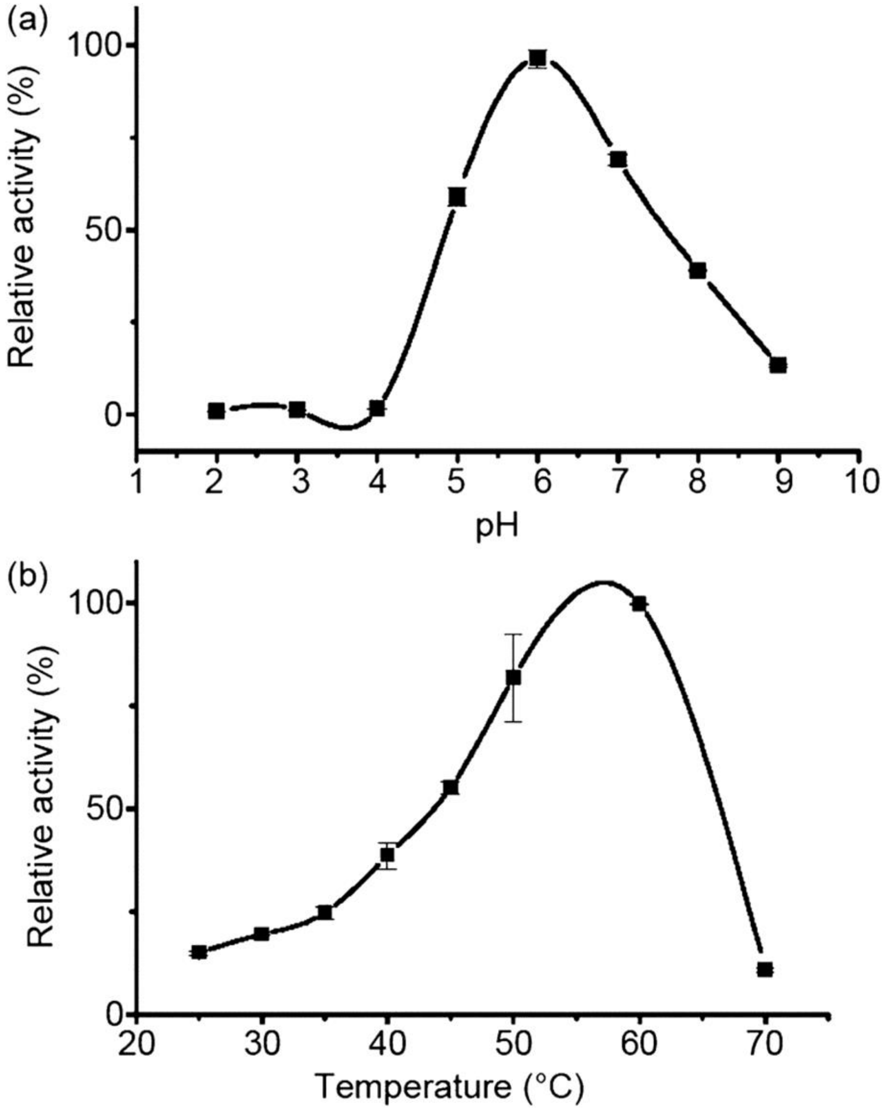
Polypeptides were separated by SDS-PAGE on 12% acrylamide gels and stained with Coomassie Blue. Lanes: 1, broad-range protein marker (Bio-Rad); 2, crude cell extract after sonication; 3, supernatant after treating cell extract with 25% $(NH_4)_2SO_4$; 4, phenyl sepharose column eluate; 5, DEAE column eluate; 6, gel filtration column eluate. From Kirkwood *et al.* (2011b).

2.2.3 Characterisation of the purified DddP enzyme

2.2.3.1 Effect of pH and temperature on DddP enzymatic activity

Prior to characterisation and enzyme kinetic studies, the effects of pH and temperature on DddP activity were ascertained, as follows. DMS assays using GC were carried out as above, with the enzyme being in MBS buffer over a range of pH values, from 2.0 to 9.0 (see Figure 2.3a).

Figure 2.3 Effect of pH and temperature on DddP activity



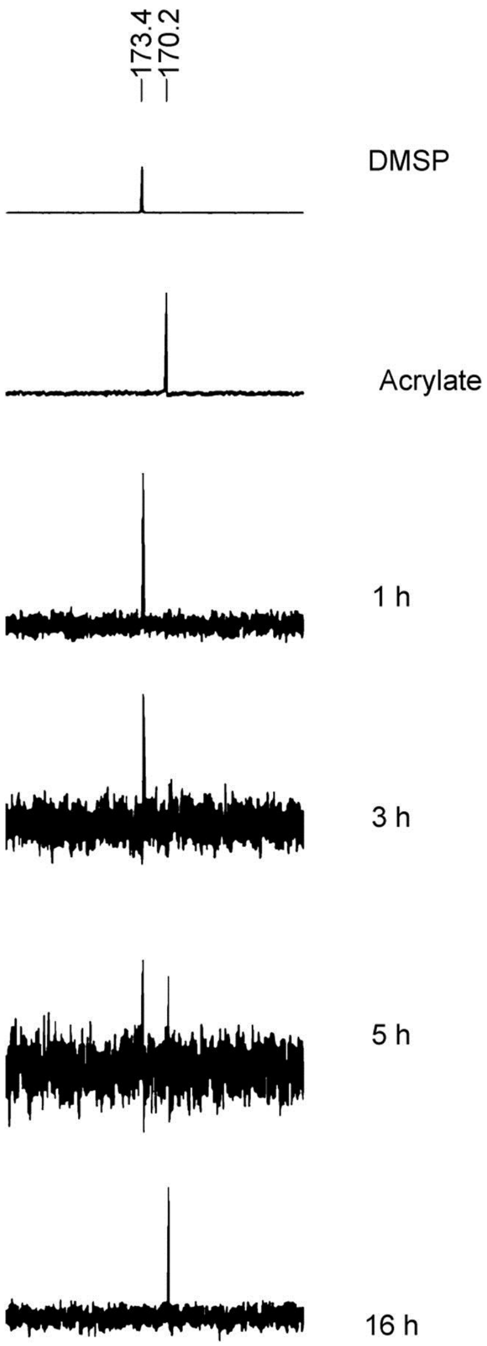
The relative activities (%) of samples of DddP were assayed by DMS production in solutions at different pH (a), and then in 50 mM MES buffer, pH 6.0 at different temperatures (b). Error bars calculated from duplicate experiments.

The highest DMS activity was observed at pH 6.0, which was then used for further studies, including the temperature-responsive activity of the DddP enzyme *in vitro* which showed that activity was lost at temperatures >60°C. All subsequent work was carried out at 30°C, to reflect the *in vivo* conditions (*R. nubinhibens* ISM is routinely cultured at 30°C).

2.2.3.2 Confirmation of DMSP lyase activity

To determine the *in vitro* activity of DddP, samples of purified protein (50 μl, 0.9 μM) amended with 5 mM labelled [1-^{13}C]DMSP were incubated for 16 hours. The ^{13}C catabolite was identified by nuclear magnetic resonance spectroscopy (NMR) and confirmed that the DMSP had been converted to a newly formed labelled compound, which exhibited an identical peak at the chemical shift of a reference sample of acrylate (Figure 2.4). This work was conducted as described in Todd *et al.* (2010).

Figure 2.4 NMR illustrating depletion of [1-^{13}C]DMSP and appearance of labelled acrylate when in the presence of purified DddP lyase



NMR spectra of the products of DddP-mediated cleavage of [1-^{13}C]DMSP. The ^{13}C NMR spectra for pure samples of DMSP and acrylate are shown as indicated, with peaks at chemical shifts of 173.4 and 170.2, respectively. The spectra below the reference compounds are from reaction mixes containing 5 mM [1-^{13}C]DMSP plus 0.9 µM DddP enzyme, sampled after 1, 3, 5 and 16 h incubation, as indicated.

To confirm that DMS was the concomitant product, gas chromatography (GC) was used. A sample of DddP (~10 μM) was incubated in a 1 ml screw cap vial in buffer containing 5 mM DMSP, at 30°C. Peaks corresponding to DMS were subsequently observed.

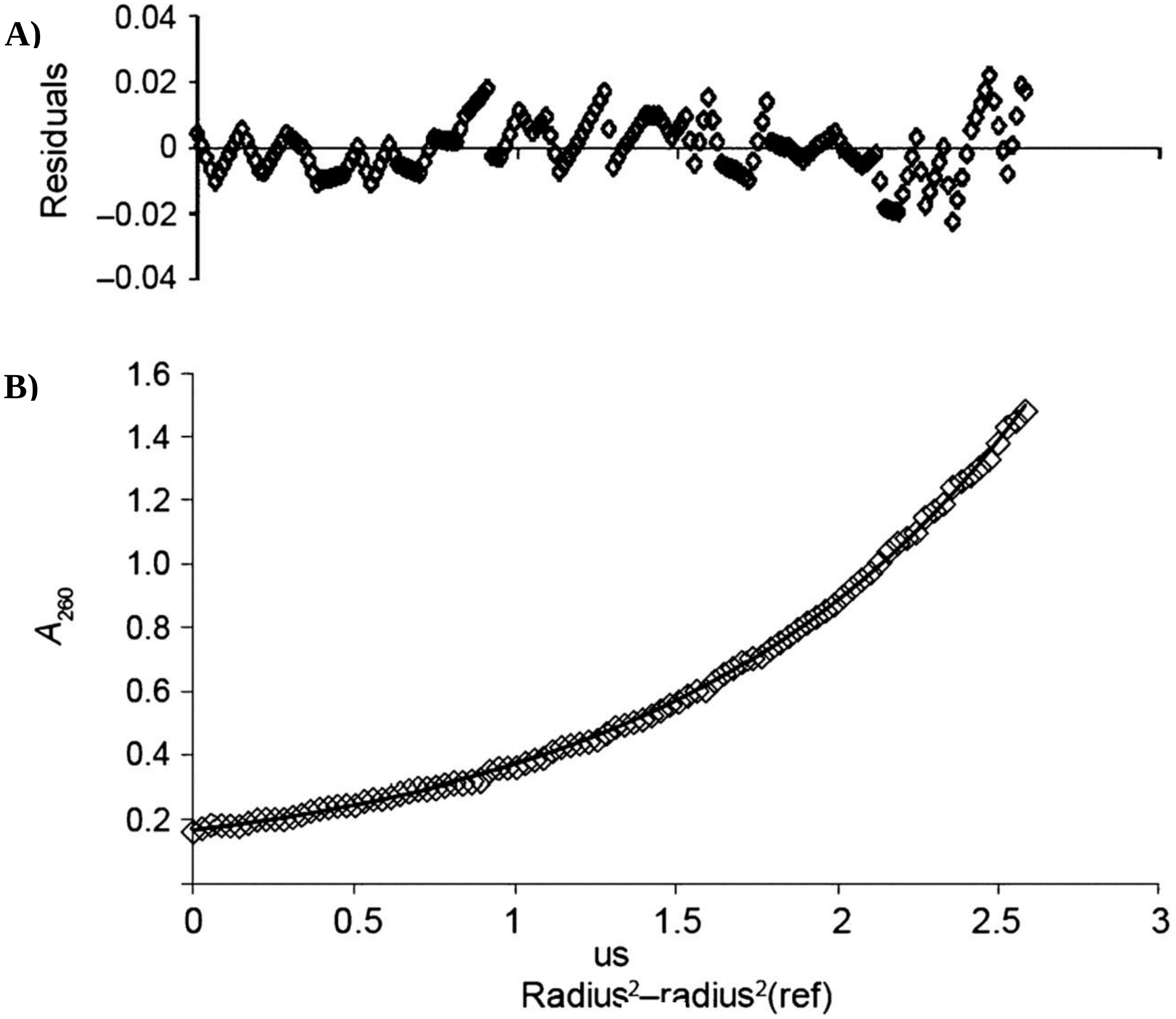
This confirms the function of DddP as a conventional lyase, which cleaves DMSP to DMS and acrylate. Approximate estimated rates of production were 0.07 and 0.185 nmol/μg/min for DMS and acrylate, respectively.

2.2.3.3 Association state of DddP

As expected from its deduced M_r (49, 972 Da), the purified DddP polypeptide was seen as a ~50 kDa band in denaturing gels. To ascertain the association state of functional DddP, this was determined using sedimentation equilibrium analytical ultracentrifugation. This technique works by centrifuging a sample of protein until the opposing forces of diffusion and sedimentation are equal, with different species (of different M_r) reaching equilibrium at different times (Cole *et al.*, 2008). This is recorded by a series of scans, and the data can then be applied to known models to ascertain structural composition of the protein. Thus, a sample of DddP (~5 μM) was spun at 12,000 rpm at 20°C in a Beckman Optima XL-1 analytical ultracentrifuge. Scans were taken every 4 hours to determine when equilibrium had been reached, at which point 5 more scans were recorded. The data were analysed (Ultrascan; Demeler, 2005) and fitted well to a one-component model, which predicted a M_r of 95, 300 ± 8000 Da, suggesting that DddP is a homodimer in solution (Figure 2.5).

The addition of 0.45 M NaCl had no obvious effect on the association state of the homodimer, implying that the interaction between the two polypeptides is relatively stable.

Figure 2.5 Sedimentation equilibrium ultracentrifugation of purified DddP



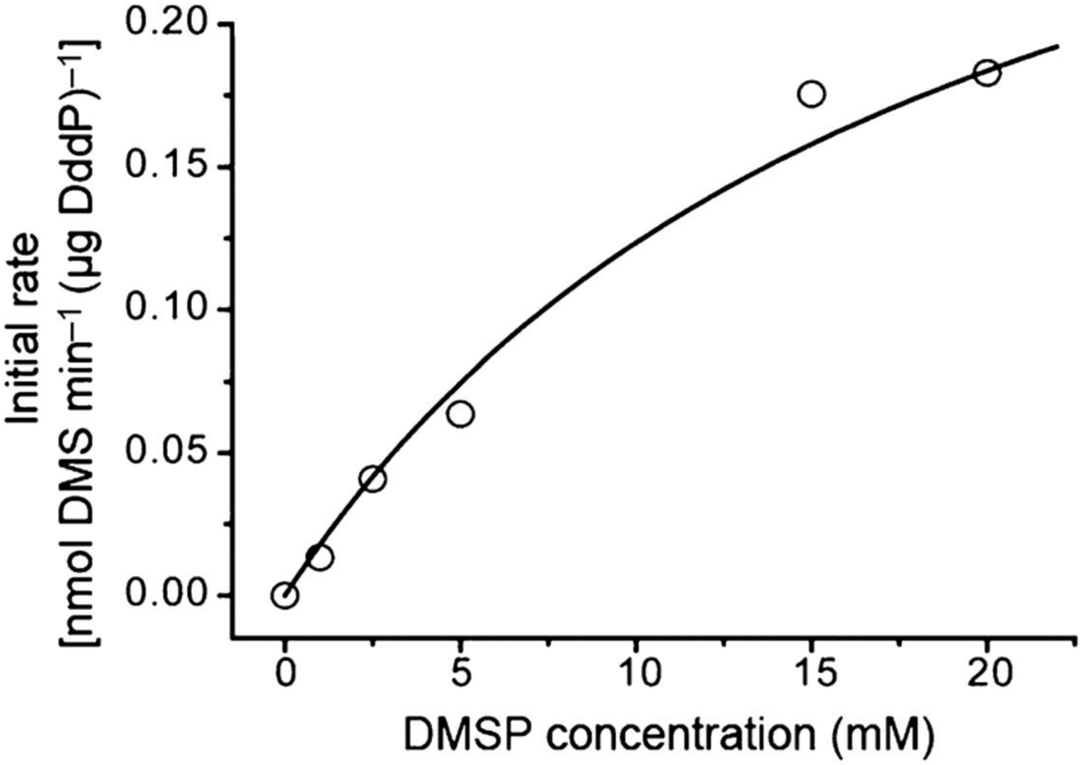
Absorbance at 260 nm against radius^2-radius^2(ref) following equilibration of purified DddP (~5 µM) at 20°C and 12,000 rpm. A) Residual difference between experimental data and fitted curve. B) A mean molecular weight of 95,300 ± 8000 Da was recorded when data were fitted to a single species (solid line).

The structure of another MEROPS M24B family member, namely creatinase from *Actinobacillus* (Padmanabhan *et al.*, 2002), has been solved and also shows a dimeric enzyme. However, most M24 family members, such as methionine aminopeptidases (M24A – EC: 3.4.11.18) are monomeric.

2.2.3.4 DddP enzyme kinetics

To determine the K_m and V_{max} values of the DddP enzyme preparation, the initial rates of DMS production were measured at intervals using ~0.3 µM DddP incubated at 30°C in MES buffer (pH 6.0), between 1 mM and 20 mM DMSP. The data fitted reasonably well to the Michaelis-Menten equation (Figure 2.6) and a K_m of DddP for DMSP of 13.8 ± 5.5 mM and a V_{max} of 0.31 ±0.06 nmol DMS min^{-1} (µg $DddP)^{-1}$ was extrapolated.

Figure 2.6 Determination of DddP K_m for DMSP



Initial rate (nmol DMS min^{-1} (µg $DddP)^{-1}$) plotted against DMSP concentration. DddP (0.3 µM) was in 50 mM MES, pH 6.0. Solid line represents a fit to the Michaelis-Menten equation.

A value of K_m value of DddP of ~14 mM seemed rather high, but the K_m of another M24B family member, creatinase is also high, at 13.3 mM for the wild type enzyme in *Pseudomonas putida* (Schumann *et al.,* 1993). Furthermore, the DmdA demethylase enzymes of *Ruegeria pomeroyi* and of *Candidatus* Pelagibacter ubique exhibit high K_m values, at 5.4 mM and 13.2 mM, respectively (Reisch *et al.,* 2008). To recall, DMSP concentrations in the open oceans can be as little as ~1-2 nM (van Duyl *et al.,* 1998), whereas significant accumulation of

DMSP occurs intracellularly in these organisms; as high as 70 mM (Reisch *et al.,* 2008). The use of DMSP as an osmoprotectant is therefore likely metabolically linked to its catabolism by the DMSP lyases such as DddP.

2.2.3.5 Metal-binding studies

Several, but not all, polypeptides in this M24B family have been shown to bind metal (usually Co or Mn) cofactors (Graham *et al.,* 2005), so I set out to determine if DddP was also metal-binding. To do this, the assays used material that contained metal-chelating compounds. Both 2,2'-bipyridyl (2.5 mM) and ethylene-diaminetetra-acetic acid (EDTA- 25 mM) were added separately to DddP samples and incubated for 15 minutes at room temperature, before adding 5 mM DMSP and carrying out GC DMS assays, as before. No discernible inhibitory effect on DMS production was noted in the presence of either compound. Note that creatinase (another M24B family enzyme, see above) from *Paracoccus,* also retains its activity in the presence of EDTA (Wang *et al.,* 2006). These findings imply that DddP does not require metal cofactors for its activity, although it cannot be wholly discounted that the metal of interest was not sequestered from the enzyme. However, EDTA is an efficient compound in sequestering transition metal ions (such as Co and Mn) from metallopeptidases, and so would be expected to have done so in this experiment (Auld, 1995).

In an attempt to identify putative cofactors (and, in particular, metal ions) more directly, inductively coupled plasma- optical emission spectroscopy (ICP-OES) was used to try to detect metal ions in a sample of DddP. Samples of active 10 µM DddP in 2.5% (v/v) nitric acid, were analysed on a Varian Vista pro CCD simultaneous ICP-OES. None of the following metals, Co, Cu, Mn, Ni and Zn was detected above background levels, consistent with the observations when EDTA was added.

2.2.3.6 DddP active site residues

The M24 family enzymes (including members of both sub-families such as methionine aminopeptidase [M24A], and creatinase [M24B]), contain a “pita bread” fold that harbours their active sites (Bazan *et al.,* 1994). Five residues in particular have been predicted to form the active site and/or coordinate metal-binding in the M24 metallopeptidases, these being D97, D108,E204, E235 H171 (Schiffman *et al.*, 2006). Significantly, all these residues are conserved in DddP, towards its C-terminal end (Figure 2.7).To determine if these residues were important in DddP, site-directed mutagenesis was carried out. The pBIO1658 plasmid, created for the over expression studies (see above), had its cloned *R. nubinhibens* ISM *dddP* gene altered, by introducing 6 different residue substitutions in individual copies of the vector. The D295, D297, D307, H371, E406 and E421 (see Figure 2.7) residues were each individually substituted for an alanine, using a Quikchange XL site-directed mutagenesis kit. Mutagenised plasmids were transformed into *E. coli* BL21 and confirmed by sequencing. Each of these site-directed mutations completely abolished DMS production, as assayed by DMS production. Thus, DddP appears to require similar active site residues as other members of the M24B enzyme family. However, unlike other M24 enzymes, and like creatinase, these residues are important for catalytic activity in a non-metal-dependant manner.

Figure 2.7 Predicted active site residues, selected for site-directed mutagenesis in DddP of *Roseovarius nubinhibens* ISM

```
     290       300       310            370       380
     390
Nterm-
EIISFDTDLIGSYGICVDISRSW...FQAQKYGCLMHGVGLCDEWPLVAYPDQAVPGSYDY

  400        410       420    446
PLEPGMVLCVEAAVGAVGGNFTIKLEDQV-Cterm
```

A section of the DddP amino acid sequence is shown. Residues highlighted in black, which are predicted to function at the active sites of M24B peptidases (Bazan *et al.*, 1994; Schiffman *et al.*, 2006), were changed to alanine by SDM (Table 8.6).

These findings further expand our understanding, in a biochemical sense, of this relatively recent addition to the DMSP lyase family. However, I wished to also investigate the evolution of this enzyme, particularly in regards to its transferral between the kingdoms, such as the fungi, and the ecological relevance of such events.

2.2.4 The presence of a functional *dddP* gene in the opportunistic coral pathogen, *Aspergillus sydowii*

Earlier work by Yoch and colleagues (Bacic *et al.,* 1998; Bacic and Yoch, 1998) had shown that some Ascomycete fungi, notably those that were isolated from decaying remains of the DMSP-producing salt-marsh grass *Spartina*, could make DMS from DMSP. Several Ascomycetes, including *Aspergillus* and *Fusarium spp.* were then shown to contain functional *dddP* genes (Todd *et al.,* 2009).

The presence of these organisms in DMSP-rich environments prompted me to investigate fungi that are associated with another DMSP-rich niche, namely coral reefs. Corals include single-celled, symbiotic photosynthetic dinoflagellates, such as *Symbiodinium*, which have massive levels (as great as 0.5 M) of intracellular DMSP (Matrai *et al.*, 1994; Raina *et al.,* 2010).

2.2.4.1 DMS assays of isolates of *Aspergillus sydowii* confirms a Ddd$^+$ phenotype

I obtained 20 isolates of *Aspergillus sydowii* from Krystal Riepen (then at Cornell University), sourced from a variety of environments. This species is a putative fungal pathogen of the sea fan *Gorgonia ventalina* (Hernández *et al.*, 2008) and so would be a good candidate for a marine *Aspergillus* species that catabolises DMSP. To test this, mycelial plugs (taken from the growing edge of a mycelium incubated for 48 hours at 28°C on Potato Dextrose Agar) of each strain were placed in liquid Vogel's medium containing 5 mM DMSP, and incubated at 28°C overnight in screw cap vials. After 6 hours, DMS was quantified by GC (Table 2.1). All of the strains exhibited a Ddd$^+$ phenotype, at varying levels of activity. There was no clear correlation between site of isolation and level of DMS release.

Table 2.1 Dimethylsulfoniopropionate-dependent dimethyl sulfide production in strains of *Aspergillus sydowii*

Strain (1)	***Source (2)***	***DMS (3)***
SOMB	**Infected *Gorgonia ventalina***	**0.83±0.09**
SABA	**Infected *G. ventalina***	**2.01±0.48**
DumpD	**Infected *G. ventalina***	**0.41±0.03**
FK11	**Infected *G. ventalina***	**0.5±0.02**
15B1	**Infected *G. ventalina***	**2.89±0.31**
NRRL 242	**Environmental**	**2.17±0.16**
NRRL 663	**Environmental**	**4.59±0.20**
NRRL 251	**Environmental**	**0.54±0.06**
NRRL 247	**Environmental**	**1.67±0.03**
KIR 382A	**Environmental**	**2.31±0.28**
SRRC 2540	**Environmental**	**2.78±0.44**
NRRL 4790	**Environmental**	**0.65±0.28**
NRRL 245	**Environmental**	**0.31±0.02**
NRRL 249	**Environmental**	**0.26±0.11**
NRRL 1732	**Environmental**	**4.31±0.04**
NRRL 5913	**Environmental**	**3.22±0.53**
NRRL 244	**Environmental**	**0.70±0.02**
NRRL 253	**Infectious—human**	**0.11± 0.02**
297072	**Infectious—human**	**1.20±0.04**
SRRC 1112	**Unknown**	**1.10±0.03**

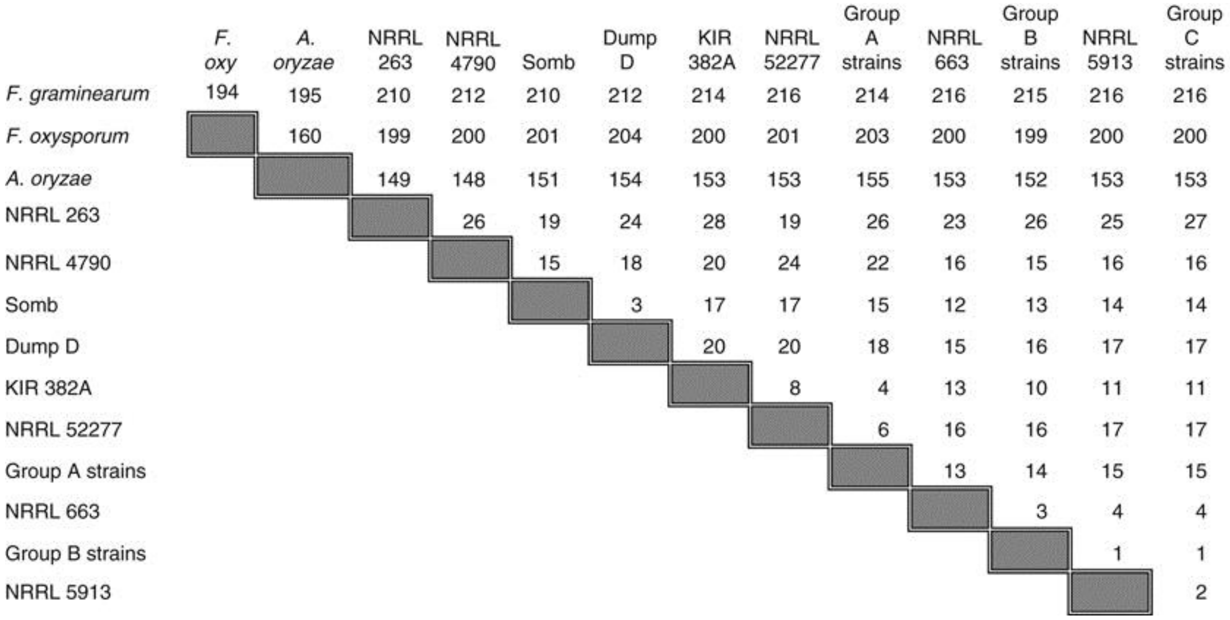
Column (1) lists the *A. sydowii* strains used in Rypien *et al.* (2008). Column (2) shows their sources, where known. Column (3) shows levels of DMSP-dependent DMS production, in nmol DMS $h^{-1}mg^{-1}$ *A. sydowii* mycelial dry weight, with standard errors from two samples. Adapted from Kirkwood *et al.* (2011a).

2.2.4.2 PCR amplification of conserved *dddP* from *A. sydowii*

To examine if these *A. sydowii* contained a *dddP* gene, the SydDddPF and SydDddPR primers (both of which had some redundancy) were designed, based on sequence conservation of the *dddP* genes of *A. oryzae, F. culmorum* and *F. graminearum.* These primers targeted an internal fragment of *dddP,* 238 bp downstream 3’ of the ATG start codon and 114 bp upstream of the stop codon.

In all 18 cases, PCR amplification of the genomic DNAs of using *PfuUltra* DNA polymerase (Stratagene) generated fragments of the expected size, *ca.* 1.2 kb. DNA sequencing of these PCR products showed them to be very similar to each other (>97 % identity at the DNA level), ~85% identical to the *dddP* gene of the Ddd$^+$ *A. oryza*e and ~80% identical to the *dddP* genes of the *Fusarium spp.* (Table 2.2; Todd *et al.,* 2009). Thus, *dddP* was likely present in the last common ancestor of *A. sydowii*. Variations in the level of homology between the *A. sydowii dddP*s did not seem to correlate with the source of each isolate (environmental, human, sea fan), supporting the suggestion (Rypien *et al.*, 2008) that the *A. sydowii* populations are panmictic.

Table 2.2 Conservation of *dddP* regions present in the Ddd$^+$ fungi



	F. oxy	*A. oryzae*	NRRL 263	NRRL 4790	Somb	Dump D	KIR 382A	NRRL 52277	Group A strains	NRRL 663	Group B strains	NRRL 5913	Group C strains
F. graminearum	194	195	210	212	210	212	214	216	214	216	215	216	216
F. oxysporum	▨	160	199	200	201	204	200	201	203	200	199	200	200
A. oryzae		▨	149	148	151	154	153	153	155	153	152	153	153
NRRL 263			▨	26	19	24	28	19	26	23	26	25	27
NRRL 4790				▨	15	18	20	24	22	16	15	16	16
Somb					▨	3	17	17	15	12	13	14	14
Dump D						▨	20	20	18	15	16	17	17
KIR 382A							▨	8	4	13	10	11	11
NRRL 52277								▨	6	16	16	17	17
Group A strains									▨	13	14	15	15
NRRL 663										▨	3	4	4
Group B strains											▨	1	1
NRRL 5913												▨	2

Numbers of nucleotide differences (out of 998, ~88% of a conserved region of *dddP*) in *A. sydowii dddP* and corresponding regions of *dddP* in *A. oryzae, Fusarium graminearum* and *F. culmorum* (Todd *et al.*, 2009) are shown, following comparisons with Megalign. Group A, group B and group C strains each have identical sets of sequences: group A; NRRL 245, NRRL 249; group B; 297072, SRRC 2540, FK11, 15B1, NRRL 251, NRRL 1732; group C; NRRL 242, NRRL 247. The analyses were carried out on 998 bps of unambiguous sequences, which are deposited at GenBank as follows: strain and accession number, respectively; 297072, GQ421799; DumpD, GQ421800; FK11, GQ421801; 15B1, GQ421802; KIR 382A, GQ421803; NRRL242, GQ421804; NRRL245, GQ421805; NRRL247, GQ421806; NRRL249, GQ421807; NRRL251, GQ421808; NRRL263, GQ421809; NRRL663, GQ421810; NRRL1732, GQ421811; NRRL4790, GQ421812; NRRL5913, GQ421813; NRRL52277, GQ421814; SRRC2540, GQ421815; Somb, GQ421816.

2.3 Conclusions

2.3.1 DddP is an atypical M24B metallopeptidase

The ability of DddP to cleave a non-peptide bond (C-S) is unusual, but not unique, among the M24B family of peptidases. For example, creatinase of *Pseudomonas putida* generates sarcosine plus urea from water plus creatine, by cleaving a non-peptide C-N bond (Bazan *et al.*, 1994). Indeed, this implicates DddP as the least typical of the peptidases encountered in this group. Many well-characterized M24 enzymes, such as the cobalt-dependent methionine aminopeptidase from *E. coli* have metal cofactors. Yet DddP does not, and so in this regard too it resembles the creatinase of *Paracoccus*, which also lacks a metal-containing active site (Wang *et al.*, 2006). It may be significant that creatinase and DddP, the two known non-metal-dependent M24B enzymes, have structurally related substrates that carry a positive charge at or close to the catalytically cleaved bond. The work described here further extends the types of enzymatic activities that can be accomplished by M24B family members and, importantly, establishes that at least one of them can cleave a C–S bond.

The novel structural features of this enzyme compared to other known lyases, such as the cupin-containing DddL, emphasised the diversity of DMSP-cleaving enzymes, and further encouraged new searches for yet more DMSP lyases that had not yet been discovered (see chapter 4).

2.3.2 Evolution of fungal *dddP*

Given the distribution and conservation between the fungal species studied, it can be concluded that *A. sydowii* likely acquired *dddP* through a HGT event, as had been proposed for the other *Aspergillus* spp., and that the distribution of the gene matches the panmictic nature of the *A. sydowii* population (Todd *et al.*, 2009; Rypien *et al.*, 2008). It is debatable if *A. sydowii* and other DddP-containing fungi are mutualistic / commensal symbionts, or opportunistic pathogens (Smith *et al.*, 1996; Geiser *et al.*, 1998; Alker *et al.*, 2001; Hernández *et al.*, 2008). Both marine and terrestrial species of fungi might benefit by using the DMSP synthesised by corals or angiosperms, respectively, and it may have been a co-habitation by these organisms that resulted in the transfer of DddP between species.

Chapter 3

Optimisation of *Ruegeria pomeroyi* DSS-3 growth and microarray parameters

3.1 Introduction

One major goal of this study was to discover novel genes in the Roseobacter clade bacterium, *Ruegeria pomeroyi* DSS-3, that respond to a number of inducers, specifically DMSP and the products of its cleavage, acrylate and DMS. Microarrays provide powerful tools to achieve this goal, but a degree of preliminary work was required to try to optimise the procedure. These included the development of suitable growth conditions for *R. pomeroyi* DSS-3, and methods for the isolation of consistent and satisfactory levels of high quality cellular material and RNA.

For this to be done, it was first necessary to establish media and growth conditions that would

(a) maximise any differences in the expression of those genes whose transcription was affected by growth of the cells in one of the potential co-inducers
(b) not be distorted by any severe inhibitory effects of these molecules

3.1.1 Existing transcriptomics studies involving DMSP

In previous work in the UEA lab's studies on the effects of DMSP- and/or acrylate-mediated induction of known genes involved in the catabolism of these substrates, concentrations of 5 mM and 2.5 mM respectively had been used, in media in which a "conventional" carbon (C) source, usually succinate, was also present. These concentrations may initially seem high. However, acrylate at concentrations of 1.3-6.5 mM has been recorded in the mucus of algal *Phaeocystis* colonies (Noordkamp *et al.*, 2000). It was therefore felt that this would be more informative than the very low levels of DMSP (80 μM) used by Bürgmann *et al.* (2007) in their transcriptomic study of the same strain. From our lab's experience it was deduced that such a low concentration would be rapidly consumed in batch cultures prior to the harvesting of the mRNA. Given the very short half-life of mRNA in bacteria, this would likely account for the low-to-absent levels of induction that were seen by Bürgmann *et al.*, even with *ddd* and *dmd* genes that are known to be induced many-fold by one or other of these substrates (see below). Additionally, only the effects of DMSP on gene expression were examined, and not of the two other co-inducers used in this study. As will be shown in chapter 5, the toxic effect of acrylate on growth of wild type *R. pomeroyi* cultures is minimal until well above several mM concentrations, although the myriad of indirect effects of adding a toxic compound may be noted in aspects of the gene expression.

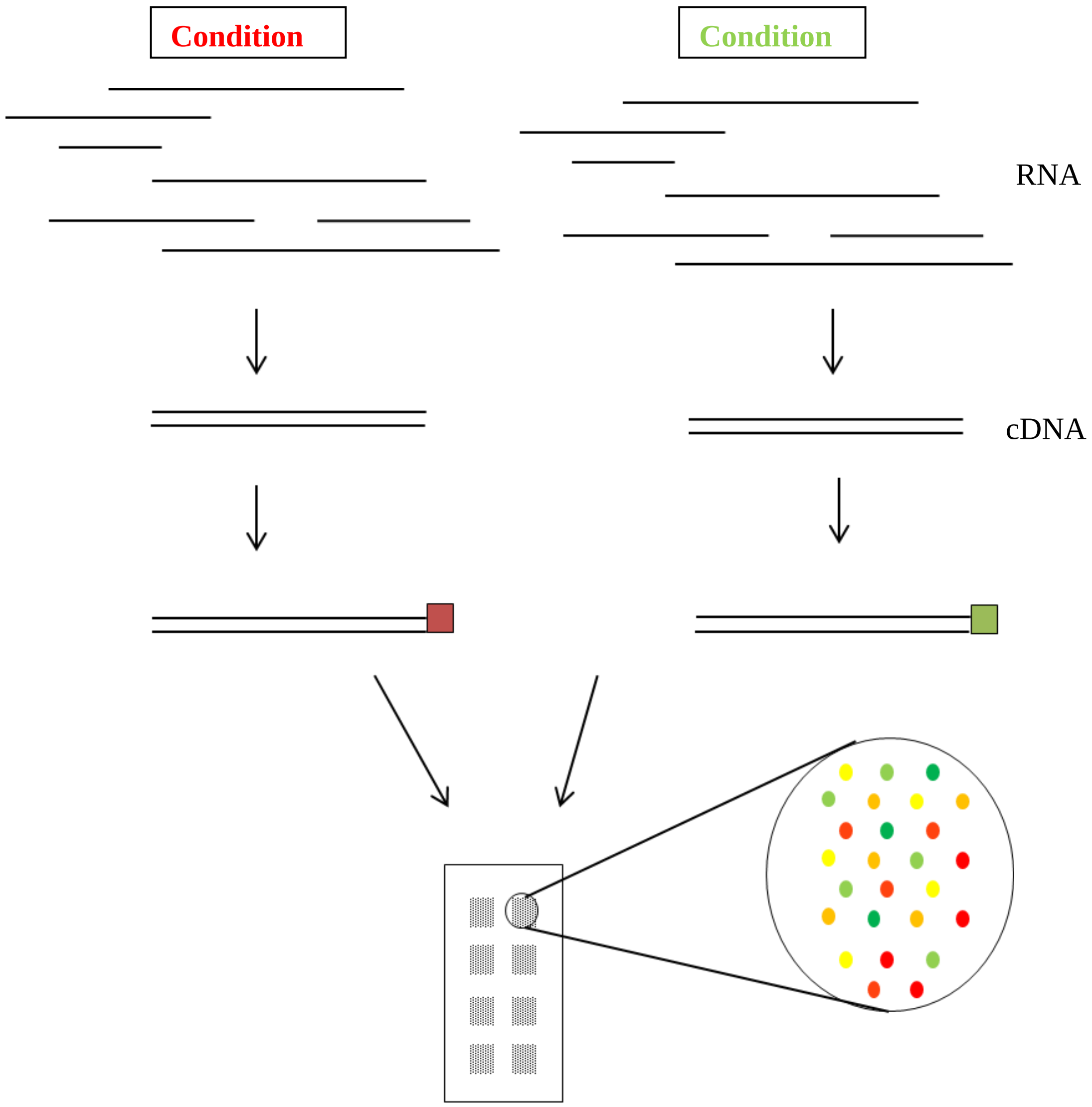
3.1.2 An introduction to microarrays

DNA microarrays provide a remarkably powerful method of quantifying the expression of a large number of genes (>10,000), sometimes the entire genome, of an organism in response to an external stimulus and/or genetic background.

The mRNA molecules obtained from the organism grown under two (or more) different conditions are reverse transcribed to cDNA, then labelled, *en masse,* with different markers – usually coloured dyes (see below). This is known as a Type I microarray experiment, and the alternative (Type II) involves the hybridisation of one of the dyes to a reference sample, such as genomic DNA, in all of the arrays (DeRisi *et al.,* 1997).

To quantify these labelled RNAs, a microarray first requires the attachment of thousands of pre-designed DNA oligonucleotide “probes” to a glass slide. The probes comprise short sequences (~60bp), or oligomers, of DNA that contain sections of the target genes. Thus, upon addition of the solution consisting of reverse-transcribed cDNA from the RNA of cells exposed to an experimental condition, these probes become bound. This level of binding infers the level of mRNA that was originally present in the sample for a given probe. The samples, hybridized to fluorophores, give a measure of the signal intensity, or initial RNA concentration, by fluorescence emission, which is detected using a scanner, such as a GeneScan (summarised in Figure 3.1).

Figure 3.1 Summary of microarray procedure



Simplified microarray procedure. RNA is isolated from cells grown in two experimental conditions. RNA is reverse-transcribed to cDNA, which is labelled using a coloured fluorophore, such as Cy3 or Cy5. Labelled cDNA is applied to DNA microchip and hybridised. Microchip is scanned, recording the ratio between the two intensities of fluorescence emissions. Red or green spots represent the abundance of one fluorophore, indicating a greater level of cDNA from one sample compared to the other. This illustrates the initial levels of RNA in the sample, and by association, the cells. Spots that appear yellow exhibit roughly equal levels of both fluorophores.

There are two general variants of the microarray procedure. A microarray study may use one, or two fluorophores to label cDNA, and these are named either single-, or dual-channel microarrays, respectively. Thus, a single channel array will provide a measurement of the relative abundance of genes in a given sample, compared to all of the other genes. In a dual-channel array, each fluorophore has a different fluorescence emission spectrum and is hybridised to a different sample, both of which are applied to the slide simultaneously (Shalon *et al.,* 1996). For example, dyes Cy3 and Cy5 have emission wavelengths of 570nm (appears green) and 670 nm (appears red), respectively. A dual-channel array uses the ratio of the intensity of each dye to assess the relative up- or down-regulation of each gene (Tang *et al.,* 2007).

Microarrays are a useful tool for analysing gene expression at a pan-genomic level, and therefore I wished to first optimise growth of *R. pomeroyi* cultures and isolation of good quality RNA for just such an experiment.

3.2 Results

3.2.1 Growth characteristics of *Ruegeria pomeroyi* DSS-3

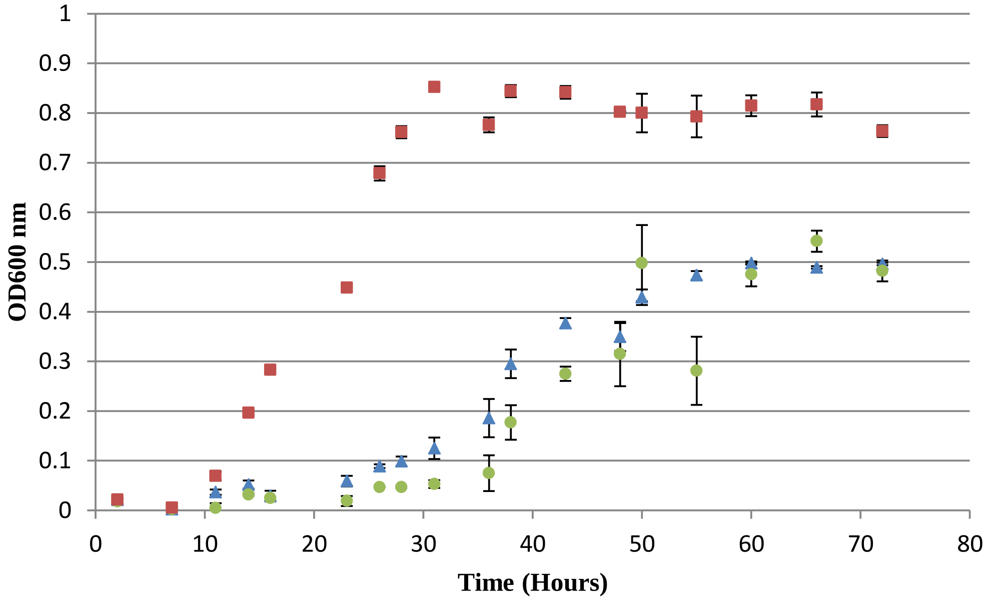
R. pomeroyi DSS-3 was originally isolated from seawater samples that had been plated onto seawater medium enriched with 10 μM DMSP, although this was not the sole C source (González *et al.,* 1999; 2003). This strain was shown to grow well on complete, ½ strength YTSS (which contains tryptone, in reconstituted seawater) with colonies forming within 2 days at 28°C (González *et al.,* 1996). It also grows readily in a marine basal medium (MBM; Baumann and Baumann, 1981); a defined, minimal growth medium that is amended with a sea salts mix plus vitamins. There is no specific requirement for the vitamins, but enhanced growth has been observed with their addition; biotin, folic acid, pyridoxine, riboflavin, thiamine nicotinic acid, pantothenic acid, cyanocobalamin and *p*-aminobenzoic acid (all of which are B-vitamins) have all been shown to improve growth, (González *et al.,* 1997).

To measure the growth of *R. pomeroyi* DSS-3 on the substrates DMSP and acrylate as sole C sources, batch culture experiments were carried out to produce growth curves. Cells were grown overnight in ½ YTSS media, then diluted 1:100 into minimal MBM medium amended with 10 mM succinate, or with 5 mM DMSP or with 2.5 mM acrylate as sole C sources. Growth of the cells was determined by spectrophotometric measurement of their optical densities at 600 nm (OD_{600}).

As shown in Figure 3.2, all three compounds acted as sole C sources, though, clearly, succinate was most effective, with a shorter lag phase (*ca*. 10 hours compared to *ca.* 20 h for acrylate and DMSP) and a higher final cell density after 60 hours incubation (OD_{600} of 0.8 for succinate and 0.5 for acrylate or DMSP). All three conditions would supply reasonable amounts of biomass for subsequent studies.

Strikingly, these observations are in contrast to those of González *et al.* (1999), who reported that this strain did not grow on acrylate and only grew on DMSP following iterative inoculations onto a medium containing these compounds. The reasons for this disparity are unclear, but perhaps stem from their higher concentration of acrylate (5 mM compared to 2.5 mM). Unfortunately, we were unable to acquire the strain of *R. pomeroyi* as isolated by González *et al.*, so the possibility that an inadvertent genetic change had occurred in the different versions of this strain cannot be discounted. Oddly, this finding was redacted in 2003 (again by González *et al.*) when it was shown that DSS-3 was indeed found to grow on acrylic acid as a sole C source following iterative inoculations in MBM medium.

Figure 3.2 Growth of *Ruegeria pomeroyi* DSS-3 in MBM minimal medium with 10 mM succinate, 5 mM DMSP or 2.5 mM acrylate as sole C sources



Batch cultures of *Ruegeria pomeroyi* strain DSS-3 were incubated at 28°C in MBM minimal media supplemented with vitamin solution and 10mM succinate (red squares), or 5mM DMSP (blue triangles), or 2.5mM acrylate (green circles) as sole C sources.

3.2.2 RNA techniques

3.2.2.1 Optimisation of *Ruegeria pomeroyi* DSS-3 growth for RNA extraction and microarray analysis

It was decided that the RNA to be used in the microarrays should be harvested from cells in their early exponential stage since, *a priori*, it was felt that any differences in the expression of genes involved in the uptake and catabolism of the different carbon sources would be greater than in cells that were approaching stationary phase, which was the case in the microarray survey by Bürgmann *et al.*, 2007.

Concerning the timescale of the induction period, it was considered to be important to choose a time that provided sufficient opportunity for the relevant genes to be induced at maximal levels or for the mRNA to decay, for those genes that were repressed by (say) acrylate or DMSP. Cells were grown using succinate as a C source; this had been shown to facilitate good growth and acceptable levels of biomass production for further experiments.

3.2.2.2 RNA extraction

Cultures of *R. pomeroyi* DSS-3 were incubated at 30°C in MBM minimal media supplemented with 10 mM succinate to an OD_{600} of ~0.4 (*ca*. 16 hours growth). The cultures were then incubated for a further 2 hours in the presence of either 5 mM DMSP, 2.5 mM acrylate, 5 mM DMS or no additional inducer. Following this, a tenth volume of phenol:ethanol (5:95) “stop solution” was added, which inhibits ribonuclease activity, and RNA was extracted. There was some difficulty in achieving adequate levels of RNA, requiring several iterations and the development of a modified SV Total RNA kit (Promega) protocol, using many of the original reagents. A detailed description is given in the Materials and Methods section, but an overview is presented here, as follows.

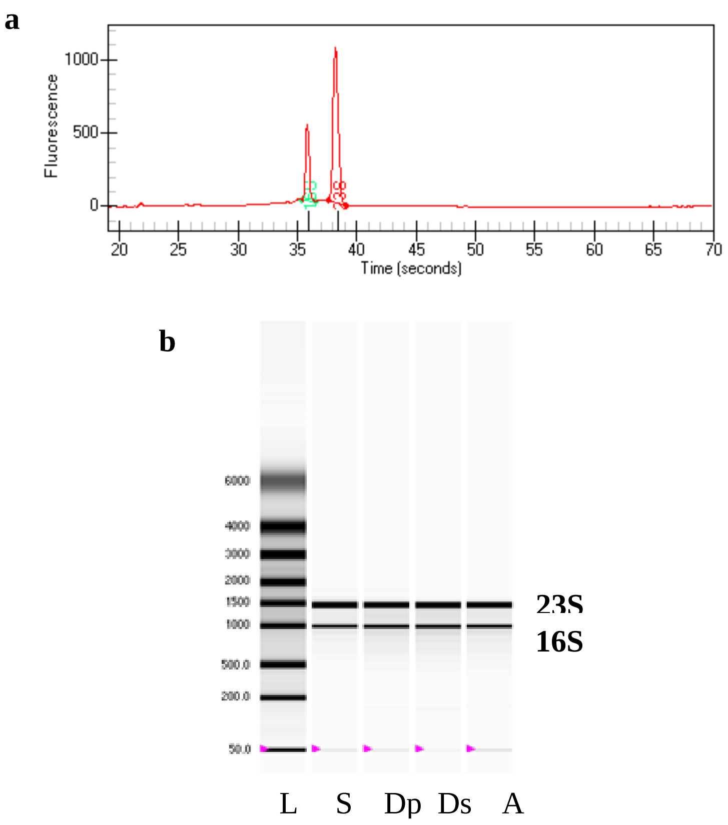
Essentially, the modified protocol involved increased lysis and additional homogenisation steps; preliminary attempts at RNA isolation without these steps were inconsistent and resulted in low final RNA levels (<100 $\mu g\ ml^{-1}$) . We first attempted to increase yield by using increased lysozyme, diluted in TE (Tris:EDTA) buffer, in order to more effectively break down the cells following pellet retrieval (100 mg/ml compared to 50 mg/ml). This improved yield but was still not sufficient for further experiments. Both freeze:thaw (using liquid nitrogen) and homogenisation (using glass beads and a ribolyser) steps were tested to improve cellular disruption and RNA retrieval. At first, each was used individually, but it was subsequently discovered that using both steps following lysozyme treatment improved RNA yield and quality significantly. Thus, 3 additional techniques were used to isolate RNA from *R. pomeroyi* at an acceptable quality and quantity. This yielded a final RNA concentration of *ca*. 0.8 - 1.5 μg ml^{-1} sample, which could be used for further procedures (microarray analysis - materials and methods).

3.2.2.3 Assessment of RNA quality

To measure the suitability of the RNA for further analyses, the quality and stability of the 16S rRNA in a 1 μl sample, was determined. An Experion automated electrophoresis platform was used, the output being in the form of a “virtual” agarose gel. Samples underwent electrophoresis within a microfluidic chip, using a gel-stain solution. Micro-channels in the chip separated the RNA fragments based on their size and charge and these were detected via a bound fluorescent dye and photodiode (Experion Automated Electrophoresis System – user manual, BioRad). The data were converted into an electropherogram (plotting fluorescence vs. time) and then as a “virtual” agarose gel, shown in Figure 3.3a, and 3.3b, respectively.

The protocol used here yielded high quality RNA, as judged by the amounts and integrity of the rRNA molecules. A microarray analysis could then be undertaken.

Figure 3.3 “Virtual” agarose gel of *Ruegeria pomeroyi* DSS-3 RNA samples



Samples of *Ruegeria pomeroyi* DSS-3 RNA were analysed using an Experion automated electrophoresis platform (BioRad), with 1 µl of RNA applied to each well.

Data were initially converted into an electropherogram, plotting fluorescence vs. time (2a), where the peaks are identified (e.g. 16S or 23S rRNA) and integrated, to calculate a concentration of RNA. Clearly defined peaks illustrate a low level of rRNA degradation.

Data can also be shown in the form of a “virtual” agarose gel (2b). L, RNA ladder, sizes shown in base pairs; S, succinate; Dp, DMSP; Ds, DMS; A, acrylate. Distinct bands corresponding to the 16S and 23S rRNA molecules are shown. The absence of smearing between the bands indicates lack of RNA degradation. Pink triangles indicate the position of the lowest ladder marker.

3.2.3 Microarray analysis

3.2.3.1 Slide design and labelling

The DNA microchip used in this study was initially designed by me *in silico* using the online tool, eArray (Agilent), by assigning short oligomeric sequences to a pre-determined grid, providing a complete, three-fold coverage of the entire *Ruegeria pomeroyi* DSS-3 genome, both the chromosome and megaplasmid (see materials and methods).

The samples of *R. pomeroyi* mRNA populations isolated above were fluorescently labelled, using a DIG-Easy Hyb kit (Roche). The RNAs from the unamended (succinate only) culture were labelled with Cy3 (red emission) and with Cy5 (green emission) for those samples from cultures containing acrylate, or DMSP or DMS. As noted in the materials and methods, a control array was conducted in which probes were hybridised to genomic DNA, in order to confirm the correct hybridisation to all of the spots on the array slide. A Type I experiment was chosen because I wished to more directly observe the changes in the RNA profile between the different growth conditions.

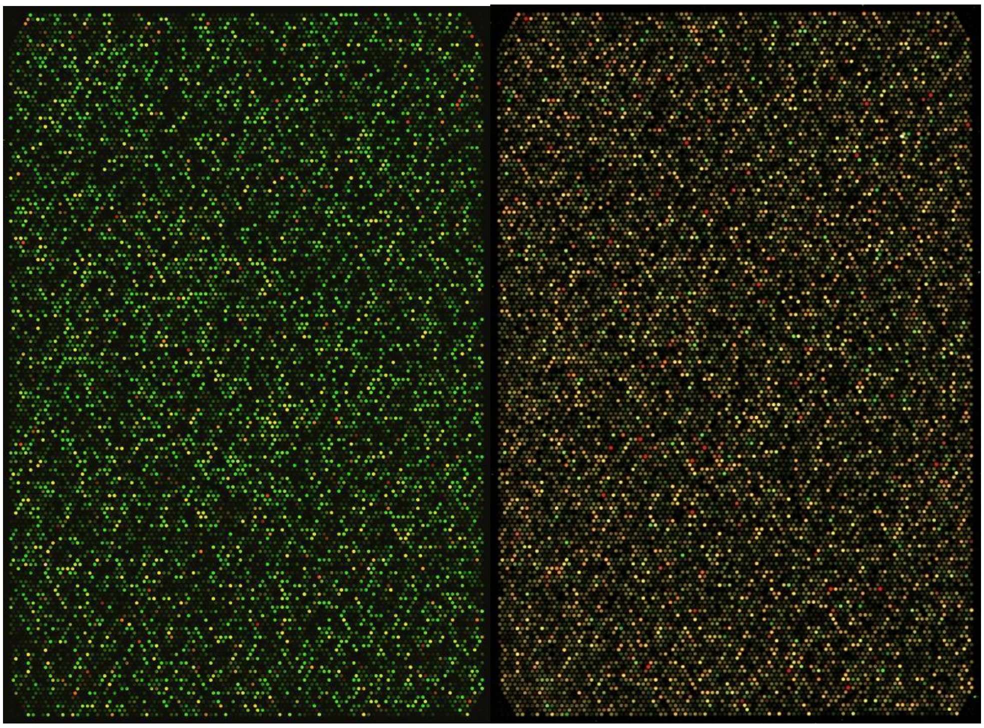
Dual-channel arrays are more useful in a study such as this, which requires the direct comparison of growth in certain conditions as a marker of gene regulation. A single channel study would require double the number of experiments to ascertain the same expression pattern, and would require additional normalisation, usually with the simultaneous assessment of pre-determined “housekeeping” genes (Stoyanova *et al.*, 2004).

3.2.3.2 Slide scanning

Once the microarray slide was hybridised and ready to scan, a number of efforts were made to improve the accuracy of any data retrieved. Firstly, samples were applied in biological duplicate, and each of the two arrays contained three distinct probes for each gene in the genome or megaplasmid, thus accounting for probe bias or incorrect binding. To reduce variation between the samples, the saturation levels and detector gain of the scanner for each fluorophore were manually calibrated using the software, GenePix (Agilent), following a preliminary scan of the slide. This process records the fluorescence of each dye, highlighting any bias and if the detector is allowing too much, or too little, light in, with the former causing saturation, represented by a white pixel on a scan image. Considering the method by which the program calculates fluorescence, by recording the intensity and wavelength of each individual pixel inside a given spot, or "feature", then white pixels would skew any subsequent results. The GenePix bioinformatics package uses a pre-made template file, which assigns a gene number to each of the features and allows identification of each spot following scanning. For this to be accurate, it is useful to carry out a manual examination of the template overlay and confirm that features are indeed bounded correctly.

Once a satisfactory alignment of template and slide was achieved, GenePix recorded the raw pixel values and fluorescence ratios for each spot on the array, and thus the expression of each gene in the *Ruegeria pomeroyi* DSS-3, in triplicate (shown in Figure 3.4). The raw data were normalised by the LOWESS (LOcally WEighted Scatterplot Smoothing algorithm) method and Marray, to calibrate inter- and intra-array variation such as dye intensity bias (Cleveland, 1979; Yang *et al.*, 2001; Dudoit and Yang, 2002; B Pearson, personal communication). LOWESS normalisation assumes that dye bias is dependent on spot intensity, and fits a smoothing curve to the dataset.

Figure 3.4 Microarray output of RNA isolated from *Ruegeria pomeroyi* DSS-3 grown in +acrylate conditions

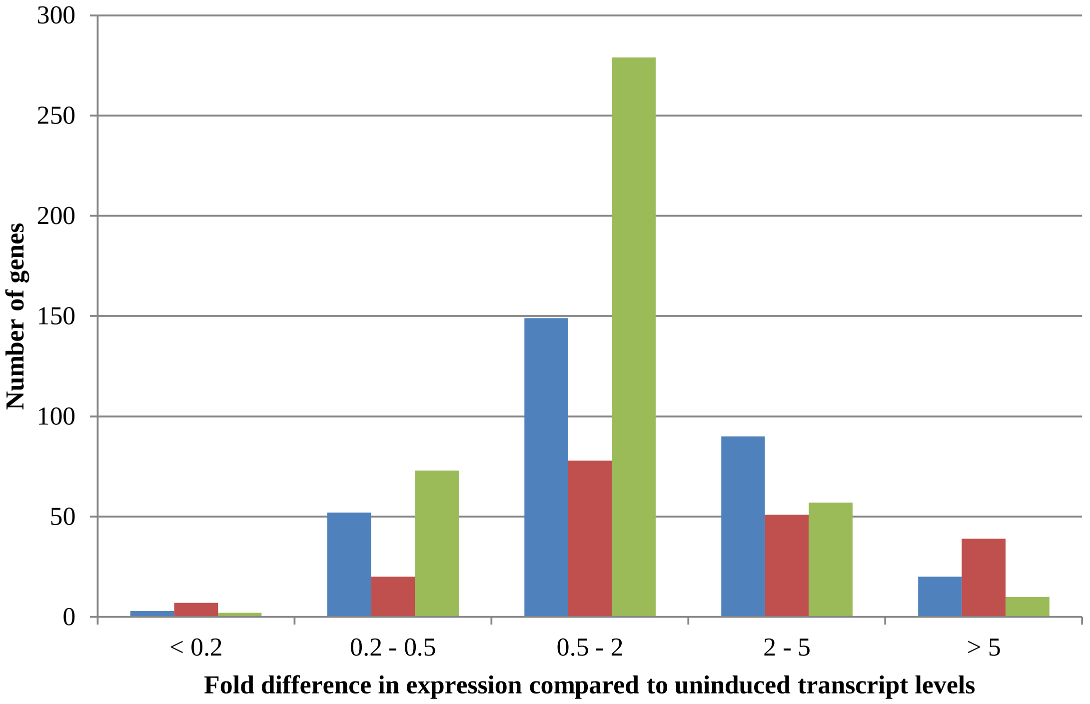


Raw data showing the output from a GeneScan scan of a microarray slide hybridised with RNA isolated from a culture of *Ruegeria pomeroyi* DSS-3 exposed to 2.5 mM acrylate. Each panel represents a separate microarray and thus, individual biological replicates. Each panel represents a three-fold coverage of the *R. pomeroyi* genome. Green spots indicate proportionally more RNA labelled from succinate conditions (Cy5), red spots indicate proportionally more RNA labelled from acrylate conditions (Cy3), and yellow spots indicate approximately equal levels of RNA from each sample. Blank spots indicate either a failed hybridisation, or more likely a control spot allocated by the template file, to allow for scanner calibration. This figure highlights the inter- and intra- array variation that may occur between samples, necessitating the need for post-array normalisation.

3.2.3.3 Summary of gene regulation in DMSP, DMS or acrylate growth conditions

In total, 31 genes were marked as having “no data” in any of the arrays following ratio calculation and normalisation, and 350 had at least one set of results absent. This data loss is most likely due to mis-binding of a number of the probes, or dyes, so that dye intensity for one spot was missing, causing the normalisation program to ignore the entire result (Yang *et al.*, 2001). The data retrieved were grouped according to the mean -fold change in expression (based on the ratio of the intensity of one dye over the other), either positively or negatively. An overview of this data is provided in Figure 3.5, or in its complete form in appendix A3. As expected, few genes were significantly (with both array results exhibiting P values of <0.05) up- or down-regulated in the presence of the compounds used.

Figure 3.5 Summary of -fold differences in gene expression in *Ruegeria pomeroyi* DSS-3 exposed to DMSP, DMS or acrylate



Numbers of genes that are up- or down-regulated relative to the control (succinate-alone) cells. Blue bars, DMSP; red bars, acrylate; green bars, DMS. Data shown includes only genes with a mean fold change as indicated, where both repeats exhibited P values <0.05.

3.2.3.4 Limitations of a microarray study

Significant variability between replicates may exist due to the limitations of the microarray technology (Dudoit and Yang, 2002). This may be introduced through factors, such as:

probe-binding bias;

imbalance in the cDNA levels between samples;

variation in the binding of the fluorophore;

uneven spot detection;

over exposure.

To try to minimise these factors, the levels of RNA are accurately measured prior to reverse transcription, along with the quality of the RNA. Triplicate probes were designed for each gene in order to avoid a binding bias of one of the replicates, and a dual channel array was chosen to give a better representation of relative expression between samples. Finally, LOWESS and Marray normalisation were used to alleviate the variation caused by spot intensity or scanning errors, by merging the two colour data and applying a smoothing adjustment that attempts to remove incorrect variation.

The disadvantage of the dual-channel microarray is the possibility of one sample being of higher quality than the other, leading to better hybridisation and a bias of results. There is also the risk of gene-specific dye bias, in both forms of array. This is difficult to normalize, due to variation in the binding of different samples to the dyes, rather than their cognate oligonucleotides (Margaritis *et al.*, 2009). Whilst the absolute levels of gene expression cannot accurately be determined using a dual-channel microarray analysis, they give a clear quantification of the ratio of gene expression between two conditions, which was what was sought here.

Difficulties may also arise from the *in silico* analyses. If either of the green or red data is missing for a particular spot, no data will be recorded for that probe, and information may be lost as a result. The normalisation may also lead to the smoothing of otherwise legitimate variation, which may mask some gene expression unnecessarily. However, the possible loss in fidelity is more than made up for by the reduction in noise that this procedure achieves. In addition to this variability, the baseline expression of a gene of interest may mislead a researcher looking only for relative -fold change in expression. Therefore, a gene that is constitutively highly expressed and involved in (for example) a DMSP catabolic pathway, will change little (if at all) in response to the substrate.

A significant disadvantage to a microarray study is the skewed measurement of the expression of the genome in response to a given condition. Because a microarray records the activities of the cells ‘transcriptome’, that is, the level of mRNAs (indeed, all RNA molecules), this is not necessarily directly comparable to the proteome. The proteome describes the complete suite of proteins that a cell may express. The relative abundance of the various mRNAs is not always directly proportional to the presence of the translated polypeptide. This may be due to factors such as mRNA or protein stability in the cell, the processing of RNA or its translated protein product, or the mRNA’s binding affinity for the ribosome, determined by the composition of the translation initiation sequence (Brown, 2002).

3.3 Conclusions

Microarrays may also have some “biological” limitations, since, for example, they may detect genes whose expression is subject to general stress rather than direct catabolic responses to a particular molecule, and, of course, in the real world organisms are rarely faced with a straightforward “either-or” pair of dramatically different environments that differ in a single parameter. They nevertheless have the potential to give a global view of gene expression that was unthinkable not too long ago.

Certainly, some of the work described in this thesis was initiated solely from the microarray data. Notable discoveries include the gene encoding a wholly new DMSP lyase, and the expression of a suite of genes involved in a rather arcane catabolic pathway with no known link to sulfur, let alone DMS(P). It has to be admitted, though, that this particular set of experiments did not yield as much useful information as was hoped. This was due, largely, to the substantial errors in the different outputs for an individual gene, meaning that several genes whose levels of expression were genuinely affected by one or more of the agents used here were missed and, conversely, perhaps, some genes that were scored as being regulated by these agents were, in reality unaffected.

With these being the first microarrays attempted in our laboratory, it is likely that given increased financial resources, time, replicates and experience, a more accurate picture of the transcriptome of this bacterium would have emerged. However, this pan-genomic inspection of the transcriptional response of *Ruegeria pomeroyi* to DMSP and to related molecules did provide some very useful data.

Chapter 4

Discovery of the Novel Lyase, DddW

4.1 Introduction

The previously described primary *ddd* genes (*dddD, dddL, dddP, dddQ* and *dddY*) had been identified by screening genomic libraries for any cosmids that conferred a Ddd$^+$ phenotype to other bacteria. In contrast, the work described in this chapter used a very different approach, in which a candidate *ddd* gene was identified, *de novo*, by its expression pattern, as revealed by the microarray analyses (see chapter 3).

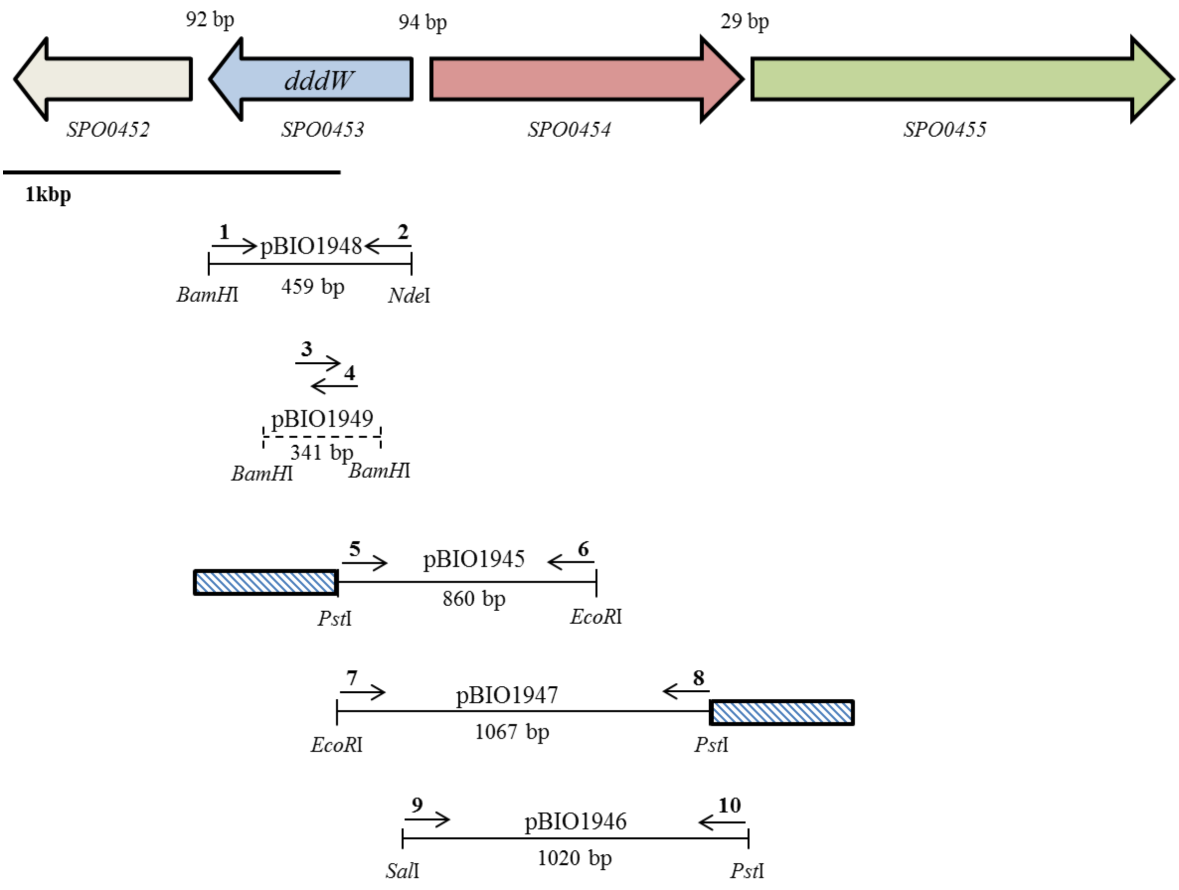
4.2 Results

4.2.1 Enhanced expression of the *SPO0453* transcript in response to DMSP

The microarray analyses showed that the *Ruegeria pomeroyi* DSS-3 gene whose expression was enhanced greatly (average 41.1-fold), following growth of the cells in the presence of DMSP compared to the control medium, was *SPO0453.* Acrylate or DMS had no detectable effect on its expression compared to the control. This gene was of particular interest, not only because of its very pronounced, and specific, induction by DMSP, but also because of the nature of its gene product – the SPO0453 polypeptide is predicted to have a cupin domain, as do two other known DMSP lyases, DddL and DddQ.

The *SPO0453* gene is transcribed divergently from *SPO0454* and is upstream of *SPO0452*, whose 5’ start is 92 bps downstream from *SPO0453* (Figure 4.1).To confirm the conclusions drawn from the microarray data, the effects of DMSP on the expression of *SPO0453* were examined, using two other, independent techniques.

Figure 4.1 Location of *dddW* and neighbouring genes in *Ruegeria pomeroyi* DSS-3



Coloured arrows show locations of *SPO0453* and neighbouring genes. The *SPO0452* gene product is a predicted tellurite resistance protein, the *SPO0453* gene product is the novel DMSP lyase, DddW, the *SPO0454*gene product is a predicted LysR type transcriptional activator and *SPO0455* encodes a predicted lysyl tRNAsynthetase. Intergenic gaps are in base pairs (bp).

The 459 bp fragment (amplified using primers Wpet1 and Wpet2 – arrows 2 and 1, respectively) containing intact *dddW* was cloned into the pET21a expression vector to form pBIO1948.

The 341 bp fragment (amplified using primers Wmut1 and Wmut2 - arrows 4 and 3, respectively) was cloned into pBIO1879 (a pK19*mob* derivative with spec^R) to form pBIO1949. This was used to disrupt genomic *dddW* through homologous recombination.

The 860 bp fragment (amplified using primers Wprom1 and Wprom2 – arrows 6 and 5, respectively) was cloned into the *lacZ* reporter plasmid, pBIO1878, to create pBIO1945, a *dddW-lacZ* reporter fusion.

The 1067 bp fragment (amplified using primers 454prom1 and 454prom2 – arrows 7 and 8, respectively) was cloned into pBIO1878 to create pBIO1947, a *SPO0454-lacZ* reporter fusion.

The 1020 bp fragment (amplified using primers 454P1 and 454P2 – arrows 10 and 9, respectively) was cloned into the expression vector pOT2 to create pBIO1946, for heterologous expression of *SPO0454* with its native promoter.

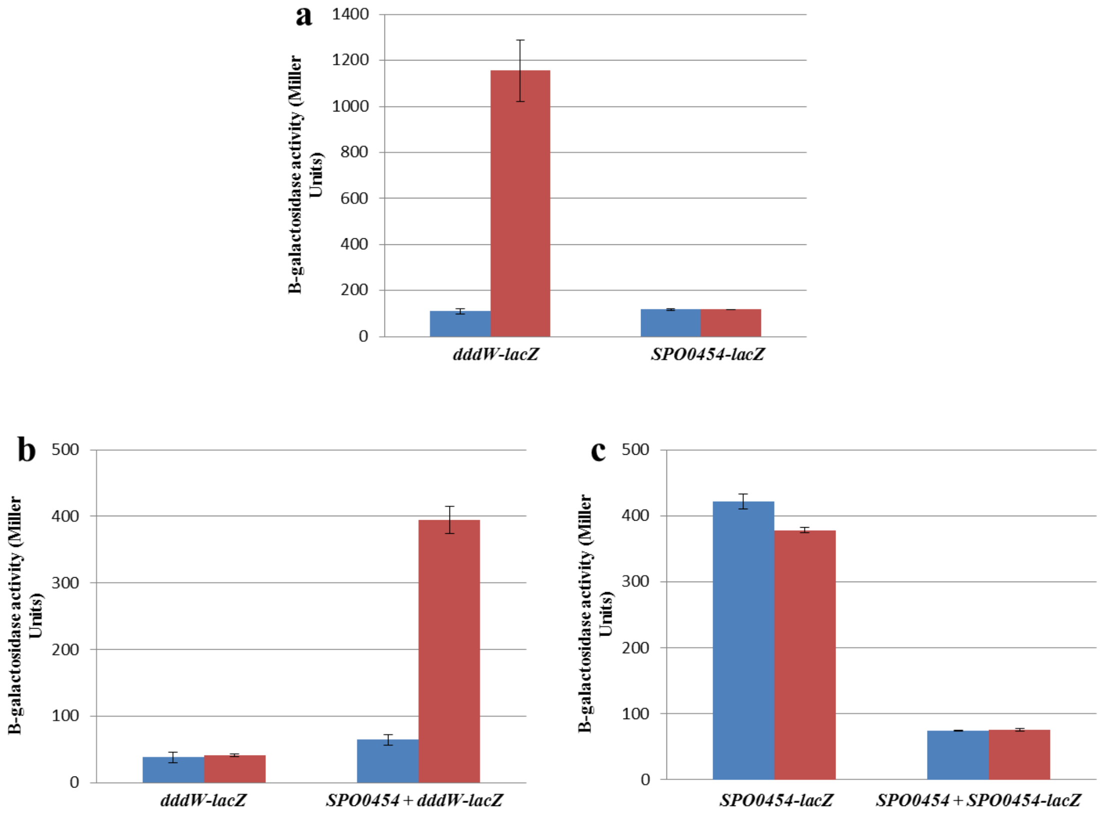
Blue striped bars indicate junction with *lacZ* of pBIO1878.

4.2.1.1 Construction and assay of a *dddW-lacZ fusion*

First, a *dddW-lacZ* transcriptional fusion was made by amplifying the intergenic region between *SPO0453* and *SPO0454*, using primers Wprom1 and Wprom2 to amplify the corresponding fragment from genomic DNA. This was cloned upstream of the promoter-less *lacZ* reporter in the wide host-range promoter-probe vector pBIO1878, cut with *EcoR*I and *Pst*I, and orientated such that the reporter *lacZ* would be under the control of the *dddW* promoter. The resulting plasmid, pBIO1945, was mobilized via a triparental conjugational mating into strain J470 (*Ruegeria pomeroyi* DSS-3 Rif^R mutant), selecting for Rif^R, Spec^R, Tet^R transconjugants. Two of these were then assayed for β-galactosidase activity after growth in minimal media that either contained or lacked 5 mM DMSP. Consistent with the microarray data, the *SPO0453-lacZ* fusion was induced 10-fold, in the DMSP-amended media, compared to the control (Figure 4.2a).

The difference in the ratios between the microarray and transcriptional fusion data could be due to the method by which expression is quantified. Microarray analyses take a snapshot of mRNA levels in a cell at a single moment in time, whereas β-galactosidase assays record the accumulation of the expressed reporter enzyme over a sustained period. Also, as noted previously, microarray data represents a ratio of uninduced:induced expression, rather than absolute levels of expression.

Figure 4.2 Regulation of the *Ruegeria pomeroyi dddW-lacZ* fusion in response to DMSP and the putative regulator, SPO0454



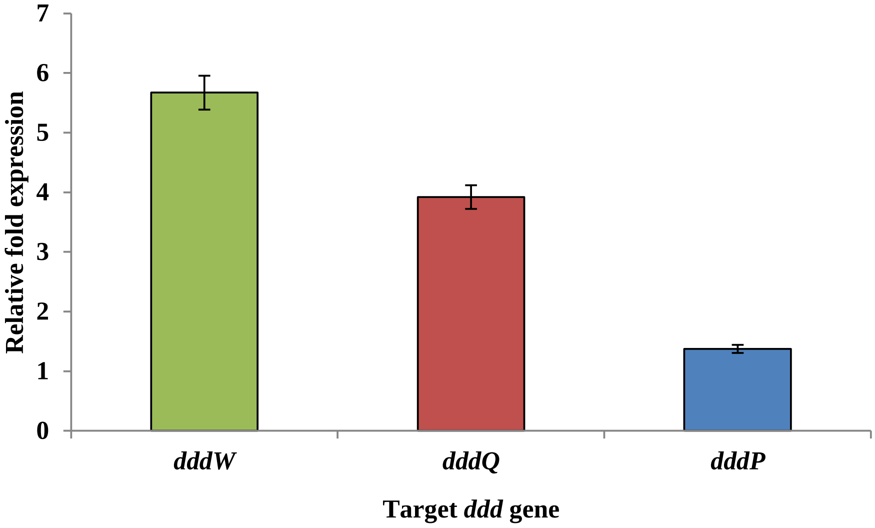
β-galactosidase activity of the *dddW-lacZ* (a, b), or *SPO0454-lacZ* (a, c) fusion plasmid when expressed by cultures of *Ruegeria pomeroyi* DSS-3 (a) or *Rhizobium leguminosarum* strain 3841 (b, c) in minimal media in the presence or absence of 5mM DMSP (blue and red bars, respectively). Error bars calculated from triplicate experiments.

4.2.1.2 qRT-PCR analysis of *dddW* transcription

DMSP-dependent induction of *SPO0453* (*dddW*) by growth in the presence of DMSP was also ratified by quantitative real-time reverse transcriptase PCR (qRT-PCR). To do this, *Ruegeria pomeroyi* DSS-3 was grown in the same manner as for the microarrays, overnight incubation followed by a 2 hour induction with/without 5 mM DMSP. The cultures were stopped for growth using phenol:ethanol and the cells frozen in liquid nitrogen. The RNA was harvested, purified and quantified using a Nanodrop 3000 (Thermo), and also checked for DNA or phenol contamination (based on the absorbance ratio at 260 nm: 280 nm and 260 nm: 230 nm, respectively).The RNA was then reverse-transcribed to cDNA and PCR-amplified using primers RTdddWF/RTdddWR, RTdddQF/RTdddQR and RTdddPF/RTdddPR, specific to *dddW, dddQ* and *dddP,* respectively (designed using Primer^{3} software – Rozen and Skaletsky, 2000). Detection of amplification was achieved by using SYBR-green fluorescent label in conjunction with a C1000 Thermal Cycler and CFX Real-Time PCR detection system (BioRad).

The relative fold change in expression was calculated in relation to *SPO2904*, which encodes a serine/threonine protein phosphatase/nucleotidase. This gene is thought to be constitutively expressed in the conditions tested, so acts as a control gene for the results to be normalised (Bürgmann *et al.*, 2007). Despite *SPO2904* being slightly down-regulated in the array (-1.36 fold) in the presence of DMSP, there was a *ca.* 6-fold increase in *SPO0453* transcript levels over *SPO2904* in cells that had been grown in DMSP (Figure 4.3). Transcript levels were also measured for the genes encoding other lyases present in *R. pomeroyi*, namely *dddQ* and *dddP*. The qRT-PCR results showed that *SPO0453* is more responsive to DMSP than either *dddQ* or *dddP*. The microarray data and qRT-PCR do not corroborate each other as well as would be hoped, but nonetheless, an increase in transcription of *dddW* is observed in both experiments.

Figure 4.3 qRT-PCR showing the increase in transcription of the primary *ddd* genes in *Ruegeria pomeroyi* DSS-3, in response to DMSP



RNA extracted from *R. pomeroyi* cultures grown in minimal (MBM) media overnight, followed by a 2 hour induction by 5 mM DMSP, or no addition, was used to carry out qRT-PCR. Primers RTdddWF/RTdddWR, RTdddQF/RTdddQR and RTdddPF/RTdddPR were used to amplify *dddW* (*SPO0453*), *dddQ* (*SPO1596*) and *dddP* (*SPO2299*), respectively. Expression ratios are shown, using the reference gene, *SPO2904,* as a baseline control. Error bars calculated from duplicate readings.

4.2.2 Demonstration that *SPO0453* encodes a novel DMSP lyase - DddW

Having confirmed that*SPO0453* was specifically induced by DMSP, the function of its product was examined directly, as follows.

4.2.2.1 DddW confers a Ddd$^+$ phenotype when expressed in *E. coli*

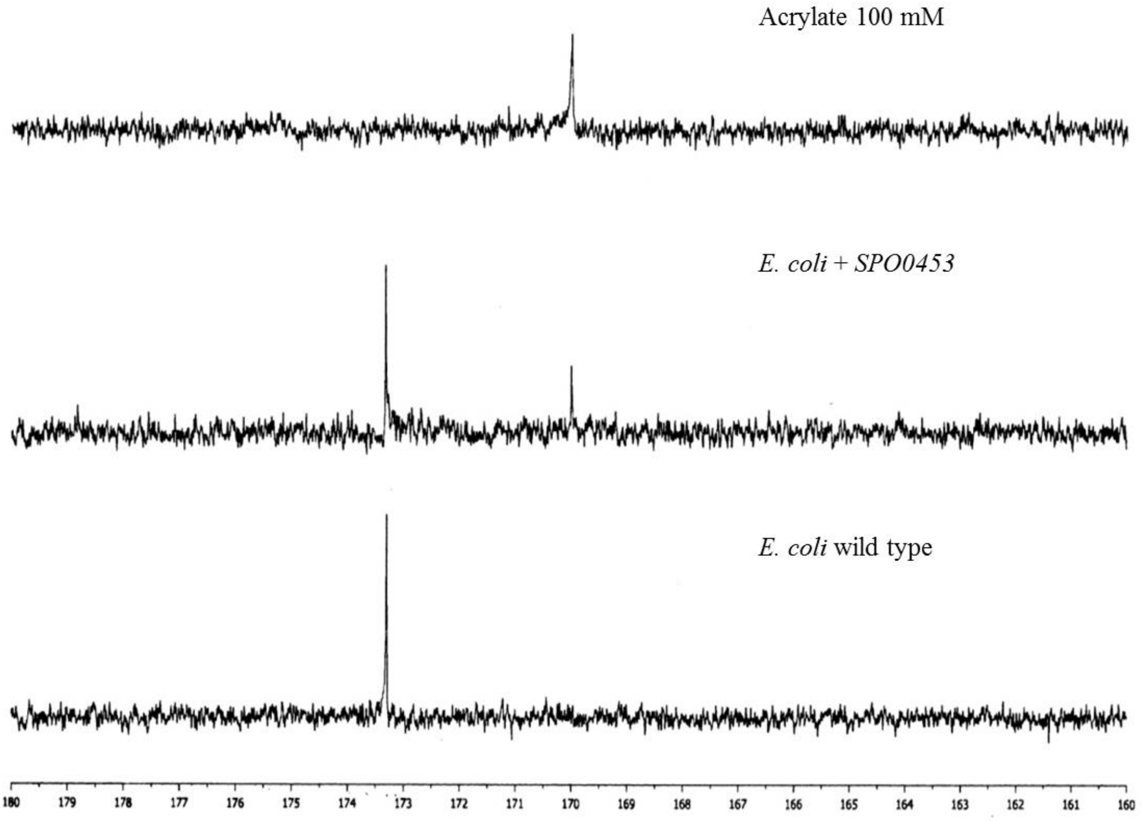
Using primers Wpet1 and Wpet2, the intact *SPO0453* gene was PCR-amplified from *R. pomeroyi* DSS-3 genomic DNA (Figure 4.1), then ligated to the expression vector pET21a, cut with *Bam*HI and *Nde*I. The ligation mix was used to transform *E. coli* strain BL21 and the cells were plated onto media containing X-gal, IPTG and ampicillin, these three compounds being used, for blue-white screens to detect inserts (X-gal), induction of the *lacZ* promoter for expression of the cloned gene (IPTG) and to screen for the transformants (ampicillin). Plasmid DNA was isolated from six white transformant colonies and these were all confirmed to contain the correct insert, as judged by *Bam*HI / *Nde*I analytical restriction digests. One of these (with a plasmid termed pBIO1948) was ratified by sequencing.

A culture of an *E.coli* transformant containing pBIO1948 was then assayed for its Ddd phenotype. This was done by sonicating the cells and incubating the cell lysate for 1 hour with 5 mM DMSP. Protein levels were calculated using a Bradford assay. The DMS product, measured by gas chromatography (GC), was made at a rate of 35 pmol^{-1} µg^{-1} protein^{-1} min^{-1}. This activity is similar to that of *E. coli* harbouring plasmids that contained either the cloned *dddP* or the cloned *dddL* genes of *R. pomeroyi* DSS-3 and *Rhodobacter sphaeroides* 2.4.1., respectively (Todd *et al.*, 2012a; S Newton-Payne, personal communication).

4.2.2.2 DddW releases acrylate from DMSP, as confirmed by NMR

Thus, it seemed that the *SPO0453* gene encoded a DMSP lyase, which liberates DMS from DMSP. To identify the C3 cleavage product, cultures of the *E. coli* strain containing the cloned *SPO0453* were grown overnight at 37°C in LB then diluted 10^{-2} into 1 ml M9 minimal medium (made up in deuterium oxide (>99.9%)], containing glycerol and 10 mM [1-^{13}C]DMSP and 0.2 mM IPTG to induce expression. Following incubation at 28°C overnight, perchloric acid (5% v/v final concentration) was added to lyse the cells. The supernatant was added to NMR tubes and proton-decoupled ^{13}C-nuclear magnetic resonance (NMR) spectra were measured at 75 MHz with a Varian Gemini 2000 in D_2O (as in Todd *et al.*, 2010). This was used to show that a proportion of the ^{13}C was converted to acrylate (Figure 4.4; J D Todd, personal communication). Thus, the *SPO0453* gene encodes a newly identified DMSP lyase, termed DddW, which cleaves DMSP into acrylate plus DMS.

Figure 4.4 Nuclear Magnetic Resonance (NMR) spectra of *Escherichia coli* containing *dddW*, fed with [1-^{13}C]DMSP



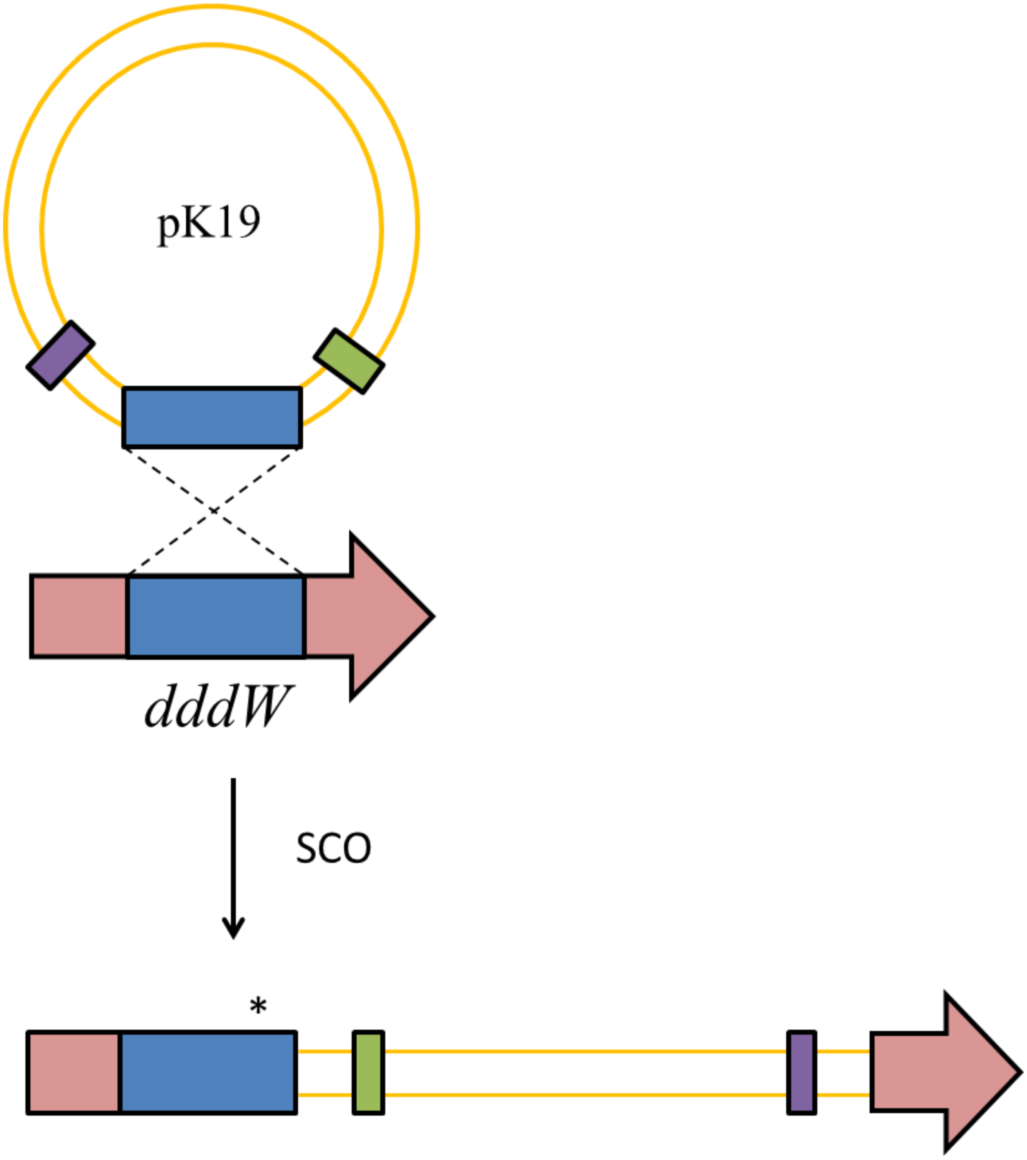
NMR spectra for pure sample of 100 mM acrylate is indicated, with a chemical shift peak at 69.9 p.p.m. The spectra below the acrylate reference, from top to bottom, shows *E. coli* expressing *SPO0453* from the pET21a plasmid, and *E. coli* wild type strain. The peak at 173.22 p.p.m. represents DMSP, added at 10 mM. Average scans recorded was 300 (J D Todd, personal communication).

4.2.2.3 An insertion mutation into *dddW* affects DMS production

To examine the role of *dddW* in DMSP catabolism in *Ruegeria pomeroyi* itself, a 341 bp internal fragment of the gene was amplified using primers Wmut1 and Wmut2, and cloned into the suicide plasmid pBIO1879, cut with *BamH*I, creating plasmid pBIO1949 (Figure 4.1). The pBIO1879 plasmid is derived from pK19*mob* (Schäfer *et al.,* 1994), and contains an extra, selectable antibiotic resistance gene (spectinomycin, Spec^R) to facilitate counter-selection in the Roseobacters, several of which are resistant to tetracycline (Todd *et al.*, 2011). The original plasmid pK19 *mob* confers resistance to kanamycin and is mobilisable by conjugation at high frequency into a wide range of host bacteria, but fails to replicate in hosts other than enterics, such as *E. coli.* Therefore, if a fragment internal to a gene of interest is cloned into the polylinker of pK19*mob* and the resultant plasmid is mobilised into the corresponding host strain, then, by selecting for an antibiotic resistance marker on the vector, transconjugants should arise by a single crossover event in which the plasmid has integrated into, and hence disrupted, the chromosomal version of the gene (Figure 4.5).

The recombinant plasmid, pBIO1949, was mobilised into strain J470 (*Ruegeria pomeroyi* DSS-3 Rif^R) via tri-parental mating (see materials and methods) and the transconjugants screened for those that were Rif^R, Kan^{R}and Spec^R. These arose at *ca*. 5.0 x 10^{3}cfu/ml and six colonies were used for genomic DNA preparation to determine if the plasmid had indeed inserted into the target gene, *dddW.* This was ratified by both PCR amplification and by Southern blotting of genomic DNA from the mutant strain, using the PCR product that was amplified to create pBIO1948 (J D Todd, personal communication).

Figure 4.5 pK19 mediated insertion mutagenesis



Blue bar indicates internal fragment of *dddW* cloned into the suicide vector pBIO1879 (pK19*mob* spec^{R}), and the corresponding region in the genomic *dddW* of *Ruegeria pomeroyi* DSS-3 (red arrow). Green and purple bars indicate orientation of inserted plasmid DNA. SCO; single crossover event via homologous recombination.* It should be noted that any part of this region may be the starting point for the SCO event, and as such, may result in the insertion of pK19 at any point along this homology.

The DddW$^-$ mutant strain was then assayed for DMSP-dependent DMS production, by growing in minimal medium containing 5 mM DMSP overnight, then assessing DMS levels using GC. It was found that the DddW$^-$ mutant released DMS at a rate ~50% lower than wild type cells. Thus, DddW makes a contribution to the overall Ddd$^+$ phenotype of *R. pomeroyi,* DSS-3, as do the other two lyases, DddQ and DddP, since mutations that abolish each of these lyases reduce, but do not abolish DMS production (Todd *et al.*, 2012a).

4.2.3 Regulation of *dddW*

As noted above, *dddW* is separated by 92 bps from the downstream gene, and is predicted to be in a single gene transcriptional unit (see Figure 4.1). The downstream *SPO0452* gene was up-regulated by 3.3-fold in the presence of DMSP, but its loose homology to a tellurite resistance protein does not appear to relate to DMSP in any significant manner. Thus, the function of this gene product is unknown.

The divergently transcribed *SPO0454* gene encodes a member of the widespread family of LysR-type transcriptional regulators (LTTRs). These proteins are responsible for regulating a diverse range of phenotypes, such as virulence, motility, quorum sensing and metabolism (Maddocks and Oyston, 2008). Another feature of many LTTRs is that they are auto-regulatory, repressing their own expression, even in the absence of the cognate co-inducer molecule. Given its location, relative to *dddW,* an attempt was made to show if the SPO0454 gene product was responsible for the DMSP-dependent regulation of *dddW.*

4.2.3.1 Difficulty in constructing a SPO0454$^-$ mutant *R. pomeroyi* strain

To do this, attempts were made to create a pK19 insertion mutant of *SPO0454* in the same way as described for *dddW.* Although transconjugants that were Rif^R, Kan^R, Spec^R were obtained, when these were checked by PCR amplification, all of them had an intact *SPO0454* gene. A possible explanation for this is that the gene immediately downstream (separated by 29 bps) of *SPO0454* is predicted to encode a lysyl-tRNA synthetase, LysS, (Figure 4.1). Aminoacyl-tRNA synthetases are essential for all living cells, because they attach ("charge") amino acids to their cognate RNA molecules, prior to their incorporation by the ribosome into peptide chains during translation. Therefore, the failure to obtain an insertion into *SPO0454* may have been due to polar effects of such a mutation on the transcription of this downstream gene (Todd *et al.,* 2012a).

4.2.3.2 Effect of cloned *SPO0454* on expression of *dddW-lacZ* in *R. leguminosarum*

I therefore adopted a different approach to test the regulatory role (if any) of the *SPO0454* gene. To do this, a "surrogate" host bacterium was employed to examine the expression of *dddW* in the presence and absence of *SPO0454*. The chosen bacterium was *Rhizobium leguminosarum* strain 3841, which was chosen for reasons already described.

First, the intact *SPO0454* gene, plus its native promoter, was cloned as a 1020 bp fragment into the wide host-range plasmid vector, pOT2, using primers 454P1 and 454P2 (see Figure 4.1), using *R. pomeroyi* genomic DNA as the template. This formed the recombinant plasmid, pBIO1946, which was then ratified by *Sal*I/ *Pst*I analytical restriction digests and by DNA sequencing of the insert. The *dddW-lacZ* fusion plasmid, pBIO1945, was transferred from *E. coli* into *R. leguminosarum* 3841 by triparental mating and then the *SPO0454*-containing plasmid, pBIO1946, was also introduced into the *R .leguminosarum* 3841/pBIO1945 by conjugation. Note that the two cloning vectors are compatible with each other and determine different antibiotic resistances (Gent^R for pOT2 and Tet^R/ Spec^R for pBIO1878).

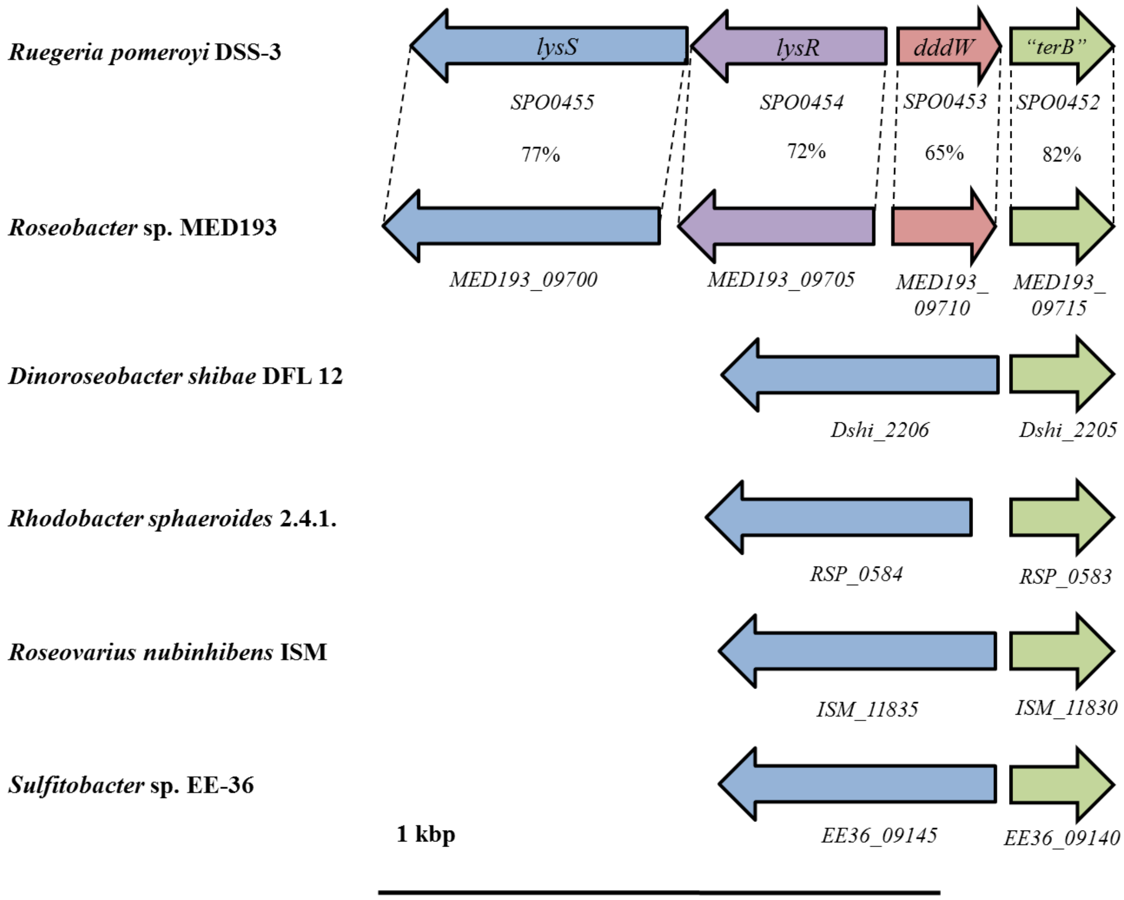
The two *Rhizobium* strains, each with the *dddW-lacZ* fusion plasmid and which either contained, or lacked, the cloned *SPO0454* gene, were each grown in the presence or absence of 5 mM DMSP and the cells were assayed for β-galactosidase activity. In the absence of the cloned *SPO0454* gene, the *dddW-lacZ* fusion was not expressed at significant levels in minimal media, either in the presence or absence of DMSP. However, in the *Rhizobium* strain containing both the fusion and the heterologously expressed SPO0454, β-galactosidase was expressed at high levels, but only when DMSP was present in the medium (Figure 4.2b). This provides strong evidence that the LysR- like *SPO0454* gene product is indeed a regulatory protein that activates transcription of *dddW* in the presence of DMSP.

As described previously, many LTTR proteins are auto-regulatory (Maddocks and Oyston, 2008). This was shown to be the case for SPO0454, as follows. A *SPO0454-lac* fusion was created by amplifying 1055 bp of the promoter region of *SPO0454*, using primers 454Prom1 and 454Prom2, and cloning the fragment into the *lacZ* reporter plasmid, pBIO1878, cut with *EcoR*I and *Pst*I, to make pBIO1947 (Figure 4.1). This was then mobilised into *R. leguminosarum* 3841. The *SPO0454-lacZ* fusion expressed β-galactosidase constitutively in *R. leguminosarum* itself. However, when pBIO1946 (pOT2 containing *SPO0454* and its native promoter) was present, the fusion was repressed ~4 fold, independent of the presence or absence of DMSP (Figure 4.2c).

4.2.4 Distribution and characteristics of DddW homologues

A BLASTp survey of the NCBI database (as at September, 2012) using DddW from *Ruegeria pomeroyi* DSS-3 as the *in silico* probe found one close homologue (65% identity at the amino acid level, $E = 3e^{-63}$) to a polypeptide (MED193_09710) in the α-proteobacterium, *Roseobacter* sp.MED193. In this strain, *dddW* is also transcribed divergently from a gene that encodes a polypeptide that closely resembles that of *SPO0454* (72% identity at peptide level, $E = 1e^{-148}$) (Figure 4.6, see later).

Figure 4.6 Comparison of the *dddW* gene clusters in several α-proteobacteria



Approximate scale provided. Gene numbers are given below, and gene names for the *R. pomeroyi* homologues are given in the arrows. Matching colours indicate homologous gene products. Identity between the gene products of *R. pomeroyi* and *Roseobacter* sp. MED193 are given between dashed lines (%).

SPO0452, Putative tellurite related, TerB-like protein;

SPO0453, DMSP lyase, DddW;

SPO0454, LysR-like transcriptional activator;

SPO0455, Class I lysyl-tRNA synthetase.

There were no other convincing DddW homologues in any other known organisms whose genome sequences are available in current databases, so DddW is rare, compared to the other Ddd lyases that have been described.

Homologues of *R. pomeroyi* DddW were also sought in metagenomic data bases, including those in the Global Ocean Survey (GOS) (Rusch *et al.,* 2007). Only four convincing homologues (40–50% identical, probability $<e^{-22}$) were found, a much lower number than DddQ and DddP, but about the same as DddL, and more than DddY. These homologues were all from the same location, a hypersaline lagoon site at Punta Cormorant in the Galapagos, the same site that contained the only DddL homologues in the GOS data set (Curson *et al.,* 2008; Todd *et al.*, 2012a).The significance, if any, of this observation remains to be determined and it also needs to be established if such divergent gene products have functional DMSP lyase activity.

Interestingly, when the *dddW* regions of the genomes of *R. pomeroyi* and *Roseobacter* sp. MED193 are compared, it appears that the *dddW-SPO0453 / MED193_09710* genes have been inserted into a region of their genomes that is conserved in other Roseobacters, as follows.

A ~4kbp region containing genes *SPO0452- SPO0455* is well conserved in both *R. pomeroyi* and *Roseobacter* sp. MED193. Of the Roseobacters interrogated, other species possessed only divergently transcribed *SPO0455* and *SPO0452* genes, without the *SPO0453-SPO0454* genes (Figure 4.6). This is supportive of a horizontal gene transfer (HGT) event involving acquisition of the *dddW* gene pair. The distribution and function of the 2 ancillary and single co-acquired genes surrounding *dddW* in this cluster will now be discussed.

4.2.5 SPO0454 and SPO0455

There were a significant number of homologues of the divergently transcribed SPO0454 detected in the NCBI database, due to the ubiquity of LysR-like regulators (Maddocks and Oyston, 2008). Many of the closest matches were to *Burkholderia* spp. and *Pseudomonas* spp. (β- and γ- proteobacteria, respectively). SPO0454 also exhibits 72% identity at the peptide level with the *Roseobacter* sp. MED193 protein, MED193_09705. The SPO0454 protein has been ratified as the regulator of *dddW* and itself in this study, and this fits well with the predicted LysR-like function of the gene product. The LysR-type SPO0454 is also very different from the LysR-type regulator, DddR in *Marinomonas* sp. MWYL1. This transcriptional activator of *dddD* is only 26% identical at the peptide level to SPO0454 (Todd *et al.,* 2007).

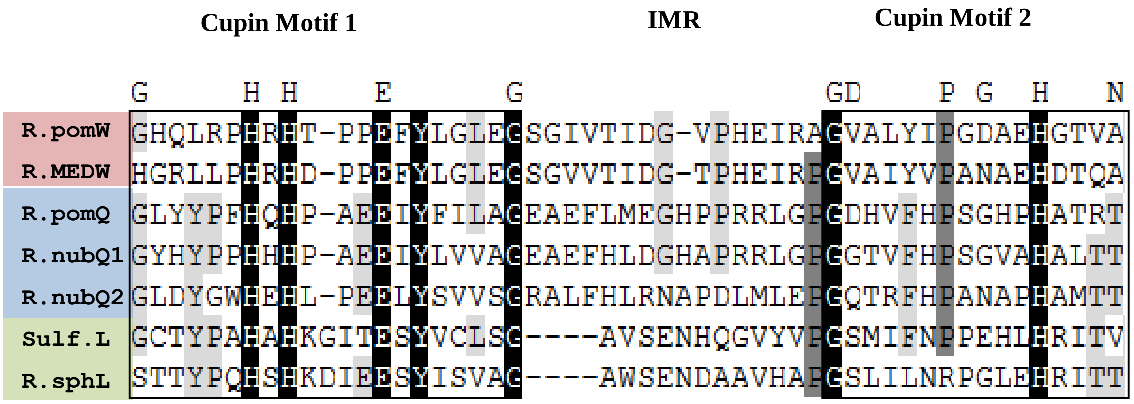
The gene directly downstream of *SPO0454* is thought to be co-transcribed, based on the polar effects of a mutation in *SPO0454* and a DOOR operon prediction (Mao *et al.,* 2008). The gene encodes a protein, SPO0455, which is 77% identical ($E = 0.0$) to the MED193_09700 peptide, a predicted Class I lysyl-tRNA synthetase, LysS. This sequence elicited a large number of homologues, due to its essential nature as a tRNA synthetase. SPO0455 has a 24 amino acid N-terminal extension, compared to the other peptides, but a SignalP analysis failed to identify a leader sequence in the peptide (Petersen *et al.*, 2011). It is unknown why this extension is present in SPO0455 at this time.

The presence of two *lys* genes in close proximity perhaps reflects the acquisition of genes to clusters that complement their activity.

4.2.6 The cupin motif in DddW

Like DddL and DddQ, the DddW polypeptide contains a predicted cupin domain (see introduction). As shown in Figure 4.7, DddW shares several of the catalytically important residues with these two other lyases, notably, the two histidines and the glutamate within motif 1, and the histidine in motif 2, all of which are implicated in metal-binding. In preliminary studies (S Newton-Payne, personal communication), the DMSP lyase activity of semi-purified DddW protein was inhibited by addition of the metal-chelating agent ethylenediaminetetra-acetic acid (EDTA), providing circumstantial evidence that DddW is indeed a metallo-protein.

Figure 4.7 Alignment of the cupin domains of DddW, DddL and DddQ



```
         G     H H    E      G                 GD    P G  H   N
R.pomW   GHQLRPHRHT-PPEFYLGLEGSGIVTIDG-VPHEIRAGVALYIPGDAEHGTVA
R.MEDW   HGRLLPHRHD-PPEFYLGLEGSGVVTIDG-TPHEIRFGVAIYVPANAEHDTQA
R.pomQ   GLYYPFHQHP-AEEIYFILAGEAEFLMEGHPPRRLGFGDHVFHPSGHPHATRT
R.nubQ1  GYHYPPHHHP-AEEIYLVVAGEAEFHLDGHAPRRLGFGGTVFHPSGVAHALTT
R.nubQ2  GLDYGWHEHL-PEELYSVVSGRALFHLRNAPDLMLEFGQTRFHPANAPHAMTT
Sulf.L   GCTYPAHAHKGITESYVCLSG----AVSENHQGVYVFGSMIFNPPEHLHRITV
R.sphL   STTYPQHSHKDIEESYISVAG----AWSENDAAVHAFGSLIILNRPGLEHRITT
```

Sequences of the predicted cupin motifs sequences of two DddW polypeptides are compared with representatives of the DddQ and DddL DMSP lyases. The amino acids that are highly conserved in all cupins are shown above the sequences (Dunwell *et al.*, 2004). *Ruegeria pomeroyi* DSS-3 (R.pomW; *SPO0453*) and *Roseobacter* sp. MED193 (R.MEDW; *MED193_09710*;), shown in pink, are aligned with the DddQ lyases from *R. pomeroyi* (R.pomQ; *SPO1596*) and *Roseovarius nubinhibens* ISM (R.nubQ1, *ISM_14090* and R.nubQ2 *ISM_14085*), shown in blue, and the DddL lyases from *Sulfitobacter* sp. EE-36 (Sulf.L *EE36_11918*) and *Rhodobacter sphaeroides* 2.4.1 (R.sphL*RSP_1433*.), shown in green. Residues highlighted in black, dark grey or light grey indicate 100%, >80% or >60% identity between sequences, respectively. IMR; Inter-Motif Region.

4.3 Conclusions

The work described illustrates the power of microarrays in the identification of genes of interest, in this case *dddW,* which encodes a novel DMSP lyase although one whose product has some similarity to those of the previously identified products of the *dddL* and *dddQ* genes. This new DMSP lyase has some features that are of interest for a number of reasons, as follows.

4.3.1 DddW is comparatively rare

The only convincing orthologue of DddW is in the closely related strain *Roseobacter* sp. MED193, which was isolated from the surface seawaters in the Northwest Mediterranean Sea (Roseobase; http://www.roseobase.org/). Few, if any, were in the GOS or any other metagenomic database. It is possible that it is more abundant in niches that have not been studied in detail – isolated or unsampled sediments for example - or it may be more frequent in clades of organism that are difficult to culture, so are under-represented in genome sequences. Or, DddW may just be rare.

4.3.2 A surfeit of enzymes that act on DMSP in *Ruegeria pomeroyi* DSS-3

The finding of a novel DMSP lyase in *Ruegeria pomeroyi* DSS-3 means that this bacterium possesses a demethylase, DmdA, an inactive DddD (see introduction) plus no less than three functional DMSP lyases. As such, *R. pomeroyi* DSS-3 has the most diversity of any single strain (to date) in its repertoire of DMSP catabolic enzymes. There are other examples of bacteria that harbour multiple Ddd$^+$ genes. – for example, *Roseovarius nubinhibens* ISM, contains *dddP, dddQ* and *dmdA* in its genome - but none has more than strain DSS-3 (see chapter 7). A recent, novel example of a non-Roseobacter with multiple DMSP-degrading systems is the γ-proteobacterium, *Oceanimonas doudoroffii*, which contains functional *dddP* and *dddD* (Curson *et al.*, 2011b).

There are several putative reasons why *R. pomeroyi* (and other strains) may have multiple DMSP lyases:

- Each enzyme may be tailored to different cellular concentrations of DMSP, for example, by having a different K_m for DMSP. This would allow a flexible, adaptive response to local environmental fluctuations. This could relate to events such as phytoplankton blooms, where large amounts of DMSP would be readily leaked into the milieu, and an enzyme with a more appropriate specificity would be required (Merzouk *et al.*, 2008);
-
- The three enzymes also differ in size, having predicted molecular weights of 16, 22 and 50kDa for DddW, DddQ and DddP, respectively and may also require different cofactors, such as metal ions. Studies have not yet conclusively determined the metal-binding abilities of DddW and DddQ, with DddP having been found to bind no known metal ions. Therefore, in conditions where there is limited availability of the necessary metal cofactors, DddP may act as the primary DMSP lyase. Then, when conditions are favourable, DddW or DddQ become dominant;

- The “response times” of the enzymes may also differ. The microarray data recorded levels of RNA present in the cells at exactly 2 hours post induction. Therefore, each of the enzymes may be induced more, or less, quickly when exposed to DMSP, or are constitutively expressed. Again, this would be important for an efficient response to short-term events such as phytoplankton blooms.

- Lastly, the different DMSP lyases might even act on different substrates, with DMSP catabolism being a secondary function.

Recent work in our laboratory has shown that far from being a model for the catabolism of DMSP, *R. pomeroyi* DSS-3 is something of an exception regarding its response to DMSP. In a survey of several different Roseobacters, it was the only one that grew well on DMSP and on acrylate as sole C sources (E Fowler, personal communication). It remains to be seen if this is connected with its unusual trio of DMSP lyases, a subject that is investigated more thoroughly in chapter 5.

4.3.3 Future work

1. Assaying the DMS production of a triple mutant strain of *R. pomeroyi* (DddW$^-$/DddQ$^-$/DddP$^-$) would confirm that no other DMSP lyases exist in this bacterium.
2. The purification of DddW would allow ratification of the proposed cupin domain and identification of any bound metal.
3. The regulatory targets of the SPO0454 protein may extend beyond *dddW*, and it would be of interest to see if other genes are affected by this regulator in *R. pomeroyi*.

Chapter 5

The role of the *acuI – dmdA* operon in *Ruegeria pomeroyi* DSS-3

5.1 Introduction

The previous chapter described the discovery of a novel DMSP lyase, DddW. This chapter will examine the *dmdA* gene and its enzymatic product, which is responsible for the initial step in the DMSP demethylation pathway. Just as with *dddW,* the initial observations on *dmdA* were obtained in the microarray analyses but were extended to yield new insights into the function and regulation of the *dmdA* gene. Additionally, an adjacent gene was found to provide novel insights into the connection between DMSP demethylation and cleavage in *R. pomeroyi*.

As shown in Figure 5.1, the *dmdA* gene (*SPO1913*) of *Ruegeria pomeroyi* DSS-3 is upstream of, and in the same orientation as, *SPO1914* from which it is separated by 77 bp. As mentioned previously, *SPO1914* encodes an enzyme that is a homologue (54% identical, E = $3e^{-112}$) of the so-called AcuI zinc dependent oxidoreductase from *Rhodobacter sphaeroides* 2.4.1, in the medium chain reductase superfamily, and which is involved in acrylate catabolism (Sullivan *et al.,* 2011). In addition, *acuI*-like genes are closely linked to several *ddd* genes that encode very different DMSP lyases and which occur in very different bacteria – *dddD* in *Halomonas, dddP* in *Oceanimonas* and *dddY* in *Alcaligenes.*

The finding of *acuI* next to a gene involved in the very different, demethylation, pathway was particularly provocative, especially since this was the case for many different Roseobacters (see below) and there are no *acuI*-like genes near the various *ddd* genes in *Ruegeria pomeroyi* or the other Roseobacters.

The work in this chapter therefore set out to uncover any links – both functional and regulatory – between the *acuI* and the adjacent *dmdA* genes in *R. pomeroyi.*

5.2 Results

5.2.1 Induction of expression of the *dmdA-SPO1914* transcriptional unit in response to DMSP and acrylate

The microarray data (appendix A3) show that the expression of both *dmdA* and *acuI* have similar responses; both are induced by 5 mM DMSP (23.3-fold for *dmdA* and 16.4-fold for *acuI*). It was striking that the *dmdA* and *acuI* also responded to the DMSP catabolite acrylate (added at 2.5 mM), their levels of expression in the microarray being enhanced 23.8- and 17.3-fold compared to the no-addition controls.

The genes that are known to be involved in the downstream steps that convert MMPA to methane thiol (MeSH), labelled *SPO2045* (*dmdB*), *SPO3804* (*dmdC*) and *SPO3805* (*dmdD*) (see introduction) were also examined. The *dmdB* gene does not appear to be induced under any condition, but *dmdC* and *dmdD* were increased in expression in +DMSP (4.6-fold and 5.3-fold, respectively). Reisch *et al.* (2011b) observed that transcripts of all these genes were increased when cells were grown with MMPA or DMSP as a sole C source. Thus, *dmdB, dmdC* and *dmdD* transcripts were increased by 2-, 5- and 6-fold in MMPA, and 5-, 2- and 3-fold in DMSP, respectively.

The gene divergently transcribed from *dmdA*, *SPO1912,* was also up-regulated in the presence of DMSP and acrylate, being increased in expression by 4.6- and 6.1-fold, respectively (see below).

The responses of *dmdA* and *acuI* to DMSP resemble previous findings that detected a potential (but not significant) up-regulation of both genes in response to DMSP (Bürgmann *et al.,* 2007). The smaller response that was reported by those authors is likely due to their use of a lower concentration (80µM) of DMSP and/or the fact that they added DMSP to cells that were approaching stationary phase, rather than the exponentially growing cells used in the present study (see introduction; chapter 3). Bürgmann *et al.* (2007) did not investigate the effects of acrylate on the transcriptome of *R. pomeroyi*.

The catabolite-mediated induction seen in the microarray is not unique. As described above, 3HP, a product of the DddD-mediated catabolism of DMSP in *Halomonas* HTNK1, induced transcription of the *ddd* genes *in situ* (Todd *et al.*, 2010). The regulation of *acuI* by acrylate also resembles the findings of Sullivan *et al.* (2011) in *Rhodobacter sphaeroides* 2.4.1. However, in the case of *Ruegeria pomeroyi dmdA-acuI*, acrylate is not an immediate, obvious catabolite of DmdA. The reasons for this unusual regulation are investigated below.

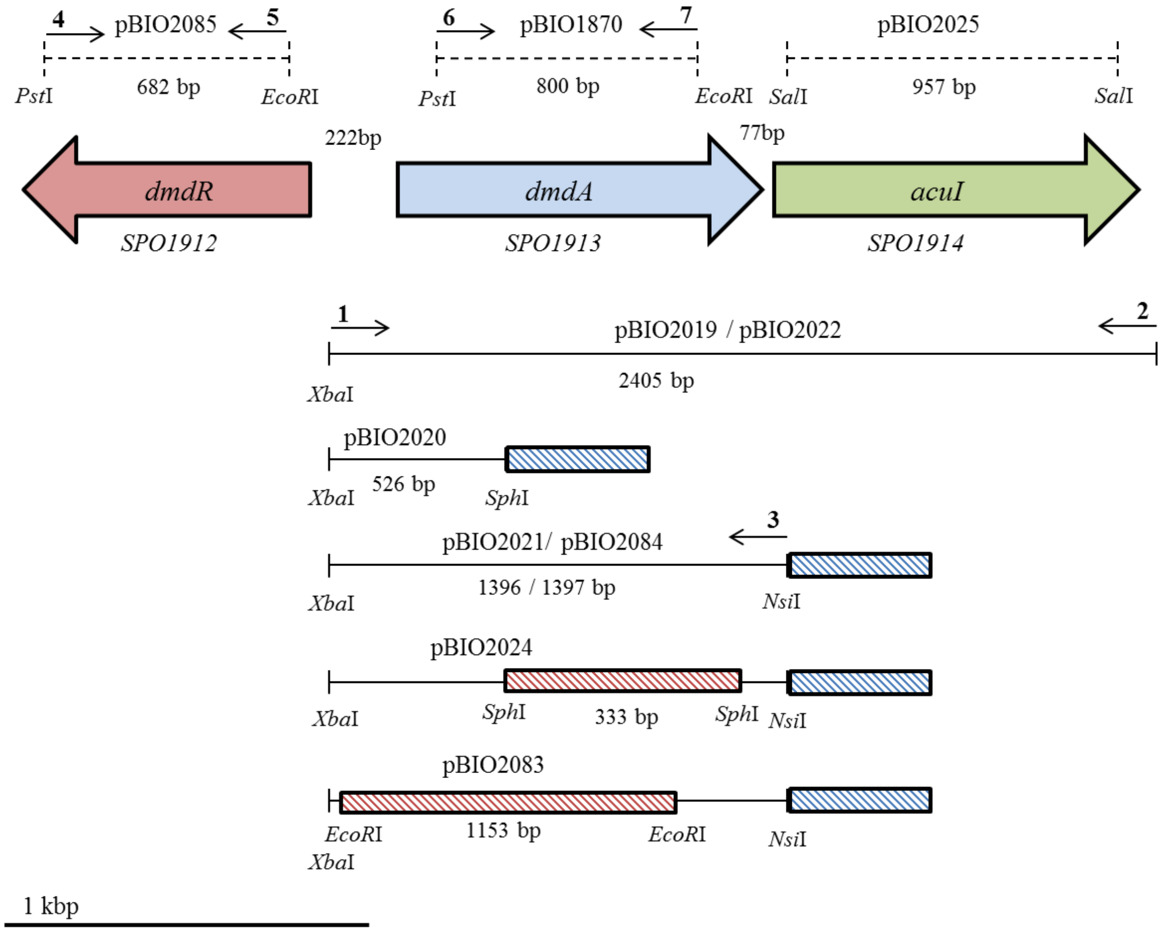
5.2.1.1 Constructing and assaying *dmdA-lacZ* and *acuI-lacZ* fusions

The microarray data and their close linkage provided good *prima facie* evidence that *dmdA* and *acuI* were co-regulated and both responded to the substrate DMSP and one of its catabolites, acrylate. To confirm this, a wholly independent measure of gene expression, namely *lacZ* reporter transcriptional fusions, was used.

In general terms, this was done by cloning fragments that spanned the *dmdA* and *acuI* promoter region into a wide host-range promoter probe plasmid, pBIO1878, and mobilising the resultant plasmids into *Ruegeria pomeroyi* DSS-3. The transconjugants were then grown in different conditions and the gene expression was measured by assaying β-galactosidase activities. The particular constructs were made as follows.

A 2405 bp fragment, which included the intact *dmdA* and *acuI* genes, plus 216 bps upstream of *dmdA* which spanned the predicted promoter region for these genes, was amplified from *Ruegeria pomeroyi* DSS-3 genomic DNA using primers SPO1913/14_XbaF and SPO1913/14_BamR (Figure 5.1). This fragment, cut with *Xba*I and *Bam*HI, was ligated into the expression vector, pBluescript SK-, digested with the same enzymes and the ligation mix was used to transform *E. coli* strain JM101. Transformants arose at *ca.* 5 x 10^2 cfu/ml and six colonies were selected for plasmid DNA preparations, followed by diagnostic restriction digests. One recombinant plasmid, termed pBIO2019, was confirmed as containing the correct fragment, cloned in the appropriate orientation, and was used as a starting point to create two individual *lacZ* reporter transcriptional fusions.

Figure 5.1 Location of *dmdA* and neighbouring genes in *Ruegeria pomeroyi* DSS-3



Genes are shown to scale, illustrating gene numbers and intergenic regions.

A 2405 bp fragment of DNA was amplified using primers SPO1913/14_XbaF (1) and SPO1913/14_BamR (2) and cloned into pBluescript SK- to create pBIO2019, or pBIO1878 (*lacZ* reporter plasmid) to form pBIO2022. This PCR product was also used as a probe for Southern blotting of *dmdA*$^{-}$ and *acuI*$^{=}$ mutants.

A 526 bp fragment of DNA was released from the pBIO2019 plasmid by digestion with *Xba*I and *Sph*I and cloned into pBIO1878 to form the *dmdA-lacZ* fusion plasmid, pBIO2020.

A 1396 bp fragment of DNA was released from the pBIO2019 plasmid by digestion with *Xba*I and *Nsi*I and cloned into pBIO1878 to form the *acuI-lacZ* fusion plasmid, pBIO2021.

Primers SPO1913/14_XbaF (1) and acuI+1_NsiR (3) were used to amplify the same fragment as for pBIO2021, with the addition of a C nucleotide upstream of the *Nsi*I cut site, in order to create a frame shift mutation reporter plasmid, pBIO2084.

A 333 bp fragment of DNA was removed from pBIO2021 (red striped bar) by restriction digestion with *Sph*I to create the *acuI-lacZ* fusion plasmid, pBIO2024.

An 1153 bp fragment of DNA was removed from pBIO2021 (red striped bar) by restriction digestion with *Eco*RI to create the fusion plasmid, pBIO2083.

Primers 1912_EcoF (5) and 1912_PstR (4) were used to PCR amplify a 682 bp internal fragment of *dmdR* to clone into the suicide vector, pBIO1879 (a pK19*mob* derivative) to make pBIO2085. This was used to create a DmdR$^-$ strain of *R. pomeroyi*.

Primers SPO1913F_Pst (6) and SPO1913R_Eco (7) were used to PCR amplify an 800 bp internal fragment of *dmdA* to clone into pBIO1879 to make pBIO1870. This was used to create a DmdA$^-$ strain of *R. pomeroyi*.

The PCR product amplified using primers SPO1913/14_XbaF (1) and SPO1913/14_BamR (2) was digested with *Sal*I to release a 957 bp internal fragment of *acuI*, cloned into pBIO1879 to create pBIO2025. This was used to create an AcuI$^-$ strain of *R. pomeroyi*.

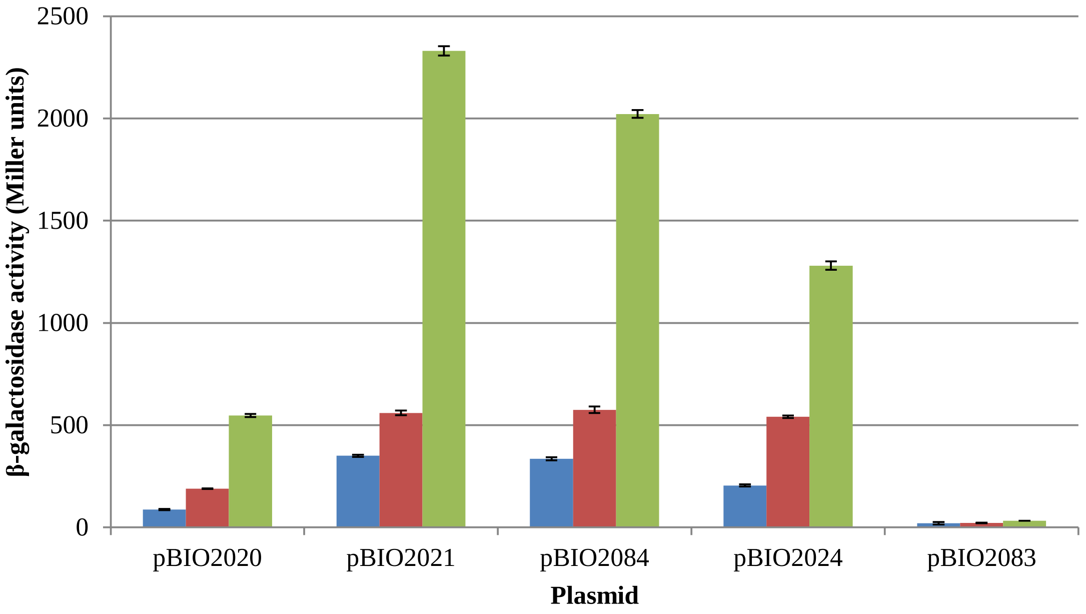
Blue striped bars indicate the junction point with *lacZ* of pBIO1878.

A *dmdA-lacZ* transcriptional fusion was created by digesting pBIO2019 DNA with *Xba*I plus *Sph*I to release a 526 bp fragment comprising 216 bp 5' upstream, and 310 bp downstream from the start of the *dmdA* gene and which therefore spans the predicted *dmdA-acuI* promoter region. This fragment was gel-extracted and ligated into the reporter plasmid pBIO1878 (see chapter 4), also digested with *Xba*I and *Sph*I, before transforming *E. coli* strain 803, selecting Tet^R (specified by pBIO1878) transformants. Restriction digests and then DNA sequencing of the plasmid DNA in six of the resulting transformants confirmed that they each contained the 526 bp fragment in the correct orientation and one of these plasmids, termed pBIO2020, was chosen for further study. A similar method was used to make the *acuI-lacZ* fusion plasmid. Thus, a 1396 bp fragment containing 216 bp upstream of *dmdA*, the entire *dmdA* gene plus 8 bp of the 5' end of *acuI* was released from pBIO2019 by restriction digest with *Xba*I and *Nsi*I, a naturally occurring restriction site within *acuI*. The *Nsi*I site was used to sub-clone into pBIO1878, which possessed *Xba*I and *Pst*I restriction sites, because the cutting of an *Nsi*I restriction site leaves sticky ends complementary to *Pst*I, an isoschizomer of *Nsi*I. The recombinant plasmid was termed pBIO2021and its integrity was confirmed as described above for pBIO2020.

The two fusion plasmids pBIO2020 and pBIO2021 were each introduced into *Ruegeria pomeroyi* strain J470 in triparental conjugational crosses, selecting for Tet^R transconjugants. For each cross, one transconjugant was purified and was then used to examine the expression of the corresponding fusion, as follows.

Cultures of *R. pomeroyi* J470/pBIO2020 and J470/pBIO2021 were grown in unsupplemented ½ YTSS medium and also in ½ YTSS that contained either 5 mM DMSP or 2.5 mM acrylate, before assaying the cultures for β-galactosidase activity. Note the use of the complete ½ YTSS medium, rather than the minimal MBM medium. This was because cell growth was considerably greater in the former and the levels of expression correspondingly greater than in the minimal medium. As shown in figure 5.2, the patterns of expression of the two fusions, as reflected in the resultant β-galactosidase activities were similar, but not identical to those seen in the microarrays.

Figure 5.2 Expression of the *R. pomeroyi* DSS-3 *dmdA-lacZ* and *acuI-lacZ* fusions in response to DMSP and acrylate



Derivatives of *Ruegeria pomeroyi* DSS-3 (J470) containing one of the various fusion plasmids as indicated were grown in ½ YTSS medium (blue bars) or in the same medium supplemented with 5 mM DMSP (red bars) or 2.5 mM acrylate (green bars). Results of triplicate assays of β-galactosidase activities are shown as Miller Units, with standard errors.

Figure 5.1 shows the dimensions of the cloned DNA in the fusion plasmids, which are:

***dmdA-lacZ* (pBIO2020);**

***acuI-lacZ* (pBIO2021);**

***acuI-lacZ* +1 (pBIO2084), a single base insertion, to create a frameshift in *lacZ* (see below);**

***acuI-lacZ* with a fragment of *dmdA* deleted but with an intact promoter region (pBIO2024);**

***acuI-lacZ* with the majority of *dmdA* and its promoter region deleted (pBIO2083).**

Thus, both fusions were induced by pre-growth in the presence of DMSP and of acrylate, compared to the values in the unsupplemented medium, and, for both fusions, acrylate was a more effective co-inducer than was DMSP. However, the ratios of increase were considerably less than those seen in the microarrays. Thus, DMSP caused a *ca.* 2-fold and 1.5-fold increase in β-galactosidase activity from, respectively, the *dmdA-lacZ* and the *acuI-lacZ* fusions compared to the control, whereas the corresponding factors of enhancement in the microarrays were, respectively *ca.* 20-fold and 15-fold. Similarly, the potency of acrylate-dependent induction was *ca.* 6-fold and 7-fold increase in β-galactosidase activity, and a *ca.* 20-fold and 15-fold in the microarray, for the *dmdA-lacZ* and *acuI-lacZ* fusions, respectively.

Whereas microarray data only present the *ratios* of the corresponding RNA molecules in the different samples, other methods, such as qRT-PCR and, as used here, the assaying of reporter fusion activities, indicate the *absolute* levels of expression of the genes under study. In the present study, the data presented in figure 5.2 show that (a) the *dmdA* and *acuI* genes are expressed at very high levels when induced by either acrylate or DMSP, since β-galactosidase activities > 1,000 Miller Units are, in our experience, towards the top end of gene activity as measured in this way and (b) perhaps most strikingly, the *acuI-lacZ* fusion was expressed at significantly greater levels than was the *dmdA-lacZ* fusion, under all three growth conditions (control, +DMSP or +acrylate).

5.2.2 Unusual expression of the *dmdA-lacZ* and *acuI-lacZ* transcriptional fusions

This expression pattern was surprising, since it had been predicted that *dmdA* and *acuI* are in a single transcriptional unit, and, while it is not unusual for downstream genes in an operon to be expressed at *lower* levels than the promoter-proximal genes, the converse is unusual. Three possible explanations for this observation were considered, and tested as follows.

5.2.2.1 The *acuI* gene has another, internal promoter that responds to DMSP and to acrylate

To examine this possibility, a new *acuI –lacZ* fusion plasmid, pBIO2083, was made (Figure 5.1). Compared to pBIO2021, the original plasmid that contains this fusion, pBIO2083 was deleted for the DNA upstream of *dmdA* and therefore lacks the promoter that is located in that region, as shown via the β-galactosidase assays. This new *acuI-lacZ* fusion plasmid was made by digesting pBIO2021 with *Eco*RI and re-ligating to remove an 1153 bp fragment that contained the majority (975 bp) of *dmdA* and its 178 bp upstream promoter region. The ligation mix was transformed into *E. coli* 803, and plasmid DNA was isolated from 10 of the resulting transformants. These plasmids were then analysed by restriction digest with *Eco*RI to identify those that had lost the appropriately sized *Eco*RI fragment. One such plasmid, termed pBIO2083, was mobilised into *R. pomeroyi* J470 and a culture derived from a purified Tet^R transconjugant was assayed for β-galactosidase activities, as described above. It was found that the “promoter-less” fusion was almost totally abolished in its activity, in all three conditions. Thus the promoter that drives the expression of *acuI* does indeed seem to be upstream of the *dmdA* gene.

5.2.2.2 The presence of an intact *dmdA* gene in the fusion plasmid may affect the expression of *acuI-lacZ*

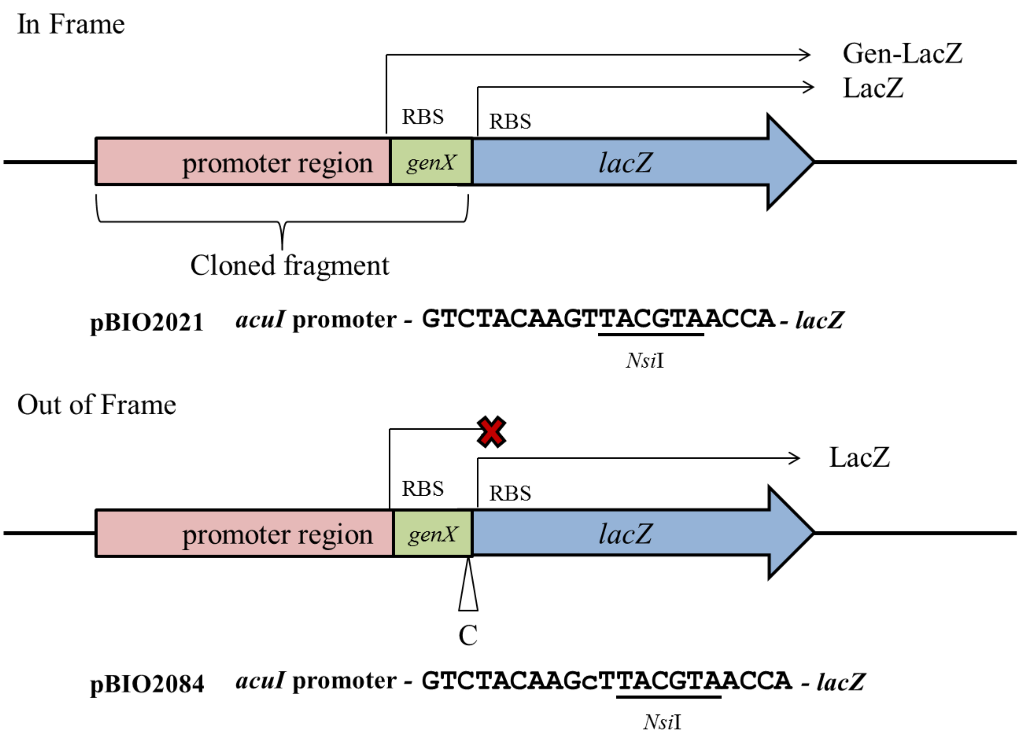
The original *acuI-lacZ* fusion plasmid, pBIO2021, contains an intact version of *dmdA,* but the *dmdA-lacZ* fusion plasmid pBIO2020 does not. In light of the interactions between the DmdA-mediated DMSP demethylation pathway and the various Ddd-mediated cleavage pathways (see below), it may be that the presence of the extra copies of *dmdA* in pBIO2021 affect the expression of the *acuI-lacZ* fusion. To examine this, another *acuI-lacZ* fusion plasmid was made, which was very similar to pBIO2021, but which lacked an intact *dmdA* gene. Thus, the new fusion would be under the control of its promoter, but would not contain a functional *dmdA* gene. This plasmid was made by digesting pBIO2021 with *Sph*I and re-ligating to remove a 333 bp fragment within *dmdA*, towards its 3’ terminus (Figure 5.1). The ligation mix was transformed into *E. coli* 803 and 10 colonies were used for plasmid DNA extraction. These plasmids were then analysed by restriction digest with *Xba*I and *Bam*HI to identify any that were appropriately truncated. One such plasmid, termed pBIO2024, was mobilised into *R. pomeroyi* J470 and a culture derived from a purified Tet^R transconjugant was assayed for β-galactosidase activities, as described above. The new fusion was found to exhibit essentially the same pattern of induction as the *acuI-lacZ* fusion, with a *ca.* 2-fold and 5-fold increase in activity in the presence of DMSP or acrylate, respectively (Figure 5.2). Activity in acrylate was not as markedly high as in the *acuI-lacZ* fusion, but it is uncertain whether this is due to the reduced levels of DmdA in the cell, or if the removal of this region affected the stability or availability of the mRNA (see chapter 7). The latter seems unlikely, given the activity of a similarly truncated transcript, in the form of pBIO2083 (see above). In any event, this result showed that the intact *dmdA* gene is likely not the sole reason for the unexpectedly high β-galactosidase activity of the *acuI-lacZ* fusion.

5.2.2.3 The *lacZ* fusion plasmid, pBIO1878, contains its own, efficient, ribosomal binding site

The promoter-probe plasmid pBIO1878 was designed to construct transcriptional fusions (the reporter *lacZ* retains its own ribosomal binding site {RBS}). However, in some cases, translational fusions can be made if the junction between the cloned gene and *lacZ* is in-frame. Therefore, in such cases, the level of β-galactosidase may be affected by the relative strength of the target gene's RBS, compared to that of *lacZ.*

To examine this possibility, the junction sequences of the *acuI-lacZ* and the *dmdA-lacZ* fusions were deduced, first *in silico* and then directly by DNA sequencing. It was found that *dmdA* was not in frame with *lacZ*, but that the *acuI-lacZ* fusion in pBIO2021 did form an in-frame fusion. To determine whether this translational fusion affected β-galactosidase activity, a +1 frame shift mutation was introduced into the junction point of the *acuI-lacZ* gene fragment. The mutagenic primer, acuI+1_NsiR, was used with SPO1913/14_XbaF to PCR amplify the fragment of the *dmdA-acuI* region from pBIO2019 used to create pBIO2021 (*acuI*-*lacZ*). The acuI+1_NsiR primer introduced an additional C nucleotide 2 base pairs 5’ of the *Nsi*I cut site, creating a +1 frame shift in the sequence, shown in Figure 5.3.

Figure 5.3 Translational and transcriptional *lacZ* fusions



When the promoter and start of a gene (*genX*) are cloned in frame with the downstream *lacZ* gene of pBIO1878, the ribosome can translate the mRNA transcript from two ribosomal binding sites (RBS), resulting in a LacZ protein product and a Gen-LacZ hybrid enzyme, because of read-through. Here, the binding efficiency of the inserted RBS may affect the outcome of a β-galactosidase assay. This was the case for pBIO2021, an *acuI-lacZ* transcriptional fusion plasmid, as indicated below the “In Frame” region.

However, if the promoter region is fused out of frame (indicated by the insertion of a C nucleotide in the figure), the RBS for this promoter region will soon hit a nonsense codon and lead to a non-functional, deleted β-galactosidase gene product. This was the case for pBIO2084, whereby a C nucleotide (lower case in the sequence) was inserted in the sequence prior to the *Nsi*I restriction site, which represents the junction point with the plasmid bound *lacZ*.

This mutagenised fusion was cloned and transformed as described for pBIO2021. A single successful transformant was confirmed by DNA sequencing as a *bona fide* +1 frame shift mutant. The resulting plasmid, pBIO2084 (Figure 5.1), was transferred via triparental conjugation to *R. pomeroyi* J470 and assayed for β-galactosidase activity, as above. The frameshift mutation had no significant effect compared to its progenitor (Figure 5.2). Therefore, the additional RBS present in pBIO1878 does not appear to affect β-galactosidase activity.

A terminator prediction using TransTermHP (Kingsford *et al.,* 2007) located a stem-loop-tail terminator motif (GGCCCCCGG ACATAGCG CCGGGGGCC, score 5.2), located 19 bps downstream of *acuI.* This was the only such predicted terminator within the entire *acuI-dmdA* region, again supporting the notion that *acuI* and *dmdA* are co-transcribed, from a promoter upstream of *dmdA.*

Given these results, it is still unclear why the *acuI-lacZ* reporter fusion exhibited higher β-galactosidase activity than the *dmdA-lacZ* reporter fusion.

5.2.3 Insertion mutations into *dmdA* and *acuI*

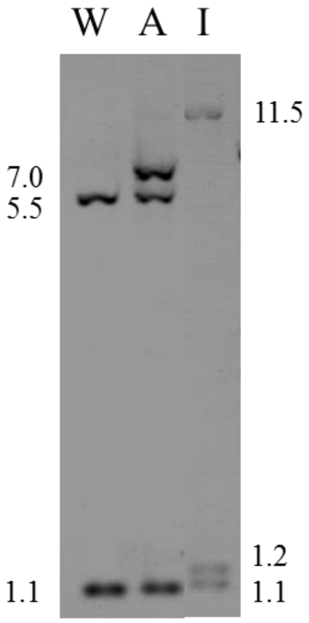
Having shown that *dmdA* and *acuI* are co-transcribed and co-regulated, the functions of these two genes were examined in some detail. This first involved the isolation of insertional mutations into each of these genes followed by phenotypic characterisation of these mutants.

5.2.3.1 Construction of DmdA$^-$ and AcuI$^-$ *R. pomeroyi* strains

To make these mutations, fragments internal to *acuI* and to *dmdA* were cloned, separately, into the suicide plasmid vector pBIO1879. The *dmdA* fragment was made by amplifying an 800 bp region from *R. pomeroyi* DSS-3 genomic DNA using primers SPO1913F_Pst and

SPO1913R_Eco (Figure 5.1), which contain *Pst*I and *EcoR*1restriction sites, respectively, prior to cloning into a similarly digested pBIO1879 vector, to form pBIO1870. A 957 bp *acuI* internal DNA fragment was made by digesting pBIO2019 (see above) with *Sal*I, which cuts twice within *acuI,* and this fragment was then cloned into *Sal*I-digested pBIO1879 to form pBIO2025. To recap, pBIO1879 is a pK19*mob* suicide vector derivative with an additional Spec^R cassette, which inserts into the host genome via homologous recombination, based on homology to an inserted fragment of DNA, and disrupts the function of the respective gene. This method was used previously in the mutagenesis of the *dddW* gene (see chapter 4). The two plasmids pBIO1870 and pBIO2025 were then each introduced by conjugation into *R. pomeroyi* J470 in triparental matings, selecting Rif^R/Spec^R/Kan^R transconjugants, which should arise via a single cross-over event within the corresponding genes (See Figure 4.5, chapter 4). Each cross generated ~50 transconjugants with the selected resistances; genomic DNA was isolated from four of these, and was digested with *Eco*RI. The fragments were separated on an agarose gel, which was then blotted to nitrocellulose and probed with a PCR product that extended from 216 bp upstream of *dmdA* to the 3' end of *acuI*. This had been generated from *R. pomeroyi* genomic DNA, using primers SPO1913/14_xbaF and SPO1913/14_BamR (Figure 5.4) and would label a ~1.1 kbp and ~5.5 kbp fragment in wild type *R. pomeroyi.* The DmdA$^-$ mutant exhibited fragments of *ca.* 1.1, 5.5 and 7 kbp in size, representing the insertion of the ~6 kb pBIO1879 plasmid into the 1.1 kb fragment. The unusual nature of the insertion of pK19 into host genomes (as described in chapter 4) makes accurately calculating the insertion difficult at times. Thus, primers located external to the *dmdA* gene were used to PCR amplify it from both the wild type and DmdA$^-$ strains. As expected of an insertion of a 6 kb fragment into *dmdA*, a PCR product for *dmdA* was amplified from the wild type, but not the DmdA$^-$ strain. The AcuI$^-$ mutant strain exhibited fragments of *ca.* 1.1, 1.2 and 11.5 kbp, consistent with the insertion of pBIO1879 into the *acuI* gene, and introduction of an *Eco*RI site from the plasmid ~1.2 kb from an existing *Eco*RI site in the genome. These mutant *Ruegeria pomeroyi* DSS-3 strains were termed J527 (AcuI$^-$) and J471 (DmdA$^-$).

Figure 5.4 Southern blot of *Ruegeria pomeroyi* DmdA$^-$ and AcuI$^-$ mutants



Genomic DNA from wild type (W), *dmdA*$^-$ (A), *acuI*$^-$ (I) strains of *Ruegeria pomeroyi* J470, digested with *Eco*RI and probed with the PCR product that was obtained using primers SPO1913/14_XbaF and SPO1913/14_BamR (see Figure 5.1.) which spans both *dmdA* and *acuI* genes. Numbers represent approximate DNA length in kilo base pairs (kbp) of the labelled bands.Note the appearance of a larger band in the DNA from the mutant strains, consistent with the insertion of the pBIO1879 plasmid into the genome.

Prior to examining these two mutants for their phenotypes, a series of plasmids was made (using the methods described above) in which the *acuI* and *dmdA* genes were each cloned alone, and also together, in the wide host-range plasmid pBIO1878, thus allowing the correction of any mutant phenotypes by the corresponding wild type genes to be determined.

To make these constructs, the PCR product (Figure 5.1) that included both *dmdA* and *acuI*, with their native promoter was cloned as a 2045 bp fragment to form pBIO2022. Then, pBIO2024 (*acuI* alone) was created by cloning pBIO2023 (itself a copy of pBIO2019 with a

*Sph*I fragment of *dmdA* deleted –see above) into pBIO1878. Plasmid pBIO2021 comprises the *acuI-lacZ* fusion, and so contains functional *dmdA* but not *acuI.*

5.2.3.2 Growth of DmdA$^-$ and AcuI$^-$ strains of *R. pomeroyi* on DMSP or acrylate

The following phenotypes were examined for the original DmdA$^-$ and AcuI$^-$ mutants and for the transconjugants in which the cloned, wild type genes had been introduced into these mutants by conjugational triparental matings.

(i) Ability to grow on acrylate as sole carbon source;
(ii) Ability to grow on DMSP as sole carbon source;
(iii) Tolerance to toxic effects of acrylate;
(iv) Levels of DMSP-dependent DMS production.

Cultures of the various strains were grown in MBM to an OD_{600} ~0.8 before being washed in fresh MBM and spotted in 20µl aliquots onto solid MBM media, in which either DMSP or acrylate (each at 5 mM) was the sole C source. In addition, aliquots of the cultures were plated on MBM containing each of these compounds, plus the “regular” C source, succinate (10 mM) to test the toxicity of DMSP and of acrylate. The results are summarized in Table 5.1.

Table 5.1 Summary of growth of wild type, DmdA^{-} and AcuI^{-} strains of *Ruegeria pomeroyi* J470 on DMSP or acrylate, and phenotypic correction with intact *dmdA* and/or *acuI*

R. pomeroyi strain	Growth on 5 mM DMSP as sole C source	Growth on 5 mM acrylate as sole C source	Growth on 10 mM succinate in the presence of 5 mM acrylate
J470	+	+	+
J471 (DmdA^{-})	-	-	-
J527 (AcuI^{-})$^{-}$	-	-	-
J471 :: pBIO2019 (cloned *dmdA* plus *acuI*)	+	+	+
J471 :: pBIO2021 (cloned *dmdA*)	-	-	-
J471 :: pBIO2024 (cloned *acuI*)	+	+	+
J527 :: pBIO2019	+	+	+
J527 :: pBIO2021	-	-	-
J527 :: pBIO2024	+	+	+

+ or – indicates growth or no growth on the tested conditions.

Data summarised from this study and Todd *et al.*, 2012b.

It was striking that both the AcuI^{-} mutant (J527) and the DmdA^{-} mutant (J471) failed to grow on either DMSP or acrylate, whereas the wild type grew well on both compounds. Not only that, but both mutants failed to grow in the presence of either of DMSP or acrylate (each at 5 mM) even when the alternative C source succinate was supplied.

In view of these observations, an attempt was made to quantify the sensitivity of the DmdA^{-} and AcuI^{-} mutants by spotting aliquots of these strains onto succinate-containing MBM plates to which varying levels of DMSP and of acrylate, from 0.2 mM to 10 mM were added. Strikingly, the wild type grew well on each of these at concentrations as high as 10 mM (DMSP) or 5 mM (acrylate). In contrast, both the mutants were inhibited for growth at concentrations of 1 mM DMSP and 0.5 mM acrylate. These initial results imply that both *dmdA* and *acuI* are involved in the catabolism of both these substrates.

It was noted that the release of DMS, the other product of the cleavage pathway, was also enhanced 5-fold, when the DmdA^- mutant was assayed for DMSP lyase activity. This could be explained by the channeling of more of the substrate DMSP into one or more of the DMSP lyase systems, since the demethylation pathway was blocked. This corroborates findings by Bürgmann *et al.* (2007) that a DmdA^- mutant of *Ruegeria pomeroyi* accumulated acrylate (the other product that is made by cleavage of DMSP by the lyase[s]) from DMSP than the wild type.

5.2.3.3 DmdA^- and AcuI^- complementation assays

To further investigate the growth phenotypes, a series of complementation tests was done. Thus, the plasmids that contained *acuI* alone (pBIO2024), *dmdA* alone (pBIO2021) or both *dmdA* plus *acuI* (pBIO2022) were introduced into the AcuI^- and the DmdA^- mutant strains and the transconjugants were examined for their growth characteristics. As expected, pBIO2022 corrected both mutants for all the defects (growth on and tolerance to DMSP and acrylate). However, both of the plasmids that contained each of the genes, alone, gave some very surprising results.

Thus, the cloned *dmdA* gene, in pBIO2021 did not correct any of the phenotypes, whereas the cloned *acuI* gene, alone in pBIO2024, corrected all of them, even the ability of the DmdA^- mutant to grow on DMSP as sole C source (Table 5.1). These results can be explained as follows.

First, it is likely that the insertion of pBIO1879 into *dmdA* has a polar effect on the transcription of the downstream *acuI* gene; therefore the DmdA$^-$ mutant would actually be defective in both DmdA and AcuI. This would explain the acrylate sensitivity and the failure to grow on this substrate in the DmdA$^-$ mutant, since the *acuI* gene of other bacteria (*Rhodobacter sphaeroides,* see above) had already been implicated in conferring acrylate resistance and, perhaps in acrylate catabolism (and see also below). It would also explain why neither of these phenotypes was corrected by the cloned *dmdA* gene, alone, but could, as expected, be corrected by the cloned *acuI* gene. The real surprise was that the failure of the DmdA$^-$ mutant to grow on DMSP could also be corrected by the cloned *acuI* gene, but *not* by the cloned *dmdA.* The implications of this are important and unexpected.

First, it means that growth of *Ruegeria pomeroyi* on DMSP can occur even in the absence of a functional demethylation pathway, indicating that growth on this compound may involve one or more of the DMSP lyases (DddP, DddQ and/or DddW). Furthermore, it seems that this system requires a functional AcuI, either to confer resistance to the acrylate that is generated as the product of these DMSP lyases, and/or to initiate a productive catabolic pathway that uses acrylate and leads to growth of the bacteria.

Taken together, the work described above provides a genetic and perhaps a physiological link between AcuI and both the DMSP demethylation and DMSP cleavage pathways. When regarding the function of the Dmd enzymes (which mediate the demethiolation pathway of DMSP catabolism, see introduction), the growth of a DmdB$^-$ mutant strain of *R. pomeroyi* on DMSP as a sole C source (Reisch *et al.,* 2011a; 2011b) provides compelling evidence that DMSP cleavage is able to sustain cellular growth by utilising acrylate via the actions of the AcuI enzyme (also see chapter 7). It was therefore important to explore the role of AcuI more thoroughly.

5.2.4 A role for AcuI

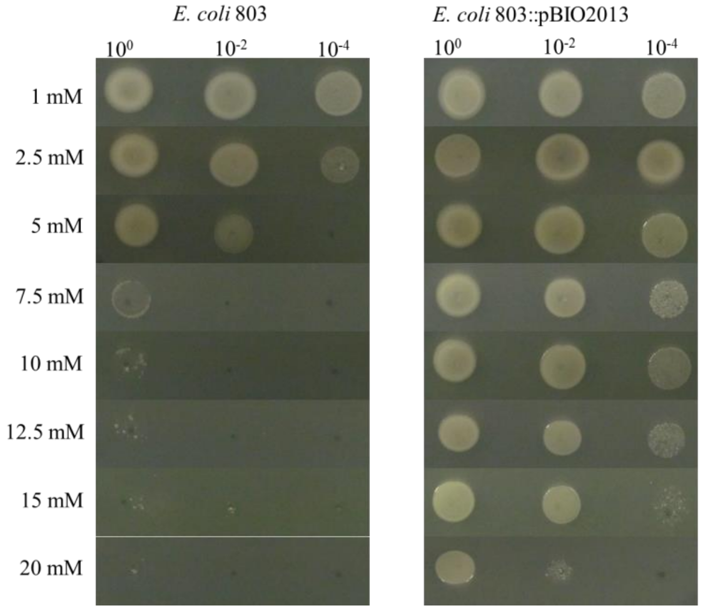
Having shown that AcuI conferred increased tolerance to acrylate and was required for growth of *Ruegeria pomeroyi* on this substrate, the effects of this gene product in other bacteria were investigated. Specifically, its effects in *Escherichia coli* were investigated, as follows.

5.2.4.1 Ectopically expressed AcuI confers acrylate resistance to *E. coli*

Primers SPO1913/14_BamR and SPO1914_NdeF were used to amplify a 1017 bp fragment containing the intact *R. pomeroyi* DSS-3 *acuI* gene (0 bp upstream of its start and 24bp downstream from its end). This was ligated into the over-expression vector, pET21a and the ligation mix was added to competent cells of *E. coli* 803, before plating for Amp^R (encoded by pET21a) transformants. These arose at *ca.* 1.0 x 10^3 cfu/ml and 6 of these were used for plasmid isolation. These plasmids were digested with *Bam*HI and *Nde*I to identify the appropriately sized insert. One of these, termed pBIO2013, was confirmed by DNA sequencing and was used to determine the effects of the cloned gene on acrylate tolerance in this heterologous host.

The *E. coli* 803::pBIO2013 strain and a control lacking the introduced plasmid were grown in LB broth to an OD_{600} nm of 1.0, serially diluted and spotted as 20 µl aliquots onto solid LB media amended with acrylate, (1 mM – 20 mM) and incubated for 24 hours at 37°C (Figure 5.5).

Figure 5.5 Effect of the cloned *acuI* gene of *Ruegeria pomeroyi* DSS-3 on the ability of *Escherichia coli* strain 803 to grow in the presence of acrylate



Cultures of wild type *E. coli* strain 803 with or without the cloned *acuI* gene from *R. pomeroyi* DSS-3, in pBIO2013, were grown in LB medium to an OD $_{600}$ nm of ~1.0. The cultures were serially diluted as indicated and 20 µL aliquots were spotted onto LB agar plates, supplemented with various levels of acrylate as indicated. Plates were incubated for 24 hours at 37^{0}C.

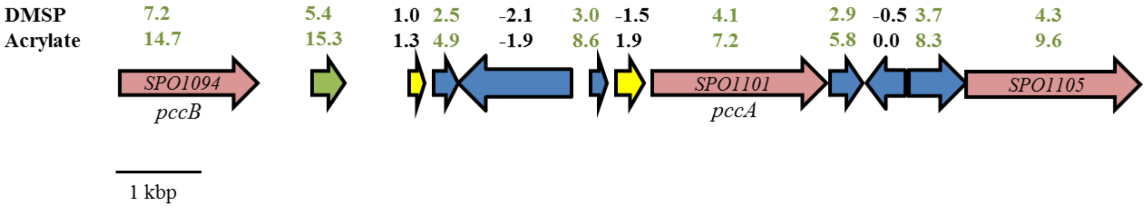
The wild type *E. coli* 803 cells showed signs of growth inhibition at 5 mM acrylate, whereas the presence of the cloned *acuI* gene in pBIO2013 made cells significantly more resistant (Figure 5.5). Cell extracts obtained from this strain were analysed by HPLC following incubation with acrylate, as in Sullivan *et al.* (2011) and Todd *et al.* (2010). The cultures of *E. coli* 803::pBIO2013 were grown overnight at 37°C in LB media, before diluting 10^{-2} into 1 ml M9 minimal medium containing 10 mM glycerol and 2.7 kBq [1- ^{14}C] acrylate, with unlabelled acrylate added to a final concentration of 2.5 mM. The cells were lysed and pelleted and the supernatant was resolved on a Dionex (Sunnyvale, CA, USA) ICE-AS6 HPLC column. The amount of acrylate dropped by 3-5% in both the wild type and pBIO2013 expressing cells. Also, no new peaks that might be attributed to a catabolite of acrylate, and mediated by the presence of the cloned *acuI* gene were seen (M J Sullivan, personal communication).

These observations resemble those of Sullivan *et al.* (2011) who were unable to detect a known catabolite released from acrylate by cell extracts of *Rhodobacter sphaeroides* 2.4.1, which harbours an AcuI homologue. Most importantly, Schneider *et al.*, (2012) showed that the AcuI of *Rhodobacter sphaeroides* 2.4.1. (the very same strain studied by Sullivan *et al.*, [2011]) could catalyse the reduction of acryloyl-CoA to propionyl-CoA. It is thought that acryloyl-CoA can act as a strong electrophile once inside the cell, making it a potentially toxic compound to any organisms that produce it (Herrmann *et al.*, 2005), and this is likely to explain the toxic effects of exogenous acrylate on AcuI$^-$ mutants.

5.2.4.2 Downstream catabolism of acryloyl-CoA

Assuming that AcuI has the same function in *Ruegeria* as in *Rhodobacter,* there must be a route by which propionyl-CoA can be further catabolised in these species. Interestingly this pathway relates directly to a cluster of several closely linked genes whose expression was much elevated by acrylate in the microarrays. As shown in Figure 5.6 and Figure 5.7 these genes were *SPO1094, SPO1101, SPO0932* and *SPO1105.*

Figure 5.6 The *SPO1094-SPO1105* region in *Ruegeria pomeroyi* DSS-3



Approximate scale provided. Arrows in red are confirmed to be involved in the catabolism of acrylate:

***SPO1094*, PccB propionyl-CoA carboxylase B sub-unit;**

***SPO1101*, PccA propionyl-CoA carboxylase A sub-unit;**

***SPO1105*, methylmalonyl-CoA mutase.**

Green arrow represents a hypothetical polypeptide containing a cupin domain.

Yellow arrows represent putative lipoproteins.

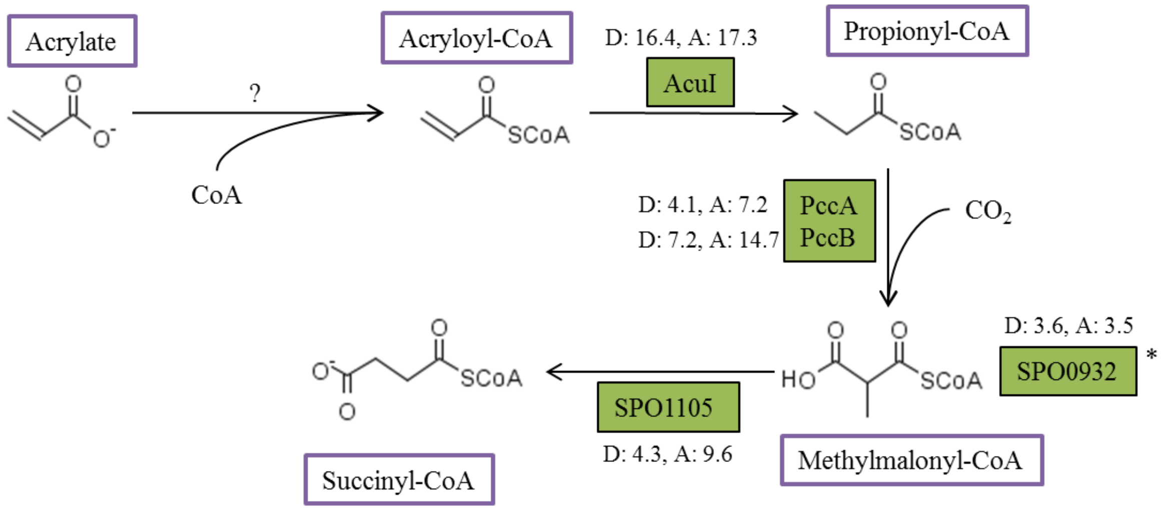
Blue arrows represent hypothetical gene products.

The regulation of each gene in the cluster by DMSP or acrylate is represented by the numbers above the genes, as indicated. Green text illustrates where there is a >2.5 fold increase in transcription over uninduced conditions.

Some of the genes that follow are only potentially (as indicated by a large variance or P-value >0.05) up-regulated in the presence of 5 mM DMSP or 2.5 mM acrylate, by up to *ca.* 15-fold. Three of these genes are strongly predicted to be involved in the conversion of propionyl-CoA to succinyl-CoA (see Figure 5.7).

The PccA and PccB gene products (encoded by *SPO1101* and *SPO1094*, respectively) are the two polypeptides in the heterodimeric enzyme propionyl carboxylase (EC 6.4.1.3), which is responsible for the conversion of propionyl-CoA to *S*-methylmalonyl-CoA. The SPO0932 (EC:5.1.99.1) gene product is annotated as a methylmalonyl-CoA epimerase, and this enzyme is responsible for the inter-conversion of the *R* and *S* forms of methylmalonyl-CoA (McCarthy *et al.*, 2001). Finally, the *SPO1105* gene encodes a methylmalonyl-CoA mutase (EC:5.4.99.2), which is responsible for the conversion of *R*-methylmalonyl-CoA to succinyl-CoA. This can then be incorporated into the citric acid cycle.

Figure 5.7 Acrylate catabolism via AcuI in *Ruegeria pomeroyi* DSS-3



A CoA group is first attached to acrylate to form acryloyl-CoA, mediated by an as-yet unknown enzyme (?). Acryloyl-CoA is reductively converted to propionyl-CoA by AcuI, and then carboxylated by the PccAB/SPO1101 heteromer to *S*-methylmalonyl-CoA. A predicted methylmalonyl epimerase, encoded by *SPO0932*, converts *S*-methylmalonyl-CoA to *R*-methylmalonyl-CoA (*). This is then acted upon by SPO1105, a methylmalonyl-CoA mutase (EC 5.4.99.2) to produce succinyl-CoA, which may be incorporated into central metabolism via the citric acid cycle.

Green boxes indicate that the genes encoding these enzymes are up-regulated in the presence of DMSP and acrylate, and the associated numbers are the fold change in expression over uninduced cells. D, DMSP; A, acrylate.

Gene numbers in *R. pomeroyi* DSS-3:

AcuI, SPO1914*;*

PccA, SPO1101*;*

PccB, SPO1094.

The gene product responsible for the initial transfer of a CoA group onto acrylate is unknown. However, an acetyl-CoA ligase (EC 6.2.1.1) from *E. coli* has been shown to exhibit low specificity, being capable of attaching CoA to acrylate and other substrate analogues (Patel and Walt, 1987). Thus, an orthologue of this gene in *R. pomeroyi* may act to carry out the initial step in this reaction.

Preliminary work by E Fowler (personal communication) has corroborated some of the microarray data. She showed that a *pccB-lacZ* transcriptional fusion was up-regulated *ca.* 4- and 7- fold in the presence of DMSP and acrylate, respectively, indicating that DMSP may have to be catabolised to acrylate to act as a co-inducer.

Importantly, she also made strains of *R. pomeroyi* with insertional mutations into the *pccA*, *pccB* and *SPO1105* genes and found that they were unable to grow on acrylate or, significantly, on DMSP as sole C source.

5.2.4.3 The *SPO1094-SPO1105* region

Despite encoding two sub-units of the same enzyme, the *pccA* and *pccB* genes are separated by several genes and large intergenic regions in *R. pomeroyi* (see Figure 5.6). These include 2 large apparently non-coding regions (~1kbp) between *SPO1094*, *SPO1095* and *SPO1096.* There are several genes encoding hypothetical proteins or lipoproteins. The two lipoproteins are encoded by *SPO1096* and *SPO1100.* SPO1096, at 45 amino acids long, has 41%-60% identity ($>e^{-9}$) to putative lipoproteins from other Roseobacter species only. The SPO1100 polypeptide has between 46%-60% identity ($>e^{-4}$) to lipoproteins from other Roseobacters also.

Two other genes that have at least some homology with proteins of known function, or contain known functional domains, are *SPO1095* and *SPO1098*. The *SPO1095* gene is predicted to be in a one-gene operon, with an intergenic region of approximately 1 kbp between its flanking genes (Figure 5.6). A BLASTp analysis retrieves weak homology to cupin domain-containing proteins sporadically distributed, such as in a SAR116 cluster bacterium (72%, 1e^{-37}) and *Azospirillum brasilense* Sp245 (66%, 9e^{-32}). Due to the possession of a cupin-containing domain like other DMSP lyases (DddL, DddQ and DddW – see introduction and chapter 4) and the induction by DMSP, an *E. coli* pET21a::*SPO1095* clone was created and tested for a Ddd$^+$ phenotype (J D Todd, personal communication). No DMS was produced when cells were amended with 5 mM DMSP overnight. However, in light of the recent findings that genes present in the same region have effects on acrylate metabolism, and this gene's increased expression in the presence of acrylate over DMSP, it would be worth revisiting this mutant in the future to assay its effect on acrylate and other related compounds.

Finally, the *SPO1098* gene encodes a hypothetical protein in *R. pomeroyi*, which has homologues in a few other Roseobacter species (>65% identity at the peptide level). There are also several considerably less well conserved matches (~26% identity, ~e^{-24}) in β and γ-proteobacteria, with most also being annotated as hypothetical. However, in one particular group of γ-proteobacteria, *Acinetobacter* spp., the homologues are annotated as DcaP-like proteins. In *Acinetobacter baumannii* AYE this gene product is described as a porin pre-cursor in catabolism of dicarboxylic acids (hence, DiCarboxylicAcid, DcaP). Porins allow the passive diffusion of hydrophilic molecules through the outer membrane (Benz and Bauer, 1988). The polypeptide was interrogated using the SignalP signal sequence search tool, and a signal peptide was predicted (mean value, 0.882), with a putative cleavage site at position 25. This implies that the gene product is indeed a porin-like protein. Interestingly, succinic acid is a dicarboxylic acid, so perhaps this relates to the other enzymes that are coded by genes in this cluster, converting propionyl-CoA to succinyl-CoA.

This unusual interruption of the propionyl-CoA carboxylase (PCC) genes is somewhat conserved between members of the Roseobacters, with a little variation. For example, *SPO1095* is only present in *R. pomeroyi.* One Genus in which the 3 "core" PCC genes are found clustered together with no interference is the α-proteobacterial *Brucella* spp. Perhaps this is indicative of their roles as progenitors for the genes found in the Roseobacters.

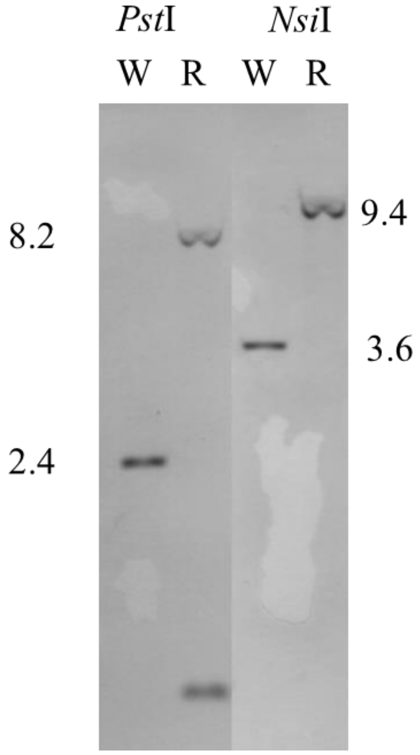
5.2.5 A putative *dmdA* regulator, SPO1912 (DmdR)

Separated by 222 bps from the translational start of *acuI* is the ATG of the divergently transcribed gene, *SPO1912* (now designated *dmdR*), which likely comprises a one-gene operon (Figure 5.1). The microarrays showed that the expression of *dmdR* was significantly induced by DMSP and acrylate, by 3.6 and 6.1-fold, respectively. The *dmdR* gene product belongs to the large family of GntR-like repressors, the originally named GntR being found in *Bacillus subtilis*, where it represses the *gnt* genes, unless relieved by addition of the co-inducer gluconate (Fujita and Fujita, 1987). These observations suggest that *dmdR* may be a regulatory gene, controlling the expression of the *dmdA*-*acuI* operon. Indeed, homologues of the *SPO1912* gene have been noted to exist upstream of 42% of *dmdA* homologues within the Roseobacter clade (Howard *et al.*, 2008).

5.2.5.1 Construction of a DmdR$^-$ mutant *R. pomeroyi* strain

To test the regulatory function of *dmdR*, an insertion mutation into the gene was created, in essentially the same way as had been done for the *acuI* and *dmdA* mutations (see above). In this case, primers SPO1912_EcoF and SPO1912_PstR were used to amplify a 682 bp fragment, internal to the *dmdR* gene, which was then cloned into the suicide plasmid pBIO1879 (see above, Figure 5.1), creating pBIO2085. This was mobilised into *R. pomeroyi* J470 via triparental mating, selecting for Rif^R/Spec^R/Kan^R. Transconjugants appeared following 2 days incubation (1.0 x 10^2 cfu/ml). Four of these were re-inoculated to fresh media and genomic DNA extracted. DNA was digested with *Pst*I and *Nsi*I and the *dmdR* PCR product was used as a probe for a Southern blot, as carried out for J471 and J527, above. This confirmed an insertion into *dmdR*, with the loss of the original *ca.* 2.4 kbp and *ca.* 3.6 kbp wild type fragments, and the appearance of mutated fragments at *ca.* 8.2 kbp and 9.4 kbp for *Pst*I and *Nsi*I digested DNA, respectively (Figure 5.8); the mutant, strain J530, was retained for further study.

Figure 5.8 Southern blot of a DmdR$^-$ mutant of *Ruegeria pomeroyi* J470



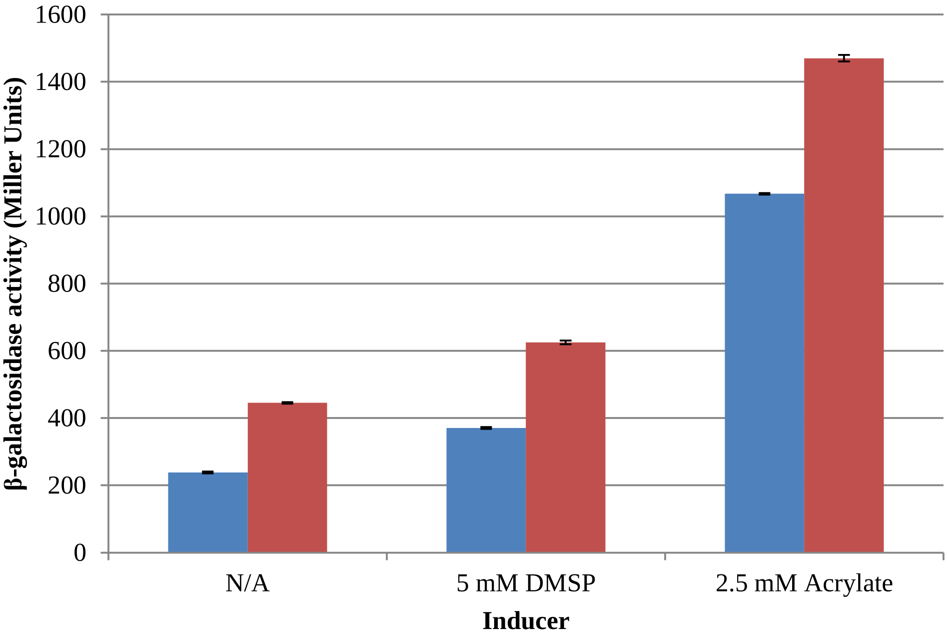
Genomic DNA samples from wild type (W) and a DmdR$^-$ mutant strain of *Ruegeria pomeroyi* J470 (R), were digested with *Pst*I or *Nsi*I and probed with the *dmdR* PCR product, amplified with primers SPO1912_EcoF and SPO1912_PstR. Numbers represent approximate DNA length in kilo base pairs (kbp) of the labelled bands. Note the larger 8.2 kb and 9.4 kb fragments in the DmdR$^-$ mutant, compared to the 2.4 kb and 3.6 kb wild type fragments, due to the insertion of the *ca.* 6 kb pBIO1879 plasmid into *dmdR*.

5.2.5.2 Effects of an insertion mutation into *dmdR* on expression of *acuI*

To determine whether a mutation in *dmdR* affected expression of the *dmdA-acuI* transcriptional unit, the *acuI-lacZ* fusion plasmid, pBIO2021, was conjugated via tri-parental mating into the newly created DmdR$^-$ *R. pomeroyi* (J530), selecting for Rif^R/Spec^R/Kan^R/Tet^R transconjugants. One of these was purified and cultures were grown in ½ YTSS medium to which either 5 mM DMSP or 2.5 mM acrylate had been added, with unsupplemented medium acting as the control. These cells were then assayed for β-galactosidase activity.

As shown in Figure 5.9, the mutation in *dmdR* had a little or no effect on the expression of the *acuI-lacZ* fusion compared to the wild type, under any of the growth conditions tested. Thus, DMSP and, to a greater extent, acrylate acted as co-inducers for the expression of the *acuI-lacZ* fusion and there was no evidence that DmdR was a positively or negatively acting transcriptional regulator.

Figure 5.9 Expression of an *acuI-lacZ* fusion in wild type and DmdR$^-$ mutant *Ruegeria pomeroyi* J470



Wild type *Ruegeria pomeroyi* J470 (blue bar) and the DmdR$^-$ mutant derivative J530 (red bar) containing the *acuI-lacZ* fusion plasmid pBIO2021 was grown in ½ YTSS medium (N/A) or in the same medium supplemented with 5 mM DMSP or 2.5 mM acrylate. Results of triplicate assays of β-galactosidase activities, in Miller Units, with standard error are shown.

5.2.5.3 The presence of a cloned *dmdR* gene affects expression of *dmdA-lacZ / acuI-lacZ* in the heterologous host*, Rhizobium leguminosarum*

Despite this result, preliminary work using *Rhizobium leguminosarum* indicated that DmdR may indeed act a transcriptional repressor of the *dmdA*-*lacZ* fusion (J D Todd, personal communication), in keeping with its homology to the GntR family of transcriptional repressors. This was shown by the fact that when the *dmdA*-*lacZ* and *acuI*-*lacZ* fusions were transferred to this heterologous host, both were expressed constitutively at high level. However when the cloned *dmdR* gene was also present, the expression of both fusions was substantially reduced by exposure of the *Rhizobium* cells to either DMSP or acrylate. Perhaps DmdR does indeed respond to these two molecules, but they may need to be converted to the *bona fide* co-inducer, perhaps by a function that is present in *Ruegeria* but not in *Rhizobium.*

5.2.5.4 MMPA also affects expression of *acuI-lacZ* in *R. pomeroyi*

Very recently, the effects of MMPA on the expression of the two fusions were examined in *Ruegeria pomeroyi* and it was found that an *acuI*-*lacZ* fusion was enhanced, *ca.* 10-fold in cells that were pre-grown in the presence of this molecule (J D Todd, personal communication) in *Ruegeria pomeroyi*. So, here is yet another example in which the product of DMSP catabolism may act as a co-inducer.

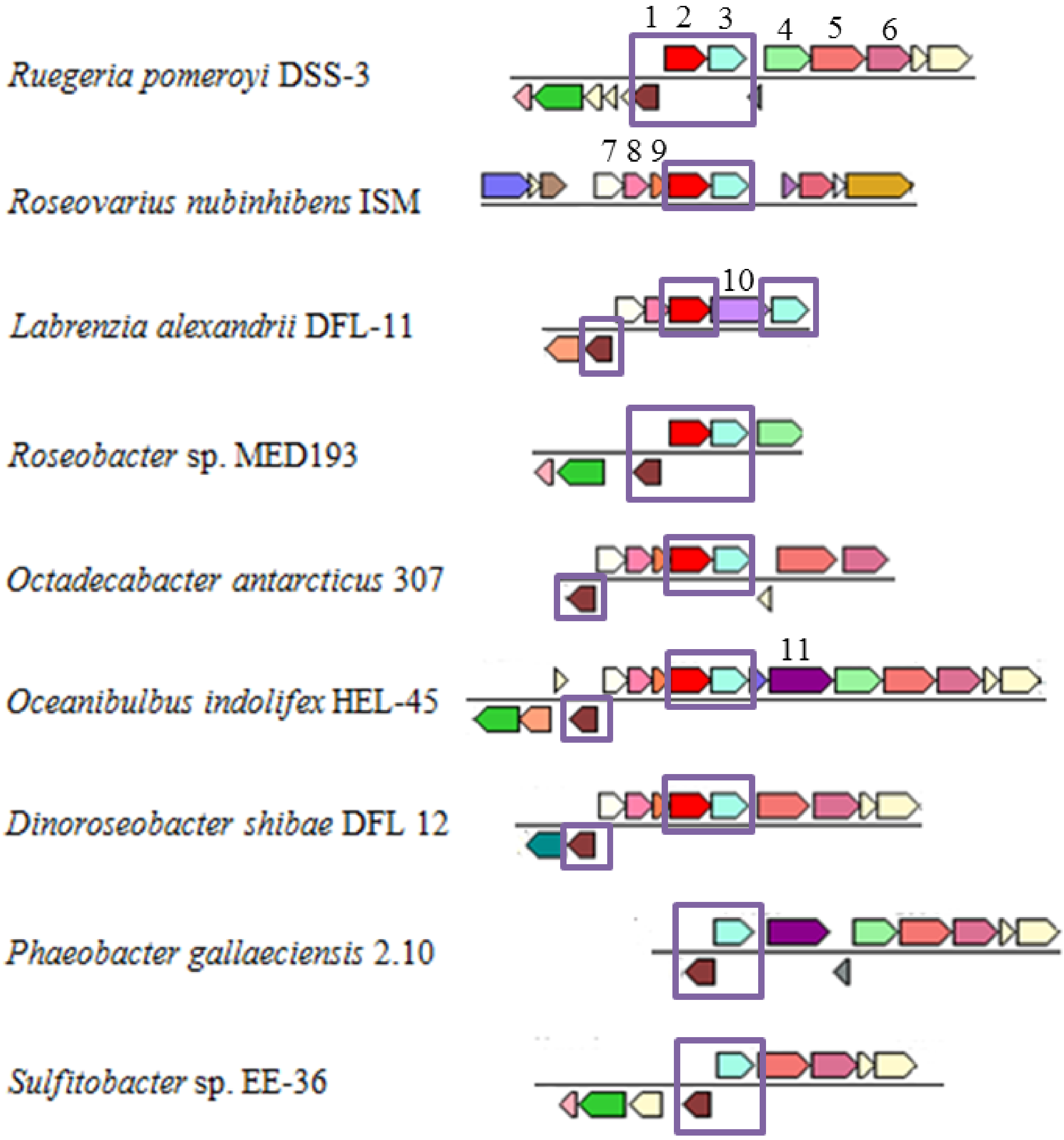
5.2.6 Distribution of the *dmdA* and *acuI* genes

It had already been well-established that the DmdA demethylase was widespread (though not universal) among the Roseobacters; of the 37 sequenced Roseobacter strains, 26 harbour a homologue of DmdA (see introduction; Howard *et al.,* 2006; 2008; 2011; Reisch *et al.,* 2008; Varaljay *et al.,* 2010). Additional homologues occur in the SAR11 and SAR116 Clades and one or two other γ- Proteobacteria. The *acuI* gene has been detected in all of the Roseobacter clade species, including *R. pomeroyi*, that contain *dmdA*. Close homologues (> 70% identical) of DmdR are found in many of the Roseobacters.

5.2.6.1 Close linkage of the *dmdA*, *acuI* and *dmdR* genes

The genes are nearly always closely linked, though there are differences in the precise genetic architecture, shown in figure 5.10.

Figure 5.10 Representative comparison of the *dmdA* and/or *acuI* regions



Gene homologues are indicated by coloured arrows. 1, DmdR; 2, DmdA; 3, AcuI; 4, aminotransferase; 5, PhrB deoxyribodipyrimidine photolyase; 6, cyclopropane-fatty-acyl-phospholipid synthase; 7, hypothetical protein; 8, hypothetical protein; 9, DinB family protein; 10, putative AMP-binding enzyme; 11, Betaine-Carnitine-Choline Transporter (BCCT family). The *dmdR*, *dmdA* and *acuI* homologues are highlighted by purple boxes. Created using IMG. (http://img.jgi.doe.gov)

Dinoroseobacter shibae DFL12 and *Sulfitobacter* sp. EE-36 harbour intervening genes between the *dmdR* and *dmdA* genes, or no *dmdA* gene at all, respectively. Of the genomes analysed, there were a few cases, such as *P. gallaeciensis* 2.10, in which *dmdR-acuI* were divergently transcribed from one another without *dmdA*, but none in which *dmdR-dmdA* were found without *acuI*. In one case, in *Roseovarius nubinhibens* ISM, a homologue of *dmdR* was not detected at all, having only the *dmdA-acuI* gene pair.

5.2.6.2 Other notable genes present in regions containing *dmdR/dmdA/acuI*

It was noted that two of the repeatedly encountered genes in the *dmdR/dmdA/acuI* clusters were concerned with DNA repair. Thus, *dinB,* found in *Oceanibulbus indolifex* HEL-45 and *Dinoroseobacter shibae* DFL 12 encodes a DNA polymerase that is important in protection from UV-induced mutagenesis in *E. coli* (Wagner *et al.,* 1999). The *phrB* gene, found in *Ruegeria pomeroyi* DSS-3 and *Octadecabacter anarcticus* 307 encodes a deoxyribodipyrimidine photolyase (EC 4.1.99.3), involved in the repair of pyrimidine dimers that occur from UV radiation (Dorrell *et al.,* 1993). With DMSP catabolising bacteria proliferating mainly in response to events such as phytoplankton blooms, there will be a significant chance that the cells utilising DMSP will be exposed to high levels of UV radiation in ocean surface waters. Indeed, Sunda *et al.,* (2002) found that UV radiation actually increased cellular DMSP and its lysis to DMS in marine algal cultures. Thus, pairing systems for UV induced DNA repair with genes involved in catabolism of a likely substrate seems evolutionarily advantageous (Levine *et al.,* 2012).

Another gene in proximity to the *dmdA-acuI* genes is a BetT BCCT family choline transporter. The DddT DMSP transporter identified from *Halomonas* HTNK1 and *Marinomonas* MWYL1 (see introduction; Todd *et al.,* 2007; Sun *et al.,* 2011) is a member of this family, so the presence of another BCCT gene near DMSP catabolic genes is enticing.

The other main group of *dmdA*-containing bacteria, *Candidatus* Pelagibacter spp. are different. It is not known why, but they do not have Ddd enzymes so do not encounter acrylate as is the case for the Roseobacters. However, all three genome-sequenced strains of Pelagibacter have homologues of AcuI (~40% identity at the peptide level to the *Rhodobacter sphaeroides* AcuI), but none is closely linked to *dmdA* (Todd *et al.*, 2012b).

5.3 Conclusion

The work described in this chapter has greatly enhanced our understanding of a gene that was, at one point, considered peripheral to the activities of *dmdA* (Howard *et al.*, 2008). Instead, *R. pomeroyi* harbours two genes, *dmdA* and *acuI*, each responsible for the activities of a different DMSP catabolic pathway, in a co-transcribed, co-regulated operon, pointing to an unexpected link between the demethylation and lyase pathways – considered more fully in Chapter 7.

5.3.1 Future work

Much work remains to fully reveal the complexity of this system, including:

1. Investigate the actions, if any of the DmdR regulator, and identify the *bona fide* cognate co-inducer molecule and its gene targets.
2. The activity of the accessory genes surrounding, and interrupting, the *dmdR-dmdA-acuI* operon could be established in regards to DMSP metabolism.

Chapter 6

Effects of DMSP, acrylate and DMS on the expression of selected genes involved in DMSP, methane thiol and carbon monoxide metabolism

6.1 Introduction

Previous chapters described genes that are directly related to the catabolism of DMSP (e.g. *dddW*, *dmdA*) or acrylate (*acuI, pccA, pccB, SPO0932, SPO1105*) in *Ruegeria pomeroyi* DSS-3. In many cases, the expression of these genes was affected by the addition of DMSP, and/or acrylate and/or other metabolically related compounds, as revealed by the microarrays. But, in addition to those genes whose products act directly on DMSP, or acrylate or some immediate downstream catabolites, several other metabolic pathways impinge (or have been proposed to impinge) on DMSP catabolism.

In this chapter, the microarray-based expression of a selection of the other genes that are predicted (though not ratified) by MetaCyc or KEGG (Caspi *et al.*, 2012; http://www.genome.jp/kegg/) to encode some of the enzymes in these “side” reactions is presented, and the implications of their differential expression are discussed.

By their very nature, microarrays are data-heavy. In this study, there were 3 separate growth conditions. This, in conjunction with the 4,252 genes present in the *Ruegeria pomeroyi* DSS-3 genome, resulted in the generation of 12,756 data points, rather too many to interpret for a single thesis. Therefore, in what follows, I will focus only on those cases that satisfy one or more of the following criteria:

1. A large difference in expression, >10 fold between one or more of the treatments
2. A predicted link with DMSP or DMS catabolism
3. Co-regulation of more than one, and ideally all, the genes in a predicted operon
4. And, in some cases, ratification of microarray data by the use of *lacZ* transcriptional fusions

There are some other caveats attached to these analyses, which represent a highly selective sample within the genome-wide response. Firstly, few pathways under consideration here have been verified by direct biochemical studies in *Ruegeria*, or indeed in any Roseobacter strain. Secondly, the approach relies heavily on the correctness of the microarray data, since, in some cases, no other criteria (e.g. qRT-PCR or β-galactosidase assays) were used to confirm the differential levels of expression that were recorded in the microarrays. This may have been due to a number of factors; difficulties in creating *lacZ* transcriptional fusions, the rapid focus onto AcuI over all else, the isolation of a gene from other genes of interest, no predicted function, lack of regulation of other genes in a putative operon, or highly variable microarray data (see chapter 3).

Despite these reservations, the genes discussed in this chapter help build a more complete picture of DMSP catabolism in *Ruegeria pomeroyi*, and in one particular case, open up avenues of research that were never expected.

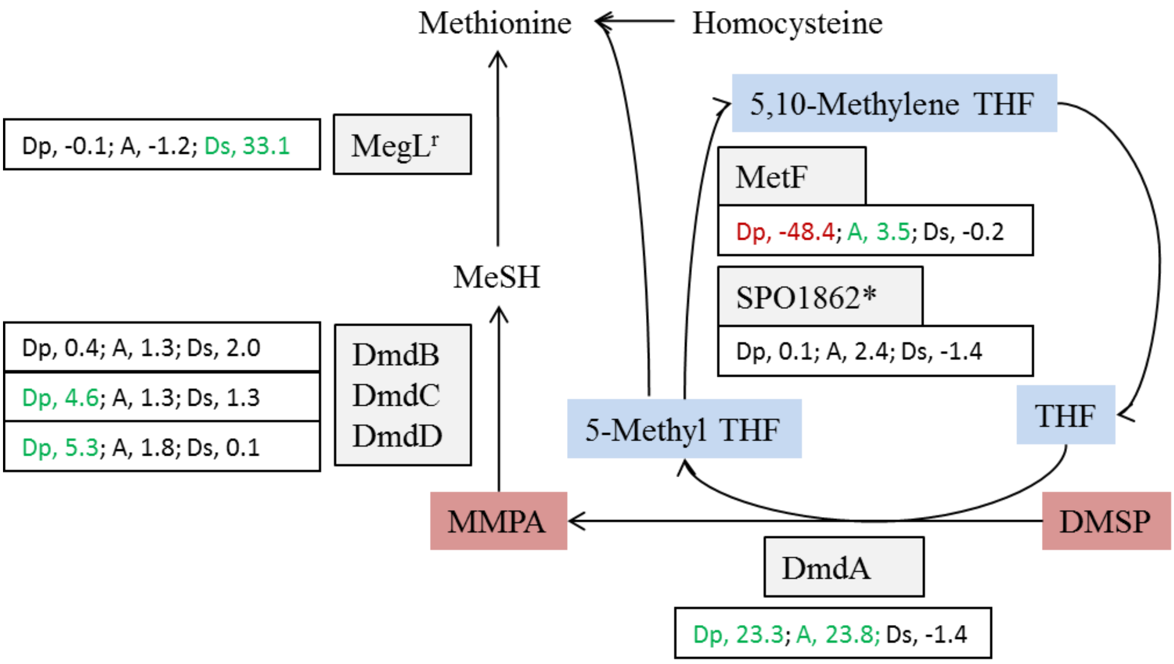
6.2 Results

6.2.1 Genes linked to THF and/or methionine

6.2.1.1 The MetF-like enzymes, SPO3016 and SPO1862

The *SPO3016* and *SPO1862* genes have potentially close links to the recycling of the tetrahydrofolate (THF) cofactor that acts as a receptor of one-carbon units from donor molecules, including methyl groups during DMSP demethylation. This has connections to methionine biosynthesis, and the interactions of the relevant gene products are summarised in Figure 6.1.

Figure 6.1 DMSP demethylation and tetrahydrofolate recycling



Gene products are highlighted grey. Fold change in expression, as shown by the microarray data, is given next to each protein: Dp, DMSP; A, acrylate; Ds, DMS. Light blue boxes highlight the various intermediate forms of the co-factor, tetrahydrofolate (THF). Red boxes indicate DMSP and its catabolic product, MMPA, released by demethylation.

*** indicates that transposon disruption of the gene affected DMSP dependent MeSH production (Bürgmann *et al.*, 2007). ^{r} indicates a hypothesized reversal of the direction of the reaction compared to that which is normally annotated for the function of this gene.**

DmdA: DMSP demethylase, SPO1913; DmdB: MMPA-CoA ligase, SPO2045; DmdC: MMPA-CoA dehydrogenase, SPO3804; DmdD: methylthioacryloyl-CoA hydratase, SPO3805;

MetF: 5,10-methylene-THF reductase, SPO3016; SPO1862: MetF-like enzyme;

MegL: methionine γ lyase, SPOA0318.

Adapted from Bürgmann *et al.*, 2007; Reisch *et al.*, 2011a.

In *R. pomeroyi,* it was recently found that the methyl group from DMSP is transferred to THF, to form 5-methyl-THF, as shown in figure 6.1 (Schuller *et al.*, 2012). The production of 5-methyl-THF by glycine cleavage T-proteins (the family to which DmdA belongs – see introduction, chapter 5) is highly unusual and, indeed, had not been previously reported. Rather, the methylated folate products normally take the form of 5,10-methylene-THF (Schübert *et al.,* 2003; Schuller *et al.,* 2012).

Bürgmann *et al.*, (2007) noted that a mutation in a gene, *SPO1862*, abolished DMSP-dependent MeSH production in *R. pomeroyi*, but MMPA-dependent MeSH production remained intact. The gene product was annotated as a MetF-like protein, with the canonical MetF (encoded by *SPO3016* in *R. pomeroyi*) being a predicted 5,10-methylene-THF reductase (E.C. 1.5.1.20). The MetF enzyme catalyses the reversible conversion of 5,10-methylene-THF to 5-methyl-THF (Figure 6.1), which may then be used by methionine γ-lyase to convert homocysteine to methionine (Matthews *et al.*, 1998). The product of the *SPO1862* gene is only 29% identical (with a rather high E value of $2e^{-7}$, over only 162/300 amino acid sequence coverage) to the SPO3016 polypeptide, and the gene encoding this protein was not induced notably in the microarray under any conditions used here. However, the *SPO3016* gene was down-regulated, 48.4-fold in the +DMSP medium, but was up-regulated, 3.5-fold, in acrylate. The *SPO3016* gene product is 43% identical ($E = 1e^{-83}$) to the canonical MetF enzyme in *E. coli* K12 and contains a well-conserved methylene-THF reductase domain ($E = 8.6e^{-91}$). Nearly all of the sequenced Roseobacters contained a gene product that was very similar (>51% identity).

A possible explanation for this regulation is as follows. The MetF (SPO3016) is down-regulated in DMSP, causing accumulation of 5-methyl-THF, a by-product of DmdA-mediated DMSP demethylation. This cofactor would then be available for the methylation of homocysteine to form methionine, and methionine has been shown to repress *metF* in *S. typhimurium* (Cowan *et al.,* 1993).Thus, MetF might mediate a negative feedback loop via the action of DmdA. The phenotype observed in the $SPO1862^-$ mutant strain may relate to a similar function to MetF, involving the cycling of THF.

6.2.1.2 The methionine γ-lyase, SPOA0318

The *SPOA0318* gene, located on the *R. pomeroyi* DSS-3 megaplasmid, was markedly enhanced (59.6-fold) in one set of data, and slightly enhanced (6.5-fold) in another set, in the presence of DMS, but not of DMSP or acrylate. The gene encodes a protein with a conserved methionine γ-lyase (EC 4.4.1.11) domain (E = 0.0). This enzyme catalyses the conversion of methionine to MeSH and 2-oxobutanoate, in many *Enterobacteriaceae* (Manukhov *et al.,* 2005). The MegL, methionine γ-lyase is an important connection between methionine synthesis and DMSP catabolism, indicated in Figure 6.1. The expression of this gene should be examined by *lacZ* fusions to ascertain whether DMSP is a true inducer or not, as this would fit perfectly with the predicted role it plays.

6.2.1.3 The trimethylamine methyltransferase-like SPO2134

The *SPO2134* gene, located in a single gene unit, was up-regulated 49-fold in the presence of DMSP. This gene encodes a putative trimethylamine methyltransferase (EC 2.1.1.-), with a highly conserved MTTB domain (E = $2.28e^{-147}$). The SPO2134 protein shares 30% identity at the peptide level with the MttB from the archaeon, *Methanosarcina barkeri* (E = $3e^{-53}$). In methanogens such as *Methanosarcina barkeri,* the MttB enzyme catalyses the conversion of trimethylamine to dimethylamine, transferring the methyl group onto a corrinoid protein, Coenzyme M (Paul *et al.,* 2000). The enzymes involved in methionine biosynthesis contain corrinoid domains and utilise the simultaneous binding of a corrinoid, THF and homocysteine to transfer the methyl moiety between intermediates, to form methionine (Matthews *et al.,* 2008). Thus, the MttB-like enzyme in *R. pomeroyi* may play a role in transferring methyl groups between corrinoid proteins for use in methionine biosynthesis, but its function is unknown at present. However, the catabolism of DMSP through to methionine is certainly allusive of this function.

6.2.2 SPO0759

Another gene that was up-regulated by 10.6-fold and 23.6-fold in DMSP and acrylate, respectively, was *SPO0759*. This gene was also down-regulated in the presence of DMS by 3.8-fold. However, the gene encodes a short (107 amino acid) peptide that has no predicted function, with only a few weak homologues (<57% identity, low sequence coverage and $E>5e^{-12}$) in other α-proteobacteria. Nearby genes include an acetyl-CoA acetyltransferase (*SPO0758*) and a 4-carboxymuconolactone carboxylase domain containing gene (*SPO0760*). However, none of the neighbouring genes is conserved between species.

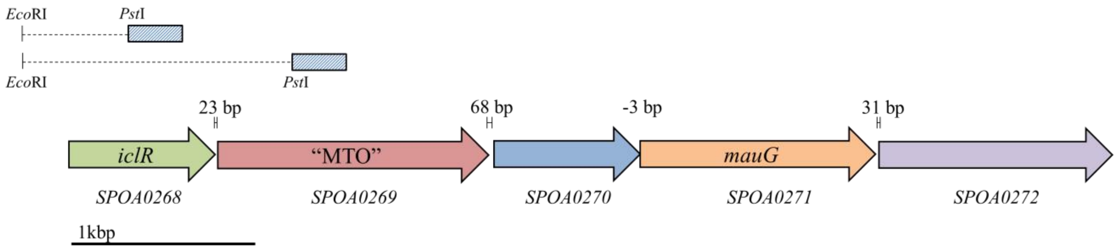
6.2.3 Ratified DMSP-regulated genes

Following discussion of the genes that had no further experimental evidence for their role in DMSP catabolism, I will discuss two sets of genes that were discovered from the microarray that have been ratified in some way. They have less direct connections to DMSP catabolism. Indeed, the latter set is a complete surprise, with no obvious connection to the pathways described up until this point.

6.2.3.1 Methane thiol oxidase genes

A cluster of genes on the resident megaplasmid was up-regulated by DMSP (*ca.* 2-8 fold increases, but with large variance). A DOOR analysis (Mao *et al.*, 2008) predicted two separate operons, comprising *SPOA0268-9* and *SPOA0270-2* (Figure 6.2).

Figure 6.2 The *SPOA0268-SPOA0272* region of *Ruegeria pomeroyi* DSS-3



Scale indicated. Gene names and/or numbers are shown. Sizes of intergenic regions are shown in base pairs (bp). Dashed lines indicate the dimensions cloned to form the *lacZ* transcriptional fusions of *SPOA0268* and *SPOA0269*, with blue boxes representing the *lacZ* junction (J D Todd, unpublished data). MTO, methane thiol oxidase.

Despite these weakly convincing microarray data, subsequent experimental validation confirmed that at least one of these operons was indeed induced by DMSP. J D Todd (Personal communication) constructed a *SPOA0269-lacZ* fusion plasmid (containing an intact *SPOA0268* gene, with its putative promoter, and the 5' region of *SPOA0269*-Figure 6.2) and found that its expression was increased, ~10-fold in DMSP-grown cells.

The *SPOA0269* gene is thought to encode a methane thiol oxidase (MTO) which is 54% identical to the corresponding Hden_0743 gene product in *Hyphomicrobium* (J D Todd, personal communication). MTO catalyses the reversible conversion of MeSH to formaldehyde, as discovered by Suylen *et al.*, 1987:

$$\mathrm{MeSH} + \mathrm{H_2O} + \mathrm{O_2} \Leftrightarrow \mathrm{CHO} + \mathrm{H_2O_2} + \mathrm{H_2S}$$

DMSP catabolism in *R. pomeroyi* leads to the production of MeSH through DMSP demethylation and possibly DMSP cleavage, so it was decided to test the effects of MeSH itself as a co-inducer. It was found that pre-growth in MeSH of *Ruegeria pomeroyi* containing the *SPOA0269-lacZ* plasmid did indeed induce expression of the fusion, but the ratio of increase was rather less than with DMSP (see above) indicating that the effect of DMSP was not mediated by its conversion to MeSH.

The related function of the neighbouring genes supports the role of SPOA0269 as a MTO, as it would act to shuttle the formaldehyde produced by the associated enzymes into less toxic intermediates. Several of the genes in this region encode hypothetical proteins, but annotated examples include SPOA0268 as an IclR transcriptional regulator, SPOA0271 as MauG, a methylamine utilisation protein, and SPOA0272 as a glutathione dependent formaldehyde dehydrogenase. The IclR family regulators are diverse, controlling the expression of genes involved in carbon metabolism, aromatic compound degradation and solvent tolerance, to name but a few (Krell *et al.*, 2006). MauG assists in maturation of the methylamine dehydrogenase required to convert formaldehyde to methylamine (van der Palen *et al.*, 1995) and SPOA0272 is a predicted *S*-(hydroxymethyl)-glutathione dehydrogenase (EC 1.1.1.284), carrying out the reaction of *S*-hydroxy-methyl-glutathione to *S*-formyl-glutathione, as described in *Rhodobacter sphaeroides* (Barber *et al.*, 1996). *S*-hydroxy-methyl-glutathione is the spontaneous product of glutathione and formaldehyde.

To investigate the role of the IclR-like regulator, J D Todd created a transcriptional fusion to the promoter region of *SPOA0268*, this time omitting the intact *SPOA0268* gene (Figure 6.2). When expressed in *Rhizobium leguminosarum* J391, the *SPOA0268-lacZ* fusion plasmid was constitutively expressed under all conditions, at *ca.* 900 Miller Units, compared to *ca.* 100 Miller Units for the *SPOA0269-lacZ* fusion, which raised to *ca.* 400 Miller units in the presence of MeSH. Therefore, SPOA0268 is a MeSH dependent repressor of the MTO in *Ruegeria pomeroyi*. A number of investigations remain, including confirming the operonic structure of this gene cluster and assaying the *Rhizobium* for MeSH removal.

6.2.3.2 Novel DMS dependent regulation of *cox* genes for carbon monoxide oxidation

In addition to those genes with some connection with DMSP and DMS catabolism or formation, the microarrays revealed some wholly unexpected sets of genes with no known link to these compounds, yet whose expression was massively affected by DMS. Among these, the *cox* genes, involved in carbon monoxide catabolism, are described here.

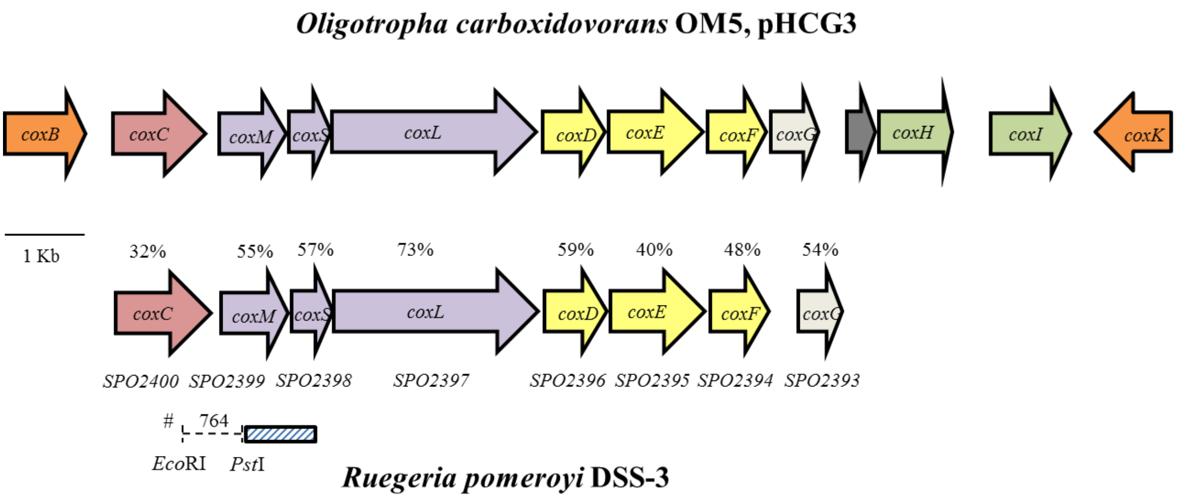
In total, a set of 7 contiguous *R. pomeroyi cox* genes, *SPO2399*- *SPO2393* inclusive, were markedly up-regulated in response to DMS addition, the factors of increase of the individual genes ranging from a remarkable 80.1-fold (*coxM – SPO2399*) to 3.5-fold (*coxE – SPO2395*), as summarised in figure 6.3 and table 6.1. To confirm this totally unexpected finding, a transcriptional fusion plasmid was made, in which *lacZ* was fused to the *coxM* (*SPO2399*) in a manner similar to those described in chapters 4 and 5. Thus, primers *SPO2399*_ecoRIF and *SPO2399_Pst*IR were used to amplify a 760 bp fragment that spanned the 3' end of the upstream gene, *coxC,* the *coxC-coxM* intergenic gap and the 5' end of *coxM* (Figure 6.3). Plausible promoter sites had been identified 58 nucleotides upstream of *coxM* in a highly similar cluster in another bacterium, *O. carboxidovorans* (see below; Santiago *et al.*, 1999) and so this fragment was predicted to contain the *coxM* promoter. The fragment was PCR-amplified from *Ruegeria pomeroyi* J470 genomic DNA, and cloned into the *lacZ* reporter plasmid, pBIO1878 (Figure 6.3). The resultant recombinant plasmid was introduced into *E. coli* 803 and transformants arose at a frequency of ~5 x10^3 cfu/ml. Six colonies were selected for analytical digestions using *Eco*RI and *Pst*I, with the plasmid DNA from one of the transformants that contained an insert of the expected size being sent for DNA sequencing to confirm that the correct fragment had been cloned. This plasmid, pBIO2086, was then introduced in a triparental mating from the *E. coli* host into *Ruegeria pomeroyi* J470 as a recipient. A purified transconjugant was then grown overnight in MBM minimal media, before splitting the culture, with one aliquot being grown for a further 5 hours in the presence of 10 mM DMS and the other being used as the control. The β-galactosidase activity was *ca.* 4-fold greater in the cultures exposed to DMS than in the control, consistent with the microarray data. The absolute level of β-galactosidase activity itself was quite low, at 145 ± 2

Miller Units for +DMS conditions, 35 ± 10 Miller Units for un-induced. Nevertheless, it was confirmed that at least one of the *cox* genes is induced in DMS-grown cells.

6.2.3.3 The *cox* gene cluster in *Ruegeria pomeroyi* and *Oligotropha carboxidovorans*

The *cox* genes have been studied in most detail in another α-proteobacterium, *Oligotropha carboxidovorans* OM5 (Meyer *et al.*, 1993). As shown in Figure 6.3, there is remarkable conservation of the *cox* gene order and of the sequences of the Cox gene products in *O. carboxidovorans* and in *R. pomeroyi.*

Figure 6.3 The *cox* gene clusters of *Oligotropha carboxidovorans* OM5 (pHCG3) and *Ruegeria pomeroyi* DSS-3



Scale bar given. Gene names given, with gene numbers for *R. pomeroyi* provided below arrows. Coloured arrows indicate known or predicted gene functions: red, putatively regulatory; purple, CO dehydrogenase enzyme; yellow, maturation; green, cytoplasmic; orange, putative trans-membrane; light grey, unknown; dark grey, pseudogene. The %age identities between the gene products in the two bacteria are shown between genes. # indicates region used to create pBIO2087, with the blue striped bar indicating fusion to the *lacZ* .

By a mixture of biochemistry and genetics it had been shown for *O. carboxidovorans* that the carbon monoxide dehydrogenase (CODH) enzyme itself is a heterotrimer, consisting of: CoxL, the large subunit; CoxM, the medium, FAD-containing polypeptide; and CoxS, the small subunit, which contains an FeS cluster; these are encoded by the corresponding genes *coxL, coxM* and *coxS*. Other Cox polypeptides (CoxD, CoxE and CoxF) are also required for the ability of CODH to oxidise CO to CO_2 and may be involved in some form of "maturation" of the enzyme. This may involve the correct insertion of a Mo-containing co-factor that is found in CODH, and also in the related enzymes aldehyde oxidase and xanthine dehydrogenase (Pelzmann *et al.,* 2009). There is also a *coxG* gene following *coxDEF*. A $CoxG^-$ mutant strain of *O. carboxidovorans* retained CO oxidising activity, however, so it is not clear why this should be called a *cox* gene (Schübel *et al.*, 1995; Santiago *et al.*, 1999).

There are striking similarities with the arrangement and composition of the gene clusters, and a high level of sequence conservation of the polypeptides in the two species, ranging from 32% to 73% identity. However, there are also some significant differences in the Cox systems of *Ruegeria pomeroyi* and *O. carboxidovorans,* as follows.

Many Roseobacters, such as *R. pomeroyi,* lack the ribulose-1,5-bisphosphate carboxylase/oxygenase required for carbon fixation, so cannot assimilate it (Moran *et al.,* 2004; Tolli *et al.,* 2006; Newton *et al.,* 2010). Also, these Roseobacters lack a homologue of an unusual, carbon monoxide-resistant cytochrome b_{561}, which allows *O. carboxidovorans* OM5 to respire even in the presence of CO. CODH generates a proton gradient by channelling electrons into a CO-insensitive respiratory chain from this cytochrome (Meyer *et al.,* 1990). The combination of these genes allows the organism to grow with H_2 plus CO_2 under chemolithoautotrophic conditions (Santiago and Meyer, 1997), but Roseobacters cannot. However, it is thought that the Roseobacter species may use CO as a potential supplementary energy source, providing some reducing equivalents and perhaps accounting for the widespread distribution of the *cox* genes in this clade (Moran *et al.*, 2004; 2007; Newton *et al.*, 2010; Cunliffe, 2010).

The *R. pomeroyi cox* gene cluster itself lacks several genes, namely *coxB, coxH, coxI* and *coxJ,* that *O. carboxidovorans* harbours (see Figure 6.3). The CoxHI proteins are thought to be involved in interaction of the CODH with the cytoplasmic membrane in *O. carboxidovorans* (Meyer *et al.,* 1990). No homologues of *coxHI* were detected within the Roseobacter Clade, and this fits with the absence of any proteins that require a proton gradient to be maintained between the CODH and the cytoplasmic membrane (see above). The CoxB and CoxK enzymes have no confirmed function at present, and are merely labelled as putative transmembrane proteins. A summary of these gene products is given in Table 6.1.

Table 6.1 Comparison of *cox* genes from *Oligotropha carboxidovorans* and *Ruegeria pomeroyi*

Gene[a]	**Predicted function of gene product**[b]	**Identity to *R. pomeroyi* homologue, *E* value**[c]	**Factor of DMS Induction**[d]
coxB	Putative transmembrane protein	No significant match in *R. pomeroyi* genome	-
coxC	Transcriptional regulator	SPO2400, 32%, 6e^{-54}	0.2
coxM	CODH medium subunit	SPO2399, 55%, 6e^{-108}	80.1
coxS	CODH small subunit	SPO2398, 57%, 3e^{-67}	31.9
coxL	CODH large subunit	SPO2397, 73%, 0.0	21.2
coxD	CODH active site maturation	SPO2396, 59%, 4e^{-112}	16.9
coxE	CODH active site maturation	SPO2395, 40%, 8e^{-91}	3.5
coxF	CODH active site maturation	SPO2394, 48%, 6e^{-78}	8.0
coxG	Unknown	SPO2393, 54%, 2e^{-42}	7.3
coxH	Possible interaction with cytoplasmic membrane	CoxC, 27%, 9e^{-16}	-
coxI	Interaction with cytoplasmic membrane	SPO2640[#] , 31%, 3e^{-38}	-
coxK	Putative transmembrane protein	No significant match in *R. pomeroyi* genome	-
lon*	Regulatory protease	SPO2613, 69%, 0.0	-

Name of gene in *Oligotropha carboxidovorans* OM5, column (a), predicted protein function (b), homology between peptides from *R. pomeroyi* and *O. carboxidovorans* OM5 (Locus tag, % identity and e value) (c) and -fold induction by DMS (d) are given. The SPO2640 ($^{\#}$) protein shares low identity with CoxI and the gene is not located in the *cox* operon. The *lon* gene (*) is not in the *cox* gene cluster (Santiago *et al.,* 1999). Grey-shaded entries indicate the genes in the *cox* cluster in *R. pomeroyi*.

6.2.3.4 Carbon monoxide dehydrogenase (CODH) activity

Despite these differences, it is nevertheless clear that the *cox* genes identified here in *Ruegeria* are critical for CODH activity. Recent work by S Newton-Payne (personal communication) isolated a SPO2397^{-} (CoxL) mutant and M Cunliffe (personal communication) showed that it was unable to oxidise CO to CO_2. However, in initial experiments, there was no evidence that pre-growth of *R. pomeroyi* in DMS-containing medium caused any increase of the actual CODH activity, as measured by the removal of CO that had been added to the cultures (M Cunliffe, personal communication). Interestingly, CODH activity is not induced by the substrate CO itself in *R. pomeroyi* (Johnson *et al.,* 2007), whereas in *O. carboxidovorans* CO does act as a co-inducer of the *cox* genes, but these are repressed if other carbon sources are available (Santiago *et al.,* 1999).

6.2.3.5 A *cox* cluster regulator

From its location relative to the structural *cox* genes, *coxC* is an *a priori* candidate for a *cox* regulatory protein. A BLASTp analysis of CoxC showed that it has two identifiable domains. The N-terminal signalling domain, contains two trans-membrane helices and is weakly predicted ($E = 2.3e^{-7}$) to be in the MHYT superfamily. It was proposed that this domain senses an exogenous signal, with some members of the family having been shown to respond to Cu or NO (Galperin *et al.,* 2001). The other, C-terminal domain, is in the LytTR superfamily ($E = 3.32e^{-21}$) of non-helix-turn-helix DNA-binding domains found in a variety of bacterial transcriptional regulators (Galperin, 2008). Experimental evidence shows that polypeptides possessing LytTR domains act as transcriptional activators, and often exist in two-component response regulator systems (Gao *et al.,* 2007; Galperin *et al.,* 2008).

There are also conserved homologues of *R. pomeroyi coxC* gene products in 12 other Roseobacter genomes, (>42% identity, $E < 3e^{-82}$), several *Bradyrhizobium* spp. (~30% identity) and *Sinorhizobium meliloti* strains (~28%), in the same locations relative to the other *cox* genes. This implies a similar (regulatory?) role for this gene in a range of different CO-oxidising bacteria, even those with no known link to DMS, as in *Bradyrhizobium* spp. It should be noted that the CoxC protein was the least conserved of all the Cox peptides, with only 32% identity, perhaps implying divergent functions in the different species.

There may well be another regulatory protein involved in the control of this gene cluster, namely the Lon protease which is encoded by the *lon* gene. This is located on the 133 kbp megaplasmid (pHCG3) of *O. carboxidovorans* OM5 (Santiago and Meyer, 1997; Santiago *et al.,* 1999; Fuhrmann *et al.,* 2003), as is the *cox* gene cluster and the ancillary *cbb* and *hox* genes for CO respiration. The Lon protein is an ATP-dependent serine protease, present throughout all life forms, with targets including the regulatory proteins such as the transcriptional activator, SoxS (Chung and Goldberg, 1981; Shah and Wolf, 2006). Mutations in the *lon* gene in pHCG3 abolished growth on CO (Santiago and Meyer, 1997; Santiago *et al.,* 1999). A BLASTp of the Lon protein from *O. carboxidovorans* retrieved a homologue (SPO2613) in *R. pomeroyi* with 69% identity at the peptide level (E = 0.0). In *R. pomeroyi,* the *lon* gene orthologue is induced by 2.2-fold by DMS, but not by any other co-inducer tested.

It is striking that several bacteria, such as *Bradyrhizobium,* as well as the model *Oligotropha* itself are almost certainly never exposed to DMS, yet, these too contain the strongly predicted CoxC and Lon regulators. Although unlikely, it needs to be established if a similar induction of their *cox* genes is also mediated by exposure to DMS. If so, then this suggests that this observation is some sort of chance molecular aberration, with no adaptive value. But, if

DMS-dependent induction of the *cox* operon is found only in the Roseobacters, then this points to some sort of functionality, and would prompt a search for the mechanism(s) involved.

This would involve the following types of experimentation:

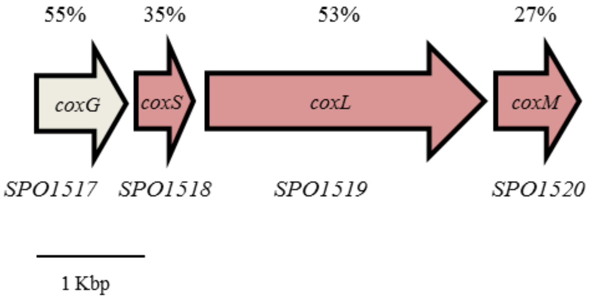
1. Isolation and characterisation of CoxC$^-$ mutants.
2. If CoxC is involved, establish (by {e.g.} two-hybrids) if it interacts with other polypeptides, such as Lon.
3. Confirm by biochemical assays if Lon does indeed act as a protease on CoxC.
4. Use *in vitro* binding studies to examine CoxC binding to possible operator sequences and establish if DMS affects this interaction.
5. Locate the promoters that are regulated by CoxC (and/or other transcriptional regulators) by RACE or primer extensions.

This story is further complicated by the fact that *R. pomeroyi* DSS-3, and several other Roseobacter strains contain not just one set of *cox* genes, but may have a second cluster, as described below.

6.2.3.6 Distribution of *cox* gene clusters

Ruegeria pomeroyi DSS-3 possesses another predicted operon that contains genes that encode Cox polypeptides that are homologues of CoxG (SPO1517), CoxS (SPO1518), CoxM (SPO1519), and CoxL (SPO1520), which are 35%, 27% and 53% identical to the corresponding products of the genes in the *SPO1517-SPO1520* cluster (Cunliffe, 2010; Figure 6.4). The genes in this second cluster encode the so-called form II CODH, and, strikingly, these too were shown in the microarrays to be up-regulated by 3.2-5.2 fold in the presence of DMS.

Figure 6.4 The *cox* form II operon present in *Ruegeria pomeroyi*



Scale indicated. Coloured arrows show carbon monoxide dehydrogenase (CODH) form II gene products. Numbers below gene names gives corresponding gene number. The %age identities to the respective form I CODH polypeptides present in *R. pomeroyi* are given above arrows.

This second group of genes is most commonly found in members of the Roseobacter Clade, Rhizobiales Order (containing *Oligotropha carboxidovorans*) and β-proteobacteria, including species of *Burkholderia* (see also Cunliffe, 2010). Many of these homologues are labelled as xanthine dehydrogenase, and *R. pomeroyi* also possesses several other xanthine dehydrogenases in its genome, including *SPO3019*, whose gene product resembles the SPO2397 (CoxL) enzyme (31% identity, $8e^{-107}$). The function of the second form of CODH is putative in *Oligotropha* (Cunliffe, 2010), although *Mesorhizobium loti* USDA 3471, which contains only the second form of CODH, is known to oxidize CO (King, 2003). The relation to xanthine dehydrogenase may stem from the similarities in the enzymes' molybdenum binding domains and active sites, although at present this is conjecture only. It would be of great interest to see if this cluster, expressed in the *Rhizobium* strain that contains the other *cox* cluster (see above), is able to restore CO oxidising activity.

6.2.3.7 Conserved promoter motifs

A MAST/MEME motif search (Bailey *et al.*, 2009) using the regions 200 bp upstream of the ATG of *R. pomeroyi* form I *coxM* and form II *coxS* (the beginning of each respective *cox* gene cluster, excluding *coxC*) did not retrieve any significant motifs that could be regarded as regulatory, e.g. inverted tandem repeats. Nor was a significant motif identified upstream of the start of the *coxG*, from *O. carboxidovorans* or *R. pomeroyi.* Note that this was the gene for which there was a considerable intergenic gap preceding it in *R. pomeroyi*, as to indicate a possible separately transcribed gene.

6.3 Conclusion

The work carried out in this chapter has touched upon a number of disparate systems in *R. pomeroyi,* with indirect and sometimes unfathomable links to DMSP and MMPA catabolism. From THF recycling, to methane thiol oxidation, to carbon monoxide oxidation, the work described opens up several highly interesting avenues of research, despite the “handicap” of high variance and inherent unreliability of the microarray data.

Chapter 7

General Discussion

7.1 Preamble

For all the (somewhat disappointing, and frustrating) problems of the high variances in the microarray data, they nonetheless revealed some novel and wholly unexpected genes whose expression was affected by one or more of the DMSP-related molecules that were tested.

In what follows, I present a brief overview of some of these newly discovered genes and/or links between previously described genes and DMS(P), reserving the most detailed discussion for a consideration of the ways in which this work, together with that of others, has thrown fresh light on the interactions between the DMSP demethylation and cleavage pathways.

7.2 The DMSP lyase, DddW

I have shown that the novel DddW lyase is rare compared to most of the other DMSP lyases, both in the deduced proteomes of known bacteria and in bacterial metagenomic data sets. Collaborative work, with Mishto Dey (University of Iowa) is now underway to obtain the crystal structure of DddW, which would be the first DMSP lyase to be studied in such detail and be informative in showing if and how this cupin-like protein interacts with a metal (if that is in fact the case).

One other striking feature of DddW is that its expression is massively induced by the DMSP substrate, this being mediated by the transcriptional regulator that is encoded by the divergently transcribed *SPO0454.* It will be of interest to show exactly how this regulatory gene product interacts with its *cis*-acting DNA target(s) and with (presumably) the co-inducer DMSP. Electrophoretic mobility shift assays would ratify the binding of this regulator to the putative gene(s) in the neighbouring region. Also, a pan-genomic study (such as chromatin immunoprecipitation or chIP-on-chip) would show if this regulator acted on any other genes in *R. pomeroyi.*

7.3 The *cox* genes

The novel and completely unexpected DMS-mediated regulation of the *cox* genes is of interest for a number of reasons, and raises a number of interesting questions, ripe for future study.

In cooperation with Michael Cunliffe (Plymouth), we will confirm the function of these gene products in *R. pomeroyi* by characterising the phenotypes of the various Cox^- mutants that have been made. Given that, unlike *Oligotropha carboxidovorans*, the Roseobacters are unable to grow on carbon monoxide – for reasons set out in chapter 6 – it will be informative to determine if the CODH enzyme(s) in these bacteria contribute some input to the energy generation, though not enough to support stand-alone growth.

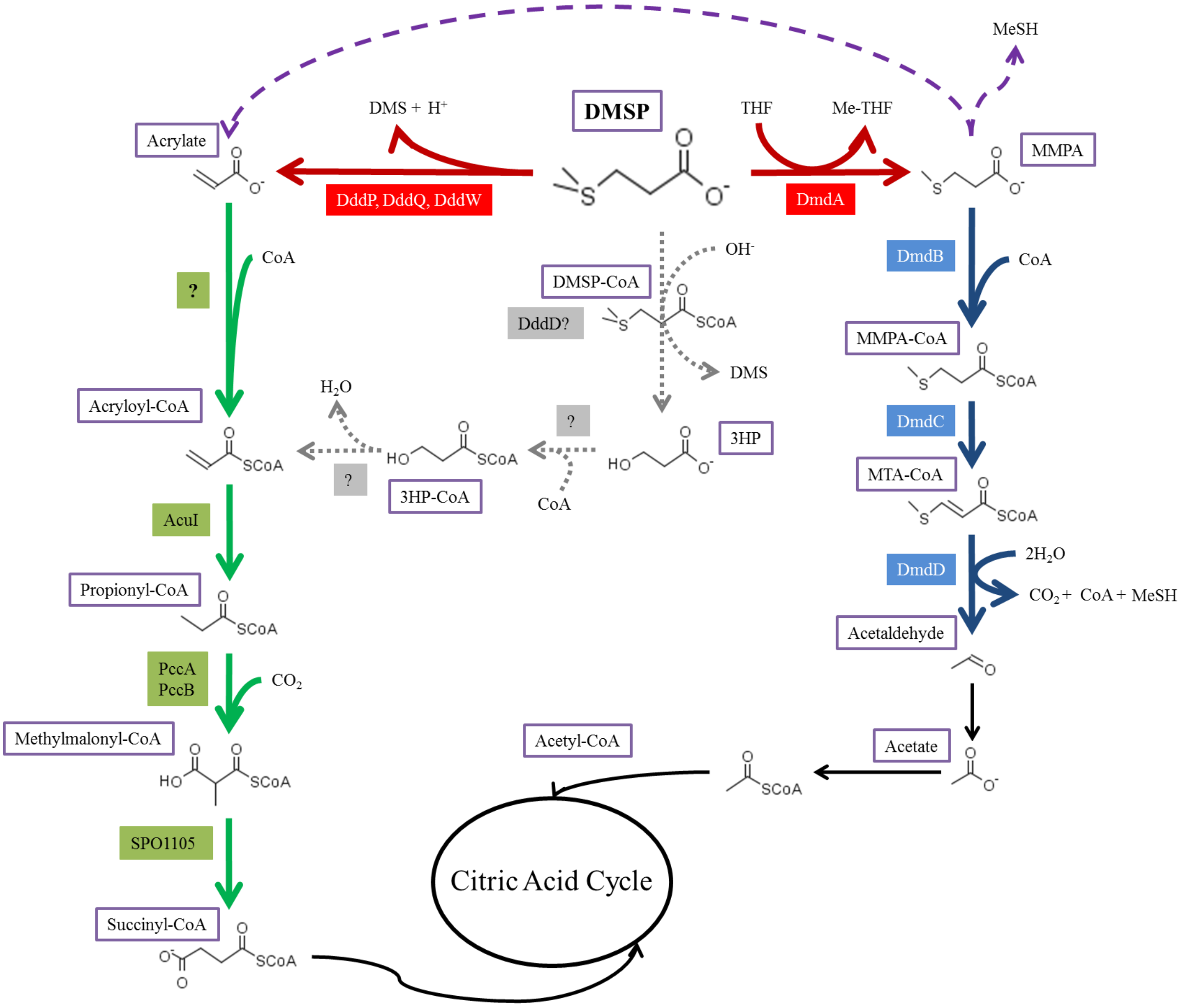
There is still much to do to understand the mechanisms that underlie the DMS-dependent regulation of the *cox* genes – how widespread is this phenomenon?, what is the transcriptional regulator?, and how does this respond to DMS?, are but some of the questions to arise from this microarray based finding.

Possibly the most far-reaching set of observations that stem from the work in this thesis relate to those that impinge on the relationship between the demethylation and the DMS-emitting cleavage pathways. These are discussed in the following section.

7.4 Interplay between demethylation and cleavage pathways for DMSP catabolism

The findings and models set out below build on the pathways – ratified and conjectured – shown in figure 7.1.

Figure 7.1 Biochemical pathways for DMSP degradation in *Ruegeria pomeroyi*



Enzymes and predicted gene products that are involved in the dimethylsulfoniopropionate (DMSP) cleavage (green boxes) and demethylation (blue boxes) pathways in *R. pomeroyi* are shown, with the primary enzymes that act on DMSP itself highlighted in red boxes.

The grey boxes highlight the putative DddD-mediated reaction that is yet to be confirmed in *R. pomeroyi*, based on known, functional DddD enzymes and a putative pathway predicted by Schneider *et al.*, 2012 (indicated by ?).

The purple, dashed arrow indicates a putative breakdown of methylmercaptopropionate (MMPA) to acrylate (or possibly propionate) and methane thiol (MeSH) – see text. MTA, methylthioacryloyl.

Gene numbers in *R. pomeroyi* DSS-3:

dddP, SPO2399; dddQ, SPO1596; dddW, SPO0453; dddD, SPO1703;

***acuI, SPO1914*; *pccA, SPO1101; pccB , SPO1094*;**

dmdA, SPO1913*; *dmdB, SPO2045; dmdC, SPO3804; dmdD, SPO3805.

Adapted from Curson *et al.*, 2011a; Reisch *et al.*, 2012a; 2011b.

7.4.1 Co-regulation of the *dmdA* and *acuI* genes

Importantly, we now know that the *dmdA* and *acuI* genes of *R. pomeroyi* are co-regulated, not only by DMSP, but by its cleavage catabolite, acrylate. Indeed, acrylate was a more potent inducer for both these genes than DMSP, implying a previously unconsidered link between DMSP cleavage and DMSP demethylation. Until now, *acuI* was relatively ignored in *R. pomeroyi*, with previous work concentrating almost solely on the *dmdA* gene (*e.g.* Howard *et al.,* 2006, Reisch *et al.,* 2008).

The genes neighbouring *dmdA* had only been touched upon prior to this thesis. Howard *et al.*, (2006) noted a predicted regulatory gene that was upstream of *dmdA* not only in *R. pomeroyi* but in several other Roseobacters, and speculated that its GntR-like product might control *dmdA* expression, but this was not checked experimentally. This surmise has now been confirmed, as shown in chapter 5. The gene that is known to be *acuI*, was described as a generic “dehydrogenase” by Howard *et al.* (2006).

7.4.2 Growth of AcuI$^-$ and DmdA$^-$ mutants on DMSP or acrylate

The phenotypes of the *acuI* and *dmdA* mutants raised some intriguing questions about the roles of these genes in the catabolism of DMSP and acrylate. This work showed that wild type *R. pomeroyi* could grow effectively on both DMSP and on acrylate as a sole C source.

Intriguingly, a mutation in *acuI* abolished growth on both compounds, yet (essentially) a mutation in *dmdA* did not. Despite the plethora of DMSP catabolic enzymes, most Roseobacters do not grow well – or at all – with DMSP or acrylate as sole C sources, at least under the laboratory conditions tested to date (E Fowler, unpublished). Indeed, for reasons that are not clear, González *et al.* (1999) originally stated that *R. pomeroyi* did not grow on acrylate, but then came to the opposite conclusion in 2003 (González *et al.*, 1999; 2003).

In my hands, not only were AcuI^{-} strains unable to utilise acrylate as a sole C source, but they were sensitive to its toxic effects. Thus, AcuI appears to protect the cells against acrylate or its catabolites (most likely acryloyl-CoA, see below) as well as allowing growth on this substrate.

7.4.3 A possible link between DMSP demethylation and cleavage

At first sight, the above observation on the mutant phenotypes might provide an explanation for a surprising result presented by Reisch *et al.* (2011b). They noted that *R. pomeroyi* DmdB^{-}, DmdC^{-} and DmdD^{-} mutants still grew on DMSP as sole C source, which rather flies in the face of the previous belief that demethylation is the primary route of C assimilation from DMSP. They apportioned this to the fact that the cleavage pathways, mediated by DddP, DddQ and/or DddW might supply sufficient acrylate for growth.

However, Reisch *et al.* also noted that the DmdC^{-} and DmdD^{-} mutants failed to use MMPA as sole C source. The growth of DmdB^{-} mutant was explained (but not checked) by their suggestion that there are two copies of *dmdB* in *R. pomeroyi*. One other striking observation by Reisch *et al*. was that not only did the DmdC^{-} and DmdD^{-} strains fail to grow on MMPA but they were sensitive to this compound. In light of the work presented in this thesis, this inhibition might be due to the build-up of potentially toxic MMPA- and/or MTA-CoA intermediates in such mutants, rather than a failure to use MMPA as a C source (see Figure 7.1). If true, this raises some doubts as to whether this pathway is indeed the most important even for the degradation of MMPA, let alone DMSP.

A closer examination of the experimental approach taken by Reisch *et al.* also casts some doubt on the nature of their conclusions. Firstly, the pathway was totally restricted to the identification of enzymes (and hence the corresponding genes) that generated catabolites that included a CoA moiety, and not the full panoply of catabolites *in toto*. Also, they did not measure the flux through this pathway, compared to that through cleavage, and/or any other routes for DMSP/MMPA catabolism, so it is not possible to assess their relative importance.

7.4.4 Consideration of an alternative MMPA degradation pathway

Prior to the identification of any of the relevant genes and enzymes, it had been thought that the demethylation pathway was the main route by which the Roseobacters *grew* on DMSP, with the cleavage pathways providing only a minor contribution to nutrition (Kiene, 1996; Kiene *et al.*, 2000). This was based on ^{35}S DMSP tracer experiments tracking the accumulation of MeSH following DMSP addition. However, the recent descriptions of the phenotypes of the mutations in the various *dmd* genes (Reisch *et al.*, 2011b), in addition to the findings in this thesis, do not appear to support this view. However, there is another, non-ratified demethylation pathway described many years ago by Kiene *et al.* (2000) who predicted that MMPA might be cleaved directly, either to MeSH and acrylate, or by a reductive cleavage to MeSH and propionate. The recent discovery of the *dmdBCD*-mediated pathway does not necessarily overturn the veracity of either of these pathways

Let us suppose that there is an (as yet unidentified) enzyme that removes the MeSH from MMPA, to form acrylate. This would provide a second, link between DMSP and acrylate, but this time, this acrylate product is generated as part of the demethylation pathway (Figure 7.1). Thus, MeSH would be seen to accumulate through DMSP demethylation, but not necessarily through the actions of the DmdB, DmdC or DmdD enzymes. This might provide an even more convincing reason why *dmdA* and *acuI* are so closely linked in the Roseobacters and why the *dmdA*-*acuI* operon in *Ruegeria pomeroyi* responds to acrylate as a co-inducer. Indeed, perhaps the reduced expression of the *dmdA*-*acuI*-*lacZ* fusion with *dmdA* removed (pBIO2024) in comparison to one with an intact *dmdA* (pBIO2021), observed in chapter 5, stems from the removal of an additional source of MMPA and thus, acrylate, in those cells. Likewise, the induction of *acuI*-*lacZ* by MMPA may relate to its eventual catabolism to acrylate. I have shown through the microarrays that the *pccA*, *pccB* and *SPO1105* genes that are responsible for the downstream conversion of acryloyl-CoA to succinyl-CoA (see Figure 7.1) are up-regulated in the presence of acrylate. Importantly, E Fowler (personal communication) then used this information to make targeted mutations in each of these genes and found that these indeed abolished growth on acrylate as sole C source. Furthermore, she used *lacZ* fusions to confirm that these genes were induced by the presence of acrylate in the medium. Thus, any acrylate formed, by whatever mechanism, could be incorporated into central metabolism for growth.

Moran and colleagues have discussed the presence of a bacterial “switch”, which may control the relative importance of the demethylation and DMS-producing cleavage pathways in response to the substrate DMSP, or perhaps UV radiation, or temperature, or any number of stimuli (Sunda *et al.,* 2002; Howard *et al.,* 2006; 2008; Levine *et al.,* 2012). The work described in this thesis shows that it is likely to be more complex than a simple on/off system. Clearly though, the elucidation of this switch, if it does exist, will be crucial to understanding the catabolism of DMSP by *R. pomeroyi*, the Roseobacters, and indeed, all DMSP catabolising organisms.

7.4.5 Future work on the demethylase- cleavage interactions

Firstly, it is important to identify the (strongly predicted) CoA ligase that is responsible for the initial transfer of CoA onto acrylate to form acryloyl-CoA. There may be several genes that are regulated by acrylate in the microarray that perhaps have annotations as CoA interacting gene products (e.g. SPO1813). Growth on acrylate could be assessed in strains with mutations in these genes, to confirm their role in this pathway. Alternatively, random transposon mutagenesis could be employed to obtain mutants that fail to grow on acrylate as a sole C source. The proposed acrylate catabolic pathway also requires biochemical ratification, using radio-labelled ^{14}C-acrylate – this will be done in the near future by others.

Another goal is to examine the flux of DMSP and acrylate through the different pathways described above, which would involve the use of different, labelled substrates, metabolomics and comparisons of the wild type and the various diagnostic mutants.

It is also important to confirm – or refute – an alternative branch to the demethylation pathway, in which MeSH is cleaved directly from MMPA. This could be done by screening cosmids from gene libraries for any that could generate MeSH from MMPA in a heterologous bacterial background.

Further work on gene regulation is also required. The exact role and function of DmdR needs to be confirmed using (for example) gel-shifts and foot-printing to identify its targets and to establish if and how it interacts with its cognate co-inducer (MMPA? Acrylate?). It would also be instructive to see if the *dmdA* genes that are not located near to *acuI* in Roseobacters and other bacteria were regulated in a similar way to that of *R. pomeroyi.* For example, Pelagibacter spp., also contain *dmdA* but do not possess *acuI* or the DMSP lyases (Todd *et al.*, 2012b).

7.5 The DMSP catabolic genes in the "model" Roseobacter, *Ruegeria pomeroyi,* and other bacteria

The work in this thesis has concentrated on the DMSP catabolic systems in *Ruegeria pomeroyi*, which has become something of a model for genetic and biochemical studies on DMSP catabolism in the Roseobacter clade. In fact, our studies indicate that this strain may actually be atypical in regard to its ability to catabolise DMSP. This is because it is one of very few strains of this clade that can use DMSP or acrylate as sole C sources (E Fowler, personal communication). Also, compared to other genome-sequenced Roseobacters it holds the record number (four – DddD, DddP, DddQ, DddW) of different *ddd* genes, although most other Roseobacters also have more than one type of DMSP lyase (see Table 7.1 and Buchan *et al*.,2005; Wagner-Döbler and Biebl, 2006). Outside the Roseobacters, the γ-proteobacterium, *Oceanimonas doudoroffii* has very recently been shown to express functional DddD and DddP enzymes, making it the first non α-proteobacterium to be able to catabolise DMSP in multiple ways (Curson *et al*., 2011b).

Despite variation in the complement of Ddd genes throughout the Rosebacters, there is excellent conservation of the acrylate degradation pathway. As such, homologues of AcuI, PccA and PccB were found together in the same species, and all of these also contained DMSP lyases and DmdA homologues. Intriguingly, the α-proteobacterium, *Candidatus* Puniceispirillum marinum IMCC1322 possesses a DmdA and AcuI homologue, but no Ddd enzyme that results in the production of acrylate. However, neither does it contain the downstream acrylate catabolic enzymes, so the importance of this finding is unknown.

Table 7.1 A selection of bacteria that catabolise DMSP by more than one mechanism

		Ddd									
Species or strain	**DmdA**	**P**	**L**	**D**	**Q**	**W**	**Y**	**AcuI**	**PccA**	**PccB**
Ruegeria pomeroyi str. DSS-3 (R)	X^{1}	X^{1}		X^{3}	X^{1}	X^{1}		X^{1}	X^{1}	X^{1}
Dinoroseobacter shibae str. DFL12 (R)	X		$X^{1,2}$	X^{3}				X	X	X
Rhodobacteraceae bacterium str. KLH11 (R)	X	X		X^{3}				X	X	X
Rhodobacteraceae bacterium HTCC2150 (R)	X	X			X			X	X	X
Roseobacter litoralis str. OCh 149 (R)	X	X						X	X	X
Phaeobacter gallaeciensis str. 2.10		X						X	X	X
Roseovarius nubinhibens str. ISM (R)	X	X^{1}			$X^{1,4}$			X	X	X
Silicibacter lacuscaerulensis str. ITI-1157 (R)	X	X			X^{1}			X	X	X
Candidatus Puniceispirillum marinum str. IMCC1322 (SAR116) (α)	X			X				X^{1}		
Oceanimonas doudoroffii (γ)		$X^{1,5}$		X^{1}						
Alcaligenes faecalis M3A (β)							X^{1}	X^{1}	X^{6}	X^{6}

In the left hand column of strains; (R) = Roseobacter; (α, β, γ) = α, β, γ-proteobacteria. Crosses indicate the presence of the corresponding polypeptide, based on BLAST hits that satisfied the following stringency tests in comparison with functionally verified DmdA, Ddd and AcuI polypeptide sequences from the Roseobacters, as follows: DmdA, $<e^{-85}$; DddP, $<e^{-86}$; DddL, $<e^{-52}$; DddD, 0.0; DddQ, $<e^{-20}$; AcuI, $<e^{-141}$; PccA, 0.0; PccB, 0.0 (PccA and PccB have e values of 63^{-147} and $7e^{-80}$ in *A. faecalis*, respectively, see below).

[1]: These proteins have been experimentally confirmed to be functional.

[2]: *Dinoroseobacter shibae* str. DFL 12 lacks a Ddd^+ phenotype under laboratory conditions examined to date, but its cloned *dddL* gene confers a Ddd^+ phenotype to *Escherichia coli.*

[3]: These three DddD homologues form an out-group from the known, functional DddD enzymes; DddD of *R. pomeroyi* str. DSS-3 lacks DMSP lyase activity under the conditions sued to date.

[4]: *Roseovarius nubinhibens* ISM has two DddQ homologues.

[5]: *Oceanimonas doudoroffii* has two DddP homologues.

[6]: *A. faecalis* has a methylcrotonyl-CoA carboxylase with 33% identity with PccB and an acetyl-CoA carboxylase with 52% identity to PccA in strain NCIB 8687 (there is no entry for M3A in the NCBI data base).

Adapted from Curson *et al.* 2011a; 2011b; Todd *et al.*, 2012b.

7.6 A widespread role for acrylate degradation enzymes

In a sense, this work started off in a rather parochial, specialised catabolic pathway for the breakdown of a rather esoteric substrate. However, it may now be addressing a phenomenon of much wider importance, namely the extreme toxicity of acrylate (or its CoA derivative) and the way that bacteria deal with it. Work by A R J Curson identified homologues of AcuI in many members of the Enterobacteria, such as *E. coli*. This homologue was termed YhdH, and is a medium chain reductase family protein (MDR012 class), that shares 54% identity with AcuI (Todd *et al.*, 2012b). An *E. coli* K12 $YhdH^-$ mutant was very markedly inhibited for growth by acrylate, and this could be relieved by introducing different *acuI* genes (including that of *R. pomeroyi*) *in trans*. It is possible that despite not encountering acrylate in its natural environment, *E. coli* and other bacteria can convert acrylate to acryloyl-CoA, as does *R. pomeroyi,* and that this can be detoxified via AcuI-like enzymes. Additionally, O Burns (personal communication) screened metagenomic libraries of bacterial populations obtained from water-treatment pipes, soil and other, non-marine sources. Several recombinant plasmids were isolated on the basis that they corrected the acrylate sensitivity of the YhdH$^-$ *E. coli* mutant. Sequencing showed that some of these contained *acuI*-like genes, but others contained genes that encoded short chain dehydrogenase/reductase family proteins (EC 1.3.1.33) and were found in a range of bacterial taxa.

Perhaps all of these genes are merely protective measures independently evolved by different bacterial species to counteract the toxic effect of acrylate (and its CoA derivative), either sourced by DMSP in marine Roseobacters, or exogenously, as may be the case for species such as *E. coli*. Clearly, there are exciting discoveries ahead for the role of acrylate in the marine food web, and beyond, and hopefully this thesis has at least hinted at things to come.

Chapter 8

Materials and Methods

8.1 Strains, plasmids, growth and media

Bacterial strains and plasmids used in this work are shown in Tables 8.4 and 8.5.

8.1.1 Preparation of culture media

All media were prepared using distilled water (dH_2O), sterilised by autoclaving at 121°C for 20 minutes. Solid media contained 1.5% (w/v) agar, unless otherwise stated.

Roseovarius nubinhibens ISM was grown routinely at 28°C in Marine Broth 2216 Difco (MB).

Ruegeria pomeroyi was routinely grown at 28°C in complete ½ YTSS media: 1.25 g Tryptone, 2 g Yeast Extract, 20 g Sea Salts per litre of dH_2O, adjusted to pH 7.0 (González *et al*., 2003).
Minimal medium for *R. pomeroyi* DSS-3 was marine basal medium (MBM):
20 g Sea Salts, 250 ml basal media [150 ml 1M Tris HCl pH 7.5, 87 mg K_2HPO_4, 1.5 g NH_4Cl, 375 ml dH_2O], 700 ml dH_2O, 10 mM succinate, prior to autoclaving and adding 50 ml FeEDTA [50 mg FeEDTA, 100 ml dH_2O], 0.1% vitamin solution [2 mg biotin, 2 mg folic acid, 10 mg pyroxidine-HCl, 5 mg riboflavin, 5 mg thiamine, 5 mg nicotinic acid, 5 mg pantothenic acid, 0.1 mg cyanocobalamin, 5 mg p-aminobenzoic acid per 100 ml dH_2O] following autoclaving (González *et al*., 1997).

Escherichia coli was routinely grown at 37°C on Luria–Bertani (LB) broth: 10 g Tryptone, 5 g Yeast Extract, 5 g NaCl and 1.5 g D-glucose per litre of dH_2O, adjusted to pH 7.2. (Sambrook *et al*., 1989).
For growth in minimal media, *E. coli* was grown in M9: 200 ml 5x M9 salts [64 g $Na_2HPO_4.7H_2O$, 15 g KH_2PO_4, 2.5 g NaCl, 5 g NH_4Cl per litre dH_2O], 0.1 mM $CaCl_2$, 2 mM $MgSO_4$, 30 mg Thiamine HCl, 10 mM succinate per litre dH_2O (an additional 15 mg

methionine per litre dH_2O was required for the Met$^-$ strain *E. coli* strain 803) (Sambrook *et al*., 1989).
Rhizobium leguminosarum was routinely grown at 28°C in TY complete media: 5 g Tryptone, 3 g Yeast Extract and 0.9 g $CaCl_2.6H_2O$ per litre of dH_2O, adjusted to pH 6.8. (Beringer, 1974).

Liquid cultures were shaken at 200 rpm.

For the purpose of blue/white screens for cloned inserts, *E. coli* JM101 was grown on LB containing ampicillin (to screen for Amp^R provided by the plasmid e.g. pBluescript), 5-bromo-4-chloro-3-indolyl-β-D-galactoside (X-gal – whose cleavage by β-galactosidase yields the blue product, 5,5'-dibromo-4,4'-dichloro-indigo), and isopropyl-β-D-thiogalactopyranoside (IPTG – a gratuitous inducer of *lacZ*, located on the plasmid).

Table 8.1 Antibiotics and supplement concentrations

Antibiotic	**Solvent**	**Stock (mg ml^{-1})**	**Final concentration (µg ml^{-1})**
Ampicillin (Amp)	dH_2O	100	100
Gentamicin (Gent)	dH_2O	10	5
Spectinomycin (Spec)	dH_2O	50	200
Streptomycin (Str)	dH_2O	200	400
Tetracycline (Tet)	70% Ethanol	5	5
Supplement	**Solvent**	**Stock (mg ml^{-1})**	**Final concentration (µg ml^{-1})**
5-Bromo-4-Chloro-3-Indolyl -β-D-galactoside (X-Gal)	2,2 Dimethyl-formamide	40	40
isopropyl-β-D-thiogalactopyranoside (IPTG)	dH_2O	200	200
Ortho-Nitrophenyl-β-galactoside (ONPG)	dH_2O	4	800
Inducer	**Solvent**	**Stock (mM)**	**Final concentration (mM)**
Dimethylsulfoniopropionate (DMSP)	dH_2O	100	5
Acrylate	dH_2O	100	2.5
Dimethylsulfide (DMS)	dH_2O	“Neat”	5
Carbon source	**Solvent**	**Stock (M)**	**Final concentration (mM)**
Succinate	dH_2O	1	10

8.1.2 Long-term storage

For long-term storage, *E. coli* cultures were grown overnight to stationary phase, glycerol added to a concentration of 25%, then flash frozen on dry ice and stored at -80°C.

R. pomeroyi required 48 hour growth and the addition of 15% dimethylsulfoxide, and 15% glycerol before flash freezing and storage at -80°C (González *et al.*, 2003).

8.1.3 Growth curves

For growth curve determination, 10 µl of a 5 ml ½ YTSS starter culture of *R. pomeroyi* DSS-3 at OD_{600} nm ~1.0 was inoculated to 10 ml MBM medium containing either; no added carbon, DMSP (5 mM) or acrylate (2.5 mM). Readings were taken at timed intervals for 72 hours.

8.2 *In vitro* and *in vivo* genetic manipulations

General handling and manipulation of bacterial DNA was carried out as described by Wexler *et al.* (2001).

8.2.1 Phenol:chloroform and midi plasmid preparations

8.2.1.1 Preparation of plasmid DNA using alkaline lysis and phenol:chloroform step

This method of plasmid preparation was used for the small-scale isolation (< 5 µg) of plasmid DNA from *E. coli* strains and yielded material of sufficient purity to be used for restriction digestion, PCR or transformation. Prior to DNA isolation, *E. coli* was cultured overnight in LB medium. All centrifugation steps were carried out at 13,000 rpm in a bench-top 5415 Microcentrifuge (Eppendorf).

The procedure is based around the optimised alkaline lysis method of Birnboim and Doly, (1979), followed by phenol: chloroform purification and elution of plasmid DNA.
Buffers P1, P2, N3, PB and PE were supplied in the QIAGEN Plasmid Miniprep spin column kit and used according to the manufacturer's instructions.

The supernatant resulting from P1, P2 and N3 treatment steps (as indicated in manufacturer's instructions) was transferred to a clean 1.5 ml microfuge tube and an equal volume (400 µl) of phenol:chloroform:isoamyl alcohol (25:24:1) added, then mixed by vortexing for 10 seconds and centrifuged for 2 minutes. The upper aqueous layer was transferred to a clean 1.5 ml microfuge tube (to remove protein from the lysate), then two volumes of room temperature 100% ethanol (700 µl) was added and mixed to precipitate the plasmid DNA. This was then centrifuged for 30 minutes and the supernatant discarded. The DNA pellet was washed with 500 µl 70% ethanol (v/v) to remove precipitated salts and centrifuged for 5 minutes. The pellet was air-dried and the DNA resuspended in 40 µl dH_2O, and stored at –20 °C.

8.2.1.2 Midi-preparation of plasmid DNA using QIAGEN columns

The QIAGEN plasmid purification procedure was used when large amounts (> 5 µg) of high purity DNA from *E. coli* strains were required for multiple procedures and sequencing. The procedure is also based around the optimised alkaline lysis method of Birnboim and Doly, (1979). It comprises three distinct steps: alkaline lysis, column purification using 'Qiagen resin', and precipitation of plasmid DNA. These preparations routinely yielded >70 µg of plasmid DNA from *E. coli* cultures, which was free of RNA and protein. Buffers P1, P2, P3, QBT, QC, and QF were supplied in the QIAGEN Plasmid Midi kit and used according to the manufacturer's instructions.

8.2.2 Preparation of genomic DNA

Wizard Mini columns (Promega) were used to prepare genomic DNA suitable for Southern blotting and PCR. The Nuclei Lysis, RNase, and Protein Precipitation solutions were supplied with the Promega kit and used according to the manufacturer's instructions for Gram Negative Bacteria.

8.2.3 Restriction enzyme digestions

DNA was digested using restriction enzymes and buffers purchased from Roche or Invitrogen and were carried out according to the manufacturers' specifications and with supplied buffers. Approximately 1 μg of plasmid DNA was routinely digested in a reaction containing 1x restriction buffer and ~10 U of restriction enzyme, made up to a total reaction volume of 20 μl with dH_2O. Digests, unless recommended otherwise, were routinely incubated at 37°C for 2-3 hours, and were stopped by heating samples to 80°C for 10 minutes.

8.2.4 Dephosphorylation of cut vectors

Shrimp alkaline phosphatase (Boehringer Mannheim) was used to dephosphorylate digested vector DNA prior to its use in ligation reactions, according to the manufacturer's specifications, and with supplied buffers. The reaction mixture contained the digested vector DNA, 1 μl shrimp alkaline phosphatase and 1X dephosphorylation buffer made up to a total volume of 20 μl with dH_2O. Reactions were incubated at 37°C for ~1 hour, and stopped by heating samples to 80°C for 10 minutes.

8.2.5 Ligation of DNA fragments

T4 DNA ligase (Roche) was used to produce recombinant plasmids from digested vector and insert DNA, according to the manufacturer's specifications and with supplied buffers. The ligation reaction mixture contained ~ 200 ng of linearised vector DNA and insert DNA, 1 µl T4 DNA ligase and 1x ligation buffer, made up to a total reaction volume of 20 µl with dH_2O. Ligation reactions were incubated overnight at 4°C.

8.2.6 DNA electrophoresis

DNA fragments were separated by electrophoresis in 1% agarose gels containing 500 ng ml^{-1} ethidium bromide (EtBr) and 1X TBE buffer (45 mM Tris-borate, 1 mM EDTA, pH 8.0). Before loading the DNA samples onto agarose gels, 0.2 volumes of 5x loading dye [0.25% bromophenol blue (v/v), 30% glycerol (v/v)] was added. Gels were run in SCIE-PLAS Mini or Midi horizontal gel tanks with 1X TBE buffer at 70-100 V for 1-2 hours with 1 kb Plus ladder (Invitrogen).

8.2.7 Recovery of DNA from agarose gels

DNA separated on agarose gels was purified from the gels using a QIAquick Gel Extraction Kit (QIAGEN). Buffers QG and PE were supplied with the QIAGEN kit and used according to the manufacturer's instructions.

8.2.8 DNA precipitation

Where necessary, DNA was precipitated from solution for sequencing. 1.1 µl Na Acetate (pH 4.8) and 28 µl 100% ethanol were added per 10 µl DNA solution in a 1.5 ml microfuge tube and mixed well. This was incubated on ice for 15 minutes then centrifuged for 15 minutes. Then, the supernatant was discarded and 500 µl 70% ethanol added and centrifuged for 5 minutes. The supernatant was carefully removed and the DNA pellet air-dried for 15 minutes.

8.2.9 Bacterial Polymerase Chain Reaction (PCR)

A Primus 2596 thermocycler machine (MWG-Biotech) was used to perform PCR. Unless otherwise stated, standard PCR reactions were set up as follows:

5 µl miniprep DNA/genomic DNA or 1 µl midiprep DNA
1 µl primer 1 (20 pmol μl^{-1})
1 µl primer 2 (20 pmol μl^{-1})
10 µl 10x reaction buffer (Roche)
2 µl deoxynucleoside triphosphates (dNTPS) (10 mM for each nucleotide) (Roche)
1 µl Taq polymerase (Roche)
dH_20 up to a final volume of 100 µl

For the specific conditions used for standard PCR see tTable 8.2, and for site-directed mutagenesis PCR, see Table 8.3. PCR products were routinely sequenced to check that they contained the correct sequence.

Table 8.2 PCR temperature cycles for standard PCR

Stage	**Cycles**		**Temperature (°C)**	**Time (seconds)**
1	**1**	(initial denature)	**95**	**240**
2	**30**	(denature)	**95**	**30**
		(anneal)	**60**	**60**
		(extend)	**72**	**90**
3	**1**	(final extend)	**72**	**300**

Table 8.3 PCR temperature cycles for site-directed mutagenic PCR

Stage	**Cycles**		**Temperature (°C)**	**Time (seconds)**
1	**1**	(denature)	**94**	**240**
		(anneal)	**50**	**120**
		(extend)	**72**	**120/kb DNA length**
2	**18**	(denature)	**94**	**30**
		(anneal)	**56**	**60**
		(extend)	**72**	**60/kb DNA length**
3	**1**	(final extend)	**72**	**300**

Cycling parameters were from the Stratagene ExSite PCR-Based Site-Directed Mutagenesis Kit protocol.

8.2.10 Methods for transforming *E. coli* with plasmid DNA

8.2.10.1 Preparation of competent cells

Competent *E. coli* cells were prepared using $CaCl_2$, as described by Sambrook *et al.* (1989). All centrifugation steps were carried out at 6,000 rpm in a bench-top centrifuge at 4°C.

A single colony of the desired *E. coli* strain was inoculated to 5 ml LB and incubated overnight at 37°C. Then, 1 ml of the overnight culture was inoculated to 100 ml LB and incubated at 37°C until OD_{600} nm was between 0.3 and 0.4. Sometimes, 100 ml LB was inoculated directly from a loop of bacteria on an LB plate grown from a single colony. The cells were cooled on ice and pelleted by centrifugation for 15 minutes. The cells were kept on ice and the supernatant was decanted, before the cells were resuspended in 15 ml of 0.1 M $CaCl_2$ and incubated for 30 minutes. The cells were pelleted by centrifugation for 15 minutes, resuspended in 2 ml 0.1 M $CaCl_2$ and stored at –4°C for at least 1 hour. Competent cells could be left at 4°C overnight if desired.

For site-directed mutagenic PCR, XL1-Blue supercompetent cells (Stratagene) were used for transformation and these required no preparation in-house.

8.2.10.2 Transformation of competent cells

Competent *E. coli* cells were routinely transformed with plasmid DNA, as follows. Plasmid DNA or ligation mix was added to 100 µl of competent cells in a clean 1.5 ml microfuge tube and incubated on ice for one hour. The cells were heat-shocked at 42°C for 3 minutes then transferred back to the ice for 2 minutes. 0.5 ml pre-warmed LB was added and incubated at 37°C for one hour, inverting the tube occasionally. The transformation mix was plated out on LB containing the appropriate antibiotics, X-gal plus IPTG as appropriate.

In transformations involving pUC18-based clones, *E. coli* strain JM101 was used to facilitate blue–white screening of transformants that contained plasmids with inserts.
E. coli strain 803 used for the transformation of large (> 10 kb) plasmids.
E. coli strain Bl-21 was the routine host for the over-expression plasmid, pET21a, used in protein purification experiments.
XL1-Blue supercompetent cells (Stratagene), used in site-directed mutagenesis, were transformed according to the manufacturer's instructions.

8.2.10.3 Plasmid constructions

Construction of specific plasmids is described in the appropriate chapters. In general, the desired gene of an organism was PCR-amplified from genomic DNA with forward and reverse primers, then ligated into the relevant plasmid, digested with restriction enzymes complementary to the sites introduced into the PCR product.

For protein purification, the PCR products were cloned into pET21a, and for transcriptional *lacZ* reporter fusions, PCR products were cloned into the reporter plasmid, pBIO1878. Sub-cloning of fusions used pBluescript as the first plasmid. A list of plasmids constructed in this work is shown in table 8.4, table 8.5 and table 8.6.

8.2.10.4 Plasmid conjugation

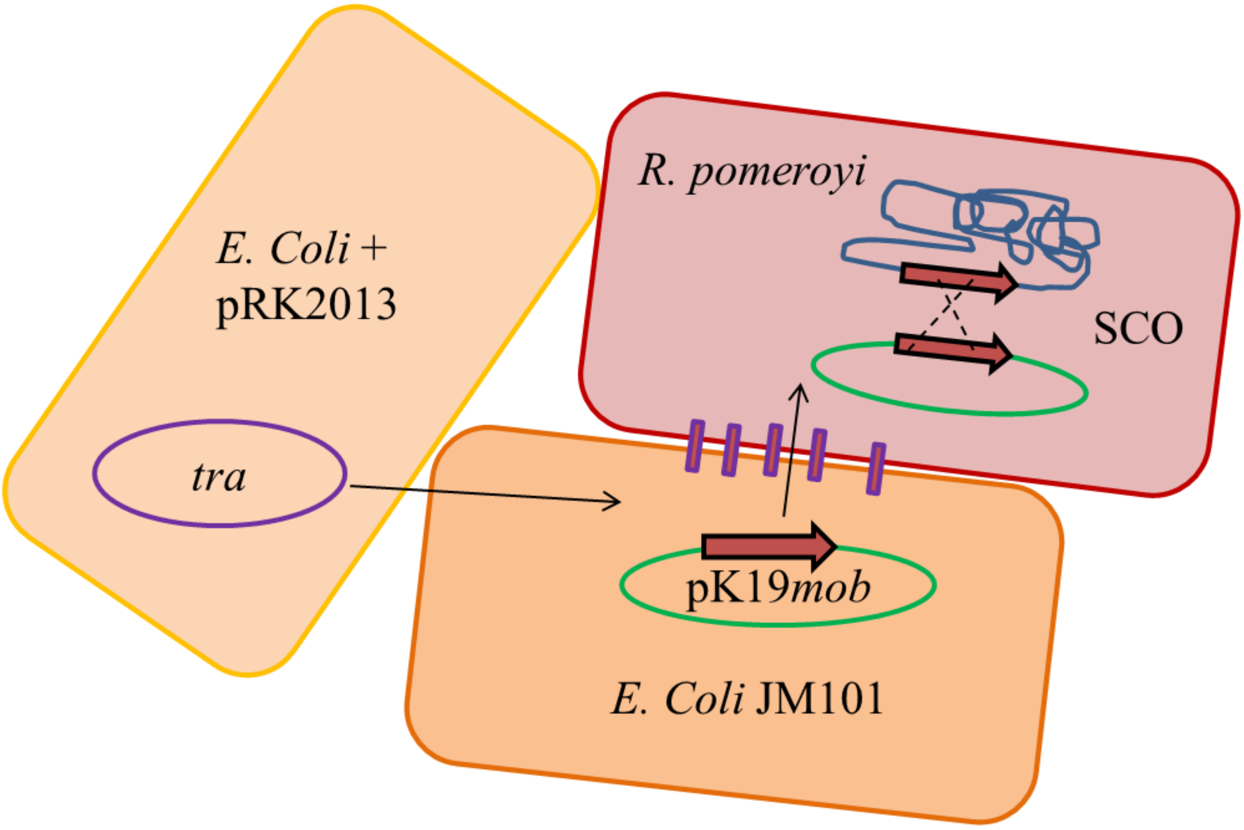
Plasmids were transferred by conjugation to *Ruegeria pomeroyi* or *Rhizobium leguminosarum* from *E. coli* using a patch cross (Johnston *et al.*, 1978). Because the vectors pOT2 and pBIO1878 are not self-transmissible (lacking the *mob* genes), this was done by using tri-parental crosses with *E. coli* 803, containing pRK2013 as a helper plasmid (Figurski and Helinski, 1979; see Figure 8.1).

The *Ruegeria pomeroyi* DSS-3 or *Rhizobium leguminosarum* recipient, *E. coli* strain 803 *lacZ*::promoter fusion donor plus *E. coli* pRK2013 (the helper strain) were separately cultured on ½ YTSS (*R. pomeroyi*), TY (*R. leguminosarum*) or LB (*E. coli*) agar plates. Loopfuls of each strain were mixed on ½ YTSS (*R. pomeroyi*) agar, or TY (*R. leguminosarum*) agar. Following overnight incubation at 28°C, the cells were streaked on selective media (½ YTSS for *R. pomeroyi*, TY for *R. leguminosarum*) with the appropriate antibiotics for the plasmid and/or strain. These plates were incubated at 28°C for ~2 days to recover the desired transconjugants.

8.2.11 Insertional mutants in *Ruegeria pomeroyi*

To generate targeted, insertional mutations into the genome of *Ruegeria pomeroyi*, a modified pK19*mob* system was used. Generally, PCR fragments internal to the gene were amplified from *R. pomeroyi* genomic DNA and then cloned into pBIO1879 using restriction enzymes complementary to the PCR primers used. The pBIO1879 plasmid is a derivative of the suicide insertion plasmid pK19*mob* (Kan^R) (Schäfer *et al*., 1994) into which a Spec^R cassette was cloned as a 2 kb fragment from pHP45W (Prentki and Krisch, 1984) into the HindIII site of pK19*mob*. The resultant plasmid was transformed into *E. coli* strain JM101 and then mobilized by triparental conjugational mating (with pRK2013) into J470 (*R. pomeroyi* DSS-3 Rif^R), selecting for transfer of Spec^R, Kan^R and the mutants selected for on ½ YTSS medium with spectinomycin, kanamycin, with the *E. coli* donor cells being eliminated by rifampicin.

Figure 8.1. Triparental mating technique for mobilisation of pK19*mob* into *Ruegeria pomeroyi*



The helper strain of *E. coli* containing pRK2013 contains the *tra* genes (coloured purple), allowing conjugation of the pK19*mob*-derived plasmid (coloured green), containing a fragment internal to the target gene – coloured red, from a host, to the recipient *R. pomeroyi*. Then, selecting for the Kan^R resistance encoded by pK19*mob spec*, a single cross-over event (SCO) can be chosen, in which the entire suicide plasmid is inserted into the target gene in the host genome (coloured blue), disrupting its function.

Because the recovery of insertional mutations was lower than that of the transfer of the plasmid itself, these conjugations were done as filter crosses, as follows (Beringer and Hopwood, 1976). *Ruegeria pomeroyi* cells were cultured overnight in ½ YTSS liquid at 28°C. *E. coli* containing the pBIO1879-derived mutagenic plasmid, and the helper *E. coli* pRK2013 were grown overnight in liquid LB at 37°C. Then, 0.5 ml of *R. pomeroyi*, 1.5 ml of *E. coli* pBIO1879 donor and 1 ml of *E. coli* pRK2013 was centrifuged, and re-suspended in 200 µl of liquid ½ YTSS. This 200 µl culture was spread on a sterile nitrocellulose filter on a non-selective ½ YTSS plate. Filters were incubated at 28°C for ~2 days, then the cells were washed off with ½ YTSS liquid, diluted as appropriate and spread onto ½ YTSS agar plates supplemented with spectinomycin, kanamycin and rifampicin. Transconjugants in which the plasmid had integrated into the gene were ratified by PCR and by Southern blot hybridizations (see below).

8.3 Methods for *in vitro* analysis of DNA, RNA and protein

8.3.1 Over-expression and purification of DddP protein.

100 ml cultures of *Escherichia coli* strain BL21 containing plasmid pBIO1658 were grown at 37 °C in LB broth containing 100 µg ampicillin ml^{-1} to an OD$_{600}$ of 0.4–0.6. To induce *dddP* expression, 10 µM IPTG was added, followed by incubation at 25 °C until cells reached the stationary phase. Cells were pelleted by centrifugation and resuspended in 0.1 vols 20 mM Tris buffer (pH 8) at 4 °C. Cells were lysed by sonication (6×10 s) and cell debris was removed by centrifugation. Then, 25% (w/v) $(NH_4)_2SO_4$ was added to the lysate and the resulting precipitate was removed by centrifugation. The supernatant was loaded onto a phenyl sepharose high-performance column (xk16/20; GE Healthcare) equilibrated with 20 mM Tris containing 25% (w/v) $(NH_4)_2SO_4$. Proteins were eluted using a 25–0% $(NH_4)_2SO_4$ gradient (flow rate 3 ml min^{-1}). The 3 x 3 ml fractions that contained DddP polypeptide were then applied to a DEAE (HiTrap, 5 ml; GE Healthcare) column equilibrated with 20 mM Tris buffer, pH 8 (flow rate 5 ml min^{-1}). Proteins were eluted in the same buffer with a linear gradient of 0–1 M NaCl. The 3 x 2 ml fractions containing DddP were concentrated to 2 ml using an Amicon Ultra 4 ml Centrifugal filter and loaded onto a Superdex 200 gel filtration column (10/300GL; GE Healthcare) equilibrated with 50 mM MES buffer, pH 6 (flow rate 1

ml min^{-1}). The 2 x 5 ml DddP-containing fractions were pooled and stored at 4 °C. DddP concentration was estimated from A_{280} measurements, using ϵ_{280} nm=76 860 M^{-1} cm^{-1}, as calculated from the numbers of tryptophan, tyrosine and cysteine residues in the protein (Gill and von Hippel, 1989).

8.3.2 Enzymic properties of DddP *in vitro*

To determine the pH optimum for DddP activity, a mixed buffer solutions (MBS) of 50 mM K_2HPO_4, sodium citrate, Tris and *N*-cyclohexyl-2-aminoethanesulfonic acid was used to generate solutions in the pH range 2.0–9.0. HCl or NaOH were used to achieve the desired pH before assaying DMS production (section 8.5.2).

The effects of temperature on DddP activity were examined by incubating the reaction mixtures in 50 mM MES buffer, pH 6.0 over a range from 25 °C to 70 °C, at 5 °C intervals.

To examine the effects of metal availability on DddP function, the metal chelators 2,2′-bipyridyl (2.5 mM) or EDTA (25 mM) were added to DddP in MES buffer pH 6 and incubated for 15 min at room temperature before adding DMSP substrate and assaying as in section 8.5.2.

K_m and V_{max} studies were done with ~0.3 μM DddP in MES buffer, pH 6, with DMSP concentrations ranging from 1 to 20 mM. Samples were incubated at 30 °C and DMS headspace measurements were taken at regular time intervals.

8.3.3 Analytical ultracentrifugation

Analytical ultracentrifugation was done at 12 000 r.p.m., 20 °C, in a Beckman Optima XL-I analytical ultracentrifuge, with absorbance optics and an An50Ti rotor. Partial specific volumes were estimated from DddP amino acid sequences using SEDNTERP software, version 1.05 (Philo, 1997). Scans were recorded every 4 h to determine when protein samples had reached equilibrium, when five scans were recorded per sample. DddP (~5 µM) was in 20 mM Tris, 100 mM NaCl, pH 8. Data were analysed using Ultrascan (Demeler, 2005) and fitted to a one-component model.

8.3.4 Southern blotting

8.3.4.1 Probe design

To ratify pK19 insertional mutations, probes were designed for Southern blots that targeted a 5-10 kbp flanking region around the gene of interest, bordered by natural restriction sites. In some cases, probes were re-appropriated from existing PCR products, for example in the use of the *SPO193-1914* fragment originally cloned into pBluescript.

8.3.4.2 Probe creation

This protocol used the DIG High Prime DNA labelling and detection starter kit (Roche). A 16 µl aliquot of the probe DNA was boiled for 10 minutes to denature the DNA, followed by a quick cooling on a salt ice mixture. Then, 4 µl of “dig1”, DIG high prime, buffer was added, vortexed and incubated overnight at 37 °C for efficient random, primed labelling of the probe DNA. Following incubation, the probe was heat-killed at 65°C for 10 minutes and stored at -20°C for use later.

8.3.4.3 Southern blot buffers

The buffers prepared for this procedure are as follows:

Denaturation solution

0.5 M NaOH

1.5 M NaCl

Neutralisation solution

1 M Tris-HCl; pH8

1.5 M NaCl

Depurination solution

0.2 M HCl

20X SSC (in 2 litres)

3 M NaCl

0.3 M Tri sodium citrate; pH7

To be diluted for use as 6X SSC

Washing Buffer

0.1 M maleic acid

0.15 M NaCl; pH 7.5

0.3% (v/v) Tween 20

Maleic acid Buffer

0.1 M maleic acid

0.15 M NaCl; adjusted with solid NaOH to pH 7.5

Post Hybridisation Buffers (PHB)

1) 0.5x SSC, 0.1% SDS

2) 0.1x SSC, 0.1% SDS

Detection Buffer

0.1 M Tris-HCl

0.1 M NaCl; pH 9.5

Blocking solution

Dilute 10x blocking solution (vial 6 in the DIG kit) 1:10 in maleic acid buffer

Antibody solution

Centrifuge anti-digoxigenin-AP (vial 4 in the DIG kit) for 5 minutes at 13,000 rpm, and pipette from surface.

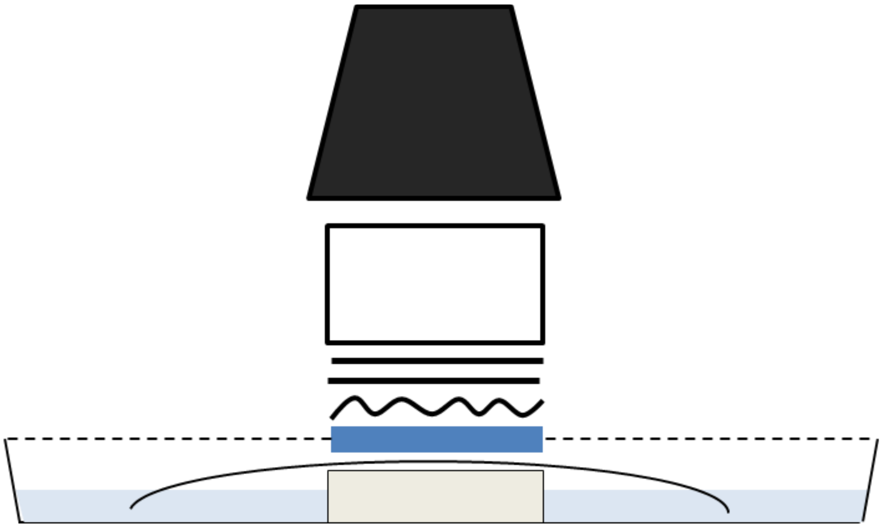
Dilute 1: 10,000 (75mU/ml) in blocking solution

8.3.4.4 Southern blot protocol

Genomic DNA preparations were digested with the relevant restriction enzymes overnight at 37°C, and the fragments, separated by agarose gel electrophoresis were photographed, together with a ruler scale.

The gel was then rinsed in dH_2O and soaked in depurination solution for 15 minutes, then rinsed in dH_2O and soaked in denaturation solution for 30 minutes. It was rinsed again and finally soaked in neutralisation solution for 30 minutes. The gel was then set up for blotting as shown in figure 8.2 below, and left overnight.

Figure 8.2 Cross section of a Southern blot hybridisation



Simplified representation of the Southern blot technique used in this study. A tray was partially filled with 6 x SSC blotting solution (light blue) and a filter paper “bridge” created (curved line) over a plastic base (light grey). Once soaked through, the agarose gel (dark blue) to be blotted was placed on top of the filter paper bridge and cling film (dashed lines) was used to seal the edges completely. This prevents the filter bridge from coming into contact with any of the other blotting components such as the blotting membrane and preventing efficient blotting. A Hybrid- N$^+$ nylon membrane (Amersham Biosciences), cut to identical dimensions as the agarose gel, was placed on top of the gel (waved line). Two similarly sized pieces of filter paper (straight line) were then placed on top of this, followed by a thick block of tissue (white rectangle). Finally, a heavy weight (black trapezium) was carefully placed on top and left overnight, to allow complete blotting to occur.

8.3.4.5 Probe hybridisation

Following blotting, the nylon filter was removed and rinsed in 2X SSC solution, air-dried, and UV cross-linked at 254 nm. A 20 ml aliquot of DIG Easy Hyb solution (kit no. 7) was pre-heated to 42°C and added to the filter in a heat-sealed hybridisation bag (Amersham Biosciences) and incubated at 42°C for 30 minutes. The DNA probe was denatured at 100°C for 10 minutes, cooled in a beaker of salted ice for 2 minutes and 3 µl was added to 3 ml of DIG Easy Hyb solution. This was added to the nylon filter in the bag, re-sealed and incubated at 42°C overnight.

8.3.4.6 Post-hybridisation and detection

Following hybridisation, the filter was washed for 2 x 5 minutes in PHB 1 at room temperature, and 2 x 15 minutes in PHB 2 at 68 °C.

The filter was then rinsed in washing buffer, and then incubated at room temperature for 30 minutes in blocking buffer. The DIG-Ap antibody mix was added to blocking buffer (4 µl in 20 ml), and was then applied to the filter and incubated for 30 minutes at room temperature. The filter was then washed 2 x 15 minutes in washing buffer and 5 minutes in detection buffer, at room temperature.

A colour substrate solution was created by adding 200 µl NBT/BCIP to 10 ml detection buffer; this was applied to the filter immediately, then stored in the dark. The filter was periodically assessed for development of bands.

8.3.5 RNA extraction

Starter cultures of *R. pomeroyi* DSS-3 were grown overnight in ½ YTSS media, washed and diluted 1:200 in MBM minimal media containing 10 mM succinate, and incubated at 28°C for 16 h to an OD_{600} nm ~ 0.4. Then, compounds whose effects on gene expression were to be determined were added (see respective chapters). Then, cultures were incubated for a further 2 hours, before harvesting 2 x 50 ml aliquots of each growth condition. 20 ml of ice-cold 5% phenol, 95% ethanol (v/v) solution was added and the culture was incubated on ice for 1 hour to stabilize RNA and prevent degradation. Cells were then pelleted and RNA was extracted using SV Total RNA isolation kit and buffers (Promega). To achieve the quality and quantity of RNA required for the microarray analysis, an amended SV Total RNA protocol was used, as follows.

Pellets were re-suspended in 200 µl TE buffer containing 100 mg/ml lysozyme, and incubated at 37°C for 10 minutes. These were then freeze/thawed 5 times using dry ice. 135 µl lysis buffer (containing β-mercaptoethanol) and 630 µl RNA dilution buffer were added to the frozen pellet and mixed by inversion. The sample was then added to a 2ml screw cap vial containing 0.6 g Sigma (≤106 µM) acid-washed glass beads and broken open ("ribolysed") in a FastPrep (MP Bio) for 40 seconds at speed setting 6.0. Samples were then heated at 70°C for 3 minutes and centrifuged at maximum speed for 10 minutes. The supernatant was transferred to a clean microfuge tube containing 200 µl 100% ethanol and mixed by pipette, before being transferred to a spin column and centrifuged at max speed for 30 seconds. The eluate was discarded and the column washed with 600 µl wash buffer before being spun again for 30 seconds. DNase mix was prepared in the following way: 5 µl 90 mM $MnCl_2$, 40 µl DNase core buffer, 5 µl DNase. Then, 50 µl of the DNase mix was applied to the column matrix and incubated at 37°C for 40 minutes, before stopping with 200 µl DNase stop mix and centrifuged for 30 seconds at 13,000 rpm. Columns were washed with 600 µl wash buffer, and centrifuged at 13,000 rpm for 30 seconds. The eluate was discarded, and the column washed again, with 250 µl wash buffer and centrifuged at 13,000 rpm for 30 seconds. The eluate was discarded and the column spun again for 1 minute, to remove any residual wash buffer. Columns were transferred to clean microfuge tubes and 70 µl RNAse-free dH_2O applied to the matrix. This was left to stand for 1 minute before being centrifuged at 4500 x g for 2 minutes and the column was discarded. The RNA sample was frozen at -80°C.

8.3.5.1 RNA quality assessment

A Nanodrop was used on 1 µl samples to estimate the DNA/RNA concentration (in ng/µl) and purity, using dH_2O as a blank. Purity was estimated by the ratios of absorbance at 280 nm (DNA levels), 260 nm (RNA levels) or 230 nm (organic solvents) in the relevant sample.

An Experion automated electrophoresis platform (BioRad) was used to assess the integrity of the RNA for use in the microarray assay, as per the manufacturer's instructions for the Experion RNA StdSens kit and an RNA StdSens Chip (BioRad). Typically, 1 µl of each sample was loaded into 1 of 11 wells on the StdSens chip. A virtual-gel output showed bands corresponding to 23S, 16S and 5S rRNA and the absence of any 'smearing' illustrated that the RNA had not degraded during the isolation process.

8.3.6 Quantitative real-time RT-PCR

The absence of genomic DNA contamination in the RNA samples was confirmed by PCR amplification, using Taq PCR Master Mix (QIAGEN) according to manufacturer's specifications. For qRT-PCR, primers (Table 8.6) were designed using Primer3 software (Rozen and Skaletsky, 2000) and used to amplify genes from total RNA isolated from cells grown in the presence or absence of 5 mM DMSP, 2.5 mM acrylate or 5 mM DMS. The data were normalised against the RNA encoded by *SPO2904,* an *Ruegeria pomeroyi* gene that encodes a serine/threonine protein phosphatase/nucleotidase, and was used in the microarray protocol of Bürgmann *et al.* (2007). The iScript™ One-step RT-PCR Kit (Bio-Rad) with SYBR® Green was used for reverse transcription followed by PCR, as described in the manufacturer's manual. Master mix and RNA solutions were added to a final volume of 25 µl, containing 50 ng of RNA, and quantification of mRNA transcripts was carried out using a CFX96 Real-time PCR Detection system (Bio-Rad).

8.3.7 Microarrays

8.3.7.1 Slide design

Agilent 8 x 15K gene expression microarray slides were used, and a GenePix Array List (GAL) file was created using eArray (https://earray.chem.agilent.com/earray/) based on the *Ruegeria pomeroyi* DSS-3 genome and megaplasmid sequences obtained from B Pearson (personal communication). Each gene was represented by 3 separate ~60 bp oligomer "probe" sequences, each designated to a particular "spot" on the array slide by eArray. Control spots were also assigned to the slide to allow calibration by the GenePix program.

8.3.7.2 RNA Labelling

A Stratagene AffinityScript Multiple Temperature reverse transcriptase kit was used. RNA was extracted and assessed for quality and quantity, as above. A 10 µg aliquot of RNA was dried using a rotary vacuum, then resuspended in 7.7 µl of RNase-free water. The RNA labelling protocol was as follows.

Random priming reactions were set up with 7.7 µl of RNA and 5 µg (1.7 µl) of random hexamers, and incubated at 70^{o}C for 5 minutes, before being put on ice for 10 minutes. Samples were centrifuged briefly.

A reverse transcription (RT) reaction mix was prepared:

2 µl of 10 x RT buffer
2 µl of 0.1 M Dithiothreitol (DTT)
0.6 µl of 50 x dNTPs (25 mM of dATP, dGTP, dTTP and 10 mM of dCTP, equivalent to 25 µl of dA, dG, dT and 10 µl of dCTP from Amersham Pharmacia 100 mM stock dNTP
2 µl of Cy3 or Cy5-dCTP (1 mM stock from Amersham Pharmacia)
4 µl of reverse transcriptase (AffinityScript, Stratagene)
Water, treated with 0.1% Diethylpyrocarbonate (DEPC) to a total volume of 20 µl.

Samples were mixed and incubated at 25^{o}C for 10 minutes, incubated overnight at 42^{o}C. The next day, 15 µl of freshly made 0.1 M NaOH was added and the RNA hydrolysed at 70^{o}C for 10 minutes. Then, 15 µl of 0.1 M HCl was added to neutralise the reaction.

8.3.7.3 Genomic DNA (gDNA) labelling reaction

A Gibco/BRL BioPrime DNA labelling kit was used. Firstly, a 2 µg aliquot of chromosomal DNA from a QIAGEN Genomic DNA Kit was added and the volume brought to 21 µl with DEPC-treated water. Then 20 µl of 2.5 x Random primer/reaction buffer mix from the Gibco kit was added. The sample was boiled for 5 minutes, then put on ice for 5 minutes. Once on ice, 5 µl of 10 x dNTP mix (1.2 mM each of dATP, dGTP, dTTP; 0.6 mM of dCTP; 10 mM Tris pH 8.0; 1 mM EDTA) plus 3 µl of Cy3 or Cy5 dCTP (1 mM stock from Amersham) and 1 µl of Klenow fragment from the kit was added. This was spun down at 13,000 rpm and incubated at 37^{o}C overnight.

8.3.7.4 RNA/gDNA Clean up

An Invitrogen PureLink PCR purification was used as follows. A 50 µl aliquot of labelled RNA/gDNA reactions was added to 200 µl of PureLink binding buffer B2 and mixed well by inversion. The sample was added to a spin column and centrifuged at 10 000X g in a microcentrifuge for 1 minute. The flow-through was discarded, and column washed with 650 µl of Wash Buffer, then spun as before. The flow-through was discarded again, and the empty spin column was spun at full speed for 3 minutes to remove all traces of wash buffer. DNA was eluted using 50 µL DEPC-treated water and spun after incubating for 1 minute at room temperature, elution was performed by centrifugation into a clean eppendorf for 2 minutes at 13,000 rpm.

8.3.7.5 Array Hybridisation

An Agilent Hi-RPM gene expression hybridisation kit was used as follows. Samples for the conditions being compared in each array were dried as before, then resuspended in 10 µl of DEPC-treated water, before being mixed. To this 20 µl sample, 25 µl of hybridisation buffer (Agilent) and 5 µl of blocking reagent (Agilent) were added, and boiled for 3 minutes before being cooled to room temperature.

A 40 µl aliquot of each sample was applied to a well on an Agilent hybridisation chamber, held in a clamp (Agilent). The array was carefully applied on top of the chamber, and clamped down firmly. This was incubated in a hybridisation oven at 65°C overnight.

8.3.7.6 Washing the hybridised arrays

The hybridisation chamber and microarray, held in the clamp was disassembled in wash buffer 1 (Agilent) away from bright light. The array was loaded into a foil covered 50 ml Falcon tube filled with Wash Buffer 1 and rotated gently for 1 minute at room temperature. The array slide was transferred to another Falcon tube containing wash buffer 2, pre-warmed to 37°C and rotated again for 2 minutes. The slide was then immersed briefly in acetonitrile and air-dried, before being placed into stabilisation buffer, air-dried and stored in the dark.

8.3.7.7 Scanning and normalisation

The array slide was scanned using a GenePix 4000B scanner, and data were acquired using GenePix 6.0 software (Axon Instruments). Laser excitation was provided by individual 635 nm and 532 nm lasers. These wavelengths correspond to the ideal wavelengths used to excite the fluorophores Cy3 and Cy5 (Amersham Pharmacia Biotech), respectively, used in this study. The intensity of each laser and the gain of the photomultiplier tube (detector) were manually calibrated, and an approximately equal fluorescence for both dyes was achieved, to negate saturation of one wavelength. Spots were scanned at a resolution of 5 μm. Spots incorrectly aligned to the template GAL file were identified manually and corrected where possible. Data from the triplicate technical, and duplicate biological replicates were processed using GeneSpring GX software, and normalised using LOWESS and Marray packages, giving the fold change in fluorescence between conditions (Cleveland, 1979; Wang *et al.*, 2002; B Pearson, personal communication). Student's *T*-tests were used to calculate P values.

8.4 Sequencing and bioinformatics

DNA sequencing was carried out at the John Innes Centre Genome Laboratory. Sequences were analysed with Artemis (http://www.sanger.ac.uk/Software/Artemis) and DNAStar (DNAStar Inc. Madison, WI) EditSeq and aligned using MegAlign and GeneDoc.

Basic Local Alignment Search Tool analyses (BLAST) utilised the BLASTp (for proteins), BLASTn (for genes) or BLASTx (nucleotide into protein) function of the NCBI BLAST online program (www.ncbi.nlm.nih.gov/BLAST/).

Genome alignment was carried out using the NMPDR database tool, the IMG database (Markowitz *et al.,* 2010) or PATRIC (Gillespie *et al.,* 2011).

Operon prediction used the DOOR database (Mao *et al.*, 2008).

Motif searches used MEME/MAST (Bailey *et al.*, 2009).

PePPER was used to predict terminators (http://pepper.molgenrug.nl/), along with TransTermHP (Kingsford *et al.*, 2007).

8.5 Gas chromatography

Gas chromatography used a flame photometric detector (GC 2010; Shimadzu, Milton Keynes, UK) and a 30 m x 0.53 mm ID-BP1 5.0 μm capillary column (SGE Europe, Milton Keynes, UK).

8.5.1 Bacterial DMS assays

To measure DMS production, bacteria were first grown overnight in the appropriate medium. Cultures were then adjusted to the same OD_{600} nm, the cells were spun down and re-suspended in complete medium containing a final concentration of 5 mM DMSP. Certain experiments involved washing three times in minimal media before re-suspending in minimal media. They were then incubated with shaking in 1ml vials (12 x 32 mm, Alltech Associates) at their appropriate growth temperature. After the necessary incubation time, DMS in the vial headspace was quantified by gas chromatography (see above). Activities are expressed as nmol DMS. min^{-1}. µg $protein^{-1}$. Protein concentrations were estimated using Bradford’s assays (BioRad).

To measure the effects of pre-growth in the presence of potential co-inducer molecules (DMSP, acrylate, DMS) on the rates of DMS production, the relevant strains were grown in minimal medium supplemented with one of these compounds, or unamended. After overnight growth, the cells were washed, and were assayed for DMS production, using fresh DMSP substrate.

8.5.2 Purified DddP DMS assays

For *in vitro* assays with purified DddP, the protein (∼10 µM) was added to an appropriate buffer solution containing different concentrations of the substrate DMSP in a sealed 1 ml vial (Alltech Associates). For routine assays, DMSP was used at a final concentration of 5 mM. Following incubation at 30 °C, the DMS in the headspace was quantified by gas chromatography as above.

8.6 β-galactosidase assays

β-galactosidase activity was used to measure the transcription of *lacZ* reporter fusions, based on the reporter plasmid pBIO1878, similar to the methods described by Sambrook *et al.* (1989) and modified by Rossen *et al.* (1985).

Ruegeria pomeroyi or *Rhizobium leguminosarum* were inoculated from a single colony to 5 ml ½ YTSS, or TY medium, respectively, and grown for ~2 days at 28°C. 1 ml of this culture was inoculated to 100 ml MBM or TY and grown for 16 hours at 28°C (until OD_{600} nm was between 0.3 and 0.6). Potential co-inducer molecules were added to 5 ml aliquots of *R. pomeroyi* or *R. leguminosarum* cultures in Sterilin 10 ml Universal containers and incubated at 28°C for a further 2 hours. Add 1 ml of culture to a 2 ml cuvette and measure the OD_{600} nm (blanked against MBM medium), to determine the cell density. Aliquots of the culture (0.1 - 0.5 ml depending on activity) were removed and added to a 2 ml microfuge tube and made up to 1 ml with Z buffer (see below). Then, 2 drops of chloroform plus 1 drop 0.1% SDS (w/v) was added to each microfuge tube and vortexed for 10 seconds, and the tubes incubated at 28°C for 5 minutes. 0.2 ml *O*-nitrophenyl-β-D-galactopyranoside (ONPG) (4 mg ml^{-1}) was added to each microfuge tube, a timer started and incubated at 28°C. When sufficient yellow colour had developed, 0.5 ml Na_2CO_3 was added to stop the reaction and the time was recorded. The tubes were centrifuged for 3 minutes at 13,000 rpm to pellet the cell debris and 1 ml of the supernatant was added to a 2 ml cuvette, with the $OD_{420\ nm}$ measured (blanked against Z buffer).

The β-galactosidase activity, in Miller units, was calculated using the following equation:
Miller units = $1000 \times OD_{420} / t \times V \times OD_{600}$
t = time
V = volume of culture used
Z-buffer contains 1 ml 3 M $Na_2HPO_4.7H_2O$, 0.5 ml 4 M $NaHPO_4.7H_2O$, 0.5 ml 1 M KCl, 0.5 ml 0.1 M $MgSO_4.7H_2O$, 175 µl mercaptoethanol, made up to a final volume of 50 ml with

dH_2O. ONPG was freshly prepared each time. OD_{600} nm and OD_{420} nm values were measured using a Unicam 8625 UV/VIS spectrophotometer.

8.7 Detection of substrates, catabolites and metals

8.7.1 High Pressure Liquid Chromatography (HPLC) and Nuclear Magnetic Resonance (NMR)

8.7.1.1 Detection of metabolites by HPLC

Labelled [1-^{14}C]DMSP (2.7 kBq) was added to cell-free extracts of *E. coli* strain BL21 to a final concentration of 1 mM. Following 2 hours incubation, labelled products were identified by HPLC. The DMSP catabolites were resolved on a Dionex (Sunnyvale, CA, USA) ICE-AS6 column (250 mm x 9 mm id.) eluted isocratically with 0.4 mM HCl at a flow rate of 1 ml min^{-1}. The column, suppressor and detection cell were maintained at 35°C. Metabolites were detected by tandem suppressed ion conductivity and UV detection at 210 nm. Ion suppression used a Dionex AMMS-ICE Micromembrane Suppressor with 5 mM tetrabutylammonium hydroxide as the solvent (flow rate of 2 ml min^{-1}). Conductivity was measured with a Dionex ED50 conductivity detector and UV absorbance with a Jasco (Tokyo, Japan) UV-975 detector.

8.7.1.2 Detection of metabolites by NMR

Cultures of *E. coli* containing cloned genes were grown overnight at 37°C in LB, adjusted to equivalent OD_{600} nm values, then diluted 10^{-2} into 1 ml M9 [made up in deuterium oxide (> 99.9%)], containing glycerol (10 mM), and 10 mM [1-^{13}C]DMSP or 5 mM [1-^{13}C]acrylate and 0.2 mM IPTG to induce expression of the cloned genes. After incubating at 28 °C overnight, cells were lysed by adding perchloric acid (5% v/v final concentration) and samples were incubated on ice for 10 min. Cell debris was spun down and the supernatant was added to NMR tubes.

For NMR of purified DddP, 50 µl (~0.9 µM) of protein was added to 5 mM [1-^{13}C]DMSP and made up to 500 µl in deuterium oxide.

Proton-decoupled ^{13}C NMR spectra were measured at 75 MHz with a Varian Gemini 2000 in D_2O. An average of 300 scans was recorded when DMSP was used and an average of 1000 scans when acrylate solutions were used. Note that ^{13}C NMR detects the ^{13}C isotope, whose natural abundance is only 1.1%.

8.7.2 Inductively coupled plasma, optical emission spectrometry (ICP-OES).

ICP-OES was carried out on samples of 10 µM DddP in 2.5% (v/v) nitric acid. A Varian Vista Pro CCD simultaneous ICP-OES, with axial torch, concentric seaspray nebuliser (Glass Expansion) and 50 ml cyclonic spray chamber was used to analyse triplicate samples. The power was 1.2 kW and the analysed wavelengths were: Co, 228.62 nm; Cu, 324.75 nm; Mn, 259.37 nm; Ni, 230.30 nm; Zn, 213.86 nm. The limits of detection for Co, Cu, Mn, Ni and Zn were 7.3, 5.3, 9.1, 206 and 10.0 nmol, respectively.

8.8 Chemical syntheses

These were carried out by Dr Y Chan (UEA chemistry department). DMSP was prepared by adding dimethylsulfide (15.3 ml, 0.21 mol) to aqueous HCl (100 ml, 2 M). Acrylic acid (10.0 g, 0.14 mol) was added, and the resulting mixture heated under reflux (95°C) for 2h. The reaction mixture was allowed to reach room temperature and concentrated under reduced pressure. The residue was triturated using a mixture of ethanol/diethyl ether, and the resulting solid was filtered, washed once with ethanol and twice with diethyl ether to yield DMSP (21.8 g, 92%). The identity and purity of DMSP was established by melting point, and by infrared and NMR spectroscopy [m.p. 134–135°C; ν_{max} (solid/cm^{-1}) 3013, 2621, 2549, 2478, 2426, 1787, 1691, 1414, 1396, 1247, 1183, 906; δ_H (400 MHz; D_2O) 2.94 (6H, s, 2 × CH_3), 2.98 (2H, t, J = 6.8 Hz), 3.53 (2H, t, J = 6.8 Hz); δ_C (75 MHz; D_2O) 24.51, 27.84, 38.05, 173.17]. [1-^{14}C]DMSP was made as described above except that ^{14}C-labelled acrylic acid (27 MBq in 0.75 ml dH_2O) was also added, and the resulting mixture heated under reflux (95°C) for 2 hours. The reaction mixture was allowed to reach room temperature and concentrated under reduced pressure. The residue was triturated using a mixture of ethanol/diethyl ether, and the resulting solid was filtered, washed once with ethanol and twice with diethyl ether to yield [1-^{14}C]DMSP. [1-^{13}C]DMSP HCl was prepared by adding ^{13}C-acrylic acid (100 mg, 1.39 mmol) to aqueous HCl (5 ml, 2 M). DMS (2.78 mmol) was added and then treated as above, for [1-^{14}C]DMSP, to yield [1-^{13}C]DMSP (210 mg, 89%).

Table 8.4 Strains used in this study

Bacteria	**Characteristics**	**Source**
Escherichia coli 803	Met^-; used as host for transformation with large plasmids	Wood (1966)
E. coli BL21	Used as host for expression from pET21a	Studier and Moffat (1986)
E. coli JM101	Used as host for expression of pBluescript and for blue white screens	(Yanisch-Perron *et al.*, 1985)
Rhizobium leguminosarum J391	Wild type; $Strep^R$ mutant	Young *et al.* (2006)
Rhizobium leguminosarum strain 3841	Wild type strain ($Strep^R$) Heterologous host for expression of *dddW*	Todd *et al.,* (2011b)
Roseovarius nubinhibens ISM	Wild type isolate	González *et al.* (2003)
Ruegeria pomeroyi DSS-3	Wild type isolate	González *et al.* (2003)
Ruegeria pomeroyi J470	*R. pomeroyi* DSS-3 Rif^R mutant	Todd *et al.,* (2011a)
Ruegeria pomeroyi J471	*R. pomeroyi* J470 with insertion in *dmdA*	This study; Todd *et al.,* (2012)
Ruegeria pomeroyi J527	*R. pomeroyi* J470 with insertion in *acuI*	This study; Todd *et al.,* (2012)
Ruegeria pomeroyi J530	*R. pomeroyi* J470 with insertion in *dmdR*	This study; Todd *et al.,* (2012)
Ruegeria pomeroyi J497	*R. pomeroyi* J470 with insertion in *dddW*	This study

Table 8.5 Plasmids used in this study

Plasmid	Description	Features	Origin
pET21a	Used for expression of cloned *ddd, dmdA* and *acuI* genes	Amp^R	Novagen
pBIO1658	*R. nubinhibens dddP* cloned in pET21a	Amp^R	Todd *et al.,* (2010)
pMP220	Broad-host-range promoter probe vector with promoterless *lacZ* reporter gene	Tet^R	Spaink *et al.,* (1987)
pBIO1878	Spc^R cassette cloned into pMP220. Used as *lacZ*-promoter fusion plasmid in *Ruegeria pomeroyi*	Tet^R Spec^R	Todd *et al.,* (2012a)
pRK2013	Used as mobilising plasmid in tri-parental crosses	Kan^R	Figurski & Helinski (1979)
pBluescript	Used for sub-cloning genes, prior to cloning into larger, low-copy vectors	Amp^R	*Stratagene*
pK19*mob*	Suicide insertion plasmid	Kan^R	Schäfer *et al.,* (1994)
pBIO1879	pK19*mob* suicide vector with added Spec^R cassette	Spec^R Kan^R	Todd *et al.,* (2011)
pBIO1887	*dddP* of *Ruegeria pomeroyi* DSS-3 cloned in pET21a	Amp^R	This work
pUC18	High copy number cloning vector	Amp^R	Vieira *et al.,* (1982)
pBIO1945	pBIO1878 containing 307 bp fragment spanning the *dddW* promoter	Contains *lacZ* reporter Tet^R, Spec^R	This study

pBIO1946	pOT2 containing *SPO0454* and its native promoter	Gent^R	This study
pBIO1947	SPO0454 promoter cloned into pBIO1878	Amp^R Spec^R	This study
pBIO1948	pET21 containing *R. pomeroyi dddW*	Amp^R	This study
pBIO1949	pBIO1879 containing internal *dddW* fragment	Spec^R Kan^R	Todd *et al.*, (2011)
pBIO1870	Internal fragment of *Ruegeria pomeroyi* DSS-3 *dmdA* cloned into pBIO1879	Spec^R Kan^R	Todd *et al.*, (2012b)
pBIO2013	*Ruegeria pomeroyi* DSS-3 *acuI* cloned in pET21a	Amp^R	Todd *et al.*, (2012b)
pBIO2019	*Ruegeria pomeroyi* DSS-3 *dmdA* and *acuI* with their native promoter, cloned in pBluescript	Amp^R	Todd *et al.*, (2012b)
pBIO2020	*Ruegeria pomeroyi* DSS-3 *dmdA-lacZ* reporter fusion plasmid	Tet^R Spec^R	Todd *et al.*, (2012b)
pBIO2021	*Ruegeria pomeroyi* DSS-3 *acuI-lacZ* reporter fusion plasmid	Tet^R Spec^R	Todd *et al.*, (2012b)
pBIO2022	*Ruegeria pomeroyi* DSS-3 *dmdA* and *acuI* with their native promoter cloned in pBIO1878	Tet^R Spec^R	Todd *et al.*, (2012b)
pBIO2023	pBIO2019 with a deletion in *dmdA*	Amp^R	Todd *et al.*, (2012b)
pBIO2024	*Ruegeria pomeroyi* DSS-3 *acuI* with its own promoter, sub-cloned from pBIO2023 into pBIO1878	Tet^R Spec^R	Todd *et al.*, (2012b)
pBIO2025	Internal fragment of *Ruegeria pomeroyi* DSS-3 *acuI* cloned into pBIO1879	Spec^R Kan^R	Todd *et al.*, (2012b)

pBIO2083	pBIO2021 digested with *EcoR*I to remove *dmdA* promoter and a large section of *dmdA*	Tet^R $Spec^R$	This study
pBIO2084	pBIO2021 with an introduced +1 frameshift prior to *lacZ*	Tet^R $Spec^R$	This study
pBIO2085	pBIO1879 containing internal *dmdR* fragment	$Spec^R$ Kan^R	This study
pBIO2086	pBIO1878 with *coxM* promoter	$Spec^R$ Tet^R	This study

Table 8.6 Primers used in this study

Primer name	**Primer sequence (5' – 3')**	**Use**
DddPF	GGAATTCCATATGAACCAGCATTACAGCG	Cloning *dddP* of *Roseovarius nubinhibens* ISM into pET21a
DddPR	GGAATTCATGCCCCGCCCTGCCCG	Cloning *dddP* of *Roseovarius nubinhibens* ISM into pET21a
SydDddPF	GGACCG/AACTCCGCTGGCGTT	Amplification of conserved regions of *dddP* in isolates of *Aspergillus sydowii*
SydDddPR	TCATAG/ACCCGTCTCCGTCAC	Amplification of conserved regions of *dddP* in isolates of *Aspergillus sydowii*
D295 For	CATCTCTTTCG**c**CACCGATCTCATCGG	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*

D295 Rev	CCGATGAGATCGGTG**g**CGAAAGAGATG	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
D297 For	CTTTCGACACCG**c**TCTCATCGGCAGC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
D297 Rev	GCTGCCGATGAGA**g**CGGTGTCGAAAG	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
D307 For	GGCATCTGCGTCG**c**CATCTCGCGCAGC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
D307 Rev	GCTGCGCGAGATG**g**CGACGCAGATGCC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
H371 For	GGCTGCCTGATGG**c**TGGGGTCGGGC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
H371 Rev	GCCCGACCCCA**g**CCATCAGGCAGCC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
E406 For	GCTCTGTGTCG**c**GGCGGCGGTCGGCG	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
E406 Rev	CGCCGACCGCCGCC**g**CGACACAGAGC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*

E421 For	CCATCAAGCTCG**c**GGATCAGGTGC	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
E421 Rev	GCACCTGATCC**g**CGAGCTTGATGG	Site directed mutagenesis of *Roseovarius nubinhibens* ISM *dddP*
Wprom 1	GCGAATTCCATCGTCAGCAGAGTC	Cloning promoter of *Ruegeria pomeroyi* DSS-3 *dddW* into pBIO1878
Wprom 2	GCCTGCAGCACCATGTCGCGCGGCG	Cloning promoter of *Ruegeria pomeroyi* DSS-3 *dddW* into pBIO1878
Wpet1	AACTGCAGCATATGACCGCCATGCT CGACAGTTTC	Amplification of *dddW* to create expression vector pBIO1948
Wpet2	ATGGATCCTCAGGCGCTGGCGGTGAACCG	Amplification of *dddW* to create expression vector pBIO1948
RTdddPF	GCTGTGGAACACCCATAA	For qRT-PCR analysis of *dddP*
RTdddPR	GCCTCGGTCGAAATAGAACA	For qRT-PCR analysis of *dddP*
RTdddQF	AAACCTTCTGGCCGAGTTTC	For qRT-PCR analysis of *dddQ*
RTdddQR	ATAGGCTGTGGTCGTCAGGT	For qRT-PCR analysis of *dddQ*
RTdddWF	GTTTCGCAACCGATCTGACT	For qRT-PCR analysis of *dddW*

RTdddWR	TCGAGGCCCAGATAGAACTC	For qRT-PCR analysis of *dddW*
SPO2904F	TAAGCTTTCCGGTCCTGATG	For qRT-PCR analysis, control
SPO2904R	ACCGTCGATTTCAGCAACTT	For qRT-PCR analysis, control
Wmut1	CGGGATCCAGCCCGGCAACCTGCCG	Cloning internal *dddW* fragment to create pBIO1949
Wmut2	CGGGATCCATAGGCAAAGCGCAGACC	Cloning internal *dddW* fragment to create pBIO1949
454P1	ATCTGCAGCAAACCGCGCTATTTGTGACT	Cloning *R. pomeroyi* DSS-3 *SPO0454* and its promoter into pOT2
454P2	ATGTCGACAGATCGGTTGCGAAACTGTCG	Cloning *R. pomeroyi* DSS-3 *SPO0454* and its promoter into pOT2
454prom1	GGCCGAATTCGGCGATGCCCAC	Cloning promoter of *SPO0454* into pBIO1878
454prom2	AACTGCAGGCGCACCAGCGCGCC	Cloning promoter of *SPO0454* into pBIO1878
SPO1913F_Pst	GCCTGCAGGGGCCCGACGCGCGCGG	For cloning fragment used in pBIO1870
SPO1913R_Eco	GCGACATTCAGCCGAATTC	For cloning fragment used in pBIO1870
SPO1913/14_XbaF	GCGTCTAGAGGTCCTGACGCCGGGTCGCAC	For cloning fragment used in pBIO2019

SPO1913/14_BamR	CGGGATCCGGGCCTCTTGCCGCTCACTTC	For cloning fragment used in pBIO2019 and pBIO2013
acuI+1_NsiR	ACCAATGCATTCGAACATCTG	For cloning fragment used in pBIO2084
Spo1914_NdeF	GGAATCCATATGTTCAATGCATTGGTGG	For cloning fragment used in pBIO2013
1912_EcoF	CGCGGAATTCCAGATCGACCCCAACAGC	For cloning fragment used in pBIO2085
1912_PstR	CGCGCTGCAGTCGTATAGCGCATCAGTTCG	For cloning fragment used in pBIO2085
SPO2399_ecoR1 for1	GCGAATTCCGGCTTTTGCAGGTGCC	For cloning fragment used in pBIO2086
SPO2399_pst1 rev1	GCCTGCAGCGCGGCTTCGCGCAGG	For cloning fragment used in pBIO2086

Sequences of the oligonucleotide primers are shown, with cloning restriction sites underlined.

All primers were synthesised by MWG Biotech. Where required, primers were supplied with phosphate groups at their 5’ ends.

Chapter 9

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Chapter 10

Appendix

A1: Abbreviations

ABC ATP-binding cassete

Acu Acrylate-utilising

AMP Adenosine monophosphate

Amp Ampicillin

Amp$^{\mathbf{R}}$ Ampicillin-resistant

ATP Adenosine triphosphate

Bp Base pair(s)

BCCT Betaine-Carnitine-Choline Transporter

BLAST Basic Local Alignment Search Tool

CCN Cloud condensation nuclei

cDNA complementary DNA

CO Carbon monoxide

CO$_2$ Carbon dioxide

CoA Coenzyme A

CODH Carbon monoxide dehydrogenase

Da Daltons

Ddd DMSP-dependent DMS

DEPC diethyl pyrocarbonate

dH2O Distilled H2O

DMS Dimethyl sulfide

DMSP Dimethylsulfoniopropionate

DMSHB ***D***-4-dimethylsulfonio-2-hydroxybutyrate

DNA Deoxyribonucleic acid

dNTP deoxynucleotide triphosphate

DTT dithiothreitol

EDTA Ethylenediaminetetra-acetic acid

EtBr Ethidium bromide

FAD flavin adenine dinucleotide

g gram

GC Gas chromatography

Gent Gentamicin

Gent$^{\mathbf{R}}$ Gentamicin- resistant

GOS Global Ocean Survey

GTP Guanosine triphosphate

HGT Horizontal gene transfer

3HP 3-hydroxypropionate

HPLC High pressure liquid chromatography

IPTG Isopropyl-β-D-thiogalactopyranoside

k kilo

Kan Kanamycin

Kan$^{\mathbf{R}}$ Kanamycin-resistant

kbp kilo base pair(s)

kDa kilo Daltons

l litre

LOWESS Locally weighted scatterplot smoothing algorithm

m milli

µ micro

M Molar

MalSA Malonate semialdehyde

Mb Megabase(s)

MBM Marine basal medium

MeSH methanethiol

MMPA methylmercaptopropionate

MPA 3-mercaptopropionate

mol moles

mRNA messenger RNA

MTHB *D*-4-methylthio-2-hydroxybutyrate

MTO Methanethiol oxidase

MTOB 4-methylthio-2-oxobutyrate

n nano

NMR Nuclear magnetic resonance

OD Optical density

ONPG *ortho*-nitrophenyl-β-D-galactopyranoside

PAGE Polyacrylamide gel electrophoresis

PCR Polymerase chain reaction

p pico

q-RTPCR quantitative real-time reverse transcriptase PCR

RBS Ribosomal binding site

Rif Rifampicin

Rif$^{\mathbf{R}}$ Rifampicin-resistant

RNA Ribonucleic acid

rRNA ribosomal RNA

RT Reverse transcriptase

SDS Sodium dodecyl sulfate

SMM *S*-methyl methionine

sp. Species

Spec Spectinomycin

Spec$^{\mathbf{R}}$ Spectionmycin-resistant

spp. Species (plural)

Str Streptomycin

Str$^{\mathbf{R}}$ Streptomycin-resistant

Tet Tetracycline

Tet$^{\mathbf{R}}$ Tetracycline-resistant

THF Tetrahydrofolate

Tris Tris (hydroxymethyl) aminomethane

UV Ultra-violet

X-gal 5-bromo-4-chloro-3-indolyl-β-D-galactoside

YTSS Yeast-Tryptone-Sea Salts

A2: Publications

Todd, J.D., Curson, A.R.J., Sullivan, M.J**., Kirkwood, M**. and Johnston, A.W.B. (2012) The *Ruegeria pomeroyi acuI* gene has a role in DMSP catabolism and resembles *yhdH* of *E. coli* and other bacteria in conferring resistance to acrylate. *PLoS One* **7:** e35947

In this paper I was responsible for sensitivity tests, whereby YhdH was shown to facilitate growth in the presence of acrylate, and much of the work presented in chapter 5 directly precedes work presented in this journal article.

Todd, J.D., Curson, A.R.J., **Kirkwood, M**., Sullivan, M.J., Green, R.T., and Johnston, A.W.B. (2011) DddQ, a novel, cupin-containing, dimethylsulfoniopropionate lyase in marine Roseobacters and in uncultured marine bacteria. *Env Microbiol* **13:** 427-438

My work for this journal article involved alignments of the DddQ and DddL peptides, and several of the DMS assays showing activity of heterologous strains.

Todd, J.D., **Kirkwood, M.**, Newton-Payne, S. and Johnston, A.W.B. (2011) DddW, a third DMSP lyase in a model Roseobacter marine bacterium, *Ruegeria pomeroyi* DSS-3. *ISME J* **6:** 223-226

Again, I was responsible for the alignment of the similar peptide regions. Also, work on heterologous expression of DddW, along with *lacZ* assays showing transcriptional regulation, were conducted by me, as shown in chapter 4 of this thesis.

Kirkwood, M., Todd, J.D., Rypien, K.L. and Johnston, A.W.B. (2010) The opportunistic coral pathogen *Aspergillus sydowii* contains *dddP* and makes dimethyl sulphide from dimethylsulfoniopropionate. *ISME J* **4:** 147-150

Kirkwood, M., Le Brun, N.E., Todd, J.D. and Johnston, A.W.B. (2010) The *dddP* gene of *Roseovarius nubinhibens* encodes a novel lyase that cleaves dimethylsulfoniopropionate into acrylate plus dimethyl sulphide. *Microbiol* **156:** 1900-1906

All work in both of these articles was carried out by me, and is presented in chapter 2.

A3: Microarray data

Table 10.1 Microarray data for the fold-change in gene expression in *Ruegeria pomeroyi* following exposure to DMSP, DMS or acrylate

Gene No.	Name	Function	Dp1	P	Dp2	P	Mean	Error	A1	P	A2	P	Mean	Error	Ds1	P	Ds2	P	Mean	Error
SPO0001	*gidA*	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	-1.23	0.04	-1.01	0.92	-1.12	0.11	-0.93	0.04	-1.46	0.00	-1.19	0.27	-1.64	0.00	-2.01	0.00	-1.83	0.19
SPO0002	*gidB*	glucose-inhibited division protein B	-1.17	X	1.17	0.33	0.00	1.17	-0.89	0.03	-1.34	0.32	-1.12	0.22	-1.31	0.09	-1.48	0.29	-1.40	0.09
SPO0003	*parA*	chromosome partitioning protein ParA	1.08	0.97	0.98	0.84	1.03	0.05	1.31	0.40	-1.28	0.26	0.02	1.30	-1.16	0.46	0.99	0.80	-0.08	1.08
SPO0004	*parB*	chromosome partitioning protein parB	1.64	0.16	-1.08	0.60	0.28	1.36	1.69	0.03	0.98	0.44	1.33	0.36	1.05	0.93	1.08	0.88	1.07	0.02
SPO0005		hypothetical protein	2.62	0.00	1.44	0.45	2.03	0.59	2.78	0.02	-1.03	0.90	0.88	1.91	-1.09	0.83	-0.98	0.86	-1.04	0.05
SPO0006		coproporphyrinogen III oxidase	-1.55	0.40	1.13	0.42	-0.21	1.34	1.68	0.15	-1.21	0.11	0.24	1.45	-1.37	0.03	-1.64	0.07	-1.51	0.14
SPO0007		deoxyribonucleotide triphosphate pyrophosphatase	-1.87	0.00	1.17	0.39	-0.35	1.52	1.21	0.07	-1.32	0.06	-0.06	1.27	-1.55	0.04	-2.07	0.00	-1.81	0.26
SPO0008	*rph*	ribonuclease PH (EC:2.7.7.56)	-1.08	0.74	1.28	0.08	0.10	1.18	2.64	0.02	-1.42	0.01	0.61	2.03	-1.37	0.00	-1.82	0.00	-1.60	0.22
SPO0009	*hrcA*	heat-inducible transcription repressor	1.51	0.00	1.20	0.01	1.36	0.16	1.76	0.00	-1.02	0.66	0.37	1.39	1.14	0.15	-1.08	0.29	0.03	1.11
SPO0010	*grpE*	co-chaperone GrpE	1.81	0.00	1.02	0.99	1.42	0.39	2.28	0.00	-1.37	0.00	0.46	1.83	-1.37	0.00	-1.38	0.00	-1.38	0.00
SPO0011	*mutS*	DNA mismatch repair protein MutS	X	X	1.06	0.59	N/A	N/A	3.80	0.00	-1.13	0.12	1.34	2.47	-1.26	0.03	-1.78	0.00	-1.52	0.26
SPO0012	*maeB*	malic enzyme (EC:1.1.1.40)	1.48	0.01	1.65	0.01	1.57	0.09	3.72	0.00	-1.26	0.01	1.23	2.49	-1.40	0.01	-1.93	0.00	-1.67	0.27
SPO0013	*rbsK*	ribokinase (EC:2.7.1.15)	1.52	0.11	1.48	0.03	1.50	0.02	2.89	0.01	-1.29	0.06	0.80	2.09	-1.01	0.79	-1.37	0.01	-1.19	0.18
SPO0014	*msrA-1*	methionine-S-sulfoxide reductase (EC:1.8.4.-)	1.30	0.15	1.18	0.22	1.24	0.06	-2.31	0.00	1.09	0.67	-0.61	1.70	-0.99	0.79	1.58	0.04	0.29	1.29
SPO0015		hypothetical protein	-1.47	0.00	1.16	0.58	-0.16	1.32	1.19	0.01	-1.17	0.49	0.01	1.18	1.15	0.03	-1.03	0.97	0.06	1.09
SPO0016		sterol carrier protein	-1.43	0.04	1.23	0.53	-0.10	1.33	-1.46	0.04	-1.26	0.02	-1.36	0.10	1.09	0.08	1.21	0.27	1.15	0.06
SPO0017		hypothetical protein	-3.41	0.04	1.29	0.20	-1.06	2.35	1.28	0.47	-1.42	0.02	-0.07	1.35	-1.26	0.26	-1.69	0.00	-1.48	0.21
SPO0018	*argG*	argininosuccinate synthase (EC:6.3.4.5)	1.54	0.04	1.40	0.06	1.47	0.07	4.84	0.00	-1.43	0.00	1.71	3.14	-1.10	0.20	-1.46	0.00	-1.28	0.18
SPO0019		hypothetical protein	-1.09	0.23	2.14	0.00	0.53	1.62	-1.39	0.08	1.07	0.52	-0.16	1.23	-1.02	0.51	-1.07	0.36	-1.05	0.03
SPO0020	*ilvA*	threonine dehydratase (EC:4.3.1.19)	1.06	0.67	1.25	0.01	1.16	0.10	1.33	0.06	-1.41	0.00	-0.04	1.37	1.10	0.28	-1.00	0.75	0.05	1.05
SPO0021		Hpt domain-containing protein	1.51	0.00	2.40	0.07	1.96	0.44	-7.49	0.00	3.39	0.00	-2.05	5.44	-1.06	0.95	1.41	0.37	0.18	1.24
SPO0022		response regulator	-1.76	0.01	1.23	0.05	-0.27	1.50	-6.04	0.00	1.49	0.07	-2.28	3.77	-1.54	0.11	-1.07	0.75	-1.31	0.23
SPO0023		NUDIX family hydrolase	-1.03	0.83	1.05	0.66	0.01	1.04	1.86	0.00	-1.54	0.00	0.16	1.70	-2.14	0.00	-2.21	0.00	-2.18	0.03
SPO0024	*hslO*	chaperonin, 33 kDa	-1.69	0.00	-1.31	0.03	-1.50	0.19	2.19	0.00	-1.33	0.00	0.43	1.76	-1.12	0.05	0.95	0.18	-0.08	1.04
SPO0025		NUDIX family hydrolase	X	X	-1.36	0.01	N/A	N/A	3.31	0.00	-1.84	0.00	0.74	2.58	1.14	0.06	-1.34	0.00	-0.10	1.24
SPO0026		poly(A) polymerase	-1.66	0.20	-1.42	0.33	-1.54	0.12	1.85	0.19	-1.66	0.28	0.10	1.76	1.05	0.88	-1.02	1.00	0.02	1.04
SPO0027		ABC transporter transmembrane ATP-binding protein	-1.27	0.75	1.56	0.10	0.15	1.42	-1.19	0.87	-1.30	0.54	-1.25	0.06	1.12	0.79	1.27	0.41	1.20	0.08
SPO0028		ABC transporter transmembrane ATP-binding protein	-1.06	0.74	-1.12	0.57	-1.09	0.03	-1.09	0.92	1.03	0.88	-0.03	1.06	-1.21	0.48	1.09	0.59	-0.06	1.15
SPO0029	*rumA*	23S rRNA (uracil-5-)-methyltransferase RumA	-1.25	0.09	1.28	0.01	0.02	1.27	2.03	0.00	-1.59	0.00	0.22	1.81	-1.08	0.28	-1.76	0.00	-1.42	0.34

		(EC:2.1.1.-)																		
SPO0030		voltage-gated sodium channel	1.80	0.03	1.11	0.48	1.46	0.35	3.07	0.00	-2.10	0.00	0.49	2.59	1.25	0.16	-1.19	0.29	0.03	1.22
SPO0031		ErfK/YbiS/YcfS/YnhG family protein	1.17	0.94	0.98	0.84	1.07	0.10	1.09	0.94	-1.23	0.34	-0.07	1.16	1.23	0.53	-1.09	0.66	0.07	1.16
SPO0032		hypothetical protein	-1.49	0.20	-1.18	0.31	-1.34	0.16	-2.13	0.01	-1.34	0.14	-1.74	0.40	-1.07	0.79	-0.92	0.74	-1.00	0.07
SPO0033		LysR family transcriptional regulator	-1.30	0.36	-1.10	0.19	-1.20	0.10	-1.10	0.25	-1.46	0.00	-1.28	0.18	-1.12	0.29	-1.42	0.10	-1.27	0.15
SPO0034		hypothetical protein	-1.14	0.62	-1.03	0.87	-1.09	0.05	-1.29	0.49	1.08	0.85	-0.11	1.19	-1.08	0.64	-1.06	0.75	-1.07	0.01
SPO0035		core-2/I-branching enzyme family protein	-1.65	0.00	-1.02	0.91	-1.34	0.32	-1.42	0.04	-1.18	0.29	-1.30	0.12	-1.15	0.34	-1.68	0.00	-1.42	0.27
SPO0036		hypothetical protein	-1.56	0.02	-1.33	0.15	-1.45	0.12	-1.60	0.08	-1.06	0.71	-1.33	0.27	-1.49	0.07	-1.25	0.30	-1.37	0.12
SPO0037		hypothetical protein	-2.03	0.00	-1.19	0.04	-1.61	0.42	-1.97	0.00	-1.10	0.21	-1.54	0.44	-1.75	0.00	-1.18	0.24	-1.47	0.29
SPO0038	*kdsB*	3-deoxy-manno-octulosonate cytidylyltransferase (EC:2.7.7.38)	-1.09	0.52	-1.04	0.67	-1.07	0.03	1.58	0.00	-1.06	0.51	0.26	1.32	1.09	0.75	1.82	0.02	1.46	0.37
SPO0039	*cysQ*	3'(2'),5'-bisphosphate nucleotidase (EC:3.1.3.7)	-1.13	0.01	1.26	0.30	0.07	1.20	2.00	0.00	1.06	0.81	1.53	0.47	-1.44	0.00	-1.33	0.06	-1.39	0.05
SPO0040		ABC transporter permease	1.19	0.42	-1.18	0.26	0.01	1.19	-1.73	0.00	1.01	0.74	-0.36	1.37	1.23	0.01	1.35	0.02	1.29	0.06
SPO0041		hypothetical protein	1.33	0.62	1.12	0.53	1.23	0.11	0.86	0.54	1.00	0.71	0.93	0.07	1.65	0.00	1.61	0.01	1.63	0.02
SPO0042		alkylated DNA repair protein	1.13	0.91	1.13	0.26	1.13	0.00	1.41	0.64	-1.38	0.14	0.02	1.40	1.26	0.10	1.11	0.40	1.19	0.08
SPO0043	*dnaK*	molecular chaperone Dna	0.97	0.69	-1.69	0.01	-0.36	1.33	2.62	0.05	-1.63	0.00	0.50	2.13	1.21	0.32	1.49	0.28	1.35	0.14
SPO0044	*dnaJ*	molecular chaperone DnaJ	-1.34	0.58	-1.19	0.28	-1.27	0.08	2.22	0.37	-1.41	0.20	0.41	1.82	1.18	0.58	1.32	0.55	1.25	0.07
SPO0045	*thiD*	phosphomethylpyrimidine kinase (EC:2.7.4.7)	-1.81	0.09	-1.01	1.00	-1.41	0.40	1.15	0.22	-2.14	0.02	-0.50	1.65	-0.97	0.82	-1.26	0.63	-1.11	0.15
SPO0046		thiamine biosynthesis oxidoreductase ThiO	-1.26	0.33	-1.11	0.57	-1.19	0.08	1.38	0.32	-1.74	0.00	-0.18	1.56	-1.55	0.01	-1.95	0.00	-1.75	0.20
SPO0046.1	*thiS*	thiamine biosynthesis protein ThiS	1.09	0.94	1.03	0.90	1.06	0.03	1.41	0.70	-1.21	0.55	0.10	1.31	-1.00	0.97	1.28	0.25	0.14	1.14
SPO0047	*thiG*	thiazole synthase	X	X	1.13	0.14	N/A	N/A	1.48	0.00	-1.95	0.02	-0.24	1.72	-1.35	0.17	X	X	N/A	N/A
SPO0048	*thiE*	thiamine-phosphate pyrophosphorylase (EC:2.5.1.3)	-1.06	0.73	1.11	0.28	0.03	1.09	1.45	0.00	-1.73	0.00	-0.14	1.59	-1.38	0.03	-2.03	0.01	-1.71	0.33
SPO0049		thiamine biosynthesis protein ThiF	X	X	-1.17	0.26	N/A	N/A	-0.97	0.01	-1.72	0.03	-1.34	0.38	-1.86	0.00	-1.13	0.97	-1.50	0.37
SPO0050		ABC transporter substrate-binding protein	-1.23	0.85	-1.06	0.81	-1.15	0.09	1.21	0.83	-1.30	0.19	-0.05	1.26	-1.42	0.07	-1.68	0.12	-1.55	0.13
SPO0051		TENA/THI-4 family protein	-1.80	0.11	1.07	0.48	-0.37	1.44	2.15	0.06	-1.25	0.08	0.45	1.70	-1.36	0.01	-1.53	0.08	-1.45	0.09
SPO0052		ABC transporter ATP-binding protein	-1.63	0.09	1.10	0.35	-0.27	1.37	1.57	0.09	-1.65	0.00	-0.04	1.61	1.09	0.82	-0.98	0.77	0.05	1.04
SPO0053		ABC transporter permease	X	X	-1.01	0.97	N/A	N/A	1.27	0.01	-1.36	0.10	-0.05	1.32	1.08	0.35	-1.13	0.74	-0.02	1.11
SPO0054	*radC*	DNA repair protein RadC	1.13	0.69	1.19	0.28	1.16	0.03	-4.31	0.00	1.44	0.01	-1.44	2.88	-1.05	0.98	-1.22	X	-1.14	0.09
SPO0055		OmpA domain-containing protein	-1.17	0.24	1.04	0.89	-0.06	1.11	2.11	0.00	1.02	0.94	1.57	0.55	1.05	0.71	1.33	0.12	1.19	0.14
SPO0056		hypothetical protein	-2.16	0.00	-1.08	0.46	-1.62	0.54	-2.96	0.00	-1.15	0.50	-2.06	0.91	-1.26	0.17	-1.19	0.89	-1.23	0.04
SPO0057	*secA*	preprotein translocase subunit SecA	-1.06	0.57	-1.42	0.00	-1.24	0.18	3.00	0.00	-1.36	0.01	0.82	2.18	-1.30	0.04	0.97	0.20	-0.16	1.14
SPO0058		peptidyl-prolyl cis-trans isomerase domain-containing protein	1.71	0.08	-1.35	0.17	0.18	1.53	2.03	0.04	-1.30	0.09	0.37	1.67	1.26	0.31	1.72	0.05	1.49	0.23
SPO0059	*argJ*	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase (EC:2.3.1.1 2.3.1.35)	1.81	0.00	-1.08	0.32	0.37	1.45	2.41	0.00	-1.32	0.01	0.55	1.87	1.54	0.00	1.04	0.41	1.29	0.25
SPO0060	*mutT*	mutator mutT protein (EC:3.6.1.-)	3.13	0.00	-1.12	0.06	1.01	2.13	3.56	0.00	-1.27	0.02	1.15	2.42	1.52	0.00	1.30	0.03	1.41	0.11
SPO0061	*infB*	translation initiation factor IF-2	1.07	0.94	1.57	0.02	1.32	0.25	3.06	0.00	-1.33	0.11	0.87	2.20	1.48	0.04	-1.32	0.21	0.08	1.40
SPO0062		hypothetical protein	-1.61	0.00	-1.24	0.04	-1.43	0.19	1.71	0.00	-1.30	0.01	0.21	1.51	-1.69	0.00	-2.20	0.00	-1.95	0.26
SPO0063	*nusA*	transcription elongation factor NusA	-1.53	0.00	0.97	0.34	-0.28	1.25	1.32	0.08	-1.48	0.00	-0.08	1.40	-1.61	0.00	-2.11	0.00	-1.86	0.25
SPO0064		hypothetical protein	-1.72	0.00	1.05	0.75	-0.34	1.39	1.34	0.02	-1.58	0.00	-0.12	1.46	-1.77	0.00	-2.65	0.00	-2.21	0.44
SPO0065		peptide/opine/nickel uptake ABC transporter	-1.48	0.00	1.05	0.73	-0.22	1.27	-1.30	0.01	1.16	0.18	-0.07	1.23	1.01	0.95	-1.07	0.49	-0.03	1.04

		substrate-binding protein																		
SPO0066	*pip*	proline iminopeptidase (EC:3.4.11.5)	1.00	0.72	1.12	0.28	1.06	0.06	1.19	0.39	1.63	0.00	1.41	0.22	1.14	0.34	1.17	0.02	1.16	0.02
SPO0067	*ubiG*	3-demethylubiquinone-9 3-methyltransferase (EC:2.1.1.64)	4.01	0.00	2.40	0.00	3.21	0.80	3.21	0.00	-1.08	0.25	1.07	2.15	1.29	0.02	-1.20	0.20	0.05	1.25
SPO0068		transcriptional regulator	-1.16	0.56	1.22	0.06	0.03	1.19	1.44	0.26	-1.28	0.01	0.08	1.36	1.22	0.09	-1.02	0.83	0.10	1.12
SPO0069		carbon-nitrogen family hydrolase	1.39	0.01	1.63	0.01	1.51	0.12	1.51	0.00	1.01	0.91	1.26	0.25	-1.18	0.07	-1.23	0.11	-1.21	0.03
SPO0070		glutaredoxin	0.88	0.70	-1.05	0.62	-0.09	0.96	-1.86	0.22	1.17	0.26	-0.35	1.52	1.05	0.92	1.03	0.90	1.04	0.01
SPO0071		competence protein F	0.97	0.15	-1.21	0.36	-0.12	1.09	-5.24	0.00	1.30	0.10	-1.97	3.27	-1.29	0.34	2.01	0.00	0.36	1.65
SPO0072		hypothetical protein	X	X	1.26	0.08	N/A	N/A	1.37	0.00	-1.25	0.04	0.06	1.31	-1.52	0.00	-2.30	0.00	-1.91	0.39
SPO0073	*hemH*	ferrochelatase (EC:4.99.1.1)	1.04	0.99	1.07	0.68	1.06	0.02	1.27	0.54	-1.44	0.00	-0.09	1.36	-1.28	0.15	-1.41	0.01	-1.35	0.06
SPO0074		hypothetical protein	1.15	0.64	1.59	0.00	1.37	0.22	1.29	0.40	0.97	0.02	1.13	0.16	1.63	0.02	1.28	0.73	1.46	0.17
SPO0075		ErfK/YbiS/YcfS/YnhG family protein	-1.16	0.37	-1.62	0.00	-1.39	0.23	1.00	0.01	1.94	0.00	1.47	0.47	0.99	0.34	1.21	0.17	1.10	0.11
SPO0076		lipoprotein	-1.18	0.01	2.61	0.00	0.72	1.90	1.10	0.33	1.22	0.04	1.16	0.06	1.42	0.01	-1.32	0.02	0.05	1.37
SPO0077	*ptsN*	PTS transporter subunit IIA-like nitrogen-regulatory protein PtsN	1.73	0.07	1.04	0.87	1.39	0.35	1.21	0.53	1.95	0.00	1.58	0.37	1.48	0.01	1.54	0.01	1.51	0.03
SPO0078		ribosomal subunit interface protein	2.34	0.04	0.98	0.70	1.66	0.68	1.25	0.06	1.98	0.00	1.62	0.37	1.83	0.00	2.42	0.00	2.13	0.30
SPO0079		ABC transporter ATP-binding protein	-1.15	0.03	-1.56	0.00	-1.36	0.21	1.77	0.00	-1.28	0.00	0.25	1.53	-1.31	0.01	-1.42	0.00	-1.37	0.05
SPO0080		hypothetical protein	1.12	0.84	-1.29	0.03	-0.09	1.21	1.93	0.00	-1.54	0.00	0.20	1.74	1.42	0.00	1.15	0.14	1.29	0.14
SPO0081		hypothetical protein	1.06	0.43	-1.51	0.08	-0.23	1.29	2.60	0.00	-1.59	0.00	0.51	2.10	-1.17	0.15	-1.21	0.01	-1.19	0.02
SPO0082	*kdsD*	arabinose 5-phosphate isomerase (EC:5.3.1.13)	1.33	0.08	-1.19	0.20	0.07	1.26	3.70	0.00	-1.36	0.00	1.17	2.53	1.17	0.27	0.97	0.15	1.07	0.10
SPO0083		exonuclease	-1.20	0.02	-1.40	0.03	-1.30	0.10	1.88	0.00	1.07	0.71	1.48	0.41	-1.24	0.04	1.07	0.72	-0.09	1.16
SPO0084	*betB*	betaine aldehyde dehydrogenase (EC:1.2.1.8)	X	X	-1.09	0.53	N/A	N/A	1.86	0.00	-2.17	0.00	-0.16	2.02	-1.50	0.00	-2.18	0.00	-1.84	0.34
SPO0085		hypothetical protein	-1.11	0.72	-1.68	0.09	-1.40	0.29	-2.58	0.00	-1.53	0.06	-2.06	0.53	1.29	0.13	2.66	0.00	1.98	0.69
SPO0086		lipoprotein	1.13	0.02	1.08	0.50	1.11	0.02	-1.45	0.15	1.05	X	-0.20	1.25	-1.21	0.35	-0.98	0.64	-1.09	0.12
SPO0087		hypothetical protein	-2.00	0.04	-1.16	0.77	-1.58	0.42	-2.18	0.42	-1.07	0.77	-1.63	0.56	-1.10	0.82	1.55	0.05	0.23	1.33
SPO0088		hypothetical protein	-1.32	0.16	-1.38	0.16	-1.35	0.03	2.84	0.20	1.04	0.83	1.94	0.90	-1.43	0.29	1.56	0.15	0.07	1.50
SPO0089		hypothetical protein	1.95	0.00	1.03	0.66	1.49	0.46	1.34	0.00	-1.35	0.04	-0.01	1.35	-1.33	0.44	1.13	0.34	-0.10	1.23
SPO0090		hypothetical protein	-1.23	0.79	-1.19	0.58	-1.21	0.02	-1.57	0.68	-0.99	0.95	-1.28	0.29	1.12	0.80	2.11	0.10	1.62	0.50
SPO0091		rhodanese-like domain-containing protein	X	X	1.25	0.00	N/A	N/A	3.59	0.00	-1.92	0.00	0.84	2.76	-1.65	0.00	-2.80	0.00	-2.23	0.58
SPO0092		molecular chaperone DnaK	-1.24	X	-1.33	0.32	-1.29	0.05	4.45	0.00	-1.70	0.07	1.38	3.08	-2.08	0.02	-1.85	0.08	-1.97	0.12
SPO0093	*pncA*	pyrazinamidase/nicotinamidase (EC:3.5.1.19)	-1.35	0.00	1.21	0.00	-0.07	1.28	-2.14	0.00	1.38	0.01	-0.38	1.76	1.54	0.03	-0.98	0.19	0.28	1.26
SPO0094		sensory box sensor histidine kinase/response regulator (EC:2.7.3.-)	-0.95	0.61	1.28	0.28	0.17	1.11	-2.44	0.28	X	X	N/A	N/A	-1.11	0.80	X	X	N/A	N/A
SPO0095	*pncB*	nicotinate phosphoribosyltransferase (EC:2.4.2.11)	-1.38	0.12	-1.14	0.54	-1.26	0.12	1.46	0.10	1.01	0.93	1.24	0.23	1.11	0.76	-1.14	0.58	-0.01	1.13
SPO0096		hypothetical protein	1.19	0.12	1.09	0.52	1.14	0.05	1.18	0.11	1.15	0.61	1.17	0.02	1.37	0.03	-1.01	0.88	0.18	1.19
SPO0097		aldehyde dehydrogenase	-1.00	0.94	1.40	0.08	0.20	1.20	-1.15	0.87	1.84	0.03	0.35	1.50	1.26	0.30	1.19	0.27	1.23	0.04
SPO0098		peptide/opine/nickel uptake ABC transporter ATP-binding protein	-1.44	0.00	-1.01	0.99	-1.23	0.21	-1.17	0.27	1.34	0.05	0.09	1.26	1.26	0.01	-1.16	0.61	0.05	1.21
SPO0099		peptide/opine/nickel uptake ABC transporter permease	-1.82	0.02	1.01	0.95	-0.41	1.42	-1.58	0.06	1.86	0.03	0.14	1.72	-1.36	0.06	-1.01	0.92	-1.19	0.18
SPO0100		peptide/opine/nickel uptake ABC transporter permease	-1.86	0.10	-1.09	0.50	-1.48	0.39	-1.94	0.00	1.50	0.01	-0.22	1.72	-1.31	0.09	-1.08	0.84	-1.20	0.12
SPO0101		peptide/opine/nickel uptake ABC transporter	1.36	0.55	-1.03	0.72	0.17	1.20	-1.83	0.00	1.90	0.01	0.03	1.87	1.36	0.09	1.95	0.02	1.66	0.29

		substrate-binding protein																		
SPO0102	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC:2.1.2.11)	1.44	0.02	-1.53	0.06	-0.05	1.49	5.27	0.00	-3.25	0.00	1.01	4.26	1.20	0.11	1.65	0.00	1.43	0.23
SPO0103	*panC*	pantoate--beta-alanine ligase (EC:6.3.2.1)	-1.11	0.73	-1.26	0.10	-1.19	0.08	1.88	0.09	-2.37	0.00	-0.25	2.13	1.71	0.01	1.79	0.00	1.75	0.04
SPO0104	*glpK*	glycerol kinase (EC:2.7.1.30)	-1.13	0.04	-1.03	0.77	-1.08	0.05	-1.14	0.20	-1.17	0.01	-1.16	0.02	-1.01	0.77	-1.04	0.64	-1.03	0.02
SPO0105		hypothetical protein	-1.06	0.59	1.01	0.96	-0.03	1.04	-1.58	0.01	1.04	0.86	-0.27	1.31	1.18	0.26	1.46	0.03	1.32	0.14
SPO0106		hypothetical protein	1.45	0.42	1.09	0.48	1.27	0.18	2.19	0.11	-1.10	0.18	0.55	1.65	1.01	0.80	-1.28	0.06	-0.14	1.15
SPO0107	*recQ*	ATP-dependent DNA helicase RecQ (EC:3.6.1.-)	-1.32	0.37	-1.06	0.76	-1.19	0.13	0.91	0.62	1.09	0.82	1.00	0.09	1.36	0.34	1.39	0.50	1.38	0.01
SPO0108		transposase, truncation	X	X	1.32	0.00	N/A	N/A	2.40	0.00	1.22	0.02	1.81	0.59	-1.85	0.00	-2.16	0.00	-2.01	0.16
SPO0109		hypothetical protein	-1.03	X	2.24	0.00	0.61	1.64	12.70	0.00	1.99	0.01	7.35	5.36	-1.34	0.10	-1.93	0.00	-1.64	0.30
SPO0110		ABC transporter ATP-binding protein/permease	X	X	2.07	0.00	N/A	N/A	21.40	0.00	1.66	0.00	11.53	9.87	-0.96	0.31	-1.37	0.35	-1.16	0.21
SPO0111		hypothetical protein	1.54	0.42	1.69	0.04	1.62	0.08	8.13	0.00	2.23	0.01	5.18	2.95	1.02	0.93	-1.06	0.92	-0.02	1.04
SPO0112		poly(3-hydroxyalkanoate) polymerase	1.22	0.14	2.41	0.00	1.82	0.60	4.63	0.00	3.24	0.00	3.94	0.70	-1.05	0.61	-1.24	0.19	-1.15	0.10
SPO0113	*fabI-1*	enoyl-ACP reductase (EC:1.3.1.10)	1.17	0.74	2.08	0.03	1.63	0.46	5.37	0.01	1.97	0.00	3.67	1.70	1.03	0.75	-1.13	0.94	-0.05	1.08
SPO0114		hypothetical protein	-1.46	0.23	1.18	0.29	-0.14	1.32	1.25	0.02	1.37	0.05	1.31	0.06	-1.60	0.00	1.22	0.37	-0.19	1.41
SPO0115		bifunctional enoyl-CoA hydratase/phosphate acetyltransferase	2.35	0.00	2.39	0.00	2.37	0.02	9.42	0.00	2.45	0.00	5.94	3.49	-1.25	0.04	-1.41	0.20	-1.33	0.08
SPO0116	*ackA*	acetate kinase (EC:2.7.2.1)	1.51	0.20	2.17	0.03	1.84	0.33	2.98	0.00	2.35	0.02	2.67	0.32	-0.98	0.69	1.10	X	0.06	1.04
SPO0118		hypothetical protein	1.68	0.00	1.08	0.32	1.38	0.30	-1.48	0.04	1.37	0.01	-0.05	1.43	-1.75	0.01	-1.27	0.24	-1.51	0.24
SPO0119		AsnC family transcriptional regulator	-1.22	0.07	1.14	0.05	-0.04	1.18	-2.18	0.00	-1.26	0.06	-1.72	0.46	-1.39	0.02	-1.94	0.00	-1.67	0.27
SPO0120		hypothetical protein	-1.18	X	-1.13	0.49	-1.16	0.03	-1.49	0.13	-1.11	X	-1.30	0.19	1.09	0.77	-1.33	X	-0.12	1.21
SPO0122		hypothetical protein	1.39	0.02	-1.85	0.00	-0.23	1.62	2.95	0.00	-1.09	0.07	0.93	2.02	-1.04	0.09	1.24	0.01	0.10	1.14
SPO0123		hypothetical protein	-1.59	0.01	-1.17	0.00	-1.38	0.21	-1.15	0.10	-1.25	0.01	-1.20	0.05	1.20	0.06	-1.20	0.14	0.00	1.20
SPO0124	*mepA*	penicillin-insensitive murein endopeptidase	-2.17	0.00	-1.42	0.04	-1.80	0.38	1.19	0.90	1.69	0.00	1.44	0.25	1.64	0.00	2.73	0.00	2.19	0.54
SPO0125		hypothetical protein	-2.14	0.00	-1.32	0.06	-1.73	0.41	1.08	0.02	1.15	0.49	1.12	0.03	1.52	0.00	1.23	0.03	1.38	0.14
SPO0126		hypothetical protein	-1.26	0.84	1.31	0.24	0.03	1.29	2.35	0.47	-5.87	0.00	-1.76	4.11	-2.18	0.03	-3.22	0.02	-2.70	0.52
SPO0127		peptidyl-tRNA hydrolase domain-containing protein	-2.84	0.00	-1.32	0.10	-2.08	0.76	-3.60	0.00	-1.01	0.58	-2.31	1.30	-1.18	0.12	-1.32	0.03	-1.25	0.07
SPO0128	*fabG*	3-ketoacyl-ACP reductase (EC:1.1.1.100)	1.13	0.92	-1.02	0.81	0.05	1.08	0.97	0.38	1.31	0.08	1.14	0.17	1.13	0.36	1.44	0.00	1.29	0.16
SPO0129		T4 family peptidase	-1.06	0.41	1.02	0.72	-0.02	1.04	1.10	0.15	-1.01	0.76	0.05	1.06	1.04	0.44	-1.03	0.82	0.01	1.04
SPO0130		cytochrome c family protein	5.48	0.00	1.76	0.01	3.62	1.86	2.60	0.00	1.57	0.01	2.09	0.52	1.26	0.01	1.66	0.06	1.46	0.20
SPO0131		isopentyl-diphosphate delta-isomerase (EC:5.3.3.2)	3.38	0.00	1.83	0.00	2.61	0.78	2.33	0.00	-1.27	0.02	0.53	1.80	1.19	0.11	1.22	0.34	1.21	0.02
SPO0132		sensor histidine kinase/response regulator (EC:2.7.3.-)	-1.10	X	1.42	0.14	0.16	1.26	-1.39	0.84	-1.16	X	-1.28	0.12	1.13	0.47	X	X	N/A	N/A
SPO0133		PAN domain-containing protein	1.21	0.73	1.14	0.20	1.18	0.04	-1.47	0.00	1.57	0.01	0.05	1.52	1.62	0.00	1.66	0.00	1.64	0.02
SPO0134		hypothetical protein	-1.35	0.00	1.10	0.29	-0.13	1.23	-1.58	0.00	1.28	0.03	-0.15	1.43	1.65	0.00	1.29	0.01	1.47	0.18
SPO0135	*pbpC*	penicillin-binding protein 1C	-1.21	X	-1.01	0.97	-1.11	0.10	-1.22	0.17	1.46	0.02	0.12	1.34	1.49	0.10	1.32	0.49	1.41	0.09
SPO0136		hypothetical protein	-1.15	0.03	-1.13	0.02	-1.14	0.01	-1.76	0.00	1.49	0.00	-0.14	1.63	1.25	0.01	1.19	0.02	1.22	0.03
SPO0137		hypothetical protein	-1.48	0.05	-1.12	0.06	-1.30	0.18	-1.72	0.00	1.40	0.00	-0.16	1.56	-1.00	0.92	-1.03	0.84	-1.02	0.02
SPO0138		hypothetical protein	-1.18	0.02	-1.10	0.04	-1.14	0.04	-1.36	0.03	1.72	0.00	0.18	1.54	1.35	0.04	1.32	0.00	1.34	0.02
SPO0139		MoxR family ATPase	0.93	0.00	-1.35	0.03	-0.21	1.14	-1.86	0.00	1.52	0.00	-0.17	1.69	1.15	0.13	1.62	0.00	1.39	0.24
SPO0140		hypothetical protein	-1.37	0.05	-1.23	0.02	-1.30	0.07	1.05	0.12	1.01	0.99	1.03	0.02	1.33	0.00	1.33	0.06	1.33	0.00

SPO0141		DNA binding protein	-1.24	0.01	-1.16	0.10	-1.20	0.04	1.88	0.00	1.14	0.20	1.51	0.37	-1.42	0.02	1.34	0.02	-0.04	1.38
SPO0142	*bktB*	beta-ketothiolase	6.45	0.01	2.25	0.00	4.35	2.10	1.67	0.00	1.96	0.00	1.82	0.15	1.74	0.00	2.31	0.00	2.03	0.29
SPO0143		(Fe-S)-binding protein	-2.39	0.00	-1.33	0.01	-1.86	0.53	-2.97	0.00	1.85	0.00	-0.56	2.41	-1.23	0.01	-1.08	0.84	-1.16	0.08
SPO0144	*ubiB*	2-polyprenylphenol 6-hydroxylase (EC:1.14.13.-)	1.20	0.03	1.85	0.00	1.53	0.33	-1.37	0.00	-1.47	0.00	-1.42	0.05	1.19	0.01	-1.60	0.00	-0.21	1.40
SPO0145	*ubiE*	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	1.72	0.01	1.36	0.08	1.54	0.18	2.50	0.00	-1.11	0.25	0.70	1.81	-1.84	0.00	-2.09	0.00	-1.97	0.13
SPO0146	*mutM*	formamidopyrimidine-DNA glycosylase (EC:3.2.2.23)	1.13	0.01	-1.14	0.07	-0.01	1.14	1.37	0.00	1.31	0.01	1.34	0.03	-1.11	0.07	-1.13	0.26	-1.12	0.01
SPO0147		enoyl-CoA hydratase (EC:4.2.1.17)	2.08	0.00	1.16	0.10	1.62	0.46	3.56	0.00	1.10	0.55	2.33	1.23	1.14	0.01	-1.26	0.10	-0.06	1.20
SPO0148	*rpsT*	30S ribosomal protein S20	1.73	0.07	-1.32	0.01	0.21	1.53	5.84	0.00	-1.37	0.01	2.24	3.61	-1.98	0.00	-2.87	0.00	-2.43	0.45
SPO0149	*dnaA*	chromosome replication initiator DnaA	1.50	0.17	1.01	0.96	1.26	0.25	1.32	0.34	1.07	0.94	1.20	0.13	-1.14	0.52	-1.18	0.48	-1.16	0.02
SPO0150	*dnaN*	DNA polymerase III subunit beta (EC:2.7.7.7)	1.27	0.08	1.28	0.07	1.28	0.01	1.66	0.00	-1.13	0.09	0.27	1.40	1.17	0.19	-1.14	0.30	0.02	1.16
SPO0151	*recF*	recombination protein F	1.31	0.11	1.20	0.00	1.26	0.06	2.27	0.00	-1.29	0.03	0.49	1.78	1.17	0.01	-1.34	0.03	-0.09	1.26
SPO0152		amino acid transporter LysE	-1.37	0.08	1.19	0.80	-0.09	1.28	1.66	0.23	-1.11	0.81	0.28	1.39	1.28	0.50	1.08	0.86	1.18	0.10
SPO0153		TetR family transcriptional regulator	-1.36	0.02	1.85	0.01	0.25	1.61	1.93	0.00	-1.08	0.32	0.43	1.51	1.25	0.01	1.19	0.17	1.22	0.03
SPO0154		quinone family NAD(P)H dehydrogenase	-2.41	0.00	2.26	0.00	-0.08	2.34	1.09	0.04	-1.94	0.00	-0.43	1.52	1.21	0.02	4.53	0.00	2.87	1.66
SPO0155	*gyrB*	DNA gyrase subunit B (EC:5.99.1.3)	1.31	0.01	-1.02	0.57	0.15	1.17	1.42	0.01	-1.45	0.00	-0.02	1.44	1.01	0.76	-1.27	0.01	-0.13	1.14
SPO0156	*rtcR*	transcriptional regulator RtcR	-1.57	0.03	-1.17	0.52	-1.37	0.20	-1.49	0.72	-1.16	0.61	-1.33	0.16	-1.09	0.85	-1.15	0.85	-1.12	0.03
SPO0157		TROVE domain-containing protein	-2.76	0.01	1.07	0.25	-0.85	1.92	1.18	0.27	1.20	0.07	1.19	0.01	-1.77	0.00	-2.50	0.00	-2.14	0.37
SPO0160		hypothetical protein	-1.00	0.73	1.15	0.11	0.08	1.08	1.36	0.00	1.04	0.59	1.20	0.16	1.14	0.13	-0.96	0.15	0.09	1.05
SPO0161		LuxR family transcriptional regulator	-1.87	0.00	-1.21	0.01	-1.54	0.33	1.10	0.18	1.09	0.29	1.10	0.01	-1.10	0.02	1.19	0.07	0.04	1.15
SPO0162		hypothetical protein	-1.02	0.63	2.35	0.00	0.67	1.69	-1.76	0.05	3.21	0.00	0.73	2.49	1.17	0.15	X	X	N/A	N/A
SPO0163		sensory box histidine kinase/response regulator	-1.18	0.79	1.43	0.19	0.13	1.31	-1.40	0.72	1.25	0.33	-0.08	1.33	1.52	0.12	1.30	0.22	1.41	0.11
SPO0164		oxidoreductase, FMN-binding/pyridine nucleotide-disulfide oxidoreductase	-1.13	0.55	-1.17	0.15	-1.15	0.02	-1.54	0.34	-1.16	0.23	-1.35	0.19	-1.28	0.06	-0.98	0.35	-1.13	0.15
SPO0165		pyrroline-5-carboxylate reductase	1.54	X	1.22	0.18	1.38	0.16	1.54	0.01	-1.01	0.88	0.27	1.28	1.17	0.15	-1.08	X	0.04	1.13
SPO0166		N-methylproline demethylase	1.27	0.37	-1.10	0.31	0.09	1.19	-1.35	0.07	-1.13	0.15	-1.24	0.11	-1.18	0.14	-1.21	0.63	-1.20	0.02
SPO0167		trimethylamine methyltransferase	1.74	0.00	-1.31	0.03	0.22	1.53	-1.56	0.00	1.27	0.17	-0.15	1.42	-1.46	0.02	-1.18	0.29	-1.32	0.14
SPO0168		TetR family transcriptional regulator	X	X	-1.43	0.00	N/A	N/A	1.80	0.00	-1.10	0.46	0.35	1.45	-1.46	0.00	-1.76	0.00	-1.61	0.15
SPO0169		Slt family transglycosylase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO0170	*flhA*	flagellar biosynthesis protein FlhA	1.54	0.00	1.33	0.06	1.44	0.11	-1.08	0.32	1.18	0.44	0.05	1.13	-1.07	0.89	X	X	N/A	N/A
SPO0171	*fliR*	flagellar biosynthetic protein FliR	-1.24	0.11	1.11	0.38	-0.06	1.18	-1.62	0.03	-1.07	X	-1.35	0.27	1.41	0.01	X	X	N/A	N/A
SPO0172	*flhB*	flagellar biosynthesis protein FlhB	X	X	-1.61	0.02	N/A	N/A	-1.06	X	-1.52	0.18	-1.29	0.23	-1.77	0.03	-1.02	0.90	-1.40	0.38
SPO0173		hypothetical protein	X	X	-1.06	X	N/A	N/A	-2.21	0.00	X	X	N/A	N/A	-1.28	0.29	X	X	N/A	N/A
SPO0174		hypothetical protein	2.04	0.00	2.64	0.00	2.34	0.30	-3.81	0.00	5.14	0.09	0.67	4.48	-1.18	0.11	X	X	N/A	N/A
SPO0175	*flgH*	flagellar basal body L-ring protein	2.13	0.00	2.44	0.01	2.29	0.16	-4.21	0.00	2.44	0.18	-0.89	3.33	-1.18	0.70	-1.65	X	-1.42	0.23
SPO0176	*flgA*	flagellar basal body P-ring biosynthesis protein FlgA	2.13	0.02	2.12	0.00	2.13	0.00	-5.39	0.00	3.74	0.00	-0.83	4.57	-1.55	0.00	X	X	N/A	N/A
SPO0177	*flgG*	flagellar basal body rod protein FlgG	2.54	0.08	1.49	0.43	2.02	0.52	-3.19	0.04	1.86	0.01	-0.67	2.53	-1.14	0.69	1.52	X	0.19	1.33
SPO0178	*flgF*	flagellar basal body rod protein FlgF	2.25	0.11	2.12	0.20	2.19	0.06	-2.68	0.40	3.18	0.07	0.25	2.93	-1.05	0.98	2.00	0.11	0.48	1.53
SPO0179	*fliQ*	flagellar biosynthetic protein FliQ	1.71	0.00	4.10	0.00	2.91	1.20	-13.70	0.00	7.01	0.00	-3.35	10.36	-1.60	0.01	X	X	N/A	N/A
SPO0180	*fliE*	flagellar hook-basal body protein FliE	2.05	0.00	2.80	0.00	2.43	0.38	-4.92	0.00	4.39	0.00	-0.27	4.66	-1.63	0.00	-1.25	X	-1.44	0.19

SPO0181	*flgC*	flagellar basal body rod protein FlgC	2.25	0.00	4.52	0.00	3.39	1.14	-13.00	0.00	5.51	0.00	-3.75	9.26	-1.66	0.06	X	X	N/A	N/A
SPO0182	*flgB*	flagellar basal-body rod protein FlgB	2.03	0.00	1.03	0.58	1.53	0.50	-5.68	0.00	1.35	0.16	-2.17	3.52	-1.05	0.89	1.47	0.02	0.21	1.26
SPO0183	*fliI*	H+-transporting two-sector ATPase, flagellum-specific (EC:3.6.3.14)	1.27	0.65	1.29	0.35	1.28	0.01	-1.13	0.85	1.11	0.63	-0.01	1.12	-0.96	0.78	1.13	0.53	0.09	1.04
SPO0184		hypothetical protein	2.69	0.00	-1.34	0.19	0.68	2.02	1.64	0.00	-1.30	0.43	0.17	1.47	-1.73	0.23	-1.68	0.30	-1.71	0.03
SPO0185		hypothetical protein	2.32	0.12	-1.48	0.02	0.42	1.90	1.76	0.38	-1.21	0.27	0.28	1.49	-2.37	0.00	-5.01	0.00	-3.69	1.32
SPO0186		hypothetical protein	1.01	0.02	-1.77	0.00	-0.38	1.39	-3.57	0.00	-1.02	0.61	-2.30	1.28	-3.34	0.00	-3.84	0.00	-3.59	0.25
SPO0187		DNA-binding response regulator	-1.53	0.00	-1.21	0.18	-1.37	0.16	-2.30	0.00	-1.04	0.75	-1.67	0.63	-1.13	0.41	1.34	0.03	0.11	1.24
SPO0188		sensor histidine kinase (EC:2.7.3.-)	1.15	0.44	1.40	0.01	1.28	0.13	-1.06	0.40	1.11	0.33	0.03	1.09	1.10	0.27	-1.22	0.22	-0.06	1.16
SPO0189		hypothetical protein	1.07	0.86	1.02	0.84	1.05	0.03	1.40	0.22	1.25	0.11	1.33	0.08	-1.40	0.34	-1.11	0.76	-1.26	0.15
SPO0190		GMC family oxidoreductase	2.33	0.00	1.45	0.12	1.89	0.44	-1.34	0.37	1.48	0.04	0.07	1.41	1.42	0.16	2.64	0.02	2.03	0.61
SPO0191	*motB*	chemotaxis protein MotB	-1.03	0.47	1.37	0.40	0.17	1.20	-3.10	0.00	1.21	0.57	-0.95	2.16	-1.14	0.65	1.20	0.45	0.03	1.17
SPO0192		flagellar hook protein FlgE	1.88	0.01	2.06	0.01	1.97	0.09	-4.65	0.00	2.66	0.01	-1.00	3.66	-1.28	0.42	-0.96	0.42	-1.12	0.16
SPO0193	*flgK*	flagellar hook-associated protein Flg	2.43	0.00	1.78	0.01	2.11	0.33	-1.24	0.83	2.14	0.04	0.45	1.69	-1.18	0.52	-1.04	0.78	-1.11	0.07
SPO0194		flagellar hook-associated protein FlgL family protein	2.10	0.00	1.37	0.11	1.74	0.37	-1.11	0.30	1.72	0.02	0.31	1.42	-1.31	0.22	-1.04	0.83	-1.18	0.14
SPO0195	*flgI*	flagellar basal body P-ring biosynthesis protein FlgA	X	X	1.50	0.09	N/A	N/A	X	X	X	X	N/A	N/A	-1.18	0.29	X	X	N/A	N/A
SPO0196	*fliP*	flagellar biosynthesis protein FliP	1.21	0.77	-1.16	0.68	0.03	1.19	1.46	0.58	1.21	0.69	1.34	0.13	-1.35	0.25	1.57	0.28	0.11	1.46
SPO0197	*fliN*	flagellar motor switch protein FliN	2.74	0.00	3.19	0.01	2.97	0.23	-4.14	0.00	4.19	0.02	0.03	4.17	-1.07	X	X	X	N/A	N/A
SPO0198		ABC transporter ATP-binding protein, flagellar	1.90	0.12	2.14	0.01	2.02	0.12	-5.06	0.00	2.06	0.07	-1.50	3.56	-1.08	0.81	1.58	0.14	0.25	1.33
SPO0199	*fliF*	flagellar MS-ring protein	3.40	0.00	1.43	0.24	2.42	0.98	-7.27	0.00	3.64	0.00	-1.82	5.46	-1.25	0.36	-0.93	0.39	-1.09	0.16
SPO0200	*fliL*	flagellar basal body protein FliL	1.17	0.68	-1.22	0.48	-0.03	1.20	-5.67	0.00	1.13	0.77	-2.27	3.40	-1.33	0.54	1.65	0.36	0.16	1.49
SPO0201		hypothetical protein	2.40	0.00	2.39	0.00	2.40	0.00	-4.81	0.00	2.28	0.00	-1.27	3.55	1.14	0.09	X	X	N/A	N/A
SPO0202		hypothetical protein	2.58	0.00	1.50	0.09	2.04	0.54	-5.84	0.00	2.15	0.00	-1.85	4.00	-1.59	0.05	-0.95	0.57	-1.27	0.32
SPO0203	*motA*	flagellar motor protein MotA	2.42	0.00	2.94	0.00	2.68	0.26	-3.46	0.00	4.86	0.00	0.70	4.16	-1.07	0.89	X	X	N/A	N/A
SPO0204		hypothetical protein	2.21	0.00	1.54	0.00	1.88	0.34	-2.23	0.00	1.10	X	-0.57	1.67	1.12	0.11	X	X	N/A	N/A
SPO0205		MmgE/PrpD family protein	43.00	0.00	-1.34	0.07	20.83	22.17	-4.63	0.00	X	X	N/A	N/A	-1.27	0.13	X	X	N/A	N/A
SPO0206		LysR family transcriptional regulator	1.33	0.01	1.14	0.04	1.24	0.10	-0.98	0.05	1.06	0.48	0.04	1.02	1.31	0.01	-1.16	0.94	0.08	1.24
SPO0207		glycine cleavage system protein T	29.60	0.00	-1.18	0.20	14.21	15.39	-1.26	0.41	1.08	0.31	-0.09	1.17	1.17	0.02	-1.38	0.32	-0.11	1.28
SPO0209		Na/Pi-cotransporter family protein	1.46	0.04	1.09	0.11	1.28	0.19	1.23	0.05	1.37	0.00	1.30	0.07	1.37	0.02	-1.02	0.31	0.18	1.20
SPO0210	*leuB*	3-isopropylmalate dehydrogenase (EC:1.1.1.85)	2.41	0.00	1.48	0.04	1.95	0.47	3.43	0.00	-1.07	0.08	1.18	2.25	-1.05	0.42	-1.32	0.00	-1.19	0.14
SPO0211		LysR family transcriptional regulator	X	X	-1.13	0.31	N/A	N/A	-1.50	0.30	-1.42	0.20	-1.46	0.04	-1.05	0.71	-1.02	0.56	-1.04	0.02
SPO0212		hypothetical protein	-2.33	0.00	-1.53	0.37	-1.93	0.40	-6.48	0.00	-1.26	0.53	-3.87	2.61	-1.06	0.95	1.44	X	0.19	1.25
SPO0213		hypothetical protein	-1.26	0.01	-1.06	0.62	-1.16	0.10	1.01	0.91	-1.23	0.21	-0.11	1.12	-0.98	0.58	-1.05	0.62	-1.01	0.04
SPO0214		hypothetical protein	-1.75	0.01	1.01	0.98	-0.37	1.38	-1.72	0.07	-1.71	0.03	-1.72	0.01	-1.18	0.36	-1.25	0.27	-1.22	0.04
SPO0215	*leuD*	isopropylmalate isomerase small subunit (EC:4.2.1.33)	1.63	0.00	1.02	0.99	1.33	0.31	3.80	0.00	-1.52	0.01	1.14	2.66	-1.30	0.16	-1.71	0.01	-1.51	0.21
SPO0216	*leuC-1*	isopropylmalate isomerase large subunit (EC:4.2.1.33)	1.55	0.18	-1.24	0.15	0.16	1.40	3.46	0.01	-1.39	0.01	1.04	2.43	1.00	0.65	-1.32	0.05	-0.16	1.16
SPO0217		hypothetical protein	X	X	-1.37	0.50	N/A	N/A	-2.85	0.07	-1.11	0.82	-1.98	0.87	-1.10	0.83	X	X	N/A	N/A
SPO0218		mechanosensitive ion channel protein MscS	-1.61	0.00	1.19	0.11	-0.21	1.40	-1.59	0.01	1.44	0.00	-0.08	1.52	1.55	0.00	1.16	0.10	1.36	0.20

SPO0219		iojap family protein	-1.45	0.00	-1.67	0.00	-1.56	0.11	0.92	0.00	1.11	0.63	1.02	0.09	2.04	0.00	1.76	0.01	1.90	0.14
SPO0220		rRNA large subunit methyltransferase	-1.02	0.80	-1.51	0.03	-1.27	0.24	1.40	0.07	-1.16	0.01	0.12	1.28	1.60	0.00	1.17	0.50	1.39	0.22
SPO0221		hypothetical protein	-1.22	0.87	-1.62	0.04	-1.42	0.20	1.95	0.61	-1.13	0.36	0.41	1.54	1.23	0.27	0.99	0.93	1.11	0.12
SPO0222	*ald*	alanine dehydrogenase (EC:1.4.1.1)	15.40	0.00	-1.21	0.16	7.10	8.31	8.29	0.00	-2.47	0.00	2.91	5.38	1.55	0.00	1.79	0.00	1.67	0.12
SPO0223		AsnC family transcriptional regulator	-1.01	0.21	-1.47	0.00	-1.24	0.23	-1.55	0.00	-1.20	0.01	-1.38	0.18	-1.29	0.00	-1.55	0.00	-1.42	0.13
SPO0224		polyphosphate kinase	1.03	0.85	-1.40	0.17	-0.19	1.22	1.40	0.20	-1.09	0.63	0.16	1.25	1.44	0.18	1.65	0.12	1.55	0.11
SPO0225		transcriptional regulator	-1.48	0.01	-1.11	0.55	-1.30	0.19	-1.10	0.26	-1.08	0.48	-1.09	0.01	-1.31	0.01	-1.82	0.00	-1.57	0.26
SPO0226		cytochrome P450 family protein	X	X	-1.06	0.57	N/A	N/A	1.44	0.00	-1.16	0.31	0.14	1.30	1.50	0.01	-1.60	X	-0.05	1.55
SPO0227		PaxA	-2.63	0.00	-2.69	0.00	-2.66	0.03	3.16	0.00	-1.37	0.00	0.90	2.27	3.28	0.00	1.87	0.00	2.58	0.70
SPO0228		hypothetical protein	4.77	0.00	1.78	0.00	3.28	1.50	-1.60	0.06	1.25	0.04	-0.18	1.43	1.21	0.22	1.67	0.03	1.44	0.23
SPO0229	*rpsU*	30S ribosomal protein S21	-1.39	0.00	1.16	0.59	-0.12	1.28	5.36	0.00	-1.39	0.00	1.99	3.38	2.15	0.00	-1.52	0.00	0.32	1.84
SPO0230		hypothetical protein	1.38	0.02	-1.10	0.27	0.14	1.24	1.81	0.00	-1.17	0.02	0.32	1.49	-1.03	0.16	-1.21	0.00	-1.12	0.09
SPO0231		alcohol dehydrogenase	2.19	0.00	1.02	0.93	1.61	0.59	2.23	0.00	-1.38	0.01	0.43	1.81	1.70	0.00	1.32	0.01	1.51	0.19
SPO0232		quinone oxidoreductase	1.13	0.59	-1.29	0.07	-0.08	1.21	-1.33	0.00	1.52	0.00	0.10	1.43	1.44	0.01	1.90	0.04	1.67	0.23
SPO0233		AsnC family transcriptional regulator	1.29	0.03	-1.03	0.88	0.13	1.16	-1.50	0.02	1.22	0.00	-0.14	1.36	-1.46	0.00	-1.46	0.02	-1.46	0.00
SPO0234		hypothetical protein	-4.02	0.00	-1.00	0.99	-2.51	1.51	-25.60	0.00	-1.23	0.56	-13.42	12.19	-1.18	0.58	1.37	0.24	0.10	1.28
SPO0235		aldehyde dehydrogenase	-3.94	0.00	-1.56	0.07	-2.75	1.19	-16.50	0.00	-1.21	0.36	-8.86	7.65	-1.27	0.16	1.76	0.00	0.25	1.52
SPO0236		glycerophosphoryl diester phosphodiesterase	-2.31	0.17	-1.29	0.20	-1.80	0.51	-2.39	0.01	-1.59	0.08	-1.99	0.40	-1.33	0.06	1.35	0.05	0.01	1.34
SPO0237	*ugpC*	glycerol-3-phosphate transporter ATP-binding subunit (EC:3.6.3.20)	1.56	0.01	1.03	0.61	1.30	0.27	1.70	0.00	-1.51	0.05	0.10	1.61	-1.15	0.32	-1.35	0.46	-1.25	0.10
SPO0238	*ugpE*	SN-glycerol-3-phosphate ABC transporter permease	-1.13	0.82	-1.07	0.65	-1.10	0.03	-0.99	0.65	-1.24	0.30	-1.12	0.12	-1.32	0.11	-1.18	0.86	-1.25	0.07
SPO0239	*ugpA*	SN-glycerol-3-phosphate ABC transporter permease	1.14	0.33	-1.21	0.42	-0.04	1.18	1.21	0.15	-1.16	0.18	0.03	1.19	-1.10	0.47	-1.12	0.94	-1.11	0.01
SPO0240	*ugpB*	SN-glycerol-3-phophate ABC transporter substrate-binding protein	-1.36	0.02	-1.53	0.02	-1.45	0.09	-1.23	0.04	-1.04	0.42	-1.14	0.10	-1.27	0.01	1.23	0.09	-0.02	1.25
SPO0241		LysR family transcriptional regulator	-1.31	0.60	-1.18	0.76	-1.25	0.07	-1.24	0.97	-1.24	0.70	-1.24	0.00	-1.17	0.79	1.12	0.77	-0.02	1.15
SPO0247	*dxs*	1-deoxy-D-xylulose-5-phosphate synthase (EC:2.2.1.7)	1.35	0.09	1.23	0.02	1.29	0.06	1.79	0.00	-1.15	0.29	0.32	1.47	-1.19	0.12	-1.60	0.01	-1.40	0.21
SPO0248	*ispA*	farnesyl diphosphate synthase (EC:2.5.1.10)	1.40	0.74	1.12	0.77	1.26	0.14	1.70	0.52	1.02	0.95	1.36	0.34	-1.07	0.79	-1.29	0.55	-1.18	0.11
SPO0249	*xseB*	exodeoxyribonuclease VII small subunit (EC:3.1.11.6)	0.99	0.53	1.06	0.76	1.03	0.04	1.13	0.41	1.03	0.85	1.08	0.05	-1.28	0.00	-2.34	0.00	-1.81	0.53
SPO0250		histone deacetylase	-1.30	0.43	-1.82	0.05	-1.56	0.26	-1.65	0.20	-1.12	0.38	-1.39	0.27	-1.86	0.03	-2.74	0.00	-2.30	0.44
SPO0251	*petR*	DNA-binding response regulator PetR	-2.15	0.08	-2.12	0.00	-2.14	0.01	-2.44	0.00	-1.14	0.08	-1.79	0.65	-2.00	0.00	-2.48	0.00	-2.24	0.24
SPO0252	*petP*	transcriptional regulator PetP	-1.62	0.00	-1.28	0.05	-1.45	0.17	-1.89	0.00	-1.02	0.48	-1.46	0.43	-1.28	0.01	-1.57	0.00	-1.43	0.14
SPO0253	*ilvE*	branched-chain amino acid aminotransferase (EC:2.6.1.42)	1.11	0.20	-1.59	0.01	-0.24	1.35	1.98	0.00	0.98	0.56	1.48	0.50	-2.19	0.00	-4.68	0.00	-3.44	1.25
SPO0254	*ohr*	organic hydroperoxide resistance protein	-1.54	0.00	1.47	0.00	-0.04	1.51	11.20	0.00	1.04	0.91	6.12	5.08	-1.86	0.00	-2.02	0.00	-1.94	0.08
SPO0255		MarR family transcriptional regulator	-1.31	0.08	1.47	0.05	0.08	1.39	1.99	0.00	1.27	0.12	1.63	0.36	1.05	0.81	-1.04	0.98	0.01	1.05
SPO0256		plastocyanin/azurin family copper binding protein	-1.04	0.94	-1.42	0.18	-1.23	0.19	1.28	0.00	-1.01	0.99	0.14	1.15	-1.01	0.98	1.60	0.14	0.30	1.31
SPO0257		hypothetical protein	-0.97	0.73	-1.60	0.05	-1.28	0.32	-1.03	0.64	1.12	0.67	0.05	1.08	1.03	0.86	2.01	0.08	1.52	0.49
SPO0258		AraC family transcriptional regulator	-1.33	0.44	-1.37	0.18	-1.35	0.02	0.87	0.66	1.23	0.48	1.05	0.18	-1.00	0.93	1.01	0.99	0.01	1.01
SPO0259		hypothetical protein	-1.19	0.04	-1.27	0.05	-1.23	0.04	1.48	0.00	-1.13	0.28	0.18	1.31	-1.15	0.20	X	X	N/A	N/A

SPO0260		alkaline phosphatase	-1.18	0.13	1.03	0.86	-0.08	1.11	-1.07	0.13	1.38	0.02	0.16	1.23	1.51	0.00	X	X	N/A	N/A
SPO0261		hypothetical protein	X	X	1.21	0.00	N/A	N/A	4.32	0.00	-1.26	0.11	1.53	2.79	-1.02	0.78	-1.63	0.01	-1.33	0.31
SPO0262	*cobO*	cob(I)alamin adenosyltransferase (EC:2.5.1.17)	1.62	0.00	1.27	0.11	1.45	0.18	4.05	0.00	1.06	0.82	2.56	1.50	1.22	0.01	-1.15	0.01	0.04	1.19
SPO0263		hypothetical protein	X	X	-1.20	0.42	N/A	N/A	-1.10	0.16	-1.02	0.94	-1.06	0.04	-1.04	0.98	-0.90	0.56	-0.97	0.07
SPO0264		CaiB/BaiF family protein	1.16	0.11	1.53	0.00	1.35	0.19	1.55	0.00	1.05	0.73	1.30	0.25	1.14	0.14	-1.22	0.16	-0.04	1.18
SPO0265		auxin efflux carrier protein	-1.46	0.38	1.36	0.60	-0.05	1.41	-1.35	0.77	-1.24	0.71	-1.30	0.06	-1.18	0.79	-1.26	0.70	-1.22	0.04
SPO0266		HD domain-containing protein	-2.51	0.01	1.03	0.86	-0.74	1.77	-2.74	0.00	-1.52	0.04	-2.13	0.61	-1.12	0.54	1.09	0.53	-0.02	1.11
SPO0267	*aroC*	chorismate synthase (EC:4.2.3.5)	-1.52	0.00	1.03	0.84	-0.25	1.28	1.49	0.00	-1.31	0.00	0.09	1.40	-1.91	0.00	-1.61	0.02	-1.76	0.15
SPO0268	*ribH-1*	riboflavin synthase subunit beta (EC:2.5.1.9)	-1.84	0.00	1.00	1.00	-0.42	1.42	1.06	0.56	1.26	0.23	1.16	0.10	-1.65	0.04	-1.39	0.24	-1.52	0.13
SPO0269		negative transcriptional regulator	-1.14	0.69	1.08	0.47	-0.03	1.11	1.10	0.25	-1.04	0.55	0.03	1.07	-1.37	0.04	-1.42	0.06	-1.40	0.02
SPO0270		glutathione S-transferase	1.40	0.00	1.01	0.95	1.21	0.19	1.27	0.03	1.00	0.66	1.13	0.14	1.10	0.31	-1.21	0.04	-0.05	1.16
SPO0271	*petA*	ubiquinol-cytochrome c reductase, iron-sulfur subunit (EC:1.10.2.2)	4.47	0.00	1.17	0.51	2.82	1.65	3.89	0.00	1.27	0.23	2.58	1.31	-1.32	0.02	0.93	0.18	-0.20	1.13
SPO0272	*petB*	ubiquinol--cytochrome c reductase, cytochrome B (EC:1.10.2.2)	6.19	0.00	1.34	0.10	3.77	2.43	5.69	0.00	1.04	0.59	3.37	2.33	1.15	0.29	1.25	0.67	1.20	0.05
SPO0273	*petC*	ubiquinol--cytochrome c reductase, cytochrome c1 (EC:1.10.2.2)	5.01	0.00	1.80	0.01	3.41	1.61	6.11	0.00	-1.46	0.00	2.33	3.79	1.11	0.67	-1.42	0.00	-0.16	1.27
SPO0274		hypothetical protein	X	X	-1.08	0.83	N/A	N/A	1.37	0.00	-1.18	0.23	0.10	1.28	-1.05	0.96	1.09	X	0.02	1.07
SPO0275		cytochrome b	1.17	0.41	1.10	0.45	1.14	0.03	1.90	0.00	1.23	0.06	1.57	0.34	1.54	0.00	1.36	0.01	1.45	0.09
SPO0276		LuxR family transcriptional regulator	-2.30	0.01	-1.08	0.71	-1.69	0.61	-2.25	0.01	-1.02	0.97	-1.64	0.62	1.07	0.59	1.43	0.11	1.25	0.18
SPO0277		MiaB-like tRNA modifying enzyme	-1.15	0.13	-1.37	0.05	-1.26	0.11	1.94	0.00	-1.36	0.01	0.29	1.65	-1.46	0.00	-1.62	0.00	-1.54	0.08
SPO0278	*dapF*	diaminopimelate epimerase (EC:5.1.1.7)	-1.30	0.00	-1.25	0.03	-1.28	0.03	1.68	0.00	-1.49	0.00	0.10	1.59	-1.06	0.36	-1.32	0.01	-1.19	0.13
SPO0280		transposase, truncation	X	X	-0.99	0.46	N/A	N/A	2.74	0.00	-1.20	0.02	0.77	1.97	-1.01	0.95	-1.39	0.20	-1.20	0.19
SPO0281		hypothetical protein	1.36	0.09	-1.23	0.15	0.07	1.30	-1.91	0.00	-1.19	0.04	-1.55	0.36	-1.07	0.30	-1.24	0.05	-1.16	0.09
SPO0282		hypothetical protein	-1.24	0.06	1.34	0.05	0.05	1.29	1.51	0.00	-1.09	0.29	0.21	1.30	-1.19	0.10	-1.52	0.03	-1.36	0.16
SPO0283		hypothetical protein	1.04	0.16	1.27	0.27	1.16	0.12	-1.41	0.00	-1.20	0.08	-1.31	0.11	1.10	0.68	1.74	0.03	1.42	0.32
SPO0284		dihydroorotase (EC:3.5.2.3)	1.41	0.00	1.30	0.03	1.36	0.05	1.81	0.00	-1.20	0.01	0.31	1.51	-1.13	0.12	-1.14	0.30	-1.14	0.01
SPO0285		hypothetical protein	1.20	0.03	1.29	0.05	1.25	0.05	1.71	0.00	-1.08	0.16	0.32	1.40	-1.28	0.02	-1.27	0.05	-1.28	0.01
SPO0286		hypothetical protein	2.29	0.00	1.36	0.00	1.83	0.47	5.23	0.00	-1.46	0.00	1.89	3.35	-1.41	0.00	-2.21	0.00	-1.81	0.40
SPO0287	*pyrB*	aspartate carbamoyltransferase (EC:2.1.3.2)	1.66	0.00	1.33	0.02	1.50	0.16	3.00	0.00	-1.43	0.00	0.79	2.22	-1.38	0.00	-1.81	0.00	-1.60	0.21
SPO0288	*udgA*	uracil-DNA glycosylase (EC:3.2.2.-)	1.02	0.97	1.00	1.00	1.01	0.01	2.34	0.00	1.38	0.00	1.86	0.48	1.49	0.00	1.05	0.46	1.27	0.22
SPO0289		Ser/Thr protein phosphatase	1.55	0.78	1.31	0.01	1.43	0.12	1.76	0.63	1.41	0.03	1.59	0.17	1.71	0.00	1.46	0.05	1.59	0.13
SPO0290		transmembrane amino acid efflux protein	1.23	0.54	1.06	0.60	1.15	0.09	1.45	0.01	1.17	0.05	1.31	0.14	1.12	0.41	1.03	0.46	1.08	0.05
SPO0291		molybdenum cofactor biosynthesis protein B	1.43	0.02	-1.07	0.13	0.18	1.25	1.53	0.00	1.51	0.01	1.52	0.01	-1.16	0.00	-1.05	0.38	-1.11	0.05
SPO0292		RND family efflux transporter MFP subunit	-1.21	0.32	1.37	0.03	0.08	1.29	1.24	0.76	1.19	0.13	1.22	0.03	1.77	0.02	1.69	0.02	1.73	0.04
SPO0293		AcrB/AcrD/AcrF family transporter	-1.53	0.00	-1.17	0.31	-1.35	0.18	-1.82	0.00	-1.13	0.37	-1.48	0.35	-1.11	0.65	1.77	0.02	0.33	1.44
SPO0294		NUDIX family hydrolase	-1.10	0.64	-1.11	0.43	-1.11	0.01	-1.09	0.42	-1.12	0.09	-1.11	0.02	1.30	0.15	1.56	0.06	1.43	0.13
SPO0295		hypothetical protein	1.17	0.04	-1.22	0.02	-0.03	1.20	1.21	0.02	-1.10	0.04	0.05	1.16	1.53	0.00	1.39	0.00	1.46	0.07
SPO0296		hypothetical protein	-1.24	0.54	1.09	0.69	-0.08	1.17	-1.24	0.00	1.11	0.68	-0.06	1.18	2.20	0.00	2.07	0.01	2.14	0.07
SPO0297		Sua5/YciO/YrdC family protein	-1.28	0.02	-1.10	0.05	-1.19	0.09	-2.96	0.00	1.04	0.92	-0.96	2.00	-1.63	0.00	-1.30	0.11	-1.47	0.17
SPO0298		acyl-CoA dehydrogenase	2.75	0.03	2.95	0.00	2.85	0.10	-1.26	0.56	1.25	0.23	-0.01	1.26	1.43	0.07	2.97	0.00	2.20	0.77

SPO0299		metallo-beta-lactamase	2.41	0.00	3.44	0.00	2.93	0.52	-1.29	0.61	-1.00	0.82	-1.14	0.15	1.20	0.06	1.65	0.00	1.43	0.23
SPO0300		hypothetical protein	1.01	0.86	1.47	0.01	1.24	0.23	-1.13	0.74	-1.05	0.19	-1.09	0.04	1.51	0.01	1.30	0.01	1.41	0.11
SPO0301		glycerophosphoryl diester phosphodiesterase	0.95	0.87	1.06	0.85	1.00	0.06	-1.23	0.77	1.16	0.43	-0.04	1.20	1.41	0.11	1.62	0.07	1.52	0.11
SPO0302		hypothetical protein	1.02	0.99	1.05	0.83	1.04	0.02	-1.22	0.51	1.24	0.29	0.01	1.23	1.02	0.92	-1.17	0.59	-0.08	1.10
SPO0303		cytochrome c oxidase subunit IV	4.12	0.00	1.75	0.00	2.94	1.19	3.56	0.00	1.35	0.00	2.46	1.11	1.07	0.77	0.95	0.07	1.01	0.06
SPO0304		lipoprotein	3.37	0.05	1.75	0.06	2.56	0.81	4.35	0.00	1.28	0.46	2.82	1.54	1.12	0.80	0.98	0.68	1.05	0.07
SPO0305		AzlC family protein	-1.58	0.05	1.21	0.01	-0.19	1.40	1.16	0.09	-1.25	0.03	-0.05	1.21	-1.15	0.31	-1.29	0.04	-1.22	0.07
SPO0306	*fdhD*	formate dehydrogenase accessory protein FdhD	1.04	0.51	-1.09	0.43	-0.03	1.07	1.21	0.00	-1.11	0.08	0.05	1.16	1.21	0.00	1.05	0.69	1.13	0.08
SPO0307	*mobA*	molybdopterin-guanine dinucleotide biosynthesis protein MobA	1.14	0.48	-1.21	0.47	-0.04	1.18	5.00	0.00	-1.19	0.44	1.91	3.10	1.06	0.83	1.16	0.55	1.11	0.05
SPO0308	*mobB*	molybdopterin-guanine dinucleotide biosynthesis protein MobB	1.18	0.01	1.11	0.11	1.15	0.03	1.34	0.00	-1.03	0.78	0.16	1.19	1.10	0.06	-1.24	0.10	-0.07	1.17
SPO0309		hypothetical protein	-1.08	0.78	1.09	0.76	0.01	1.09	1.02	0.77	1.02	0.98	1.02	0.00	1.29	0.32	1.06	0.74	1.18	0.12
SPO0310	*moeA*	molybdopterin biosynthesis protein MoeA	-1.72	0.02	-1.34	0.14	-1.53	0.19	-1.81	0.00	1.04	0.95	-0.39	1.43	1.02	0.99	2.15	0.02	1.59	0.57
SPO0311		hypothetical protein	1.25	0.52	1.31	0.29	1.28	0.03	2.50	0.04	-1.30	0.30	0.60	1.90	-1.11	0.58	-1.55	0.14	-1.33	0.22
SPO0312	*greA*	transcription elongation factor GreA	-1.42	0.14	1.00	0.78	-0.21	1.21	0.99	0.06	1.03	0.51	1.01	0.02	-1.68	0.00	-1.34	0.00	-1.51	0.17
SPO0313		glyoxalase	-1.57	0.01	-1.38	0.01	-1.48	0.10	1.59	0.01	1.01	0.96	1.30	0.29	-1.24	0.03	-1.58	0.00	-1.41	0.17
SPO0314	*soxR*	redox-sensitive transcriptional activator SoxR	-1.46	0.22	-1.11	0.73	-1.29	0.17	-1.37	0.65	-1.45	0.15	-1.41	0.04	1.25	0.18	1.32	0.14	1.29	0.04
SPO0315		hypothetical protein	-2.05	0.00	-1.42	0.01	-1.74	0.32	-3.08	0.00	1.81	0.00	-0.64	2.45	1.41	0.01	1.76	0.01	1.59	0.17
SPO0316		electrotransfer ubiquinone oxidoreductase	1.48	0.08	1.16	0.54	1.32	0.16	1.54	0.08	1.00	0.68	1.27	0.27	-1.24	0.22	1.24	0.59	0.00	1.24
SPO0317		hypothetical protein	-1.33	0.00	-1.05	0.54	-1.19	0.14	1.40	0.01	1.22	0.06	1.31	0.09	1.85	0.00	1.59	0.01	1.72	0.13
SPO0318	*ispE*	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC:2.7.1.148)	-1.41	0.00	-1.22	0.04	-1.32	0.10	1.68	0.00	1.15	0.11	1.42	0.27	1.81	0.00	1.32	0.01	1.57	0.25
SPO0319	*ddsA*	decaprenyl diphosphate synthase (EC:2.5.1.31)	-1.15	0.01	1.22	0.09	0.04	1.19	2.53	0.00	-1.35	0.01	0.59	1.94	-1.29	0.00	-1.59	0.05	-1.44	0.15
SPO0320		hypothetical protein	-1.77	0.12	1.04	0.74	-0.37	1.41	-1.46	0.16	-1.27	0.07	-1.37	0.10	1.04	0.50	-1.23	0.33	-0.10	1.14
SPO0321		hypothetical protein	-1.37	0.00	-1.10	0.46	-1.24	0.14	1.68	0.00	1.28	0.07	1.48	0.20	-1.41	0.04	-1.36	0.13	-1.39	0.02
SPO0322		hypothetical protein	1.03	0.20	-1.16	0.11	-0.06	1.10	-1.62	0.00	2.18	0.00	0.28	1.90	-1.11	0.42	1.66	0.04	0.28	1.39
SPO0323		hypothetical protein	-1.36	0.21	1.86	0.01	0.25	1.61	-1.57	0.55	-1.46	0.14	-1.52	0.06	1.28	0.09	-1.20	0.73	0.04	1.24
SPO0324		DNA-binding transcriptional activator GcvA	-1.12	0.22	1.25	0.00	0.06	1.19	1.20	0.00	1.05	0.40	1.13	0.08	-1.68	0.00	-2.06	X	-1.87	0.19
SPO0325	*phbB*	acetoacetyl-CoA reductase (EC:1.1.1.36)	1.43	0.62	1.66	0.04	1.55	0.12	0.87	0.02	2.35	0.00	1.61	0.74	0.98	0.33	1.18	0.76	1.08	0.10
SPO0326	*phbA*	acetyl-CoA acetyltransferase (EC:2.3.1.9)	3.58	0.01	1.37	0.07	2.48	1.11	2.90	0.00	1.77	0.00	2.34	0.57	1.20	0.03	1.65	0.00	1.43	0.23
SPO0327		diguanylate phosphodiesterase	X	X	1.20	0.16	N/A	N/A	X	X	X	X	N/A	N/A	-1.28	0.28	X	X	N/A	N/A
SPO0328		hypothetical protein	1.48	0.00	-1.18	0.04	0.15	1.33	-2.23	0.00	1.29	0.06	-0.47	1.76	1.38	0.01	2.46	0.00	1.92	0.54
SPO0329		hypothetical protein	1.00	0.53	-1.67	0.00	-0.34	1.34	-3.20	0.00	1.36	0.01	-0.92	2.28	-1.12	0.11	2.27	0.00	0.58	1.70
SPO0330	*ccpA*	cytochrome c peroxidase (EC:1.11.1.5)	-1.07	0.24	1.02	0.89	-0.03	1.05	-1.85	0.00	1.08	0.55	-0.39	1.47	1.37	0.00	1.30	0.15	1.34	0.04
SPO0331		thiol:disulfide interchange protein	1.11	0.26	-1.09	0.45	0.01	1.10	1.72	0.00	-1.05	0.52	0.34	1.39	-1.03	0.80	-1.05	0.92	-1.04	0.01
SPO0332	*argH*	argininosuccinate lyase (EC:4.3.2.1)	-2.20	0.00	1.49	0.03	-0.36	1.85	-1.30	0.02	-1.23	0.09	-1.27	0.04	1.52	0.00	1.09	0.32	1.31	0.21
SPO0333		lipoprotein	1.87	0.02	1.46	0.06	1.67	0.21	2.06	0.00	-1.16	0.27	0.45	1.61	1.46	0.03	1.18	0.28	1.32	0.14
SPO0334	*lysA*	diaminopimelate decarboxylase (EC:4.1.1.20)	-1.18	0.13	1.13	0.10	-0.03	1.16	4.21	0.00	-1.64	0.00	1.29	2.93	-1.92	0.00	-2.48	0.00	-2.20	0.28
SPO0335		hypothetical protein	1.02	0.68	-1.19	0.12	-0.09	1.11	-2.41	0.00	1.65	0.00	-0.38	2.03	1.25	0.04	1.56	0.00	1.41	0.16
SPO0336		hypothetical protein	-1.25	0.02	1.03	0.77	-0.11	1.14	-1.63	0.00	-1.36	0.01	-1.50	0.14	1.22	0.01	-1.01	0.74	0.11	1.12

SPO0337	*ftsE*	cell division ATP-binding protein FtsE	1.08	0.11	1.21	0.02	1.15	0.06	2.47	0.00	-1.29	0.01	0.59	1.88	-1.14	0.11	-1.66	0.00	-1.40	0.26
SPO0338		cell division permease FtsX	-1.33	0.01	1.26	0.06	-0.04	1.30	1.51	0.00	-1.33	0.29	0.09	1.42	-1.06	0.61	-1.15	0.76	-1.11	0.04
SPO0339		acyltransferase	1.21	0.09	1.41	0.04	1.31	0.10	2.55	0.00	-1.25	0.05	0.65	1.90	1.52	0.01	-1.00	0.98	0.26	1.26
SPO0340	*lpdA*	2-oxoglutarate dehydrogenase E3 (EC:1.8.1.4)	1.18	0.80	1.53	0.00	1.36	0.18	6.21	0.00	3.31	0.00	4.76	1.45	-1.25	0.06	0.90	0.05	-0.18	1.08
SPO0341		hypothetical protein	-1.10	0.70	1.64	0.06	0.27	1.37	1.64	0.01	2.01	0.01	1.83	0.19	-1.35	0.04	1.69	X	0.17	1.52
SPO0342		hypothetical protein	-2.62	0.00	1.39	0.05	-0.62	2.01	1.10	0.07	3.15	0.00	2.13	1.03	-1.25	0.09	1.77	0.05	0.26	1.51
SPO0343	*sucB*	dihydrolipoamide succinyltransferase (EC:2.3.1.61)	1.54	0.50	1.79	0.00	1.67	0.13	6.11	0.02	3.66	0.00	4.89	1.23	-1.04	0.33	-1.15	0.08	-1.10	0.05
SPO0344	*sucA*	2-oxoglutarate dehydrogenase E1 (EC:1.2.4.2)	1.37	0.01	1.45	0.01	1.41	0.04	4.70	0.00	3.44	0.00	4.07	0.63	-1.59	0.00	-1.55	0.00	-1.57	0.02
SPO0345		hypothetical protein	1.29	0.68	2.04	0.00	1.67	0.38	5.93	0.00	4.38	0.00	5.16	0.78	-1.10	0.03	1.04	0.53	-0.03	1.07
SPO0346	*sucD*	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5)	1.37	0.02	2.04	0.00	1.71	0.33	6.69	0.00	3.45	0.00	5.07	1.62	1.19	0.08	1.20	0.63	1.20	0.01
SPO0347	*sucC*	succinyl-CoA synthetase subunit beta (EC:6.2.1.5)	1.72	0.03	1.44	0.05	1.58	0.14	7.46	0.00	4.59	0.00	6.03	1.44	-1.42	0.00	0.89	0.01	-0.27	1.16
SPO0348		hypothetical protein	-1.88	0.00	-1.15	0.31	-1.52	0.37	1.26	0.01	-1.06	0.27	0.10	1.16	1.37	0.00	-1.15	0.23	0.11	1.26
SPO0349	*mdh*	malate dehydrogenase (EC:1.1.1.37)	2.67	0.00	1.52	0.03	2.10	0.58	5.12	0.00	1.07	0.89	3.10	2.03	1.24	0.12	0.91	0.02	1.07	0.17
SPO0350		hypothetical protein	2.01	0.00	1.73	0.00	1.87	0.14	1.28	0.00	-0.97	0.60	0.15	1.13	-0.99	0.73	-1.60	0.06	-1.30	0.30
SPO0351		hypothetical protein	1.42	0.00	1.18	0.34	1.30	0.12	-1.40	0.74	2.69	0.00	0.65	2.05	-0.98	0.55	-1.03	0.81	-1.00	0.03
SPO0352	*citE*	citrate lyase subunit beta (EC:4.1.3.34 4.1.3.6)	-1.74	0.00	1.39	0.04	-0.18	1.57	2.03	0.00	1.04	0.78	1.54	0.50	-1.36	0.02	-1.52	0.00	-1.44	0.08
SPO0353		NnrU family protein	1.11	0.90	1.15	0.10	1.13	0.02	1.86	0.00	0.99	0.38	1.43	0.43	-1.36	0.03	-1.42	0.00	-1.39	0.03
SPO0354		hypothetical protein	1.45	0.43	1.21	0.19	1.33	0.12	1.39	0.54	1.18	0.13	1.29	0.11	-1.30	0.00	-1.19	0.02	-1.25	0.06
SPO0355		hypothetical protein	1.66	0.00	1.65	0.01	1.66	0.01	1.47	0.00	-1.19	0.02	0.14	1.33	-1.01	0.98	-1.49	0.02	-1.25	0.24
SPO0356		hypothetical protein	1.06	0.92	1.20	0.27	1.13	0.07	1.74	0.05	1.15	0.24	1.45	0.30	1.26	0.05	-1.06	0.44	0.10	1.16
SPO0357		von Willebrand factor A	-1.38	0.34	1.03	0.88	-0.18	1.21	-2.23	0.00	1.39	0.15	-0.42	1.81	-1.10	0.65	-1.20	0.43	-1.15	0.05
SPO0358	*sdhC*	succinate dehydrogenase, cytochrome b556 subunit (EC:1.3.99.1)	3.07	0.00	1.40	0.01	2.24	0.84	4.46	0.00	1.94	0.00	3.20	1.26	-1.04	0.43	1.09	0.69	0.03	1.07
SPO0359	*sdhD*	succinate dehydrogenase, hydrophobic membrane anchor protein (EC:1.3.99.1)	3.31	0.00	1.85	0.00	2.58	0.73	4.69	0.00	2.38	0.00	3.54	1.16	-1.18	0.00	-1.20	0.04	-1.19	0.01
SPO0360	*sdhA*	succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1)	3.22	0.00	1.24	0.34	2.23	0.99	4.82	0.00	2.43	0.00	3.63	1.20	-1.20	0.02	0.94	0.03	-0.13	1.07
SPO0361	*sdhB*	succinate dehydrogenase iron-sulfur subunit (EC:1.3.99.1)	3.05	0.06	2.07	0.01	2.56	0.49	5.68	0.00	2.29	0.01	3.99	1.70	-1.12	0.57	-1.31	0.09	-1.22	0.10
SPO0362		type I secretion target repeat-containing protein	-1.35	0.00	1.47	0.05	0.06	1.41	1.11	0.88	1.61	0.00	1.36	0.25	-1.51	0.01	-1.45	0.03	-1.48	0.03
SPO0363		hypothetical protein	3.14	0.00	3.76	0.00	3.45	0.31	12.90	0.00	4.58	0.00	8.74	4.16	-1.65	0.02	-1.09	0.45	-1.37	0.28
SPO0364		decarboxylase, pyridoxal-dependent	-0.96	0.45	-1.02	1.00	-0.99	0.03	-1.20	0.75	-1.45	0.32	-1.33	0.13	-1.80	0.03	-1.96	0.03	-1.88	0.08
SPO0365		hypothetical protein	3.24	0.02	1.59	0.03	2.42	0.83	1.35	0.16	-1.07	0.84	0.14	1.21	1.19	0.25	-1.44	0.54	-0.13	1.32
SPO0366	*deoD*	purine nucleoside phosphorylase (EC:2.4.2.1)	-1.36	0.19	1.31	0.05	-0.03	1.34	1.94	0.06	-1.16	0.11	0.39	1.55	1.60	0.01	1.10	0.84	1.35	0.25
SPO0367		H-NS family DNA-binding protein	-1.48	0.00	-1.12	0.42	-1.30	0.18	1.74	0.00	-1.09	0.06	0.33	1.42	0.99	0.19	1.05	0.53	1.02	0.03
SPO0368		methylmalonyl-CoA mutase (EC:5.4.99.2)	-1.59	0.09	1.29	0.09	-0.15	1.44	-1.36	0.12	1.25	0.23	-0.06	1.31	-1.12	0.35	-1.41	0.04	-1.27	0.14
SPO0369		acyltransferase	-1.36	0.55	-1.10	0.90	-1.23	0.13	-1.01	0.72	1.05	0.95	0.02	1.03	-1.03	0.99	2.41	0.11	0.69	1.72
SPO0370	*ccrA*	crotonyl-CoA reductase	-3.94	0.00	1.58	0.04	-1.18	2.76	-1.51	0.02	1.46	0.02	-0.03	1.49	1.04	0.94	1.23	0.33	1.14	0.10
SPO0371	*luxR-1*	LuxR family transcriptional regulator	-1.80	0.26	3.01	0.01	0.61	2.41	-5.51	0.01	5.46	0.00	-0.02	5.49	1.13	0.63	1.73	0.10	1.43	0.30
SPO0372		autoinducer synthesis protein	-1.72	0.00	2.47	0.01	0.38	2.10	-3.54	0.00	4.09	0.00	0.28	3.82	-1.14	0.56	-0.89	0.59	-1.01	0.13
SPO0373		helicase, ATP-dependent	-1.70	0.00	-1.17	0.46	-1.44	0.27	2.52	0.05	1.00	0.86	1.76	0.76	-1.03	0.82	-1.17	0.33	-1.10	0.07
SPO0374		hypothetical protein	1.06	0.98	1.13	0.68	1.10	0.03	1.43	0.37	1.03	0.98	1.23	0.20	1.41	0.17	1.05	0.93	1.23	0.18

SPO0375		hypothetical protein	-1.02	0.87	-1.16	0.37	-1.09	0.07	1.58	0.28	-1.03	0.77	0.28	1.31	-1.04	0.75	-1.05	0.75	-1.05	0.01
SPO0376		sugar ABC transporter permease	-1.01	0.86	1.09	0.52	0.04	1.05	1.03	0.74	-1.71	0.01	-0.34	1.37	1.15	0.27	1.01	0.92	1.08	0.07
SPO0377		sugar ABC transporter permease	-1.45	0.00	-1.11	0.14	-1.28	0.17	-1.35	0.01	-1.63	0.00	-1.49	0.14	-1.07	0.10	1.01	0.99	-0.03	1.04
SPO0378		sugar ABC transporter ATP-binding protein	-1.37	0.41	-1.18	0.25	-1.28	0.10	-1.48	0.00	-1.49	0.01	-1.49	0.01	-1.09	0.31	1.26	0.19	0.09	1.18
SPO0379		sugar ABC transporter substrate-binding protein	-1.34	0.00	-1.63	0.00	-1.49	0.15	-1.55	0.00	-1.47	0.00	-1.51	0.04	-1.02	0.43	1.20	0.23	0.09	1.11
SPO0380		ribosomal-protein-alanine acetyltransferase	-1.72	0.00	-1.19	0.42	-1.46	0.26	-1.86	0.00	1.03	0.88	-0.42	1.45	-1.44	0.03	1.60	0.01	0.08	1.52
SPO0381		protease	1.01	0.95	1.03	0.90	1.02	0.01	1.33	0.66	-1.07	0.85	0.13	1.20	-1.01	0.97	1.35	0.45	0.17	1.18
SPO0382		NifU domain-containing protein	0.92	0.08	1.29	0.08	1.11	0.18	0.84	0.00	1.03	0.66	0.94	0.09	1.30	0.00	1.10	0.75	1.20	0.10
SPO0383		ACP phosphodieterase	-1.45	0.23	-1.25	0.56	-1.35	0.10	-2.19	0.00	-1.24	0.54	-1.72	0.48	1.34	0.39	2.63	0.02	1.99	0.65
SPO0384		hypothetical protein	-2.48	0.00	-1.22	0.30	-1.85	0.63	-1.08	0.87	1.30	0.06	0.11	1.19	-1.28	0.06	-1.30	0.07	-1.29	0.01
SPO0385		2-hydroxychromene-2-carboxylate isomerase	1.57	0.00	1.11	0.52	1.34	0.23	1.55	0.00	1.12	0.20	1.34	0.22	1.25	0.01	-1.14	0.11	0.06	1.20
SPO0386		universal stress family protein	1.39	0.10	1.12	0.32	1.26	0.14	1.32	0.10	1.19	0.14	1.26	0.07	1.27	0.04	1.31	0.03	1.29	0.02
SPO0387		hypothetical protein	-1.89	0.00	-1.39	0.22	-1.64	0.25	-2.07	0.00	-1.11	0.67	-1.59	0.48	-1.21	0.14	-1.06	0.98	-1.14	0.08
SPO0388		aminotransferase	1.09	0.98	-1.54	0.02	-0.23	1.32	-1.35	0.00	1.02	0.77	-0.17	1.19	-1.05	0.50	-1.57	0.00	-1.31	0.26
SPO0389		AsnC family transcriptional regulator	-1.74	0.16	-1.36	0.03	-1.55	0.19	-2.40	0.05	-1.07	0.65	-1.74	0.67	-1.40	0.01	1.13	0.22	-0.14	1.27
SPO0390		glutamate/leucine/phenylalanine/valine dehydrogenase	-1.15	0.76	1.36	0.43	0.11	1.26	0.84	0.62	-1.61	0.19	-0.39	1.22	1.24	0.41	1.56	0.30	1.40	0.16
SPO0391	*bphC3*	biphenyl-2,3-diol 1,2-dioxygenase III (EC:1.13.11.39)	1.45	0.05	1.48	0.01	1.47	0.02	1.19	0.09	-1.14	0.36	0.03	1.17	-1.29	0.02	-1.53	0.05	-1.41	0.12
SPO0392	*trpS*	tryptophanyl-tRNA synthetase (EC:6.1.1.2)	1.18	0.78	1.09	0.67	1.14	0.04	1.29	0.59	-1.52	0.01	-0.12	1.41	-1.63	0.02	-2.24	0.00	-1.94	0.31
SPO0393		rhomboid family protein	-1.03	0.13	1.03	0.96	0.00	1.03	1.43	0.00	-1.27	0.04	0.08	1.35	1.29	0.00	1.25	0.34	1.27	0.02
SPO0394		hypothetical protein	1.97	0.00	-1.10	0.41	0.44	1.54	-1.29	0.11	-1.10	0.45	-1.20	0.10	-1.07	0.81	2.43	0.00	0.68	1.75
SPO0395		cyclic nucleotide-binding protein	-1.28	0.49	1.09	0.72	-0.10	1.19	1.15	0.63	-0.99	0.99	0.08	1.07	1.41	0.02	1.12	0.70	1.27	0.14
SPO0396	*mviN*	integral membrane protein MviN	1.10	0.46	1.18	0.53	1.14	0.04	1.52	0.04	-1.02	0.81	0.25	1.27	1.40	0.00	-0.93	0.13	0.24	1.16
SPO0397	*glnD*	PII uridylyl-transferase (EC:2.7.7.59)	-1.24	0.07	1.17	0.24	-0.04	1.21	1.26	0.04	1.07	0.71	1.17	0.10	1.10	0.43	-1.11	0.66	-0.01	1.11
SPO0398		hypothetical protein	-1.32	0.24	1.06	0.84	-0.13	1.19	1.51	0.02	1.24	0.34	1.38	0.14	1.19	0.36	1.17	0.68	1.18	0.01
SPO0399		tetrapyrrole methylase	1.06	0.37	1.75	0.00	1.41	0.35	1.34	0.01	-1.02	0.73	0.16	1.18	1.30	0.00	-0.94	0.22	0.18	1.12
SPO0400		hypothetical protein	-1.00	0.43	1.63	0.00	0.32	1.31	1.31	0.01	1.38	0.14	1.35	0.03	-1.08	0.48	-1.09	0.92	-1.09	0.01
SPO0401	*gshB*	glutathione synthetase (EC:6.3.2.3)	1.62	0.13	1.13	0.35	1.38	0.25	2.81	0.00	-1.23	0.01	0.79	2.02	1.13	0.34	-1.21	0.05	-0.04	1.17
SPO0402	*comM*	competence protein ComM	1.47	0.30	2.36	0.00	1.92	0.44	1.23	0.78	1.97	0.00	1.60	0.37	-1.02	0.96	1.18	0.58	0.08	1.10
SPO0403		hypothetical protein	2.43	0.00	2.90	0.00	2.67	0.24	4.44	0.00	1.13	0.11	2.79	1.66	1.51	0.00	-0.94	0.19	0.29	1.22
SPO0404		phosphoglycerate mutase	-1.07	0.25	1.39	0.01	0.16	1.23	4.29	0.00	1.06	0.38	2.68	1.62	-1.17	0.02	-1.73	0.00	-1.45	0.28
SPO0405		cobinamide kinase/cobinamide phosphate guanylyltransferase	-1.02	0.89	1.07	0.56	0.03	1.05	1.44	0.00	1.16	0.10	1.30	0.14	-1.49	0.00	-1.84	0.00	-1.67	0.18
SPO0406	*rpoH2*	RNA polymerase factor sigma-32	1.08	0.16	-2.19	0.00	-0.56	1.64	0.90	0.02	1.02	0.96	0.96	0.06	1.21	0.02	-1.02	0.85	0.10	1.12
SPO0407		hypothetical protein	1.20	0.92	-1.07	0.67	0.06	1.14	1.26	0.85	1.34	0.18	1.30	0.04	1.37	0.13	1.15	0.40	1.26	0.11
SPO0408	*coaBC*	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase (EC:4.1.1.36 6.3.2.5)	-1.21	0.43	1.08	0.68	-0.06	1.15	1.12	0.91	1.19	0.39	1.16	0.03	1.14	0.34	1.22	0.28	1.18	0.04
SPO0409	*dut*	deoxyuridine 5'-triphosphate nucleotidohydrolase (EC:3.6.1.23)	1.06	1.00	1.38	0.08	1.22	0.16	1.65	0.47	1.04	0.85	1.35	0.31	1.45	0.01	1.03	0.72	1.24	0.21
SPO0410		molybdopterin biosynthesis protein MoeB	-1.61	0.26	1.12	0.45	-0.25	1.37	-1.33	0.69	-1.34	0.03	-1.34	0.01	1.08	0.31	-1.48	0.02	-0.20	1.28

SPO0411		hypothetical protein	-1.80	0.01	-1.04	0.55	-1.42	0.38	-1.63	0.00	1.02	0.84	-0.31	1.33	1.06	0.41	1.29	0.01	1.18	0.12
SPO0412		hypothetical protein	-1.00	0.62	1.08	0.21	0.04	1.04	3.60	0.00	1.43	0.00	2.52	1.09	1.79	0.00	1.22	0.00	1.51	0.29
SPO0413		Cys/Met metabolism PLP-dependent enzyme family protein	1.29	0.02	-1.66	0.00	-0.19	1.48	-2.02	0.00	2.13	0.00	0.05	2.08	1.23	0.00	1.27	0.07	1.25	0.02
SPO0414		peptidyl-dipeptidase	1.44	0.42	1.09	0.66	1.27	0.18	1.77	0.13	-1.11	0.10	0.33	1.44	1.92	0.00	1.58	0.00	1.75	0.17
SPO0415		D-isomer specific 2-hydroxyacid dehydrogenase	-1.04	0.80	-1.20	0.49	-1.12	0.08	1.12	0.63	1.02	0.86	1.07	0.05	-1.47	0.04	-1.25	0.16	-1.36	0.11
SPO0416	*mreD*	rod shape-determining protein MreD	1.36	0.15	1.19	0.31	1.28	0.09	1.72	0.04	-1.11	0.33	0.31	1.42	-1.08	0.55	-1.43	0.04	-1.26	0.18
SPO0417	*pbpA*	penicillin-binding protein 2	-1.15	0.01	1.04	0.77	-0.05	1.10	1.14	0.01	-1.08	0.14	0.03	1.11	-1.01	0.50	-1.33	0.00	-1.17	0.16
SPO0418		hypothetical protein	-1.10	0.80	1.51	0.00	0.21	1.31	1.17	0.10	-1.02	0.48	0.08	1.10	1.19	0.02	-1.30	0.01	-0.06	1.25
SPO0419	*mreC*	rod shape-determining protein MreC	-1.07	0.21	1.18	0.14	0.05	1.13	1.28	0.02	-1.14	0.18	0.07	1.21	1.08	0.19	-1.17	0.12	-0.04	1.13
SPO0420	*mreB*	rod shape-determining protein MreB	-1.40	0.00	-1.26	0.02	-1.33	0.07	3.51	0.00	-1.27	0.00	1.12	2.39	-1.54	0.00	-1.48	0.00	-1.51	0.03
SPO0421		hypothetical protein	-1.63	0.01	1.23	0.22	-0.20	1.43	-1.28	0.29	1.04	0.76	-0.12	1.16	-1.26	0.07	-1.37	0.08	-1.32	0.06
SPO0422	*leuA*	2-isopropylmalate synthase (EC:2.3.3.13)	1.54	0.00	1.12	0.24	1.33	0.21	3.69	0.00	-1.09	0.03	1.30	2.39	-1.10	0.33	-1.40	0.00	-1.25	0.15
SPO0423		DNA-binding protein	-1.71	0.04	1.10	0.70	-0.31	1.41	1.10	0.73	-1.39	0.23	-0.15	1.25	-1.29	0.02	-0.91	0.14	-1.10	0.19
SPO0424		hypothetical protein	-2.05	0.02	1.03	0.80	-0.51	1.54	-3.83	0.00	-1.27	0.20	-2.55	1.28	-1.32	0.07	-0.99	0.57	-1.16	0.16
SPO0425		MORN repeat-containing protein	0.94	0.00	1.02	1.00	0.98	0.04	0.94	0.00	1.23	0.15	1.09	0.14	1.10	0.17	1.07	0.71	1.09	0.02
SPO0426	*nadE*	NAD synthetase (EC:6.3.1.5)	1.85	0.00	1.29	0.17	1.57	0.28	3.15	0.00	-1.03	0.51	1.06	2.09	-1.14	0.38	-1.50	0.00	-1.32	0.18
SPO0427		hypothetical protein	1.88	0.00	2.21	0.00	2.05	0.17	-1.74	0.00	2.37	0.00	0.32	2.06	-1.02	0.68	-1.31	0.03	-1.17	0.14
SPO0428		amino acid deaminase	-1.26	0.33	1.65	0.00	0.20	1.46	-1.10	0.86	-1.11	0.08	-1.11	0.01	-1.10	0.37	-1.05	0.76	-1.08	0.03
SPO0429		metallo-beta-lactamase	1.46	0.01	-1.01	0.99	0.23	1.24	-1.10	0.61	2.99	0.00	0.95	2.05	1.60	0.01	1.21	0.38	1.41	0.20
SPO0430	*gltX*	glutamyl-tRNA synthetase (EC:6.1.1.17)	-1.02	X	1.18	0.33	0.08	1.10	5.68	0.00	-1.31	0.01	2.19	3.50	-1.42	0.00	-1.61	0.01	-1.52	0.10
SPO0431		hypothetical protein	1.14	0.33	1.42	0.46	1.28	0.14	1.93	0.17	1.09	0.87	1.51	0.42	-1.32	0.61	-1.52	0.51	-1.42	0.10
SPO0432		rrf2 family protein	1.07	0.46	1.36	0.03	1.22	0.15	7.87	0.00	1.05	0.63	4.46	3.41	1.31	0.05	-1.36	0.00	-0.03	1.34
SPO0433		ABC transporter permease	-0.97	0.88	-1.21	0.36	-1.09	0.12	1.53	0.18	-1.60	0.05	-0.04	1.57	-0.98	0.69	-1.00	0.92	-0.99	0.01
SPO0434		ABC transporter ATP-binding protein	-1.05	0.08	-1.42	0.00	-1.24	0.19	1.35	0.03	-1.64	0.00	-0.15	1.50	1.53	0.00	1.32	0.02	1.43	0.11
SPO0435		acyl-CoA thioesterase	1.21	0.67	1.07	0.44	1.14	0.07	1.36	0.01	1.10	0.20	1.23	0.13	1.41	0.00	1.15	0.05	1.28	0.13
SPO0436		hypothetical protein	1.10	0.38	1.23	0.00	1.17	0.06	-1.09	0.96	-1.03	0.71	-1.06	0.03	1.32	0.01	1.12	0.11	1.22	0.10
SPO0437		cold shock family protein	-1.46	0.00	1.27	0.10	-0.10	1.37	1.65	0.00	-1.17	0.17	0.24	1.41	1.42	0.11	1.20	0.78	1.31	0.11
SPO0438		ErfK/YbiS/YcfS/YnhG family protein	1.17	0.23	-1.05	0.04	0.06	1.11	-2.54	0.00	1.07	0.83	-0.74	1.81	0.99	0.67	1.15	0.28	1.07	0.08
SPO0439		hypothetical protein	1.15	0.37	-1.09	0.40	0.03	1.12	-1.61	0.03	-1.14	0.19	-1.38	0.24	-1.84	0.00	-1.55	0.06	-1.70	0.15
SPO0440		thioesterase	-1.27	0.01	1.50	0.02	0.12	1.39	-1.20	0.46	-1.29	0.36	-1.25	0.05	1.18	0.07	-1.10	0.92	0.04	1.14
SPO0441		hypothetical protein	1.22	0.39	-1.02	0.89	0.10	1.12	1.15	0.50	-1.34	0.22	-0.10	1.25	-1.12	0.15	1.29	0.13	0.09	1.21
SPO0442		thioredoxin	1.08	0.23	-1.23	0.17	-0.08	1.16	-1.22	0.58	-1.52	0.01	-1.37	0.15	1.13	0.06	-0.92	0.11	0.11	1.02
SPO0443		hypothetical protein	-1.03	0.89	-1.16	0.66	-1.10	0.06	-1.13	0.69	-1.30	0.34	-1.22	0.09	1.22	0.51	1.88	0.16	1.55	0.33
SPO0444		hypothetical protein	1.02	0.51	-1.12	0.52	-0.05	1.07	-1.88	0.00	1.03	0.99	-0.43	1.46	-1.10	0.41	-1.17	0.56	-1.14	0.03
SPO0445		hypothetical protein	1.09	0.51	1.12	0.67	1.11	0.02	-2.03	0.05	-1.02	0.95	-1.53	0.51	-1.17	0.64	X	X	N/A	N/A
SPO0446		ABC transporter ATP-binding protein	1.62	0.00	0.98	0.87	1.30	0.32	2.22	0.00	-1.33	0.07	0.45	1.78	-1.40	0.01	-1.50	0.01	-1.45	0.05
SPO0447		hypothetical protein	X	X	-1.31	0.03	N/A	N/A	-1.00	0.01	-1.30	0.05	-1.15	0.15	-1.46	0.00	X	X	N/A	N/A
SPO0448		MOSC domain-containing protein	1.32	0.92	1.15	0.74	1.24	0.09	1.42	0.86	-1.14	0.78	0.14	1.28	1.14	0.76	1.59	0.44	1.37	0.23
SPO0449	*nadD*	nicotinic acid mononucleotide adenylyltransferase	-1.67	0.48	1.15	0.78	-0.26	1.41	1.84	0.39	0.99	0.93	1.41	0.43	1.11	0.83	-1.27	0.56	-0.08	1.19

		(EC:2.7.7.18)																		
SPO0450		hypothetical protein	1.17	0.27	1.46	0.17	1.32	0.15	1.84	0.09	-1.40	0.05	0.22	1.62	-1.33	0.03	-1.81	0.00	-1.57	0.24
SPO0451	*dacB*	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase (EC:3.4.16.4)	-1.49	0.12	1.11	0.45	-0.19	1.30	-1.98	0.07	1.21	0.14	-0.39	1.60	1.18	0.06	1.29	0.01	1.24	0.06
SPO0452		hypothetical protein	4.61	0.00	1.98	0.01	3.30	1.32	2.57	0.01	1.24	0.38	1.91	0.67	1.24	0.10	1.07	0.94	1.16	0.09
SPO0453	*dddW*	dimethylsulfoniopropionate lyase	36.60	0.00	45.60	0.00	41.10	4.50	2.66	0.01	-1.12	0.34	0.77	1.89	-1.72	0.00	X	X	N/A	N/A
SPO0454		LysR family transcriptional regulator	3.30	0.00	2.09	0.00	2.70	0.61	-0.95	0.27	-1.22	0.14	-1.08	0.14	1.04	0.76	1.08	0.51	1.06	0.02
SPO0455	*lysK*	lysyl-tRNA synthetase (EC:6.1.1.6)	1.51	0.47	1.34	0.30	1.43	0.09	3.38	0.07	-1.68	0.01	0.85	2.53	-1.39	0.02	-1.66	0.00	-1.53	0.14
SPO0456		hypothetical protein	1.71	0.00	1.12	0.53	1.42	0.29	-1.44	0.00	1.39	0.00	-0.03	1.42	-1.23	0.00	-1.17	0.01	-1.20	0.03
SPO0457		hypothetical protein	1.51	0.00	1.01	0.97	1.26	0.25	-1.78	0.00	1.69	0.01	-0.05	1.74	-1.74	0.00	-1.10	0.51	-1.42	0.32
SPO0458		hypothetical protein	-1.82	0.12	-1.00	0.94	-1.41	0.41	-1.84	0.53	2.07	0.03	0.12	1.96	-1.46	0.23	1.17	0.12	-0.15	1.32
SPO0459		hypothetical protein	1.28	0.03	1.32	0.05	1.30	0.02	-1.08	0.73	3.15	0.00	1.04	2.12	-1.16	0.28	-2.14	0.00	-1.65	0.49
SPO0460		hypothetical protein	-1.06	0.20	1.28	0.46	0.11	1.17	-7.99	0.00	1.24	X	-3.38	4.62	-1.46	0.07	X	X	N/A	N/A
SPO0461		ParA family protein	2.60	0.05	2.78	0.00	2.69	0.09	5.50	0.00	-1.46	0.00	2.02	3.48	1.40	0.03	1.21	0.01	1.31	0.10
SPO0462		antibiotic biosynthesis monooxygenase domain-containing protein	0.99	0.00	1.10	0.22	1.05	0.05	-3.75	0.00	1.19	0.03	-1.28	2.47	1.15	0.14	1.15	0.06	1.15	0.00
SPO0463		universal stress family protein	1.49	0.01	1.32	0.03	1.41	0.09	3.25	0.00	1.02	0.95	2.14	1.12	1.51	0.01	1.13	0.17	1.32	0.19
SPO0464		hypothetical protein	1.79	0.00	1.18	0.10	1.49	0.31	1.46	0.00	1.24	0.11	1.35	0.11	1.12	0.18	1.34	0.17	1.23	0.11
SPO0465		pyridoxamine 5'-phosphate oxidase	X	X	1.13	0.10	N/A	N/A	X	X	1.28	X	N/A	N/A	1.14	0.06	-1.17	X	-0.02	1.16
SPO0466		formate/nitrate transporter	-1.10	0.05	-1.35	0.15	-1.23	0.13	1.69	0.02	1.04	0.87	1.37	0.33	-1.08	0.65	1.31	0.26	0.12	1.20
SPO0467		GntR family transcriptional regulator	1.19	0.28	-1.06	0.90	0.06	1.13	1.36	0.65	-1.13	0.76	0.12	1.25	-1.21	0.56	-1.19	0.86	-1.20	0.01
SPO0468	*phnG*	alkylphosphonate utilization protein PhnG	1.32	0.90	-1.01	0.98	0.16	1.17	1.27	0.88	1.03	0.96	1.15	0.12	-1.08	0.88	1.61	0.42	0.27	1.35
SPO0469	*phnH*	carbon-phosphorus lyase complex subunit	1.03	0.99	-1.12	0.24	-0.05	1.08	-2.40	0.00	-1.15	0.49	-1.78	0.63	-1.46	0.05	-1.18	0.76	-1.32	0.14
SPO0470	*phnI*	alkylphosphonate utilization protein PhnI	1.21	0.22	-1.03	0.85	0.09	1.12	-2.15	0.01	1.08	0.49	-0.54	1.62	-1.59	0.00	-1.76	0.00	-1.68	0.09
SPO0471	*phnJ*	alkylphosphonate utilization protein PhnJ	1.36	0.31	1.12	0.59	1.24	0.12	-1.61	0.14	-1.22	0.52	-1.42	0.20	1.08	0.76	-1.11	0.96	-0.02	1.10
SPO0472	*phnK*	phosphonate C-P lyase system protein Phn	1.49	0.15	1.14	0.09	1.32	0.18	-1.41	0.46	-1.11	0.26	-1.26	0.15	-1.10	0.87	-1.39	0.03	-1.25	0.14
SPO0473	*phnL*	alkylphosphonate utilization protein PhnL	-0.99	0.92	1.17	0.12	0.09	1.08	-1.66	0.16	-1.13	0.47	-1.40	0.27	-0.97	0.69	-1.54	0.58	-1.26	0.28
SPO0474	*phnN*	alkylphosphonate utilization protein PhnN	1.19	0.91	1.20	0.34	1.20	0.01	0.99	0.98	-0.99	0.93	0.00	0.99	1.07	0.62	1.13	0.72	1.10	0.03
SPO0475		hypothetical protein	-1.25	0.11	1.13	0.52	-0.06	1.19	1.51	0.00	-1.55	0.09	-0.02	1.53	-1.32	0.27	-1.49	0.11	-1.41	0.09
SPO0476	*phnM*	alkylphosphonate utilization protein PhnM	-1.03	0.98	1.04	0.86	0.01	1.04	-1.32	0.80	-1.29	0.30	-1.31	0.02	-0.97	0.81	-1.00	0.71	-0.98	0.02
SPO0477		hypothetical protein	1.05	0.07	1.26	0.10	1.16	0.11	-3.09	0.00	1.24	0.05	-0.93	2.17	-2.25	0.00	-1.54	0.03	-1.90	0.36
SPO0478		hypothetical protein	1.92	0.00	-1.24	0.15	0.34	1.58	-1.27	0.07	-1.74	0.00	-1.51	0.24	-1.37	0.00	-1.41	0.09	-1.39	0.02
SPO0479		ISSpo8, transposase	1.08	0.11	1.99	0.00	1.54	0.46	-1.15	0.40	X	X	N/A	N/A	-1.07	0.78	-1.60	X	-1.34	0.27
SPO0481		acetyltransferase	X	X	1.26	0.12	N/A	N/A	4.51	0.00	-1.28	0.04	1.62	2.90	1.13	0.08	-1.48	0.01	-0.18	1.31
SPO0482		NADH-ubiquinone oxidoreductase	1.33	0.74	1.23	0.04	1.28	0.05	2.28	0.00	0.99	0.18	1.63	0.65	1.19	0.25	1.02	0.15	1.11	0.09
SPO0483		microcystin dependent protein	-1.30	0.00	-1.83	0.00	-1.57	0.27	-3.98	0.00	1.12	0.45	-1.43	2.55	1.62	0.00	3.22	0.00	2.42	0.80
SPO0484	*rplB*	50S ribosomal protein L2	-1.61	0.00	-1.48	0.00	-1.55	0.07	11.70	0.00	-1.62	0.01	5.04	6.66	-2.07	0.00	-3.55	0.00	-2.81	0.74
SPO0485	*rpsS*	30S ribosomal protein S19	-1.49	0.00	-1.65	0.00	-1.57	0.08	11.80	0.00	-1.70	0.00	5.05	6.75	-2.02	0.00	-3.71	0.00	-2.87	0.85
SPO0486	*rplV*	50S ribosomal protein L22	-1.42	0.00	-1.17	0.15	-1.30	0.13	13.20	0.00	-1.78	0.00	5.71	7.49	-1.17	0.02	-2.35	0.00	-1.76	0.59
SPO0487	*rpsC*	30S ribosomal protein S3	-1.96	0.00	-1.15	0.26	-1.56	0.41	11.20	0.00	-1.98	0.00	4.61	6.59	-1.09	0.00	-2.07	0.00	-1.58	0.49

SPO0488	*rplP*	50S ribosomal protein L16	-2.08	0.03	2.24	0.00	0.08	2.16	1.79	0.01	-2.03	0.00	-0.12	1.91	1.97	0.00	1.01	0.19	1.49	0.48
SPO0489		ISSpo2, transposase	-1.00	0.85	-1.04	0.94	-1.02	0.02	-1.52	0.56	1.14	0.36	-0.19	1.33	-1.24	0.26	-1.20	0.81	-1.22	0.02
SPO0490		calcium-binding domain-containing protein	1.44	0.30	1.61	0.30	1.53	0.09	-4.41	0.00	2.15	0.06	-1.13	3.28	-1.09	0.81	1.44	0.38	0.18	1.27
SPO0491		hypothetical protein	-0.95	0.06	1.08	0.60	0.07	1.01	6.88	0.00	-1.03	0.51	2.93	3.96	-1.59	0.00	-2.51	0.00	-2.05	0.46
SPO0492		cyclic nucleotide-binding protein	-1.36	0.01	1.11	0.42	-0.13	1.24	-1.33	0.01	1.05	0.65	-0.14	1.19	1.41	0.00	1.17	0.01	1.29	0.12
SPO0493	*rpmC*	50S ribosomal protein L29	1.26	0.02	-1.34	0.20	-0.04	1.30	8.43	0.00	-1.73	0.00	3.35	5.08	-2.65	0.00	-4.38	0.00	-3.52	0.87
SPO0494	*rpsQ*	30S ribosomal protein S17	-1.04	0.15	-1.26	0.08	-1.15	0.11	7.67	0.00	-1.57	0.00	3.05	4.62	-2.24	0.00	-4.81	0.00	-3.53	1.29
SPO0495	*rplN*	50S ribosomal protein L14	-1.08	0.56	-1.07	0.32	-1.08	0.01	11.30	0.00	-1.44	0.00	4.93	6.37	-1.56	0.01	-2.61	0.00	-2.09	0.53
SPO0496	*rplX*	50S ribosomal protein L24	1.05	0.63	1.25	0.25	1.15	0.10	10.60	0.00	-1.08	0.04	4.76	5.84	1.28	0.03	-1.64	0.00	-0.18	1.46
SPO0497	*rplE*	50S ribosomal protein L5	1.05	0.95	-1.27	0.10	-0.11	1.16	9.38	0.00	-1.64	0.00	3.87	5.51	-1.34	0.01	-2.81	0.00	-2.08	0.74
SPO0498	*rpsN*	30S ribosomal protein S14	1.38	0.52	0.99	0.82	1.19	0.19	11.00	0.00	-1.80	0.00	4.60	6.40	-1.33	0.00	-2.99	0.00	-2.16	0.83
SPO0499	*rpsH*	30S ribosomal protein S8	1.04	0.69	-1.18	0.00	-0.07	1.11	10.30	0.00	-1.78	0.00	4.26	6.04	-1.38	0.00	-2.99	0.00	-2.19	0.81
SPO0500	*rplF*	50S ribosomal protein L6	0.93	0.01	-1.20	0.08	-0.14	1.06	7.63	0.00	-1.51	0.00	3.06	4.57	-1.26	0.00	-2.24	0.00	-1.75	0.49
SPO0501	*rplR*	50S ribosomal protein L18	-1.05	0.06	1.05	0.96	0.00	1.05	9.72	0.00	-1.21	0.02	4.26	5.47	-1.22	0.05	-1.83	0.00	-1.53	0.31
SPO0502	*rpsE*	30S ribosomal protein S5	1.12	0.62	0.97	0.52	1.04	0.08	7.63	0.00	-1.48	0.00	3.08	4.56	1.21	0.14	-1.63	0.00	-0.21	1.42
SPO0503	*rpmD*	50S ribosomal protein L30	1.74	0.02	1.25	0.11	1.50	0.24	5.33	0.00	-2.52	0.00	1.41	3.93	1.28	0.06	-2.53	0.00	-0.63	1.91
SPO0504		hypothetical protein	X	X	-1.20	0.50	N/A	N/A	1.27	X	-1.59	0.24	-0.16	1.43	-1.24	0.06	1.24	X	0.00	1.24
SPO0505	*rplO*	50S ribosomal protein L15	1.08	0.80	1.06	0.91	1.07	0.01	7.38	0.00	-1.84	0.00	2.77	4.61	-1.18	0.04	-2.07	0.00	-1.63	0.44
SPO0506	*secY*	preprotein translocase subunit SecY	1.74	0.00	-1.17	0.22	0.29	1.46	3.67	0.00	-1.43	0.00	1.12	2.55	-1.50	0.00	-1.55	0.00	-1.53	0.03
SPO0507	*adk*	adenylate kinase (EC:2.7.4.3)	-1.21	0.11	1.00	0.78	-0.11	1.10	1.04	0.35	-1.30	0.03	-0.13	1.17	-1.41	0.02	-1.77	0.00	-1.59	0.18
SPO0508		hypothetical protein	-1.53	0.05	1.13	0.38	-0.20	1.33	1.62	0.00	-1.40	0.00	0.11	1.51	-1.42	0.08	-2.02	0.00	-1.72	0.30
SPO0509	*rpsM*	30S ribosomal protein S13	-1.22	0.27	-1.69	0.03	-1.46	0.23	2.39	0.01	-1.15	0.01	0.62	1.77	-1.68	0.00	-1.95	0.00	-1.82	0.14
SPO0510	*rpsK*	30S ribosomal protein S11	-1.40	0.00	-1.14	0.14	-1.27	0.13	5.74	0.00	-1.71	0.00	2.02	3.73	-1.30	0.01	-1.77	0.00	-1.54	0.24
SPO0511	*rpoA*	DNA-directed RNA polymerase subunit alpha (EC:2.7.7.6)	-1.22	0.28	-1.20	0.11	-1.21	0.01	5.35	0.00	-1.39	0.00	1.98	3.37	-1.64	0.00	-1.75	0.00	-1.70	0.06
SPO0512	*rplQ*	50S ribosomal protein L17	-1.17	0.81	1.56	0.12	0.20	1.37	11.70	0.05	-1.28	0.25	5.21	6.49	1.06	0.90	-2.00	0.01	-0.47	1.53
SPO0513		hypothetical protein	-3.43	0.00	-1.41	0.05	-2.42	1.01	-2.31	0.00	-1.12	0.52	-1.72	0.60	1.13	0.40	1.17	0.36	1.15	0.02
SPO0514		serine protease	1.91	0.00	1.38	0.00	1.65	0.27	1.96	0.00	-1.42	0.01	0.27	1.69	1.17	0.36	-1.13	0.21	0.02	1.15
SPO0515		recombination factor protein RarA	-1.08	0.79	1.02	0.72	-0.03	1.05	1.17	0.00	-1.13	0.17	0.02	1.15	1.51	0.01	-1.15	0.41	0.18	1.33
SPO0516	*rluC*	ribosomal large subunit pseudouridine synthase C (EC:4.2.1.70)	1.15	0.24	1.00	0.97	1.08	0.08	4.30	0.00	-1.40	0.02	1.45	2.85	-1.37	0.03	-2.27	0.00	-1.82	0.45
SPO0517		HAD family hydrolase	-1.21	0.76	-1.11	0.46	-1.16	0.05	3.02	0.02	-1.33	0.04	0.85	2.18	-1.57	0.00	-2.17	0.00	-1.87	0.30
SPO0518		hypothetical protein	-1.32	0.63	-1.05	0.76	-1.19	0.14	2.94	0.04	-1.55	0.12	0.70	2.25	-1.42	0.08	-2.37	0.01	-1.90	0.48
SPO0519		glutamate/glutamine/aspartate/asparagine ABC transporter substrate-binding protein	-2.19	0.00	-2.27	0.00	-2.23	0.04	-2.32	0.00	-1.30	0.00	-1.81	0.51	1.25	0.22	1.42	0.05	1.34	0.09
SPO0520		glutamate/glutamine/aspartate/asparagine ABC transporter permease	-1.60	0.49	-1.95	0.00	-1.78	0.18	-1.25	0.05	-1.16	0.10	-1.21	0.05	1.13	0.68	1.12	0.96	1.13	0.00
SPO0521		glutamate/glutamine/aspartate/asparagine ABC transporter permease	-1.42	0.27	-2.44	0.00	-1.93	0.51	-1.28	0.36	-1.22	0.02	-1.25	0.03	-1.14	0.06	1.06	0.65	-0.04	1.10
SPO0522		glutamate/glutamine/aspartate/asparagine ABC transporter ATP-binding protein	-1.63	0.07	-2.28	0.02	-1.96	0.33	0.89	0.48	1.01	0.89	0.95	0.06	1.01	0.93	1.02	0.78	1.02	0.01
SPO0523		phosphoglycerate mutase	-1.12	0.04	1.32	0.00	0.10	1.22	-1.25	0.05	1.47	0.00	0.11	1.36	1.43	0.00	1.18	0.01	1.31	0.13
SPO0524		hypothetical protein	3.55	0.00	-1.01	0.94	1.27	2.28	2.79	0.00	1.21	0.22	2.00	0.79	-1.29	0.00	-1.22	0.20	-1.26	0.04

SPO0525		sterol desaturase-like protein	-1.19	0.03	1.16	0.28	-0.02	1.18	1.70	0.00	1.13	0.12	1.42	0.28	-1.05	0.33	-1.43	0.01	-1.24	0.19
SPO0526	*argB*	acetylglutamate kinase (EC:2.7.2.8)	1.10	0.03	1.77	0.00	1.44	0.34	2.05	0.00	1.14	0.27	1.60	0.46	-1.41	0.03	-1.63	0.04	-1.52	0.11
SPO0527		short chain dehydrogenase/reductase oxidoreductase	1.72	0.00	1.55	0.00	1.64	0.09	1.80	0.00	1.09	0.21	1.45	0.36	1.20	0.03	-1.29	0.01	-0.05	1.25
SPO0528		hypothetical protein	1.13	0.71	3.45	0.00	2.29	1.16	2.11	0.00	1.31	0.02	1.71	0.40	-1.34	0.02	3.35	0.00	1.01	2.35
SPO0529		hypothetical protein	1.20	0.96	2.27	0.00	1.74	0.54	1.45	0.11	1.68	0.00	1.57	0.12	-1.15	0.01	3.01	0.00	0.93	2.08
SPO0530	*engB*	ribosome biogenesis GTP-binding protein YsxC	1.28	0.22	1.50	0.01	1.39	0.11	1.85	0.00	-1.21	0.04	0.32	1.53	-1.65	0.01	-2.17	0.00	-1.91	0.26
SPO0531		MOSC domain-containing protein	-1.06	0.92	1.27	0.14	0.11	1.17	4.08	0.00	-1.07	0.47	1.51	2.58	-1.69	0.00	-2.50	0.00	-2.10	0.41
SPO0532		inner membrane protein translocase component YidC	-1.12	0.30	1.32	0.15	0.10	1.22	4.19	0.00	-1.09	0.49	1.55	2.64	-1.52	0.04	-1.59	0.04	-1.56	0.04
SPO0533		diguanylate cyclase	1.28	0.01	1.63	0.01	1.46	0.17	-2.79	0.02	1.71	0.00	-0.54	2.25	-1.19	0.14	-0.97	0.28	-1.08	0.11
SPO0534		C32 tRNA thiolase	-1.26	0.06	1.37	0.07	0.06	1.32	1.81	0.00	-1.10	0.45	0.36	1.46	-1.01	0.79	1.25	0.55	0.12	1.13
SPO0535		K+-dependent Na+/Ca+ exchanger-like protein	X	X	-1.36	0.00	N/A	N/A	2.78	0.00	-2.02	0.00	0.38	2.40	1.54	0.00	1.32	0.00	1.43	0.11
SPO0536		hypothetical protein	1.29	0.44	-1.07	0.76	0.11	1.18	2.92	0.00	1.13	0.62	2.03	0.90	1.36	0.09	1.43	0.26	1.40	0.03
SPO0537		ribonuclease P protein component (EC:3.1.26.5)	X	X	1.73	0.00	N/A	N/A	6.91	0.00	-1.79	0.00	2.56	4.35	-1.55	0.00	-3.75	0.00	-2.65	1.10
SPO0538	*rpmH*	50S ribosomal protein L34	1.02	0.64	1.45	0.08	1.24	0.22	5.47	0.00	-1.57	0.00	1.95	3.52	-1.09	0.14	-1.59	0.00	-1.34	0.25
SPO0539		hypothetical protein	-2.77	0.04	1.10	0.29	-0.84	1.94	-3.20	0.00	-1.11	0.64	-2.16	1.05	-1.27	0.16	1.20	0.17	-0.04	1.24
SPO0540		mercuric reductase	1.13	0.28	-1.06	0.66	0.03	1.10	2.00	0.00	1.11	0.39	1.56	0.44	1.11	0.47	1.17	0.25	1.14	0.03
SPO0541		sensor histidine kinase (EC:2.7.3.-)	-1.02	0.96	1.14	0.36	0.06	1.08	1.65	0.00	-1.14	0.37	0.26	1.40	1.15	0.03	-1.25	0.31	-0.05	1.20
SPO0543		hypothetical protein	2.71	0.00	1.19	0.15	1.95	0.76	-0.89	0.00	-1.01	0.95	-0.95	0.06	-1.23	0.01	-0.98	0.68	-1.11	0.12
SPO0544		glycine cleavage system protein T	3.68	0.00	1.68	0.00	2.68	1.00	-1.19	0.45	1.40	0.01	0.11	1.30	-1.10	0.39	X	X	N/A	N/A
SPO0545	*uvrB*	excinuclease ABC subunit B	-1.69	0.15	-1.26	0.15	-1.48	0.21	1.10	0.40	-1.12	0.08	-0.01	1.11	1.14	0.13	1.28	0.03	1.21	0.07
SPO0546		hypothetical protein	-1.15	0.50	1.02	0.80	-0.06	1.09	1.38	0.12	1.26	0.07	1.32	0.06	-1.10	0.26	-1.09	0.95	-1.10	0.01
SPO0547		hypothetical protein	-1.32	0.69	1.10	0.68	-0.11	1.21	-1.81	0.63	1.30	0.31	-0.26	1.56	-1.18	0.84	1.47	X	0.15	1.33
SPO0548		hypothetical protein	-2.04	0.09	-1.05	0.45	-1.55	0.50	-1.18	0.10	-1.04	0.54	-1.11	0.07	1.61	0.01	-1.01	0.84	0.30	1.31
SPO0549		hypothetical protein	1.39	0.69	1.26	0.01	1.33	0.06	1.99	0.46	-1.05	0.58	0.47	1.52	-1.14	0.09	-1.07	0.61	-1.11	0.03
SPO0550		hypothetical protein	1.86	0.01	1.18	0.51	1.52	0.34	-1.73	0.00	-1.08	0.34	-1.41	0.33	1.04	0.70	1.45	0.19	1.25	0.20
SPO0551		hypothetical protein	1.10	0.94	-1.34	0.14	-0.12	1.22	2.70	0.00	-1.27	0.34	0.72	1.99	-1.09	0.61	2.25	0.05	0.58	1.67
SPO0552		phosphoglycerate mutase	1.65	0.11	1.26	0.15	1.46	0.19	-1.01	0.21	-1.27	0.02	-1.14	0.13	-1.10	0.63	-1.38	0.08	-1.24	0.14
SPO0553		group 1 family glycosyltransferase	1.07	0.41	1.53	0.00	1.30	0.23	1.42	0.01	-1.06	0.16	0.18	1.24	-1.34	0.01	-1.68	0.00	-1.51	0.17
SPO0554		glycoside hydrolase	1.16	0.06	1.35	0.20	1.26	0.10	1.17	0.06	-1.36	0.03	-0.10	1.27	-1.01	0.98	-1.48	0.06	-1.25	0.23
SPO0555		hypothetical protein	1.24	0.02	1.23	0.09	1.24	0.01	1.12	0.08	-1.55	0.00	-0.22	1.34	-1.05	0.53	-1.40	0.04	-1.23	0.17
SPO0556		UDP-glucose/GDP-mannose dehydrogenase	-1.71	0.00	-1.02	0.77	-1.37	0.35	-1.46	0.01	-1.01	0.57	-1.24	0.23	-1.54	0.00	-1.64	0.00	-1.59	0.05
SPO0557		mechanosensitive ion channel protein MscS	-1.06	0.65	1.03	0.96	-0.02	1.05	1.16	0.82	1.19	0.64	1.18	0.02	1.23	0.47	1.68	0.26	1.46	0.22
SPO0558		oligopeptide ABC transporter permease	1.24	0.01	1.05	0.64	1.15	0.10	1.03	0.53	1.53	0.01	1.28	0.25	1.18	0.00	1.15	0.07	1.17	0.02
SPO0559		oligopeptide ABC transporter permease	1.50	0.70	-1.15	0.40	0.18	1.33	1.59	0.63	1.30	0.48	1.45	0.15	-1.10	0.70	-1.03	0.87	-1.07	0.04
SPO0560		oligopeptide ABC transporter substrate-binding protein	-1.63	0.08	1.03	0.89	-0.30	1.33	-2.39	0.00	1.26	0.16	-0.57	1.83	1.21	0.01	1.06	0.34	1.14	0.08
SPO0562		hypothetical protein	-1.17	0.70	-1.07	0.59	-1.12	0.05	1.84	0.00	-1.55	0.00	0.15	1.70	-1.20	0.05	-1.43	0.20	-1.32	0.12
SPO0563		glutathione S-transferase	3.06	0.00	1.35	0.02	2.21	0.86	1.37	0.01	-1.12	0.13	0.13	1.25	1.36	0.00	1.40	0.00	1.38	0.02
SPO0564		glycine cleavage system protein T	1.16	0.18	-1.25	0.16	-0.05	1.21	-1.69	0.01	-1.64	0.00	-1.67	0.03	1.34	0.07	1.22	0.06	1.28	0.06

SPO0565		trimethylamine methyltransferase	-1.35	0.25	-1.11	0.56	-1.23	0.12	-1.46	0.46	-1.27	0.05	-1.37	0.10	1.23	0.26	1.29	0.02	1.26	0.03
SPO0566		TetR family transcriptional regulator	1.21	0.00	-1.16	0.14	0.03	1.19	2.69	0.00	1.03	0.54	1.86	0.83	-1.02	0.83	-1.09	0.87	-1.06	0.04
SPO0567		oxidoreductase, FAD-binding	1.36	0.00	1.10	0.09	1.23	0.13	1.59	0.00	1.07	0.37	1.33	0.26	1.40	0.02	-1.21	0.34	0.10	1.31
SPO0568		2-oxoacid ferredoxin oxidoreductase	2.54	0.00	-1.47	0.41	0.54	2.01	-8.32	0.00	-1.48	0.66	-4.90	3.42	-1.45	0.36	-1.11	X	-1.28	0.17
SPO0569		AsnC family transcriptional regulator	3.97	0.00	1.04	0.82	2.51	1.47	-1.79	0.03	-1.81	0.01	-1.80	0.01	-1.43	0.00	-1.24	X	-1.34	0.10
SPO0570		hypothetical protein	2.26	0.02	1.24	0.27	1.75	0.51	1.12	0.22	1.20	0.28	1.16	0.04	-0.98	0.67	-0.91	0.33	-0.95	0.03
SPO0571		PKD domain-containing protein	1.05	0.96	1.08	0.53	1.07	0.02	2.45	0.12	1.19	0.41	1.82	0.63	-1.13	0.62	1.31	0.35	0.09	1.22
SPO0572		guanylate cyclase	-1.49	0.02	1.04	0.85	-0.23	1.27	-1.80	0.00	-1.02	1.00	-1.41	0.39	-1.10	0.38	1.22	0.01	0.06	1.16
SPO0573		hypothetical protein	-3.04	0.01	-1.31	0.12	-2.18	0.87	-5.98	0.00	-1.16	0.46	-3.57	2.41	1.64	0.01	2.16	0.00	1.90	0.26
SPO0574		ABC transporter transmembrane ATP-binding protein	-1.28	0.00	1.10	0.57	-0.09	1.19	-2.34	0.00	1.24	0.26	-0.55	1.79	1.06	0.53	1.07	0.61	1.07	0.01
SPO0575	*acdA-1*	acyl-CoA dehydrogenase (EC:1.3.99.-)	1.10	0.51	-1.10	0.80	0.00	1.10	-1.27	0.05	-1.20	0.42	-1.24	0.04	1.13	0.29	-1.22	0.77	-0.05	1.18
SPO0576		TetR family transcriptional regulator	-1.55	0.01	-1.39	0.01	-1.47	0.08	-2.28	0.00	-1.49	0.00	-1.89	0.40	-1.29	0.01	-1.25	0.23	-1.27	0.02
SPO0577		hypothetical protein	1.31	0.01	1.12	0.18	1.22	0.10	-2.34	0.00	-0.97	0.71	-1.66	0.68	1.12	0.23	-0.89	0.39	0.12	1.00
SPO0578		acetyl-CoA carboxylase carboxyltransferase	0.98	0.00	1.22	0.03	1.10	0.12	-4.96	0.00	-1.05	0.96	-3.01	1.96	1.34	0.00	X	X	N/A	N/A
SPO0579		acetyl-CoA carboxylase, biotin carboxylase	1.60	0.05	1.01	0.96	1.31	0.30	0.99	0.97	-1.14	0.75	-0.08	1.07	1.30	0.29	1.45	0.12	1.38	0.08
SPO0580		2-nitropropane dioxygenase	-1.83	0.34	-1.17	0.53	-1.50	0.33	-3.09	0.00	-1.39	0.33	-2.24	0.85	1.12	0.79	1.84	0.22	1.48	0.36
SPO0581		hypothetical protein	-1.05	0.21	-1.15	0.53	-1.10	0.05	-2.70	0.00	-1.16	0.59	-1.93	0.77	1.21	0.12	1.96	0.04	1.59	0.38
SPO0582	*acdA-2*	acyl-CoA dehydrogenase (EC:1.3.99.-)	4.18	0.05	1.41	0.06	2.80	1.39	-2.07	0.22	1.88	0.02	-0.10	1.98	1.40	0.07	3.86	0.00	2.63	1.23
SPO0583		LysR family transcriptional regulator	-2.42	0.03	-1.07	0.68	-1.75	0.68	-2.64	0.00	-1.06	0.85	-1.85	0.79	-1.12	0.63	1.13	0.19	0.00	1.13
SPO0584	*aspC-1*	aspartate aminotransferase (EC:2.6.1.1)	1.53	0.02	-1.07	0.92	0.23	1.30	-1.97	0.17	-1.02	0.95	-1.50	0.48	-1.31	0.24	1.05	X	-0.13	1.18
SPO0585		dehydrogenase/transketolase	1.15	0.62	1.26	0.10	1.21	0.06	1.33	0.24	-1.25	0.09	0.04	1.29	-1.15	0.32	-1.45	0.11	-1.30	0.15
SPO0586		acyl carrier protein	-1.38	0.01	1.20	0.07	-0.09	1.29	1.01	1.00	-1.24	0.03	-0.12	1.13	-1.18	0.03	-1.01	0.31	-1.10	0.09
SPO0587		hypothetical protein	1.16	0.28	1.12	0.31	1.14	0.02	2.62	0.00	-1.12	0.49	0.75	1.87	-1.03	0.87	1.10	0.23	0.04	1.07
SPO0588		LysR family transcriptional regulator	1.03	0.20	-1.54	0.19	-0.26	1.29	-0.98	0.89	-1.25	0.53	-1.12	0.13	-1.54	0.16	-1.37	0.58	-1.46	0.09
SPO0589		oxidoreductase, NAD-binding/iron-sulfur cluster-binding protein	-1.57	0.00	-1.32	0.67	-1.45	0.13	-1.10	0.49	1.22	0.52	0.06	1.16	-1.36	0.51	1.44	0.37	0.04	1.40
SPO0590	*hpsR*	LacI family transcriptional regulator	X	X	1.39	0.00	N/A	N/A	-1.21	0.69	-1.57	0.01	-1.39	0.18	1.07	0.33	-1.01	X	0.03	1.04
SPO0591	*hpsK*	dihydroxypropanesulfonateTRAP transporter	-5.75	0.00	-1.68	0.08	-3.72	2.04	-6.29	0.00	1.28	0.12	-2.51	3.79	1.08	0.35	-1.16	0.98	-0.04	1.12
SPO0592	*hpsL*	dihydroxypropanesulfonateTRAP transporter	1.17	0.73	-1.26	0.05	-0.05	1.22	1.76	0.01	-1.34	0.11	0.21	1.55	-1.22	0.44	1.40	0.02	0.09	1.31
SPO0593	*hpsM*	dihydroxypropanesulfonateTRAP transporter	X	X	X	X	N/A	N/A	-2.32	0.00	X	X	N/A	N/A	-1.11	0.68	X	X	N/A	N/A
SPO0594	*hpsN*	dihydroxypropanesulfonate-3-dehydrogenase (EC:1.1.1.23)	X	X	-1.28	0.19	N/A	N/A	-2.23	0.00	-1.12	X	-1.68	0.56	-0.99	0.55	X	X	N/A	N/A
SPO0595	*hpsO*	R or S-dihydroxypropanesulfonate-2-dehydrogenase (EC:1.1.1.69)	X	X	1.05	0.60	N/A	N/A	-1.44	0.58	X	X	N/A	N/A	-1.02	0.74	X	X	N/A	N/A
SPO0596	*hpsP*	S or R-dihydroxypropanesulfonate-2-dehydrogenase	X	X	-1.49	0.03	N/A	N/A	-1.75	0.45	1.18	0.13	-0.29	1.47	-1.54	0.01	X	X	N/A	N/A
SPO0597	*hpsQ*	UspA family stress protein	-2.57	0.01	-1.30	0.15	-1.94	0.63	-4.91	0.00	-1.02	0.99	-2.97	1.95	-1.20	0.11	1.24	0.06	0.02	1.22
SPO0598	*slcD*	membrane-bound sulfolactate dehydrogenase	1.53	0.01	-1.33	0.17	0.10	1.43	2.68	0.00	-1.19	0.29	0.75	1.94	-1.24	0.24	1.76	0.11	0.26	1.50
SPO0599	*speB-1*	agmatinase (EC:3.5.3.11)	1.22	0.02	1.32	0.03	1.27	0.05	1.30	0.00	-1.21	0.04	0.05	1.26	-1.52	0.00	-1.96	0.00	-1.74	0.22
SPO0600	*nspC*	carboxynorspermidine decarboxylase	-1.14	0.31	1.11	0.38	-0.01	1.13	0.98	0.88	1.17	0.14	1.08	0.09	-2.10	0.00	-2.19	0.00	-2.15	0.04
SPO0601		saccharopine dehydrogenase (EC:1.5.1.7)	1.38	0.66	1.06	0.87	1.22	0.16	1.46	0.58	1.50	0.02	1.48	0.02	-1.33	0.02	-1.12	0.30	-1.23	0.11

SPO0602	*speA*	arginine decarboxylase (EC:4.1.1.19)	-1.05	0.81	1.06	0.85	0.01	1.06	1.47	0.13	1.23	0.34	1.35	0.12	-2.13	0.00	-2.02	0.02	-2.08	0.05
SPO0603		hypothetical protein	-1.18	0.20	-1.59	0.04	-1.39	0.21	-1.09	0.44	-1.45	0.07	-1.27	0.18	-1.43	0.00	-1.63	0.01	-1.53	0.10
SPO0604		hypothetical protein	-1.45	0.01	-1.86	0.00	-1.66	0.21	-1.56	0.01	-1.27	0.01	-1.42	0.14	-1.49	0.01	-1.48	0.00	-1.49	0.01
SPO0605		MarR family transcriptional regulator	-2.15	0.00	-1.96	0.00	-2.06	0.10	-1.58	0.04	-1.46	0.01	-1.52	0.06	-1.88	0.00	-1.86	0.00	-1.87	0.01
SPO0606		hypothetical protein	1.04	0.99	-1.14	0.67	-0.05	1.09	-1.60	0.58	1.51	0.18	-0.05	1.56	-1.08	0.76	1.12	0.38	0.02	1.10
SPO0607		proline racemase	0.95	0.89	1.16	0.14	1.06	0.10	-3.10	0.35	1.36	0.03	-0.87	2.23	1.23	0.10	1.16	0.12	1.20	0.04
SPO0608		sugar ABC transporter substrate-binding protein	-3.13	0.01	-1.77	0.01	-2.45	0.68	-39.50	0.00	1.22	0.01	-19.14	20.36	1.43	0.00	-1.02	0.36	0.21	1.23
SPO0609		sugar ABC transporter ATP-binding protein	-1.83	0.06	-1.00	0.78	-1.41	0.42	-7.07	0.00	-1.07	0.80	-4.07	3.00	-0.96	0.56	-1.77	X	-1.37	0.41
SPO0610		sugar ABC transporter ATP-binding protein	-1.62	0.01	-1.27	0.08	-1.45	0.18	-2.62	0.00	-1.22	0.50	-1.92	0.70	-1.35	0.31	1.57	0.07	0.11	1.46
SPO0611		sugar ABC transporter permease	-1.85	0.07	-1.19	0.79	-1.52	0.33	-6.24	0.00	-0.99	0.97	-3.61	2.63	-1.18	0.78	1.53	0.50	0.18	1.36
SPO0612		sugar ABC transporter permease	-1.42	0.01	1.10	0.67	-0.16	1.26	-4.07	0.00	-1.01	0.97	-2.54	1.53	1.06	0.54	-1.01	0.65	0.03	1.04
SPO0613		hypothetical protein	-1.11	0.00	-1.11	0.75	-1.11	0.00	-2.96	0.00	-1.04	0.95	-2.00	0.96	1.15	0.30	-0.89	0.27	0.13	1.02
SPO0614		transcriptional regulator	-1.36	0.03	0.99	0.67	-0.19	1.17	-3.33	0.00	1.25	0.14	-1.04	2.29	1.16	0.17	1.35	0.11	1.26	0.10
SPO0615		hypothetical protein	-1.31	0.01	1.04	0.67	-0.14	1.18	-2.82	0.00	1.13	0.31	-0.85	1.98	1.25	0.01	1.15	0.06	1.20	0.05
SPO0616		zinc-binding dehydrogenase oxidoreductase	-1.18	0.03	1.10	0.04	-0.04	1.14	-1.19	0.33	1.22	0.19	0.02	1.21	-1.03	0.95	-1.33	0.49	-1.18	0.15
SPO0618		AraC family transcriptional regulator	-2.48	0.00	-1.34	0.12	-1.91	0.57	-3.81	0.00	-1.02	0.92	-2.42	1.40	-1.36	0.28	1.77	0.01	0.21	1.57
SPO0619		sterol desaturase	1.09	X	1.08	0.76	1.09	0.01	1.26	0.38	-1.09	0.79	0.09	1.18	-1.18	0.55	-0.95	0.32	-1.07	0.11
SPO0620		hypothetical protein	-0.99	0.89	-1.07	0.79	-1.03	0.04	-1.88	0.13	-0.99	0.92	-1.44	0.45	-1.08	0.78	1.31	0.22	0.12	1.20
SPO0621		ankyrin repeat-containing protein	-1.60	0.06	1.05	0.83	-0.28	1.33	-2.22	0.03	1.18	0.43	-0.52	1.70	1.15	0.49	-0.97	0.70	0.09	1.06
SPO0622		ISSpo1, transposase	-2.30	0.40	-1.16	0.79	-1.73	0.57	-3.74	0.28	-0.99	0.99	-2.37	1.37	-1.15	0.78	1.31	0.68	0.08	1.23
SPO0623		cytochrome c oxidase domain-containing protein	-1.22	0.29	1.05	0.57	-0.09	1.14	1.30	0.11	-1.02	0.93	0.14	1.16	-1.34	0.25	-1.97	0.04	-1.66	0.32
SPO0624		hypothetical protein	-1.04	0.86	-1.27	0.03	-1.16	0.12	1.55	0.03	-1.04	0.51	0.26	1.30	-1.59	0.01	-1.81	0.00	-1.70	0.11
SPO0628		transposase, degenerate	-2.41	0.03	-1.56	0.09	-1.99	0.43	-3.17	0.00	1.12	0.52	-1.03	2.15	-1.17	0.56	1.73	0.04	0.28	1.45
SPO0629		ISSpo3, transposase	0.90	0.01	-1.38	0.03	-0.24	1.14	-2.49	0.00	1.19	0.03	-0.65	1.84	-1.31	0.01	-1.27	0.03	-1.29	0.02
SPO0631		hypothetical protein	0.92	0.00	-1.09	0.07	-0.08	1.01	0.75	0.00	-1.18	0.01	-0.22	0.97	1.08	0.65	-1.14	0.00	-0.03	1.11
SPO0632		2-hydroxyacid dehydrogenase	2.08	0.00	2.40	0.00	2.24	0.16	1.58	0.01	1.53	0.01	1.56	0.03	1.39	0.00	1.11	0.36	1.25	0.14
SPO0633	*ggt*	gamma-glutamyltranspeptidase (EC:2.3.2.2)	-1.59	0.00	-1.29	0.05	-1.44	0.15	-5.72	0.00	1.94	0.00	-1.89	3.83	-1.13	0.34	1.98	0.01	0.43	1.56
SPO0634		oxidoreductase, FAD-binding	-1.24	0.00	-1.25	0.15	-1.25	0.01	-1.81	0.00	1.19	0.14	-0.31	1.50	1.07	0.43	1.55	0.05	1.31	0.24
SPO0635		glycine cleavage system protein T	-1.55	0.03	1.70	0.02	0.08	1.63	-2.14	0.02	-1.34	0.08	-1.74	0.40	-1.24	0.01	-1.46	0.01	-1.35	0.11
SPO0636		EF hand domain-containing protein	X	X	1.15	0.71	N/A	N/A	-1.14	0.18	X	X	N/A	N/A	-1.35	0.18	X	X	N/A	N/A
SPO0637		hypothetical protein	2.08	0.00	1.50	0.00	1.79	0.29	-2.92	0.00	-1.14	0.04	-2.03	0.89	-0.98	0.77	-1.36	0.02	-1.17	0.19
SPO0638		hypothetical protein	2.61	0.00	-1.01	0.88	0.80	1.81	-3.79	0.00	-1.08	0.08	-2.44	1.36	-1.63	0.00	-2.01	0.00	-1.82	0.19
SPO0639		LysR family transcriptional regulator	-2.54	X	-0.99	0.67	-1.76	0.78	-1.38	0.15	-1.35	0.06	-1.37	0.01	-1.26	0.00	-1.19	X	-1.23	0.04
SPO0640		alkylhydroperoxidase	X	X	1.56	0.07	N/A	N/A	3.29	0.00	-1.09	0.68	1.10	2.19	1.18	0.15	-1.14	0.98	0.02	1.16
SPO0641		hypothetical protein	1.58	0.00	1.12	0.03	1.35	0.23	3.21	0.00	1.24	0.00	2.23	0.98	-1.02	0.75	-1.12	0.41	-1.07	0.05
SPO0642		oxidoreductase, FAD-binding	-1.00	0.98	1.30	0.24	0.15	1.15	1.47	0.38	1.21	0.08	1.34	0.13	1.68	0.00	1.32	0.03	1.50	0.18
SPO0643		aldo/keto reductase	-1.60	0.00	-1.03	0.52	-1.32	0.29	1.41	0.00	-1.01	0.75	0.20	1.21	1.02	0.91	-1.43	0.00	-0.21	1.23
SPO0644		hypothetical protein	0.97	0.08	1.07	0.23	1.02	0.05	-1.80	0.00	1.50	0.00	-0.15	1.65	1.34	0.00	1.56	0.00	1.45	0.11
SPO0645		multidrug resistance efflux pump	1.20	0.80	1.47	0.02	1.34	0.14	-1.32	0.02	1.19	0.23	-0.07	1.26	1.76	0.00	1.34	0.01	1.55	0.21

SPO0646		hypothetical protein	-2.33	0.00	1.21	0.20	-0.56	1.77	1.29	0.00	-1.00	0.89	0.15	1.15	1.49	0.03	-1.24	0.30	0.13	1.37
SPO0647		hypothetical protein	-1.72	0.06	-1.15	0.19	-1.44	0.28	1.05	0.74	-1.01	0.93	0.02	1.03	1.07	0.54	-1.39	0.01	-0.16	1.23
SPO0648		bmp family protein	1.12	0.86	0.98	0.57	1.05	0.07	0.87	0.00	1.31	0.02	1.09	0.22	0.97	0.33	1.52	0.00	1.24	0.28
SPO0649		sugar ABC transporter permease	-2.16	0.00	-1.66	0.01	-1.91	0.25	-4.21	0.00	1.34	0.05	-1.44	2.78	-1.58	0.00	-1.15	0.00	-1.37	0.22
SPO0650		sugar ABC transporter permease	-1.41	0.00	1.32	0.03	-0.04	1.37	-2.78	0.00	-1.03	0.76	-1.91	0.88	-1.16	0.01	-1.40	0.00	-1.28	0.12
SPO0651		sugar ABC transporter ATP-binding protein	-1.59	0.00	1.24	0.12	-0.18	1.42	-3.30	0.00	1.03	0.98	-1.14	2.17	1.27	0.03	1.64	0.05	1.46	0.18
SPO0652	*xdhC*	xanthine dehydrogenase accessory factor	-2.21	0.00	1.04	0.47	-0.59	1.63	-5.21	0.00	1.23	0.02	-1.99	3.22	1.04	0.49	-1.20	0.33	-0.08	1.12
SPO0653	*xdhB*	xanthine dehydrogenase subunit B (EC:1.17.1.4)	-1.54	0.01	1.11	0.39	-0.22	1.33	-3.53	0.00	-0.97	0.79	-2.25	1.28	1.21	0.18	1.25	0.01	1.23	0.02
SPO0654	*xdhA*	xanthine dehydrogenase, A subunit (EC:1.17.1.4)	-1.87	0.00	1.11	0.01	-0.38	1.49	-5.18	0.00	1.34	0.06	-1.92	3.26	-1.14	0.13	-1.15	0.93	-1.15	0.01
SPO0655		hypothetical protein	1.14	0.62	1.65	0.19	1.40	0.26	-1.18	0.96	-1.11	0.79	-1.15	0.03	1.37	0.09	-0.94	0.86	0.22	1.15
SPO0656	*dnaE*	DNA polymerase III subunit alpha (EC:2.7.7.7)	1.31	0.02	-1.16	0.12	0.08	1.24	2.94	0.00	1.06	0.59	2.00	0.94	1.07	0.53	-1.27	0.00	-0.10	1.17
SPO0657	*naaT*	metallochaperone	-2.66	0.00	-1.29	0.03	-1.98	0.69	-3.95	0.00	-1.15	0.71	-2.55	1.40	-1.03	0.94	1.66	0.08	0.32	1.35
SPO0658	*naaS*	N-acetyltaurine amidohydrolas	1.13	0.06	-1.08	0.82	0.02	1.11	-2.01	0.01	-1.09	0.56	-1.55	0.46	-0.99	0.75	1.31	0.03	0.16	1.15
SPO0659	*naaR*	LysR family transcriptional regulator	-2.47	0.01	-1.16	0.70	-1.82	0.66	-3.55	0.00	-1.17	0.68	-2.36	1.19	1.09	0.42	1.20	0.21	1.15	0.05
SPO0660	*naaA*	N-acetyltaurine ABC transporter substrate-binding protein	-1.56	0.29	-1.23	0.56	-1.40	0.17	-3.69	0.00	1.23	0.40	-1.23	2.46	1.26	0.34	1.23	0.19	1.25	0.02
SPO0661	*naaB*	N-acetyltaurine	-1.44	0.02	-1.19	0.38	-1.32	0.13	-2.42	0.07	-1.30	0.38	-1.86	0.56	-1.04	0.92	-1.22	X	-1.13	0.09
SPO0662	*naaB'*	N-acetyltaurine ABC transporter permease	-1.07	0.95	1.04	0.84	-0.02	1.06	-1.32	0.96	X	X	N/A	N/A	-1.01	0.69	X	X	N/A	N/A
SPO0663	*naaC*	N-acetyltaurine ABC transporter ATP-binding protein	-1.23	0.81	-1.04	0.90	-1.14	0.10	-1.52	0.72	1.06	0.67	-0.23	1.29	-1.03	0.99	1.62	0.04	0.30	1.33
SPO0664	*naaC'*	N-acetyltaurine ABC transporter ATP-binding protein	-0.97	0.91	-1.14	0.86	-1.05	0.09	-1.09	0.69	-1.29	0.47	-1.19	0.10	-0.96	0.70	1.72	0.40	0.38	1.34
SPO0665		SlyX protein	-1.04	0.57	-1.12	0.07	-1.08	0.04	1.88	0.00	1.05	0.75	1.47	0.42	-1.24	0.14	-1.70	0.00	-1.47	0.23
SPO0666		enoyl-CoA hydratase (EC:4.2.1.17)	1.82	0.01	1.14	0.48	1.48	0.34	-1.57	0.32	2.08	0.00	0.26	1.83	2.19	0.01	4.35	0.00	3.27	1.08
SPO0667	*hisS*	histidyl-tRNA synthetase (EC:6.1.1.21)	0.87	0.00	1.08	0.82	0.98	0.10	-2.60	0.00	-1.15	0.26	-1.88	0.73	1.08	0.69	1.78	0.01	1.43	0.35
SPO0668	*hisZ*	ATP phosphoribosyltransferase	-2.75	0.00	1.89	0.00	-0.43	2.32	-3.34	0.00	-1.76	0.00	-2.55	0.79	-1.14	0.15	-1.50	0.07	-1.32	0.18
SPO0669	*hisG*	ATP phosphoribosyltransferase (EC:2.4.2.17)	1.40	0.05	2.21	0.00	1.81	0.41	2.32	0.00	-1.55	0.00	0.39	1.94	1.23	0.04	-1.84	0.00	-0.31	1.54
SPO0670		DNA polymerase III subunit alpha	-1.98	0.07	-1.39	0.51	-1.69	0.29	-2.76	0.03	-1.03	0.97	-1.90	0.86	-1.08	0.84	1.99	0.29	0.46	1.54
SPO0671		hypothetical protein	X	X	-1.16	0.61	N/A	N/A	1.41	0.00	-1.16	0.31	0.13	1.29	1.17	0.01	X	X	N/A	N/A
SPO0672		hypothetical protein	-1.93	X	-1.07	0.86	-1.50	0.43	-2.03	0.01	-1.10	X	-1.57	0.47	1.12	0.49	1.09	X	1.11	0.02
SPO0673	*tpa*	taurine--pyruvate aminotransferase (EC:2.6.1.77)	2.01	0.00	1.21	0.05	1.61	0.40	1.26	0.24	0.97	0.18	1.12	0.14	1.17	0.03	1.56	0.01	1.37	0.20
SPO0674	*tauA*	taurine ABC transporter substrate-binding protein	-4.95	0.00	-1.38	0.00	-3.17	1.79	-15.30	0.00	-1.08	0.28	-8.19	7.11	1.36	0.02	1.35	0.00	1.36	0.01
SPO0675	*tauB*	taurine ABC transporter ATP-binding protein	-3.37	0.08	-1.42	0.45	-2.40	0.98	-4.47	0.05	-1.15	0.74	-2.81	1.66	-1.12	0.82	1.16	0.67	0.02	1.14
SPO0676	*tauC*	taurine ABC transporter permease	-2.14	0.00	1.11	0.08	-0.52	1.63	-1.09	0.82	-1.22	0.11	-1.16	0.06	1.33	0.03	-1.17	0.88	0.08	1.25
SPO0677		acyl-CoA synthetase (EC:2.3.1.86)	-1.06	0.72	-1.09	0.83	-1.08	0.02	-1.55	0.15	1.04	0.91	-0.26	1.30	1.20	0.44	1.08	0.72	1.14	0.06
SPO0678		agmatinase	1.00	0.61	-1.17	0.36	-0.09	1.09	-1.72	0.04	1.30	0.31	-0.21	1.51	-1.15	0.41	1.04	0.87	-0.05	1.10
SPO0679	*hmgC*	maleylacetoacetate isomerase (EC:5.2.1.2)	-2.24	0.00	-1.16	0.03	-1.70	0.54	-1.91	0.00	1.12	0.23	-0.40	1.52	-1.42	0.00	-1.15	0.71	-1.29	0.14
SPO0680		glyoxalase	-1.21	0.02	1.02	0.81	-0.10	1.12	1.24	0.02	1.03	0.77	1.14	0.11	-1.11	0.47	-1.35	0.01	-1.23	0.12
SPO0681		hypothetical protein	1.03	0.81	-1.32	0.07	-0.15	1.18	1.41	0.57	1.09	0.59	1.25	0.16	-1.40	0.05	-1.41	0.10	-1.41	0.01
SPO0682		FAD-dependent oxidoreductase	-1.16	0.01	-1.28	0.30	-1.22	0.06	1.11	0.38	-1.11	0.41	0.00	1.11	1.27	0.23	1.95	0.03	1.61	0.34
SPO0683		metallo-beta-lactamase	-1.46	0.01	1.07	0.78	-0.20	1.27	-1.58	0.02	1.26	0.28	-0.16	1.42	-1.12	0.28	-1.18	0.40	-1.15	0.03

SPO0684		glyoxalase	-1.38	0.27	1.02	0.75	-0.18	1.20	-1.60	0.00	1.00	0.72	-0.30	1.30	-1.32	0.00	-1.74	0.01	-1.53	0.21
SPO0685	*hmgB*	fumarylacetoacetase (EC:3.7.1.2)	-1.33	0.02	-1.02	0.77	-1.18	0.16	-1.52	0.00	-1.01	0.57	-1.27	0.25	-1.16	0.03	-1.17	0.07	-1.17	0.01
SPO0686	*hmgA*	homogentisate 1,2-dioxygenase (EC:1.13.11.5)	-1.98	0.00	-1.22	0.20	-1.60	0.38	-2.57	0.00	1.17	0.15	-0.70	1.87	-1.64	0.00	-1.53	0.01	-1.59	0.05
SPO0687		MarR family transcriptional regulator	-3.22	0.00	-1.17	0.01	-2.20	1.03	-3.84	0.00	-1.26	0.08	-2.55	1.29	-1.56	0.00	-1.60	0.01	-1.58	0.02
SPO0688		guanylate cyclase	1.03	0.99	-1.09	0.18	-0.03	1.06	1.52	0.01	-1.18	0.04	0.17	1.35	1.19	0.02	1.02	0.99	1.11	0.09
SPO0689		hypothetical protein	-1.07	X	1.01	0.84	-0.03	1.04	1.70	0.01	-1.22	0.02	0.24	1.46	-1.17	0.00	-1.84	0.00	-1.51	0.34
SPO0690		hypothetical protein	X	X	1.97	0.00	N/A	N/A	4.08	0.00	-1.37	0.01	1.36	2.73	-1.04	0.71	-3.24	0.15	-2.14	1.10
SPO0691	*era*	GTP-binding protein Era	1.31	0.48	1.19	0.34	1.25	0.06	3.58	0.01	-1.17	0.00	1.21	2.38	-1.20	0.09	-1.34	0.06	-1.27	0.07
SPO0692		multicopper oxidase	1.17	0.17	1.51	0.01	1.34	0.17	-1.10	0.59	-1.14	0.61	-1.12	0.02	1.12	0.07	1.60	X	1.36	0.24
SPO0693		isobutyryl-CoA dehydrogenase	-2.10	0.00	1.34	0.03	-0.38	1.72	-1.08	0.97	-1.01	0.91	-1.05	0.04	1.16	0.13	-1.25	0.44	-0.05	1.21
SPO0694		hypothetical protein	1.14	0.21	-1.31	0.01	-0.09	1.23	2.37	0.00	1.06	0.52	1.72	0.66	1.04	0.44	1.45	0.01	1.25	0.20
SPO0695		hypothetical protein	-1.58	0.00	1.29	0.00	-0.15	1.44	1.14	0.02	1.16	0.03	1.15	0.01	-1.14	0.23	-1.48	0.00	-1.31	0.17
SPO0697	*modC*	molybdate ABC transporter ATP-binding protein (EC:3.6.3.29)	1.65	0.03	-1.12	0.60	0.27	1.39	1.51	0.04	1.13	0.37	1.32	0.19	-1.34	0.12	-1.22	0.70	-1.28	0.06
SPO0698	*modB*	molybdate ABC transporter permease	X	X	-1.08	0.74	N/A	N/A	-1.28	0.54	-1.13	0.45	-1.21	0.08	-1.06	0.89	-0.91	0.13	-0.98	0.08
SPO0699	*modA*	molybdate ABC transporter substrate-binding protein	-1.49	0.13	-1.14	0.67	-1.32	0.18	1.13	0.84	1.09	0.79	1.11	0.02	-1.44	0.26	1.09	0.69	-0.18	1.27
SPO0700		molybdenum-binding transcriptional regulator	1.16	0.63	-1.08	0.35	0.04	1.12	1.07	0.37	1.99	0.00	1.53	0.46	1.07	0.39	-0.97	0.49	0.05	1.02
SPO0701	*gap-1*	glyceraldehyde-3-phosphate dehydrogenase, type I (EC:1.2.1.-)	1.82	0.00	1.96	0.00	1.89	0.07	-1.88	0.00	13.40	0.00	5.76	7.64	-2.12	0.00	-3.88	0.00	-3.00	0.88
SPO0702		oligopeptide ABC transporter ATP-binding protein	1.11	0.04	-1.08	0.66	0.02	1.10	-1.55	0.01	-1.21	0.11	-1.38	0.17	-1.49	0.00	-1.64	0.00	-1.57	0.08
SPO0703		oligopeptide ABC transporter ATP-binding protein	-1.68	0.12	-1.10	0.68	-1.39	0.29	-8.57	0.00	-1.22	0.31	-4.90	3.68	-1.04	0.83	-1.17	0.65	-1.11	0.06
SPO0704		oligopeptide ABC transporter permease	1.21	0.56	1.10	0.47	1.16	0.05	-1.01	0.81	-1.42	0.09	-1.22	0.21	1.17	0.23	-1.26	0.52	-0.05	1.22
SPO0705		oligopeptide ABC transporter permease	-1.09	0.66	-1.23	0.16	-1.16	0.07	-1.88	0.00	-1.45	0.00	-1.67	0.21	-1.27	0.07	-1.42	0.11	-1.35	0.08
SPO0706		oligopeptide ABC transporter substrate-binding protein	-1.40	0.00	-1.43	0.30	-1.42	0.02	-4.58	0.00	0.98	0.64	-1.80	2.78	-1.07	0.69	1.32	0.44	0.13	1.20
SPO0707		DeoR family transcriptional regulator	-1.97	0.00	-1.57	0.00	-1.77	0.20	-6.57	0.00	-1.12	0.31	-3.85	2.73	-1.33	0.02	0.98	0.43	-0.18	1.15
SPO0708		invasion protein IbeA	10.90	0.00	1.46	0.07	6.18	4.72	1.55	0.00	-1.23	0.14	0.16	1.39	-1.07	0.80	-1.35	0.63	-1.21	0.14
SPO0709	*pckA*	phosphoenolpyruvate carboxykinase (EC:4.1.1.49)	1.10	0.99	1.03	1.00	1.07	0.04	1.41	0.59	-2.59	0.07	-0.59	2.00	-1.04	0.84	-1.15	0.64	-1.10	0.05
SPO0710	*chvI*	DNA-binding response regulator ChvI	-1.64	0.07	-1.38	0.11	-1.51	0.13	-2.32	0.01	1.18	0.22	-0.57	1.75	-1.19	0.04	-1.16	0.02	-1.18	0.02
SPO0711	*chvG*	sensor histidine kinase ChvG (EC:2.7.3.-)	1.04	0.76	-1.16	0.43	-0.06	1.10	1.03	0.80	1.08	0.88	1.06	0.03	1.55	0.07	1.09	0.85	1.32	0.23
SPO0712		Hpr serine kinase/phosphatase domain-containing protein	-1.19	0.01	-1.31	0.65	-1.25	0.06	-1.16	0.86	1.08	0.89	-0.04	1.12	-1.03	0.96	-1.19	0.78	-1.11	0.08
SPO0713		hypothetical protein	1.53	0.00	1.03	0.88	1.28	0.25	2.04	0.00	-1.03	0.68	0.51	1.54	-1.10	0.28	-1.13	0.53	-1.12	0.01
SPO0714		PTS system mannose subfamily IIA subunit	-1.20	0.00	-1.36	0.00	-1.28	0.08	1.04	0.29	1.07	0.84	1.06	0.02	-1.33	0.02	-1.19	0.15	-1.26	0.07
SPO0715		phosphocarrier protein HPr	1.06	0.11	1.11	0.48	1.09	0.03	0.94	0.02	1.21	0.18	1.08	0.13	1.08	0.63	-1.05	0.22	0.02	1.07
SPO0716		hypothetical protein	1.39	0.24	1.33	0.43	1.36	0.03	2.55	0.03	-1.23	0.47	0.66	1.89	-1.02	0.87	-1.47	0.15	-1.25	0.22
SPO0717	*bhbD*	3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157)	2.32	0.00	1.94	0.00	2.13	0.19	2.55	0.00	1.09	0.47	1.82	0.73	-1.02	0.67	-1.32	0.01	-1.17	0.15
SPO0718		hypothetical protein	-1.15	0.60	-1.19	0.52	-1.17	0.02	-2.83	0.00	1.01	1.00	-0.91	1.92	-1.04	0.91	2.23	0.01	0.60	1.64
SPO0719	*etfA*	electron transfer flavoprotein subunit alpha	2.45	0.00	2.23	0.00	2.34	0.11	4.03	0.00	0.99	0.38	2.51	1.52	1.18	0.04	-1.43	0.01	-0.13	1.31
SPO0720	*etfB*	electron transfer flavoprotein subunit beta	1.24	0.61	1.76	0.00	1.50	0.26	1.84	0.00	1.07	0.90	1.46	0.38	1.33	0.03	1.22	0.14	1.28	0.06
SPO0721		glyoxalase	-1.81	0.00	1.19	0.01	-0.31	1.50	-7.43	0.00	1.29	0.03	-3.07	4.36	1.36	0.02	-1.09	0.72	0.14	1.23

SPO0722		ATP:cob(I)alamin adenosyltransferase	1.51	0.42	1.72	0.18	1.62	0.11	2.03	0.08	-1.05	0.76	0.49	1.54	1.07	0.87	-1.62	0.09	-0.28	1.35
SPO0723		hypothetical protein	1.91	0.24	1.33	0.08	1.62	0.29	3.44	0.02	-1.14	0.04	1.15	2.29	-1.26	0.00	-1.76	0.00	-1.51	0.25
SPO0724		short chain dehydrogenase/reductase oxidoreductase	1.41	0.44	1.51	0.06	1.46	0.05	1.46	0.27	-1.16	0.13	0.15	1.31	-1.07	0.65	-1.48	0.04	-1.28	0.21
SPO0725		hypothetical protein	X	X	-1.21	0.25	N/A	N/A	-2.04	0.01	1.33	0.31	-0.36	1.69	-1.45	0.00	X	X	N/A	N/A
SPO0726	*parC*	DNA topoisomerase IV subunit A (EC:5.99.1.-)	-1.46	0.05	1.04	0.83	-0.21	1.25	-1.04	0.81	-1.06	0.15	-1.05	0.01	1.23	0.14	-1.06	0.33	0.09	1.15
SPO0727		hypothetical protein	1.33	0.04	1.00	0.87	1.17	0.17	2.35	0.00	-1.36	0.07	0.50	1.86	1.03	0.99	-1.36	0.00	-0.17	1.20
SPO0728	*tuf-1*	elongation factor Tu (EC:3.6.5.3)	1.92	0.00	-1.12	0.12	0.40	1.52	7.16	0.00	-1.65	0.00	2.76	4.41	1.03	0.79	-1.55	0.00	-0.26	1.29
SPO0729		hypothetical protein	-1.48	0.02	1.09	0.59	-0.20	1.29	1.94	0.00	-1.49	0.01	0.23	1.72	1.40	0.00	-1.00	0.88	0.20	1.20
SPO0731	*glpR*	glycerol-3-phosphate regulon repressor	-1.18	0.09	-1.03	0.78	-1.11	0.08	-0.96	0.00	-1.54	0.01	-1.25	0.29	-1.22	0.04	-1.47	0.08	-1.35	0.13
SPO0732	*glpD*	glycerol-3-phosphate dehydrogenase (EC:1.1.5.3)	-1.53	0.00	-1.09	0.68	-1.31	0.22	-1.76	0.00	-1.45	0.01	-1.61	0.16	-1.09	0.19	-1.41	0.16	-1.25	0.16
SPO0733		esterase	-1.20	0.00	-1.03	0.42	-1.12	0.09	2.35	0.00	1.14	0.05	1.75	0.61	-1.22	0.00	-1.19	0.02	-1.21	0.02
SPO0734		PaaX domain-containing protein	-2.14	0.00	-1.25	0.21	-1.70	0.45	-3.14	0.00	1.23	0.16	-0.96	2.19	-1.30	0.02	1.24	0.22	-0.03	1.27
SPO0735	*paaZ*	bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	-1.44	0.00	-1.06	0.77	-1.25	0.19	-2.51	0.00	1.34	0.04	-0.59	1.93	-1.19	0.27	1.30	0.14	0.06	1.25
SPO0736		TRAP dicarboxylate transporter subunit DctM	-1.08	0.91	-1.19	0.75	-1.14	0.05	-1.13	0.95	-1.11	0.85	-1.12	0.01	-1.21	0.71	1.25	0.30	0.02	1.23
SPO0737		TRAP dicarboxylate transporter subunit DctQ	X	X	-1.13	0.27	N/A	N/A	-1.04	0.01	X	X	N/A	N/A	-1.09	0.72	-1.12	X	-1.11	0.02
SPO0738		TRAP dicarboxylate transporter subunit DctP	-2.02	0.00	-1.61	0.00	-1.82	0.21	-2.20	0.00	-1.14	0.26	-1.67	0.53	-1.45	0.02	-1.13	0.93	-1.29	0.16
SPO0739		enoyl-CoA hydratase	-2.29	0.01	-1.31	0.04	-1.80	0.49	-3.24	0.00	-1.49	0.01	-2.37	0.88	-1.16	0.22	1.47	0.03	0.16	1.32
SPO0740	*paaB*	enoyl-CoA hydratase (EC:4.2.1.17)	-2.27	0.12	-1.09	0.80	-1.68	0.59	-3.89	0.00	1.05	0.79	-1.42	2.47	-1.12	0.77	1.28	0.50	0.08	1.20
SPO0741	*paaD*	phenylacetic acid degradation protein PaaD	-1.18	0.02	-1.03	0.66	-1.11	0.08	-3.04	0.00	1.44	0.01	-0.80	2.24	-1.13	0.62	1.60	0.01	0.24	1.37
SPO0742	*paaF*	phenylacetate-CoA ligase (EC:6.2.1.30)	0.95	0.02	-1.09	0.35	-0.07	1.02	-2.98	0.00	1.39	0.00	-0.80	2.19	-1.00	0.88	-1.11	0.23	-1.06	0.06
SPO0743		TetR family transcriptional regulator	-1.11	0.15	-1.18	0.41	-1.15	0.03	-1.13	0.78	-1.07	0.49	-1.10	0.03	-1.55	0.00	-2.14	0.00	-1.85	0.29
SPO0744		hypothetical protein	-1.22	0.08	1.25	0.32	0.02	1.24	-1.75	0.07	1.57	0.19	-0.09	1.66	1.06	0.77	-1.66	0.05	-0.30	1.36
SPO0745		hypothetical protein	-1.08	0.08	-1.16	0.36	-1.12	0.04	-2.50	0.00	1.31	0.21	-0.60	1.91	-1.68	0.02	1.19	0.42	-0.25	1.44
SPO0746		hypothetical protein	-1.09	0.39	-1.26	0.01	-1.18	0.09	-2.40	0.00	1.52	0.00	-0.44	1.96	-1.61	0.00	-1.29	0.06	-1.45	0.16
SPO0747		peroxidase	X	X	-1.28	0.09	N/A	N/A	-2.79	0.01	-1.14	0.55	-1.97	0.83	-1.07	0.87	1.87	0.06	0.40	1.47
SPO0748		hypothetical protein	-2.07	0.17	-1.17	0.66	-1.62	0.45	-1.98	0.34	-1.10	0.88	-1.54	0.44	-1.20	0.36	1.30	X	0.05	1.25
SPO0749		hypothetical protein	-4.98	0.00	-1.55	0.02	-3.27	1.72	-6.10	0.00	X	X	N/A	N/A	-1.45	0.27	1.08	X	-0.19	1.27
SPO0750		hypothetical protein	-1.91	0.48	-1.12	0.87	-1.52	0.39	-1.77	0.58	1.19	0.76	-0.29	1.48	1.08	0.89	1.48	0.51	1.28	0.20
SPO0751		guanylate cyclase	-1.12	0.84	-1.01	0.98	-1.07	0.06	-2.02	0.47	-1.00	0.99	-1.51	0.51	1.20	0.65	-1.02	0.95	0.09	1.11
SPO0752		phenylacetic acid degradation protein	1.19	0.21	1.15	0.47	1.17	0.02	-2.00	0.00	1.39	0.06	-0.31	1.70	-1.22	0.12	1.12	0.49	-0.05	1.17
SPO0753	*paaK*	phenylacetic acid degradation oxidoreductase Paa	1.30	0.72	1.22	0.69	1.26	0.04	-3.32	0.07	1.91	0.15	-0.71	2.62	-1.11	0.72	1.22	0.55	0.05	1.17
SPO0754	*paaJ*	phenylacetic acid degradation protein PaaJ	1.38	0.00	1.22	0.02	1.30	0.08	-3.53	0.00	1.81	0.00	-0.86	2.67	-1.44	0.00	-1.23	0.17	-1.34	0.11
SPO0755	*paaI*	phenylacetic acid degradation protein PaaI	1.17	0.96	1.53	0.19	1.35	0.18	-2.01	0.23	2.06	0.06	0.03	2.04	-1.31	0.32	-1.15	0.80	-1.23	0.08
SPO0756	*paaB*	phenylacetate-CoA oxygenase subunit PaaB	1.15	0.63	1.78	0.01	1.47	0.32	-3.18	0.00	2.20	0.00	-0.49	2.69	-1.05	0.52	-1.14	0.63	-1.10	0.04
SPO0757	*paaA*	phenylacetate-CoA oxygenase subunit PaaA	0.99	0.58	1.12	0.40	1.06	0.06	-5.10	0.00	2.48	0.00	-1.31	3.79	-1.39	0.07	1.11	0.57	-0.14	1.25
SPO0758		beta-ketoadipyl CoA thiolase (EC:2.3.1.-)	-1.24	0.51	1.89	0.00	0.33	1.57	1.26	0.19	1.41	0.01	1.34	0.08	-1.31	0.06	-1.35	0.24	-1.33	0.02
SPO0759		hypothetical protein	9.36	0.00	11.80	0.00	10.58	1.22	32.00	0.00	15.10	0.00	23.55	8.45	-2.70	0.00	-4.97	0.00	-3.84	1.14
SPO0760		alkylhydroperoxidase	-1.71	0.14	-1.42	0.56	-1.57	0.15	-3.40	0.01	-1.34	0.54	-2.37	1.03	1.12	0.79	-1.05	0.98	0.04	1.09

SPO0761		cyclase	-1.94	0.00	-2.08	0.00	-2.01	0.07	-9.45	0.00	1.08	0.55	-4.19	5.27	-1.29	0.04	1.09	0.60	-0.10	1.19
SPO0762		GntR family transcriptional regulator	-1.57	0.00	-1.05	0.61	-1.31	0.26	1.09	0.09	1.06	0.32	1.08	0.02	1.27	0.04	-0.91	0.09	0.18	1.09
SPO0763		glutamine amidotransferase	-1.56	0.05	-1.06	0.68	-1.31	0.25	-5.36	0.00	-1.33	0.06	-3.35	2.02	-1.43	0.00	-1.00	0.23	-1.22	0.22
SPO0764		cytochrome P450 family protein	-1.48	0.01	-1.01	0.92	-1.25	0.23	-4.80	0.00	-1.14	0.24	-2.97	1.83	-1.31	0.02	-1.14	0.98	-1.23	0.09
SPO0765		glutamine synthetase	-1.38	0.00	-1.15	0.18	-1.27	0.12	-3.03	0.00	1.13	0.19	-0.95	2.08	-1.15	0.10	-1.35	0.28	-1.25	0.10
SPO0766		(Fe-S)-binding protein	-1.09	0.95	-1.03	0.95	-1.06	0.03	-1.32	0.96	1.35	0.15	0.02	1.34	1.13	0.47	-1.28	0.25	-0.08	1.21
SPO0767		FkbM family methyltransferase	-1.40	0.00	1.01	0.96	-0.20	1.21	1.06	0.89	-1.14	0.30	-0.04	1.10	1.27	0.23	0.98	0.64	1.12	0.15
SPO0768		IclR family transcriptional regulator	-1.76	0.00	1.01	0.89	-0.38	1.39	1.32	0.01	-1.27	0.03	0.03	1.30	-1.51	0.00	-1.83	0.00	-1.67	0.16
SPO0769		hypothetical protein	-3.02	0.03	-1.98	0.00	-2.50	0.52	-7.23	0.00	1.11	0.25	-3.06	4.17	-1.32	0.07	1.16	0.09	-0.08	1.24
SPO0770		hypothetical protein	-2.17	0.07	-1.54	0.46	-1.86	0.32	-3.30	0.15	-1.07	0.89	-2.19	1.12	-0.98	0.94	1.43	0.43	0.22	1.21
SPO0771		hypothetical protein	X	X	-1.06	0.71	N/A	N/A	-1.69	0.01	X	X	N/A	N/A	1.22	0.05	X	X	N/A	N/A
SPO0772		enoyl-CoA hydratase	1.99	0.00	-1.10	0.67	0.45	1.55	-3.78	0.00	1.23	0.41	-1.28	2.51	1.27	0.19	1.74	0.05	1.51	0.24
SPO0773		acetyl-CoA acyltransferase/thiolase	1.31	0.86	-1.10	0.59	0.11	1.21	-2.86	0.00	1.37	0.06	-0.75	2.12	1.26	0.25	2.24	0.00	1.75	0.49
SPO0774		acyl-CoA dehydrogenase	1.49	0.00	-1.27	0.00	0.11	1.38	-4.07	0.00	1.30	0.04	-1.39	2.69	1.15	0.14	1.44	0.00	1.30	0.15
SPO0775		acyl-CoA dehydrogenase	1.17	0.79	-1.22	0.32	-0.03	1.20	-4.10	0.00	1.73	0.07	-1.19	2.92	1.29	0.39	1.50	0.16	1.40	0.11
SPO0776		hypothetical protein	1.06	0.99	-1.17	0.66	-0.05	1.12	-3.33	0.01	1.40	0.15	-0.97	2.37	1.22	0.51	1.35	0.25	1.29	0.07
SPO0777		enoyl-CoA hydratase (EC:4.2.1.17)	0.98	0.87	1.04	0.89	1.01	0.03	-1.74	0.41	1.28	0.46	-0.23	1.51	1.25	0.45	1.74	0.12	1.50	0.24
SPO0778		long-chain-fatty-acid--CoA ligase	1.17	0.87	-1.01	1.00	0.08	1.09	-2.48	0.22	1.42	0.38	-0.53	1.95	1.13	0.75	1.57	0.15	1.35	0.22
SPO0779	*rpe*	ribulose-phosphate 3-epimerase (EC:5.1.3.1)	-1.13	0.07	1.62	0.01	0.25	1.38	4.09	0.00	-1.12	0.07	1.49	2.61	-1.32	0.02	-1.84	0.00	-1.58	0.26
SPO0780	*phoC*	phosphonate ABC transporter ATP-binding protein	X	X	X	X	N/A	N/A	-1.58	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO0781	*phnD*	phosphonate ABC transporter substrate-binding protein	-1.19	0.16	1.10	0.46	-0.04	1.15	-0.96	0.02	-0.96	0.35	-0.96	0.00	1.20	0.03	-1.11	X	0.04	1.16
SPO0782	*phoE*	phosphonate ABC transporter permease	-1.92	0.00	-1.14	0.75	-1.53	0.39	-1.70	0.03	-1.64	0.45	-1.67	0.03	-1.27	0.69	1.14	0.86	-0.07	1.21
SPO0783	*phnE*	phosphonate ABC transporter permease	-1.13	0.13	-1.23	0.09	-1.18	0.05	1.61	0.03	-1.30	0.47	0.16	1.46	-1.30	0.03	-0.92	0.42	-1.11	0.19
SPO0784		chloramphenicol acetyltransferase	-1.43	0.41	1.14	0.19	-0.15	1.29	11.80	0.00	-1.05	X	5.38	6.43	-1.13	0.69	X	X	N/A	N/A
SPO0785		2-dehydro-3-deoxygalactonokinase	1.75	0.71	1.06	0.78	1.41	0.35	1.75	0.66	-1.30	0.34	0.23	1.53	-1.12	0.85	-1.04	0.98	-1.08	0.04
SPO0786		thioesterase	2.10	0.00	1.95	0.00	2.03	0.08	2.39	0.00	1.07	0.23	1.73	0.66	-1.23	0.09	-1.90	0.00	-1.57	0.34
SPO0787	*gph-1*	phosphoglycolate phosphatase (EC:3.1.3.18)	1.38	0.02	1.36	0.00	1.37	0.01	2.59	0.00	-1.07	0.21	0.76	1.83	-1.38	0.01	-1.69	0.00	-1.54	0.16
SPO0788		metallo-beta-lactamase	-1.29	0.55	-1.33	0.22	-1.31	0.02	-3.49	0.07	1.40	0.09	-1.05	2.45	1.12	0.09	1.59	0.14	1.36	0.24
SPO0789		hypothetical protein	X	X	1.09	0.65	N/A	N/A	-0.93	0.12	-1.09	0.81	-1.01	0.08	-1.13	0.31	1.72	0.19	0.30	1.43
SPO0790		hypothetical protein	X	X	1.22	0.04	N/A	N/A	-1.24	0.25	X	X	N/A	N/A	-1.00	0.76	X	X	N/A	N/A
SPO0791		hypothetical protein	1.21	0.07	1.44	0.00	1.33	0.12	3.94	0.00	-1.50	0.00	1.22	2.72	1.35	0.00	-1.31	0.01	0.02	1.33
SPO0792		6-phosphogluconate dehydrogenase	-1.02	0.51	1.35	0.04	0.17	1.19	3.73	0.00	-1.12	0.12	1.31	2.43	1.00	0.85	-1.08	0.19	-0.04	1.04
SPO0793	*cueR*	Cu(I)-responsive transcriptional regulator	1.08	0.70	1.03	0.81	1.06	0.03	1.38	0.04	-1.04	0.92	0.17	1.21	-1.12	0.53	1.42	0.20	0.15	1.27
SPO0794		copper-translocating P-type ATPase (EC:3.6.3.4)	1.13	0.87	1.41	0.06	1.27	0.14	1.61	0.44	1.81	0.00	1.71	0.10	-1.10	0.30	-1.03	0.83	-1.07	0.04
SPO0795		short chain dehydrogenase/reductase oxidoreductase	X	X	-1.39	0.35	N/A	N/A	X	X	-1.39	0.31	N/A	N/A	-1.09	0.85	1.37	0.62	0.14	1.23
SPO0796		hypothetical protein	-1.00	0.54	1.01	0.90	0.01	1.01	1.26	0.01	-1.07	0.74	0.10	1.17	-0.97	0.55	-1.09	0.78	-1.03	0.06
SPO0797		bile acid transporter family protein	1.12	0.70	-1.35	0.35	-0.12	1.24	1.71	0.00	-1.19	0.58	0.26	1.45	1.18	0.42	1.24	0.47	1.21	0.03
SPO0798		monooxygenase domain-containing protein	-1.46	0.62	-1.79	0.36	-1.63	0.16	-2.25	0.46	-0.98	0.95	-1.61	0.64	-1.24	0.66	1.27	0.68	0.02	1.26

SPO0799		TetR family transcriptional regulator	-1.67	0.26	-1.02	0.99	-1.35	0.33	-1.79	0.45	-1.26	0.23	-1.53	0.27	1.14	0.66	-1.14	0.94	0.00	1.14
SPO0800		choline sulfatase	-0.99	0.91	-1.14	0.75	-1.07	0.08	-2.22	0.00	1.60	0.07	-0.31	1.91	-1.17	0.18	-0.93	0.74	-1.05	0.12
SPO0801	*fadD*	4-coumarate--CoA ligase (EC:6.2.1.12)	1.35	0.46	-1.08	0.58	0.14	1.22	-2.40	0.06	1.48	0.04	-0.46	1.94	-1.17	0.26	1.22	0.10	0.03	1.20
SPO0802	*rpsA*	30S ribosomal protein S1	-1.33	0.55	1.11	0.72	-0.11	1.22	3.87	0.04	-1.98	0.00	0.95	2.93	1.05	0.98	-1.50	0.01	-0.23	1.28
SPO0803		NUDIX domain-containing protein (EC:6.-.-.-)	-1.30	0.00	-1.18	0.48	-1.24	0.06	-1.28	0.04	-1.07	0.67	-1.18	0.11	1.05	0.85	1.46	0.19	1.26	0.21
SPO0804	*ihfB*	integration host factor subunit beta	-1.68	0.00	1.50	0.00	-0.09	1.59	-2.57	0.00	1.36	0.00	-0.61	1.97	1.15	0.19	1.31	0.00	1.23	0.08
SPO0805		hypothetical protein	1.45	0.00	1.67	0.00	1.56	0.11	-1.48	0.00	1.23	0.02	-0.13	1.36	1.69	0.00	1.49	0.00	1.59	0.10
SPO0806	*trpF*	N-(5'-phosphoribosyl)anthranilate isomerase (EC:5.3.1.24)	1.62	0.01	1.53	0.01	1.58	0.05	1.51	0.00	-1.17	0.05	0.17	1.34	1.52	0.00	-1.09	0.66	0.22	1.31
SPO0807		hypothetical protein	1.45	0.04	1.06	0.81	1.26	0.20	-1.43	0.27	-1.00	0.86	-1.21	0.22	1.30	0.02	-1.06	X	0.12	1.18
SPO0808	*trpB*	tryptophan synthase subunit beta (EC:4.2.1.20)	1.96	0.17	1.27	0.23	1.62	0.35	2.75	0.01	1.12	0.61	1.94	0.82	1.00	0.81	-1.18	0.13	-0.09	1.09
SPO0809		hypothetical protein	1.33	0.08	1.20	0.13	1.27	0.07	-1.73	0.01	1.26	0.01	-0.24	1.50	1.10	0.13	1.08	0.07	1.09	0.01
SPO0810		6-aminohexanoate-dimer hydrolase	1.48	0.73	1.04	0.88	1.26	0.22	0.86	0.70	1.11	0.17	0.99	0.12	1.13	0.38	1.73	0.00	1.43	0.30
SPO0811	*pth*	peptidyl-tRNA hydrolase (EC:3.1.1.29)	-1.35	0.21	-1.08	0.46	-1.22	0.14	1.87	0.00	-1.23	0.03	0.32	1.55	-1.37	0.00	-1.67	0.00	-1.52	0.15
SPO0812	*rplY*	50S ribosomal protein L25	-1.23	0.48	1.03	0.92	-0.10	1.13	3.95	0.00	-1.29	0.00	1.33	2.62	-1.25	0.00	-1.36	0.03	-1.31	0.06
SPO0813		L-lactate dehydrogenase	1.43	0.11	1.06	0.68	1.25	0.18	0.93	0.50	2.85	0.00	1.89	0.96	-1.10	0.45	1.18	0.60	0.04	1.14
SPO0814		acyl dehydratase MaoC	-1.45	0.01	1.09	0.32	-0.18	1.27	1.12	0.01	1.48	0.00	1.30	0.18	-1.03	0.67	-1.06	0.78	-1.05	0.02
SPO0815	*trpA*	tryptophan synthase subunit alpha (EC:4.2.1.20)	1.91	0.00	1.18	0.14	1.55	0.37	4.09	0.00	-1.27	0.01	1.41	2.68	-1.38	0.02	-2.04	0.00	-1.71	0.33
SPO0816		hypothetical protein	-1.94	X	-1.39	0.24	-1.67	0.27	-1.44	0.68	-1.70	0.17	-1.57	0.13	-1.14	0.69	1.21	0.42	0.04	1.18
SPO0817	*ychF*	GTP-dependent nucleic acid-binding protein EngD	-0.99	0.98	1.38	0.10	0.19	1.19	4.05	0.10	-1.54	0.02	1.26	2.80	-1.91	0.00	-2.45	0.00	-2.18	0.27
SPO0818		MAPEG family protein	-0.96	0.09	1.27	0.00	0.16	1.11	2.00	0.00	-1.12	0.14	0.44	1.56	-1.03	0.84	-1.68	0.02	-1.36	0.32
SPO0819		amidohydrolase	0.98	0.19	2.14	0.01	1.56	0.58	-8.19	0.00	1.29	0.45	-3.45	4.74	1.16	0.10	1.16	X	1.16	0.00
SPO0820		CAIB/BAIF family protein	1.25	0.00	1.25	0.11	1.25	0.00	2.47	0.00	-1.47	0.01	0.50	1.97	-1.71	0.00	-2.83	0.00	-2.27	0.56
SPO0821		MarR family transcriptional regulator	1.08	0.98	1.25	0.56	1.17	0.09	1.56	0.68	-1.36	0.29	0.10	1.46	1.18	0.70	1.01	0.98	1.10	0.09
SPO0822		branched-chain amino acid ABC transporter ATP-binding protein	-1.35	0.00	1.09	0.02	-0.13	1.22	-3.02	0.00	-1.22	0.12	-2.12	0.90	1.37	0.01	-0.98	0.34	0.19	1.18
SPO0823		branched-chain amino acid ABC transporter ATP-binding protein	1.06	0.28	1.02	0.73	1.04	0.02	-2.19	0.00	-1.18	0.23	-1.69	0.50	1.41	0.03	1.22	0.06	1.32	0.10
SPO0824		branched-chain amino acid ABC transporter permease	-1.48	0.33	-1.16	0.43	-1.32	0.16	-2.20	0.06	-1.19	0.37	-1.70	0.51	1.12	0.53	1.19	0.32	1.16	0.03
SPO0825		branched-chain amino acid ABC transporter substrate-binding protein	-2.44	0.13	-1.48	0.06	-1.96	0.48	-11.80	0.00	1.42	0.01	-5.19	6.61	1.04	0.58	1.34	0.01	1.19	0.15
SPO0826		hypothetical protein	-1.42	0.00	1.25	0.00	-0.09	1.34	-4.23	0.00	1.39	0.03	-1.42	2.81	-1.16	0.01	-1.08	0.84	-1.12	0.04
SPO0827		hypothetical protein	-1.19	0.33	1.25	0.01	0.03	1.22	-3.13	0.00	1.32	0.02	-0.91	2.23	-1.06	0.35	-1.37	0.18	-1.22	0.16
SPO0828		hypothetical protein	-1.74	0.00	1.51	0.00	-0.12	1.63	-4.39	0.00	1.17	0.24	-1.61	2.78	-0.99	0.32	X	X	N/A	N/A
SPO0829		hypothetical protein	-1.79	0.03	1.10	0.68	-0.35	1.45	-2.98	0.03	1.10	0.66	-0.94	2.04	-0.98	0.86	1.18	0.29	0.10	1.08
SPO0830		xanthine dehydrogenase, small/large subunits	-1.99	0.00	1.03	0.87	-0.48	1.51	-8.22	0.00	1.10	0.69	-3.56	4.66	-1.15	0.43	1.43	0.16	0.14	1.29
SPO0831		xanthine dehydrogenase, medium subunit	-2.06	0.01	-1.17	0.01	-1.62	0.45	-4.29	0.00	-1.23	0.28	-2.76	1.53	-0.97	0.70	1.60	0.00	0.32	1.28
SPO0832		LysR family transcriptional regulator	X	X	1.07	0.12	N/A	N/A	X	X	1.23	0.07	N/A	N/A	1.20	0.03	-1.13	X	0.04	1.17
SPO0833		formate dehydrogenase subunit beta (EC:1.2.1.2)	3.81	0.00	1.20	0.21	2.51	1.31	2.09	0.00	-7.13	0.00	-2.52	4.61	-1.33	0.01	1.18	0.31	-0.08	1.26
SPO0834		formate dehydrogenase subunit alpha (EC:1.2.1.2)	3.05	0.00	1.36	0.04	2.21	0.85	1.65	0.01	-6.36	0.00	-2.36	4.01	-1.21	0.02	-1.44	0.01	-1.33	0.12
SPO0835		cyclase	1.88	0.00	1.26	0.02	1.57	0.31	1.71	0.00	-1.05	0.13	0.33	1.38	1.02	0.94	1.02	0.44	1.02	0.00

SPO0836		hypothetical protein	1.13	0.85	1.32	0.10	1.23	0.10	1.18	0.60	1.09	0.49	1.14	0.04	-1.13	0.25	0.98	0.81	-0.08	1.05
SPO0837		hypothetical protein	2.07	0.00	2.09	0.00	2.08	0.01	-1.08	0.40	1.58	0.00	0.25	1.33	-1.16	0.19	-1.40	0.44	-1.28	0.12
SPO0838		sugar transferase	20.60	0.00	3.27	0.00	11.94	8.67	2.07	0.00	-1.02	0.98	0.53	1.55	-1.17	0.10	-1.84	0.05	-1.51	0.34
SPO0839		exopolysaccharide biosynthesis domain-containing protein	2.96	0.00	2.17	0.00	2.57	0.39	-2.90	0.00	1.22	0.24	-0.84	2.06	-1.27	0.17	-1.18	0.37	-1.23	0.05
SPO0840		chain length determinant protein	0.99	0.84	1.15	0.32	1.07	0.08	-2.08	0.00	1.10	0.25	-0.49	1.59	-1.00	0.77	1.16	0.17	0.08	1.08
SPO0841		polysaccharide biosynthesis protein	-1.11	0.63	1.41	0.00	0.15	1.26	-1.00	0.47	1.06	0.31	0.03	1.03	1.15	0.07	1.16	0.07	1.16	0.01
SPO0842		glycoside hydrolase	-0.94	0.26	1.19	0.55	0.13	1.06	-0.91	0.04	-1.41	0.18	-1.16	0.25	1.40	0.18	-1.07	0.75	0.17	1.24
SPO0843		glycosyl transferase family protein	1.08	0.64	1.71	0.05	1.40	0.31	-1.00	0.35	-1.09	0.85	-1.05	0.05	1.78	0.06	-1.00	0.54	0.39	1.39
SPO0844		hypothetical protein	-1.02	0.98	1.31	0.04	0.15	1.17	-1.08	0.50	-1.06	0.56	-1.07	0.01	1.15	0.06	-0.95	0.09	0.10	1.05
SPO0845		hypothetical protein	-1.14	0.14	-1.05	0.58	-1.10	0.04	-1.17	0.31	-1.00	0.86	-1.09	0.09	-1.40	0.01	1.04	0.65	-0.18	1.22
SPO0846		phosphopantetheinyl transferase PptA	1.21	0.89	1.15	0.59	1.18	0.03	-1.15	0.93	1.21	0.37	0.03	1.18	-1.32	0.16	-1.17	0.70	-1.25	0.08
SPO0847		non-ribosomal peptide synthetase	1.16	0.51	1.02	0.91	1.09	0.07	-2.14	0.00	1.22	0.06	-0.46	1.68	-1.60	0.01	-1.43	0.00	-1.52	0.09
SPO0848		glycosyl transferase family protein	-1.82	0.00	1.07	0.77	-0.38	1.45	-3.45	0.00	1.11	0.59	-1.17	2.28	-1.86	0.12	-1.25	0.62	-1.56	0.30
SPO0849		non-ribosomal peptide synthase	1.04	0.97	1.37	0.23	1.21	0.17	-1.28	0.83	1.16	0.69	-0.06	1.22	-1.15	0.52	-1.17	0.65	-1.16	0.01
SPO0850		hypothetical protein	0.99	0.83	1.25	0.56	1.12	0.13	-2.24	0.21	1.24	0.47	-0.50	1.74	-1.44	0.12	-1.17	0.51	-1.31	0.14
SPO0851		WecB/TagA/CpsF family glycosyl transferase	-1.20	0.79	1.18	0.66	-0.01	1.19	1.11	0.90	-1.40	0.51	-0.15	1.26	1.49	0.46	-0.97	0.87	0.26	1.23
SPO0852		Gfo/Idh/MocA family oxidoreductase	1.10	0.37	1.41	0.25	1.26	0.16	-1.26	0.51	1.03	0.69	-0.12	1.15	-1.53	0.06	-1.58	0.16	-1.56	0.03
SPO0853		glycosyl transferase family protein	-1.20	0.31	1.14	0.14	-0.03	1.17	-1.88	0.02	-1.00	0.91	-1.44	0.44	-2.02	0.01	-1.55	0.11	-1.79	0.24
SPO0854		glycoside hydrolase	1.02	0.85	1.12	0.28	1.07	0.05	-1.39	0.02	-1.03	0.63	-1.21	0.18	-1.98	0.01	-2.45	0.01	-2.22	0.24
SPO0855	*xylB*	xylulokinase (EC:2.7.1.17)	-1.69	0.01	-1.60	0.23	-1.65	0.04	-3.19	0.01	-1.37	0.22	-2.28	0.91	-1.43	0.27	1.24	0.60	-0.10	1.34
SPO0856	*xylA*	xylose isomerase (EC:5.3.1.5)	-1.25	0.79	-1.22	0.53	-1.24	0.02	-3.10	0.00	-1.42	0.41	-2.26	0.84	-1.01	0.92	-1.06	0.76	-1.04	0.03
SPO0857	*galM*	aldose 1-epimerase (EC:5.1.3.3)	-1.18	0.57	-1.17	0.62	-1.18	0.01	-1.45	0.49	-1.21	0.49	-1.33	0.12	-1.15	0.62	1.35	0.28	0.10	1.25
SPO0858		methylamine utilization protein MauG	2.05	0.01	-1.10	0.82	0.48	1.58	2.03	0.01	-1.16	X	0.44	1.60	-1.33	0.14	X	X	N/A	N/A
SPO0859		hypothetical protein	-1.10	0.13	1.12	0.49	0.01	1.11	-1.45	0.08	1.20	0.22	-0.13	1.33	1.08	0.13	-1.28	0.10	-0.10	1.18
SPO0860		xylose repressor	0.97	0.19	1.15	0.21	1.06	0.09	-1.34	0.07	1.28	0.06	-0.03	1.31	1.25	0.11	-1.15	0.28	0.05	1.20
SPO0861	*xylF*	xylose ABC transporter substrate-binding protein	1.17	0.91	-2.16	0.00	-0.50	1.67	-8.32	0.01	-1.02	0.57	-4.67	3.65	1.11	0.50	-1.07	0.50	0.02	1.09
SPO0862	*xylH*	xylose ABC transporter permease	1.75	0.05	-1.22	0.66	0.27	1.49	2.21	0.00	-1.18	0.46	0.52	1.70	-1.28	0.74	1.10	0.87	-0.09	1.19
SPO0863	*xylG*	xylose ABC transporter ATP-binding protein	1.04	0.89	-1.12	0.17	-0.04	1.08	-2.90	0.09	-1.08	0.75	-1.99	0.91	-1.05	0.83	-1.00	0.83	-1.03	0.03
SPO0864		glucokinase	1.21	0.58	1.28	0.22	1.25	0.04	1.31	0.61	-1.37	0.31	-0.03	1.34	1.20	0.45	-0.93	0.51	0.14	1.07
SPO0865		Gfo/Idh/MocA family oxidoreductase	1.04	0.87	-1.10	0.90	-0.03	1.07	-1.91	0.32	-1.06	0.94	-1.49	0.43	-1.00	0.98	1.30	0.77	0.15	1.15
SPO0866		gamma-glutamyltranspeptidase	1.71	0.00	1.04	0.66	1.38	0.34	2.32	0.01	-1.01	0.93	0.66	1.67	-1.00	0.96	-1.46	0.09	-1.23	0.23
SPO0867		hypothetical protein	1.72	0.02	1.04	0.56	1.38	0.34	1.55	0.02	1.37	0.04	1.46	0.09	-1.06	0.29	-1.02	0.53	-1.04	0.02
SPO0868		OMP85 family outer membrane protein	1.01	0.76	-1.06	0.79	-0.03	1.04	-1.28	0.19	-1.08	0.64	-1.18	0.10	1.04	0.88	1.11	0.44	1.08	0.04
SPO0869		hypothetical protein	-1.27	0.08	-1.27	0.74	-1.27	0.00	-1.84	0.28	1.18	0.58	-0.33	1.51	-1.32	0.79	-1.09	0.84	-1.21	0.12
SPO0870		LysR family transcriptional regulator	-1.14	0.50	-1.38	0.01	-1.26	0.12	1.18	0.86	-1.32	0.23	-0.07	1.25	-1.09	0.69	1.34	0.07	0.13	1.22
SPO0871		transthyretin family protein	-1.13	0.88	1.51	0.27	0.19	1.32	-1.69	0.72	1.14	0.71	-0.28	1.42	-0.97	0.82	-1.54	0.36	-1.25	0.29
SPO0872		polysaccharide deacetylase	1.43	0.11	1.42	0.06	1.43	0.01	-2.40	0.01	1.20	0.25	-0.60	1.80	-1.25	0.16	-1.57	0.05	-1.41	0.16
SPO0873	*allA*	ureidoglycolate hydrolase (EC:3.5.3.19)	1.47	0.52	1.79	0.02	1.63	0.16	-2.45	0.05	1.08	0.63	-0.69	1.77	-1.17	0.34	-1.53	0.10	-1.35	0.18
SPO0874		xanthine/uracil permease	1.60	0.02	-1.06	0.59	0.27	1.33	-2.42	0.00	1.09	0.47	-0.67	1.76	1.19	0.04	1.76	0.05	1.48	0.29

SPO0875	*gap-2*	glyceraldehyde-3-phosphate dehydrogenase, type I (EC:1.2.1.-)	1.44	0.00	-1.20	0.48	0.12	1.32	1.48	0.04	-1.21	0.03	0.14	1.35	-1.35	0.08	-1.38	0.02	-1.37	0.01
SPO0876		hypothetical protein	1.43	0.26	-1.77	0.10	-0.17	1.60	-3.15	0.02	-1.32	0.37	-2.24	0.92	1.27	0.49	1.32	0.53	1.30	0.03
SPO0877		hypothetical protein	-1.14	0.81	1.45	0.32	0.16	1.30	-1.04	0.91	1.32	0.45	0.14	1.18	1.53	0.28	-1.11	0.98	0.21	1.32
SPO0878	*gcvH-1*	glycine cleavage system H protein	1.58	0.79	1.09	0.68	1.34	0.25	1.01	0.82	1.44	0.19	1.23	0.21	1.37	0.15	1.32	0.06	1.35	0.03
SPO0879		acyl-CoA dehydrogenase	2.09	0.08	1.01	0.92	1.55	0.54	-1.44	0.04	1.85	0.04	0.21	1.65	1.50	0.20	2.85	0.02	2.18	0.68
SPO0880		hypothetical protein	1.08	0.99	1.13	0.57	1.11	0.02	-1.73	0.09	1.91	0.00	0.09	1.82	1.10	0.17	1.86	0.01	1.48	0.38
SPO0881		hypothetical protein	-2.70	0.26	-1.04	0.78	-1.87	0.83	-2.16	0.07	-1.40	0.13	-1.78	0.38	1.06	0.79	-1.44	0.03	-0.19	1.25
SPO0882		hypothetical protein	-4.40	0.12	1.12	0.86	-1.64	2.76	-8.69	0.05	-1.18	0.88	-4.94	3.76	-1.04	0.99	-1.12	X	-1.08	0.04
SPO0883		hypothetical protein	1.32	0.15	1.08	0.32	1.20	0.12	2.29	0.01	1.19	0.37	1.74	0.55	1.55	0.12	1.39	0.11	1.47	0.08
SPO0884		hypothetical protein	-1.07	0.10	1.22	0.33	0.08	1.15	1.36	0.24	1.05	0.94	1.21	0.16	1.91	0.06	1.43	0.12	1.67	0.24
SPO0885		alpha/beta hydrolase	-1.19	0.78	-1.03	0.94	-1.11	0.08	1.38	0.68	1.07	0.91	1.23	0.15	1.08	0.89	1.13	0.65	1.11	0.02
SPO0886	*groES*	co-chaperonin GroES	-1.27	0.04	-3.46	0.01	-2.37	1.10	5.38	0.01	-10.60	0.00	-2.61	7.99	-1.59	0.07	-1.70	0.04	-1.65	0.05
SPO0887	*groEL*	molecular chaperone GroEL	1.06	0.81	-1.96	0.04	-0.45	1.51	7.89	0.00	-9.38	0.01	-0.75	8.64	1.97	0.00	1.47	0.33	1.72	0.25
SPO0888		acetyltransferase	1.42	0.17	-1.15	0.53	0.14	1.29	1.88	0.09	1.06	0.86	1.47	0.41	1.73	0.03	1.16	0.23	1.45	0.29
SPO0889		hypothetical protein	1.04	0.97	1.02	0.98	1.03	0.01	1.48	0.90	-1.04	0.90	0.22	1.26	1.21	0.77	1.80	0.37	1.51	0.30
SPO0890		lipase	X	X	1.18	0.11	N/A	N/A	5.62	0.00	-1.56	0.01	2.03	3.59	-1.57	0.02	-2.40	0.03	-1.99	0.42
SPO0891		alkylphosphonate utilization protein PhnM	X	X	1.11	0.28	N/A	N/A	2.88	0.00	-1.52	0.02	0.68	2.20	-1.87	0.09	-1.92	0.21	-1.90	0.02
SPO0892	*purK*	phosphoribosylaminoimidazole carboxylase ATPase subunit (EC:4.1.1.21)	1.40	0.07	1.85	0.01	1.63	0.23	2.36	0.01	-1.06	0.48	0.65	1.71	1.07	0.28	-1.68	0.04	-0.31	1.38
SPO0893	*purE*	phosphoribosylaminoimidazole carboxylase catalytic subunit (EC:4.1.1.21)	1.95	0.03	1.48	0.09	1.72	0.24	5.06	0.00	-1.03	0.44	2.02	3.05	-1.13	0.02	-1.83	0.02	-1.48	0.35
SPO0894		hypothetical protein	-1.47	0.00	1.21	0.30	-0.13	1.34	-2.39	0.00	1.34	0.16	-0.53	1.87	1.04	0.83	-1.12	0.35	-0.04	1.08
SPO0895		heat shock protein 20	-1.27	0.06	-1.95	0.00	-1.61	0.34	1.29	0.46	-1.27	0.24	0.01	1.28	1.40	0.05	1.39	0.03	1.40	0.01
SPO0896		hypothetical protein	1.23	0.61	-1.32	0.22	-0.05	1.28	1.63	0.04	-1.24	0.11	0.20	1.44	1.61	0.01	1.49	0.06	1.55	0.06
SPO0897		PhzF family phenazine biosynthesis protein	1.07	0.63	1.14	0.40	1.11	0.03	1.71	0.02	-1.20	0.08	0.26	1.46	1.03	0.91	-1.06	0.27	-0.02	1.05
SPO0898		hypothetical protein	1.18	0.11	-1.04	0.91	0.07	1.11	1.29	0.08	-1.41	0.21	-0.06	1.35	1.22	0.19	1.38	0.39	1.30	0.08
SPO0899		hypothetical protein	2.38	0.46	1.60	0.02	1.99	0.39	-1.57	0.08	1.94	0.01	0.19	1.76	1.48	0.05	1.57	0.03	1.53	0.05
SPO0900	*sat*	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase (EC:2.7.1.25 2.7.7.4)	1.31	0.67	0.98	0.89	1.14	0.17	7.68	0.05	1.44	0.14	4.56	3.12	-1.32	0.15	-1.91	0.10	-1.62	0.30
SPO0901		guanylate cyclase	-1.04	0.66	-1.08	0.90	-1.06	0.02	-2.28	0.00	1.46	0.04	-0.41	1.87	1.34	0.08	1.16	0.36	1.25	0.09
SPO0902		hypothetical protein	1.39	0.90	1.28	0.16	1.34	0.05	2.42	0.68	-1.17	0.13	0.63	1.80	1.32	0.09	1.07	0.94	1.20	0.13
SPO0903	*trxB*	thioredoxin-disulfide reductase (EC:1.8.1.9)	0.98	0.45	1.06	0.63	1.02	0.04	2.22	0.02	-1.16	0.13	0.53	1.69	1.25	0.22	1.23	0.48	1.24	0.01
SPO0904		leucine-responsive regulatory protein	-2.25	0.01	-1.36	0.10	-1.81	0.45	1.49	0.03	-1.06	0.22	0.22	1.28	-1.13	0.26	-1.42	0.06	-1.28	0.14
SPO0905		hypothetical protein	3.58	0.00	1.81	0.01	2.70	0.88	-1.23	0.14	-1.01	0.77	-1.12	0.11	-1.70	0.01	-1.46	0.08	-1.58	0.12
SPO0906		hypothetical protein	-1.78	0.06	1.09	0.63	-0.35	1.44	-1.47	0.24	1.21	0.13	-0.13	1.34	1.05	0.71	-1.19	0.08	-0.07	1.12
SPO0907		hypothetical protein	-1.33	0.17	-1.22	0.44	-1.28	0.06	-1.13	0.68	1.15	0.37	0.01	1.14	-1.19	0.29	1.25	0.42	0.03	1.22
SPO0908	*lgt*	prolipoprotein diacylglyceryl transferase (EC:2.4.99.-)	1.06	0.99	-1.71	0.01	-0.33	1.39	1.53	0.05	-1.33	0.11	0.10	1.43	1.20	0.66	1.30	0.42	1.25	0.05
SPO0909		hypothetical protein	1.52	0.77	1.34	0.34	1.43	0.09	1.77	0.62	-1.07	0.06	0.35	1.42	1.55	0.19	1.26	0.33	1.41	0.15
SPO0910		hypothetical protein	1.96	0.11	1.60	0.14	1.78	0.18	-2.27	0.01	2.29	0.00	0.01	2.28	1.41	0.03	1.83	0.03	1.62	0.21
SPO0911	*proC*	pyrroline-5-carboxylate reductase (EC:1.5.1.2)	2.19	0.18	1.28	0.37	1.74	0.46	1.80	0.59	1.29	0.35	1.55	0.26	-1.25	0.15	-1.10	0.36	-1.18	0.08

SPO0912	*csaA*	chaperonin csaA	2.00	0.02	1.09	0.34	1.55	0.46	2.73	0.00	1.24	0.21	1.99	0.75	1.05	0.91	-1.14	0.04	-0.04	1.10
SPO0913		D-isomer specific 2-hydroxyacid dehydrogenase	1.60	0.01	1.30	0.03	1.45	0.15	1.56	0.07	-1.10	0.33	0.23	1.33	1.14	0.06	-1.10	0.24	0.02	1.12
SPO0914	*tdk*	thymidine kinase (EC:2.7.1.21)	-1.16	0.35	-1.02	0.79	-1.09	0.07	4.75	0.01	-1.36	0.03	1.70	3.06	-1.63	0.01	-2.69	0.01	-2.16	0.53
SPO0915		hypothetical protein	1.01	0.10	-1.05	0.47	-0.02	1.03	-1.74	0.01	1.08	0.94	-0.33	1.41	-1.06	0.52	1.01	0.26	-0.03	1.04
SPO0916		hypothetical protein	1.17	0.70	1.21	0.66	1.19	0.02	1.34	0.30	1.21	0.27	1.28	0.07	1.25	0.26	1.13	0.75	1.19	0.06
SPO0917		glyoxalase	X	X	-1.07	0.68	N/A	N/A	-0.85	0.04	1.10	0.39	0.12	0.98	-1.08	0.64	-1.14	X	-1.11	0.03
SPO0918	*fabH-1*	3-oxoacyl-ACP synthase (EC:2.3.1.41)	-1.32	0.00	-1.41	0.18	-1.37	0.04	0.89	0.05	1.70	0.04	1.30	0.40	-1.14	0.16	1.57	0.01	0.22	1.36
SPO0919		MarR family transcriptional regulator	1.11	0.31	-1.42	0.40	-0.16	1.27	2.61	0.00	-1.21	0.36	0.70	1.91	-1.34	0.17	-1.28	0.63	-1.31	0.03
SPO0920		RND family efflux transporter MFP subunit	0.98	0.09	-1.10	0.37	-0.06	1.04	-1.73	0.03	-1.15	0.28	-1.44	0.29	-1.22	0.06	-1.77	0.06	-1.50	0.27
SPO0921		AcrB/AcrD/AcrF family transporter	1.59	0.16	-1.18	0.61	0.21	1.39	2.55	0.03	-1.41	0.07	0.57	1.98	-1.14	0.26	-1.29	0.26	-1.22	0.08
SPO0922		hypothetical protein	-1.11	0.43	-1.10	0.48	-1.11	0.01	-1.64	0.02	1.40	0.32	-0.12	1.52	-1.04	0.66	1.11	0.59	0.04	1.08
SPO0923	*carB*	carbamoyl phosphate synthase large subunit (EC:6.3.5.5)	1.63	0.07	1.41	0.10	1.52	0.11	2.03	0.01	-1.12	0.12	0.46	1.58	-1.26	0.04	-1.55	0.05	-1.41	0.15
SPO0924	*pabB*	aminodeoxychorismate synthase (EC:2.6.1.85)	-1.48	0.10	1.16	0.20	-0.16	1.32	5.09	0.00	-1.59	0.04	1.75	3.34	-1.22	0.17	-2.27	0.02	-1.75	0.52
SPO0925		hypothetical protein	1.10	0.87	1.37	0.09	1.24	0.14	1.71	0.47	-1.10	0.66	0.31	1.41	-1.36	0.06	-1.75	0.05	-1.56	0.19
SPO0926	*aspS*	aspartyl-tRNA synthetase (EC:6.1.1.12)	-1.20	X	1.30	0.06	0.05	1.25	8.33	0.00	-1.97	0.05	3.18	5.15	-1.07	0.64	-2.38	0.00	-1.73	0.65
SPO0927		hypothetical protein	1.15	X	1.42	0.19	1.29	0.14	4.69	0.02	-1.79	0.02	1.45	3.24	1.00	0.79	-2.34	0.02	-0.67	1.67
SPO0928		hypothetical protein	-1.57	0.02	-1.20	0.21	-1.39	0.19	-2.46	0.01	-1.03	0.73	-1.75	0.72	-1.22	0.10	-1.00	0.97	-1.11	0.11
SPO0929		type II DNA modification methyltransferase	-2.33	0.00	-1.23	0.63	-1.78	0.55	-1.74	0.02	1.43	0.33	-0.16	1.59	-1.02	0.85	1.00	0.94	-0.01	1.01
SPO0930		hypothetical protein	1.94	0.00	1.51	0.04	1.73	0.21	-2.43	0.01	2.28	0.00	-0.08	2.36	1.42	0.07	2.31	0.03	1.87	0.45
SPO0931		response regulator	1.45	0.07	1.08	0.75	1.27	0.19	1.53	0.08	1.54	0.18	1.54	0.01	-1.35	0.05	1.53	0.07	0.09	1.44
SPO0932		methylmalonyl-CoA epimerase (EC:5.1.99.1)	5.45	0.00	1.76	0.04	3.61	1.85	8.10	0.00	-1.08	0.14	3.51	4.59	-1.47	0.01	-1.74	0.02	-1.61	0.14
SPO0933		hypothetical protein	3.59	0.00	2.08	0.10	2.84	0.76	5.18	0.01	1.32	0.05	3.25	1.93	-1.19	0.09	-1.48	0.15	-1.34	0.14
SPO0934		hypothetical protein	1.11	0.90	1.08	0.66	1.10	0.02	1.80	0.33	-1.55	0.02	0.13	1.68	1.43	0.05	1.21	0.30	1.32	0.11
SPO0935		nitroreductase	1.00	0.47	-1.33	0.23	-0.17	1.16	1.71	0.10	-1.84	0.00	-0.07	1.78	1.17	0.24	1.48	0.24	1.33	0.15
SPO0936		hypothetical protein	1.02	0.03	1.12	0.06	1.07	0.05	-4.41	0.00	1.61	0.01	-1.40	3.01	-1.38	0.04	-1.45	0.12	-1.42	0.04
SPO0937		hypothetical protein	1.11	0.93	1.18	0.69	1.15	0.03	-1.03	0.89	-1.00	0.99	-1.01	0.02	1.41	0.50	-1.13	0.91	0.14	1.27
SPO0938		hypothetical protein	-1.33	0.06	-1.34	0.16	-1.34	0.01	1.00	0.16	1.36	0.22	1.18	0.18	1.33	0.08	1.21	0.19	1.27	0.06
SPO0939		M48 family peptidase	1.34	0.71	-1.09	0.32	0.13	1.22	0.96	0.71	1.12	0.83	1.04	0.08	-1.11	0.65	1.00	0.80	-0.06	1.05
SPO0940		hypothetical protein	1.45	0.06	1.20	0.40	1.33	0.13	1.04	0.82	1.11	0.60	1.08	0.04	1.16	0.22	-1.05	0.58	0.05	1.11
SPO0941		hypothetical protein	1.91	0.01	1.45	0.03	1.68	0.23	8.20	0.00	-1.25	0.23	3.48	4.73	1.42	0.03	-1.13	0.37	0.15	1.28
SPO0942		hypothetical protein	1.65	0.26	2.01	0.14	1.83	0.18	2.89	0.24	1.39	0.52	2.14	0.75	1.23	0.48	-1.09	X	0.07	1.16
SPO0943		hypothetical protein	1.46	0.68	1.13	0.54	1.30	0.16	1.24	0.65	2.23	0.02	1.74	0.50	1.44	0.27	1.33	0.30	1.39	0.05
SPO0944	*rimO*	30S ribosomal protein S12 methylthiotransferase	-1.30	0.86	-1.02	0.94	-1.16	0.14	1.40	0.80	-1.22	0.43	0.09	1.31	-1.63	0.22	-1.95	0.18	-1.79	0.16
SPO0945		AsmA family protein	1.29	0.24	-1.34	0.21	-0.03	1.32	0.88	0.01	1.32	0.21	1.10	0.22	1.81	0.03	2.26	0.11	2.04	0.22
SPO0946	*algC*	phosphomannomutase (EC:5.4.2.2 5.4.2.8)	1.35	0.11	1.07	0.54	1.21	0.14	1.78	0.01	1.00	0.76	1.39	0.39	1.11	0.33	-1.18	0.24	-0.03	1.15
SPO0947	*kdsA*	2-dehydro-3-deoxyphosphooctonate aldolase (EC:2.5.1.55)	1.31	0.40	-1.29	0.28	0.01	1.30	1.87	0.10	1.14	0.64	1.51	0.37	-1.43	0.02	-1.22	0.11	-1.33	0.11
SPO0948	*kpsE*	capsule polysaccharide exporter	1.39	0.03	-1.09	0.25	0.15	1.24	-1.11	0.78	-1.05	0.45	-1.08	0.03	-1.72	0.04	-2.02	0.02	-1.87	0.15
SPO0949	*kpsT*	capsular polysaccharide export ATP-binding protein (EC:3.6.3.38)	1.06	0.84	-1.54	0.30	-0.24	1.30	-1.30	0.35	1.13	0.84	-0.09	1.22	-1.54	0.24	-1.32	0.32	-1.43	0.11

SPO0950		uracil-DNA glycosylase	-2.01	0.23	-1.16	0.37	-1.59	0.43	-2.92	0.03	-1.06	0.70	-1.99	0.93	1.04	0.85	2.22	0.13	1.63	0.59
SPO0951		hypothetical protein	1.14	0.99	2.06	0.23	1.60	0.46	1.41	0.88	1.15	0.73	1.28	0.13	-1.01	0.95	-1.16	0.77	-1.09	0.08
SPO0952		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO0953		glutathione S-transferase	1.51	0.03	1.05	0.29	1.28	0.23	1.69	0.04	1.03	0.87	1.36	0.33	1.59	0.05	1.35	0.17	1.47	0.12
SPO0954		hypothetical protein	1.01	0.24	1.50	0.07	1.26	0.25	-2.28	0.02	1.15	0.19	-0.57	1.72	-1.15	0.51	-1.46	0.03	-1.31	0.16
SPO0955		amidohydrolase	1.10	0.72	-1.04	0.25	0.03	1.07	-3.74	0.01	2.39	0.00	-0.68	3.07	1.01	1.00	1.36	0.01	1.19	0.18
SPO0956		hypothetical protein	-1.13	0.26	1.31	0.41	0.09	1.22	1.96	0.11	-1.31	0.06	0.33	1.64	1.20	0.56	-1.27	0.14	-0.04	1.24
SPO0957		ABC transporter permease	-0.97	0.30	1.14	0.65	0.09	1.06	2.00	0.16	-1.91	0.12	0.05	1.96	1.29	0.30	-1.42	0.40	-0.06	1.36
SPO0958		hypothetical protein	2.06	0.42	1.10	0.85	1.58	0.48	-1.23	0.44	1.28	0.69	0.03	1.26	1.04	0.97	2.13	0.19	1.59	0.55
SPO0959		hypothetical protein	X	X	1.24	0.46	N/A	N/A	2.25	0.06	1.20	0.59	1.73	0.52	-1.10	0.69	-1.46	0.15	-1.28	0.18
SPO0960		MerR family transcriptional regulator	-1.64	0.01	-1.24	0.38	-1.44	0.20	-1.28	0.27	1.11	0.48	-0.09	1.20	1.43	0.09	-1.22	0.46	0.11	1.33
SPO0961		hypothetical protein	-2.92	0.02	-1.04	0.81	-1.98	0.94	-3.33	0.00	1.24	0.46	-1.05	2.29	1.25	0.38	1.33	0.49	1.29	0.04
SPO0962	*argD*	acetylornithine transaminase (EC:2.6.1.11)	3.18	0.13	1.25	0.30	2.22	0.97	1.78	0.10	1.35	0.14	1.57	0.22	-1.51	0.02	-1.52	0.14	-1.52	0.01
SPO0963	*argF*	ornithine carbamoyltransferase (EC:2.1.3.3)	1.59	0.50	1.39	0.04	1.49	0.10	1.28	0.79	1.18	0.21	1.23	0.05	-1.27	0.01	-1.83	0.01	-1.55	0.28
SPO0964	*argC-1*	N-acetyl-gamma-glutamyl-phosphate reductase (EC:1.2.1.38)	1.09	0.71	1.44	0.08	1.27	0.18	1.24	0.02	-1.45	0.19	-0.11	1.35	-1.50	0.05	-2.27	0.03	-1.89	0.39
SPO0965		acetyltransferase	-1.67	0.24	1.32	0.52	-0.18	1.50	-1.28	0.93	-1.68	0.42	-1.48	0.20	-1.03	0.97	-0.95	0.88	-0.99	0.04
SPO0966	*panE-1*	2-dehydropantoate 2-reductase (EC:1.1.1.169)	1.16	0.37	-1.13	0.59	0.02	1.15	-2.26	0.01	1.39	0.07	-0.44	1.83	-1.30	0.08	-1.09	0.93	-1.20	0.11
SPO0967		phosphate transporter family protein	-1.66	X	1.42	0.09	-0.12	1.54	2.49	0.01	-1.62	0.05	0.44	2.06	-1.36	0.14	-1.41	0.48	-1.39	0.02
SPO0968		NUDIX family hydrolase	-1.26	0.02	-1.36	0.03	-1.31	0.05	-2.62	0.00	-2.32	0.01	-2.47	0.15	1.04	0.96	1.05	0.19	1.05	0.01
SPO0970	*apqZ*	aquaporin Z	1.85	0.07	-1.21	0.21	0.32	1.53	2.23	0.03	2.52	0.01	2.38	0.15	1.48	0.05	1.71	0.18	1.60	0.12
SPO0971		GMC family oxidoreductase	-1.17	0.86	-1.12	0.52	-1.15	0.02	0.97	0.98	1.37	0.03	1.17	0.20	-1.01	0.89	1.04	0.50	0.02	1.03
SPO0972	*hrpB*	ATP-dependent helicase HrpB	X	X	-1.01	0.99	N/A	N/A	2.65	0.02	-1.20	0.53	0.73	1.93	-1.32	0.08	-1.69	0.17	-1.51	0.19
SPO0973		arginine/ornithine transport system ATPase (EC:2.7.-.-)	1.11	0.92	2.17	0.00	1.64	0.53	1.69	0.13	1.10	0.62	1.40	0.29	-1.07	0.19	1.05	0.75	-0.01	1.06
SPO0974	*rpmB*	50S ribosomal protein L28	-1.08	0.92	1.10	0.83	0.01	1.09	5.44	0.00	-1.52	0.07	1.96	3.48	-1.49	0.10	-1.60	0.13	-1.55	0.06
SPO0975		hypothetical protein	2.58	0.01	1.37	0.50	1.98	0.61	1.86	0.03	-1.04	X	0.41	1.45	-1.41	0.14	1.36	X	-0.02	1.39
SPO0976		hypothetical protein	3.67	0.00	3.64	0.01	3.66	0.01	3.29	0.00	1.34	0.07	2.32	0.98	1.78	0.00	5.25	0.01	3.52	1.74
SPO0977		ornithine cyclodeaminase/mu-crystallin family protein	1.31	0.01	1.68	0.04	1.50	0.18	-1.05	0.87	1.37	0.05	0.16	1.21	1.53	0.13	1.35	0.08	1.44	0.09
SPO0978		NAD-dependent deacetylase	1.08	0.92	1.63	0.14	1.36	0.28	-1.19	0.76	1.65	0.02	0.23	1.42	1.41	0.03	1.45	0.02	1.43	0.02
SPO0979		low molecular weight phosphotyrosine protein phosphatase (EC:3.1.3.48)	1.07	0.50	1.58	0.05	1.33	0.25	1.80	0.06	-1.12	0.18	0.34	1.46	1.05	0.56	-2.05	0.01	-0.50	1.55
SPO0980		LysR family transcriptional regulator	1.23	0.89	1.05	0.65	1.14	0.09	1.67	0.62	-1.07	0.49	0.30	1.37	1.09	0.30	-1.91	0.05	-0.41	1.50
SPO0981	*hisD*	histidinol dehydrogenase (EC:1.1.1.23)	-1.96	0.72	-1.17	0.91	-1.57	0.40	-2.02	0.76	1.10	0.96	-0.46	1.56	-1.05	0.97	2.51	0.10	0.73	1.78
SPO0982		hypothetical protein	-1.71	0.07	1.07	0.76	-0.32	1.39	-1.26	0.32	2.05	0.01	0.40	1.66	1.37	0.31	1.07	0.74	1.22	0.15
SPO0983	*lepA*	GTP-binding protein LepA	-1.32	0.60	1.51	0.39	0.10	1.42	2.15	0.18	-1.40	0.50	0.38	1.78	-1.15	0.71	-1.96	0.32	-1.56	0.41
SPO0984	*znuB*	zinc ABC transporter permease	-2.81	0.24	1.07	0.60	-0.87	1.94	1.10	0.85	-1.28	0.39	-0.09	1.19	1.31	0.38	1.27	0.48	1.29	0.02
SPO0985	*znuC*	zinc ABC transporter ATP-binding protein	-6.66	0.01	-1.09	0.25	-3.88	2.79	-1.04	0.38	-1.10	0.38	-1.07	0.03	-1.03	0.78	-1.16	0.24	-1.10	0.06
SPO0986	*zur*	zinc uptake regulation protein	-5.15	0.00	-1.33	0.19	-3.24	1.91	-1.20	0.30	1.16	0.46	-0.02	1.18	-1.16	0.15	1.05	0.93	-0.05	1.11
SPO0987	*znuA*	zinc ABC transporter substrate-binding protein	-11.90	0.00	-1.30	0.03	-6.60	5.30	-3.48	0.00	-1.21	0.18	-2.35	1.14	-1.29	0.04	-1.00	0.42	-1.15	0.15
SPO0988		hypothetical protein	-1.27	0.80	-1.03	0.95	-1.15	0.12	-2.47	0.08	1.15	0.84	-0.66	1.81	1.38	0.51	1.50	0.61	1.44	0.06

SPO0989		transcriptional regulator SoxR	-1.73	0.01	-1.07	0.53	-1.40	0.33	1.66	0.03	-1.45	0.06	0.11	1.56	-1.19	0.07	-1.86	0.01	-1.53	0.34
SPO0990	*soxS*	regulatory protein SoxS	-2.14	0.03	-1.43	0.04	-1.79	0.35	-2.58	0.06	1.67	0.02	-0.46	2.13	-0.98	0.76	-1.31	0.67	-1.15	0.16
SPO0991	*soxV*	sulfur oxidation V protein	-1.87	0.23	-1.36	0.33	-1.62	0.25	-3.45	0.02	1.01	0.78	-1.22	2.23	0.99	0.85	2.84	0.02	1.92	0.92
SPO0992	*soxW*	thioredoxin	1.05	0.39	-2.59	0.01	-0.77	1.82	-5.72	0.00	1.27	0.22	-2.23	3.50	-1.59	0.03	-1.29	0.10	-1.44	0.15
SPO0993	*soxX*	monoheme cytochrome c SoxX	-3.25	0.07	-2.33	0.01	-2.79	0.46	-14.50	0.00	1.73	0.04	-6.39	8.12	-1.20	0.03	1.16	0.55	-0.02	1.18
SPO0994	*soxY*	sulfur oxidation protein SoxY	-1.92	0.25	-1.45	0.37	-1.69	0.23	-4.86	0.09	1.96	0.05	-1.45	3.41	1.08	0.85	1.45	0.31	1.27	0.19
SPO0995	*soxZ*	sulfur oxidation Z protein	-2.29	0.01	-2.17	0.03	-2.23	0.06	-8.62	0.00	1.56	0.11	-3.53	5.09	-1.50	0.08	0.95	0.37	-0.28	1.22
SPO0996	*soxA*	diheme cytochrome c SoxA	-2.55	0.00	-1.95	0.02	-2.25	0.30	-6.96	0.00	1.38	0.07	-2.79	4.17	1.04	0.71	1.07	0.54	1.06	0.02
SPO0997	*soxB*	sulfur oxidation B protein	-1.43	0.12	-1.49	0.19	-1.46	0.03	-3.98	0.02	1.39	0.15	-1.30	2.69	-1.54	0.21	-0.93	0.34	-1.24	0.30
SPO0998	*soxC*	sulfur oxidation molybdopterin C protein	-1.31	0.08	-1.33	0.09	-1.32	0.01	-2.89	0.02	1.49	0.07	-0.70	2.19	-0.99	0.73	1.14	0.11	0.08	1.06
SPO0999	*soxD*	diheme cytochrome c SoxD	-1.37	0.52	-1.02	0.96	-1.20	0.18	-1.66	0.12	1.28	0.22	-0.19	1.47	1.24	0.29	-0.97	0.31	0.13	1.11
SPO1000	*soxE*	diheme cytochrome c SoxE	-2.81	0.00	-1.62	0.04	-2.22	0.60	-2.72	0.00	1.41	0.10	-0.66	2.07	-1.03	0.87	-1.43	0.10	-1.23	0.20
SPO1001	*soxF*	sulfur oxidation F protein	-2.10	0.11	-2.12	0.04	-2.11	0.01	-5.90	0.04	1.92	0.04	-1.99	3.91	1.59	0.01	1.19	0.10	1.39	0.20
SPO1002		AraC family transcriptional regulator	-1.05	0.38	1.39	0.22	0.17	1.22	-1.20	0.58	1.24	0.23	0.02	1.22	-1.06	0.91	-1.27	0.61	-1.17	0.11
SPO1003	*clpP*	ATP-dependent Clp protease proteolytic subunit (EC:3.4.21.92)	1.43	0.51	0.98	0.63	1.20	0.23	2.26	0.04	1.21	0.28	1.74	0.53	1.21	0.30	1.42	0.13	1.32	0.11
SPO1004	*clpX*	ATP-dependent protease ATP-binding subunit ClpX	1.01	0.26	1.09	0.70	1.05	0.04	1.39	0.69	1.13	0.84	1.26	0.13	1.43	0.30	1.08	0.88	1.26	0.18
SPO1005		endoribonuclease L-PSP	2.04	0.01	1.14	0.49	1.59	0.45	2.16	0.03	-1.16	0.07	0.50	1.66	1.39	0.07	-1.20	0.11	0.10	1.30
SPO1006		NADH dehydrogenase (EC:1.6.99.3)	2.13	0.01	1.38	0.22	1.76	0.38	1.93	0.01	0.97	0.47	1.45	0.48	1.17	0.54	0.98	0.52	1.07	0.10
SPO1007		hypothetical protein	1.50	0.01	1.67	0.23	1.59	0.09	1.50	0.05	1.17	0.45	1.34	0.17	1.38	0.03	0.97	0.42	1.18	0.20
SPO1008		hypothetical protein	1.69	0.44	2.34	0.12	2.02	0.33	2.09	0.30	1.05	0.99	1.57	0.52	2.04	0.07	1.22	0.36	1.63	0.41
SPO1009	*aat*	leucyl/phenylalanyl-tRNA--protein transferase (EC:2.3.2.6)	-1.03	0.98	-1.08	0.62	-1.06	0.03	2.94	0.04	-1.08	0.10	0.93	2.01	-1.29	0.14	-1.86	0.03	-1.58	0.28
SPO1010	*accC*	acetyl-CoA carboxylase biotin carboxylase subunit (EC:6.4.1.2)	-1.14	0.01	-1.07	0.17	-1.11	0.03	2.38	0.08	-1.21	0.05	0.59	1.80	-1.23	0.04	-1.76	0.03	-1.50	0.27
SPO1011	*accB*	acetyl-CoA carboxylase, biotin carboxyl carrier protein (EC:6.4.1.2)	-1.36	0.06	-1.37	0.18	-1.37	0.01	1.51	0.04	-1.08	0.34	0.22	1.30	-1.26	0.17	0.92	0.26	-0.17	1.09
SPO1012		LuxR family transcriptional regulator	-1.77	0.50	-1.38	0.30	-1.58	0.20	-1.48	0.65	1.53	0.11	0.03	1.51	1.15	0.69	1.07	0.86	1.11	0.04
SPO1013		acetyl-CoA acetyltransferase (EC:2.3.1.9)	1.01	0.03	1.55	0.17	1.28	0.27	0.94	0.07	5.36	0.00	3.15	2.21	2.48	0.02	5.87	0.02	4.18	1.70
SPO1014		AMP-binding protein	0.94	0.01	2.42	0.00	1.68	0.74	-1.83	0.02	8.44	0.00	3.31	5.14	3.44	0.01	6.04	0.00	4.74	1.30
SPO1015		3-hydroxybutyrate dehydrogenase	-1.73	0.02	1.63	0.12	-0.05	1.68	-1.46	0.01	5.75	0.00	2.15	3.61	1.97	0.01	4.78	0.00	3.38	1.41
SPO1016		hypothetical protein	-1.41	0.06	1.14	0.11	-0.14	1.28	-1.49	0.18	1.62	0.07	0.07	1.56	1.05	0.84	-1.31	0.44	-0.13	1.18
SPO1017		branched-chain amino acid ABC transporter ATP-binding protein	6.01	0.00	-1.01	0.86	2.50	3.51	-1.47	0.00	26.40	0.00	12.47	13.94	2.06	0.01	1.54	0.12	1.80	0.26
SPO1018		branched-chain amino acid ABC transporter ATP-binding protein	9.26	0.00	-1.50	0.59	3.88	5.38	-1.77	0.31	21.80	0.01	10.02	11.79	1.98	0.06	2.66	0.10	2.32	0.34
SPO1019		branched-chain amino acid ABC transporter permease	8.42	0.00	-2.77	X	2.83	5.60	-1.74	0.12	47.90	0.01	23.08	24.82	2.27	0.16	X	X	N/A	N/A
SPO1020		branched-chain amino acid ABC transporter permease	7.83	0.02	-1.87	0.05	2.98	4.85	-2.25	0.17	42.40	0.00	20.08	22.33	2.42	0.01	2.58	0.04	2.50	0.08
SPO1021		branched-chain amino acid ABC transporter substrate-binding protein	4.59	0.12	-2.82	0.09	0.89	3.71	-8.57	0.03	57.80	0.00	24.62	33.19	2.49	0.01	3.57	0.00	3.03	0.54
SPO1022		transcriptional regulator	5.16	0.02	-1.07	0.66	2.05	3.12	2.96	0.06	5.91	0.00	4.44	1.48	1.40	0.17	-1.53	0.06	-0.07	1.47
SPO1023		response regulator	-1.11	0.71	-1.28	0.53	-1.20	0.09	-1.70	0.32	2.17	0.15	0.24	1.94	1.62	0.04	1.65	0.42	1.64	0.01

SPO1024	hypothetical protein	-1.55	0.01	-1.30	0.19	-1.43	0.13	-2.54	0.01	2.47	0.01	-0.03	2.51	1.73	0.02	1.54	0.10	1.64	0.10
SPO1025	sensor histidine kinase (EC:2.7.3.-)	X	X	1.07	0.29	N/A	N/A	-1.35	0.97	X	X	N/A	N/A	1.29	X	X	X	N/A	N/A
SPO1026	hypothetical protein	-1.02	0.87	-1.11	0.52	-1.07	0.05	-1.77	0.41	1.35	0.58	-0.21	1.56	-1.03	0.98	1.61	0.33	0.29	1.32
SPO1027	hypothetical protein	-1.16	0.16	1.12	0.40	-0.02	1.14	0.92	0.28	-1.28	0.32	-0.18	1.10	1.00	0.74	0.95	0.72	0.98	0.02
SPO1028	hypothetical protein	0.92	0.93	-1.35	0.62	-0.21	1.14	0.91	0.93	1.00	0.89	0.96	0.04	1.70	0.31	2.38	0.14	2.04	0.34
SPO1029	hypothetical protein	-1.18	0.31	-1.54	0.03	-1.36	0.18	-1.37	0.30	-1.40	0.02	-1.39	0.01	1.15	0.06	1.24	0.05	1.20	0.05
SPO1030	metallo-beta-lactamase	-1.30	0.56	-1.98	0.01	-1.64	0.34	-1.87	0.04	-1.15	0.22	-1.51	0.36	-1.17	0.15	1.49	0.26	0.16	1.33
SPO1031	hypothetical protein	-1.51	0.15	1.14	0.58	-0.19	1.33	2.73	0.11	1.05	0.87	1.89	0.84	1.35	0.14	1.33	0.13	1.34	0.01
SPO1032	hypothetical protein	-2.13	0.02	1.45	0.05	-0.34	1.79	1.19	0.35	-1.58	0.00	-0.20	1.39	-1.02	0.69	-1.40	0.15	-1.21	0.19
SPO1033	hypothetical protein	1.58	0.57	1.32	0.46	1.45	0.13	4.06	0.10	-1.32	0.22	1.37	2.69	1.05	0.93	-1.50	0.16	-0.23	1.28
SPO1034	hypothetical protein	1.04	0.68	1.17	0.47	1.11	0.06	1.13	0.61	1.01	0.80	1.07	0.06	1.17	0.18	0.97	0.65	1.07	0.10
SPO1036	phage integrase site specific recombinase	-1.29	0.81	-1.31	0.61	-1.30	0.01	-2.26	0.54	1.15	0.64	-0.56	1.71	-1.13	0.67	1.03	0.97	-0.05	1.08
SPO1037	hypothetical protein	1.38	0.19	1.18	0.15	1.28	0.10	-1.73	0.11	1.27	0.26	-0.23	1.50	1.22	0.25	-1.08	0.64	0.07	1.15
SPO1038	hypothetical protein	X	X	-1.29	0.57	N/A	N/A	-1.17	0.70	-1.09	X	-1.13	0.04	-1.04	0.94	X	X	N/A	N/A
SPO1039	hypothetical protein	-2.86	X	-1.29	0.65	-2.08	0.78	-1.55	0.83	-1.49	X	-1.52	0.03	-1.04	1.00	1.06	X	0.01	1.05
SPO1040	hypothetical protein	-2.71	0.00	-1.43	0.36	-2.07	0.64	-3.73	0.01	-1.32	0.69	-2.53	1.21	-1.34	0.26	1.26	0.74	-0.04	1.30
SPO1041	hypothetical protein	-2.22	0.13	-1.81	0.43	-2.02	0.20	-2.27	0.17	1.04	0.96	-0.62	1.66	-1.45	0.64	1.57	0.72	0.06	1.51
SPO1042	hypothetical protein	-2.33	0.01	-1.79	0.13	-2.06	0.27	-1.99	0.07	1.48	0.01	-0.26	1.74	-1.47	0.01	-1.40	0.26	-1.44	0.04
SPO1043	hypothetical protein	X	X	-1.25	0.60	N/A	N/A	-1.81	0.26	X	X	N/A	N/A	-1.02	0.89	X	X	N/A	N/A
SPO1044	hypothetical protein	-1.68	0.29	-1.18	0.67	-1.43	0.25	-2.23	0.18	1.07	0.86	-0.58	1.65	-1.05	0.94	-1.01	0.86	-1.03	0.02
SPO1045	hypothetical protein	0.91	0.84	-1.16	0.23	-0.12	1.04	-1.81	0.34	1.18	0.77	-0.32	1.50	1.32	0.15	1.10	0.86	1.21	0.11
SPO1046	hypothetical protein	0.96	0.36	-1.18	0.73	-0.11	1.07	-2.40	0.11	1.43	0.45	-0.49	1.92	-1.07	0.71	0.96	0.77	-0.06	1.02
SPO1047	RNA-dependent DNA polymerase	1.08	0.86	-1.21	0.26	-0.06	1.15	-1.55	0.27	1.61	0.14	0.03	1.58	1.07	0.69	1.09	0.52	1.08	0.01
SPO1048	hypothetical protein	-1.30	0.55	-1.05	0.96	-1.18	0.13	-1.33	0.04	1.65	0.04	0.16	1.49	1.04	0.95	1.21	0.44	1.13	0.09
SPO1049	C-5 cytosine-specific family DNA methylase	-1.66	0.01	-1.30	0.05	-1.48	0.18	-1.85	0.03	1.07	0.86	-0.39	1.46	-1.29	0.14	-1.08	0.41	-1.19	0.11
SPO1050	phage integrase site specific recombinase	X	X	-1.07	0.81	N/A	N/A	X	X	-1.24	X	N/A	N/A	-1.11	0.60	X	X	N/A	N/A
SPO1051	hypothetical protein	-1.98	0.79	-1.17	0.83	-1.58	0.41	-2.48	0.74	-1.04	0.98	-1.76	0.72	1.32	0.38	1.27	0.63	1.30	0.03
SPO1052	hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	1.31	X	X	X	N/A	N/A
SPO1053	hypothetical protein	1.19	0.14	1.12	0.41	1.16	0.03	2.10	0.06	-1.00	0.97	0.55	1.55	-1.60	0.05	-1.94	0.05	-1.77	0.17
SPO1054	hypothetical protein	X	X	X	X	N/A	N/A	-1.10	0.70	X	X	N/A	N/A	-1.35	0.18	X	X	N/A	N/A
SPO1055	hypothetical protein	X	X	X	X	N/A	N/A	-1.02	0.09	X	X	N/A	N/A	-1.03	0.84	X	X	N/A	N/A
SPO1056	hypothetical protein	1.09	0.65	-1.50	0.44	-0.21	1.30	1.20	0.34	1.09	0.83	1.15	0.05	-1.39	0.11	2.05	0.32	0.33	1.72
SPO1057	AraC family transcriptional regulator	-1.49	0.01	-1.20	0.50	-1.35	0.15	-1.68	0.18	1.09	0.61	-0.30	1.39	-1.03	0.76	1.27	0.53	0.12	1.15
SPO1058	acyltransferase	1.41	0.02	-1.06	0.37	0.18	1.24	3.58	0.00	-1.47	0.03	1.06	2.53	-1.11	0.22	-1.63	0.30	-1.37	0.26
SPO1059	serine/threonine protein kinase (EC:2.7.1.-)	-1.73	0.03	-1.19	0.43	-1.46	0.27	-1.91	0.04	-7.34	0.02	-4.63	2.72	-1.63	0.01	-2.12	0.05	-1.88	0.25
SPO1060	hypothetical protein	-0.99	0.98	-1.28	0.05	-1.14	0.14	1.12	0.29	-13.80	0.00	-6.34	7.46	-2.30	0.00	-3.63	0.02	-2.97	0.67
SPO1061	LysM domain-containing protein	1.02	0.86	-1.55	0.07	-0.27	1.29	1.07	0.96	-11.10	0.00	-5.02	6.09	-2.43	0.02	-3.17	0.02	-2.80	0.37
SPO1062	LysM domain-containing protein	-1.15	0.18	-1.75	0.02	-1.45	0.30	1.32	0.35	-11.30	0.00	-4.99	6.31	-1.60	0.16	-1.85	0.09	-1.73	0.13
SPO1063	hypothetical protein	-1.11	0.33	-1.66	0.05	-1.39	0.28	1.21	0.38	-9.18	0.00	-3.99	5.20	-1.77	0.10	-2.59	0.02	-2.18	0.41

SPO1064		serine/threonine protein phosphatase	-1.16	0.81	-1.87	0.09	-1.52	0.36	1.26	0.59	-10.40	0.02	-4.57	5.83	-2.63	0.02	-3.95	0.03	-3.29	0.66
SPO1065		hypothetical protein	-1.39	0.03	-1.21	0.08	-1.30	0.09	-0.98	0.17	-4.20	0.00	-2.59	1.61	-1.25	0.06	-1.64	0.04	-1.45	0.20
SPO1066		hypothetical protein	X	X	1.62	0.01	N/A	N/A	3.48	0.01	-2.07	0.03	0.71	2.78	-1.23	0.12	-2.73	0.01	-1.98	0.75
SPO1067		hypothetical protein	1.27	0.80	1.23	0.65	1.25	0.02	1.74	0.30	-1.06	0.58	0.34	1.40	-1.23	0.18	-1.13	0.50	-1.18	0.05
SPO1068		hypothetical protein	-1.13	0.60	1.04	0.97	-0.04	1.09	-1.05	0.92	-8.24	0.03	-4.65	3.60	-2.39	0.06	-4.30	0.08	-3.35	0.96
SPO1069		hypothetical protein	-1.20	0.73	-1.38	0.21	-1.29	0.09	-1.28	0.66	-4.94	0.02	-3.11	1.83	-2.05	0.05	-1.75	0.15	-1.90	0.15
SPO1070		FAD-binding dehydrogenase	-1.16	0.24	-1.73	0.05	-1.45	0.29	-3.16	0.01	1.79	0.07	-0.69	2.48	1.24	0.20	2.20	0.03	1.72	0.48
SPO1071		glutamine amidotransferase (EC:6.3.5.2)	X	X	1.13	0.56	N/A	N/A	2.90	0.00	-1.50	0.03	0.70	2.20	-1.14	0.44	-1.89	0.10	-1.52	0.38
SPO1072		hypothetical protein	1.13	0.96	1.06	0.89	1.10	0.03	1.98	0.36	-1.18	0.10	0.40	1.58	-1.30	0.02	-1.91	0.00	-1.61	0.31
SPO1073		hypothetical protein	-3.40	0.00	-1.53	0.13	-2.47	0.94	-15.10	0.00	-1.33	0.17	-8.22	6.89	1.40	0.19	1.66	0.02	1.53	0.13
SPO1074		hypothetical protein	-1.14	0.78	-1.09	0.83	-1.12	0.02	1.05	0.95	-1.24	0.54	-0.10	1.15	1.39	0.32	1.44	0.13	1.42	0.03
SPO1075		hypothetical protein	-1.09	X	1.06	0.93	-0.02	1.08	-2.01	X	1.03	X	-0.49	1.52	-1.09	0.90	1.35	X	0.13	1.22
SPO1076		TrkA domain-containing protein	-1.46	0.09	1.06	0.84	-0.20	1.26	1.18	0.63	1.03	0.96	1.11	0.08	1.29	0.43	1.19	0.53	1.24	0.05
SPO1077		nitroreductase	-0.97	0.88	-1.14	0.77	-1.05	0.09	1.47	0.31	1.13	0.74	1.30	0.17	-1.18	0.54	-1.24	0.66	-1.21	0.03
SPO1078		chromosome replication initiation inhibitor protein	-1.06	0.87	-1.16	0.69	-1.11	0.05	-1.20	0.95	-1.36	0.41	-1.28	0.08	-1.36	0.24	-1.29	0.57	-1.33	0.04
SPO1079		L-lysine exporter	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.48	X	X	X	N/A	N/A
SPO1080		hypothetical protein	1.15	1.00	-1.18	0.77	-0.02	1.17	1.17	0.98	-1.25	0.64	-0.04	1.21	-1.12	0.83	1.54	0.59	0.21	1.33
SPO1081		hypothetical protein	1.38	0.04	1.13	0.16	1.26	0.13	2.46	0.08	-1.07	0.55	0.70	1.77	1.18	0.28	-1.20	0.79	-0.01	1.19
SPO1082	*betI*	transcriptional regulator BetI	-1.23	0.01	-1.19	0.10	-1.21	0.02	1.12	0.19	-1.38	0.07	-0.13	1.25	-1.16	0.28	-1.72	0.01	-1.44	0.28
SPO1083	*betC-1*	choline sulfatase (EC:3.1.6.6)	1.20	0.55	-1.16	0.54	0.02	1.18	1.34	0.13	-1.33	0.12	0.01	1.34	-1.13	0.31	-1.50	0.20	-1.32	0.19
SPO1084		hypothetical protein	-1.26	0.09	1.18	0.57	-0.04	1.22	-1.46	0.33	1.18	0.78	-0.14	1.32	-1.02	0.93	X	X	N/A	N/A
SPO1085		hypothetical protein	1.54	0.77	1.26	0.44	1.40	0.14	0.92	0.26	-1.07	0.40	-0.07	1.00	1.23	0.07	-1.01	0.75	0.11	1.12
SPO1086		TetR family transcriptional regulator	-1.23	0.17	-1.07	0.67	-1.15	0.08	1.74	0.01	1.15	0.15	1.45	0.30	1.03	0.85	-1.14	0.03	-0.05	1.09
SPO1087		hypothetical protein	-1.42	0.32	-1.40	0.37	-1.41	0.01	-1.91	0.43	-1.16	0.67	-1.54	0.38	-1.54	0.28	-1.07	0.96	-1.31	0.23
SPO1088	*betA*	choline dehydrogenase (EC:1.1.99.1)	1.16	X	-1.34	0.56	-0.09	1.25	1.44	0.43	-1.14	0.80	0.15	1.29	-1.34	0.40	1.47	0.39	0.06	1.41
SPO1089		hypothetical protein	-1.32	0.01	1.26	0.54	-0.03	1.29	5.28	0.00	-1.22	0.58	2.03	3.25	1.43	0.15	1.18	0.65	1.31	0.13
SPO1090		DNA-binding protein	1.23	0.84	-1.50	0.33	-0.14	1.37	-1.43	0.88	-1.33	0.34	-1.38	0.05	-1.04	0.72	-1.05	0.98	-1.05	0.01
SPO1091		hypothetical protein	1.90	0.32	-1.18	0.74	0.36	1.54	-1.55	0.78	X	X	N/A	N/A	1.12	0.12	X	X	N/A	N/A
SPO1092		LysR family transcriptional regulator	-1.65	0.83	-1.20	0.86	-1.43	0.23	-1.79	0.76	-1.44	0.68	-1.62	0.17	1.17	0.88	1.21	0.84	1.19	0.02
SPO1093		Bcr/CflA subfamily drug resistance transporter	-1.33	0.31	-1.43	0.02	-1.38	0.05	1.10	0.23	-1.50	0.04	-0.20	1.30	1.38	0.01	1.41	0.04	1.40	0.02
SPO1094	*pccB*	propionyl-CoA carboxylase subunit beta (EC:6.4.1.3)	10.00	0.00	4.44	0.00	7.22	2.78	4.44	0.00	25.00	0.00	14.72	10.28	1.07	0.43	1.95	0.02	1.51	0.44
SPO1095		hypothetical protein	6.27	0.00	4.49	0.00	5.38	0.89	6.51	0.01	24.10	0.00	15.31	8.80	1.74	0.01	1.74	0.01	1.74	0.00
SPO1096		lipoprotein	0.97	0.07	1.06	0.78	1.02	0.04	1.15	0.05	1.43	0.01	1.29	0.14	1.18	0.12	-2.00	0.00	-0.41	1.59
SPO1097		hypothetical protein	3.41	0.61	1.67	0.20	2.54	0.87	3.09	0.45	6.60	0.01	4.85	1.76	1.26	0.51	1.17	0.91	1.22	0.05
SPO1098		hypothetical protein	-2.80	0.50	-1.48	0.64	-2.14	0.66	-2.65	0.61	-1.20	0.78	-1.93	0.73	-1.01	0.99	1.59	0.41	0.29	1.30
SPO1099		hypothetical protein	4.50	0.01	1.51	0.10	3.01	1.50	5.31	0.01	11.80	0.00	8.56	3.25	1.06	0.18	-1.31	0.38	-0.13	1.19
SPO1100		lipoprotein	-1.18	0.03	-1.85	0.04	-1.52	0.33	2.86	0.01	0.95	0.33	1.90	0.96	1.54	0.06	1.32	0.35	1.43	0.11
SPO1101	*pccA*	propionyl-CoA carboxylase subunit alpha (EC:6.4.1.3)	6.30	0.07	1.90	0.07	4.10	2.20	5.43	0.07	8.86	0.01	7.15	1.72	1.16	0.29	1.11	0.46	1.14	0.02

SPO1102		lipoprotein	3.83	0.36	1.89	0.05	2.86	0.97	3.95	0.31	7.62	0.01	5.79	1.84	1.23	0.19	1.13	0.51	1.18	0.05
SPO1103		hypothetical protein	0.96	0.47	-1.94	0.06	-0.49	1.45	-1.23	0.02	1.16	0.10	-0.04	1.20	1.14	0.13	1.52	0.02	1.33	0.19
SPO1104		hypothetical protein	5.51	0.01	1.78	0.03	3.65	1.87	3.03	0.02	13.60	0.00	8.32	5.29	-2.03	0.01	-1.34	0.06	-1.69	0.34
SPO1105		methylmalonyl-CoA mutase (EC:5.4.99.2)	5.91	0.00	2.65	0.00	4.28	1.63	4.04	0.00	15.20	0.00	9.62	5.58	1.39	0.06	1.46	0.04	1.43	0.04
SPO1106		hypothetical protein	-1.18	0.75	1.14	0.32	-0.02	1.16	-1.04	0.55	4.50	0.09	1.73	2.77	-0.97	0.71	1.20	0.06	0.12	1.08
SPO1107		phosphinothricin N-acetyltransferase	-1.44	0.22	-1.39	0.20	-1.42	0.03	-2.16	0.18	1.23	0.49	-0.47	1.70	1.20	0.63	1.50	0.41	1.35	0.15
SPO1108		DnaJ-like protein DjlA	1.45	0.03	1.34	0.27	1.40	0.05	2.07	0.04	1.23	0.26	1.65	0.42	1.08	0.67	1.19	0.19	1.14	0.05
SPO1109		hypothetical protein	1.15	0.09	1.99	0.02	1.57	0.42	2.14	0.02	1.29	0.17	1.72	0.43	1.33	0.11	-1.33	0.58	0.00	1.33
SPO1110		LysR family transcriptional regulator	1.35	0.69	-1.05	0.95	0.15	1.20	1.39	0.57	1.29	0.35	1.34	0.05	1.07	0.35	-1.02	0.83	0.03	1.05
SPO1111		hypothetical protein	X	X	1.69	0.00	N/A	N/A	-0.92	0.16	1.30	0.40	0.19	1.11	1.25	0.19	-1.24	X	0.01	1.25
SPO1112		TRAP transporter, periplasmic protein	-1.03	0.88	1.67	0.01	0.32	1.35	1.39	0.00	2.04	0.04	1.72	0.33	1.20	0.15	1.70	0.04	1.45	0.25
SPO1113		TRAP transporter, transmembrane protein	1.09	0.17	1.63	0.09	1.36	0.27	-1.12	0.59	1.67	0.07	0.28	1.40	1.50	0.02	1.30	0.05	1.40	0.10
SPO1114		TRAP dicarboxylate transporter subunit DctM	-2.64	0.07	1.44	0.47	-0.60	2.04	-1.26	0.98	1.34	0.51	0.04	1.30	1.49	0.36	1.24	0.72	1.37	0.13
SPO1115		hypothetical protein	-1.45	0.06	1.37	0.09	-0.04	1.41	-1.80	0.13	1.60	0.05	-0.10	1.70	-0.98	0.66	1.32	X	0.17	1.15
SPO1116		hypothetical protein	-1.57	0.51	-1.97	0.34	-1.77	0.20	-1.81	0.44	1.45	0.58	-0.18	1.63	1.66	0.40	1.67	0.41	1.67	0.01
SPO1117		Ppx/GppA phosphatase	2.86	0.05	1.61	0.03	2.24	0.63	1.55	0.11	1.66	0.02	1.61	0.05	-1.12	0.34	0.98	0.43	-0.07	1.05
SPO1118		hypothetical protein	1.61	0.03	1.07	0.57	1.34	0.27	2.39	0.01	-1.55	0.06	0.42	1.97	-1.39	0.21	-1.83	0.01	-1.61	0.22
SPO1119		hypothetical protein	0.99	0.33	1.06	0.16	1.03	0.03	1.00	0.96	-1.02	0.57	-0.01	1.01	-1.11	0.06	-1.37	0.02	-1.24	0.13
SPO1120		hypothetical protein	1.07	0.98	-1.08	0.79	-0.01	1.08	1.36	0.77	-0.99	0.87	0.18	1.18	-1.13	0.18	-1.35	0.18	-1.24	0.11
SPO1121	*proS*	prolyl-tRNA synthetase (EC:6.1.1.15)	1.76	0.54	1.13	0.48	1.45	0.32	3.36	0.24	-1.05	0.20	1.16	2.21	-1.14	0.25	-1.29	0.13	-1.22	0.08
SPO1122		hypothetical protein	1.61	0.00	1.44	0.03	1.53	0.09	-1.31	0.07	1.10	0.77	-0.11	1.21	-1.53	0.00	-1.24	0.17	-1.39	0.14
SPO1123	*lolE*	lipoprotein releasing system transmembrane protein LolE	-1.55	0.01	-1.03	0.90	-1.29	0.26	2.97	0.01	-1.51	0.01	0.73	2.24	-1.06	0.39	-1.69	0.01	-1.38	0.32
SPO1124	*lolD*	lipoprotein releasing system ATP-binding protein	-1.27	0.03	-1.07	0.46	-1.17	0.10	3.41	0.00	-1.60	0.05	0.91	2.51	1.27	0.02	-1.48	0.01	-0.11	1.38
SPO1125		hypothetical protein	-1.55	X	1.07	0.74	-0.24	1.31	1.72	0.04	-1.59	0.23	0.06	1.66	1.33	0.29	-1.30	0.56	0.02	1.32
SPO1126		cytochrome c family protein	1.53	0.05	1.12	0.33	1.33	0.20	2.33	0.01	-1.00	0.76	0.67	1.66	-1.03	0.97	-1.48	0.23	-1.26	0.23
SPO1127		cytochrome c family protein	-1.39	0.78	1.35	0.34	-0.02	1.37	-2.85	0.32	1.36	0.53	-0.75	2.11	2.02	0.17	1.65	0.14	1.84	0.18
SPO1128		hypothetical protein	1.67	0.02	1.04	0.72	1.36	0.32	1.17	0.21	1.58	0.12	1.38	0.21	-1.04	0.72	1.09	0.04	0.03	1.07
SPO1129		hypothetical protein	1.40	0.87	1.08	0.90	1.24	0.16	1.13	0.95	1.40	0.45	1.27	0.14	1.15	0.87	1.16	0.62	1.16	0.01
SPO1130		thioesterase	-1.76	0.35	-1.10	0.72	-1.43	0.33	-1.21	0.84	1.25	0.60	0.02	1.23	-1.15	0.55	-0.99	0.96	-1.07	0.08
SPO1131		glycine betaine/proline ABC transporter substrate-binding protein	-1.22	0.06	-1.81	0.00	-1.52	0.29	-1.69	0.00	1.30	0.05	-0.20	1.50	1.79	0.07	2.04	0.08	1.92	0.13
SPO1132		glycine betaine/proline ABC transporter ATP-binding protein (EC:3.6.3.32)	-1.71	0.00	-1.72	0.06	-1.72	0.01	-1.44	0.07	-1.06	0.63	-1.25	0.19	1.23	0.08	1.31	0.10	1.27	0.04
SPO1133		glycine betaine/proline ABC transporter permease	-1.52	0.02	-1.31	0.19	-1.42	0.11	1.08	0.03	1.10	0.32	1.09	0.01	1.83	0.00	-0.98	0.60	0.43	1.40
SPO1134		NnrU family protein	-1.08	0.85	1.01	0.91	-0.04	1.05	1.53	0.27	1.31	0.26	1.42	0.11	1.16	0.31	1.10	0.46	1.13	0.03
SPO1135		hypothetical protein	-1.19	0.58	1.16	0.24	-0.02	1.18	1.21	0.12	-1.30	0.25	-0.05	1.26	1.37	0.09	-1.08	0.81	0.15	1.23
SPO1136	*doeD*	diaminobutyric acid transaminase	-1.16	0.08	1.35	0.42	0.10	1.26	-1.19	0.67	-1.05	0.76	-1.12	0.07	-1.07	0.49	-0.94	0.25	-1.01	0.06
SPO1137	*doeC*	aspartate-semialdehyde dehydrogenase (EC:1.2.1.16)	-1.38	0.35	1.18	0.59	-0.10	1.28	-2.12	0.31	-0.99	0.78	-1.55	0.57	1.07	0.63	1.35	X	1.21	0.14
SPO1138	*doeX*	transcriptional regulator	2.68	X	1.30	0.25	1.99	0.69	1.62	0.05	1.49	0.12	1.56	0.07	1.15	0.37	1.11	X	1.13	0.02
SPO1139	*doeB*	Na-acetyl-L-2,4-diaminobutyric acid deacetylase	-1.47	0.01	1.30	0.04	-0.09	1.39	-2.71	0.00	-1.01	0.91	-1.86	0.85	1.27	0.33	1.06	0.82	1.17	0.11

SPO1140	*doeA*	ectoine hydrolase	2.37	0.25	1.36	0.44	1.87	0.50	-1.15	0.91	1.26	0.62	0.06	1.21	-1.20	0.67	-0.99	0.95	-1.10	0.10
SPO1141		ectoine utilization protein EutC (EC:4.3.1.12)	-1.52	0.28	-1.25	0.09	-1.39	0.14	-3.03	0.01	-1.12	0.26	-2.08	0.95	-1.13	0.22	2.14	0.00	0.51	1.64
SPO1142		threonine dehydratase (EC:4.3.1.19)	1.50	0.04	1.10	0.03	1.30	0.20	-1.26	0.09	-1.15	0.12	-1.21	0.06	-1.01	0.99	1.13	0.31	0.06	1.07
SPO1143		ectoine utilization protein EutA	1.08	0.80	-1.00	0.88	0.04	1.04	-1.55	0.21	-1.24	0.25	-1.40	0.16	-1.40	0.02	-1.39	X	-1.40	0.01
SPO1144		universal stress protein family protein	-1.33	0.07	-1.21	0.28	-1.27	0.06	-2.61	0.04	-0.99	0.81	-1.80	0.81	-1.70	0.03	-1.34	0.39	-1.52	0.18
SPO1145	*uehC*	TRAP transporter periplasmic binding protein	X	X	-1.38	0.76	N/A	N/A	-1.38	0.96	-1.25	0.85	-1.32	0.06	-1.27	0.68	1.01	X	-0.13	1.14
SPO1146	*uehB*	TRAP transporter small integral membrane protein	1.99	0.03	-1.32	0.59	0.34	1.66	-1.35	0.05	-1.18	X	-1.27	0.09	-1.06	0.95	-1.27	X	-1.17	0.11
SPO1147	*uehA*	TRAP transporter large integral membrane protein	1.12	0.92	-1.22	0.87	-0.05	1.17	-2.11	0.50	-1.04	0.96	-1.58	0.54	-1.40	0.65	-1.05	1.00	-1.23	0.17
SPO1148	*gntR*	family transcriptional regulator	-1.60	0.16	-1.30	0.42	-1.45	0.15	-2.08	0.27	1.16	0.76	-0.46	1.62	-1.46	0.28	-1.14	0.80	-1.30	0.16
SPO1150		RNA methyltransferase	-1.32	0.41	1.13	0.62	-0.10	1.23	2.00	0.11	1.11	0.74	1.56	0.44	-1.16	0.39	-1.10	0.67	-1.13	0.03
SPO1151		hypothetical protein	-0.98	0.67	1.03	0.81	0.03	1.00	2.51	0.02	-1.16	0.31	0.68	1.84	1.43	0.06	1.14	0.46	1.29	0.15
SPO1152		twin-arginine translocation pathway signal sequence domain-containing protein	1.04	0.99	1.60	0.04	1.32	0.28	1.54	0.08	1.17	0.30	1.36	0.19	-1.07	0.39	-1.76	0.02	-1.42	0.35
SPO1153		CoA-binding domain-containing protein	-1.04	0.97	-1.04	0.73	-1.04	0.00	1.17	0.73	1.02	0.96	1.10	0.08	-1.00	0.97	-1.05	0.84	-1.03	0.03
SPO1154		lipoprotein	1.24	0.30	-1.11	0.36	0.06	1.18	1.94	0.03	0.99	0.45	1.47	0.47	-1.06	0.48	-1.12	0.14	-1.09	0.03
SPO1155	*hisE*	pyrophosphatase (EC:3.6.1.31)	1.86	0.09	1.63	0.10	1.75	0.12	4.10	0.00	-1.22	0.11	1.44	2.66	1.09	0.49	-1.65	0.10	-0.28	1.37
SPO1156	*hisF*	glycerol phosphate synthase subunit HisF	1.27	0.30	1.15	0.53	1.21	0.06	3.36	0.01	-1.04	0.39	1.16	2.20	-1.24	0.05	1.29	0.55	0.03	1.27
SPO1157		hypothetical protein	-1.24	0.01	2.43	0.10	0.60	1.84	-2.07	0.00	2.07	0.07	0.00	2.07	1.55	0.02	1.58	0.18	1.57	0.02
SPO1158	*hisA*	imidazole-4-carboxamide isomerase (EC:5.3.1.16)	2.14	0.35	2.22	0.17	2.18	0.04	3.87	0.31	1.05	0.98	2.46	1.41	-1.03	0.90	-1.22	0.50	-1.13	0.10
SPO1159		hypothetical protein	1.29	0.41	-2.04	0.04	-0.38	1.67	-2.57	0.03	1.08	0.83	-0.75	1.83	2.07	0.01	3.09	0.00	2.58	0.51
SPO1160		hypothetical protein	1.44	0.07	1.41	0.02	1.43	0.02	2.04	0.02	1.83	0.05	1.94	0.11	1.27	0.28	-1.05	0.58	0.11	1.16
SPO1161		AraC family transcriptional regulator	-1.39	0.06	-1.12	0.44	-1.26	0.14	-1.18	0.08	1.34	0.03	0.08	1.26	1.45	0.16	1.31	0.11	1.38	0.07
SPO1162	*hisH*	glycerol phosphate synthase subunit HisH (EC:2.4.2.-)	1.26	0.20	1.28	0.03	1.27	0.01	3.70	0.02	-1.42	0.03	1.14	2.56	-1.14	0.21	-1.94	0.00	-1.54	0.40
SPO1163	*hisB*	dehydratase (EC:4.2.1.19)	1.07	0.89	1.11	0.70	1.09	0.02	2.05	0.19	-1.28	0.26	0.39	1.67	-1.80	0.00	-2.00	0.06	-1.90	0.10
SPO1164		hypothetical protein	1.76	0.37	1.24	0.07	1.50	0.26	1.57	0.09	1.09	0.43	1.33	0.24	-1.22	0.06	-1.16	0.29	-1.19	0.03
SPO1165		hypothetical protein	-1.87	0.14	-1.12	0.67	-1.50	0.38	-6.31	0.02	-1.09	0.74	-3.70	2.61	-1.21	0.15	1.57	0.11	0.18	1.39
SPO1166		aminotransferase	1.64	0.01	1.65	0.12	1.65	0.01	1.56	0.14	-1.62	0.04	-0.03	1.59	1.15	0.54	1.05	0.92	1.10	0.05
SPO1168		hypothetical protein	-1.22	0.03	1.30	0.05	0.04	1.26	-1.54	0.13	1.41	0.07	-0.07	1.48	1.28	0.11	1.27	0.13	1.28	0.01
SPO1171	*pyc*	carboxylase (EC:6.4.1.1)	-1.16	0.30	1.22	0.49	0.03	1.19	0.79	0.02	1.23	0.30	1.01	0.22	1.25	0.28	1.27	0.03	1.26	0.01
SPO1172		FMN-dependent alpha-hydroxy acid dehydrogenase	1.12	0.35	-1.18	0.30	-0.03	1.15	4.73	0.00	1.22	0.26	2.98	1.76	0.97	0.28	-1.13	0.08	-0.08	1.05
SPO1173		diguanylate cyclase	-2.30	X	-1.73	X	-2.02	0.29	-3.48	X	-1.13	X	-2.31	1.18	1.02	X	1.70	X	1.36	0.34
SPO1174		DNA helicase II	-1.51	0.23	-1.19	0.27	-1.35	0.16	1.03	0.92	-1.18	0.12	-0.08	1.11	1.07	0.57	1.46	0.03	1.27	0.19
SPO1175		hypothetical protein	X	X	1.34	0.06	N/A	N/A	1.95	0.04	1.33	0.27	1.64	0.31	1.12	0.29	X	X	N/A	N/A
SPO1176		Ser/Thr protein phosphatase	2.48	0.01	1.64	0.07	2.06	0.42	-1.21	0.35	1.07	0.65	-0.07	1.14	-1.47	0.04	-1.59	0.07	-1.53	0.06
SPO1177		hypothetical protein	10.60	0.04	4.53	0.03	7.57	3.04	35.90	0.01	3.13	0.03	19.52	16.39	-1.02	0.98	1.12	0.95	0.05	1.07
SPO1178		cell division protein MraZ	0.99	0.86	-1.85	0.09	-0.43	1.42	1.56	0.72	1.05	0.91	1.31	0.25	1.14	0.78	1.29	0.42	1.22	0.08
SPO1179	*mraW*	MraW (EC:2.1.1.-)	-1.26	0.37	-1.40	0.23	-1.33	0.07	1.33	0.37	1.06	0.94	1.20	0.14	1.08	0.80	-1.31	0.23	-0.12	1.20
SPO1180		hypothetical protein	-1.16	0.08	-1.34	0.11	-1.25	0.09	0.96	0.24	-1.05	0.43	-0.05	1.00	-1.15	0.39	-1.55	0.06	-1.35	0.20
SPO1181		penicillin-binding protein	-1.13	0.14	-1.19	0.17	-1.16	0.03	0.88	0.05	-1.11	0.21	-0.12	0.99	1.12	0.59	1.07	0.91	1.10	0.03

SPO1182	*murE*	ligase (EC:6.3.2.13)	1.12	0.40	-1.14	0.40	-0.01	1.13	1.53	0.02	-1.58	0.08	-0.03	1.56	-1.12	0.05	-2.24	0.01	-1.68	0.56
SPO1183	*murF*	ligase (EC:6.3.2.10)	1.62	0.00	-1.06	0.64	0.28	1.34	1.20	0.39	1.01	0.90	1.11	0.10	1.13	0.54	1.51	0.25	1.32	0.19
SPO1184	*mraY*	(EC:2.7.8.13)	-1.49	0.06	-1.12	0.65	-1.31	0.18	1.46	0.01	-1.31	0.39	0.08	1.39	-1.03	0.87	1.72	0.18	0.35	1.38
SPO1185		hypothetical protein	1.21	0.41	1.15	0.09	1.18	0.03	-1.44	0.14	1.52	0.02	0.04	1.48	-1.08	0.13	0.99	0.54	-0.05	1.03
SPO1186		hypothetical protein	-1.16	0.25	1.16	0.16	0.00	1.16	-1.45	0.08	1.51	0.17	0.03	1.48	-1.16	0.35	-1.13	0.25	-1.15	0.02
SPO1187	*murD*	synthetase (EC:6.3.2.9)	-1.52	0.69	1.29	0.27	-0.12	1.41	-1.55	0.26	-1.18	0.44	-1.37	0.19	1.13	0.65	-1.10	0.90	0.01	1.12
SPO1188		hypothetical protein	-1.05	0.91	-1.15	0.25	-1.10	0.05	2.07	0.03	-1.34	0.08	0.37	1.71	-1.70	0.04	-2.33	0.02	-2.02	0.31
SPO1189		hypothetical protein	2.83	0.02	1.34	0.20	2.09	0.75	-4.16	0.02	-1.41	0.10	-2.79	1.38	1.05	0.77	1.57	0.03	1.31	0.26
SPO1190		transcriptional regulator family protein	-2.61	0.04	-1.19	0.28	-1.90	0.71	-1.35	0.21	1.56	0.10	0.11	1.46	1.03	0.70	1.16	0.51	1.10	0.06
SPO1191	*gst*	S-transferase (EC:2.5.1.18)	1.01	0.30	-2.71	0.00	-0.85	1.86	2.34	0.00	-1.01	0.79	0.67	1.68	1.64	0.01	2.14	0.01	1.89	0.25
SPO1192		hypothetical protein	1.26	0.39	-2.49	0.05	-0.62	1.88	2.74	0.00	1.21	0.16	1.98	0.77	1.37	0.05	1.89	0.02	1.63	0.26
SPO1193		4-oxalocrotonate tautomerase	1.14	0.62	-1.30	0.29	-0.08	1.22	3.06	0.01	1.12	0.17	2.09	0.97	1.58	0.03	1.88	0.05	1.73	0.15
SPO1194		cell division protein FtsW	0.96	0.31	-1.40	0.05	-0.22	1.18	1.04	0.63	-1.17	0.09	-0.06	1.11	1.22	0.03	1.05	0.32	1.14	0.09
SPO1195	*murG*	beta-N-acetylglucosaminyltransferase (EC:2.4.1.227)	-1.26	0.00	-1.46	0.02	-1.36	0.10	0.82	0.01	-1.26	0.28	-0.22	1.04	-1.12	0.41	-1.29	0.49	-1.21	0.09
SPO1196	*murC*	ligase (EC:6.3.2.8)	-1.09	0.51	-1.28	0.39	-1.19	0.10	1.22	0.77	-1.27	0.44	-0.03	1.25	1.03	0.99	-1.57	0.32	-0.27	1.30
SPO1197		amino acid permease	1.34	0.93	1.33	0.80	1.34	0.01	1.62	0.77	-1.12	0.87	0.25	1.37	1.36	0.75	1.50	0.75	1.43	0.07
SPO1198		hypothetical protein	-1.30	0.42	1.36	0.39	0.03	1.33	1.23	0.70	-1.20	0.58	0.02	1.22	1.52	0.29	-1.18	0.73	0.17	1.35
SPO1199		hypothetical protein	1.18	0.59	1.06	0.88	1.12	0.06	-1.43	0.05	1.12	0.70	-0.16	1.28	1.14	0.62	-1.01	0.94	0.06	1.08
SPO1200	*murB*	reductase (EC:1.1.1.158)	-1.31	0.22	-1.02	0.89	-1.17	0.14	1.07	0.24	1.09	0.45	1.08	0.01	-1.69	0.18	-1.78	0.12	-1.74	0.05
SPO1201	*ddl*	ligase (EC:6.3.2.4)	-2.92	0.00	-1.58	0.02	-2.25	0.67	-1.67	0.00	-1.13	0.16	-1.40	0.27	1.13	0.25	-1.22	0.08	-0.05	1.18
SPO1202		cell division protein FtsQ	-2.05	0.00	-1.73	0.01	-1.89	0.16	0.88	0.07	-1.37	0.04	-0.25	1.13	1.35	0.01	-1.11	0.02	0.12	1.23
SPO1203	*ftsA*	division protein FtsA	-1.54	0.04	-1.36	0.05	-1.45	0.09	0.86	0.10	-1.83	0.01	-0.49	1.34	1.13	0.95	-1.12	0.47	0.00	1.13
SPO1204	*ftsZ*	division protein FtsZ	-1.38	0.03	-1.28	0.38	-1.33	0.05	0.93	0.01	1.09	0.98	1.01	0.08	1.93	0.01	1.84	0.18	1.89	0.04
SPO1205	*lpxC*	N-acetylglucosamine deacetylase (EC:3.5.1.-)	3.42	0.17	1.28	0.47	2.35	1.07	0.92	0.23	-2.57	0.00	-0.83	1.74	1.33	0.33	-1.59	0.01	-0.13	1.46
SPO1206		competence lipoprotein ComL	1.18	0.63	1.02	0.99	1.10	0.08	1.72	0.05	-1.15	0.14	0.29	1.44	1.18	0.10	1.23	0.29	1.21	0.03
SPO1207	*recN*	repair protein RecN	1.20	0.57	1.00	0.95	1.10	0.10	-1.68	0.00	-1.14	0.23	-1.41	0.27	-1.01	0.71	1.61	0.03	0.30	1.31
SPO1208		voltage-gated chloride channel family protein	1.23	0.62	1.02	0.93	1.13	0.11	-2.05	0.23	-1.14	0.62	-1.60	0.46	1.06	0.49	1.44	0.04	1.25	0.19
SPO1209		MlrC domain-containing protein	1.27	0.54	-1.03	0.88	0.12	1.15	-1.55	0.04	1.48	0.18	-0.04	1.52	1.55	0.15	1.47	0.13	1.51	0.04
SPO1210		oligopeptide ABC transporter substrate-binding protein	-2.15	0.00	-1.35	0.03	-1.75	0.40	-3.20	0.00	1.29	0.05	-0.96	2.25	2.00	0.00	2.60	0.00	2.30	0.30
SPO1211		oligopeptide ABC transporter permease	-1.98	0.01	-1.10	0.81	-1.54	0.44	-2.15	0.01	1.22	0.31	-0.47	1.69	-1.19	0.02	-1.06	0.09	-1.13	0.06
SPO1212		oligopeptide ABC transporter permease	-1.52	0.57	1.06	0.89	-0.23	1.29	-1.82	0.41	1.23	0.64	-0.30	1.53	1.38	0.40	1.39	0.46	1.39	0.01
SPO1213		oligopeptide ABC transporter ATP-binding protein	-1.35	0.16	1.09	0.83	-0.13	1.22	-1.31	0.06	1.36	0.10	0.03	1.34	-1.04	0.74	1.19	0.36	0.08	1.12
SPO1214		hippurate hydrolase (EC:3.5.1.32)	-1.31	0.01	0.99	0.92	-0.16	1.15	-1.62	0.00	1.89	0.04	0.14	1.76	1.22	0.46	1.59	0.22	1.41	0.19
SPO1215		carboxypeptidase (EC:3.4.17.11)	-1.20	0.83	1.07	0.82	-0.06	1.14	-1.89	0.36	1.54	0.10	-0.18	1.72	1.45	0.15	1.45	0.16	1.45	0.00
SPO1216		hypothetical protein	-1.66	X	-1.35	0.47	-1.51	0.16	-1.53	0.12	1.29	0.32	-0.12	1.41	-1.18	0.42	X	X	N/A	N/A
SPO1217		DNA-binding protein	-2.09	0.29	1.33	0.12	-0.38	1.71	-1.21	0.81	1.16	0.88	-0.03	1.19	1.39	0.15	-0.96	0.66	0.22	1.18
SPO1218		phage integrase site specific recombinase	-1.16	0.21	-1.12	0.37	-1.14	0.02	-1.79	0.02	-1.08	0.80	-1.44	0.36	-1.01	0.83	X	X	N/A	N/A
SPO1219		phage integrase site specific recombinase	-1.11	0.66	1.01	0.81	-0.05	1.06	-4.30	0.04	-1.52	0.06	-2.91	1.39	-1.24	0.23	-1.75	0.05	-1.50	0.26

SPO1220		hypothetical protein	-1.01	0.91	1.43	0.26	0.21	1.22	-1.57	0.51	1.28	0.49	-0.15	1.43	-1.14	0.67	-1.05	0.91	-1.10	0.04
SPO1221		hypothetical protein	1.34	0.83	1.18	0.52	1.26	0.08	-1.42	0.74	1.51	0.17	0.05	1.47	1.03	0.95	-1.03	0.95	0.00	1.03
SPO1222		resolvase site-specific recombinase	-2.07	0.15	-1.29	0.75	-1.68	0.39	-2.76	0.21	-1.18	0.81	-1.97	0.79	-1.19	0.81	-0.96	0.85	-1.07	0.12
SPO1223		hypothetical protein	X	X	1.07	0.52	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1224		hypothetical protein	X	X	X	X	N/A	N/A	-2.42	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1225		hypothetical protein	X	X	-1.05	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1226		lipoprotein	1.08	0.90	1.01	0.97	1.05	0.04	-4.17	0.11	2.17	0.10	-1.00	3.17	-1.15	0.53	1.13	0.59	-0.01	1.14
SPO1227		hypothetical protein	-1.34	0.36	1.00	0.99	-0.17	1.17	0.99	0.94	1.56	0.09	1.28	0.28	1.14	0.39	1.15	0.29	1.15	0.01
SPO1228		hypothetical protein	-0.95	0.56	-1.13	0.31	-1.04	0.09	1.16	0.12	1.04	0.82	1.10	0.06	-1.04	0.89	-0.97	0.48	-1.00	0.04
SPO1229		hypothetical protein	1.42	0.11	1.47	0.04	1.45	0.03	-1.04	0.63	1.81	0.00	0.39	1.43	1.30	0.02	-1.06	0.64	0.12	1.18
SPO1230		hypothetical protein	1.21	0.95	-1.03	0.75	0.09	1.12	-1.53	0.68	1.88	0.03	0.18	1.71	1.09	0.59	1.53	0.14	1.31	0.22
SPO1231		hypothetical protein	1.23	0.89	-1.12	0.91	0.05	1.18	-1.35	0.92	1.11	0.63	-0.12	1.23	-1.13	0.89	-1.31	X	-1.22	0.09
SPO1232		H-NS family DNA-binding protein	-1.39	0.11	-1.36	0.22	-1.38	0.01	-1.77	0.03	1.94	0.02	0.09	1.86	-1.08	0.41	1.55	0.12	0.24	1.32
SPO1233		hypothetical protein	1.63	0.60	1.38	0.73	1.51	0.13	-1.78	0.43	2.43	0.35	0.33	2.11	1.14	0.85	1.60	0.42	1.37	0.23
SPO1234		hypothetical protein	1.33	0.67	1.01	1.00	1.17	0.16	0.99	0.90	1.99	0.09	1.49	0.50	-1.14	0.42	-1.16	0.47	-1.15	0.01
SPO1235		hypothetical protein	1.19	0.82	-1.27	0.23	-0.04	1.23	-1.20	0.51	1.60	0.12	0.20	1.40	-1.34	0.12	-1.41	0.16	-1.38	0.03
SPO1236		hypothetical protein	-1.23	0.49	-1.36	0.56	-1.30	0.07	1.23	0.75	1.27	0.68	1.25	0.02	-1.05	0.91	-1.24	0.73	-1.15	0.10
SPO1237		hypothetical protein	1.07	0.49	-1.16	0.19	-0.04	1.12	1.38	0.02	1.21	0.35	1.30	0.09	-1.40	0.02	-1.29	0.07	-1.35	0.05
SPO1239	*pcm-1*	O-methyltransferase (EC:2.1.1.77)	1.71	0.45	1.17	0.47	1.44	0.27	3.23	0.06	1.09	0.86	2.16	1.07	1.16	0.30	1.00	0.15	1.08	0.08
SPO1240		TolC family type I secretion outer membrane protein	1.62	0.18	-1.39	0.05	0.12	1.51	1.58	0.10	1.10	0.56	1.34	0.24	-1.15	0.10	1.10	0.47	-0.02	1.13
SPO1241		hypothetical protein	1.10	0.59	1.20	0.43	1.15	0.05	-1.76	0.06	1.51	0.12	-0.13	1.64	1.22	0.52	1.27	0.64	1.25	0.03
SPO1242	*cobQ*	acid synthase	2.34	0.03	1.64	0.09	1.99	0.35	2.84	0.00	-1.18	0.22	0.83	2.01	1.11	0.17	-1.24	0.66	-0.06	1.18
SPO1243		hypothetical protein	1.33	0.03	0.98	0.70	1.15	0.18	3.24	0.02	1.70	0.02	2.47	0.77	-1.22	0.03	1.04	0.61	-0.09	1.13
SPO1244	*efp*	factor P	1.48	0.18	1.67	0.38	1.58	0.10	4.63	0.03	-1.28	0.08	1.68	2.96	1.07	0.76	-1.73	0.02	-0.33	1.40
SPO1245		ABC transporter permease	1.62	0.21	-1.11	0.40	0.26	1.37	1.52	0.07	1.31	0.07	1.42	0.11	-1.05	0.68	-1.12	0.54	-1.09	0.04
SPO1246		glycine cleavage system protein T	1.19	0.46	-1.11	0.12	0.04	1.15	1.49	0.04	1.27	0.19	1.38	0.11	-1.04	0.26	-1.05	0.55	-1.05	0.01
SPO1247		glycosyl transferase family protein	-1.12	0.91	1.14	0.67	0.01	1.13	1.24	0.86	1.10	0.60	1.17	0.07	1.40	0.27	-0.98	0.85	0.21	1.19
SPO1249		paraquat-inducible protein	1.10	0.38	1.34	0.26	1.22	0.12	1.58	0.04	1.03	0.96	1.31	0.28	1.21	0.30	-1.17	0.43	0.02	1.19
SPO1250		lipoprotein	-1.18	0.59	1.25	0.21	0.04	1.22	-1.07	0.94	-1.16	0.60	-1.12	0.04	1.49	0.06	1.17	0.44	1.33	0.16
SPO1251		hypothetical protein	1.48	0.35	-1.04	0.92	0.22	1.26	1.67	0.67	1.20	0.60	1.44	0.23	1.25	0.58	1.17	0.59	1.21	0.04
SPO1252		hypothetical protein	-1.10	0.11	1.00	0.99	-0.05	1.05	-1.89	0.00	1.01	0.96	-0.44	1.45	-1.21	0.14	-1.17	0.17	-1.19	0.02
SPO1253	*parE*	topoisomerase IV subunit B (EC:5.99.1.-)	-1.04	0.42	1.03	0.84	-0.01	1.04	1.01	0.98	1.03	0.96	1.02	0.01	1.10	0.23	-1.27	0.24	-0.09	1.19
SPO1254		hypothetical protein	0.97	0.78	-1.22	0.38	-0.13	1.10	-3.10	0.18	1.07	0.78	-1.02	2.09	-1.01	0.89	1.63	0.07	0.31	1.32
SPO1255		alkylhydroperoxidase	-1.08	0.35	-1.12	0.27	-1.10	0.02	1.57	0.05	1.88	0.01	1.73	0.16	-1.25	0.19	-1.10	0.18	-1.18	0.08
SPO1256	*ppk2*	kinase (EC:2.7.4.1)	1.17	0.95	1.14	0.59	1.16	0.02	3.15	0.37	1.28	0.54	2.22	0.94	-1.17	0.56	-1.17	0.71	-1.17	0.00
SPO1257		glutathione S-transferase	1.21	0.68	1.20	0.66	1.21	0.01	-1.74	0.10	1.64	0.07	-0.05	1.69	1.48	0.15	1.67	0.07	1.58	0.10
SPO1258		alpha/beta hydrolase	0.95	0.73	-1.20	0.28	-0.13	1.07	-3.51	0.02	2.07	0.02	-0.72	2.79	-1.62	0.01	1.03	0.55	-0.30	1.33
SPO1259		hypothetical protein	1.15	0.97	-1.29	0.26	-0.07	1.22	-2.33	0.01	1.31	0.39	-0.51	1.82	1.05	0.90	1.77	0.03	1.41	0.36
SPO1260		MATE efflux family protein	1.18	0.26	1.46	0.20	1.32	0.14	2.14	0.11	-1.57	0.16	0.29	1.86	1.21	0.53	-1.21	0.69	0.00	1.21

SPO1261		MarR family transcriptional regulator	1.45	0.10	-1.02	0.99	0.22	1.24	2.02	0.01	-1.07	0.23	0.48	1.55	1.07	0.32	-1.23	0.66	-0.08	1.15
SPO1262		hypothetical protein	-1.57	0.28	-1.16	0.37	-1.37	0.21	-1.64	0.30	-1.20	0.45	-1.42	0.22	-1.03	0.89	1.61	0.02	0.29	1.32
SPO1263		hypothetical protein	-1.37	0.06	1.43	0.07	0.03	1.40	0.95	0.27	-1.02	0.49	-0.04	0.98	1.15	0.39	-1.38	0.17	-0.12	1.27
SPO1264	*aspC-2*	aminotransferase (EC:2.6.1.1)	1.25	0.08	1.20	0.53	1.23	0.03	1.93	0.01	1.13	0.24	1.53	0.40	-1.26	0.02	-1.39	0.14	-1.33	0.06
SPO1265		DNA-binding protein	2.74	0.38	1.94	0.31	2.34	0.40	4.73	0.24	1.48	0.42	3.11	1.63	1.26	0.62	1.12	0.96	1.19	0.07
SPO1266		hypothetical protein	2.67	0.01	1.51	0.12	2.09	0.58	3.58	0.01	-1.04	0.76	1.27	2.31	-1.38	0.03	-1.73	0.01	-1.56	0.18
SPO1267		MarR family transcriptional regulator	-1.25	0.11	2.35	0.03	0.55	1.80	-4.45	0.01	1.14	0.07	-1.66	2.80	-1.19	0.21	-1.07	0.88	-1.13	0.06
SPO1268		lipoprotein	-1.37	0.05	-1.00	0.88	-1.18	0.19	-1.29	0.16	1.04	0.86	-0.13	1.17	-1.05	0.59	-0.93	0.37	-0.99	0.06
SPO1269		hypothetical protein	-1.21	0.31	-1.02	0.93	-1.12	0.10	1.16	0.15	1.21	0.06	1.19	0.03	1.03	0.91	1.06	0.62	1.05	0.02
SPO1270		lactoylglutathione lyase	1.25	0.48	1.04	0.94	1.15	0.11	1.23	0.72	2.01	0.01	1.62	0.39	-1.03	0.20	1.27	0.37	0.12	1.15
SPO1271		hypothetical protein	-1.75	0.40	-1.38	0.08	-1.57	0.19	-1.63	0.19	1.13	0.12	-0.25	1.38	-1.53	0.04	-2.23	0.02	-1.88	0.35
SPO1272		hypothetical protein	-1.56	0.21	-1.45	0.09	-1.51	0.06	-2.86	0.04	-1.23	0.09	-2.05	0.82	-1.54	0.02	-1.44	0.04	-1.49	0.05
SPO1273	*thyX*	thymidylate synthase (EC:2.1.1.148)	1.93	0.35	1.15	0.70	1.54	0.39	1.74	0.03	1.17	0.41	1.46	0.28	-1.08	0.54	-1.59	0.03	-1.34	0.26
SPO1274		hypothetical protein	1.26	0.69	-1.05	0.94	0.11	1.16	-4.47	0.00	1.44	0.24	-1.52	2.96	-1.01	0.98	1.10	0.72	0.05	1.06
SPO1275		cold shock family protein	1.36	0.42	-1.30	0.30	0.03	1.33	1.66	0.12	1.50	0.07	1.58	0.08	1.85	0.01	2.42	0.06	2.14	0.29
SPO1276		ArsC family protein	1.59	0.03	-1.11	0.58	0.24	1.35	1.98	0.03	-1.04	0.07	0.47	1.51	-1.08	0.02	-1.64	0.01	-1.36	0.28
SPO1277		hypothetical protein	1.18	0.38	1.15	0.13	1.17	0.02	1.34	0.13	-1.12	0.23	0.11	1.23	1.53	0.03	1.14	0.14	1.34	0.20
SPO1278		hypothetical protein	1.69	0.02	1.14	0.72	1.42	0.27	0.94	0.29	-1.06	0.70	-0.06	1.00	-1.27	0.20	-1.04	0.96	-1.16	0.12
SPO1279		hypothetical protein	1.42	0.26	1.12	0.28	1.27	0.15	-1.65	0.09	1.09	0.24	-0.28	1.37	-2.42	0.00	-2.41	0.01	-2.42	0.00
SPO1280		hypothetical protein	-1.17	0.39	1.30	0.06	0.07	1.24	3.13	0.01	1.06	0.79	2.10	1.04	-1.24	0.13	-1.36	0.37	-1.30	0.06
SPO1281		hypothetical protein	1.74	0.37	1.39	0.17	1.57	0.18	1.25	0.85	1.89	0.07	1.57	0.32	1.58	0.07	1.42	0.07	1.50	0.08
SPO1282	*thrS*	synthetase (EC:6.1.1.3)	X	X	1.26	0.26	N/A	N/A	2.70	0.01	-2.25	0.01	0.23	2.48	-1.07	0.77	-1.48	0.14	-1.28	0.21
SPO1283		hypothetical protein	-1.45	0.08	1.00	0.97	-0.23	1.23	-2.36	0.01	-1.27	0.06	-1.82	0.55	-1.09	0.30	-1.08	0.35	-1.09	0.01
SPO1284		ArsR family transcriptional regulator	-1.65	0.01	-1.45	0.10	-1.55	0.10	-3.53	0.00	-1.47	0.03	-2.50	1.03	-1.54	0.08	-1.22	0.07	-1.38	0.16
SPO1285		hypothetical protein	-1.28	0.43	1.01	0.99	-0.14	1.15	-1.47	0.31	1.25	0.66	-0.11	1.36	1.05	0.81	1.52	0.62	1.29	0.23
SPO1286		hypothetical protein	-1.05	0.54	1.26	0.15	0.11	1.16	-1.15	0.56	1.62	0.02	0.24	1.39	1.65	0.07	1.41	0.02	1.53	0.12
SPO1287		glyoxalase	1.22	0.17	1.28	0.06	1.25	0.03	-1.11	0.52	1.81	0.01	0.35	1.46	1.24	0.23	-1.02	0.73	0.11	1.13
SPO1288		hypothetical protein	1.04	0.77	1.09	0.39	1.07	0.03	-1.15	0.73	1.66	0.01	0.26	1.41	-1.25	0.04	-1.63	0.01	-1.44	0.19
SPO1289		alpha/beta hydrolase	1.07	0.92	1.30	0.50	1.19	0.12	1.28	0.80	1.44	0.43	1.36	0.08	1.66	0.18	1.57	0.12	1.62	0.04
SPO1290		hypothetical protein	-1.09	0.83	1.15	0.83	0.03	1.12	-1.28	0.65	2.07	0.45	0.40	1.68	1.60	0.58	1.77	0.56	1.69	0.09
SPO1291	*phaZ*	depolymerase	1.71	0.15	-1.31	0.35	0.20	1.51	1.73	0.03	1.72	0.13	1.73	0.01	-1.19	0.06	1.34	0.16	0.08	1.27
SPO1292	*phaC*	polymerase	6.67	0.00	1.19	0.55	3.93	2.74	1.65	0.01	1.86	0.02	1.76	0.11	-1.29	0.17	1.28	0.15	-0.01	1.29
SPO1293	*phaP*	PhaP	4.33	0.17	1.19	0.65	2.76	1.57	12.30	0.01	-3.79	0.00	4.26	8.05	1.70	0.13	2.63	0.00	2.17	0.47
SPO1294		polyhydroxyalkanoate synthesis repressor PhaR	-1.52	0.01	-1.20	0.31	-1.36	0.16	-2.14	0.01	1.34	0.14	-0.40	1.74	-1.22	0.05	1.15	0.53	-0.04	1.19
SPO1295		aminotransferase	3.77	0.18	-1.03	0.80	1.37	2.40	1.72	0.56	1.46	0.41	1.59	0.13	1.10	0.78	1.45	0.37	1.28	0.18
SPO1298		oxidoreductase, aldo/keto reductase	1.74	0.05	1.19	0.18	1.47	0.28	-1.41	0.66	1.61	0.09	0.10	1.51	1.06	0.29	-1.18	0.87	-0.06	1.12
SPO1299		LysR family transcriptional regulator	-1.26	0.26	1.03	0.70	-0.12	1.15	-1.16	0.90	1.08	0.54	-0.04	1.12	-1.38	0.21	-1.65	0.09	-1.52	0.14
SPO1300		glutamine synthetase	1.00	0.30	1.60	0.05	1.30	0.30	0.94	0.68	-1.26	0.03	-0.16	1.10	-1.12	0.29	-1.55	0.01	-1.34	0.22
SPO1301		glutamine amidotransferase	-1.39	0.02	1.10	0.46	-0.15	1.25	-2.34	0.01	1.33	0.18	-0.51	1.84	-1.85	0.05	-1.81	0.01	-1.83	0.02

SPO1302		glutamine synthetase	-0.99	0.45	1.18	0.12	0.10	1.08	-1.45	0.18	-2.11	0.00	-1.78	0.33	-1.95	0.00	-2.34	0.01	-2.15	0.20
SPO1303		fructosyl-amino acid oxidase	1.22	0.26	-1.02	0.86	0.10	1.12	2.29	0.01	-1.02	0.89	0.64	1.66	-1.16	0.12	-1.87	0.07	-1.52	0.36
SPO1304		His/Glu/Gln/Arg/opine family ABC transporter permease	-1.26	0.10	-1.18	0.41	-1.22	0.04	-0.94	0.06	-1.05	0.39	-1.00	0.06	-1.39	0.04	-1.31	0.06	-1.35	0.04
SPO1305		ABC transporter permease	-1.08	0.54	-1.11	0.50	-1.10	0.02	1.22	0.32	1.13	0.76	1.18	0.05	-1.24	0.39	-1.07	0.51	-1.16	0.09
SPO1306		His/Glu/Gln/Arg/opine family ABC transporter substrate-binding protein	-2.57	0.01	-1.56	0.07	-2.07	0.51	-2.90	0.00	-1.11	0.41	-2.01	0.90	-2.41	0.32	-1.58	0.06	-2.00	0.42
SPO1307		His/Glu/Gln/Arg/opine family ABC transporter ATP-binding protein	-1.31	0.17	-1.34	0.25	-1.33	0.02	1.36	0.19	1.29	0.05	1.33	0.04	-1.63	0.03	-1.33	0.06	-1.48	0.15
SPO1308		hypothetical protein	1.18	0.70	-1.06	0.76	0.06	1.12	1.12	0.72	1.29	0.42	1.21	0.09	-1.29	0.24	-1.25	0.29	-1.27	0.02
SPO1309		hypothetical protein	1.79	0.73	1.30	0.41	1.55	0.25	2.16	0.64	1.71	0.11	1.94	0.23	1.58	0.14	1.30	0.27	1.44	0.14
SPO1310		hypothetical protein	0.97	0.86	-1.04	0.41	-0.03	1.01	1.00	0.44	1.42	0.07	1.21	0.21	1.06	0.93	1.29	0.11	1.18	0.12
SPO1311		renal dipeptidase	1.22	0.09	-1.07	0.23	0.08	1.15	1.18	0.08	1.62	0.01	1.40	0.22	1.69	0.01	1.64	0.06	1.67	0.03
SPO1312	*pyrG*	synthetase (EC:6.3.4.2)	2.25	0.11	1.75	0.49	2.00	0.25	2.48	0.03	-1.71	0.03	0.39	2.10	-1.17	0.02	-1.36	0.22	-1.27	0.10
SPO1313	*secG*	translocase subunit SecG	-1.13	0.91	-1.09	0.60	-1.11	0.02	5.26	0.00	-1.27	0.11	2.00	3.27	0.99	0.71	-1.29	0.10	-0.15	1.14
SPO1314	*nthA*	hydratase subunit alpha (EC:4.2.1.84)	1.35	0.86	-1.12	0.78	0.12	1.24	1.84	0.61	1.19	0.79	1.52	0.33	1.15	0.69	1.88	0.47	1.52	0.37
SPO1315	*nthB*	hydratase subunit beta (EC:4.2.1.84)	1.28	0.12	1.17	0.05	1.23	0.06	2.41	0.01	1.17	0.30	1.79	0.62	2.07	0.00	1.39	0.02	1.73	0.34
SPO1316		hypothetical protein	1.34	0.36	1.29	0.09	1.32	0.03	2.56	0.04	1.39	0.21	1.98	0.59	1.53	0.08	1.36	0.07	1.45	0.09
SPO1317		hypothetical protein	-1.14	X	2.10	0.04	0.48	1.62	3.41	0.42	-1.26	0.23	1.08	2.34	-1.04	0.68	-1.66	0.16	-1.35	0.31
SPO1318	*purA*	synthetase (EC:6.3.4.4)	1.00	0.67	1.86	0.02	1.43	0.43	2.31	0.03	-1.26	0.20	0.53	1.79	1.04	0.99	1.12	0.90	1.08	0.04
SPO1319		hypothetical protein	-1.28	0.02	1.02	0.85	-0.13	1.15	-1.44	0.01	1.00	0.59	-0.22	1.22	1.17	0.05	1.15	0.07	1.16	0.01
SPO1320		lipoprotein	1.40	0.31	1.53	0.11	1.47	0.07	-1.51	0.08	1.36	0.17	-0.08	1.44	1.14	0.38	1.19	0.62	1.17	0.03
SPO1321		thiamine pyrophosphokinase (EC:2.7.6.2)	-1.39	0.05	1.10	0.68	-0.15	1.25	-1.36	0.31	1.34	0.15	-0.01	1.35	-1.03	0.81	-1.16	0.77	-1.10	0.06
SPO1322		hypothetical protein	-1.46	0.30	-1.07	0.92	-1.27	0.19	1.54	0.17	1.39	0.68	1.47	0.08	-1.26	0.66	1.39	0.67	0.06	1.33
SPO1323	*sdaA*	ammonia-lyase (EC:4.3.1.17)	2.44	0.02	-1.05	0.43	0.70	1.75	2.25	0.00	-1.07	0.23	0.59	1.66	-2.20	0.00	-2.48	0.03	-2.34	0.14
SPO1324		glutathione S-transferase	1.13	0.63	-1.24	0.47	-0.06	1.19	1.54	0.21	-1.06	0.64	0.24	1.30	-2.29	0.01	-1.80	0.10	-2.05	0.25
SPO1325		lipoprotein	-1.39	0.84	-1.60	0.02	-1.50	0.11	-1.32	0.89	-1.16	0.54	-1.24	0.08	-1.01	0.97	-1.16	0.09	-1.09	0.08
SPO1326		MarR family transcriptional regulator	-1.45	0.14	-1.46	0.04	-1.46	0.01	2.05	0.00	-1.53	0.04	0.26	1.79	-1.03	0.79	-2.00	0.02	-1.52	0.49
SPO1327	*rpiA*	isomerase A (EC:5.3.1.6)	-1.56	0.05	-1.09	0.85	-1.33	0.24	1.68	0.01	-1.03	0.15	0.33	1.36	-1.31	0.02	-1.59	0.04	-1.45	0.14
SPO1328	*gor*	reductase (EC:1.8.1.7)	-1.18	0.11	-1.70	0.01	-1.44	0.26	2.50	0.02	-1.35	0.02	0.58	1.93	-1.06	0.97	1.29	0.12	0.12	1.18
SPO1329		HflK protein	1.39	0.81	-1.35	0.02	0.02	1.37	2.62	0.03	1.30	0.10	1.96	0.66	1.19	0.06	1.58	0.04	1.39	0.20
SPO1330	*hflC*	protein	1.06	0.53	1.36	0.17	1.21	0.15	2.29	0.00	-1.24	0.07	0.53	1.77	1.63	0.05	1.02	0.77	1.33	0.31
SPO1331		hypothetical protein	-1.50	0.01	1.00	0.98	-0.25	1.25	-1.06	0.88	-1.01	0.84	-1.04	0.03	-1.08	0.54	-1.07	0.94	-1.08	0.01
SPO1332		hypothetical protein	-0.98	0.92	-1.09	0.82	-1.04	0.05	1.47	0.03	-1.10	0.40	0.19	1.29	1.29	0.12	1.44	0.32	1.37	0.08
SPO1333		serine protease	1.11	0.17	-1.28	0.31	-0.09	1.20	1.56	0.09	1.47	0.02	1.52	0.05	2.37	0.01	2.76	0.00	2.57	0.20
SPO1334		hypothetical protein	-1.29	0.54	-1.71	0.19	-1.50	0.21	-1.34	0.69	1.04	0.94	-0.15	1.19	1.20	0.67	1.05	0.79	1.13	0.08
SPO1335		Crp/Fnr family transcriptional regulator	0.98	0.92	1.06	0.89	1.02	0.04	1.24	0.91	1.25	0.29	1.25	0.01	1.63	0.19	1.57	0.28	1.60	0.03
SPO1336	*ispZ*	septation protein A	1.28	0.23	-1.20	0.40	0.04	1.24	2.90	0.04	-1.19	0.06	0.86	2.05	1.28	0.27	1.10	0.81	1.19	0.09
SPO1337		hypothetical protein	-1.13	0.81	-1.10	0.38	-1.12	0.01	-0.94	0.11	-1.07	0.60	-1.01	0.06	-1.74	0.00	-1.77	0.03	-1.76	0.02
SPO1339	*ftsY*	recognition particle-docking protein FtsY	1.36	0.05	1.00	0.81	1.18	0.18	1.18	0.32	-1.05	0.55	0.06	1.12	-1.42	0.10	-1.12	0.10	-1.27	0.15
SPO1340		hypothetical protein	1.50	0.77	1.24	0.48	1.37	0.13	1.25	0.85	1.50	0.13	1.38	0.13	-1.03	0.92	1.80	0.23	0.39	1.42

SPO1341		alkane-1 monooxygenase	-1.00	0.89	1.18	0.12	0.09	1.09	1.38	0.01	1.45	0.20	1.42	0.04	-1.07	0.46	-1.08	0.98	-1.08	0.01
SPO1342		hypothetical protein	-1.24	0.13	1.01	0.91	-0.12	1.13	-1.67	0.04	1.06	0.53	-0.31	1.37	1.41	0.12	1.51	0.07	1.46	0.05
SPO1343		glutathione S-transferase	1.14	0.05	-1.15	0.13	-0.01	1.15	1.24	0.03	1.34	0.11	1.29	0.05	-1.47	0.01	-1.54	0.01	-1.51	0.04
SPO1344	*xseA*	VII large subunit (EC:3.1.11.6)	-1.24	0.73	-1.11	0.83	-1.18	0.06	1.41	0.73	1.30	0.68	1.36	0.05	1.07	0.94	1.29	0.74	1.18	0.11
SPO1345	*purD*	ligase (EC:6.3.4.13)	2.46	0.01	1.94	0.03	2.20	0.26	7.44	0.00	-1.48	0.03	2.98	4.46	1.43	0.01	-1.67	0.08	-0.12	1.55
SPO1346		LuxR family transcriptional regulator	1.03	0.85	1.07	0.83	1.05	0.02	-1.47	0.03	1.35	0.13	-0.06	1.41	1.50	0.16	1.37	0.02	1.44	0.06
SPO1347		hypothetical protein	-1.05	0.60	-1.03	0.69	-1.04	0.01	1.25	0.48	-1.27	0.14	-0.01	1.26	-1.21	0.33	-1.11	0.36	-1.16	0.05
SPO1348		(Fe-S)-binding protein	1.29	0.44	1.15	0.65	1.22	0.07	3.05	0.02	-1.45	0.05	0.80	2.25	1.10	0.70	1.00	0.15	1.05	0.05
SPO1349		lipoprotein	-1.27	0.32	1.19	0.74	-0.04	1.23	-2.34	0.07	1.24	0.73	-0.55	1.79	1.42	0.36	1.03	0.98	1.23	0.19
SPO1350		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1351	*metZ*	sulfhydrylase (EC:4.2.99.-)	-3.17	0.00	-1.43	0.03	-2.30	0.87	10.20	0.00	2.34	0.01	6.27	3.93	-3.08	0.02	-1.87	0.01	-2.48	0.61
SPO1352		GTP cyclohydrolase	1.21	0.24	-1.28	0.03	-0.04	1.25	1.85	0.08	-1.17	0.05	0.34	1.51	1.76	0.05	1.42	0.01	1.59	0.17
SPO1353	*trkH-1*	system potassium uptake protein TrkH	1.23	0.66	1.15	0.61	1.19	0.04	2.98	0.07	-1.17	0.16	0.91	2.08	1.38	0.03	1.28	0.22	1.33	0.05
SPO1354		peptidoglycan binding domain-containing protein	-1.16	0.58	1.22	0.44	0.03	1.19	1.35	0.53	1.02	0.76	1.19	0.17	1.38	0.14	1.51	0.16	1.45	0.07
SPO1355	*glyQ*	synthetase subunit alpha (EC:6.1.1.14)	1.34	0.29	1.00	0.91	1.17	0.17	5.16	0.00	-1.53	0.06	1.82	3.35	-1.29	0.11	-1.72	0.01	-1.51	0.22
SPO1356		FkbM family methyltransferase	1.10	1.00	-1.03	0.24	0.04	1.07	0.87	0.11	-1.10	0.34	-0.12	0.98	-1.59	0.04	-1.86	0.02	-1.73	0.14
SPO1357	*gltS*	symporter	1.03	0.97	1.14	0.57	1.09	0.05	1.62	0.03	-1.08	0.34	0.27	1.35	-1.65	0.08	-2.67	0.01	-2.16	0.51
SPO1358	*glyS*	synthetase subunit beta (EC:6.1.1.14)	-1.00	0.96	1.28	0.35	0.14	1.14	1.50	0.07	-1.15	0.03	0.18	1.33	-1.29	0.12	-1.22	0.24	-1.26	0.04
SPO1359	*ppdK*	phosphate dikinase (EC:2.7.9.1)	1.47	0.71	1.19	0.66	1.33	0.14	1.55	0.59	1.10	0.75	1.33	0.23	1.09	0.73	1.06	0.76	1.08	0.02
SPO1360		hypothetical protein	-1.17	0.02	-1.31	0.14	-1.24	0.07	2.69	0.01	1.87	0.04	2.28	0.41	-1.40	0.02	1.33	0.58	-0.03	1.37
SPO1361		multicopper oxidase domain-containing protein	1.66	0.09	-1.27	0.09	0.20	1.47	2.33	0.04	1.75	0.03	2.04	0.29	-1.27	0.09	-1.27	0.24	-1.27	0.00
SPO1362		dihydroneopterin aldolase	1.13	0.43	1.27	0.57	1.20	0.07	1.97	0.02	-1.16	0.23	0.41	1.57	1.18	0.52	-1.32	0.13	-0.07	1.25
SPO1363	*folP*	synthase (EC:2.5.1.15)	-1.79	0.30	-1.21	0.52	-1.50	0.29	-2.28	0.00	-1.19	0.23	-1.74	0.55	-1.05	0.67	1.21	0.71	0.08	1.13
SPO1364	*glmM*	mutase (EC:5.4.2.10)	1.25	0.13	1.12	0.33	1.19	0.06	2.31	0.00	-1.10	0.21	0.61	1.71	1.66	0.03	1.36	0.02	1.51	0.15
SPO1365		hypothetical protein	-1.07	0.88	1.52	0.06	0.23	1.30	1.67	0.07	1.09	0.29	1.38	0.29	1.32	0.08	-1.12	0.73	0.10	1.22
SPO1366	*ilvC*	reductoisomerase (EC:1.1.1.86)	1.10	0.25	1.01	0.93	1.06	0.05	-2.77	0.00	-6.63	0.01	-4.70	1.93	-1.12	0.05	-1.60	0.17	-1.36	0.24
SPO1367		AsnC family transcriptional regulator	-1.52	0.52	-1.21	0.34	-1.37	0.16	-1.55	0.72	-2.35	0.05	-1.95	0.40	-1.34	0.04	-1.69	0.12	-1.52	0.17
SPO1368		AsnC family transcriptional regulator	1.21	0.98	-1.08	0.83	0.06	1.15	0.87	0.72	-1.50	0.09	-0.31	1.19	1.05	0.34	-1.04	0.84	0.01	1.05
SPO1369		GntR family transcriptional regulator	2.08	0.02	1.09	0.69	1.59	0.50	2.98	0.00	-1.33	0.08	0.83	2.16	1.21	0.06	-1.82	0.04	-0.31	1.52
SPO1370		aminotransferase	5.41	0.00	1.73	0.00	3.57	1.84	2.63	0.01	1.22	0.30	1.93	0.71	1.27	0.09	-1.03	0.64	0.12	1.15
SPO1371		2-octaprenyl-6-methoxyphenyl hydroxylase	2.52	0.08	2.71	0.07	2.62	0.10	5.70	0.03	1.29	0.43	3.50	2.21	1.35	0.59	1.15	0.58	1.25	0.10
SPO1372		hypothetical protein	5.85	0.00	2.52	0.01	4.19	1.67	10.70	0.01	1.41	0.03	6.06	4.65	1.55	0.01	1.96	0.01	1.76	0.21
SPO1373		hypothetical protein	-2.03	0.16	1.04	0.61	-0.50	1.54	-2.58	0.05	1.30	0.20	-0.64	1.94	1.36	0.02	-0.95	0.16	0.20	1.16
SPO1374		pyrimidine 5'-nucleotidase	1.34	0.23	-1.79	0.02	-0.23	1.57	3.02	0.02	-1.20	0.24	0.91	2.11	-1.47	0.72	-1.24	0.59	-1.36	0.12
SPO1375		GntR family transcriptional regulator	-1.15	0.09	-1.77	0.10	-1.46	0.31	0.97	0.36	-1.17	0.41	-0.10	1.07	-1.30	0.22	-1.19	0.14	-1.25	0.06
SPO1376		glycosyl transferase family protein	-1.33	0.00	4.05	0.00	1.36	2.69	-6.87	0.03	4.16	0.01	-1.36	5.52	-0.98	0.47	X	X	N/A	N/A
SPO1377	*carA*	phosphate synthase small subunit (EC:6.3.5.5)	1.59	0.01	1.64	0.01	1.62	0.02	7.26	0.00	-1.22	0.09	3.02	4.24	-1.38	0.00	-2.99	0.01	-2.19	0.81
SPO1378		GatB/YqeY domain-containing protein	1.20	0.97	1.24	0.24	1.22	0.02	1.30	0.88	1.15	0.74	1.23	0.08	1.44	0.29	1.41	0.53	1.43	0.02
SPO1379		prephenate dehydrogenase	-2.15	0.57	-1.18	0.90	-1.67	0.48	-2.15	0.59	-1.47	0.63	-1.81	0.34	-1.03	0.94	2.03	0.53	0.50	1.53

SPO1380		hypothetical protein	1.64	0.70	1.08	0.70	1.36	0.28	1.17	0.86	1.29	0.26	1.23	0.06	-1.38	0.37	-1.04	0.94	-1.21	0.17
SPO1381		hypothetical protein	1.66	0.03	1.29	0.16	1.48	0.18	2.70	0.00	-1.01	0.76	0.85	1.86	-1.04	0.77	-1.66	0.01	-1.35	0.31
SPO1382		hypothetical protein	-1.36	0.27	-1.15	0.41	-1.26	0.11	0.91	0.49	-1.04	0.28	-0.07	0.97	-1.27	0.12	1.02	0.80	-0.13	1.15
SPO1383	*ctaD*	c oxidase, aa3-type, subunit I (EC:1.9.3.1)	5.30	0.05	1.37	0.18	3.34	1.97	3.84	0.06	1.31	0.25	2.58	1.27	1.11	0.76	1.21	0.98	1.16	0.05
SPO1384		MarR family transcriptional regulator	-2.08	0.10	-1.10	0.86	-1.59	0.49	1.15	0.03	1.25	0.73	1.20	0.05	1.19	0.58	-1.24	0.78	-0.03	1.22
SPO1385		twin-arginine translocation pathway signal sequence domain-containing protein	-1.36	0.84	-1.18	0.87	-1.27	0.09	1.07	0.97	1.07	0.96	1.07	0.00	-1.29	0.81	1.14	0.89	-0.08	1.22
SPO1386		HIT family protein	2.60	0.00	1.35	0.01	1.98	0.63	2.93	0.00	1.21	0.14	2.07	0.86	-1.21	0.14	-1.18	0.14	-1.20	0.02
SPO1387		cation efflux system protein	1.37	0.64	1.15	0.03	1.26	0.11	1.42	0.58	-1.18	0.30	0.12	1.30	1.41	0.09	1.26	0.23	1.34	0.08
SPO1388		LuxR family transcriptional regulator	-3.30	0.00	1.02	0.82	-1.14	2.16	-1.28	0.35	1.29	0.18	0.01	1.29	1.26	0.08	-0.93	0.23	0.17	1.09
SPO1389	*lipB*	ligase B	1.97	0.21	1.00	1.00	1.49	0.49	5.86	0.02	-1.14	0.26	2.36	3.50	1.19	0.32	-1.28	0.26	-0.05	1.24
SPO1390		thioredoxin	2.61	0.34	-1.50	0.05	0.56	2.06	3.02	0.31	1.01	0.97	2.02	1.01	1.13	0.83	-1.09	0.73	0.02	1.11
SPO1392		alkylhydroperoxidase	1.07	0.81	-1.06	0.70	0.01	1.07	1.61	0.12	-1.41	0.09	0.10	1.51	1.06	0.55	-1.03	0.74	0.02	1.05
SPO1393		Rrf2 family protein	-1.27	0.25	-1.62	0.07	-1.45	0.18	-1.60	0.33	-1.09	0.62	-1.35	0.26	-1.16	0.28	-1.90	0.02	-1.53	0.37
SPO1394		beta-lactamase	-1.14	0.55	-1.10	0.19	-1.12	0.02	1.60	0.03	-1.22	0.39	0.19	1.41	-1.23	0.09	-0.93	0.12	-1.08	0.15
SPO1395		AraC family transcriptional regulator	X	X	-1.12	0.67	N/A	N/A	1.83	X	-0.98	0.52	0.43	1.40	1.16	0.24	-1.07	X	0.04	1.12
SPO1396		transporter	1.35	0.65	1.72	0.35	1.54	0.18	-1.43	0.64	1.15	0.61	-0.14	1.29	1.42	0.10	1.60	0.14	1.51	0.09
SPO1397		hydrophobe/amphiphile efflux-1 family protein	1.26	0.35	1.70	0.04	1.48	0.22	-2.27	0.00	-1.01	0.72	-1.64	0.63	1.22	0.56	1.50	0.01	1.36	0.14
SPO1398		RND family efflux transporter MFP subunit	1.69	0.01	2.10	0.03	1.90	0.20	-2.77	0.01	1.16	0.30	-0.81	1.97	1.14	0.09	1.62	0.04	1.38	0.24
SPO1399		AraC family transcriptional regulator	-1.58	0.00	-1.19	0.35	-1.39	0.20	-1.74	0.11	1.15	0.50	-0.30	1.45	-1.10	0.22	1.46	0.27	0.18	1.28
SPO1400		hypothetical protein	2.26	0.02	-1.12	0.59	0.57	1.69	-0.98	0.08	1.26	0.66	0.14	1.12	-1.11	0.57	1.39	0.74	0.14	1.25
SPO1401		hypothetical protein	2.66	0.01	1.22	0.16	1.94	0.72	1.35	0.11	1.38	0.04	1.37	0.01	-1.13	0.19	-1.47	0.17	-1.30	0.17
SPO1402		hypothetical protein	1.20	0.97	1.46	0.03	1.33	0.13	-3.74	0.00	1.62	0.31	-1.06	2.68	1.00	0.14	1.07	0.89	1.04	0.04
SPO1403	*metG*	synthetase (EC:6.1.1.10)	1.53	0.48	1.36	0.32	1.45	0.09	4.63	0.02	-1.14	0.19	1.75	2.89	-1.08	0.20	-1.45	0.07	-1.27	0.19
SPO1404		hypothetical protein	-1.62	0.30	-1.03	0.57	-1.33	0.30	-1.94	0.01	1.10	0.83	-0.42	1.52	-1.15	0.54	1.85	0.16	0.35	1.50
SPO1405		tyrosinase domain-containing protein	0.97	0.04	1.27	0.16	1.12	0.15	-2.70	0.02	1.96	0.00	-0.37	2.33	1.60	0.01	2.07	0.10	1.84	0.24
SPO1406		hypothetical protein	1.26	0.07	1.32	0.39	1.29	0.03	-1.35	0.27	1.78	0.19	0.22	1.57	1.84	0.29	1.55	X	1.70	0.15
SPO1407		hypothetical protein	-1.05	0.39	1.19	0.10	0.07	1.12	2.39	0.01	-1.09	0.37	0.65	1.74	1.03	0.87	-1.21	0.40	-0.09	1.12
SPO1408	*rluD*	large subunit pseudouridine synthase D (EC:4.2.1.70)	X	X	1.12	0.81	N/A	N/A	2.52	0.04	-1.35	0.46	0.59	1.94	-1.49	0.23	-2.36	0.28	-1.93	0.44
SPO1409	*rpoH-2*	polymerase factor sigma-32	-1.14	0.02	-1.92	0.04	-1.53	0.39	3.86	0.00	1.33	0.02	2.60	1.27	2.31	0.02	2.44	0.00	2.38	0.06
SPO1410		renal dipeptidase	1.53	0.57	1.11	0.88	1.32	0.21	-1.19	1.00	1.71	0.34	0.26	1.45	1.78	0.14	2.78	0.09	2.28	0.50
SPO1411		hypothetical protein	-2.67	0.30	-1.13	0.61	-1.90	0.77	-3.84	0.01	1.47	0.18	-1.19	2.66	1.48	0.16	1.63	0.04	1.56	0.08
SPO1412		DNA modification methyltransferase domain-containing protein	-1.22	0.65	-1.23	0.84	-1.23	0.01	-1.46	0.85	1.14	0.70	-0.16	1.30	1.16	0.61	1.30	0.47	1.23	0.07
SPO1413	*pepF*	F (EC:3.4.24.-)	1.48	0.39	-1.53	0.12	-0.03	1.51	2.83	0.06	1.04	0.83	1.94	0.90	1.34	0.11	1.55	0.25	1.45	0.11
SPO1414		alpha/beta hydrolase	0.99	0.61	-1.56	0.01	-0.29	1.27	1.81	0.09	1.40	0.07	1.61	0.20	1.58	0.00	1.68	0.12	1.63	0.05
SPO1415		sterol carrier family protein	1.40	0.02	0.99	0.81	1.19	0.21	1.80	0.01	1.45	0.05	1.63	0.18	2.05	0.00	2.39	0.04	2.22	0.17
SPO1416		hypothetical protein	-2.36	0.03	-1.19	0.14	-1.78	0.59	-1.51	0.15	1.50	0.06	-0.01	1.51	1.03	0.90	1.22	0.58	1.13	0.10
SPO1417		helicase	2.48	0.00	1.13	0.65	1.81	0.68	2.59	0.01	1.07	0.99	1.83	0.76	1.13	0.80	1.43	0.54	1.28	0.15
SPO1418		S4 domain-containing protein	1.19	0.97	1.96	0.21	1.58	0.39	1.78	0.76	-1.08	0.70	0.35	1.43	1.60	0.44	1.22	0.74	1.41	0.19

SPO1419		(Fe-S)-binding protein	1.09	0.73	1.16	0.30	1.13	0.03	4.40	0.00	1.19	0.25	2.80	1.61	-1.09	0.37	-1.34	0.15	-1.22	0.13
SPO1420		CarD family transcriptional regulator	-1.61	0.01	-1.14	0.39	-1.38	0.24	0.92	0.04	1.33	0.18	1.13	0.21	1.01	0.24	1.32	0.16	1.17	0.16
SPO1421		cation channel family protein	2.30	0.24	2.57	0.01	2.44	0.14	1.70	0.05	1.66	0.03	1.68	0.02	-1.17	0.39	-1.09	0.55	-1.13	0.04
SPO1422		cobalamin 5'-phosphate synthase (EC:2.7.8.26)	X	X	1.33	0.03	N/A	N/A	2.67	0.02	-1.35	0.05	0.66	2.01	1.09	0.24	-1.61	0.09	-0.26	1.35
SPO1423	*cobT*	phosphoribosyltransferase (EC:2.4.2.21)	X	X	2.14	0.00	N/A	N/A	2.84	0.00	-1.37	0.13	0.74	2.11	-1.17	0.33	-3.13	0.00	-2.15	0.98
SPO1424		glutathione-regulated potassium-efflux system protein	-1.16	0.05	1.26	0.08	0.05	1.21	1.04	0.14	1.01	0.91	1.03	0.02	-1.05	0.68	-1.18	0.08	-1.12	0.06
SPO1425		AsnC family transcriptional regulator	-1.30	0.21	-1.42	0.42	-1.36	0.06	-1.40	0.12	-1.07	0.78	-1.24	0.17	1.08	0.88	1.11	0.84	1.10	0.02
SPO1426	*hppD*	dioxygenase (EC:1.13.11.27)	-3.11	0.01	-1.02	0.95	-2.07	1.05	-7.49	0.00	-1.25	0.15	-4.37	3.12	-1.47	0.02	-1.01	0.62	-1.24	0.23
SPO1427		hypothetical protein	1.07	0.18	1.21	0.21	1.14	0.07	-1.03	0.82	1.09	0.54	0.03	1.06	1.16	0.31	1.07	0.29	1.12	0.04
SPO1428		hypothetical protein	-3.02	0.02	-1.34	0.12	-2.18	0.84	-3.64	0.01	-1.36	0.36	-2.50	1.14	-1.44	0.09	-1.11	X	-1.28	0.17
SPO1429	*omp28*	membrane protein, 28	0.99	0.09	-2.83	0.03	-0.92	1.91	2.48	0.00	1.05	0.69	1.77	0.72	3.40	0.01	3.38	0.01	3.39	0.01
SPO1430		antibiotic efflux protein	-1.09	0.59	1.16	0.66	0.03	1.13	1.14	0.28	1.49	0.15	1.32	0.18	1.99	0.02	1.61	0.16	1.80	0.19
SPO1431		O-acetylhomoserine aminocarboxypropyltransferase (EC:2.5.1.49)	1.92	0.08	-1.28	0.37	0.32	1.60	1.42	0.41	1.16	0.42	1.29	0.13	-1.24	0.09	-1.19	0.03	-1.22	0.03
SPO1432		rhodanese domain-containing protein	-1.22	0.71	-1.22	0.21	-1.22	0.00	-1.48	0.54	1.26	0.51	-0.11	1.37	-1.54	0.13	-1.27	0.36	-1.41	0.14
SPO1433		aldo/keto reductase	1.13	0.58	-1.15	0.04	-0.01	1.14	2.36	0.03	1.39	0.06	1.88	0.49	-1.25	0.03	-1.14	0.12	-1.20	0.06
SPO1434		AraC family transcriptional regulator	2.03	0.04	-1.18	0.04	0.43	1.61	4.12	0.02	-1.16	0.23	1.48	2.64	-1.49	0.01	-2.07	0.01	-1.78	0.29
SPO1435		hypothetical protein	11.90	0.00	1.95	0.04	6.93	4.98	-1.55	0.01	1.09	0.52	-0.23	1.32	-1.47	0.01	-2.02	0.05	-1.75	0.27
SPO1436		bifunctional 3-hydroxyacyl-CoA dehydrogenase/thioesterase (EC:1.1.1.35)	16.30	0.00	2.21	0.00	9.26	7.05	-1.12	0.61	-1.03	0.87	-1.08	0.05	-1.29	0.62	-1.90	0.01	-1.60	0.31
SPO1437	*fabG*	reductase (EC:1.1.1.100)	3.46	0.10	1.47	0.28	2.47	1.00	-1.38	0.59	-1.02	0.99	-1.20	0.18	-0.98	0.90	1.27	0.27	0.15	1.12
SPO1438		hypothetical protein	-1.68	0.27	-1.26	0.61	-1.47	0.21	-4.74	0.03	2.22	0.08	-1.26	3.48	1.09	0.88	1.36	0.53	1.23	0.14
SPO1439		DNA binding protein	-1.15	0.92	-1.34	0.55	-1.25	0.10	-1.05	0.94	-1.43	0.44	-1.24	0.19	1.10	0.81	-1.23	0.82	-0.06	1.17
SPO1440		hypothetical protein	7.46	0.01	1.26	0.55	4.36	3.10	1.38	0.04	-1.26	0.70	0.06	1.32	-0.98	0.53	1.18	0.88	0.10	1.08
SPO1441		fatty acid desaturase	X	X	-1.05	0.89	N/A	N/A	1.41	X	X	X	N/A	N/A	-1.07	0.93	X	X	N/A	N/A
SPO1442		hypothetical protein	-0.94	0.39	1.17	0.34	0.11	1.06	2.97	0.03	-1.44	0.05	0.77	2.21	1.74	0.03	-1.35	0.05	0.20	1.55
SPO1443	*rhlE*	RNA helicase RhlE	1.51	0.11	-1.10	0.27	0.21	1.31	2.65	0.01	1.03	0.58	1.84	0.81	-1.09	0.25	-1.13	0.03	-1.11	0.02
SPO1444		hypothetical protein	1.46	0.14	-1.21	0.59	0.13	1.34	1.84	0.05	1.43	0.08	1.64	0.21	-1.20	0.18	-1.17	0.79	-1.19	0.02
SPO1445		short chain dehydrogenase/reductase oxidoreductase	-1.20	0.18	-1.02	0.80	-1.11	0.09	-2.90	0.01	1.54	0.01	-0.68	2.22	-1.43	0.24	-1.90	0.06	-1.67	0.23
SPO1446		cyclase	1.07	0.92	1.19	0.04	1.13	0.06	-2.60	0.01	1.24	0.16	-0.68	1.92	-1.08	0.34	-1.39	0.08	-1.24	0.16
SPO1447		short chain dehydrogenase/reductase oxidoreductase	1.31	0.92	1.28	0.34	1.30	0.02	-1.52	0.84	1.36	0.15	-0.08	1.44	1.03	0.82	-1.28	0.23	-0.13	1.16
SPO1448		hypothetical protein	-1.04	0.35	1.15	0.05	0.05	1.10	-1.87	0.02	1.13	0.62	-0.37	1.50	-1.01	1.00	-1.36	0.05	-1.19	0.18
SPO1449		AMP-binding protein	-1.39	0.02	-1.08	0.53	-1.24	0.16	-3.87	0.01	1.14	0.55	-1.37	2.51	-1.46	0.09	-1.86	0.02	-1.66	0.20
SPO1450		aromatic 1,2-dioxygenase subunit beta	1.06	0.36	-1.17	0.72	-0.05	1.12	-3.67	0.00	-1.01	0.94	-2.34	1.33	-1.17	0.42	1.06	0.86	-0.05	1.12
SPO1451		aromatic 1,2-dioxygenase subunit alpha	1.29	0.64	-1.19	0.46	0.05	1.24	-6.08	0.00	1.33	0.05	-2.38	3.71	-1.54	0.54	-1.48	0.03	-1.51	0.03
SPO1452		oxidoreductase	-1.10	0.83	-1.14	0.70	-1.12	0.02	-4.34	0.17	-1.01	0.95	-2.68	1.67	-1.21	0.70	-1.26	0.67	-1.24	0.03
SPO1453		MarR family transcriptional regulator	1.06	0.97	1.01	0.95	1.04	0.03	1.05	0.91	1.17	0.67	1.11	0.06	1.04	0.84	-1.12	0.88	-0.04	1.08
SPO1454		TRAP dicarboxylate transporter subunit DctP	1.41	0.87	-1.19	0.26	0.11	1.30	-2.85	0.51	1.28	0.34	-0.79	2.07	1.75	0.05	1.93	0.04	1.84	0.09
SPO1455		TRAP dicarboxylate transporter subunit DctQ	1.10	0.58	-0.99	0.78	0.06	1.04	-2.94	0.00	-1.02	1.00	-1.98	0.96	1.26	0.20	-1.43	0.08	-0.09	1.35

SPO1456		TRAP C4-dicarboxylate transport system permease DctM	-1.89	0.01	-1.43	0.20	-1.66	0.23	-1.73	0.07	0.99	0.67	-0.37	1.36	-1.18	0.46	2.39	0.08	0.61	1.79
SPO1457		thioesterase	1.10	0.52	1.14	0.59	1.12	0.02	3.16	0.01	-1.53	0.02	0.82	2.35	1.07	0.31	-1.67	0.05	-0.30	1.37
SPO1458		MarR family transcriptional regulator	-1.63	0.22	-1.03	0.98	-1.33	0.30	-2.74	0.11	-1.36	0.78	-2.05	0.69	-1.15	0.86	-1.10	0.97	-1.13	0.02
SPO1459		indolepyruvate oxidoreductase, IorA subunit	-1.20	0.41	1.17	0.18	-0.02	1.19	-1.71	0.12	-1.21	0.11	-1.46	0.25	-1.14	0.18	-1.12	0.88	-1.13	0.01
SPO1460		indolepyruvate oxidoreductase subunit B (EC:1.2.7.8)	-1.25	0.07	1.22	0.58	-0.02	1.24	-1.33	0.30	-1.32	0.49	-1.33	0.01	-0.97	0.84	-1.31	0.43	-1.14	0.17
SPO1461		hypothetical protein	1.04	0.99	-1.20	0.61	-0.08	1.12	-2.43	0.10	1.03	0.93	-0.70	1.73	1.06	0.70	1.29	0.18	1.18	0.12
SPO1462		OmpA family protein	-1.36	0.03	1.10	0.48	-0.13	1.23	-1.45	0.05	1.24	0.36	-0.11	1.35	1.20	0.11	1.30	0.17	1.25	0.05
SPO1463		TRAP dicarboxylate transporter subunit DctM	-1.53	0.01	-1.23	0.10	-1.38	0.15	-2.59	0.01	1.20	0.32	-0.70	1.90	1.08	0.28	1.35	0.50	1.22	0.14
SPO1464		TRAP dicarboxylate transporter subunit DctQ	-4.08	0.00	-1.84	0.06	-2.96	1.12	-9.78	0.00	-1.40	0.25	-5.59	4.19	-1.41	0.09	2.05	0.13	0.32	1.73
SPO1465		TRAP dicarboxylate transporter subunit DctP	-3.13	0.02	-1.84	0.29	-2.49	0.65	-8.27	0.01	-1.01	0.83	-4.64	3.63	1.28	0.17	2.64	0.13	1.96	0.68
SPO1466		opine dehydrogenase	1.17	0.69	-1.33	0.12	-0.08	1.25	-2.69	0.18	-1.12	0.72	-1.91	0.79	1.27	0.38	-0.93	0.26	0.17	1.10
SPO1467		3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157)	1.38	0.00	-1.02	0.90	0.18	1.20	-1.61	0.23	-1.32	X	-1.47	0.15	1.08	0.51	X	X	N/A	N/A
SPO1468		aminotransferase	-1.31	0.23	1.11	0.56	-0.10	1.21	-2.37	0.03	-1.05	0.83	-1.71	0.66	-1.18	0.50	-1.27	0.44	-1.23	0.05
SPO1469		3-ketosteroid dehydrogenase	-1.21	X	1.10	0.56	-0.05	1.16	-1.09	0.16	X	X	N/A	N/A	1.41	0.08	X	X	N/A	N/A
SPO1470		isocitrate lyase	-1.26	0.31	-1.24	0.43	-1.25	0.01	-2.57	0.02	1.03	0.77	-0.77	1.80	-1.24	0.19	-1.64	0.01	-1.44	0.20
SPO1471		isochorismatase	-1.03	0.87	-1.27	0.36	-1.15	0.12	-2.28	0.07	-0.99	0.82	-1.64	0.65	-1.25	0.10	-1.71	0.04	-1.48	0.23
SPO1472	*hyuA*	utilization protein A	-1.09	0.13	-1.37	0.04	-1.23	0.14	-2.49	0.01	-1.08	0.59	-1.79	0.71	-1.20	0.04	-1.18	0.20	-1.19	0.01
SPO1473		hydantoin utilization protein B	-1.13	0.55	-1.33	0.03	-1.23	0.10	-2.37	0.06	-1.25	0.39	-1.81	0.56	1.16	0.25	-1.24	0.64	-0.04	1.20
SPO1474		tautomerase	-1.43	0.02	-1.33	0.23	-1.38	0.05	-2.62	0.00	-1.28	0.13	-1.95	0.67	-0.99	0.68	X	X	N/A	N/A
SPO1475		GntR family transcriptional regulator	-1.02	0.96	-1.14	0.38	-1.08	0.06	-0.99	0.56	1.19	0.35	0.10	1.09	1.22	0.29	-1.01	0.60	0.11	1.12
SPO1476	*leuC-2*	isomerase large subunit (EC:4.2.1.33)	-1.38	0.07	-1.39	0.35	-1.39	0.01	-1.30	0.61	1.11	0.51	-0.10	1.21	1.19	0.30	-0.92	0.58	0.14	1.05
SPO1477	*leuD-2*	dehydratase small subunit (EC:4.2.1.33)	-2.05	0.12	-1.16	0.61	-1.61	0.45	-1.85	0.18	-0.99	0.98	-1.42	0.43	1.34	0.04	1.30	0.33	1.32	0.02
SPO1478		RNA polymerase sigma factor RpoE	1.73	0.02	-1.13	0.21	0.30	1.43	-1.49	0.01	1.11	0.67	-0.19	1.30	1.14	0.62	1.67	0.11	1.41	0.27
SPO1479		transcriptional activator	1.20	0.62	-1.22	0.10	-0.01	1.21	-2.80	0.00	-0.99	0.92	-1.89	0.91	-1.00	0.96	1.24	0.24	0.12	1.12
SPO1480		short chain dehydrogenase/reductase oxidoreductase	1.91	0.49	1.08	0.87	1.50	0.42	-2.17	0.69	-0.97	0.91	-1.57	0.60	-0.99	0.93	-1.02	X	-1.01	0.01
SPO1481		hypothetical protein	3.34	0.00	-1.19	X	1.08	2.27	-1.56	0.11	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1482		hypothetical protein	3.47	0.01	-1.27	0.86	1.10	2.37	-5.44	0.02	-1.10	0.95	-3.27	2.17	-1.54	0.78	1.21	0.88	-0.17	1.38
SPO1483		cyclopropane-fatty-acyl-phospholipid synthase	2.70	0.21	1.18	0.56	1.94	0.76	-4.12	0.13	-1.00	0.91	-2.56	1.56	-0.96	0.81	-1.15	0.53	-1.05	0.10
SPO1484		hypothetical protein	2.32	0.01	-1.02	0.95	0.65	1.67	-3.53	0.02	X	X	N/A	N/A	-1.00	0.64	X	X	N/A	N/A
SPO1485		sodium:galactoside symporter family protein	2.71	0.02	-1.23	0.09	0.74	1.97	-3.95	0.01	-1.06	0.93	-2.51	1.45	-1.54	0.15	-1.06	0.68	-1.30	0.24
SPO1486		hypothetical protein	4.64	0.01	1.11	0.53	2.88	1.77	-1.94	0.03	-0.98	0.79	-1.46	0.48	-1.27	0.19	-1.05	0.75	-1.16	0.11
SPO1487		hypothetical protein	2.51	0.02	-1.21	0.67	0.65	1.86	-1.35	0.50	-1.02	X	-1.19	0.17	-0.99	0.90	X	X	N/A	N/A
SPO1488		LuxR family transcriptional regulator	-1.23	0.58	-1.05	0.93	-1.14	0.09	-1.92	0.22	1.14	0.89	-0.39	1.53	1.06	0.91	1.32	0.68	1.19	0.13
SPO1489		indole acetimide hydrolase (EC:3.5.1.-)	-1.62	X	-1.04	0.98	-1.33	0.29	-2.82	0.02	-1.16	X	-1.99	0.83	-1.09	0.83	X	X	N/A	N/A
SPO1490		regulatory protein	X	X	X	X	N/A	N/A	-1.63	0.45	X	X	N/A	N/A	-0.98	0.66	X	X	N/A	N/A
SPO1491		branched-chain amino acid ABC transporter permease	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1492		branched-chain amino acid ABC transporter permease/ATP-binding protein	1.06	0.81	-1.09	0.69	-0.02	1.08	1.21	0.19	-1.12	0.80	0.04	1.17	-1.26	0.62	-1.07	0.81	-1.17	0.10

SPO1493		branched-chain amino acid ABC transporter ATP-binding protein	X	X	-1.26	0.77	N/A	N/A	-1.53	0.45	-1.59	X	-1.56	0.03	-1.18	0.33	1.51	X	0.17	1.35
SPO1494		2-hydroxychromene-2-carboxylate isomerase	-1.25	0.10	1.21	0.13	-0.02	1.23	-1.70	0.01	1.26	0.21	-0.22	1.48	-1.06	0.84	-1.29	0.50	-1.18	0.12
SPO1495		ABC transporter ATP-binding protein	4.19	0.15	2.19	0.03	3.19	1.00	2.36	0.18	1.48	0.07	1.92	0.44	1.33	0.27	1.50	0.18	1.42	0.09
SPO1496		ABC transporter permease	4.93	0.07	2.20	0.04	3.57	1.37	2.80	0.12	1.49	0.30	2.15	0.65	1.67	0.09	1.73	0.10	1.70	0.03
SPO1497		RND family efflux transporter MFP subunit	2.76	0.18	1.28	0.56	2.02	0.74	1.42	0.62	1.26	0.65	1.34	0.08	1.75	0.28	2.84	0.15	2.30	0.55
SPO1498		fumarate hydratase, class I	1.21	0.80	2.26	0.02	1.74	0.53	1.22	0.38	1.04	0.93	1.13	0.09	1.57	0.03	1.20	0.49	1.39	0.19
SPO1499		alpha/beta hydrolase	1.35	0.14	-1.17	0.30	0.09	1.26	1.23	0.02	1.43	0.11	1.33	0.10	-1.05	0.70	1.05	0.55	0.00	1.05
SPO1500	*pqqE*	quinone biosynthesis protein PqqE	-1.16	0.14	3.25	0.03	1.05	2.21	-13.70	0.00	1.07	0.68	-6.32	7.39	2.11	0.02	1.97	0.05	2.04	0.07
SPO1501	*pqqD*	PQQ synthesis protein D	-1.10	0.84	3.43	0.11	1.17	2.27	-4.40	0.27	-1.18	0.77	-2.79	1.61	3.51	0.06	2.65	0.13	3.08	0.43
SPO1502	*pqqC*	quinone biosynthesis protein PqqC	1.04	0.34	2.33	0.11	1.69	0.65	-8.58	0.00	-1.26	0.39	-4.92	3.66	3.52	0.00	2.30	0.14	2.91	0.61
SPO1503	*pqqB*	quinone biosynthesis protein PqqB	-1.16	0.33	4.75	0.03	1.80	2.96	-10.70	0.04	-1.16	0.73	-5.93	4.77	4.41	0.03	3.30	0.05	3.86	0.55
SPO1504	*pqqA*	PQQ biosynthesis protein A	0.81	0.01	4.72	0.00	2.77	1.95	-47.00	0.00	1.43	0.10	-22.79	24.22	3.69	0.00	7.03	0.00	5.36	1.67
SPO1505		sensor histidine kinase/response regulator (EC:2.7.3.-)	1.00	0.21	1.07	0.53	1.03	0.04	-5.09	0.00	1.11	0.78	-1.99	3.10	1.41	0.05	1.33	0.58	1.37	0.04
SPO1506		GfdT protein	-1.77	0.01	-1.12	0.03	-1.45	0.33	-7.45	0.00	1.32	0.10	-3.07	4.39	1.23	0.23	1.09	0.45	1.16	0.07
SPO1507		LuxR family transcriptional regulator	-1.17	0.09	3.53	0.06	1.18	2.35	-13.90	0.00	-1.03	0.83	-7.47	6.44	2.80	0.02	2.17	0.02	2.49	0.32
SPO1508		quinoprotein ethanol dehydrogenase (EC:1.1.99.-)	-2.08	0.07	2.96	0.08	0.44	2.52	-65.20	0.00	-1.01	0.87	-33.11	32.10	4.50	0.06	5.52	0.08	5.01	0.51
SPO1509		cytochrome c family protein	-2.11	0.01	1.39	0.41	-0.36	1.75	-56.80	0.00	-1.37	0.15	-29.09	27.72	2.11	0.02	X	X	N/A	N/A
SPO1510		ABC transporter permease	-1.06	0.06	1.76	0.01	0.35	1.41	-9.02	0.00	1.06	0.21	-3.98	5.04	1.85	0.01	1.22	0.12	1.54	0.31
SPO1511		ABC transporter ATP-binding protein	1.03	0.74	2.22	0.01	1.63	0.60	-4.46	0.09	1.12	0.16	-1.67	2.79	3.11	0.00	2.02	0.01	2.57	0.54
SPO1512		hypothetical protein	1.02	0.40	2.58	0.00	1.80	0.78	-11.50	0.00	1.13	0.20	-5.19	6.32	2.30	0.00	1.99	0.03	2.15	0.16
SPO1513		hypothetical protein	1.19	0.93	6.07	0.00	3.63	2.44	-17.00	0.00	-1.47	0.17	-9.24	7.77	5.50	0.00	3.95	0.03	4.73	0.78
SPO1514		hypothetical protein	-1.60	0.34	4.34	0.01	1.37	2.97	-21.80	0.00	-1.62	0.33	-11.71	10.09	6.01	0.02	4.48	0.02	5.25	0.76
SPO1515		cytochrome c550	-1.21	0.02	7.22	0.00	3.01	4.22	-35.80	0.00	-1.50	0.08	-18.65	17.15	7.73	0.00	5.27	0.00	6.50	1.23
SPO1516		amino acid ABC transporter substrate-binding protein	1.15	0.88	3.97	0.12	2.56	1.41	-12.00	0.01	1.09	0.93	-5.46	6.55	4.57	0.09	2.62	0.21	3.60	0.97
SPO1517	*coxG*	monoxide dehydrogenase operon G protein	-1.31	0.28	4.37	0.00	1.53	2.84	-12.40	0.00	1.34	0.14	-5.53	6.87	4.23	0.00	4.91	0.00	4.57	0.34
SPO1518	*coxS-1*	dehydrogenase, small subunit (EC:1.2.99.2)	-2.58	0.00	1.56	0.04	-0.51	2.07	-30.10	0.00	2.51	0.01	-13.80	16.31	3.27	0.01	6.00	0.00	4.64	1.37
SPO1519	*coxL-1*	monoxide dehydrogenase, large subunit (EC:1.2.99.2)	0.91	0.01	1.79	0.05	1.35	0.44	-23.10	0.00	2.60	0.01	-10.25	12.85	4.11	0.02	6.22	0.00	5.17	1.06
SPO1520	*coxM-1*	carbon monoxide dehydrogenase, medium subunit	-1.46	0.07	1.56	0.08	0.05	1.51	-16.10	0.00	2.23	0.01	-6.94	9.17	2.57	0.02	3.78	0.00	3.18	0.60
SPO1521		regulatory protein	-1.74	0.01	3.31	0.02	0.79	2.53	-10.50	0.00	1.16	0.23	-4.67	5.83	2.12	0.08	-1.27	X	0.43	1.70
SPO1522		hypothetical protein	1.24	0.54	1.48	0.08	1.36	0.12	2.29	0.00	1.06	0.77	1.68	0.62	1.73	0.02	1.41	0.04	1.57	0.16
SPO1523		metallo-beta-lactamase	-1.97	0.00	1.97	0.01	0.00	1.97	-29.80	0.00	1.07	0.38	-14.37	15.44	2.78	0.01	2.08	0.03	2.43	0.35
SPO1524		hypothetical protein	-1.93	0.01	2.80	0.00	0.44	2.37	-44.50	0.00	-1.01	0.99	-22.76	21.75	5.56	0.00	2.81	0.02	4.19	1.38
SPO1525		AcrB/AcrD/AcrF family transporter	1.33	0.92	1.02	0.96	1.18	0.16	1.60	0.84	-0.99	0.88	0.31	1.29	1.24	0.40	-0.88	0.11	0.18	1.06
SPO1526		RND family efflux transporter MFP subunit	1.48	0.32	-1.17	0.81	0.16	1.33	1.59	0.10	-1.25	0.79	0.17	1.42	-0.99	0.97	1.49	0.59	0.25	1.24
SPO1527		hypothetical protein	1.90	0.09	-1.22	0.90	0.34	1.56	-3.18	0.05	X	X	N/A	N/A	-1.18	0.71	2.00	X	0.41	1.59
SPO1528		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.12	0.34	X	X	N/A	N/A
SPO1529		hypothetical protein	-1.14	0.43	-1.16	0.50	-1.15	0.01	-2.47	0.05	1.04	0.89	-0.72	1.76	-1.19	0.85	1.11	0.42	-0.04	1.15
SPO1530		integral membrane protein MviN	1.03	0.99	1.19	0.72	1.11	0.08	-1.01	0.91	1.24	0.63	0.12	1.13	1.99	0.32	1.52	X	1.76	0.24

SPO1531		hypothetical protein	-1.15	0.67	1.33	0.34	0.09	1.24	-1.58	0.69	1.20	X	-0.19	1.39	1.18	0.63	X	X	N/A	N/A
SPO1532		hypothetical protein	-1.02	1.00	1.01	0.77	-0.01	1.02	1.16	0.44	1.54	0.03	1.35	0.19	1.25	0.23	-0.92	0.38	0.16	1.09
SPO1533		glycoside hydrolase	-1.35	0.60	1.01	0.93	-0.17	1.18	-1.10	0.73	-1.12	0.53	-1.11	0.01	1.31	0.28	-1.45	0.03	-0.07	1.38
SPO1534		sugar transferase	1.30	0.08	1.15	0.28	1.23	0.08	-1.56	0.03	1.28	0.29	-0.14	1.42	1.25	0.18	1.57	0.10	1.41	0.16
SPO1535		polysaccharide deacetylase	1.36	0.88	1.39	0.21	1.38	0.01	1.14	0.95	1.24	0.32	1.19	0.05	2.03	0.12	2.09	0.03	2.06	0.03
SPO1536		group 1 family glycosyltransferase	1.43	0.16	1.50	0.09	1.47	0.04	-1.32	0.00	1.63	0.01	0.16	1.48	1.31	0.06	1.21	0.20	1.26	0.05
SPO1537		twin-arginine translocation pathway signal sequence domain-containing protein	1.88	0.08	1.45	0.01	1.67	0.21	-0.93	0.10	1.79	0.02	0.43	1.36	1.33	0.03	-1.29	0.23	0.02	1.31
SPO1538		chain length determinant protein	1.26	0.15	1.44	0.04	1.35	0.09	-1.01	0.56	1.91	0.07	0.45	1.46	1.53	0.01	1.32	0.07	1.43	0.11
SPO1539		O-antigen polymerase	1.32	0.11	-1.06	0.88	0.13	1.19	-1.69	0.03	1.49	0.02	-0.10	1.59	1.10	0.34	1.20	0.15	1.15	0.05
SPO1540		glycosyl transferase family protein	1.16	0.76	1.13	0.44	1.15	0.02	-1.21	0.97	1.50	0.02	0.15	1.36	-1.10	0.77	1.21	0.13	0.05	1.16
SPO1541		LysR family transcriptional regulator	-4.93	0.00	-2.05	0.01	-3.49	1.44	-1.17	0.95	-1.55	0.12	-1.36	0.19	-1.41	0.01	-1.24	0.21	-1.33	0.09
SPO1542		renal dipeptidase	-2.93	0.27	-3.79	0.14	-3.36	0.43	-10.40	0.09	1.50	0.58	-4.45	5.95	1.09	0.92	1.02	0.95	1.06	0.04
SPO1543		peptide/opine/nickel uptake ABC transporter substrate-binding protein	-3.79	0.00	-6.49	0.00	-5.14	1.35	-20.40	0.00	1.41	0.21	-9.50	10.91	1.38	0.35	1.78	0.19	1.58	0.20
SPO1544		peptide/opine/nickel uptake ABC transporter permease	-4.28	0.01	-2.90	0.12	-3.59	0.69	-13.00	0.01	1.49	0.48	-5.76	7.25	-1.00	0.98	-1.16	0.73	-1.08	0.08
SPO1545		peptide/opine/nickel uptake ABC transporter permease	-2.17	0.08	-3.08	0.12	-2.63	0.46	-4.17	0.16	1.41	0.46	-1.38	2.79	1.26	0.30	-1.26	0.59	0.00	1.26
SPO1546		peptide/opine/nickel uptake ABC transporter ATP-binding protein	-2.82	0.00	-3.25	0.01	-3.04	0.22	-8.41	0.01	1.34	0.16	-3.54	4.88	1.29	0.10	-1.48	0.07	-0.10	1.39
SPO1547		peptide/opine/nickel uptake ABC transporter ATP-binding protein	-3.31	0.01	-2.81	0.02	-3.06	0.25	-10.30	0.00	1.32	0.06	-4.49	5.81	1.12	0.75	-1.74	0.05	-0.31	1.43
SPO1548		glycine betaine/proline ABC transporter substrate-binding protein	-2.22	0.00	-1.72	0.07	-1.97	0.25	-6.14	0.00	1.16	0.12	-2.49	3.65	-1.23	0.15	-1.03	0.32	-1.13	0.10
SPO1549		glycine betaine/proline ABC transporter ATP-binding protein (EC:3.6.3.32)	-2.01	0.01	-1.86	0.04	-1.94	0.07	3.42	0.01	-1.34	0.30	1.04	2.38	-1.06	0.81	1.64	0.26	0.29	1.35
SPO1550		glycine betaine/proline ABC transporter permease	-2.12	X	-1.55	0.82	-1.84	0.29	-1.83	0.83	-1.28	X	-1.56	0.27	1.16	0.84	1.56	X	1.36	0.20
SPO1551		flavin-containing monooxygenase	-1.06	0.88	-1.48	0.32	-1.27	0.21	-1.29	0.80	-1.01	0.99	-1.15	0.14	-1.02	1.00	-0.95	0.50	-0.99	0.03
SPO1552		ABC transporter substrate-binding protein	-2.08	0.04	-1.14	0.52	-1.61	0.47	-2.09	0.04	1.13	0.79	-0.48	1.61	-1.02	0.92	1.38	0.55	0.18	1.20
SPO1553		GntR family transcriptional regulator	-1.63	0.27	-1.13	0.85	-1.38	0.25	1.06	0.96	1.22	0.82	1.14	0.08	-1.04	0.93	1.09	0.93	0.03	1.07
SPO1554		ammonium transporter	-1.68	0.03	-1.17	0.20	-1.43	0.26	-1.62	0.11	-1.03	0.97	-1.33	0.30	-1.29	0.21	1.35	0.12	0.03	1.32
SPO1555		formate dehydrogenase subunit beta (EC:1.2.1.2)	3.84	0.09	1.34	0.58	2.59	1.25	2.23	0.23	-6.94	0.06	-2.36	4.59	1.09	0.94	1.50	0.66	1.30	0.21
SPO1556		formate dehydrogenase subunit alpha (EC:1.2.1.2)	2.34	0.01	-1.03	0.94	0.66	1.69	1.15	0.63	-1.25	0.42	-0.05	1.20	-1.55	0.12	-1.15	0.71	-1.35	0.20
SPO1557	*fhs-1*	ligase (EC:6.3.4.3)	11.90	0.00	2.36	0.04	7.13	4.77	1.23	0.20	-2.30	0.00	-0.54	1.77	-1.52	0.06	-1.80	0.04	-1.66	0.14
SPO1558		chorismate mutase	5.55	0.33	2.39	0.08	3.97	1.58	1.48	0.83	-1.30	0.45	0.09	1.39	-1.27	0.45	-1.43	0.33	-1.35	0.08
SPO1559		bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	11.70	0.21	2.54	0.01	7.12	4.58	3.71	0.01	-1.23	0.16	1.24	2.47	-1.17	0.31	-1.70	0.01	-1.44	0.27
SPO1560	*folD*	5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	1.08	X	1.64	0.01	1.36	0.28	3.87	0.01	-1.32	0.05	1.28	2.60	-1.25	0.07	-2.22	0.00	-1.74	0.49
SPO1561		hypothetical protein	-0.97	0.57	1.54	0.03	0.29	1.25	1.81	0.00	-1.11	0.72	0.35	1.46	1.24	0.21	-1.55	X	-0.16	1.40
SPO1562		glycine cleavage system T protein	1.79	0.12	1.21	0.04	1.50	0.29	1.14	0.37	1.36	0.13	1.25	0.11	1.02	0.62	-0.96	0.26	0.03	0.99
SPO1563		hypothetical protein	1.45	0.21	1.28	0.03	1.37	0.09	2.23	0.02	1.19	0.09	1.71	0.52	1.67	0.05	-1.01	0.31	0.33	1.34
SPO1564		MOFRL domain-containing protein	1.19	0.08	1.23	0.44	1.21	0.02	1.27	0.13	-4.03	0.04	-1.38	2.65	1.86	0.01	1.97	0.02	1.92	0.05

SPO1565		citrate lyase	1.46	0.07	2.01	0.00	1.74	0.27	-1.11	0.83	-5.12	0.00	-3.12	2.01	1.37	0.12	1.62	0.01	1.50	0.13
SPO1566		LuxR family transcriptional regulator	-1.36	0.21	-1.34	0.54	-1.35	0.01	-1.49	0.20	-1.61	0.07	-1.55	0.06	-1.42	0.09	-0.97	0.28	-1.20	0.22
SPO1567		aminotransferase	1.64	0.52	-1.18	0.36	0.23	1.41	-1.76	0.52	-1.35	0.20	-1.56	0.20	-1.15	0.63	1.42	0.36	0.14	1.29
SPO1568	*sucC*	ligase subunit beta (EC:6.2.1.5)	2.15	0.02	-1.38	0.05	0.39	1.77	-3.62	0.01	-1.18	0.13	-2.40	1.22	-1.26	0.05	-1.12	0.72	-1.19	0.07
SPO1569		succinyl-CoA synthetase subunit alpha (EC:6.2.1.5)	2.24	0.03	-1.50	0.22	0.37	1.87	-2.17	0.10	-1.36	0.16	-1.77	0.41	-1.17	0.41	-1.16	0.69	-1.17	0.01
SPO1570		2-hydroxyacid dehydrogenase	1.89	0.04	-1.17	0.39	0.36	1.53	-1.70	0.11	-1.52	0.04	-1.61	0.09	1.07	0.61	-1.00	0.54	0.04	1.03
SPO1571	*ppc*	carboxylase (EC:4.1.1.31)	-1.12	0.74	-1.22	0.35	-1.17	0.05	-1.20	0.55	-1.25	0.09	-1.23	0.03	-0.99	0.85	1.30	X	0.16	1.14
SPO1572	*glyA*	hydroxymethyltransferase (EC:2.1.2.1)	3.16	0.00	2.03	0.07	2.60	0.57	3.58	0.01	-1.58	0.01	1.00	2.58	-2.09	0.01	-2.06	0.01	-2.08	0.01
SPO1573	*glnT*	synthetase (EC:6.3.1.2)	X	X	-1.20	0.24	N/A	N/A	-1.13	0.42	-1.21	0.46	-1.17	0.04	1.17	0.31	-1.06	X	0.05	1.12
SPO1574		glutamate synthase	1.08	0.81	-1.23	0.37	-0.08	1.16	-1.66	0.02	-1.06	0.66	-1.36	0.30	-1.35	0.24	1.29	0.50	-0.03	1.32
SPO1575		FwdC/FmdC family protein	-1.16	0.89	-1.13	0.25	-1.15	0.02	-1.85	0.05	1.05	0.85	-0.40	1.45	-1.70	0.02	-1.57	0.01	-1.64	0.06
SPO1576		glutamine amidotransferase	1.74	0.61	1.04	0.88	1.39	0.35	-1.13	0.88	1.08	0.80	-0.02	1.11	-1.56	0.16	-1.52	0.24	-1.54	0.02
SPO1577		hypothetical protein	-1.48	0.38	1.13	0.17	-0.18	1.31	-1.39	0.10	1.18	0.33	-0.11	1.29	-1.02	0.95	-1.43	0.37	-1.23	0.20
SPO1578		ammonium transporter	-1.41	X	1.09	0.79	-0.16	1.25	-2.27	X	1.50	X	-0.39	1.89	-0.96	0.85	X	X	N/A	N/A
SPO1579		glycine cleavage system protein T	-1.37	0.29	-1.48	0.47	-1.43	0.05	-2.53	0.12	1.73	0.22	-0.40	2.13	-1.02	0.92	1.16	0.66	0.07	1.09
SPO1580		hypothetical protein	1.03	0.58	-1.17	0.03	-0.07	1.10	-1.94	0.04	1.65	0.03	-0.15	1.80	1.02	0.89	1.10	0.05	1.06	0.04
SPO1581		oxidoreductase	-1.03	0.44	-1.17	0.14	-1.10	0.07	-1.78	0.02	1.80	0.07	0.01	1.79	-1.03	0.54	-1.03	0.47	-1.03	0.00
SPO1582		hypothetical protein	1.50	0.37	-1.01	0.99	0.25	1.26	-1.13	0.56	1.53	0.13	0.20	1.33	1.30	0.32	1.23	0.18	1.27	0.04
SPO1583		DNA-binding protein	1.06	0.92	1.40	0.23	1.23	0.17	1.92	0.22	1.13	0.62	1.53	0.40	1.12	0.61	-1.58	0.05	-0.23	1.35
SPO1584		AraC family transcriptional regulator	0.98	0.95	1.03	0.92	1.00	0.03	-1.27	0.88	-1.00	0.97	-1.13	0.14	1.34	0.32	1.25	0.39	1.30	0.05
SPO1585		sarcosine oxidase subunit gamma	1.92	0.84	1.41	0.24	1.67	0.26	1.23	0.90	2.15	0.24	1.69	0.46	1.21	0.42	X	X	N/A	N/A
SPO1586		sarcosine oxidase subunit alpha	3.09	0.00	-1.04	0.90	1.03	2.07	-0.89	0.05	1.36	0.36	0.24	1.13	-1.35	0.53	-0.96	0.49	-1.15	0.20
SPO1587		sarcosine oxidase subunit delta	1.43	0.88	1.07	0.82	1.25	0.18	-2.22	0.70	2.69	0.04	0.24	2.46	-1.23	0.52	-1.74	0.17	-1.49	0.26
SPO1588		sarcosine oxidase subunit beta	6.19	0.01	1.19	0.21	3.69	2.50	1.33	0.26	X	X	N/A	N/A	-1.15	0.57	X	X	N/A	N/A
SPO1589		carboxymuconolactone decarboxylase	1.72	0.01	1.12	0.10	1.42	0.30	1.29	0.02	1.15	0.36	1.22	0.07	1.04	0.74	-1.12	0.31	-0.04	1.08
SPO1590		Rieske (2Fe-2S) domain-containing protein	5.28	0.15	1.27	0.09	3.28	2.01	-1.23	0.58	-1.79	0.06	-1.51	0.28	-1.17	0.50	-1.82	0.09	-1.50	0.33
SPO1591		SIS domain-containing protein	3.67	0.00	1.07	0.13	2.37	1.30	-1.70	0.10	-1.62	0.08	-1.66	0.04	-1.83	0.03	-2.51	0.01	-2.17	0.34
SPO1592		glycine cleavage system protein T	5.15	0.04	1.24	0.14	3.20	1.96	-1.29	0.72	-1.60	0.00	-1.45	0.16	-0.98	0.58	-1.55	0.31	-1.26	0.29
SPO1593		alcohol dehydrogenase	3.12	0.01	1.05	0.50	2.09	1.04	6.05	0.00	-1.26	0.06	2.40	3.66	-1.44	0.06	-1.32	0.50	-1.38	0.06
SPO1594		mandelate racemase	3.20	0.06	1.47	0.40	2.34	0.87	-0.89	0.55	-1.45	0.28	-1.17	0.28	1.12	0.61	-1.35	0.49	-0.12	1.24
SPO1595		mandelate racemase	-1.56	0.14	-1.30	0.68	-1.43	0.13	-2.70	0.01	-1.13	0.79	-1.92	0.79	-1.04	0.79	2.11	0.06	0.54	1.58
SPO1596	*dddQ*	lyase	2.84	0.02	1.14	0.22	1.99	0.85	3.96	0.00	1.18	0.29	2.57	1.39	1.15	0.25	-1.06	0.99	0.04	1.11
SPO1597	*hemL*	2,1-aminomutase (EC:5.4.3.8)	2.40	0.17	1.30	0.22	1.85	0.55	-1.06	0.99	1.16	0.42	0.05	1.11	1.11	0.03	-1.02	0.97	0.05	1.07
SPO1598		hypothetical protein	2.75	0.01	2.84	0.03	2.80	0.04	2.85	0.01	1.57	0.05	2.21	0.64	-1.01	0.92	1.20	0.61	0.10	1.11
SPO1599		MmgE/PrpD family protein	-1.90	0.34	-1.49	0.34	-1.70	0.21	-2.75	0.08	-1.13	0.56	-1.94	0.81	-1.38	0.64	1.93	0.53	0.28	1.66
SPO1600		fumarylacetoacetate hydrolase	1.13	0.15	-1.27	0.23	-0.07	1.20	1.55	0.02	-1.34	0.51	0.11	1.45	-1.94	0.07	-2.56	0.17	-2.25	0.31
SPO1601	*panE-2*	2-reductase (EC:1.1.1.169)	-1.01	X	-1.03	1.00	-1.02	0.01	-1.07	0.44	-1.08	X	-1.08	0.01	1.23	0.27	X	X	N/A	N/A
SPO1602		trimethylamine methyltransferase	-1.11	0.54	-1.36	0.73	-1.24	0.13	2.27	0.04	-1.14	0.78	0.57	1.71	1.17	0.52	1.67	0.59	1.42	0.25
SPO1603		malate/L-lactate dehydrogenase	-1.67	0.09	-1.00	0.92	-1.33	0.34	-2.22	0.05	1.44	0.53	-0.39	1.83	-1.38	0.29	-0.97	0.92	-1.17	0.21

SPO1604		LysR family transcriptional regulator	1.62	0.21	-1.04	0.94	0.29	1.33	-1.84	0.30	1.28	0.29	-0.28	1.56	-0.97	0.85	-1.06	0.94	-1.01	0.05
SPO1605		hypothetical protein	-1.04	0.15	1.02	0.72	-0.01	1.03	-3.07	0.01	1.78	0.01	-0.65	2.43	-1.08	0.47	-1.15	0.53	-1.12	0.03
SPO1606	*potD*	ABC transporter substrate-binding protein	-1.28	0.24	-1.61	0.02	-1.45	0.17	-3.16	0.09	1.70	0.04	-0.73	2.43	1.34	0.25	1.90	0.04	1.62	0.28
SPO1607		spermidine/putrescine ABC transporter permease	-1.40	0.05	-2.08	0.14	-1.74	0.34	-2.67	0.08	1.72	0.06	-0.48	2.20	-1.37	0.18	1.27	0.64	-0.05	1.32
SPO1608	*potB*	ABC transporter permease	1.13	0.27	-1.01	0.98	0.06	1.07	-1.62	0.49	1.55	0.14	-0.04	1.59	1.58	0.11	1.15	0.29	1.37	0.22
SPO1609	*potA*	ABC transporter ATP-binding component	-1.22	0.72	-1.34	0.66	-1.28	0.06	-2.59	0.37	1.62	0.44	-0.49	2.11	1.07	0.92	1.30	0.67	1.19	0.12
SPO1610		LuxR family transcriptional regulator	X	X	1.07	0.12	N/A	N/A	2.24	0.07	-1.31	0.29	0.47	1.78	1.07	0.31	X	X	N/A	N/A
SPO1611		hypothetical protein	1.17	0.97	-1.08	0.95	0.04	1.13	1.61	0.83	-1.35	X	0.13	1.48	-1.23	0.90	1.79	X	0.28	1.51
SPO1612		twin-arginine translocation pathway signal sequence domain-containing protein	-2.53	X	1.03	0.88	-0.75	1.78	-2.14	0.34	X	X	N/A	N/A	-1.44	0.34	-1.22	0.68	-1.33	0.11
SPO1613		hypothetical protein	X	X	-1.29	0.34	N/A	N/A	-1.05	0.64	X	X	N/A	N/A	1.16	0.36	X	X	N/A	N/A
SPO1614		hypothetical protein	1.15	0.98	1.14	0.69	1.15	0.01	1.53	0.83	-1.32	0.64	0.11	1.43	1.48	0.18	1.16	0.33	1.32	0.16
SPO1615		cyclic nucleotide-binding protein	5.33	0.04	3.35	0.00	4.34	0.99	5.38	0.01	1.51	0.07	3.45	1.94	1.18	0.12	-0.99	0.45	0.10	1.09
SPO1616		transcriptional regulator	X	X	-1.52	0.05	N/A	N/A	2.09	0.00	-1.52	0.05	0.29	1.81	1.08	0.57	X	X	N/A	N/A
SPO1617		type I secretion target repeat-containing protein	X	X	-1.02	X	N/A	N/A	-1.11	X	X	X	N/A	N/A	-1.13	X	X	X	N/A	N/A
SPO1618		hypothetical protein	-1.82	0.08	-1.38	0.63	-1.60	0.22	-1.62	0.10	-1.54	0.60	-1.58	0.04	-1.26	0.62	-1.22	0.84	-1.24	0.02
SPO1619		hypothetical protein	X	X	-1.04	0.95	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1620		glyoxalase	1.38	0.16	1.08	0.87	1.23	0.15	2.32	0.03	-2.12	0.02	0.10	2.22	1.06	0.66	-1.49	0.10	-0.22	1.28
SPO1621		TfoX domain-containing protein	-1.12	0.11	-1.04	0.88	-1.08	0.04	-1.54	0.12	1.39	0.13	-0.08	1.47	1.49	0.02	1.41	0.02	1.45	0.04
SPO1622		cytochrome P450 family protein	5.05	0.01	2.27	0.02	3.66	1.39	1.82	0.03	1.66	0.01	1.74	0.08	1.20	0.18	1.43	0.01	1.32	0.12
SPO1623		sensor histidine kinase (EC:2.7.3.-)	-1.75	0.02	-1.30	0.54	-1.53	0.23	1.81	0.11	1.17	0.61	1.49	0.32	-1.12	0.65	1.47	0.10	0.18	1.30
SPO1624		DNA-binding response regulator	-1.19	0.10	-1.25	0.33	-1.22	0.03	6.62	0.00	1.03	0.99	3.83	2.80	-1.27	0.10	-1.85	0.04	-1.56	0.29
SPO1625		serine protease	-2.43	0.24	-1.44	0.16	-1.94	0.50	8.94	0.01	2.12	0.02	5.53	3.41	1.01	0.77	1.14	0.31	1.08	0.06
SPO1626		type I secretion target repeat-containing protein	4.49	0.00	2.89	0.10	3.69	0.80	-0.99	0.43	1.65	0.03	0.33	1.32	-1.26	0.01	-1.55	0.01	-1.41	0.15
SPO1627		hypothetical protein	1.76	0.05	1.31	0.34	1.54	0.22	1.29	0.26	1.21	0.41	1.25	0.04	1.44	0.06	1.41	0.21	1.43	0.02
SPO1628		glycine cleavage system protein T	6.71	0.01	2.76	0.03	4.74	1.98	-2.77	0.06	-1.36	0.54	-2.07	0.71	-1.27	0.42	-1.18	0.81	-1.23	0.05
SPO1629		hypothetical protein	-1.35	0.06	-1.06	0.88	-1.21	0.15	-1.36	0.05	-1.17	0.69	-1.27	0.10	1.18	0.28	1.46	0.43	1.32	0.14
SPO1630		hypothetical protein	X	X	-1.12	0.72	N/A	N/A	1.77	0.00	-1.42	0.09	0.18	1.60	1.47	0.08	-0.97	0.69	0.25	1.22
SPO1631		hypothetical protein	1.02	0.99	1.00	0.69	1.01	0.01	1.43	0.17	-1.28	0.11	0.08	1.36	1.60	0.01	1.04	0.86	1.32	0.28
SPO1632	*xerD*	recombinase XerD	-1.38	0.02	-1.81	0.02	-1.60	0.21	1.23	0.39	1.01	0.32	1.12	0.11	1.03	0.93	1.31	0.34	1.17	0.14
SPO1633		hypothetical protein	-2.19	X	-1.38	0.68	-1.79	0.41	-2.23	0.56	-1.17	0.81	-1.70	0.53	-1.04	0.97	1.52	X	0.24	1.28
SPO1634	*aroK*	kinase (EC:2.7.1.71)	1.17	0.37	2.28	0.08	1.73	0.56	2.04	0.01	1.23	0.31	1.64	0.41	-1.26	0.18	-1.32	0.20	-1.29	0.03
SPO1635	*aroB*	synthase (EC:4.2.3.4)	-1.30	0.31	1.95	0.05	0.33	1.63	0.98	0.80	-1.26	0.20	-0.14	1.12	1.37	0.03	-1.09	0.67	0.14	1.23
SPO1636		SREBP protease	-1.36	0.71	1.01	0.99	-0.18	1.19	1.50	0.62	-1.05	0.90	0.23	1.28	1.41	0.63	1.13	0.90	1.27	0.14
SPO1637	*ssb*	binding protein	1.19	0.97	-1.26	0.27	-0.04	1.23	1.91	0.11	1.08	0.97	1.50	0.42	1.26	0.21	1.62	0.12	1.44	0.18
SPO1638		transglycosylase	-1.15	0.17	1.02	1.00	-0.06	1.09	2.65	0.00	0.99	0.84	1.82	0.83	1.32	0.09	-1.13	0.56	0.10	1.23
SPO1639		FadB domain-containing protein	X	X	1.32	0.31	N/A	N/A	2.42	0.02	-1.17	0.56	0.63	1.80	1.15	0.12	-1.37	0.33	-0.11	1.26
SPO1640		LysR family transcriptional regulator	-1.46	0.01	-1.15	0.35	-1.31	0.16	-1.13	0.72	-1.42	0.07	-1.28	0.14	1.09	0.40	-1.42	0.07	-0.17	1.26
SPO1641		beta-lactamase	-1.21	0.27	-1.32	0.29	-1.27	0.06	-2.01	0.20	1.09	0.79	-0.46	1.55	-1.30	0.16	-1.29	0.79	-1.30	0.01
SPO1642		hypothetical protein	-2.03	0.12	-1.41	0.40	-1.72	0.31	-2.13	0.12	-1.02	0.89	-1.58	0.56	-1.28	0.56	1.48	0.47	0.10	1.38

SPO1643		selenium-binding protein	-1.41	0.33	-1.78	0.27	-1.60	0.18	-3.40	0.07	2.09	0.16	-0.66	2.75	1.45	0.26	1.97	0.16	1.71	0.26
SPO1644		oligopeptide/dipeptide ABC transporter ATP-binding protein	8.89	0.03	1.06	0.81	4.98	3.92	-1.43	0.87	1.21	X	-0.11	1.32	-1.14	0.64	X	X	N/A	N/A
SPO1645		oligopeptide/dipeptide ABC transporter permease	8.33	0.04	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1646		oligopeptide/dipeptide ABC transporter permease	6.88	0.04	-1.04	0.98	2.92	3.96	-1.28	1.00	-1.02	1.00	-1.15	0.13	-0.95	0.90	-0.99	0.74	-0.97	0.02
SPO1647		oligopeptide/dipeptide ABC transporter substrate-binding protein	4.98	0.22	-1.02	0.99	1.98	3.00	-2.15	0.45	1.35	0.79	-0.40	1.75	1.07	0.94	1.21	0.90	1.14	0.07
SPO1648		glycine cleavage system protein T	4.31	0.03	1.25	X	2.78	1.53	-0.90	0.29	-1.24	X	-1.07	0.17	-1.42	X	X	X	N/A	N/A
SPO1649		invasion protein IbeA	X	X	1.29	0.40	N/A	N/A	-1.13	0.57	-1.14	X	-1.14	0.01	-1.23	0.50	X	X	N/A	N/A
SPO1650		hypothetical protein	1.06	0.62	1.12	0.37	1.09	0.03	-2.19	0.10	-1.08	0.86	-1.64	0.56	1.33	0.15	2.74	X	2.04	0.71
SPO1651		hypothetical protein	X	X	1.03	0.83	N/A	N/A	-1.05	0.05	1.26	0.27	0.11	1.16	-0.97	0.50	X	X	N/A	N/A
SPO1652		transposase, truncation	X	X	-1.18	0.47	N/A	N/A	-2.24	0.03	-0.96	0.67	-1.60	0.64	-1.33	0.24	-1.06	X	-1.20	0.14
SPO1655		hypothetical protein	X	X	-1.26	0.43	N/A	N/A	-2.57	X	-1.07	X	-1.82	0.75	-1.09	0.94	1.37	X	0.14	1.23
SPO1656		oligopeptide/dipeptide ABC transporter ATP-binding protein	-1.34	0.19	-1.67	0.02	-1.51	0.17	-2.30	0.03	1.62	0.05	-0.34	1.96	1.27	0.17	1.49	0.03	1.38	0.11
SPO1657		oligopeptide/dipeptide ABC transporter permease	-1.07	0.06	-1.63	0.02	-1.35	0.28	-2.19	0.00	1.25	0.09	-0.47	1.72	1.38	0.08	1.89	0.02	1.64	0.26
SPO1658		oligopeptide/dipeptide ABC transporter permease	-1.17	0.89	-1.88	0.12	-1.53	0.36	-2.49	0.25	1.40	0.38	-0.55	1.95	1.29	0.40	1.70	0.17	1.50	0.20
SPO1659		oligopeptide/dipeptide ABC transporter substrate-binding protein	-1.60	0.02	-1.82	0.08	-1.71	0.11	-3.05	0.00	2.29	0.01	-0.38	2.67	1.20	0.25	3.02	0.01	2.11	0.91
SPO1660		AraC family transcriptional regulator	-1.23	X	1.05	0.86	-0.09	1.14	1.08	X	1.21	0.71	1.15	0.06	-1.03	0.98	-1.30	0.70	-1.17	0.14
SPO1661	*miaA*	delta(2)-isopentenylpyrophosphate transferase (EC:2.5.1.75)	1.34	X	1.03	0.88	1.19	0.16	1.73	0.55	1.18	0.54	1.46	0.27	-1.02	0.92	-1.40	0.40	-1.21	0.19
SPO1662	*pyrH*	kinase (EC:2.7.4.-)	1.01	0.14	0.96	0.71	0.99	0.02	1.27	0.59	1.28	0.14	1.28	0.01	1.16	0.60	1.89	0.01	1.53	0.37
SPO1663		hypothetical protein	1.51	0.11	1.34	0.42	1.43	0.09	1.17	0.70	-1.24	0.54	-0.04	1.21	-1.25	0.50	-1.71	0.14	-1.48	0.23
SPO1664	*frr*	recycling factor	1.00	0.03	-1.20	0.37	-0.10	1.10	1.59	0.00	1.23	0.36	1.41	0.18	-1.19	0.02	0.90	0.12	-0.14	1.05
SPO1665	*uppS*	diphosphate synthase (EC:2.5.1.31)	-1.09	0.22	1.13	0.34	0.02	1.11	1.93	0.00	1.07	0.63	1.50	0.43	1.07	0.77	-1.21	0.12	-0.07	1.14
SPO1666	*cdsA*	cytidylyltransferase (EC:2.7.7.41)	-1.63	0.01	1.37	0.16	-0.13	1.50	1.24	0.07	-1.16	0.14	0.04	1.20	1.32	0.10	-1.22	0.05	0.05	1.27
SPO1667	*dxr*	5-phosphate reductoisomerase (EC:1.1.1.267)	1.40	0.04	-1.09	0.56	0.16	1.25	1.94	0.04	-1.08	0.34	0.43	1.51	-1.25	0.26	-1.44	0.09	-1.35	0.10
SPO1668		zinc metalloprotease	1.49	0.91	-1.07	0.92	0.21	1.28	1.67	0.83	-1.23	0.75	0.22	1.45	1.31	0.71	1.22	0.88	1.27	0.05
SPO1669		hypothetical protein	2.41	0.20	1.59	0.18	2.00	0.41	0.80	0.17	-1.09	0.46	-0.14	0.95	1.85	0.08	-1.43	0.13	0.21	1.64
SPO1670		OMP85 family outer membrane protein	2.12	0.00	1.38	0.02	1.75	0.37	2.29	0.01	1.20	0.20	1.75	0.55	1.08	0.41	-1.06	0.30	0.01	1.07
SPO1671		hypothetical protein	1.27	0.55	1.37	0.14	1.32	0.05	1.12	0.67	1.15	0.38	1.14	0.01	1.00	0.85	-1.07	0.16	-0.04	1.04
SPO1672	*fabZ*	dehydratase (EC:4.2.1.-)	1.40	0.22	1.09	0.78	1.25	0.15	1.75	0.07	1.04	0.86	1.40	0.36	1.06	0.90	1.06	0.75	1.06	0.00
SPO1673	*lpxA*	acyltransferase (EC:2.3.1.129)	1.38	0.01	1.36	0.02	1.37	0.01	2.26	0.01	-1.05	0.19	0.61	1.66	1.06	0.78	-1.33	0.07	-0.14	1.20
SPO1674		hypothetical protein	1.22	0.95	1.29	0.59	1.26	0.04	1.41	0.86	-1.05	0.76	0.18	1.23	1.44	0.37	1.31	0.40	1.38	0.06
SPO1675	*lpxB*	synthase (EC:2.4.1.182)	1.35	0.14	1.33	0.34	1.34	0.01	2.17	0.02	1.00	0.64	1.59	0.59	1.00	0.59	-1.35	0.08	-0.18	1.17
SPO1676		acetyltransferase	-2.19	0.27	-1.53	0.46	-1.86	0.33	-1.46	0.06	-1.12	0.65	-1.29	0.17	1.23	0.02	1.05	0.29	1.14	0.09
SPO1677	*mnmA*	2-thiouridylase MnmA (EC:2.1.1.61)	-1.13	0.48	1.06	0.77	-0.03	1.10	1.73	0.02	-1.13	0.12	0.30	1.43	1.59	0.03	-1.12	0.31	0.24	1.36
SPO1678		hypothetical protein	-1.41	0.04	-1.22	0.44	-1.32	0.10	1.63	0.40	1.41	0.17	1.52	0.11	-1.08	0.45	-1.07	0.70	-1.08	0.01
SPO1679	*ctrA*	response regulator CtrA	-1.40	0.02	2.22	0.09	0.41	1.81	-4.64	0.01	4.54	0.02	-0.05	4.59	-1.22	0.33	1.55	0.21	0.17	1.39
SPO1680	*ligA*	DNA ligase (EC:6.5.1.2)	1.01	0.99	1.20	0.55	1.11	0.10	1.29	0.82	-1.09	0.63	0.10	1.19	1.45	0.16	1.60	0.60	1.53	0.08
SPO1681	*recG*	DNA helicase RecG (EC:3.6.1.-)	1.12	0.19	1.12	0.62	1.12	0.00	1.38	0.42	-1.01	0.92	0.19	1.20	-1.21	0.65	-1.39	0.25	-1.30	0.09

SPO1682		hypothetical protein	0.99	0.87	-1.10	0.59	-0.05	1.05	-1.28	0.03	-1.34	0.11	-1.31	0.03	3.43	0.01	6.47	0.00	4.95	1.52
SPO1683		hypothetical protein	-1.18	0.55	1.01	0.99	-0.09	1.10	-1.46	0.39	-1.19	0.65	-1.33	0.14	1.75	0.25	1.98	0.26	1.87	0.12
SPO1684	*hisI*	cyclohydrolase (EC:3.5.4.19)	-1.12	0.14	1.35	0.25	0.12	1.24	-1.19	0.26	-1.18	0.48	-1.19	0.01	1.25	0.12	-0.99	0.93	0.13	1.12
SPO1685		tRNA synthetase, class I family protein	-1.15	0.53	1.07	0.92	-0.04	1.11	1.72	0.10	-1.21	0.56	0.26	1.47	-1.17	0.64	-1.27	0.47	-1.22	0.05
SPO1686	*gid*	(uracil-5-)-methyltransferase Gid	1.34	0.63	-1.10	0.54	0.12	1.22	4.51	0.10	-1.52	0.34	1.50	3.02	-1.22	0.66	-1.54	0.37	-1.38	0.16
SPO1687		enoyl-CoA hydratase	2.54	0.01	1.83	0.08	2.19	0.35	1.96	0.02	1.68	0.00	1.82	0.14	1.30	0.01	1.50	0.04	1.40	0.10
SPO1688		thioesterase	1.86	0.02	1.13	0.26	1.50	0.37	-1.19	0.51	1.36	0.06	0.09	1.28	1.25	0.04	1.33	0.04	1.29	0.04
SPO1689		hypothetical protein	-2.33	0.00	1.06	0.41	-0.64	1.70	2.16	0.01	1.05	0.87	1.61	0.56	-1.08	0.09	1.68	0.05	0.30	1.38
SPO1690		GntR family transcriptional regulator	-2.11	0.01	-1.13	0.27	-1.62	0.49	1.20	0.52	-1.43	0.06	-0.12	1.32	1.07	0.53	-1.14	0.55	-0.03	1.11
SPO1691	*rplM*	ribosomal protein L13	-2.40	0.00	-1.35	0.16	-1.88	0.53	8.47	0.00	-2.04	0.00	3.22	5.26	-1.67	0.00	-3.26	0.00	-2.47	0.80
SPO1692	*rpsI*	ribosomal protein S9	-1.63	0.19	1.00	0.77	-0.32	1.31	13.10	0.02	-2.49	0.06	5.31	7.80	1.05	0.98	-2.69	0.06	-0.82	1.87
SPO1693		hypothetical protein	1.51	0.47	1.19	0.16	1.35	0.16	1.03	0.72	1.67	0.06	1.35	0.32	1.14	0.17	1.20	0.24	1.17	0.03
SPO1694		carbohydrate kinase	1.19	0.71	-1.18	0.39	0.01	1.19	1.20	0.86	1.62	0.09	1.41	0.21	-1.06	0.78	1.08	0.92	0.01	1.07
SPO1695		hydantoin utilization protein	1.95	0.01	1.46	0.03	1.71	0.24	-0.99	0.38	-1.10	0.15	-1.04	0.06	-1.49	0.06	-1.90	0.06	-1.70	0.21
SPO1696		hydantoinase/oxoprolinase	1.78	0.01	1.41	0.30	1.60	0.18	-0.97	0.02	-1.12	0.41	-1.05	0.07	-1.12	0.27	-1.37	0.13	-1.25	0.13
SPO1697		class I and II aminotransferase	1.19	0.81	1.53	0.01	1.36	0.17	-1.41	0.13	1.02	0.93	-0.20	1.22	-1.15	0.35	-1.18	0.19	-1.17	0.02
SPO1698		Asp/Glu/Hydantoin racemase	2.95	0.01	1.40	0.12	2.18	0.78	1.38	0.03	-1.02	0.74	0.18	1.20	-1.19	0.06	-1.26	0.17	-1.23	0.04
SPO1699		MmgE/PrpD family protein	3.10	0.00	1.34	0.11	2.22	0.88	1.47	0.03	1.20	0.11	1.34	0.14	-1.41	0.09	-1.50	0.15	-1.46	0.05
SPO1700		D-isomer specific 2-hydroxyacid dehydrogenase	1.24	0.66	1.14	0.70	1.19	0.05	-1.55	0.36	1.49	0.35	-0.03	1.52	-1.44	0.27	-1.23	0.51	-1.34	0.11
SPO1701		dihydrodipicolinate synthase	1.13	0.88	1.13	0.37	1.13	0.00	-1.33	0.52	1.78	0.07	0.23	1.56	-1.37	0.13	-1.20	0.53	-1.29	0.09
SPO1702		hypothetical protein	-1.01	0.96	-1.35	0.45	-1.18	0.17	-1.86	0.22	1.31	0.24	-0.28	1.59	1.04	0.75	-0.91	0.58	0.06	0.98
SPO1703		CaiB/BaiF family protein	-1.03	1.00	-1.40	0.33	-1.22	0.19	-1.21	0.98	1.07	0.85	-0.07	1.14	-1.57	0.47	1.14	0.68	-0.22	1.36
SPO1704		AraC family transcriptional regulator	-1.44	0.49	1.07	0.71	-0.19	1.26	-1.25	0.94	1.18	0.74	-0.04	1.22	-1.39	0.49	-1.15	0.97	-1.27	0.12
SPO1705		phage head morphogenesis domain-containing protein	1.06	1.00	-1.08	0.93	-0.01	1.07	-1.76	0.74	1.35	0.78	-0.21	1.56	-1.80	0.52	-1.48	0.69	-1.64	0.16
SPO1707		branched-chain amino acid ABC transporter ATP-binding protein	-2.16	0.38	-1.12	0.57	-1.64	0.52	-3.35	0.22	1.04	0.85	-1.16	2.20	-1.06	0.84	1.74	0.09	0.34	1.40
SPO1708		branched-chain amino acid ABC transporter permease	-3.78	0.02	-1.46	0.10	-2.62	1.16	-4.70	0.00	-1.21	0.14	-2.96	1.75	-1.42	0.03	1.26	0.12	-0.08	1.34
SPO1709		branched-chain amino acid ABC transporter permease	-1.51	0.84	-1.04	0.99	-1.28	0.24	-1.87	0.81	-1.04	X	-1.46	0.42	-1.44	0.89	1.96	X	0.26	1.70
SPO1710		branched-chain amino acid ABC transporter substrate-binding protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1711	*ureD*	accessory protein UreD	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.35	X	X	X	N/A	N/A
SPO1712	*ureA*	subunit gamma (EC:3.5.1.5)	-1.33	0.54	1.08	0.68	-0.13	1.21	-0.94	0.57	-1.25	0.31	-1.09	0.16	-1.34	0.09	X	X	N/A	N/A
SPO1713	*ureB*	subunit beta	1.05	0.16	-1.26	0.73	-0.11	1.16	0.76	0.00	-1.17	0.83	-0.20	0.97	-1.38	0.46	-1.15	0.93	-1.27	0.12
SPO1714	*ureC*	subunit alpha (EC:3.5.1.5)	-2.30	X	-1.14	0.87	-1.72	0.58	-2.79	0.49	-1.26	0.75	-2.03	0.77	-1.68	0.38	-1.27	0.78	-1.48	0.20
SPO1715	*ureE*	accessory protein ureE	2.44	X	-1.09	0.93	0.68	1.77	-1.51	0.79	1.21	0.61	-0.15	1.36	-1.32	0.45	1.25	X	-0.04	1.29
SPO1716	*ureF*	accessory protein UreF	-1.06	0.93	-1.16	0.20	-1.11	0.05	-1.96	0.05	1.10	0.36	-0.43	1.53	-1.81	0.04	-1.81	0.03	-1.81	0.00
SPO1717	*ureG*	accessory protein UreG	X	X	-1.04	0.88	N/A	N/A	X	X	1.08	X	N/A	N/A	-1.01	0.67	X	X	N/A	N/A
SPO1718		hypothetical protein	-1.65	0.13	1.14	0.50	-0.26	1.40	1.34	0.03	1.16	0.11	1.25	0.09	-1.33	0.13	-1.70	0.08	-1.52	0.18
SPO1719		TRAP dicarboxylate transporter subunit DctM	X	X	1.17	0.22	N/A	N/A	-1.47	0.68	1.13	0.45	-0.17	1.30	-1.45	0.13	X	X	N/A	N/A

SPO1720		TRAP dicarboxylate transporter subunit DctQ	1.01	0.99	1.04	0.90	1.03	0.02	1.25	0.91	1.06	0.90	1.16	0.10	-1.08	0.79	-0.99	0.87	-1.03	0.05
SPO1721		TRAP dicarboxylate transporter subunit DctP	-2.67	0.01	-1.16	0.62	-1.92	0.75	-3.67	0.01	0.98	0.87	-1.34	2.33	-1.13	0.62	-1.21	0.63	-1.17	0.04
SPO1722		GntR family transcriptional regulator	-2.64	0.17	-1.06	0.53	-1.85	0.79	-3.78	0.01	-1.18	0.14	-2.48	1.30	-1.24	0.15	-2.09	0.06	-1.67	0.43
SPO1723	*uxuA*	dehydratase (EC:4.2.1.8)	-1.45	0.05	-1.11	0.75	-1.28	0.17	4.25	0.01	-1.48	0.05	1.39	2.87	-1.07	0.85	1.39	0.14	0.16	1.23
SPO1724	*uxuB*	oxidoreductase (EC:1.1.1.57)	-2.13	0.69	-1.29	0.88	-1.71	0.42	-2.58	0.56	-1.24	0.89	-1.91	0.67	-1.21	0.92	1.66	X	0.23	1.44
SPO1725		hypothetical protein	-1.09	0.05	1.09	0.77	0.00	1.09	0.93	0.11	1.43	0.11	1.18	0.25	1.09	0.74	1.11	0.95	1.10	0.01
SPO1727		polyphosphate kinase	-1.07	0.04	-1.43	0.11	-1.25	0.18	-1.39	0.10	1.15	0.26	-0.12	1.27	-1.24	0.04	-1.13	0.37	-1.19	0.06
SPO1728		esterase	1.25	0.07	-1.21	0.44	0.02	1.23	3.02	0.01	-1.27	0.04	0.88	2.15	-1.56	0.05	-1.39	0.11	-1.48	0.09
SPO1729	*metA*	O-succinyltransferase (EC:2.3.1.46)	-1.25	0.03	-1.58	0.04	-1.42	0.17	1.76	0.05	-1.33	0.01	0.22	1.55	-1.59	0.11	-1.78	0.04	-1.69	0.10
SPO1732	*recJ*	exonuclease RecJ (EC:3.1.-.-)	1.10	0.50	1.06	0.88	1.08	0.02	2.13	0.04	-1.23	0.45	0.45	1.68	1.13	0.66	-1.18	0.75	-0.03	1.16
SPO1733	*glpX*	1,6-bisphosphatase II (EC:3.1.3.11)	1.63	0.63	1.69	0.01	1.66	0.03	1.59	0.61	-1.13	0.11	0.23	1.36	1.11	0.76	-1.50	0.03	-0.20	1.31
SPO1734	*hom*	dehydrogenase (EC:1.1.1.3)	1.26	0.76	1.20	0.28	1.23	0.03	3.08	0.06	-1.08	0.09	1.00	2.08	-1.34	0.20	-1.70	0.02	-1.52	0.18
SPO1735		hypothetical protein	1.11	0.24	-1.51	0.15	-0.20	1.31	1.01	0.16	1.09	0.83	1.05	0.04	-1.79	0.05	-1.47	0.10	-1.63	0.16
SPO1736		TetR family transcriptional regulator	-3.05	0.00	-1.33	0.10	-2.19	0.86	1.05	0.75	-1.15	0.13	-0.05	1.10	1.01	0.99	-1.02	0.99	-0.01	1.02
SPO1737		pirin	1.18	0.57	-1.12	0.21	0.03	1.15	1.19	0.31	1.03	0.84	1.11	0.08	1.32	0.14	-0.96	0.41	0.18	1.14
SPO1738		dehalogenase	-1.17	0.69	-1.05	0.89	-1.11	0.06	1.34	0.64	2.03	0.19	1.69	0.34	1.02	0.96	-1.20	0.71	-0.09	1.11
SPO1739		hypothetical protein	1.10	0.11	1.19	0.54	1.15	0.04	-2.09	0.00	-1.15	0.04	-1.62	0.47	1.22	0.13	1.02	0.94	1.12	0.10
SPO1740		hypothetical protein	2.02	0.03	1.55	0.25	1.79	0.24	-2.32	0.03	1.33	0.09	-0.50	1.83	-1.74	0.00	-1.52	0.13	-1.63	0.11
SPO1741		hypothetical protein	3.05	0.17	1.28	0.24	2.17	0.89	-2.10	0.18	1.04	0.96	-0.53	1.57	-1.51	0.35	-1.20	0.56	-1.36	0.16
SPO1742		hypothetical protein	2.59	0.04	-1.11	0.46	0.74	1.85	-3.42	0.00	1.03	0.91	-1.20	2.23	-2.68	0.03	-1.86	0.01	-2.27	0.41
SPO1743		glutamate dehydrogenase (EC:1.4.1.3)	-3.93	0.00	-3.50	0.03	-3.72	0.22	-1.51	0.02	1.09	0.94	-0.21	1.30	1.50	0.09	0.90	0.23	1.20	0.30
SPO1744		sarcosine oxidase subunit beta	7.26	0.00	1.76	0.06	4.51	2.75	-1.51	0.25	1.06	0.90	-0.23	1.29	-1.01	0.94	1.09	0.75	0.04	1.05
SPO1745		sarcosine oxidase subunit delta	6.86	0.03	2.18	0.11	4.52	2.34	-1.18	0.79	1.26	0.51	0.04	1.22	1.17	0.61	-1.03	0.94	0.07	1.10
SPO1746		sarcosine oxidase subunit alpha	5.11	0.32	1.62	0.26	3.37	1.75	-1.55	0.39	1.35	0.26	-0.10	1.45	-1.04	0.87	1.19	0.63	0.08	1.12
SPO1747		sarcosine oxidase subunit gamma	5.88	0.25	1.76	0.10	3.82	2.06	-1.38	0.31	-1.10	0.71	-1.24	0.14	-1.02	0.98	1.37	0.60	0.18	1.20
SPO1748		hypothetical protein	1.68	0.01	1.19	0.62	1.44	0.24	1.85	0.00	1.08	0.85	1.47	0.39	1.20	0.05	1.11	0.81	1.16	0.04
SPO1749	*dnaG*	DNA primase (EC:2.7.7.-)	1.02	0.13	-1.82	0.01	-0.40	1.42	1.46	0.01	1.16	0.40	1.31	0.15	-1.19	0.36	0.97	0.46	-0.11	1.08
SPO1750	*rpoD*	RNA polymerase sigma factor RpoD	1.96	0.04	-1.56	0.18	0.20	1.76	1.25	0.92	1.24	0.19	1.25	0.01	-1.09	0.27	1.20	0.79	0.05	1.15
SPO1751		hypothetical protein	1.22	0.38	0.99	0.47	1.11	0.11	1.13	0.78	1.00	0.70	1.07	0.06	1.24	0.26	1.72	0.04	1.48	0.24
SPO1752		hypothetical protein	-1.13	0.76	-1.23	0.42	-1.18	0.05	1.01	0.94	1.02	0.99	1.02	0.01	-1.12	0.43	1.35	0.04	0.12	1.24
SPO1753	*nrdR*	transcriptional regulator NrdR	1.41	0.76	-1.08	0.57	0.17	1.25	-1.56	0.05	1.07	0.96	-0.25	1.32	1.13	0.71	1.14	0.63	1.14	0.01
SPO1754	*ribD*	riboflavin biosynthesis protein RibD (EC:1.1.1.193 3.5.4.26)	1.48	0.79	1.25	0.75	1.37	0.12	1.36	0.83	-1.15	0.72	0.11	1.26	1.57	0.33	1.20	0.72	1.39	0.19
SPO1755	*kpsC*	capsular polysaccharide export protein	-1.18	0.13	-1.59	0.07	-1.39	0.21	-2.00	0.03	-1.36	0.02	-1.68	0.32	-1.35	0.16	-1.77	0.22	-1.56	0.21
SPO1756		polysaccharide biosynthesis/export protein	0.87	0.05	-1.38	0.27	-0.25	1.13	-1.42	0.01	1.25	0.12	-0.09	1.34	-1.05	0.05	1.24	0.07	0.10	1.15
SPO1757	*kpsS*	capsular polysaccharide export protein	1.10	0.25	1.25	0.04	1.18	0.08	-1.75	0.02	1.08	0.52	-0.34	1.42	-1.23	0.00	-1.56	0.02	-1.40	0.17
SPO1758		hypothetical protein	X	X	1.22	X	N/A	N/A	-1.69	X	X	X	N/A	N/A	-1.46	X	X	X	N/A	N/A
SPO1759	*ribE*	riboflavin synthase subunit alpha (EC:2.5.1.9)	1.37	0.06	1.23	0.36	1.30	0.07	2.32	0.05	1.06	0.98	1.69	0.63	-1.30	0.01	-1.20	0.20	-1.25	0.05
SPO1760		hypothetical protein	1.05	0.89	1.36	0.17	1.21	0.16	1.93	0.07	-1.28	0.18	0.33	1.61	1.15	0.07	-1.28	0.07	-0.07	1.22
SPO1761		3,4-dihydroxy-2-butanone 4-phosphate synthase	1.50	0.62	1.25	0.28	1.38	0.13	2.12	0.47	-1.07	0.43	0.53	1.60	-1.54	0.08	-1.25	0.10	-1.40	0.14

SPO1762	*ribH*	6,7-dimethyl-8-ribityllumazine synthase (EC:2.5.1.9)	1.52	0.01	1.36	0.70	1.44	0.08	1.98	0.00	-1.07	0.07	0.46	1.53	-2.04	0.00	-1.88	0.02	-1.96	0.08
SPO1763	*nusB*	transcription antitermination factor NusB	1.40	0.02	1.38	0.27	1.39	0.01	5.02	0.00	-1.19	0.02	1.92	3.11	-1.29	0.05	-1.88	0.01	-1.59	0.30
SPO1764		LuxR family transcriptional regulator	1.41	0.02	-1.04	0.59	0.19	1.23	1.30	0.19	1.30	0.19	1.30	0.00	-1.03	0.87	-1.00	0.53	-1.01	0.02
SPO1765		hypothetical protein	2.20	0.59	2.11	0.12	2.16	0.05	-1.11	0.51	1.49	0.11	0.19	1.30	1.51	0.13	1.96	0.04	1.74	0.23
SPO1766		hypothetical protein	-2.33	0.01	-1.31	0.30	-1.82	0.51	-2.93	0.00	-1.09	0.86	-2.01	0.92	1.14	0.75	2.00	0.16	1.57	0.43
SPO1767		acetyltransferase	-1.06	0.29	1.00	0.94	-0.03	1.03	-1.37	0.08	1.59	0.02	0.11	1.48	-1.23	0.08	-1.09	0.84	-1.16	0.07
SPO1769		hypothetical protein	-1.82	0.36	-1.15	0.16	-1.49	0.34	-1.69	0.10	1.10	0.75	-0.30	1.40	-1.13	0.60	-1.20	0.26	-1.17	0.04
SPO1770		hypothetical protein	-1.87	0.01	-1.22	0.43	-1.55	0.33	0.93	0.25	-1.02	0.67	-0.05	0.97	1.33	0.08	1.55	0.03	1.44	0.11
SPO1771		TRAP dicarboxylate transporter subunit DctM	-1.01	0.93	-1.04	0.67	-1.03	0.02	-0.98	0.25	1.21	0.23	0.12	1.09	1.16	0.03	-0.93	0.21	0.12	1.05
SPO1772		TRAP dicarboxylate transporter subunit DctQ	-1.51	0.58	-1.56	0.07	-1.54	0.03	-1.24	0.25	1.04	0.99	-0.10	1.14	1.01	0.97	1.49	0.08	1.25	0.24
SPO1773		TRAP dicarboxylate transporter subunit DctP	-2.16	0.02	-2.71	0.02	-2.44	0.27	-4.89	0.01	1.11	0.67	-1.89	3.00	-1.28	0.15	1.22	0.54	-0.03	1.25
SPO1774		3-hydroxyanthranilate 3,4-dioxygenase (EC:1.13.11.6)	0.86	0.14	-1.62	0.25	-0.38	1.24	0.76	0.00	-1.05	0.69	-0.15	0.90	-1.06	0.80	1.19	0.50	0.06	1.13
SPO1775		hypothetical protein	1.02	0.59	-1.18	0.17	-0.08	1.10	-2.69	0.00	1.18	0.28	-0.76	1.94	1.36	0.18	1.15	0.47	1.26	0.11
SPO1776		oxidoreductase	-7.21	0.00	-2.44	0.01	-4.83	2.39	-38.20	0.00	-3.31	0.01	-20.76	17.45	1.33	0.27	1.47	0.03	1.40	0.07
SPO1777		dihydropyrimidine dehydrogenase (EC:1.3.1.1)	-5.10	0.02	-2.83	0.05	-3.97	1.14	-32.60	0.01	-3.74	0.02	-18.17	14.43	1.35	0.41	1.15	0.51	1.25	0.10
SPO1778		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1779		major facilitator superfamily transporter	1.92	0.01	1.45	0.17	1.69	0.23	1.72	0.01	-1.33	0.12	0.20	1.53	1.13	0.14	-1.44	0.14	-0.16	1.29
SPO1780		TetR family transcriptional regulator	-1.93	0.03	1.18	0.65	-0.38	1.56	-1.23	0.91	-1.65	0.31	-1.44	0.21	-1.06	0.49	-1.56	0.20	-1.31	0.25
SPO1781		allantoate amidohydrolase	-2.03	0.04	-1.15	0.67	-1.59	0.44	-9.75	0.01	-1.59	0.01	-5.67	4.08	1.64	0.01	1.38	0.19	1.51	0.13
SPO1782		hypothetical protein	-3.03	0.04	-1.58	0.10	-2.31	0.73	-12.90	0.00	-1.71	0.06	-7.31	5.60	1.14	0.40	1.28	0.22	1.21	0.07
SPO1783	*hydA*	phenylhydantoinase (EC:3.5.2.2)	-4.78	0.00	-1.83	0.01	-3.31	1.48	-17.40	0.00	-1.66	0.03	-9.53	7.87	1.23	0.11	1.55	0.01	1.39	0.16
SPO1784		hypothetical protein	-1.06	0.33	1.09	0.32	0.02	1.08	-2.50	0.00	1.60	0.12	-0.45	2.05	-1.00	0.95	-0.98	0.51	-0.99	0.01
SPO1785		ABC transporter ATP-binding protein	-3.07	0.00	1.01	0.91	-1.03	2.04	-7.01	0.00	-1.83	0.04	-4.42	2.59	1.42	0.06	-1.08	0.91	0.17	1.25
SPO1786		ABC transporter permease	-2.03	0.00	-1.00	0.76	-1.51	0.52	-4.56	0.00	-1.19	0.54	-2.88	1.69	1.18	0.04	-0.98	0.17	0.10	1.08
SPO1787		ABC transporter permease	-2.01	0.11	-1.44	0.04	-1.73	0.29	-3.35	0.01	1.03	0.84	-1.16	2.19	-1.23	0.07	1.19	0.21	-0.02	1.21
SPO1788		ABC transporter substrate-binding protein	-2.36	0.09	1.07	0.80	-0.65	1.72	-4.90	0.01	-1.27	0.36	-3.09	1.82	1.99	0.02	2.24	0.00	2.12	0.13
SPO1789		sulfate/tungstate ABC transporter permease	1.15	0.65	1.34	0.07	1.25	0.10	-1.36	0.07	-3.18	0.00	-2.27	0.91	1.74	0.06	2.03	0.01	1.89	0.15
SPO1790		sulfate/tungstate ABC transporter ATP-binding protein	2.10	0.70	1.46	0.19	1.78	0.32	1.89	0.76	-3.65	0.06	-0.88	2.77	1.52	0.39	1.55	0.15	1.54	0.02
SPO1791		sulfate/tungstate ABC transporter substrate-binding protein	1.92	0.03	2.15	0.01	2.04	0.12	1.68	0.01	-6.44	0.00	-2.38	4.06	1.62	0.02	1.19	0.60	1.41	0.22
SPO1792		excisionase	1.47	0.26	1.25	0.51	1.36	0.11	-0.99	0.76	1.08	0.82	0.05	1.03	1.67	0.34	1.45	0.30	1.56	0.11
SPO1793		hypothetical protein	-1.16	0.84	1.13	0.16	-0.02	1.15	-7.51	0.01	6.06	0.00	-0.73	6.79	1.27	0.12	1.20	0.18	1.24	0.04
SPO1794		formate dehydrogenase subunit gamma (EC:1.2.1.2)	1.35	0.26	1.08	0.34	1.22	0.14	-6.34	0.02	6.25	0.02	-0.04	6.30	2.38	0.00	2.18	0.06	2.28	0.10
SPO1795		formate dehydrogenase, iron-sulfur subunit	-1.75	0.01	-1.32	0.02	-1.54	0.21	-13.90	0.00	6.57	0.00	-3.67	10.24	2.97	0.00	2.94	0.00	2.96	0.02
SPO1796		formate dehydrogenase subunit alpha	-3.16	0.00	-1.73	0.01	-2.45	0.72	-27.60	0.00	6.77	0.00	-10.42	17.19	2.79	0.01	3.27	0.00	3.03	0.24
SPO1797		twin-arginine translocation pathway signal sequence domain-containing protein	-1.77	0.00	-2.33	0.04	-2.05	0.28	-15.70	0.00	4.86	0.01	-5.42	10.28	1.76	0.00	3.25	0.02	2.51	0.75
SPO1798		chaperone TorD	-1.17	0.09	-1.35	0.21	-1.26	0.09	-10.40	0.00	3.88	0.02	-3.26	7.14	1.91	0.06	2.03	0.04	1.97	0.06
SPO1799		hypothetical protein	-1.58	0.01	-1.50	0.02	-1.54	0.04	-10.90	0.00	5.29	0.00	-2.81	8.10	1.75	0.02	1.98	0.01	1.87	0.12

SPO1800		(Fe-S)-binding protein	-1.35	0.01	1.23	0.18	-0.06	1.29	-2.83	0.00	1.09	0.65	-0.87	1.96	1.23	0.09	2.15	0.03	1.69	0.46
SPO1801		hypothetical protein	-1.91	0.02	-1.32	0.04	-1.62	0.30	-1.54	0.02	1.23	0.19	-0.16	1.39	1.27	0.05	1.09	0.26	1.18	0.09
SPO1802		hypothetical protein	1.19	0.77	-1.30	0.01	-0.06	1.25	1.35	0.09	1.27	0.56	1.31	0.04	1.06	0.91	1.52	0.03	1.29	0.23
SPO1803		Mrp/NBP35 family protein	1.14	0.76	1.04	0.93	1.09	0.05	1.59	0.05	1.20	0.42	1.40	0.20	1.94	0.02	2.18	0.07	2.06	0.12
SPO1804		hypothetical protein	-1.23	0.17	1.03	0.97	-0.10	1.13	1.22	0.58	-1.04	0.39	0.09	1.13	1.63	0.02	1.86	0.06	1.75	0.12
SPO1805		hypothetical protein	1.06	0.93	1.05	0.85	1.06	0.01	1.10	0.98	1.08	0.74	1.09	0.01	1.76	0.06	1.46	0.16	1.61	0.15
SPO1806		flavin reductase domain-containing protein	-1.26	0.51	1.03	0.97	-0.12	1.15	-1.51	0.30	-1.22	0.46	-1.37	0.15	-1.59	0.20	-1.07	0.90	-1.33	0.26
SPO1807		DNA polymerase III subunit epsilon	2.54	0.05	-1.15	0.41	0.70	1.85	2.26	0.18	8.85	0.00	5.56	3.30	1.22	0.30	1.25	0.23	1.24	0.02
SPO1808		hypothetical protein	7.42	0.00	1.10	0.20	4.26	3.16	3.82	0.00	9.73	0.00	6.78	2.96	1.19	0.08	1.37	0.23	1.28	0.09
SPO1809		nucleotidyltransferase/CBS/cyclic nucleotide-binding domain-containing protein	25.30	0.01	1.23	0.07	13.27	12.04	11.70	0.00	17.80	0.00	14.75	3.05	2.37	0.03	1.66	0.17	2.02	0.35
SPO1810		sodium/solute symporter family protein	15.40	0.01	-1.27	0.10	7.07	8.34	5.37	0.03	15.50	0.00	10.44	5.07	2.29	0.01	2.29	0.01	2.29	0.00
SPO1811		hypothetical protein	25.20	0.01	-1.50	0.10	11.85	13.35	7.91	0.02	17.50	0.00	12.71	4.80	1.35	0.31	1.75	0.12	1.55	0.20
SPO1812	*adk-2*	adenylate kinase (EC:2.7.4.3)	7.69	0.10	-1.19	0.70	3.25	4.44	3.17	0.20	9.84	0.01	6.51	3.34	2.05	0.12	2.13	0.24	2.09	0.04
SPO1813	*acs*	acetyl-coenzyme A synthetase (EC:6.2.1.1)	7.34	0.01	-1.61	0.13	2.87	4.48	2.61	0.05	7.80	0.00	5.21	2.60	1.85	0.09	2.32	0.02	2.09	0.24
SPO1814		TRAP dicarboxylate transporter subunit DctP	-1.45	0.03	-1.90	0.02	-1.68	0.23	-4.89	0.00	2.07	0.01	-1.41	3.48	1.69	0.03	2.58	0.01	2.14	0.45
SPO1815		TRAP dicarboxylate transporter subunit DctQ	1.01	0.08	-1.88	0.01	-0.44	1.45	1.13	0.59	1.97	0.03	1.55	0.42	1.69	0.03	2.05	0.05	1.87	0.18
SPO1816		TRAP dicarboxylate transporter subunit DctM	-1.30	0.09	-1.48	0.13	-1.39	0.09	-1.69	0.04	1.26	0.34	-0.22	1.48	1.40	0.06	1.21	0.15	1.31	0.10
SPO1817		hypothetical protein	1.09	0.70	1.00	0.98	1.04	0.05	1.37	0.01	-1.38	0.21	0.00	1.38	1.14	0.40	2.12	0.03	1.63	0.49
SPO1818		hypothetical protein	1.00	0.55	1.01	0.98	1.00	0.01	1.10	0.98	1.03	0.96	1.07	0.04	-0.99	0.93	1.62	0.15	0.32	1.30
SPO1819		phosphodiesterase	1.62	0.17	-1.22	0.83	0.20	1.42	1.60	0.17	1.23	X	1.42	0.19	-1.00	0.97	1.78	X	0.39	1.39
SPO1820		sugar ABC transporter substrate-binding protein	-1.73	0.08	-1.44	0.61	-1.59	0.15	-1.63	0.55	1.05	0.75	-0.29	1.34	-1.74	0.18	1.25	0.69	-0.25	1.50
SPO1821		sugar ABC transporter permease	X	X	-1.53	0.20	N/A	N/A	X	X	X	X	N/A	N/A	-1.13	0.56	X	X	N/A	N/A
SPO1822		sugar ABC transporter permease	-1.05	0.97	-1.18	0.72	-1.12	0.06	-1.30	0.94	-1.23	0.17	-1.27	0.04	-1.14	0.81	1.15	0.69	0.01	1.15
SPO1823		sugar ABC transporter ATP-binding protein	-2.16	0.01	-1.26	0.54	-1.71	0.45	5.77	0.01	X	X	N/A	N/A	-1.08	0.91	1.19	X	0.05	1.14
SPO1824		LysR family transcriptional regulator	1.37	0.18	-1.34	0.17	0.02	1.36	1.41	0.09	1.08	0.82	1.25	0.16	-1.13	0.63	1.90	0.40	0.39	1.52
SPO1825		glutamine synthetase	-3.22	0.32	-1.14	0.55	-2.18	1.04	-3.91	0.17	-1.11	0.56	-2.51	1.40	1.06	0.79	2.19	0.05	1.63	0.57
SPO1826		RpiR family transcriptional regulator	-2.44	0.00	-1.28	0.44	-1.86	0.58	-2.25	0.00	-1.29	0.08	-1.77	0.48	-1.12	0.19	-1.62	0.06	-1.37	0.25
SPO1827		N-formylglutamate amidohydrolase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1828		isochorismatase	-2.64	0.02	1.07	0.39	-0.79	1.86	-2.19	0.04	-1.17	0.36	-1.68	0.51	1.30	0.01	-1.24	0.58	0.03	1.27
SPO1829		branched-chain amino acid ABC transporter ATP-binding protein	-3.25	0.00	-1.14	0.23	-2.20	1.06	-3.52	0.00	1.16	0.06	-1.18	2.34	-1.13	0.62	1.36	0.18	0.12	1.25
SPO1830		branched chain amino acid ABC transporter substrate-binding protein	-4.20	0.00	-1.47	0.06	-2.84	1.37	-4.26	0.00	-1.02	0.79	-2.64	1.62	1.33	0.02	1.47	0.10	1.40	0.07
SPO1831	*livF-1*	branched-chain amino acid ABC transporter ATP-binding protein	-1.77	0.01	-1.10	0.70	-1.44	0.34	-1.25	0.29	-1.00	0.97	-1.13	0.13	1.17	0.11	1.31	0.13	1.24	0.07
SPO1832		branched-chain amino acid ABC transporter permease	-3.05	0.30	-1.01	0.96	-2.03	1.02	-2.17	0.09	-1.24	0.45	-1.71	0.47	1.44	0.32	-1.38	X	0.03	1.41
SPO1833		branched-chain amino acid ABC transporter permease	-1.33	0.12	-1.01	0.95	-1.17	0.16	-1.14	0.93	-1.04	0.89	-1.09	0.05	1.44	0.15	-0.99	0.51	0.23	1.21
SPO1834		acetamidase/formamidase	-2.29	0.00	-1.14	0.59	-1.72	0.58	-2.07	0.05	1.31	0.11	-0.38	1.69	1.09	0.24	-0.94	0.50	0.08	1.01
SPO1835		sugar ABC transporter ATP-binding protein	-1.22	0.46	-1.40	0.14	-1.31	0.09	-2.83	0.03	-1.10	0.49	-1.97	0.87	-0.99	0.98	-1.05	0.92	-1.02	0.03
SPO1836		Gfo/Idh/MocA family oxidoreductase	-1.51	0.31	-1.94	0.01	-1.73	0.21	-3.66	0.03	1.26	0.14	-1.20	2.46	-1.29	0.03	-1.26	0.29	-1.28	0.02

SPO1837		sugar ABC transporter permease	-1.20	0.21	-1.57	0.01	-1.39	0.19	-3.22	0.01	-1.39	0.16	-2.31	0.92	1.12	0.26	-1.12	0.78	0.00	1.12
SPO1838		sugar ABC transporter permease	-1.40	0.16	-2.42	0.00	-1.91	0.51	-4.66	0.00	1.02	0.92	-1.82	2.84	-1.18	0.15	1.19	0.24	0.01	1.19
SPO1839		sugar ABC transporter substrate-binding protein	-1.81	0.03	-2.88	0.02	-2.35	0.54	-7.70	0.00	1.05	0.99	-3.33	4.38	1.17	0.30	1.34	0.21	1.26	0.09
SPO1840	*murQ*	N-acetylmuramic acid 6-phosphate etherase	-2.59	0.00	-2.57	0.01	-2.58	0.01	-8.22	0.00	1.21	0.11	-3.51	4.72	-1.58	0.07	0.97	0.54	-0.31	1.28
SPO1841		BadF/BadG/BcrA/BcrD ATPase	-2.49	0.01	-1.40	0.02	-1.95	0.55	-3.18	0.00	-1.40	0.03	-2.29	0.89	1.61	0.03	-1.02	0.76	0.30	1.32
SPO1842		GntR family transcriptional regulator	-2.05	0.08	-1.50	0.15	-1.78	0.28	-4.03	0.02	-1.11	0.58	-2.57	1.46	-1.41	0.03	1.07	0.88	-0.17	1.24
SPO1843		SIS domain-containing protein	-1.45	0.32	-1.39	0.12	-1.42	0.03	-2.58	0.25	-1.31	0.25	-1.95	0.64	-1.05	0.74	-1.64	0.02	-1.35	0.30
SPO1844	*nagA*	N-acetylglucosamine-6-phosphate deacetylase (EC:3.5.1.25)	1.04	0.98	-1.04	0.96	0.00	1.04	-1.23	0.89	-1.11	0.85	-1.17	0.06	1.50	0.45	1.22	0.68	1.36	0.14
SPO1845		molybdopterin-binding oxidoreductase	-1.49	0.09	-1.53	0.16	-1.51	0.02	-4.07	0.01	1.47	0.30	-1.30	2.77	1.20	0.60	2.60	0.05	1.90	0.70
SPO1846		branched-chain amino acid ABC transporter substrate-binding protein	-1.82	0.01	-2.30	0.03	-2.06	0.24	-9.76	0.01	1.46	0.08	-4.15	5.61	1.50	0.04	3.14	0.00	2.32	0.82
SPO1847		AMP-binding protein	-2.39	0.00	-4.66	0.00	-3.53	1.14	-26.50	0.00	1.03	0.98	-12.74	13.77	-1.56	0.05	1.79	0.02	0.12	1.68
SPO1848		branched-chain amino acid ABC transporter ATP-binding protein	-2.17	0.09	-3.47	0.01	-2.82	0.65	-16.00	0.00	1.17	0.41	-7.42	8.59	-1.01	0.72	2.31	0.00	0.65	1.66
SPO1849		branched-chain amino acid ABC transporter ATP-binding protein	-2.00	0.50	-3.22	0.02	-2.61	0.61	-11.40	0.14	1.01	0.97	-5.20	6.21	1.24	0.48	2.64	0.01	1.94	0.70
SPO1850		branched-chain amino acid ABC transporter permease	-2.87	0.02	-2.70	0.11	-2.79	0.09	-13.30	0.03	-1.03	0.88	-7.17	6.14	1.20	0.44	2.37	0.10	1.79	0.59
SPO1851		branched-chain amino acid ABC transporter permease	-3.27	0.00	-2.11	0.11	-2.69	0.58	-14.10	0.00	1.04	0.87	-6.53	7.57	1.90	0.01	2.88	0.01	2.39	0.49
SPO1852		zinc-binding dehydrogenase oxidoreductase	-2.51	0.00	-1.57	0.11	-2.04	0.47	-3.38	0.00	1.29	0.07	-1.05	2.34	1.94	0.01	2.26	0.01	2.10	0.16
SPO1853		TetR family transcriptional regulator	-2.76	0.10	-1.71	0.38	-2.24	0.53	-7.08	0.05	1.51	0.48	-2.79	4.30	-1.13	0.61	1.41	0.51	0.14	1.27
SPO1854		hypothetical protein	-1.82	0.28	1.04	0.95	-0.39	1.43	-2.11	0.34	1.51	0.69	-0.30	1.81	1.59	0.49	1.22	0.70	1.41	0.19
SPO1855		hypothetical protein	1.41	0.02	-1.56	0.01	-0.08	1.49	2.22	0.01	-1.21	0.13	0.51	1.72	2.78	0.02	2.59	0.00	2.69	0.10
SPO1856		ribonuclease BN	-1.19	0.49	-1.05	0.75	-1.12	0.07	-1.62	0.01	-1.41	0.18	-1.52	0.11	1.28	0.08	1.49	0.01	1.39	0.11
SPO1857		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1858	*rrmJ*	ribosomal RNA large subunit methyltransferase J (EC:2.1.1.-)	-1.15	0.71	-1.03	0.79	-1.09	0.06	3.07	0.01	-1.41	0.02	0.83	2.24	-1.30	0.20	-1.51	0.22	-1.41	0.11
SPO1859		Ppx/GppA phosphatase	-1.07	0.86	1.01	0.99	-0.03	1.04	1.28	0.62	1.04	0.98	1.16	0.12	1.65	0.32	1.39	0.55	1.52	0.13
SPO1860		twin-arginine translocation pathway signal sequence domain-containing protein	1.80	0.11	1.05	0.77	1.43	0.38	-2.55	0.00	1.37	0.29	-0.59	1.96	1.30	0.51	1.50	0.13	1.40	0.10
SPO1861		hypothetical protein	1.18	0.76	1.13	0.63	1.16	0.03	3.19	0.00	1.39	0.21	2.29	0.90	-1.30	0.05	-1.51	0.15	-1.41	0.11
SPO1862		MetF-like protein	1.31	0.08	-1.18	0.16	0.07	1.25	2.98	0.00	1.77	0.02	2.38	0.61	-1.62	0.01	-1.22	0.25	-1.42	0.20
SPO1863		methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase	0.98	0.83	-1.07	0.43	-0.04	1.03	3.58	0.01	1.23	0.26	2.41	1.18	-1.02	0.39	-1.10	0.11	-1.06	0.04
SPO1864		hypothetical protein	-1.49	0.01	1.29	0.38	-0.10	1.39	1.60	0.04	-1.38	0.03	0.11	1.49	-1.30	0.06	-2.27	0.02	-1.79	0.49
SPO1865	*tkt*	transketolase (EC:2.2.1.1)	1.52	0.33	1.39	0.57	1.46	0.07	5.63	0.05	-1.33	0.46	2.15	3.48	0.98	0.90	-1.20	0.55	-0.11	1.09
SPO1866		hypothetical protein	0.92	0.03	1.24	0.45	1.08	0.16	1.00	0.12	1.49	0.05	1.25	0.24	1.54	0.07	1.66	0.01	1.60	0.06
SPO1867		hypothetical protein	1.11	0.46	1.21	0.42	1.16	0.05	-1.33	0.08	1.20	0.41	-0.07	1.27	1.70	0.01	1.18	0.16	1.44	0.26
SPO1868		glutaredoxin-like protein	2.43	0.38	1.13	0.44	1.78	0.65	1.79	0.24	1.00	0.57	1.40	0.40	0.97	0.48	0.99	0.27	0.98	0.01
SPO1869		BolA family protein	3.16	0.00	0.99	0.84	2.08	1.08	1.66	0.01	-1.19	0.14	0.24	1.43	-1.80	0.01	-1.32	0.02	-1.56	0.24
SPO1870	*purL*	phosphoribosylformylglycinamidine synthase II (EC:6.3.5.3)	1.28	0.31	1.39	0.22	1.34	0.05	6.42	0.00	-1.23	0.08	2.60	3.83	-1.14	0.33	-1.50	0.10	-1.32	0.18
SPO1871		mechanosensitive ion channel protein MscS	0.96	0.21	1.03	0.92	1.00	0.03	-1.43	0.01	1.87	0.01	0.22	1.65	1.14	0.56	1.61	0.03	1.38	0.24

SPO1872		LysR family transcriptional regulator	1.08	0.32	-1.01	0.96	0.04	1.05	2.27	0.03	-1.33	0.17	0.47	1.80	-1.40	0.07	-1.70	0.11	-1.55	0.15
SPO1873		indolepyruvate ferredoxin oxidoreductase (EC:1.2.7.8)	-0.99	0.99	-1.47	0.06	-1.23	0.24	-1.54	0.17	-1.29	0.20	-1.42	0.13	-0.99	0.96	-1.18	0.23	-1.09	0.10
SPO1874		acyltransferase domain-containing protein	1.42	0.11	1.38	0.03	1.40	0.02	2.84	0.03	-1.38	0.04	0.73	2.11	1.27	0.28	-1.64	0.04	-0.19	1.46
SPO1875	*murI*	glutamate racemase (EC:5.1.1.3)	1.91	0.01	1.36	0.03	1.64	0.28	4.87	0.00	-1.21	0.10	1.83	3.04	1.05	0.88	-1.49	0.08	-0.22	1.27
SPO1876	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase (EC:1.2.1.38)	1.33	0.18	1.05	0.81	1.19	0.14	1.49	0.02	-1.27	0.09	0.11	1.38	-1.11	0.21	1.53	0.09	0.21	1.32
SPO1877	*ccmE*	cytochrome c-type biogenesis protein CcmE	1.96	0.00	1.66	0.03	1.81	0.15	2.31	0.03	1.02	0.84	1.67	0.65	1.62	0.17	1.74	0.03	1.68	0.06
SPO1878		hypothetical protein	X	X	1.98	0.00	N/A	N/A	1.16	X	4.55	0.03	2.86	1.70	1.42	0.07	X	X	N/A	N/A
SPO1879		hypothetical protein	1.01	0.55	-1.00	0.97	0.01	1.00	1.20	0.92	1.09	0.87	1.15	0.05	-1.13	0.87	1.39	0.17	0.13	1.26
SPO1880	*ccmF*	cytochrome c-type biogenesis protein CcmF	2.57	0.41	1.82	0.07	2.20	0.38	3.27	0.03	1.04	0.96	2.16	1.12	1.59	0.02	1.25	0.16	1.42	0.17
SPO1881		cytochrome c biogenesis family protein	2.35	0.01	2.19	0.01	2.27	0.08	2.80	0.01	1.30	0.09	2.05	0.75	1.27	0.12	1.10	0.58	1.19	0.09
SPO1882		enoyl-CoA hydratase	1.19	0.72	1.32	0.47	1.26	0.07	1.21	0.47	1.40	0.39	1.31	0.10	-1.02	0.82	1.19	0.56	0.09	1.11
SPO1883		hypothetical protein	-1.86	0.02	-1.00	0.92	-1.43	0.43	-2.20	0.02	1.34	0.34	-0.43	1.77	1.46	0.11	1.29	0.04	1.38	0.09
SPO1884		methionine synthase I (EC:2.1.1.13)	-6.01	0.00	-1.93	0.02	-3.97	2.04	2.56	0.01	1.32	0.04	1.94	0.62	-1.12	0.12	-1.11	0.06	-1.12	0.01
SPO1885		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO1886		hypothetical protein	3.16	0.01	1.45	0.03	2.31	0.86	2.19	0.01	1.16	0.45	1.68	0.52	1.30	0.04	1.27	0.30	1.29	0.02
SPO1887	*purC*	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC:6.3.2.6)	1.16	0.53	1.42	0.16	1.29	0.13	2.31	0.03	0.97	0.15	1.64	0.67	-1.07	0.55	-1.20	0.21	-1.14	0.06
SPO1888	*purS*	phosphoribosylformylglycinamidine synthase subunit PurS	1.09	0.47	1.57	0.10	1.33	0.24	4.77	0.00	-1.32	0.01	1.73	3.05	1.00	0.77	-1.80	0.04	-0.40	1.40
SPO1889		alcohol dehydrogenase (EC:1.1.1.1)	-1.10	0.52	1.42	0.08	0.16	1.26	3.10	0.01	0.97	0.16	2.04	1.07	-1.60	0.01	-2.02	0.01	-1.81	0.21
SPO1890	*purQ*	phosphoribosylformylglycinamidine synthase I (EC:6.3.5.3)	1.60	0.08	-1.18	0.18	0.21	1.39	2.38	0.03	0.96	0.54	1.67	0.71	-1.87	0.02	-1.78	0.03	-1.83	0.05
SPO1891		C4-dicarboxylate transport sensor protein DctB	-1.28	0.63	-2.42	0.02	-1.85	0.57	-1.34	0.16	1.14	0.50	-0.10	1.24	-1.16	0.05	1.05	0.59	-0.05	1.11
SPO1892	*dctD-1*	C4-dicarboxylate transport transcriptional regulatory protein DctD	0.96	0.03	-1.23	0.03	-0.14	1.09	2.52	0.00	1.34	0.08	1.93	0.59	1.71	0.08	1.88	0.04	1.80	0.09
SPO1893		ribonuclease (EC:3.4.24.-)	-1.34	0.03	-1.05	0.28	-1.20	0.15	1.48	0.03	-1.10	0.11	0.19	1.29	1.25	0.08	1.21	0.22	1.23	0.02
SPO1895		SirA family protein	-1.15	0.32	1.41	0.01	0.13	1.28	1.48	0.09	1.08	0.73	1.28	0.20	-1.58	0.74	-1.98	0.04	-1.78	0.20
SPO1896	*ccdA*	cytochrome c-type biogenesis protein CcdA	1.60	0.43	1.37	0.39	1.49	0.12	1.98	0.11	-1.53	0.26	0.23	1.76	1.24	0.23	1.25	0.70	1.25	0.01
SPO1897		hypothetical protein	-1.23	0.08	-1.06	0.31	-1.15	0.09	-1.79	0.02	1.13	0.31	-0.33	1.46	-1.06	0.51	-0.98	0.16	-1.02	0.04
SPO1898		cytochrome P450 family protein	-1.39	0.00	1.18	0.42	-0.11	1.29	-1.44	0.07	1.12	0.34	-0.16	1.28	-1.02	0.91	-1.39	0.18	-1.21	0.18
SPO1899	*fda*	fructose-1,6-bisphosphate aldolase (EC:4.1.2.13)	-1.36	0.06	1.30	0.10	-0.03	1.33	2.16	0.01	-1.84	0.01	0.16	2.00	1.05	0.88	-1.13	0.27	-0.04	1.09
SPO1900	*tag*	DNA-3-methyladenine glycosylase I (EC:3.2.2.20)	-1.16	0.67	-1.17	0.42	-1.17	0.01	1.60	0.10	-1.31	0.06	0.15	1.46	-1.02	0.62	0.98	0.57	-0.02	1.00
SPO1901		hypothetical protein	-1.12	0.07	-1.19	0.43	-1.16	0.03	1.35	0.24	-1.08	0.28	0.14	1.22	1.17	0.25	1.02	0.83	1.10	0.08
SPO1902		TetR family transcriptional regulator	1.07	0.89	-1.43	0.10	-0.18	1.25	1.93	0.09	-1.43	0.04	0.25	1.68	-1.52	0.01	-1.61	0.04	-1.57	0.05
SPO1903		hypothetical protein	1.08	0.90	-1.52	0.04	-0.22	1.30	1.18	0.35	1.25	0.08	1.22	0.04	1.27	0.37	1.22	0.11	1.25	0.03
SPO1904		hypothetical protein	1.02	0.95	-1.59	0.15	-0.29	1.31	1.03	1.00	1.14	0.73	1.09	0.05	1.07	0.57	1.04	0.94	1.06	0.02
SPO1905	*fumC*	fumarate hydratase (EC:4.2.1.2)	-1.45	0.08	-1.99	0.05	-1.72	0.27	-1.62	0.13	1.29	0.56	-0.17	1.46	-1.38	0.46	1.18	0.72	-0.10	1.28
SPO1906		hypothetical protein	-1.35	0.00	-1.04	0.60	-1.20	0.16	-1.85	0.00	1.46	0.02	-0.20	1.66	1.18	0.08	1.64	0.05	1.41	0.23
SPO1907		hypothetical protein	-1.23	0.12	1.33	0.06	0.05	1.28	-1.40	0.01	1.50	0.06	0.05	1.45	1.46	0.11	1.65	0.02	1.56	0.10
SPO1908		chromate transporter	1.05	0.44	1.08	0.44	1.07	0.02	-1.11	0.48	1.18	0.11	0.03	1.15	-1.28	0.09	-1.26	0.21	-1.27	0.01
SPO1909		hypothetical protein	-1.26	0.26	1.73	0.16	0.24	1.50	-8.67	0.01	3.19	0.02	-2.74	5.93	-1.27	0.23	1.42	0.41	0.08	1.35

SPO1911		hypothetical protein	1.30	0.74	3.87	0.12	2.59	1.29	1.35	0.60	8.62	0.08	4.99	3.64	-0.99	0.96	1.26	0.34	0.13	1.13
SPO1912		GntR family transcriptional regulator	3.24	0.04	3.86	0.05	3.55	0.31	4.64	0.01	7.45	0.02	6.05	1.41	1.14	0.50	1.33	0.56	1.24	0.10
SPO1913	*dmdA*	dimethyl sulfoniopropionate demethylase	29.60	0.00	17.00	0.00	23.30	6.30	12.50	0.00	35.00	0.00	23.75	11.25	-1.23	0.17	-1.60	0.08	-1.42	0.19
SPO1914	*acuI*	acrylate utilisation protein	16.30	0.01	16.40	0.00	16.35	0.05	8.23	0.00	26.30	0.00	17.27	9.04	1.23	0.18	1.21	0.49	1.22	0.01
SPO1915		glyoxalase	1.29	0.02	1.98	0.01	1.64	0.35	-1.10	0.70	2.78	0.07	0.84	1.94	1.13	0.37	-1.30	0.61	-0.09	1.22
SPO1916		class V aminotransferase	1.95	0.02	1.06	0.46	1.51	0.45	2.97	0.04	-1.18	0.12	0.90	2.08	-1.32	0.02	-1.30	0.06	-1.31	0.01
SPO1917	*phrB*	deoxyribodipyrimidine photolyase (EC:4.1.99.3)	-1.33	0.71	-0.99	0.95	-1.16	0.17	-1.64	0.60	1.06	0.70	-0.29	1.35	-1.02	0.98	1.37	0.21	0.18	1.20
SPO1918	*cfa*	cyclopropane-fatty-acyl-phospholipid synthase (EC:2.1.1.79)	-1.12	0.30	-1.61	0.23	-1.37	0.24	-2.07	0.02	1.44	0.42	-0.32	1.76	1.59	0.09	1.88	0.20	1.74	0.15
SPO1919	*trgA*	tellurite resistance protein	1.36	0.80	1.04	0.87	1.20	0.16	1.46	0.64	1.08	0.70	1.27	0.19	1.28	0.17	1.30	0.22	1.29	0.01
SPO1920	*trgB*	tellurite resistance protein	-1.22	0.60	-1.03	0.84	-1.13	0.10	2.63	0.15	-1.33	0.41	0.65	1.98	1.34	0.51	1.04	0.99	1.19	0.15
SPO1921		cysteine synthase A	2.47	0.33	1.21	0.50	1.84	0.63	3.30	0.02	1.02	0.77	2.16	1.14	1.09	0.38	1.02	0.26	1.06	0.04
SPO1922		mechanosensitive ion channel protein MscS	-1.37	0.44	1.25	0.14	-0.06	1.31	1.08	0.85	1.22	0.20	1.15	0.07	1.32	0.01	1.11	0.34	1.22	0.11
SPO1923		hypothetical protein	1.58	0.26	1.11	0.74	1.35	0.23	2.18	0.10	1.18	0.28	1.68	0.50	1.14	0.10	-1.02	0.48	0.06	1.08
SPO1925		hypothetical protein	1.94	0.01	-1.20	0.23	0.37	1.57	1.27	0.22	1.49	0.09	1.38	0.11	1.19	0.16	1.26	0.40	1.23	0.04
SPO1926		hypothetical protein	1.71	0.73	-1.38	0.73	0.17	1.55	1.00	0.92	1.36	0.75	1.18	0.18	-1.66	0.11	-1.40	0.56	-1.53	0.13
SPO1927		phage integrase site specific recombinase	1.80	0.29	-1.51	0.25	0.15	1.66	1.22	0.74	-1.50	0.24	-0.14	1.36	1.16	0.62	-1.05	0.82	0.05	1.11
SPO1928		Tat pathway signal sequence domain-containing protein	-2.66	0.02	1.52	0.19	-0.57	2.09	2.16	0.06	1.33	0.12	1.75	0.42	2.24	0.00	1.66	0.03	1.95	0.29
SPO1929		peptidoglycan binding protein	0.93	0.08	-1.34	0.23	-0.21	1.13	-2.97	0.01	-1.15	0.14	-2.06	0.91	-1.90	0.01	0.94	0.59	-0.48	1.42
SPO1930	*lpxD*	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase (EC:2.3.1.-)	1.25	0.13	-1.34	0.27	-0.05	1.30	1.67	0.04	-1.18	0.20	0.25	1.43	-1.13	0.48	-1.10	0.15	-1.12	0.01
SPO1931		acyl carrier protein	2.11	0.09	1.67	0.01	1.89	0.22	5.64	0.01	-1.32	0.06	2.16	3.48	1.13	0.64	-1.69	0.07	-0.28	1.41
SPO1932		beta-ketoacyl synthase	2.09	0.07	1.53	0.19	1.81	0.28	5.24	0.07	-1.07	0.45	2.09	3.16	-1.39	0.27	-1.80	0.03	-1.60	0.21
SPO1933		invasion associated family protein	1.70	0.01	1.35	0.08	1.53	0.18	2.70	0.00	1.14	0.45	1.92	0.78	-1.15	0.06	-1.24	0.05	-1.20	0.05
SPO1934		hypothetical protein	-1.11	0.24	1.05	0.87	-0.03	1.08	-1.10	0.69	-1.18	0.26	-1.14	0.04	1.11	0.36	-1.08	0.20	0.02	1.10
SPO1935		branched-chain amino acid ABC transporter permease	X	X	-1.10	0.59	N/A	N/A	2.15	0.00	-1.87	0.01	0.14	2.01	1.38	0.06	-1.04	0.82	0.17	1.21
SPO1936		branched-chain amino acid ABC transporter permease	-1.22	0.74	-1.36	0.13	-1.29	0.07	1.29	0.32	-1.56	0.03	-0.14	1.43	-1.17	0.35	-1.17	0.24	-1.17	0.00
SPO1937		branched-chain amino acid ABC transporter ATP-binding protein	-1.20	0.64	-1.56	0.11	-1.38	0.18	1.13	0.65	-1.70	0.06	-0.29	1.42	1.15	0.56	-1.04	0.68	0.05	1.10
SPO1938		branched-chain amino acid ABC transporter ATP-binding protein	-1.77	0.05	-1.89	0.05	-1.83	0.06	-1.03	0.70	-1.68	0.03	-1.36	0.32	-1.34	0.06	-1.06	0.54	-1.20	0.14
SPO1939		branched-chain amino acid ABC transporter substrate-binding protein	-2.15	0.02	-1.84	0.01	-2.00	0.16	0.98	0.10	1.15	0.84	1.07	0.08	1.65	0.09	2.80	0.01	2.23	0.58
SPO1940		hypothetical protein	1.29	0.39	1.12	0.60	1.21	0.09	-1.61	0.24	1.36	0.02	-0.13	1.49	1.53	0.09	1.46	0.29	1.50	0.04
SPO1941		AraC family transcriptional regulator	-1.70	0.00	-1.35	0.25	-1.53	0.18	1.24	0.04	1.44	0.07	1.34	0.10	-1.75	0.04	-1.41	0.09	-1.58	0.17
SPO1942		3-deoxy-7-phosphoheptulonate synthase (EC:2.5.1.54)	1.38	0.07	1.14	0.72	1.26	0.12	3.21	0.01	1.28	0.34	2.25	0.97	1.17	0.53	1.16	0.94	1.17	0.01
SPO1943		hypothetical protein	-2.07	0.23	2.28	0.03	0.11	2.18	-1.87	0.02	2.86	0.02	0.50	2.37	1.43	0.12	2.04	0.07	1.74	0.31
SPO1944		hypothetical protein	1.09	0.59	1.04	0.92	1.07	0.03	1.77	0.01	1.19	0.65	1.48	0.29	-1.61	0.02	-1.45	0.00	-1.53	0.08
SPO1945	*gmk*	guanylate kinase (EC:2.7.4.8)	1.20	0.75	1.10	0.73	1.15	0.05	1.75	0.22	1.26	0.47	1.51	0.25	-1.68	0.14	-1.88	0.23	-1.78	0.10
SPO1946		transferase	1.01	0.94	1.35	0.18	1.18	0.17	1.84	0.03	1.14	0.47	1.49	0.35	-1.06	0.27	-1.20	0.18	-1.13	0.07

SPO1947		phosphate regulon sensor histidine kinase	-1.68	0.08	1.45	0.17	-0.12	1.57	-1.25	0.55	-1.20	0.51	-1.23	0.03	-1.02	0.92	-1.16	0.81	-1.09	0.07
SPO1948	*pstS*	phosphate ABC transporter substrate-binding protein	5.57	0.02	1.37	0.22	3.47	2.10	3.35	0.01	1.88	0.02	2.62	0.73	-1.25	0.03	-1.11	0.47	-1.18	0.07
SPO1949	*pstC*	phosphate ABC transporter permease	2.47	0.28	1.09	0.69	1.78	0.69	1.40	0.20	1.68	0.10	1.54	0.14	-1.69	0.07	-1.19	0.12	-1.44	0.25
SPO1950	*pstA*	phosphate ABC transporter permease	1.83	0.39	-1.09	0.60	0.37	1.46	1.17	0.86	1.27	0.55	1.22	0.05	-1.62	0.08	1.06	0.96	-0.28	1.34
SPO1951	*pstB*	phosphate transporter ATP-binding protein (EC:3.6.3.27)	0.97	0.66	-1.16	0.65	-0.10	1.06	-1.24	0.36	1.20	0.53	-0.02	1.22	-1.34	0.21	1.08	0.92	-0.13	1.21
SPO1952	*phoU*	phosphate transport system regulatory protein PhoU	2.72	0.01	1.28	0.05	2.00	0.72	2.36	0.01	1.32	0.14	1.84	0.52	-1.19	0.24	-1.47	0.02	-1.33	0.14
SPO1953	*phoB*	phosphate regulon transcriptional regulatory protein PhoB	2.08	0.00	1.43	0.21	1.76	0.33	2.18	0.00	1.18	0.18	1.68	0.50	1.05	0.51	-1.32	0.08	-0.14	1.19
SPO1954		LysR family transcriptional regulator	-3.34	0.00	-1.79	0.01	-2.57	0.78	-1.46	0.03	1.29	0.19	-0.09	1.38	-1.60	0.01	-1.31	0.51	-1.46	0.15
SPO1955	*gcdH*	glutaryl-CoA dehydrogenase (EC:1.3.99.7)	1.97	0.53	1.18	0.27	1.58	0.40	1.71	0.42	1.37	0.09	1.54	0.17	1.28	0.19	1.24	0.29	1.26	0.02
SPO1956	*sulP*	sulfate permease	X	X	1.16	0.38	N/A	N/A	-1.17	0.89	X	X	N/A	N/A	-1.00	0.84	X	X	N/A	N/A
SPO1957		short chain dehydrogenase/reductase oxidoreductase	1.36	0.17	1.07	0.32	1.22	0.15	-1.57	0.09	1.11	0.35	-0.23	1.34	1.08	0.43	1.22	0.16	1.15	0.07
SPO1958		acyl-CoA thioesterase	-0.95	0.63	1.22	0.05	0.14	1.08	1.60	0.05	-1.19	0.31	0.21	1.40	-1.24	0.32	-1.54	0.08	-1.39	0.15
SPO1959		acetoacetyl-CoA synthetase (EC:6.2.1.1)	-1.98	0.52	1.11	0.11	-0.44	1.55	0.94	0.37	1.03	0.92	0.98	0.05	-1.12	0.61	-1.11	0.58	-1.12	0.01
SPO1960		beta-lactamase	-1.15	0.01	-1.24	0.17	-1.20	0.05	-1.46	0.01	1.97	0.05	0.26	1.72	-1.04	0.72	1.50	0.05	0.23	1.27
SPO1961		IclR family transcriptional regulator	-1.62	0.14	-1.18	0.05	-1.40	0.22	-5.48	0.06	1.07	0.43	-2.21	3.28	1.19	0.08	-0.96	0.31	0.12	1.07
SPO1962		phosphotransferase	1.39	0.00	-1.16	0.19	0.12	1.28	-1.96	0.03	1.22	0.19	-0.37	1.59	-1.02	0.61	1.09	0.43	0.04	1.06
SPO1963		phosphoglycerate mutase	1.67	0.00	-1.28	0.41	0.20	1.48	-2.68	0.01	-1.08	0.30	-1.88	0.80	-1.41	0.12	-1.20	0.36	-1.31	0.11
SPO1964		hypothetical protein	1.80	0.02	-1.27	0.18	0.27	1.54	-1.74	0.05	1.04	0.85	-0.35	1.39	1.09	0.60	1.10	0.23	1.10	0.01
SPO1965		short chain dehydrogenase/reductase oxidoreductase	1.62	0.00	-1.59	0.13	0.02	1.61	-2.33	0.01	-1.12	0.07	-1.73	0.61	-1.25	0.02	1.25	0.10	0.00	1.25
SPO1966		short chain dehydrogenase/reductase oxidoreductase	1.33	0.54	-1.33	0.11	0.00	1.33	-2.35	0.21	-1.07	0.62	-1.71	0.64	1.01	0.98	1.22	0.28	1.12	0.11
SPO1967		acyl-CoA dehydrogenase	1.57	0.80	-1.60	0.11	-0.02	1.59	-2.80	0.07	1.01	0.91	-0.90	1.91	1.04	0.90	1.49	0.10	1.27	0.23
SPO1968		acyl-CoA dehydrogenase	1.10	0.98	-1.45	0.08	-0.18	1.28	-3.24	0.01	-1.05	0.27	-2.15	1.10	1.30	0.03	1.26	0.07	1.28	0.02
SPO1969		zinc-binding dehydrogenase oxidoreductase	-1.21	0.04	-1.47	0.36	-1.34	0.13	-2.90	0.02	-1.50	0.45	-2.20	0.70	1.60	0.03	1.89	0.22	1.75	0.15
SPO1970		phosphoglycerate mutase	1.10	0.99	1.01	1.00	1.06	0.05	1.17	0.97	1.13	0.71	1.15	0.02	1.28	0.39	1.65	0.15	1.47	0.19
SPO1971		enoyl-CoA hydratase (EC:4.2.1.17)	-1.12	0.46	-1.81	0.08	-1.47	0.35	-4.12	0.04	-1.04	0.60	-2.58	1.54	-1.13	0.47	1.45	0.15	0.16	1.29
SPO1972		nodulation protein N	-1.09	0.69	-1.53	0.50	-1.31	0.22	-2.74	0.16	-1.01	0.95	-1.88	0.87	1.10	0.86	1.74	0.36	1.42	0.32
SPO1973	*aroQ*	3-dehydroquinate dehydratase (EC:4.2.1.10)	-2.50	0.04	-1.04	0.80	-1.77	0.73	-1.35	0.24	-1.32	0.42	-1.34	0.02	-1.08	0.66	1.11	0.93	0.02	1.10
SPO1974		LuxR family transcriptional regulator	-2.43	0.00	-1.02	0.84	-1.73	0.71	-1.21	0.08	-1.19	0.20	-1.20	0.01	-1.23	0.30	-1.14	0.19	-1.19	0.05
SPO1975	*tsf*	elongation factor Ts	-1.15	0.43	1.64	0.07	0.25	1.40	1.10	0.83	-3.81	0.01	-1.36	2.46	1.69	0.01	-2.15	0.02	-0.23	1.92
SPO1976	*rpsB*	30S ribosomal protein S2	-2.23	0.26	-1.34	0.12	-1.79	0.45	4.64	0.04	-2.22	0.01	1.21	3.43	-1.51	0.20	-3.15	0.00	-2.33	0.82
SPO1977		hypothetical protein	-2.74	0.00	-1.15	0.23	-1.95	0.80	-3.13	0.01	1.34	0.22	-0.90	2.24	1.08	0.05	1.19	0.21	1.14	0.05
SPO1978		hypothetical protein	-2.92	0.00	-1.15	0.41	-2.04	0.88	-2.74	0.00	1.52	0.03	-0.61	2.13	1.21	0.08	1.52	0.04	1.37	0.16
SPO1979		acyltransferase	-3.83	0.01	1.16	0.40	-1.34	2.50	-2.25	0.03	-1.67	0.10	-1.96	0.29	-1.04	0.96	-1.35	X	-1.20	0.16
SPO1980		hypothetical protein	X	X	1.12	0.22	N/A	N/A	2.26	0.01	-1.87	0.02	0.20	2.07	-1.22	0.26	-1.91	0.08	-1.57	0.35
SPO1981		hypothetical protein	1.34	0.12	1.45	0.07	1.40	0.05	1.40	0.13	1.33	0.05	1.37	0.03	-1.20	0.08	-1.36	0.10	-1.28	0.08
SPO1982		hypothetical protein	1.18	0.19	1.01	0.97	1.10	0.09	1.64	0.03	1.02	0.99	1.33	0.31	-2.02	0.01	-1.95	0.03	-1.99	0.04

SPO1983		hypothetical protein	1.28	0.77	2.34	0.05	1.81	0.53	-1.48	0.03	2.46	0.05	0.49	1.97	1.27	0.20	1.17	0.58	1.22	0.05
SPO1984	*proA*	gamma-glutamyl phosphate reductase (EC:1.2.1.41)	2.59	0.06	1.02	0.96	1.81	0.79	2.73	0.06	0.98	0.13	1.86	0.87	1.16	0.45	1.22	0.18	1.19	0.03
SPO1985	*proB*	gamma-glutamyl kinase (EC:2.7.2.11)	-1.20	0.02	1.02	0.98	-0.09	1.11	1.95	0.00	-1.12	0.11	0.42	1.54	-1.09	0.40	0.94	0.51	-0.08	1.01
SPO1986	*obgE*	GTPase ObgE	-1.20	0.08	0.99	0.88	-0.10	1.10	1.27	0.13	-1.34	0.06	-0.04	1.31	1.43	0.08	1.26	0.29	1.35	0.09
SPO1987		acetyltransferase	-2.09	0.02	-2.72	0.02	-2.41	0.31	-1.52	0.04	-1.12	0.46	-1.32	0.20	1.71	0.17	2.44	0.05	2.08	0.36
SPO1988		amino acid transporter LysE	-1.46	0.49	-2.09	0.12	-1.78	0.31	1.02	0.65	-1.07	0.78	-0.03	1.05	1.77	0.13	2.54	0.09	2.16	0.38
SPO1989	*rpmA*	50S ribosomal protein L27	-1.28	0.02	1.11	0.70	-0.09	1.20	5.98	0.00	-1.77	0.02	2.11	3.88	1.20	0.45	-1.79	0.01	-0.30	1.50
SPO1990	*rplU*	50S ribosomal protein L21	-2.76	0.00	1.13	0.46	-0.82	1.95	4.80	0.00	-1.62	0.06	1.59	3.21	-1.49	0.85	-1.39	0.06	-1.44	0.05
SPO1991		hypothetical protein	1.01	0.16	-1.00	1.00	0.01	1.01	1.09	0.31	1.22	0.13	1.16	0.06	1.96	0.00	1.14	0.14	1.55	0.41
SPO1992		hypothetical protein	-1.32	0.00	-1.15	0.06	-1.24	0.09	-1.22	0.09	1.30	0.10	0.04	1.26	1.57	0.21	1.47	0.03	1.52	0.05
SPO1994		HlyD family type I secretion membrane fusion protein	-1.75	0.29	-1.12	0.74	-1.44	0.32	-1.44	0.50	1.61	0.07	0.09	1.53	1.22	0.46	1.28	0.25	1.25	0.03
SPO1995		ABC transporter ATP-binding protein/permease	0.98	0.88	-1.18	0.12	-0.10	1.08	-1.34	0.64	1.46	0.16	0.06	1.40	1.36	0.05	1.69	0.03	1.53	0.17
SPO1996		hypothetical protein	-3.06	0.00	-1.48	0.08	-2.27	0.79	-1.82	0.02	1.85	0.04	0.02	1.84	1.00	0.59	1.54	0.05	1.27	0.27
SPO1997		hypothetical protein	-1.93	0.08	-1.41	0.05	-1.67	0.26	-2.71	0.03	1.41	0.13	-0.65	2.06	-1.24	0.29	1.66	0.22	0.21	1.45
SPO1998		hypothetical protein	-1.06	0.79	-1.47	0.16	-1.27	0.20	1.14	0.19	1.82	0.03	1.48	0.34	-1.14	0.34	-1.32	0.32	-1.23	0.09
SPO1999		hypothetical protein	X	X	1.06	0.77	N/A	N/A	-3.40	X	-1.07	X	-2.24	1.17	-1.15	0.77	X	X	N/A	N/A
SPO2000		endoribonuclease L-PSP	0.92	0.37	1.10	0.84	1.01	0.09	0.82	0.40	1.53	0.23	1.17	0.36	1.62	0.10	1.48	0.12	1.55	0.07
SPO2001		oxidoreductase, FAD-binding	-1.79	0.40	-1.37	0.44	-1.58	0.21	-2.42	0.04	-1.11	0.76	-1.77	0.65	-1.24	0.59	1.47	0.62	0.12	1.36
SPO2002		acetylpolyamine aminohydrolase	-1.56	0.69	1.03	0.95	-0.27	1.30	-1.65	0.77	-1.65	0.32	-1.65	0.00	1.14	0.77	1.18	0.75	1.16	0.02
SPO2003		acetyltransferase	-1.18	0.74	1.04	0.75	-0.07	1.11	-1.50	0.43	-0.98	0.83	-1.24	0.26	1.23	0.48	1.64	X	1.44	0.20
SPO2004		hypothetical protein	X	X	-1.08	0.68	N/A	N/A	-1.43	0.55	-1.04	0.97	-1.24	0.20	1.07	0.75	X	X	N/A	N/A
SPO2005		class III aminotransferase	-1.31	X	-0.99	0.62	-1.15	0.16	-1.43	0.02	1.65	0.14	0.11	1.54	1.13	0.30	X	X	N/A	N/A
SPO2006		spermidine/putrescine ABC transporter ATP-binding protein	-2.11	0.03	-1.43	0.39	-1.77	0.34	-2.73	0.03	1.10	0.75	-0.82	1.92	-1.06	0.94	1.29	0.66	0.12	1.18
SPO2007		spermidine/putrescine ABC transporter substrate-binding protein	-2.26	0.00	-1.40	0.41	-1.83	0.43	-3.55	0.03	1.01	0.96	-1.27	2.28	-1.07	0.83	1.15	0.73	0.04	1.11
SPO2008		spermidine/putrescine ABC transporter permease	-2.06	0.01	-1.30	0.42	-1.68	0.38	-2.31	0.05	-1.02	0.92	-1.67	0.65	1.09	0.36	-1.10	0.75	-0.01	1.10
SPO2009		spermidine/putrescine ABC transporter permease	-1.47	X	-1.40	0.61	-1.44	0.04	-2.58	0.19	X	X	N/A	N/A	-1.09	0.83	X	X	N/A	N/A
SPO2010		LysR family transcriptional regulator	-2.12	0.00	-1.36	0.07	-1.74	0.38	-1.75	0.04	-1.15	0.27	-1.45	0.30	-1.44	0.06	-1.66	0.04	-1.55	0.11
SPO2013		hypothetical protein	1.78	0.05	1.13	0.45	1.46	0.32	1.50	0.10	1.44	0.07	1.47	0.03	-1.07	0.52	1.20	0.72	0.06	1.14
SPO2014	*sufS*	cysteine desulfurase	1.48	0.31	1.40	0.03	1.44	0.04	2.44	0.01	-1.12	0.12	0.66	1.78	1.29	0.22	-1.48	0.09	-0.10	1.39
SPO2015		hypothetical protein	1.41	0.64	1.06	0.79	1.24	0.18	2.18	0.04	-1.43	0.06	0.38	1.81	-1.25	0.03	-1.16	0.04	-1.21	0.05
SPO2016		hypothetical protein	1.38	0.07	-1.32	0.01	0.03	1.35	1.93	0.02	-1.20	0.09	0.37	1.57	1.04	0.89	1.25	0.30	1.15	0.11
SPO2017		FeS assembly protein SufD	1.33	0.64	-1.24	0.51	0.05	1.29	1.75	0.34	1.04	0.88	1.40	0.36	1.10	0.60	1.00	0.61	1.05	0.05
SPO2018	*sufC*	FeS assembly ATPase SufC	1.10	0.93	-1.13	0.22	-0.01	1.12	1.06	0.98	-1.22	0.10	-0.08	1.14	-1.43	0.15	-1.34	0.07	-1.39	0.04
SPO2019		exoV domain-containing protein	1.11	0.35	-1.12	0.21	-0.01	1.12	1.75	0.07	-1.06	0.75	0.35	1.41	-1.35	0.04	-1.18	0.18	-1.27	0.09
SPO2020		FkbM family methyltransferase	1.05	0.99	1.20	0.49	1.13	0.08	-1.13	0.85	-1.13	0.52	-1.13	0.00	-1.20	0.23	-1.47	0.02	-1.34	0.14
SPO2021		hypothetical protein	1.03	0.54	1.02	0.99	1.03	0.01	1.06	0.49	0.99	0.50	1.02	0.04	1.14	0.03	1.32	0.15	1.23	0.09
SPO2022		hypothetical protein	0.99	0.39	1.02	0.82	1.00	0.02	1.31	0.07	-1.16	0.29	0.08	1.24	-1.18	0.31	-1.13	0.24	-1.16	0.03
SPO2023	*sufB*	cysteine desulfurase	-1.11	0.89	1.04	0.93	-0.04	1.08	1.06	0.76	-1.41	0.10	-0.18	1.24	1.12	0.64	-1.12	0.49	0.00	1.12

SPO2025		iron-sulfur cluster assembly transcription factor IscR	1.16	0.67	1.21	0.45	1.19	0.03	-1.99	0.07	-1.37	0.02	-1.68	0.31	-1.06	0.14	-1.34	0.42	-1.20	0.14
SPO2026		hypothetical protein	1.11	0.93	-1.36	0.05	-0.13	1.24	2.52	0.01	-1.10	0.35	0.71	1.81	-1.47	0.04	0.99	0.58	-0.24	1.23
SPO2027		hypothetical protein	1.14	0.54	1.09	0.43	1.12	0.02	3.46	0.01	1.07	0.96	2.27	1.20	1.49	0.11	1.19	0.39	1.34	0.15
SPO2028		HD domain-containing protein	0.98	0.98	-1.04	0.78	-0.03	1.01	1.79	0.81	-1.06	0.62	0.37	1.43	1.37	0.34	1.04	0.93	1.21	0.17
SPO2029		glutamine amidotransferase	-1.29	0.50	-1.42	0.19	-1.36	0.06	1.31	0.55	0.99	0.82	1.15	0.16	-1.11	0.55	-1.31	0.29	-1.21	0.10
SPO2030		SMR family multidrug efflux pump	1.62	0.53	1.55	0.18	1.59	0.04	1.60	0.61	-1.19	0.34	0.21	1.40	-1.03	0.72	-1.19	0.36	-1.11	0.08
SPO2031	*typA*	GTP-binding protein TypA	1.36	0.33	1.25	0.69	1.31	0.06	6.38	0.00	-1.47	0.02	2.46	3.93	-1.57	0.02	-1.84	0.01	-1.71	0.14
SPO2032		hypothetical protein	1.70	0.18	1.28	0.41	1.49	0.21	2.83	0.08	-1.07	0.60	0.88	1.95	1.04	0.98	-1.16	0.27	-0.06	1.10
SPO2033	*alaS*	alanyl-tRNA synthetase (EC:6.1.1.7)	1.18	0.67	-1.14	0.54	0.02	1.16	2.08	0.02	1.01	0.46	1.55	0.54	1.09	0.48	1.44	0.06	1.27	0.18
SPO2034	*recA*	recombinase A	1.68	0.02	1.15	0.75	1.42	0.27	-1.86	0.01	0.97	0.77	-0.44	1.42	1.18	0.50	1.56	0.27	1.37	0.19
SPO2035		hypothetical protein	1.20	0.41	-1.02	0.95	0.09	1.11	1.01	0.74	1.05	0.97	1.03	0.02	-1.10	0.82	-1.50	0.51	-1.30	0.20
SPO2036		sensory box sensor histidine kianse/response regulator (EC:2.7.3.-)	-1.51	0.67	1.78	0.05	0.14	1.65	-2.51	0.02	1.16	0.58	-0.68	1.84	1.07	0.64	-1.10	1.00	-0.02	1.09
SPO2037		NOL1/NOP2/sun family protein	X	X	1.19	0.11	N/A	N/A	3.12	0.00	-1.26	0.08	0.93	2.19	-1.52	0.02	-2.81	0.01	-2.17	0.65
SPO2038		metallo-beta-lactamase	1.13	0.85	1.48	0.29	1.31	0.18	4.66	0.13	-1.37	0.44	1.65	3.02	1.04	0.96	-2.25	0.24	-0.61	1.65
SPO2039	*guaB*	inosine-5'-monophosphate dehydrogenase (EC:1.1.1.205)	1.62	0.00	1.33	0.24	1.48	0.15	7.13	0.00	-1.34	0.10	2.90	4.24	1.23	0.03	-1.18	0.16	0.03	1.21
SPO2040		CaiB/BaiF family protein	1.14	X	1.23	0.08	1.19	0.05	4.57	0.00	-1.44	0.15	1.57	3.01	-1.00	0.94	-1.52	0.15	-1.26	0.26
SPO2041		(Fe-S)-binding protein	2.54	0.06	1.35	0.09	1.95	0.60	4.06	0.03	-1.44	0.03	1.31	2.75	-1.31	0.22	-2.03	0.03	-1.67	0.36
SPO2042		UbiE/COQ5 family methlytransferase	-1.50	0.14	-1.11	0.68	-1.31	0.19	0.97	0.97	1.57	0.03	1.27	0.30	-1.32	0.17	-1.31	0.14	-1.32	0.01
SPO2044		lipoprotein	-1.52	0.24	1.34	0.22	-0.09	1.43	-1.85	0.01	1.25	0.02	-0.30	1.55	-1.18	0.12	1.67	0.04	0.25	1.43
SPO2045	*dmdB*	3-methylmercaptopropionyl-CoA ligase (EC:6.2.1.-)	1.80	0.51	-1.03	0.94	0.39	1.42	0.98	0.84	1.60	0.43	1.29	0.31	1.46	0.31	2.45	0.18	1.96	0.50
SPO2046	*pgi*	glucose-6-phosphate isomerase (EC:5.3.1.9)	1.22	0.30	1.68	0.03	1.45	0.23	1.44	0.06	1.53	0.04	1.49	0.05	-1.04	0.60	-1.18	0.28	-1.11	0.07
SPO2047	*pgl*	6-phosphogluconolactonase (EC:3.1.1.31)	1.02	0.38	1.38	0.18	1.20	0.18	1.31	0.24	2.07	0.01	1.69	0.38	-1.03	0.76	-1.42	0.06	-1.23	0.19
SPO2048	*zwf-1*	glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49)	-1.34	0.63	1.15	0.67	-0.10	1.25	1.53	0.22	1.57	0.22	1.55	0.02	-1.39	0.38	-2.01	0.12	-1.70	0.31
SPO2049		radical SAM domain-containing protein	-1.55	0.02	1.00	0.93	-0.28	1.27	2.48	0.00	-1.09	0.62	0.70	1.79	-1.50	0.02	-1.28	0.10	-1.39	0.11
SPO2050		Usg	-1.66	0.11	1.28	0.26	-0.19	1.47	-11.30	0.02	1.27	0.36	-5.02	6.29	1.10	0.32	-1.47	0.49	-0.19	1.29
SPO2051	*gyrA*	DNA gyrase subunit A (EC:5.99.1.3)	-1.33	0.02	1.01	0.96	-0.16	1.17	1.07	0.74	-1.07	0.36	0.00	1.07	1.00	0.77	-1.16	0.09	-0.08	1.08
SPO2052		hypothetical protein	1.58	0.01	1.58	0.03	1.58	0.00	-5.83	0.00	2.07	0.04	-1.88	3.95	-1.31	0.05	-1.51	0.18	-1.41	0.10
SPO2053		thermostable carboxypeptidase (EC:3.4.17.19)	2.03	0.05	1.53	0.04	1.78	0.25	3.42	0.01	-1.46	0.08	0.98	2.44	1.14	0.34	-1.47	0.01	-0.17	1.31
SPO2054		cytochrome c oxidase assembly protein	1.77	0.03	1.33	0.07	1.55	0.22	2.28	0.00	-1.12	0.14	0.58	1.70	-1.12	0.35	1.14	0.71	0.01	1.13
SPO2055		RNA methyltransferase	-1.16	0.66	1.45	0.15	0.15	1.31	3.50	0.02	-1.64	0.03	0.93	2.57	-1.11	0.40	-2.13	0.04	-1.62	0.51
SPO2056		thiamine-phosphate pyrophosphorylase	1.36	0.93	1.43	0.15	1.40	0.03	3.46	0.56	-1.50	0.10	0.98	2.48	1.14	0.67	-1.28	0.27	-0.07	1.21
SPO2057		hypothetical protein	1.10	0.83	1.28	0.41	1.19	0.09	-1.05	0.59	1.08	0.51	0.02	1.07	2.12	0.02	-1.04	0.72	0.54	1.58
SPO2058		hypothetical protein	-1.69	0.15	-1.06	0.81	-1.38	0.32	-1.86	0.02	1.29	0.23	-0.29	1.58	-1.02	0.58	1.88	0.04	0.43	1.45
SPO2059		glutathione S-transferase	-1.67	0.03	-1.18	0.29	-1.43	0.25	1.37	0.17	1.45	0.15	1.41	0.04	1.13	0.65	1.21	0.13	1.17	0.04
SPO2060		PfkB family kinase	-0.98	0.70	-1.17	0.43	-1.08	0.09	2.70	0.01	1.01	0.66	1.86	0.85	-1.98	0.01	-1.79	0.03	-1.89	0.10
SPO2061		indigoidine synthase A family protein	-1.12	0.80	1.03	0.93	-0.05	1.08	2.55	0.05	-1.27	0.13	0.64	1.91	-1.73	0.04	-2.33	0.02	-2.03	0.30
SPO2062		hypothetical protein	1.18	0.12	-1.68	0.01	-0.25	1.43	2.13	0.02	-1.35	0.03	0.39	1.74	1.04	0.96	1.09	0.89	1.07	0.03

SPO2063		acetyltransferase	-1.34	0.17	-1.10	0.19	-1.22	0.12	1.67	0.02	1.15	0.31	1.41	0.26	1.38	0.06	-1.07	0.97	0.16	1.23
SPO2064		patatin family phospholipase	1.58	0.65	1.07	0.50	1.33	0.25	2.81	0.32	1.03	0.96	1.92	0.89	1.39	0.28	1.45	0.33	1.42	0.03
SPO2065	*bdh-1*	D-beta-hydroxybutyrate dehydrogenase (EC:1.1.1.30)	2.03	0.42	1.08	0.63	1.56	0.48	4.05	0.03	1.43	0.08	2.74	1.31	1.11	0.65	1.73	0.12	1.42	0.31
SPO2066		ABC transporter substrate-binding protein	-1.92	0.14	-1.36	0.20	-1.64	0.28	1.00	0.93	-1.29	0.11	-0.15	1.15	1.12	0.21	-1.23	0.29	-0.05	1.18
SPO2067		hypothetical protein	3.75	0.01	3.42	0.00	3.59	0.17	10.20	0.00	1.56	0.02	5.88	4.32	1.39	0.10	1.08	0.23	1.24	0.16
SPO2068		DNA-binding protein	X	X	1.09	0.76	N/A	N/A	4.30	0.01	-1.31	0.26	1.50	2.81	-1.03	0.89	-1.60	0.06	-1.32	0.29
SPO2069		benzoate-coenzyme A ligase	-1.06	0.89	-1.28	0.25	-1.17	0.11	1.69	0.45	1.46	0.13	1.58	0.12	-1.63	0.15	-1.49	0.06	-1.56	0.07
SPO2070		DSBA-like thioredoxin family protein	-1.95	0.05	-1.43	0.15	-1.69	0.26	-2.47	0.01	-1.08	0.41	-1.78	0.70	-1.30	0.09	1.33	0.12	0.02	1.32
SPO2071		Bcr/CflA subfamily drug resistance transporter	-1.81	0.00	-1.59	0.02	-1.70	0.11	1.84	0.00	1.18	0.21	1.51	0.33	-1.57	0.14	-2.21	0.00	-1.89	0.32
SPO2072		hypothetical protein	1.08	0.77	-1.12	0.76	-0.02	1.10	-1.54	0.09	1.56	0.13	0.01	1.55	1.19	0.60	1.38	0.50	1.29	0.10
SPO2073		hypothetical protein	-1.20	0.03	1.02	0.83	-0.09	1.11	-1.44	0.06	1.61	0.04	0.09	1.53	1.15	0.33	-1.04	0.99	0.05	1.10
SPO2074	*mfd*	transcription-repair coupling factor	1.57	0.09	1.19	0.13	1.38	0.19	4.22	0.01	-1.51	0.05	1.36	2.87	-1.18	0.20	-1.59	0.10	-1.39	0.21
SPO2075		hypothetical protein	1.14	0.81	-1.09	0.58	0.02	1.12	3.21	0.09	-1.44	0.14	0.89	2.33	-1.50	0.32	-1.48	0.02	-1.49	0.01
SPO2076	*hemB*	delta-aminolevulinic acid dehydratase (EC:4.2.1.24)	3.51	0.01	1.45	0.03	2.48	1.03	3.52	0.02	1.35	0.17	2.44	1.09	1.11	0.50	1.05	0.91	1.08	0.03
SPO2077		twin-arginine translocation pathway signal sequence domain-containing protein	-2.35	0.00	-1.90	0.01	-2.13	0.23	1.18	0.21	-1.13	0.07	0.03	1.16	1.47	0.17	1.12	0.27	1.30	0.18
SPO2078		penicillin amidase	-1.08	0.82	1.05	0.87	-0.02	1.07	-1.83	0.44	-1.60	0.06	-1.72	0.12	1.24	0.13	-1.37	0.30	-0.07	1.31
SPO2079		Na(+)/H(+) antiporter-like protein	X	X	1.08	0.19	N/A	N/A	2.02	0.01	-1.23	0.05	0.40	1.63	1.09	0.12	-1.51	0.17	-0.21	1.30
SPO2080	*hflX*	GTP-binding protein HflX	-1.16	0.03	-1.04	0.80	-1.10	0.06	2.87	0.01	1.17	0.38	2.02	0.85	1.25	0.07	1.04	0.89	1.15	0.11
SPO2081	*hfq*	RNA-binding protein Hfq	0.91	0.31	-1.06	0.07	-0.08	0.98	1.32	0.92	1.37	0.19	1.35	0.03	1.28	0.26	1.85	0.13	1.57	0.29
SPO2082	*trkH-2*	Trk system potassium uptake protein TrkH	1.26	0.68	1.28	0.10	1.27	0.01	1.48	0.02	1.53	0.05	1.51	0.03	1.05	0.76	-1.14	0.70	-0.04	1.10
SPO2083	*trkA*	potassium transporter peripheral membrane protein	1.02	0.96	1.05	0.71	1.04	0.02	1.35	0.10	-1.24	0.16	0.06	1.30	1.24	0.41	-1.22	0.39	0.01	1.23
SPO2084		hypothetical protein	1.32	0.32	1.70	0.02	1.51	0.19	-1.47	0.22	-0.98	0.77	-1.22	0.25	1.33	0.06	-1.09	0.69	0.12	1.21
SPO2085	*ntrX*	nitrogen assimilation regulatory protein NtrX	-1.91	0.04	-1.41	0.25	-1.66	0.25	-1.52	0.04	1.48	0.15	-0.02	1.50	1.41	0.24	1.57	0.12	1.49	0.08
SPO2086	*ntrY*	nitrogen regulation protein ntrY (EC:2.7.3.-)	-2.03	0.00	-1.48	0.18	-1.76	0.28	-1.77	0.03	1.47	0.08	-0.15	1.62	1.04	0.74	1.58	0.31	1.31	0.27
SPO2087	*ntrC*	nitrogen regulation protein NtrC	1.55	0.10	-1.05	0.89	0.25	1.30	2.33	0.02	-1.16	0.33	0.59	1.75	-1.15	0.55	-1.80	0.02	-1.48	0.33
SPO2088	*ntrB*	nitrogen regulation protein NtrB (EC:2.7.3.-)	X	X	-1.04	0.44	N/A	N/A	1.81	0.01	-1.22	0.50	0.30	1.52	-1.39	0.12	-1.26	0.59	-1.33	0.06
SPO2089		tRNA-dihydrouridine synthase	-1.17	0.78	-1.14	0.58	-1.16	0.02	1.48	0.33	-1.10	0.61	0.19	1.29	-1.20	0.28	-1.27	0.45	-1.24	0.04
SPO2090	*ispDF*	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC:2.7.7.60 4.6.1.12)	-1.53	0.24	1.33	0.05	-0.10	1.43	-1.37	0.35	-1.07	0.43	-1.22	0.15	-1.22	0.04	-1.62	0.07	-1.42	0.20
SPO2091		phosphatidylglycerophosphatase	1.49	0.75	1.35	0.18	1.42	0.07	1.52	0.72	-1.31	0.44	0.11	1.42	-1.38	0.23	-1.53	0.12	-1.46	0.08
SPO2092		competence/damage inducible protein CinA	2.34	0.01	1.36	0.03	1.85	0.49	2.77	0.00	1.03	0.96	1.90	0.87	-1.30	0.01	-1.98	0.00	-1.64	0.34
SPO2093	*amt-1*	ammonium transporter	X	X	1.89	0.27	N/A	N/A	5.56	0.11	1.34	X	3.45	2.11	-1.15	0.62	1.37	X	0.11	1.26
SPO2094		ACT domain-containing protein	1.21	0.49	1.25	0.04	1.23	0.02	2.34	0.02	1.44	0.12	1.89	0.45	2.02	0.01	1.19	0.21	1.61	0.42
SPO2095		MmgE/PrpD family protein	-1.03	0.82	1.01	0.89	-0.01	1.02	1.94	0.00	1.20	0.37	1.57	0.37	1.14	0.15	-1.13	0.42	0.01	1.14
SPO2096		aromatic-rich family protein	-1.56	X	-1.01	0.97	-1.29	0.28	2.03	0.02	-1.37	0.37	0.33	1.70	-1.10	0.30	-1.08	0.93	-1.09	0.01
SPO2097	*hpt*	hypoxanthine phosphoribosyltransferase (EC:2.4.2.8)	-1.34	0.07	1.34	0.01	0.00	1.34	2.57	0.01	1.02	0.77	1.80	0.78	1.20	0.16	-1.15	0.13	0.03	1.18
SPO2098		LysR family transcriptional regulator	-1.12	0.85	1.25	0.12	0.06	1.19	1.08	0.90	1.10	0.37	1.09	0.01	1.71	0.12	1.38	0.16	1.55	0.16
SPO2099	*cycF*	cytochrome c-554	1.03	0.67	1.16	0.66	1.10	0.06	-1.69	0.24	2.31	0.05	0.31	2.00	2.14	0.11	2.27	0.06	2.21	0.06

SPO2100	*cycG*	diheme cytochrome c-type	-1.50	0.49	-1.28	0.04	-1.39	0.11	-2.05	0.04	2.48	0.02	0.22	2.27	1.04	0.88	1.49	0.02	1.27	0.23
SPO2101		amidohydrolase	2.13	0.01	1.90	0.00	2.02	0.12	2.04	0.01	2.07	0.10	2.06	0.01	1.14	0.38	1.20	0.45	1.17	0.03
SPO2102	*lipA*	lipoyl synthase	2.87	0.01	1.85	0.03	2.36	0.51	5.27	0.00	4.01	0.00	4.64	0.63	1.14	0.41	1.12	0.91	1.13	0.01
SPO2103		anti-oxidant AhpCTSA family protein	1.92	0.41	1.85	0.14	1.89	0.03	10.70	0.03	-1.28	0.08	4.71	5.99	1.09	0.67	-1.38	0.18	-0.15	1.24
SPO2104		hypothetical protein	-1.37	0.06	-1.04	0.59	-1.21	0.17	-1.81	0.01	1.26	0.41	-0.28	1.54	-1.14	0.17	-1.01	0.89	-1.08	0.06
SPO2105		LysR family transcriptional regulator	-1.81	0.02	-1.91	0.09	-1.86	0.05	-1.86	0.04	1.32	0.03	-0.27	1.59	-1.37	0.03	-1.18	0.39	-1.28	0.10
SPO2106		hypothetical protein	-1.35	0.05	-1.08	0.93	-1.22	0.14	-6.97	0.02	2.41	0.16	-2.28	4.69	1.16	0.70	1.68	0.40	1.42	0.26
SPO2107		hypothetical protein	-1.78	0.04	1.74	0.03	-0.02	1.76	-6.19	0.01	6.68	0.00	0.25	6.44	-1.18	0.44	X	X	N/A	N/A
SPO2108		trimethylamine methyltransferase	3.64	0.01	2.41	0.02	3.03	0.61	-1.17	0.40	-1.51	0.10	-1.34	0.17	-1.23	0.11	-1.65	0.07	-1.44	0.21
SPO2109	*guaA*	GMP synthase (EC:6.3.5.2)	1.46	0.12	1.03	0.95	1.25	0.21	3.38	0.01	-1.19	0.01	1.10	2.29	-2.24	0.01	-2.44	0.02	-2.34	0.10
SPO2110		hypothetical protein	-2.08	0.59	1.14	0.69	-0.47	1.61	2.27	0.61	-1.33	0.31	0.47	1.80	-1.30	0.30	-1.10	0.88	-1.20	0.10
SPO2111		OmpP1/FadL/TodX family outer membrane transporter	X	X	-1.14	0.87	N/A	N/A	1.28	X	1.02	X	1.15	0.13	-1.19	0.40	-1.32	X	-1.26	0.07
SPO2112		transmembrane drug/metabolite transporter family protein	1.39	0.58	-1.40	0.32	-0.01	1.40	1.57	0.26	-1.14	0.52	0.22	1.36	1.01	0.92	2.33	0.02	1.67	0.66
SPO2113		hypothetical protein	-1.22	0.77	1.12	0.39	-0.05	1.17	1.36	0.23	-1.16	0.23	0.10	1.26	-1.37	0.24	-1.48	0.06	-1.43	0.05
SPO2116		DedA family protein	2.23	0.02	1.41	0.01	1.82	0.41	3.98	0.01	-1.26	0.16	1.36	2.62	1.45	0.06	0.97	0.15	1.21	0.24
SPO2117		DsbB family disulfide bond formation protein	0.93	0.89	1.24	0.17	1.09	0.15	1.07	0.95	-1.16	0.12	-0.04	1.12	1.58	0.21	2.05	0.02	1.82	0.24
SPO2118		AsnC family transcriptional regulator	1.17	0.63	1.08	0.81	1.13	0.04	1.03	0.96	-1.04	0.88	-0.01	1.04	1.11	0.75	-1.12	0.79	-0.01	1.12
SPO2119	*rocF*	arginase (EC:3.5.3.1)	X	X	1.08	X	N/A	N/A	X	X	X	X	N/A	N/A	-2.37	0.09	X	X	N/A	N/A
SPO2120		amidinotransferase	-7.66	0.00	1.47	0.01	-3.10	4.57	-9.99	0.00	-1.71	0.04	-5.85	4.14	-1.69	0.03	-1.46	0.06	-1.58	0.12
SPO2121	*arcB*	ornithine cyclodeaminase (EC:4.3.1.12)	-4.73	0.00	1.51	0.10	-1.61	3.12	-8.00	0.00	-0.98	0.71	-4.49	3.51	-1.04	0.81	-1.26	0.23	-1.15	0.11
SPO2122	*phnA*	alkylphosphonate utilization protein PhnA	-1.10	0.75	1.30	0.25	0.10	1.20	1.39	0.49	-1.43	0.21	-0.02	1.41	-1.36	0.27	-1.44	0.47	-1.40	0.04
SPO2123		HNH endonuclease	1.02	0.83	1.15	0.72	1.09	0.06	-1.69	0.18	1.76	0.32	0.04	1.73	1.54	0.40	1.42	0.31	1.48	0.06
SPO2124		RNA pseudouridylate synthase	X	X	-1.23	0.21	N/A	N/A	1.90	0.03	-1.27	0.08	0.32	1.59	-1.90	0.01	-2.35	0.00	-2.13	0.23
SPO2125		acetyltransferase	-1.62	0.02	1.85	0.02	0.12	1.74	-3.16	0.02	-1.30	0.16	-2.23	0.93	1.11	0.31	-2.11	0.00	-0.50	1.61
SPO2126		phospholipase/carboxylesterase	2.11	0.03	1.76	0.06	1.94	0.18	4.53	0.00	1.07	0.89	2.80	1.73	1.34	0.21	1.03	0.98	1.19	0.16
SPO2127		DNA-3-methyladenine glycosylase II	-1.36	0.31	-1.03	0.84	-1.20	0.17	-1.01	0.48	-1.19	0.36	-1.10	0.09	1.03	0.83	1.25	0.05	1.14	0.11
SPO2128		transporter	1.64	0.18	1.16	0.59	1.40	0.24	2.12	0.09	-1.01	0.92	0.56	1.57	1.16	0.15	1.06	0.65	1.11	0.05
SPO2129		hypothetical protein	1.07	0.99	1.41	0.49	1.24	0.17	1.38	0.86	-1.46	0.45	-0.04	1.42	-1.03	0.93	-1.10	0.89	-1.07	0.04
SPO2130		alpha-isopropylmalate synthase	1.12	0.94	1.53	0.42	1.33	0.20	2.13	0.55	-1.60	0.31	0.27	1.87	1.03	0.96	-1.21	0.67	-0.09	1.12
SPO2131	*cysS*	cysteinyl-tRNA synthetase (EC:6.1.1.16)	1.23	0.42	1.32	0.12	1.28	0.05	1.87	0.16	-1.27	0.19	0.30	1.57	-1.25	0.25	-1.25	0.21	-1.25	0.00
SPO2132	*aspC-3*	aspartate aminotransferase (EC:2.6.1.1)	X	X	1.55	0.14	N/A	N/A	3.18	0.04	-1.10	0.82	1.04	2.14	1.75	0.19	X	X	N/A	N/A
SPO2133		hypothetical protein	-2.55	0.01	-1.43	0.08	-1.99	0.56	2.16	0.01	-2.10	0.00	0.03	2.13	3.39	0.01	1.53	0.48	2.46	0.93
SPO2134		trimethylamine methyltransferase	82.40	0.00	15.60	0.00	49.00	33.40	-1.64	0.02	-1.37	0.46	-1.51	0.14	-1.34	0.16	-2.12	0.09	-1.73	0.39
SPO2135		hypothetical protein	-1.62	0.02	-1.66	0.09	-1.64	0.02	1.39	0.78	-1.95	0.02	-0.28	1.67	3.12	0.03	3.12	0.01	3.12	0.00
SPO2136	*nrdJ*	ribonucleotide-diphosphate reductase subunit alpha (EC:1.17.4.1)	2.54	0.02	1.38	0.04	1.96	0.58	1.92	0.04	2.05	0.00	1.99	0.06	1.11	0.55	1.28	0.13	1.20	0.09
SPO2137		lipoprotein	1.16	0.87	1.26	0.24	1.21	0.05	1.05	0.65	1.30	0.07	1.18	0.13	-1.18	0.15	-1.18	0.05	-1.18	0.00
SPO2139		hypothetical protein	1.37	0.32	-1.20	0.04	0.09	1.29	2.32	0.05	1.14	0.22	1.73	0.59	-1.02	0.76	-1.13	0.40	-1.08	0.05
SPO2140		cold shock DNA-binding domain-containing protein	-1.03	0.95	-1.13	0.24	-1.08	0.05	2.01	0.05	-1.07	0.15	0.47	1.54	1.03	0.97	1.03	0.75	1.03	0.00

SPO2141		pyridoxamine 5''-phosphate oxidase	0.94	0.05	1.04	0.93	0.99	0.05	-1.24	0.02	1.40	0.08	0.08	1.32	1.38	0.03	1.70	0.01	1.54	0.16
SPO2142	*fabI-2*	enoyl-ACP reductase (EC:1.3.1.10)	0.93	0.45	-1.28	0.14	-0.17	1.11	2.77	0.00	1.04	0.84	1.91	0.87	-1.38	0.22	-1.21	0.31	-1.30	0.09
SPO2143	*gpt*	xanthine-guanine phosphoribosyltransferase (EC:2.4.2.22)	1.11	0.96	-1.07	0.65	0.02	1.09	3.28	0.04	1.56	0.03	2.42	0.86	1.02	0.60	1.08	0.27	1.05	0.03
SPO2144		hypothetical protein	1.06	0.40	1.03	0.91	1.05	0.02	3.62	0.00	1.05	0.92	2.34	1.29	1.01	0.94	-1.23	0.23	-0.11	1.12
SPO2145		hypothetical protein	1.86	0.25	1.06	0.86	1.46	0.40	3.38	0.05	-1.05	0.41	1.17	2.22	-1.27	0.04	0.94	0.05	-0.17	1.10
SPO2146	*trpE*	synthase component I (EC:4.1.3.27)	-1.17	0.10	0.98	0.77	-0.09	1.08	2.14	0.02	-1.15	0.24	0.50	1.65	-1.45	0.13	-1.40	0.31	-1.43	0.03
SPO2147		hypothetical protein	X	X	1.13	0.01	N/A	N/A	3.42	0.01	-1.41	0.35	1.01	2.42	-1.30	0.17	-1.62	0.12	-1.46	0.16
SPO2148		hypothetical protein	-1.14	0.17	-1.12	0.44	-1.13	0.01	-1.27	0.00	1.04	0.91	-0.12	1.16	1.22	0.33	1.26	0.38	1.24	0.02
SPO2149	*trpG*	synthase component II (EC:4.1.3.27)	1.06	0.72	1.07	0.87	1.07	0.01	1.78	0.01	1.09	0.66	1.44	0.35	-1.33	0.06	-1.31	0.07	-1.32	0.01
SPO2150	*trpD*	phosphoribosyltransferase (EC:2.4.2.18)	-1.08	0.18	1.31	0.10	0.12	1.20	1.33	0.27	1.05	0.99	1.19	0.14	-1.06	0.15	-1.24	0.26	-1.15	0.09
SPO2151	*trpC*	phosphate synthase (EC:4.1.1.48)	1.04	0.44	-1.20	0.13	-0.08	1.12	1.29	0.07	1.10	0.70	1.20	0.10	-1.77	0.02	-1.75	0.03	-1.76	0.01
SPO2152	*moaC*	cofactor biosynthesis protein MoaC	1.03	0.89	1.36	0.40	1.20	0.17	0.88	0.53	1.01	0.86	0.94	0.07	1.33	0.20	1.26	0.66	1.30	0.04
SPO2153	*moaA*	cofactor biosynthesis protein A	1.30	0.04	1.11	0.49	1.21	0.10	2.64	0.03	-1.16	0.21	0.74	1.90	-1.16	0.59	-2.32	0.03	-1.74	0.58
SPO2154	*lexA*	repressor (EC:3.4.21.88)	-1.13	0.77	1.04	0.89	-0.04	1.09	-2.43	0.34	-1.63	0.09	-2.03	0.40	1.32	0.48	2.03	0.06	1.68	0.36
SPO2155		competence protein	0.98	0.51	1.10	0.72	1.04	0.06	-1.21	0.34	1.34	0.43	0.07	1.28	1.28	0.23	1.49	0.20	1.39	0.11
SPO2156	*gltX*	synthetase (EC:6.1.1.17)	3.64	0.33	1.04	0.98	2.34	1.30	5.24	0.20	-1.14	0.84	2.05	3.19	-1.16	0.78	-1.65	0.57	-1.41	0.25
SPO2157	*gltA*	synthase I (EC:2.3.3.1)	4.40	0.10	1.43	0.26	2.92	1.49	3.14	0.04	1.27	0.19	2.21	0.94	1.20	0.40	1.39	0.17	1.30	0.10
SPO2158		hypothetical protein	3.28	0.11	3.68	0.00	3.48	0.20	-1.08	0.95	1.70	0.01	0.31	1.39	-1.08	0.62	-1.59	0.16	-1.34	0.26
SPO2159		radical SAM domain-containing protein	-1.23	X	-1.18	0.48	-1.21	0.03	1.37	0.01	-1.06	0.94	0.16	1.22	1.36	0.29	1.61	0.06	1.49	0.13
SPO2160		corrinoid methyltransferase	3.14	0.10	1.90	0.10	2.52	0.62	4.27	0.05	1.50	0.08	2.89	1.39	-1.41	0.10	-1.94	0.02	-1.68	0.27
SPO2161		hypothetical protein	2.25	0.39	-1.60	0.02	0.33	1.93	1.44	0.22	0.99	0.56	1.22	0.22	-1.62	0.05	-1.51	0.05	-1.57	0.06
SPO2162		hypothetical protein	1.96	0.30	1.13	0.45	1.55	0.42	-1.67	0.01	1.07	0.61	-0.30	1.37	-1.03	0.84	-1.00	0.75	-1.01	0.02
SPO2163		hypothetical protein	1.54	X	1.11	0.59	1.33	0.21	-0.97	0.30	1.19	0.16	0.11	1.08	-1.27	0.23	1.12	0.49	-0.08	1.20
SPO2164		hypothetical protein	X	X	-1.17	0.30	N/A	N/A	-0.88	0.12	1.33	0.06	0.23	1.10	-1.48	0.02	X	X	N/A	N/A
SPO2165		Fe-S metabolism associated family protein	-1.21	0.06	1.16	0.32	-0.03	1.19	1.60	0.02	-1.17	0.04	0.22	1.39	1.41	0.04	1.09	0.87	1.25	0.16
SPO2166		lipoprotein	1.67	0.02	1.38	0.11	1.53	0.15	1.84	0.00	-1.45	0.04	0.20	1.65	1.35	0.05	-1.06	0.58	0.15	1.21
SPO2167	*rnd*	D (EC:3.1.26.3)	-1.57	0.38	-1.42	0.14	-1.50	0.08	1.26	0.84	-1.33	0.12	-0.04	1.30	-1.18	0.24	-1.42	0.04	-1.30	0.12
SPO2168	*purN*	formyltransferase (EC:2.1.2.2)	-1.09	0.49	1.50	0.12	0.21	1.30	2.63	0.01	-1.35	0.26	0.64	1.99	-1.59	0.18	-2.15	0.05	-1.87	0.28
SPO2169	*purM*	synthetase (EC:6.3.3.1)	-1.26	0.03	1.49	0.07	0.12	1.38	4.86	0.00	-1.20	0.22	1.83	3.03	-1.77	0.04	-2.08	0.01	-1.93	0.16
SPO2170		metallo-beta-lactamase	-2.36	0.00	-2.50	0.06	-2.43	0.07	1.02	0.68	-2.15	0.02	-0.57	1.59	2.30	0.04	6.78	0.00	4.54	2.24
SPO2171		LysR family transcriptional regulator	-1.15	0.82	-1.69	0.01	-1.42	0.27	2.47	0.01	-1.23	0.39	0.62	1.85	1.03	0.70	1.42	0.04	1.23	0.19
SPO2173		sensor histidine kinase (EC:2.7.3.-)	-1.24	0.25	-1.22	0.56	-1.23	0.01	1.07	0.43	1.04	0.57	1.06	0.02	-1.18	0.26	-0.99	0.79	-1.08	0.10
SPO2174		metallo-beta-lactamase	-1.02	0.64	1.09	0.35	0.04	1.06	1.04	0.39	1.01	0.87	1.03	0.02	-1.20	0.12	-1.45	0.13	-1.33	0.13
SPO2176		hypothetical protein	-1.47	0.04	-1.15	0.04	-1.31	0.16	-1.41	0.20	1.25	0.13	-0.08	1.33	1.30	0.02	1.13	0.13	1.22	0.09
SPO2177	*acuC*	utilization protein AcuC	1.10	0.99	1.18	0.79	1.14	0.04	1.90	0.76	1.21	0.40	1.56	0.35	1.54	0.41	1.24	0.35	1.39	0.15
SPO2178	*cls*	synthetase (EC:2.7.8.-)	-1.63	0.55	1.02	0.69	-0.31	1.33	-1.27	0.94	-0.97	0.75	-1.12	0.15	-1.12	0.63	-1.56	0.10	-1.34	0.22
SPO2179		hypothetical protein	1.03	0.90	1.22	0.47	1.13	0.10	1.42	0.23	1.50	0.03	1.46	0.04	1.77	0.02	1.99	0.09	1.88	0.11
SPO2180		hypothetical protein	-2.42	0.24	-2.17	0.01	-2.30	0.13	-1.42	0.09	1.14	0.72	-0.14	1.28	1.02	0.96	1.54	0.30	1.28	0.26
SPO2181		ABC transporter ATP-binding protein	-1.05	0.65	1.57	0.05	0.26	1.31	1.32	0.18	1.34	0.08	1.33	0.01	1.14	0.19	1.48	0.16	1.31	0.17

SPO2182		permease	1.63	X	2.05	0.12	1.84	0.21	3.06	0.09	1.83	0.03	2.45	0.61	1.40	0.13	1.26	0.19	1.33	0.07
SPO2183		hypothetical protein	1.60	0.83	1.53	0.31	1.57	0.04	1.85	0.76	1.19	0.59	1.52	0.33	1.28	0.12	1.24	0.58	1.26	0.02
SPO2184		hypothetical protein	-1.85	0.02	-1.13	0.09	-1.49	0.36	-1.29	0.26	1.37	0.08	0.04	1.33	1.28	0.09	1.14	0.18	1.21	0.07
SPO2185		universal stress protein family protein	-3.84	0.00	-1.43	0.13	-2.64	1.21	-1.46	0.00	1.30	0.02	-0.08	1.38	-1.44	0.01	-1.31	0.02	-1.38	0.06
SPO2186		TRAP transporter, 4TM/12TM fusion protein	-2.60	0.00	-1.98	0.00	-2.29	0.31	1.14	0.16	-1.12	0.20	0.01	1.13	1.10	0.41	1.05	0.52	1.08	0.03
SPO2187		TRAP transporter solute receptor TAXI family protein	-2.37	0.00	-2.23	0.02	-2.30	0.07	1.69	0.02	1.34	0.08	1.52	0.17	1.39	0.14	1.48	0.20	1.44	0.05
SPO2188		acetyltransferase	-1.35	0.66	1.18	0.68	-0.09	1.27	1.13	0.66	-0.98	0.95	0.07	1.06	1.31	0.31	-1.08	0.99	0.12	1.20
SPO2189		AsnC family transcriptional regulator	-2.01	0.00	1.10	0.40	-0.46	1.56	1.19	0.15	-1.20	0.19	-0.01	1.20	-1.07	0.13	-1.26	0.25	-1.17	0.10
SPO2190	*hutC*	utilization repressor	-1.30	0.78	-1.05	0.93	-1.18	0.13	-2.01	0.61	-1.26	0.36	-1.64	0.38	-1.14	0.07	1.19	0.64	0.03	1.17
SPO2191	*hutI*	(EC:3.5.2.7)	1.13	0.72	1.07	0.17	1.10	0.03	-2.65	0.07	-1.07	0.60	-1.86	0.79	-1.40	0.05	-1.39	0.24	-1.40	0.01
SPO2192	*hutH*	ammonia-lyase (EC:4.3.1.3)	1.35	0.88	-1.11	0.50	0.12	1.23	0.92	0.86	-1.25	0.43	-0.17	1.08	-1.37	0.25	1.19	0.28	-0.09	1.28
SPO2193	*hutU*	hydratase (EC:4.2.1.49)	1.34	0.04	1.00	0.97	1.17	0.17	-2.55	0.02	-1.59	0.04	-2.07	0.48	-1.21	0.06	1.20	0.48	-0.01	1.21
SPO2194	*hutF*	deiminase (EC:3.5.3.13)	-1.10	0.73	1.24	0.18	0.07	1.17	-1.69	0.40	-1.51	0.21	-1.60	0.09	1.17	0.17	-1.38	0.36	-0.11	1.28
SPO2195		amidohydrolase	-1.12	0.42	-0.99	0.34	-1.06	0.06	1.24	0.08	-1.13	0.40	0.06	1.19	-1.28	0.16	-1.44	0.46	-1.36	0.08
SPO2196		diaminopropionate ammonia-lyase (EC:4.3.1.15)	-1.10	0.91	1.16	0.77	0.03	1.13	1.61	0.38	-1.21	0.74	0.20	1.41	1.13	0.84	-1.16	0.88	-0.02	1.15
SPO2197		hypothetical protein	1.79	0.16	1.17	0.51	1.48	0.31	1.79	0.10	1.01	0.73	1.40	0.39	1.34	0.08	1.77	0.08	1.56	0.21
SPO2198	*gap-3*	dehydrogenase, type I (EC:1.2.1.-)	1.06	0.96	-1.15	0.52	-0.04	1.11	1.10	0.88	-8.43	0.03	-3.67	4.77	1.90	0.23	1.63	0.42	1.77	0.14
SPO2199		hypothetical protein	-1.09	0.70	1.59	0.05	0.25	1.34	2.20	0.03	1.06	0.76	1.63	0.57	1.62	0.15	-1.22	0.09	0.20	1.42
SPO2200	*coaD*	adenylyltransferase (EC:2.7.7.3)	1.87	0.03	2.14	0.02	2.01	0.14	1.39	0.22	1.83	0.03	1.61	0.22	1.16	0.59	1.01	0.75	1.09	0.08
SPO2201		hypothetical protein	1.17	0.92	1.38	0.21	1.28	0.11	-1.86	0.01	1.71	0.02	-0.08	1.79	1.55	0.01	1.63	0.09	1.59	0.04
SPO2202		LysR family transcriptional regulator	1.27	0.31	1.10	0.32	1.19	0.09	-1.15	0.64	1.46	0.02	0.16	1.31	1.07	0.75	-1.34	0.11	-0.14	1.21
SPO2203	*mmsA*	dehydrogenase (EC:1.2.1.27)	10.30	0.00	2.39	0.04	6.35	3.96	1.96	0.02	6.98	0.01	4.47	2.51	1.14	0.37	1.03	1.00	1.09	0.05
SPO2204		hypothetical protein	2.88	0.01	1.19	0.29	2.04	0.85	1.94	0.02	1.46	0.04	1.70	0.24	1.11	0.36	-1.32	0.20	-0.11	1.22
SPO2205		ErfK/YbiS/YcfS/YnhG family protein	2.40	0.00	1.12	0.37	1.76	0.64	1.81	0.02	1.45	0.13	1.63	0.18	-1.32	0.13	-1.40	0.04	-1.36	0.04
SPO2206		hypothetical protein	2.58	0.30	1.01	0.98	1.80	0.79	-1.22	0.82	-1.17	0.79	-1.20	0.03	1.16	0.74	-1.19	0.87	-0.02	1.18
SPO2207		hypothetical protein	1.41	0.19	-1.30	0.40	0.05	1.36	-2.09	0.02	1.38	0.46	-0.36	1.74	1.10	0.81	1.33	0.45	1.22	0.12
SPO2208		hypothetical protein	1.13	0.43	1.03	0.90	1.08	0.05	3.27	0.00	-1.22	0.32	1.03	2.25	-1.32	0.06	-1.93	0.13	-1.63	0.31
SPO2209		carboxylate-amine ligase	-1.18	0.64	-1.11	0.62	-1.15	0.03	-1.46	0.50	1.61	0.27	0.08	1.54	1.13	0.79	1.38	0.42	1.26	0.13
SPO2210		BNR/Asp-box repeat-containing protein	0.91	0.15	2.62	0.00	1.76	0.86	-2.32	0.00	2.83	0.01	0.26	2.58	1.64	0.01	2.00	0.00	1.82	0.18
SPO2211		acyl-CoA dehydrogenase (EC:1.3.99.-)	1.10	0.99	-1.02	0.90	0.04	1.06	-1.90	0.08	4.62	0.00	1.36	3.26	1.16	0.18	1.13	0.45	1.15	0.02
SPO2212		enoyl-CoA hydratase	1.83	0.59	1.12	0.73	1.48	0.36	-1.04	0.97	3.53	0.14	1.25	2.29	1.19	0.70	1.34	0.65	1.27	0.08
SPO2213	*mmsB-1*	dehydrogenase (EC:1.1.1.31)	1.02	0.59	-1.16	0.59	-0.07	1.09	-1.64	0.03	1.21	0.74	-0.22	1.43	2.17	0.02	1.36	0.02	1.77	0.41
SPO2214	*betC-2*	sulfatase (EC:3.1.6.6)	2.12	0.21	-1.26	0.55	0.43	1.69	2.28	0.11	1.09	0.60	1.69	0.60	1.09	0.68	1.93	0.03	1.51	0.42
SPO2215		glyoxalase	1.66	0.02	-1.54	0.02	0.06	1.60	-1.80	0.10	2.14	0.01	0.17	1.97	1.17	0.05	1.17	0.11	1.17	0.00
SPO2216		DNA-binding protein	-1.05	0.75	-1.07	0.53	-1.06	0.01	-1.96	0.20	1.17	0.58	-0.40	1.57	-1.03	0.92	1.35	0.03	0.16	1.19
SPO2217		hypothetical protein	-1.42	0.55	-1.31	0.38	-1.37	0.05	-1.02	0.92	-1.02	0.92	-1.02	0.00	1.07	0.92	2.03	0.14	1.55	0.48
SPO2218	*uvrA*	ABC subunit A	1.10	0.95	-1.21	0.51	-0.05	1.16	1.78	0.25	1.06	0.91	1.42	0.36	1.28	0.20	1.87	0.15	1.58	0.29
SPO2219		rhodanese-like domain-containing protein	1.01	0.96	-1.06	0.92	-0.03	1.04	2.47	0.54	-1.24	0.64	0.62	1.86	1.26	0.54	1.24	0.55	1.25	0.01
SPO2220		hypothetical protein	1.16	0.91	1.30	0.20	1.23	0.07	-1.41	0.82	1.51	0.07	0.05	1.46	1.29	0.05	1.13	0.30	1.21	0.08

SPO2221		von Willebrand factor A	X	X	1.05	0.38	N/A	N/A	3.03	0.01	-1.16	0.58	0.94	2.10	1.13	0.03	-0.89	0.22	0.12	1.01
SPO2222		dihydrolipoamide dehydrogenase (EC:1.8.1.4)	2.26	0.10	1.70	0.17	1.98	0.28	4.17	0.02	1.37	0.03	2.77	1.40	1.21	0.70	1.69	0.10	1.45	0.24
SPO2223		hypothetical protein	1.81	0.05	1.95	0.01	1.88	0.07	2.26	0.05	1.16	0.27	1.71	0.55	1.31	0.27	1.10	0.60	1.21	0.11
SPO2224		hypothetical protein	2.81	0.00	1.27	0.63	2.04	0.77	-2.08	0.01	1.21	0.25	-0.44	1.65	1.11	0.58	0.92	0.32	1.02	0.09
SPO2225		hypothetical protein	3.11	0.02	1.75	0.04	2.43	0.68	2.05	0.02	-1.56	0.10	0.25	1.81	-1.08	0.85	-1.43	0.29	-1.26	0.18
SPO2226	*queA*	ribosyltransferase-isomerase	X	X	1.35	0.68	N/A	N/A	3.31	0.40	-1.73	0.58	0.79	2.52	-1.51	0.59	-2.45	0.44	-1.98	0.47
SPO2227		hypothetical protein	1.11	0.79	-1.19	0.11	-0.04	1.15	1.07	0.39	1.26	0.44	1.17	0.10	1.36	0.15	-1.04	0.93	0.16	1.20
SPO2228		AhpC/TSA family protein	-1.36	0.75	-1.26	0.54	-1.31	0.05	1.60	0.30	1.38	0.34	1.49	0.11	-1.13	0.50	0.98	0.70	-0.07	1.06
SPO2229		hypothetical protein	1.25	0.14	-1.48	0.05	-0.12	1.37	2.15	0.08	1.09	0.60	1.62	0.53	-1.25	0.57	-1.58	0.04	-1.42	0.17
SPO2230		M24/M37 family peptidase	1.21	0.92	-1.35	0.19	-0.07	1.28	1.68	0.14	1.40	0.10	1.54	0.14	-1.74	0.00	-1.34	0.14	-1.54	0.20
SPO2231		hypothetical protein	0.96	0.62	0.99	0.55	0.97	0.01	1.60	0.14	1.34	0.08	1.47	0.13	1.23	0.35	1.42	0.52	1.33	0.10
SPO2232		hypothetical protein	-2.30	0.00	1.53	0.01	-0.39	1.92	-1.98	0.04	1.81	0.11	-0.09	1.90	1.13	0.42	X	X	N/A	N/A
SPO2233		cyclophilin type peptidyl-prolyl cis-trans isomerase	0.95	0.55	1.70	0.03	1.33	0.37	2.83	0.01	-1.10	0.23	0.87	1.97	1.79	0.01	1.42	0.04	1.61	0.18
SPO2234		cyclophilin type peptidyl-prolyl cis-trans isomerase	0.98	0.67	-1.39	0.06	-0.21	1.18	2.82	0.12	-1.50	0.09	0.66	2.16	-1.16	0.30	-1.34	0.01	-1.25	0.09
SPO2235	*pgk*	kinase (EC:2.7.2.3)	-1.31	0.12	1.12	0.38	-0.10	1.22	-1.81	0.03	1.09	0.83	-0.36	1.45	-1.27	0.85	1.90	0.02	0.32	1.59
SPO2236		hypothetical protein	-1.70	0.43	-1.40	0.07	-1.55	0.15	-1.68	0.70	-1.20	0.55	-1.44	0.24	1.50	0.02	X	X	N/A	N/A
SPO2237		hypothetical protein	1.39	0.07	-1.67	0.30	-0.14	1.53	-1.05	0.56	-1.40	0.30	-1.23	0.17	1.18	0.31	1.08	0.45	1.13	0.05
SPO2238		LysR family transcriptional regulator	X	X	-1.64	0.02	N/A	N/A	1.84	0.01	-1.11	0.71	0.37	1.48	-0.98	0.45	-1.00	0.81	-0.99	0.01
SPO2239		hypothetical protein	-1.71	0.01	-1.36	0.05	-1.54	0.17	-1.63	0.01	-1.27	0.25	-1.45	0.18	-1.05	0.65	1.12	0.64	0.04	1.09
SPO2240	*pdhA*	dehydrogenase complex, E1 component subunit alpha (EC:1.2.4.1)	1.97	0.06	-1.28	0.49	0.35	1.63	2.02	0.01	0.96	0.53	1.49	0.53	-1.64	0.08	1.06	0.71	-0.29	1.35
SPO2241	*pdhB*	dehydrogenase subunit beta (EC:1.2.4.1)	3.69	0.16	-1.12	0.17	1.29	2.41	5.51	0.00	1.36	0.38	3.44	2.08	-1.24	0.11	1.53	0.12	0.15	1.39
SPO2242	*pdhC*	alpha-keto acid dehydrogenase E2 subunit (EC:2.3.1.12)	3.48	0.00	1.08	0.80	2.28	1.20	4.30	0.00	1.13	0.43	2.72	1.59	-1.24	0.07	1.17	0.79	-0.04	1.21
SPO2243		hypothetical protein	1.28	0.14	1.18	0.01	1.23	0.05	2.38	0.02	1.58	0.01	1.98	0.40	1.17	0.11	1.62	0.06	1.40	0.23
SPO2244		hypothetical protein	1.29	0.21	1.10	0.60	1.20	0.10	-1.01	0.38	1.49	0.27	0.24	1.25	-1.05	0.95	-1.47	0.52	-1.26	0.21
SPO2245		hypothetical protein	2.53	0.33	1.84	0.02	2.19	0.35	-1.79	0.58	1.42	0.37	-0.19	1.61	-1.41	0.48	-1.10	0.88	-1.26	0.16
SPO2246	*cysK*	synthase A (EC:2.5.1.47)	1.37	0.78	-1.70	0.19	-0.17	1.54	5.11	0.04	2.40	0.02	3.76	1.36	1.14	0.71	1.59	0.10	1.37	0.23
SPO2247	*cysE*	O-acetyltransferase (EC:2.3.1.30)	1.52	0.34	-1.90	0.12	-0.19	1.71	1.89	0.14	1.61	0.04	1.75	0.14	1.53	0.04	2.09	0.04	1.81	0.28
SPO2248		dnaK suppressor protein	-1.10	0.24	-1.00	0.93	-1.05	0.05	-0.96	0.23	1.32	0.03	0.18	1.14	1.19	0.22	-1.15	0.85	0.02	1.17
SPO2249		hypothetical protein	X	X	1.14	0.47	N/A	N/A	1.51	X	1.49	0.31	1.50	0.01	1.29	0.37	X	X	N/A	N/A
SPO2250		hypothetical protein	-2.32	0.26	-1.21	0.19	-1.77	0.56	-3.11	0.06	1.96	0.16	-0.58	2.54	1.04	0.88	1.59	0.05	1.32	0.28
SPO2251		hypothetical protein	1.09	X	1.35	0.29	1.22	0.13	-1.01	0.75	3.88	0.03	1.44	2.45	1.17	0.25	-1.05	0.86	0.06	1.11
SPO2252		hypothetical protein	X	X	1.10	0.22	N/A	N/A	X	X	2.78	0.04	N/A	N/A	1.15	0.45	1.34	X	1.25	0.10
SPO2253		hypothetical protein	-1.18	0.60	1.27	0.27	0.05	1.23	-2.10	0.06	2.63	0.01	0.27	2.37	1.24	0.14	-1.16	0.57	0.04	1.20
SPO2255		hypothetical protein	1.61	0.13	1.41	0.13	1.51	0.10	2.65	0.04	4.39	0.00	3.52	0.87	1.04	0.75	-1.28	0.67	-0.12	1.16
SPO2256		hypothetical protein	-1.12	0.14	1.14	0.53	0.01	1.13	-1.25	0.06	2.41	0.02	0.58	1.83	1.07	0.25	-1.01	0.84	0.03	1.04
SPO2257		TP901-1 family major tail protein	2.23	0.16	1.15	0.26	1.69	0.54	1.65	0.02	2.97	0.00	2.31	0.66	1.16	0.19	-2.76	0.01	-0.80	1.96
SPO2258		hypothetical protein	1.27	0.95	1.09	0.87	1.18	0.09	1.44	0.89	3.56	0.14	2.50	1.06	-1.03	0.96	-1.47	0.74	-1.25	0.22
SPO2259		head-tail adaptor	1.32	0.83	1.22	0.68	1.27	0.05	1.24	0.80	2.61	0.03	1.93	0.69	1.32	0.24	1.06	0.86	1.19	0.13

SPO2260		hypothetical protein	1.20	0.77	1.29	0.39	1.25	0.05	-1.17	0.50	2.99	0.02	0.91	2.08	1.15	0.59	-1.43	0.54	-0.14	1.29
SPO2261		HK97 family major capsid protein	-1.54	0.03	1.09	0.75	-0.23	1.32	-4.29	0.01	3.87	0.00	-0.21	4.08	-1.37	0.00	-2.74	0.02	-2.06	0.69
SPO2262		HK97 family phage prohead protease	1.97	0.11	1.14	0.51	1.56	0.42	-1.06	0.52	4.35	0.00	1.65	2.71	-1.37	0.05	-2.56	0.01	-1.97	0.60
SPO2263		hypothetical protein	-1.13	0.79	-1.14	0.81	-1.14	0.01	-1.44	0.20	3.54	0.02	1.05	2.49	-1.25	0.23	-1.18	0.80	-1.22	0.04
SPO2264		HK97 family portal protein	X	X	1.05	0.80	N/A	N/A	-0.95	0.15	1.90	0.01	0.47	1.43	1.07	0.58	-3.30	0.04	-1.12	2.19
SPO2266		terminase large subunit	1.73	0.37	-1.23	0.67	0.25	1.48	1.65	0.32	-1.11	0.78	0.27	1.38	1.26	0.38	1.68	0.04	1.47	0.21
SPO2267		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2268		hypothetical protein	-1.20	0.70	-1.39	0.20	-1.30	0.10	1.06	0.48	-1.10	0.12	-0.02	1.08	1.22	0.38	1.07	0.38	1.15	0.08
SPO2269		hypothetical protein	-1.48	0.01	-1.06	0.71	-1.27	0.21	-1.67	0.04	-0.97	0.67	-1.32	0.35	-1.02	0.96	1.65	0.36	0.32	1.34
SPO2270		hypothetical protein	1.42	0.01	-1.08	0.29	0.17	1.25	2.44	0.02	-1.29	0.02	0.58	1.87	-1.11	0.01	0.97	0.56	-0.07	1.04
SPO2271	*fabF*	synthase (EC:2.3.1.41)	2.09	0.00	-1.07	0.69	0.51	1.58	4.16	0.00	-1.06	0.09	1.55	2.61	1.08	0.62	0.99	0.50	1.04	0.04
SPO2272		phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	5.00	0.00	1.45	0.06	3.23	1.78	-1.72	0.09	-1.08	0.33	-1.40	0.32	1.82	0.00	1.23	0.04	1.53	0.30
SPO2273		acetyltransferase	-1.08	0.20	1.12	0.69	0.02	1.10	1.30	0.04	-1.11	0.32	0.10	1.21	2.02	0.00	1.52	0.15	1.77	0.25
SPO2274	*acpP*	carrier protein	1.49	0.03	1.04	1.00	1.27	0.23	3.92	0.02	-1.73	0.14	1.10	2.83	1.46	0.13	0.99	0.20	1.22	0.24
SPO2275	*fabG*	reductase (EC:1.1.1.100)	1.49	0.02	1.14	0.31	1.32	0.18	2.91	0.00	-1.90	0.10	0.51	2.41	1.21	0.35	0.93	0.07	1.07	0.14
SPO2276	*fabD*	S-malonyltransferase (EC:2.3.1.39)	1.57	0.07	-1.20	0.37	0.19	1.39	2.62	0.01	0.99	0.54	1.81	0.81	-1.17	0.27	-1.14	0.10	-1.16	0.02
SPO2277		cytochrome	1.09	0.58	-1.27	0.05	-0.09	1.18	-1.43	0.19	-1.24	0.50	-1.34	0.10	-1.17	0.03	-0.97	0.38	-1.07	0.10
SPO2278		hypothetical protein	-1.14	0.92	-1.22	0.90	-1.18	0.04	1.29	0.85	1.30	0.84	1.30	0.01	1.06	0.97	1.21	0.72	1.14	0.08
SPO2279		hypothetical protein	-1.39	0.28	-2.03	0.09	-1.71	0.32	1.01	0.76	-1.51	0.29	-0.25	1.26	1.42	0.11	1.41	0.21	1.42	0.01
SPO2280		hypothetical protein	1.38	0.19	1.28	0.20	1.33	0.05	-2.43	0.01	1.28	0.09	-0.58	1.86	-1.48	0.01	0.98	0.24	-0.25	1.23
SPO2281	*rpsF*	ribosomal protein S6	-2.02	0.01	-1.72	0.03	-1.87	0.15	7.75	0.00	-5.03	0.00	1.36	6.39	-2.06	0.02	-4.15	0.00	-3.11	1.05
SPO2282	*rpsR*	ribosomal protein S18	-1.48	0.00	-1.27	0.12	-1.38	0.11	8.93	0.00	-5.14	0.00	1.90	7.04	-1.86	0.00	-2.94	0.03	-2.40	0.54
SPO2283	*rplI*	ribosomal protein L9	1.09	1.00	1.49	0.35	1.29	0.20	5.00	0.18	-7.10	0.00	-1.05	6.05	1.56	0.09	-2.03	0.08	-0.24	1.80
SPO2284		transglycosylase	2.22	0.49	1.01	0.83	1.62	0.61	3.56	0.02	1.20	0.59	2.38	1.18	1.33	0.03	1.30	0.22	1.32	0.02
SPO2285		DNA-binding protein	1.62	0.01	1.04	0.92	1.33	0.29	0.89	0.06	1.45	0.07	1.17	0.28	1.35	0.02	1.79	0.02	1.57	0.22
SPO2286	*luxR-2*	family transcriptional regulator	-1.29	0.54	-1.26	0.62	-1.28	0.02	-1.35	0.47	1.65	0.47	0.15	1.50	-1.08	0.83	1.11	0.99	0.02	1.10
SPO2287		autoinducer synthesis protein	0.88	0.01	-1.19	0.47	-0.16	1.03	-1.83	0.00	2.42	0.01	0.30	2.13	1.54	0.00	1.89	0.02	1.72	0.18
SPO2288	*tig*	factor (EC:5.2.1.8)	1.43	0.41	1.48	0.29	1.46	0.03	5.87	0.02	-1.67	0.15	2.10	3.77	-1.05	0.83	-1.41	0.33	-1.23	0.18
SPO2289		hypothetical protein	1.00	0.82	-4.01	0.26	-1.51	2.50	1.45	0.48	-2.93	0.31	-0.74	2.19	1.24	0.85	1.75	0.69	1.50	0.26
SPO2290		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2292		hypothetical protein	-1.11	0.25	1.52	0.05	0.21	1.32	-0.98	0.22	1.22	0.41	0.12	1.10	-1.40	0.39	-1.76	0.09	-1.58	0.18
SPO2293		hypothetical protein	1.37	0.06	-1.27	0.49	0.05	1.32	1.88	0.05	-1.26	0.08	0.31	1.57	1.28	0.25	1.53	0.10	1.41	0.13
SPO2294	*glnB-1*	regulatory protein P-II	2.29	0.01	-1.53	0.08	0.38	1.91	6.56	0.00	1.63	0.01	4.10	2.47	-1.72	0.00	-1.58	0.00	-1.65	0.07
SPO2295	*glnA*	synthetase, type I (EC:6.3.1.2)	1.49	0.74	-1.27	0.16	0.11	1.38	4.33	0.07	1.51	0.14	2.92	1.41	-1.31	0.81	-1.53	0.23	-1.42	0.11
SPO2296		hypothetical protein	-1.75	0.17	-1.45	0.07	-1.60	0.15	-1.61	0.12	1.65	0.06	0.02	1.63	-1.32	0.04	-1.18	0.04	-1.25	0.07
SPO2297		hypothetical protein	2.56	0.03	1.30	0.06	1.93	0.63	-2.16	0.01	1.46	0.04	-0.35	1.81	-1.28	0.13	1.63	0.01	0.18	1.46
SPO2298		hypothetical protein	-1.36	0.01	-1.10	0.72	-1.23	0.13	-2.71	0.00	1.16	0.29	-0.78	1.94	-1.16	0.58	1.32	0.06	0.08	1.24
SPO2299	*dddP*	DMSP lyase	13.30	0.02	4.01	0.06	8.66	4.65	-1.62	0.37	1.34	0.40	-0.14	1.48	1.33	0.48	1.16	0.15	1.25	0.09
SPO2300		hypothetical protein	-1.04	0.98	-1.07	0.96	-1.06	0.02	4.40	0.07	1.54	0.17	2.97	1.43	1.15	0.44	1.33	0.29	1.24	0.09

SPO2301		osmC-like family protein	-1.14	0.13	-1.14	0.74	-1.14	0.00	-1.28	0.07	1.18	0.31	-0.05	1.23	-1.55	0.03	-1.17	0.87	-1.36	0.19
SPO2302		bioY family protein	3.66	0.00	1.45	0.20	2.56	1.11	4.88	0.00	1.36	0.36	3.12	1.76	1.59	0.10	1.90	0.10	1.75	0.16
SPO2303		hypothetical protein	1.98	0.01	1.38	0.23	1.68	0.30	2.49	0.00	-1.27	0.07	0.61	1.88	-1.50	0.07	-1.79	0.06	-1.65	0.15
SPO2304		hypothetical protein	1.16	0.78	1.77	0.08	1.47	0.31	1.77	0.05	-1.45	0.01	0.16	1.61	-1.02	0.87	-1.11	0.04	-1.07	0.05
SPO2305	*purB*	lyase (EC:4.3.2.2)	1.60	0.09	1.41	0.02	1.51	0.10	9.61	0.00	-1.28	0.10	4.17	5.45	-1.49	0.12	-1.95	0.01	-1.72	0.23
SPO2306		hypothetical protein	-1.90	0.20	-1.22	0.04	-1.56	0.34	-7.32	0.01	2.00	0.08	-2.66	4.66	1.21	0.40	2.24	0.01	1.73	0.52
SPO2307		hypothetical protein	1.15	0.45	1.17	0.64	1.16	0.01	-2.53	0.00	1.89	0.01	-0.32	2.21	1.47	0.02	1.28	0.19	1.38	0.10
SPO2308	*fliG*	motor switch protein FliG	1.75	0.27	1.13	0.33	1.44	0.31	-1.76	0.38	1.57	0.03	-0.10	1.67	1.11	0.32	X	X	N/A	N/A
SPO2309		hypothetical protein	-1.41	X	-1.10	0.92	-1.26	0.16	1.23	0.87	-1.82	0.42	-0.30	1.53	-1.26	0.80	1.12	0.92	-0.07	1.19
SPO2310		lipid A biosynthesis lauroyl acyltransferase	-1.35	0.01	1.09	0.42	-0.13	1.22	1.96	0.01	-1.07	0.31	0.45	1.52	1.13	0.58	-1.05	0.33	0.04	1.09
SPO2311		hypothetical protein	X	X	X	X	N/A	N/A	X	X	1.13	X	N/A	N/A	-1.35	X	X	X	N/A	N/A
SPO2312	*acnA*	hydratase (EC:4.2.1.3)	6.55	0.03	1.23	0.29	3.89	2.66	4.67	0.00	1.65	0.10	3.16	1.51	-1.12	0.09	-1.62	0.06	-1.37	0.25
SPO2313		hypothetical protein	-1.21	0.39	1.15	0.76	-0.03	1.18	-3.22	0.01	-1.25	0.78	-2.24	0.98	1.05	0.64	1.52	X	1.29	0.23
SPO2314		DsbE subfamily periplasmic protein thiol:disulfide oxidoreductase	2.13	0.04	1.34	0.15	1.74	0.40	2.37	0.02	0.99	0.87	1.68	0.69	1.17	0.72	1.26	0.44	1.22	0.05
SPO2315	*ccmC*	exporter protein CcmC	2.62	0.02	1.28	0.17	1.95	0.67	4.08	0.02	-1.03	0.71	1.53	2.56	1.33	0.37	0.98	0.51	1.16	0.17
SPO2316	*ccmB*	exporter protein CcmB	1.89	0.68	1.48	0.26	1.69	0.20	3.25	0.44	-1.22	0.42	1.02	2.24	-1.23	0.35	-1.36	0.32	-1.30	0.07
SPO2317	*ccmA*	c biogenesis protein CcmA	1.07	1.00	1.81	0.23	1.44	0.37	1.82	0.44	1.03	0.98	1.43	0.40	1.28	0.49	1.12	0.84	1.20	0.08
SPO2318		hypothetical protein	1.25	X	1.55	0.15	1.40	0.15	2.51	0.05	-1.13	0.44	0.69	1.82	-1.47	0.09	-2.07	0.10	-1.77	0.30
SPO2319		hypothetical protein	-1.19	0.53	-1.03	0.92	-1.11	0.08	1.01	0.81	-1.12	0.65	-0.06	1.07	-1.00	0.99	1.54	0.08	0.27	1.27
SPO2320	*secF*	translocase subunit SecF	1.28	0.08	1.65	0.01	1.47	0.19	6.96	0.00	-1.37	0.08	2.80	4.17	1.37	0.02	-1.14	0.13	0.12	1.26
SPO2321	*secD*	translocase subunit SecD	1.15	0.04	-1.13	0.54	0.01	1.14	5.96	0.00	-1.14	0.06	2.41	3.55	-1.13	0.27	0.97	0.38	-0.08	1.05
SPO2322	*yajC*	translocase subunit YajC	1.18	0.40	-1.42	0.20	-0.12	1.30	4.38	0.00	1.20	0.11	2.79	1.59	-1.10	0.47	1.11	0.08	0.01	1.11
SPO2323		mechanosensitive ion channel protein MscS	-1.36	0.61	-1.03	0.95	-1.20	0.17	-2.05	0.41	1.49	0.45	-0.28	1.77	1.23	0.63	1.78	0.35	1.51	0.28
SPO2324		hypothetical protein	17.50	0.00	3.07	0.06	10.29	7.22	-1.66	0.06	1.43	0.04	-0.12	1.55	1.25	0.40	1.10	0.46	1.18	0.08
SPO2325	*serS*	synthetase (EC:6.1.1.11)	1.79	0.19	1.00	0.70	1.39	0.40	2.79	0.11	-1.24	0.04	0.78	2.02	-1.19	0.09	-1.28	0.21	-1.24	0.05
SPO2326		hypothetical protein	1.05	0.65	-1.15	0.03	-0.05	1.10	0.95	0.12	1.22	0.35	1.08	0.14	1.16	0.50	1.65	0.05	1.41	0.25
SPO2327		fatty acid desaturase	1.58	0.66	-1.21	0.51	0.19	1.40	1.42	0.76	1.49	0.33	1.46	0.04	1.25	0.69	1.92	0.14	1.59	0.34
SPO2328	*engA*	protein EngA	-1.67	0.00	1.04	0.76	-0.32	1.36	2.48	0.00	-1.42	0.01	0.53	1.95	-1.54	0.02	-2.09	0.01	-1.82	0.27
SPO2329		PQQ repeat-containing protein	1.42	0.16	1.43	0.22	1.43	0.01	2.42	0.02	-1.20	0.50	0.61	1.81	1.66	0.07	1.32	0.19	1.49	0.17
SPO2330		hypothetical protein	1.02	0.74	1.06	0.88	1.04	0.02	2.36	0.03	-1.16	0.34	0.60	1.76	1.04	0.98	-1.30	0.05	-0.13	1.17
SPO2331		RND family efflux transporter MFP subunit	0.98	0.88	-1.52	0.10	-0.27	1.25	2.53	0.06	-1.23	0.42	0.65	1.88	1.38	0.25	3.33	0.02	2.36	0.98
SPO2332		AcrB/AcrD/AcrF family transporter	1.07	0.98	-2.16	0.03	-0.55	1.62	2.79	0.01	-1.62	0.10	0.59	2.21	-1.11	0.33	2.69	0.02	0.79	1.90
SPO2333		hypothetical protein	-1.12	0.75	-1.43	0.11	-1.28	0.16	2.05	0.09	-1.85	0.03	0.10	1.95	1.06	0.77	1.68	0.05	1.37	0.31
SPO2334		CAAX amino terminal protease	-1.23	0.88	1.20	0.76	-0.02	1.22	-2.14	0.69	-1.18	0.82	-1.66	0.48	-1.06	0.93	-1.01	0.96	-1.04	0.03
SPO2335		ABC transporter ATP-binding protein/permease	1.19	0.14	1.05	0.83	1.12	0.07	2.63	0.01	-1.22	0.08	0.71	1.93	-1.17	0.20	-1.67	0.16	-1.42	0.25
SPO2336		lysM domain-containing protein	1.30	0.06	1.16	0.22	1.23	0.07	1.83	0.00	1.09	0.52	1.46	0.37	-1.20	0.06	-1.12	0.03	-1.16	0.04
SPO2337		decarboxylase	2.21	0.22	1.03	0.93	1.62	0.59	4.07	0.01	-1.19	0.17	1.44	2.63	-1.12	0.08	-1.47	0.16	-1.30	0.18
SPO2338	*rarD-1*	RarD	1.07	0.87	1.41	0.11	1.24	0.17	1.83	0.20	-1.22	0.17	0.31	1.53	1.12	0.43	-1.41	0.06	-0.15	1.27
SPO2339		enoyl-CoA hydratase	-1.31	0.66	-1.11	0.75	-1.21	0.10	-1.22	0.76	1.21	0.68	-0.01	1.22	1.85	0.16	1.73	0.38	1.79	0.06

SPO2340	*sodB*	dismutase, Fe (EC:1.15.1.1)	1.57	0.34	-1.18	0.76	0.20	1.38	2.12	0.18	-1.52	0.41	0.30	1.82	1.29	0.76	0.93	0.80	1.11	0.18
SPO2341		FkbM family methyltransferase	-1.45	0.59	1.21	0.37	-0.12	1.33	1.85	0.25	-1.04	0.76	0.41	1.45	1.14	0.40	-1.33	0.34	-0.10	1.24
SPO2342		hypothetical protein	1.98	0.06	1.29	0.26	1.64	0.35	1.13	0.78	1.96	0.02	1.55	0.42	1.03	0.93	1.84	0.04	1.44	0.41
SPO2343		hypothetical protein	2.01	0.25	1.22	0.52	1.62	0.40	0.87	0.57	2.17	0.04	1.52	0.65	-1.37	0.25	1.45	0.37	0.04	1.41
SPO2344		sarcosine oxidase subunit gamma	4.53	0.00	1.70	0.08	3.12	1.42	1.85	0.04	-1.15	0.24	0.35	1.50	-1.05	0.41	-1.20	0.17	-1.13	0.08
SPO2345		sarcosine oxidase subunit alpha	4.21	0.01	2.24	0.01	3.23	0.99	1.75	0.17	1.09	0.82	1.42	0.33	1.21	0.15	1.04	0.96	1.13	0.09
SPO2346		sarcosine oxidase subunit delta	2.54	0.55	2.71	0.01	2.63	0.09	1.39	0.28	1.19	0.36	1.29	0.10	1.18	0.15	1.06	0.99	1.12	0.06
SPO2347		hypothetical protein	2.38	0.01	1.76	0.13	2.07	0.31	1.41	0.02	1.61	0.03	1.51	0.10	-1.03	0.79	1.22	0.50	0.10	1.13
SPO2348		sarcosine oxidase subunit beta	3.12	0.38	2.85	0.00	2.99	0.14	1.60	0.11	1.51	0.02	1.56	0.05	1.22	0.33	1.31	0.05	1.27	0.05
SPO2349	*cycH*	c-type biogenesis protein CycH	1.09	0.90	1.73	0.03	1.41	0.32	4.52	0.00	1.10	0.63	2.81	1.71	1.67	0.01	1.78	0.03	1.73	0.06
SPO2350		Holliday junction resolvase-like protein	1.37	0.11	1.94	0.09	1.66	0.29	2.77	0.01	1.17	0.05	1.97	0.80	1.43	0.08	1.16	0.50	1.30	0.14
SPO2351		hypothetical protein	3.01	0.01	1.89	0.02	2.45	0.56	2.28	0.00	1.27	0.21	1.78	0.51	1.30	0.16	-1.21	0.19	0.05	1.26
SPO2352		type I secretion target repeat-containing protein	-1.22	X	1.47	0.09	0.13	1.35	-1.39	0.93	-1.06	X	-1.23	0.16	1.14	0.56	X	X	N/A	N/A
SPO2353		hypothetical protein	X	X	1.26	0.19	N/A	N/A	1.96	0.06	-1.03	0.78	0.47	1.50	-1.02	0.92	-1.14	0.93	-1.08	0.06
SPO2354		hypothetical protein	-1.03	0.90	1.24	0.47	0.11	1.14	1.66	0.05	-1.01	0.93	0.33	1.34	1.03	0.94	-1.06	0.90	-0.02	1.05
SPO2355	*iseR*	dissimilation regulator	1.21	0.27	1.19	0.03	1.20	0.01	1.90	0.01	1.13	0.14	1.52	0.39	1.29	0.05	-1.30	0.09	-0.01	1.30
SPO2356	*iseM*	TRAP transporter	-1.21	0.69	-1.10	0.16	-1.16	0.05	-0.92	0.19	4.98	0.00	2.03	2.95	1.17	0.25	-1.06	0.68	0.05	1.12
SPO2357	*iseL*	TRAP transporter	-1.40	0.46	-1.47	0.61	-1.44	0.04	-1.47	0.55	2.16	0.27	0.35	1.82	-1.06	0.92	1.34	0.67	0.14	1.20
SPO2358	*iseK*	TRAP transporter	-1.42	0.83	-1.65	0.67	-1.54	0.12	-1.82	0.76	4.75	0.14	1.47	3.29	1.20	0.83	1.30	0.75	1.25	0.05
SPO2359	*iseJ*	dehydrogenase	-1.09	0.94	-1.03	0.98	-1.06	0.03	1.67	0.23	6.12	0.01	3.90	2.23	-1.26	0.47	-1.05	X	-1.16	0.11
SPO2361		sensor histidine kinase/response regulator (EC:2.7.3.-)	-1.34	0.13	-1.37	0.21	-1.36	0.02	-1.75	0.01	-1.14	0.64	-1.45	0.31	-1.04	0.97	1.20	0.41	0.08	1.12
SPO2362		amino acid ABC transporter substrate-binding protein	-1.93	0.01	-1.04	0.54	-1.49	0.45	-1.86	0.31	1.43	0.10	-0.22	1.65	-1.00	0.98	-1.01	0.42	-1.01	0.01
SPO2363	*serB-1*	phosphatase (EC:3.1.3.3)	-1.57	0.19	-1.30	0.60	-1.44	0.14	-2.52	0.05	-1.11	0.87	-1.82	0.71	1.10	0.76	1.64	0.21	1.37	0.27
SPO2364		amino acid ABC transporter substrate-binding protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2365		amino acid ABC transporter permease	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2366		amino acid ABC transporter permease	X	X	-1.13	X	N/A	N/A	-1.52	0.60	X	X	N/A	N/A	-1.24	0.66	X	X	N/A	N/A
SPO2367		amino acid ABC transporter ATP-binding protein	1.00	0.78	-1.10	0.92	-0.05	1.05	1.40	0.71	-1.02	0.93	0.19	1.21	-1.16	0.92	1.19	0.83	0.02	1.18
SPO2368		Na/Pi-cotransporter family protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2369		LuxR family transcriptional regulator	1.03	0.89	-1.21	0.07	-0.09	1.12	1.05	0.30	-1.05	0.66	0.00	1.05	-1.21	0.22	-1.19	0.34	-1.20	0.01
SPO2370		sodium:alanine symporter family protein	-2.34	0.43	-1.33	0.26	-1.84	0.51	-1.86	0.24	-2.41	0.08	-2.14	0.27	1.20	0.68	-1.38	0.32	-0.09	1.29
SPO2371		universal stress protein family protein	-5.95	0.04	-3.26	0.03	-4.61	1.35	-2.92	0.00	-4.18	0.00	-3.55	0.63	-1.20	0.05	-1.44	0.02	-1.32	0.12
SPO2372		AsnC family transcriptional regulator	-1.36	0.06	-1.27	0.60	-1.32	0.05	-2.28	0.03	-1.47	0.30	-1.88	0.41	-1.08	0.55	-1.40	0.59	-1.24	0.16
SPO2373		hypothetical protein	1.25	0.14	1.13	0.16	1.19	0.06	1.16	0.11	-1.57	0.07	-0.21	1.37	-1.12	0.36	-2.17	0.00	-1.65	0.53
SPO2374		tRNA-dihydrouridine synthase A	-1.20	0.23	-1.26	0.28	-1.23	0.03	1.39	0.04	-1.16	0.21	0.12	1.28	1.27	0.35	1.16	0.74	1.22	0.06
SPO2376		CoA-binding domain-containing protein	1.40	0.21	1.16	0.75	1.28	0.12	-1.22	0.82	1.20	0.53	-0.01	1.21	1.07	0.79	1.28	0.28	1.18	0.11
SPO2377		ferredoxin	1.39	0.22	1.05	0.12	1.22	0.17	-1.33	0.40	1.49	0.19	0.08	1.41	-1.45	0.00	-1.35	0.16	-1.40	0.05
SPO2378		selenium-binding protein	1.29	0.68	-1.22	0.53	0.04	1.26	-1.72	0.48	1.50	0.27	-0.11	1.61	-1.17	0.25	-1.11	0.75	-1.14	0.03
SPO2380		acyl-CoA dehydrogenase (EC:1.3.99.13)	-0.97	0.94	-1.23	0.72	-1.10	0.13	-1.51	0.57	-1.11	0.83	-1.31	0.20	-1.50	0.26	1.17	0.88	-0.17	1.34

SPO2381		LysR family transcriptional regulator	-1.37	0.76	-1.46	0.68	-1.42	0.04	-2.09	0.55	-1.16	0.83	-1.63	0.47	-1.13	0.87	1.51	0.69	0.19	1.32
SPO2382		tricarboxylate transporter family protein	-2.49	0.04	-1.90	0.03	-2.20	0.29	-4.62	0.02	-1.22	0.42	-2.92	1.70	1.19	0.34	1.48	0.07	1.34	0.14
SPO2383		hypothetical protein	-1.61	X	-1.61	0.25	-1.61	0.00	-1.36	0.62	-1.41	0.06	-1.39	0.02	1.72	0.04	-1.14	1.00	0.29	1.43
SPO2384		tricarboxylate transporter family protein	X	X	-1.03	0.95	N/A	N/A	-2.38	0.05	X	X	N/A	N/A	-1.35	0.17	X	X	N/A	N/A
SPO2385		benzaldehyde lyase	-1.02	0.93	-1.48	0.43	-1.25	0.23	-1.17	0.82	-1.23	0.59	-1.20	0.03	-1.22	0.60	-1.18	0.88	-1.20	0.02
SPO2386		hypothetical protein	X	X	-1.23	0.08	N/A	N/A	-1.15	0.51	-1.04	0.99	-1.10	0.05	-1.08	0.56	X	X	N/A	N/A
SPO2387		oxidoreductase, FAD-binding	-1.79	X	-1.13	0.90	-1.46	0.33	-1.63	0.67	-1.07	0.23	-1.35	0.28	-1.21	0.71	1.02	X	-0.10	1.12
SPO2388		LysE family translocator protein	X	X	-1.35	0.71	N/A	N/A	-1.34	X	X	X	N/A	N/A	1.06	X	X	X	N/A	N/A
SPO2389		molybdopterin-binding oxidoreductase	2.32	0.12	1.02	0.95	1.67	0.65	1.40	0.17	1.23	0.30	1.32	0.09	-1.25	0.31	-1.04	0.99	-1.15	0.11
SPO2390		phage integrase site specific recombinase	X	X	-1.62	X	N/A	N/A	-2.51	X	-1.12	X	-1.82	0.70	-1.12	0.89	X	X	N/A	N/A
SPO2392		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2393	*coxG*	carbon monoxide dehydrogenase G protein	2.21	0.60	-1.33	0.84	0.44	1.77	-1.65	0.80	1.30	0.86	-0.18	1.48	5.79	0.13	8.82	0.12	7.31	1.52
SPO2394	*coxF*	carbon monoxide dehydrogenase F protein	2.56	0.11	-1.25	0.19	0.66	1.91	-1.22	0.49	X	X	N/A	N/A	7.32	0.00	8.63	0.01	7.98	0.66
SPO2395	*coxE*	carbon monoxide dehydrogenase E protein	-0.98	0.18	-1.46	0.48	-1.22	0.24	-3.38	0.01	-1.02	0.98	-2.20	1.18	3.46	0.02	3.46	0.01	3.46	0.00
SPO2396	*coxD*	carbon monoxide dehydrogenase D protein	5.59	0.04	-1.11	0.67	2.24	3.35	-1.43	0.86	-1.04	1.00	-1.24	0.20	10.50	0.02	23.30	0.00	16.90	6.40
SPO2397	*coxL-2*	carbon monoxide dehydrogenase, large subunit (EC:1.2.99.2)	12.90	0.08	-1.17	0.76	5.87	7.04	-1.19	0.98	1.28	0.67	0.05	1.24	21.00	0.02	21.30	0.03	21.15	0.15
SPO2398	*coxS-2*	carbon monoxide dehydrogenase, small subunit (EC:1.2.99.2)	2.26	0.01	-1.35	0.24	0.46	1.81	-7.07	0.01	1.26	0.54	-2.91	4.17	18.80	0.01	44.90	0.00	31.85	13.05
SPO2399	*coxM*	carbon monoxide dehydrogenase, medium subunit (EC:1.2.99.2)	27.60	0.00	-1.36	0.72	13.12	14.48	-1.93	0.16	1.19	X	-0.37	1.56	35.20	0.02	125.00	0.01	80.10	44.90
SPO2400	*coxC*	carbon monoxide dehydrogenase operon C protein	-1.40	0.64	-1.10	0.67	-1.25	0.15	-1.23	0.67	1.43	0.30	0.10	1.33	1.26	0.39	-0.97	0.79	0.14	1.12
SPO2401		type I secretion target repeat-containing protein	1.39	0.37	1.51	0.14	1.45	0.06	1.85	0.11	1.47	0.15	1.66	0.19	-1.30	0.06	-1.70	0.01	-1.50	0.20
SPO2403		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2405		phage integrase site specific recombinase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2406		ISSpo6, transposase orf A	-1.39	0.01	-1.27	0.43	-1.33	0.06	-1.38	0.09	-1.12	0.06	-1.25	0.13	-1.09	0.45	-1.45	0.23	-1.27	0.18
SPO2407		ISSpo6, transposase orfB	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2408		hypothetical protein	-1.77	0.78	-1.09	0.97	-1.43	0.34	-2.57	0.55	1.16	0.59	-0.71	1.87	-1.24	0.92	2.03	X	0.40	1.64
SPO2409		short chain dehydrogenase/reductase oxidoreductase	1.64	0.04	-1.10	0.65	0.27	1.37	-1.37	0.12	1.47	0.07	0.05	1.42	-1.00	0.87	-1.21	0.61	-1.10	0.11
SPO2410		dihydroxy-acid dehydratase (EC:4.2.1.9)	1.95	0.21	1.03	0.75	1.49	0.46	-1.48	0.06	1.15	0.29	-0.17	1.32	1.58	0.01	1.99	0.02	1.79	0.20
SPO2411		hypothetical protein	1.10	0.20	-1.25	0.76	-0.08	1.18	-1.44	0.45	1.19	0.71	-0.13	1.32	-1.83	0.16	-2.59	X	-2.21	0.38
SPO2412		aldolase	1.07	0.82	-1.44	0.53	-0.19	1.26	-1.06	0.55	1.29	0.68	0.12	1.18	-1.06	0.86	-0.96	0.50	-1.01	0.05
SPO2413		short chain dehydrogenase/reductase oxidoreductase	1.22	0.21	-1.47	0.08	-0.13	1.35	-0.98	0.24	1.68	0.17	0.35	1.33	-1.46	0.03	-1.43	X	-1.45	0.02
SPO2414		mandelate racemase	1.31	0.01	-1.25	0.36	0.03	1.28	-2.67	0.01	-0.98	0.90	-1.83	0.84	1.49	0.32	1.44	0.24	1.47	0.03
SPO2415		phytanoyl-CoA dioxygenase	1.43	0.07	-1.24	0.28	0.10	1.34	-2.66	0.02	1.29	0.36	-0.69	1.98	-1.04	0.91	1.13	0.32	0.04	1.09
SPO2416		3-hydroxyisobutyrate dehydrogenase	1.62	0.28	-1.48	0.02	0.07	1.55	-2.33	0.04	1.54	0.03	-0.40	1.94	-1.04	0.94	-1.29	0.59	-1.17	0.13
SPO2417	*idnO*	gluconate 5-dehydrogenase (EC:1.1.1.69)	-1.15	0.73	-1.34	0.82	-1.25	0.10	-2.63	0.26	1.24	0.87	-0.70	1.94	-1.08	0.95	1.38	0.81	0.15	1.23
SPO2418		amino acid transporter LysE	1.21	0.36	-1.47	0.04	-0.13	1.34	-1.39	0.28	1.44	0.09	0.03	1.42	-1.53	0.10	-1.23	0.30	-1.38	0.15
SPO2419		hypothetical protein	1.29	0.27	1.05	0.73	1.17	0.12	-1.83	0.10	1.78	0.08	-0.03	1.81	-1.41	0.12	-1.43	0.12	-1.42	0.01
SPO2420	*kdgK*	2-dehydro-3-deoxygluconokinase (EC:2.7.1.45)	1.61	0.12	-1.01	0.79	0.30	1.31	-1.46	0.07	-0.98	0.59	-1.22	0.24	-1.30	0.23	-1.48	0.42	-1.39	0.09

SPO2421		hypothetical protein	-1.15	0.18	-1.12	0.42	-1.14	0.01	-2.85	0.00	1.13	0.67	-0.86	1.99	-1.14	0.74	1.17	0.79	0.02	1.16
SPO2422		D-isomer specific 2-hydroxyacid dehydrogenase	-1.24	0.54	-1.42	0.33	-1.33	0.09	-1.48	0.41	1.04	0.90	-0.22	1.26	-1.37	0.34	1.26	0.35	-0.06	1.32
SPO2423		hypothetical protein	1.20	0.12	-1.33	0.25	-0.07	1.27	-1.38	0.16	1.29	0.19	-0.04	1.34	-1.73	0.05	-2.21	0.13	-1.97	0.24
SPO2424	*idnD*	L-idonate 5-dehydrogenase (EC:1.1.1.264)	1.09	0.48	-1.13	0.50	-0.02	1.11	1.90	0.02	1.18	0.33	1.54	0.36	-1.44	0.01	-1.25	0.49	-1.35	0.10
SPO2425	*aroE*	shikimate 5-dehydrogenase (EC:1.1.1.25)	-1.52	X	-1.23	0.62	-1.38	0.14	-1.93	0.11	1.07	0.70	-0.43	1.50	-1.21	0.51	1.45	0.36	0.12	1.33
SPO2426		hypothetical protein	X	X	-1.08	0.53	N/A	N/A	-1.15	0.26	1.06	0.82	-0.04	1.11	-1.18	0.14	1.29	0.20	0.06	1.24
SPO2427		short chain dehydrogenase/reductase oxidoreductase	1.00	0.91	-1.36	0.37	-0.18	1.18	-3.06	0.24	1.33	0.24	-0.87	2.20	-1.01	0.99	1.13	0.63	0.06	1.07
SPO2428		6-phosphogluconate dehydrogenase	1.40	0.83	-1.36	0.47	0.02	1.38	-1.81	0.69	1.45	0.21	-0.18	1.63	1.23	0.40	1.14	0.60	1.19	0.05
SPO2429		Gfo/Idh/MocA family oxidoreductase	X	X	-1.46	X	N/A	N/A	-0.92	0.11	1.07	X	0.08	0.99	-1.06	0.96	1.24	X	0.09	1.15
SPO2430		UxaA family hydrolase	X	X	-1.59	0.76	N/A	N/A	X	X	1.12	0.86	N/A	N/A	-1.14	X	1.90	X	0.38	1.52
SPO2431		TRAP dicarboxylate transporter subunit DctM	1.18	0.65	-1.01	0.93	0.09	1.10	-1.68	0.25	1.58	0.17	-0.05	1.63	-1.12	0.66	-1.45	0.44	-1.29	0.16
SPO2432		TRAP dicarboxylate transporter subunit DctQ	1.92	0.41	-2.10	0.04	-0.09	2.01	-1.25	0.77	1.54	0.03	0.15	1.40	-1.25	0.25	-1.38	0.08	-1.32	0.06
SPO2433		TRAP dicarboxylate transporter subunit DctP	X	X	X	X	N/A	N/A	-1.10	X	-1.01	X	-1.06	0.05	X	X	X	X	N/A	N/A
SPO2434		GntR family transcriptional regulator	1.21	0.03	-1.36	0.22	-0.08	1.29	1.39	0.02	1.12	0.55	1.26	0.14	-2.22	0.03	-1.89	0.02	-2.06	0.17
SPO2435		fumarylacetoacetate hydrolase	1.95	0.02	-1.42	0.13	0.27	1.69	2.45	0.01	1.66	0.03	2.06	0.39	-1.58	0.01	-1.15	0.16	-1.37	0.22
SPO2436		FAD-dependent oxidoreductase	1.05	X	-1.03	0.99	0.01	1.04	-1.06	0.99	-1.44	0.51	-1.25	0.19	1.13	0.71	-1.05	X	0.04	1.09
SPO2437		Asp/Glu/Hydantoin racemase	1.17	X	-1.05	0.95	0.06	1.11	-1.92	0.74	1.13	0.88	-0.40	1.53	-1.34	0.64	-1.67	X	-1.51	0.17
SPO2438		phytanoyl-CoA dioxygenase	2.43	0.05	-1.19	0.17	0.62	1.81	-2.37	0.04	1.09	0.65	-0.64	1.73	-1.32	0.38	-1.26	0.49	-1.29	0.03
SPO2439		GntR family transcriptional regulator	-1.73	0.19	-1.31	0.47	-1.52	0.21	-1.70	0.08	-1.38	0.06	-1.54	0.16	-1.53	0.01	-1.55	0.17	-1.54	0.01
SPO2440		M24 family metallopeptidase	-1.29	0.72	-1.29	0.06	-1.29	0.00	-2.08	0.08	-1.20	0.49	-1.64	0.44	-1.39	0.03	-1.07	0.99	-1.23	0.16
SPO2441		glycine betaine/L-proline ABC transporter substrate-binding protein	-1.95	0.03	-2.87	0.01	-2.41	0.46	-1.71	0.02	-1.96	0.02	-1.84	0.13	-1.05	0.77	-1.19	0.20	-1.12	0.07
SPO2442		glycine betaine/proline ABC transporter permease	-1.97	0.03	-1.63	0.05	-1.80	0.17	3.82	0.00	-1.24	0.41	1.29	2.53	-1.21	0.39	1.13	0.46	-0.04	1.17
SPO2443		glycine betaine/proline ABC transporter ATP-binding protein	X	X	-1.53	0.20	N/A	N/A	1.89	0.04	-1.24	0.28	0.33	1.57	-1.49	0.02	-1.13	0.91	-1.31	0.18
SPO2444	*ndk*	nucleoside diphosphate kinase (EC:2.7.4.6)	1.04	0.81	0.99	0.69	1.01	0.03	6.08	0.01	-1.28	0.10	2.40	3.68	-1.60	0.00	-2.16	0.01	-1.88	0.28
SPO2445		Bcr/CflA subfamily drug resistance transporter	-1.30	0.57	1.10	0.84	-0.10	1.20	-1.56	0.63	-1.37	0.63	-1.47	0.10	-1.20	0.67	-1.15	0.94	-1.18	0.03
SPO2446		ABC transporter ATP-binding protein	X	X	1.14	0.46	N/A	N/A	7.06	0.00	-1.45	0.02	2.81	4.26	1.02	0.98	-2.01	0.03	-0.50	1.52
SPO2447		acetyltransferase	-1.04	1.00	1.15	0.63	0.05	1.10	4.00	0.08	-1.12	0.62	1.44	2.56	-1.55	0.14	-2.27	0.08	-1.91	0.36
SPO2448		multiple antibiotic resistance protein MarC	1.18	0.98	1.02	1.00	1.10	0.08	1.79	0.83	-1.49	0.41	0.15	1.64	-1.19	0.66	-1.23	0.67	-1.21	0.02
SPO2449		hypothetical protein	-1.69	0.01	-1.53	0.02	-1.61	0.08	-1.21	0.17	-1.11	0.41	-1.16	0.05	1.10	0.62	1.30	0.18	1.20	0.10
SPO2450		Asp/Glu/Hydantoin racemase	2.75	0.00	1.82	0.08	2.29	0.47	3.20	0.02	-1.12	0.71	1.04	2.16	1.19	0.05	-1.08	0.90	0.05	1.14
SPO2451		acyltransferase	1.92	0.08	-1.10	0.27	0.41	1.51	2.71	0.03	-1.48	0.26	0.62	2.10	-1.25	0.24	1.24	0.25	-0.01	1.25
SPO2452		DNA polymerase III subunit chi	1.16	0.95	1.13	0.47	1.15	0.02	1.16	0.92	1.14	0.78	1.15	0.01	2.22	0.09	1.73	0.12	1.98	0.25
SPO2453	*pepA*	leucyl aminopeptidase (EC:3.4.11.1)	1.45	0.11	-1.37	0.09	0.04	1.41	1.85	0.07	1.83	0.04	1.84	0.01	1.44	0.16	1.74	0.01	1.59	0.15
SPO2454		YjgP/YjgQ family permease	-0.99	0.97	1.23	0.03	0.12	1.11	2.56	0.02	1.02	0.75	1.79	0.77	1.17	0.12	-1.17	0.15	0.00	1.17
SPO2455		organic solvent tolerance protein	1.30	0.73	1.00	0.87	1.15	0.15	1.33	0.67	1.21	0.52	1.27	0.06	-1.39	0.26	-1.17	0.21	-1.28	0.11
SPO2456		peptidyl-prolyl cis-trans isomerase domain-containing protein	1.33	0.03	-1.11	0.46	0.11	1.22	1.70	0.03	0.96	0.17	1.33	0.37	-1.22	0.02	1.20	0.65	-0.01	1.21
SPO2457	*pdxA*	4-hydroxythreonine-4-phosphate dehydrogenase (EC:1.1.1.262)	1.38	0.40	1.30	0.09	1.34	0.04	1.35	0.10	1.18	0.19	1.27	0.09	-1.15	0.35	-1.42	0.01	-1.29	0.14

SPO2458	*ksgA*	dimethyladenosine transferase (EC:2.1.1.-)	1.27	0.96	1.42	0.63	1.35	0.08	2.07	0.78	-1.20	0.75	0.44	1.64	1.08	0.93	-1.14	0.87	-0.03	1.11
SPO2459		hypothetical protein	-1.29	0.13	-1.78	0.04	-1.54	0.25	2.24	0.04	-1.16	0.32	0.54	1.70	-1.96	0.05	-1.35	0.06	-1.66	0.30
SPO2460		HemK family modification methylase	X	X	1.73	0.02	N/A	N/A	2.64	0.01	-1.99	0.02	0.33	2.32	1.23	0.17	-2.43	0.00	-0.60	1.83
SPO2461	*prfA*	peptide chain release factor 1	-1.07	0.91	1.35	0.04	0.14	1.21	1.75	0.13	-1.69	0.02	0.03	1.72	1.12	0.13	-1.62	0.07	-0.25	1.37
SPO2462		hypothetical protein	-1.50	0.08	1.08	0.46	-0.21	1.29	-1.79	0.06	-1.10	0.77	-1.45	0.35	-1.00	0.89	X	X	N/A	N/A
SPO2463		hypothetical protein	X	X	1.08	0.67	N/A	N/A	2.64	0.01	1.17	0.45	1.91	0.74	-0.99	0.79	-1.33	0.28	-1.16	0.17
SPO2464	*speB-2*	agmatinase (EC:3.5.3.11)	1.62	0.19	1.39	0.22	1.51	0.12	2.22	0.04	1.10	0.56	1.66	0.56	-1.08	0.38	-1.39	0.05	-1.24	0.16
SPO2465		hypothetical protein	-1.70	0.07	-1.10	0.76	-1.40	0.30	1.19	0.16	-1.35	0.15	-0.08	1.27	1.39	0.30	-1.23	X	0.08	1.31
SPO2466		glyoxalase	-3.01	0.00	-1.37	0.01	-2.19	0.82	-1.74	0.06	1.10	0.10	-0.32	1.42	1.08	0.84	1.04	0.90	1.06	0.02
SPO2467	*speB-3*	agmatinase (EC:3.5.3.11)	2.53	0.25	1.24	0.45	1.89	0.65	2.22	0.04	1.04	0.96	1.63	0.59	-1.03	0.81	0.97	0.54	-0.03	1.00
SPO2468		amidohydrolase	2.30	0.01	1.29	0.12	1.80	0.51	1.65	0.01	1.17	0.22	1.41	0.24	-1.08	0.08	-1.32	0.05	-1.20	0.12
SPO2469	*mazG*	nucleoside triphosphate pyrophosphohydrolase (EC:3.6.1.19)	1.83	0.03	1.00	0.97	1.42	0.42	2.79	0.02	-1.06	0.61	0.87	1.93	-1.66	0.01	-1.74	0.03	-1.70	0.04
SPO2470	*iunH*	inosine-uridine preferring nucleoside hydrolase (EC:3.2.2.1)	1.60	0.04	1.02	1.00	1.31	0.29	1.71	0.04	1.44	0.24	1.58	0.14	-1.63	0.07	-1.41	0.08	-1.52	0.11
SPO2471		acetyltransferase	1.45	0.04	1.30	0.40	1.38	0.08	1.57	0.08	1.24	0.15	1.41	0.17	-1.10	0.52	-1.33	0.13	-1.22	0.12
SPO2472		hypothetical protein	X	X	-1.67	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.50	0.41	X	X	N/A	N/A
SPO2473		haloacid dehalogenase	-1.16	0.60	1.61	0.00	0.23	1.39	1.68	0.03	-1.49	0.10	0.10	1.59	1.45	0.06	1.01	0.99	1.23	0.22
SPO2474	*eno*	phosphopyruvate hydratase (EC:4.2.1.11)	2.36	0.00	1.30	0.42	1.83	0.53	5.63	0.00	-1.20	0.05	2.22	3.42	1.03	0.80	0.96	0.25	0.99	0.04
SPO2475		hypothetical protein	X	X	1.70	0.01	N/A	N/A	7.51	0.00	-1.61	0.02	2.95	4.56	1.08	0.18	-1.55	0.04	-0.24	1.32
SPO2476		lipoprotein	1.07	0.92	1.16	0.50	1.12	0.04	-3.96	0.01	1.64	0.01	-1.16	2.80	1.27	0.09	1.09	0.22	1.18	0.09
SPO2477		FUR family transcriptional regulator	-1.14	0.67	1.43	0.17	0.15	1.29	1.15	0.71	-1.10	0.26	0.02	1.13	1.27	0.10	-1.25	0.29	0.01	1.26
SPO2479		hypothetical protein	1.15	0.14	1.23	0.49	1.19	0.04	-0.95	0.24	1.38	0.19	0.21	1.17	-1.20	0.84	-1.30	0.37	-1.25	0.05
SPO2480		hypothetical protein	-1.28	0.17	-2.04	0.11	-1.66	0.38	1.57	0.17	1.08	0.81	1.33	0.24	-1.23	0.11	1.20	0.57	-0.02	1.22
SPO2481		drug/metabolite exporter family protein	-1.61	0.73	-1.04	0.92	-1.33	0.28	-1.59	0.80	1.02	0.93	-0.29	1.31	1.28	0.31	1.12	0.82	1.20	0.08
SPO2482		hypothetical protein	-1.11	0.42	1.33	0.46	0.11	1.22	1.54	0.03	1.21	0.06	1.38	0.17	-1.27	0.14	-1.52	0.03	-1.40	0.13
SPO2483	*anmK*	anhydro-N-acetylmuramic acid kinase	-1.23	0.34	1.15	0.30	-0.04	1.19	-1.26	0.44	-1.07	0.28	-1.17	0.10	1.15	0.68	1.64	0.16	1.40	0.24
SPO2484	*tyrS*	tyrosyl-tRNA synthetase (EC:6.1.1.1)	-1.60	0.64	1.08	0.84	-0.26	1.34	0.95	0.85	-1.19	0.27	-0.12	1.07	-1.28	0.30	-1.36	0.30	-1.32	0.04
SPO2485		hypothetical protein	1.34	0.55	1.11	0.74	1.23	0.12	1.50	0.46	-1.14	0.81	0.18	1.32	1.05	0.59	1.54	0.13	1.30	0.25
SPO2486		hypothetical protein	-1.01	X	1.12	0.62	0.06	1.07	-1.40	X	1.25	X	-0.08	1.33	-1.11	0.94	-1.16	X	-1.14	0.02
SPO2487		3-hydroxyacyl-CoA dehydrogenase (EC:1.1.1.35)	-1.08	0.91	-1.31	0.68	-1.20	0.12	-1.21	0.79	-1.00	0.99	-1.10	0.11	1.59	0.53	1.13	0.79	1.36	0.23
SPO2488		ABC transporter ATP-binding protein	-1.28	0.62	1.06	0.80	-0.11	1.17	1.25	0.47	-1.50	0.00	-0.13	1.38	-1.55	0.06	-2.03	0.05	-1.79	0.24
SPO2489		hypothetical protein	-1.25	0.68	-1.15	0.83	-1.20	0.05	0.89	0.80	1.32	0.76	1.11	0.21	1.81	0.35	2.36	0.32	2.09	0.27
SPO2490		SmpA/OmlA family lipoprotein	1.35	0.52	0.99	0.90	1.17	0.18	1.98	0.13	1.65	0.00	1.82	0.17	-1.24	0.05	0.90	0.21	-0.17	1.07
SPO2491		hypothetical protein	-1.06	0.93	-1.13	0.87	-1.10	0.03	1.54	0.03	-1.20	0.14	0.17	1.37	-2.45	0.07	-2.41	0.03	-2.43	0.02
SPO2492	*rpmF*	50S ribosomal protein L32	1.37	0.55	-1.16	0.04	0.11	1.27	6.90	0.00	-1.63	0.01	2.64	4.27	-1.30	0.19	-1.54	0.07	-1.42	0.12
SPO2493	*plsX*	glycerol-3-phosphate acyltransferase PlsX	1.04	0.96	-1.06	0.33	-0.01	1.05	3.01	0.12	-1.53	0.26	0.74	2.27	0.99	0.61	-1.25	0.08	-0.13	1.12
SPO2494	*fabH-2*	3-oxoacyl-ACP synthase (EC:2.3.1.41)	-1.62	0.03	0.98	0.49	-0.32	1.30	2.79	0.01	-1.11	0.20	0.84	1.95	1.19	0.44	-1.46	0.04	-0.14	1.33
SPO2495	*ihfA*	integration host factor subunit alpha	-1.43	0.01	-1.11	0.53	-1.27	0.16	-2.72	0.00	1.23	0.12	-0.75	1.98	1.21	0.24	1.56	0.05	1.39	0.18
SPO2496		MerR family transcriptional regulator	1.02	0.70	-1.49	0.11	-0.24	1.26	-2.02	0.13	1.17	0.74	-0.43	1.60	-1.12	0.93	1.56	0.11	0.22	1.34

SPO2498		2'-deoxycytidine 5'-triphosphate deaminase (EC:3.5.4.13)	-1.16	0.48	1.34	0.03	0.09	1.25	1.32	0.19	-1.17	0.28	0.08	1.25	-1.24	0.09	-1.29	0.19	-1.27	0.03
SPO2499		hypothetical protein	1.12	0.51	-1.75	0.12	-0.32	1.44	1.03	0.38	1.16	0.25	1.10	0.06	1.02	0.51	1.35	0.22	1.19	0.17
SPO2500	*scpB*	segregation and condensation protein B	1.01	0.94	-1.60	0.46	-0.30	1.31	1.09	0.96	1.03	0.96	1.06	0.03	1.43	0.60	1.11	0.97	1.27	0.16
SPO2501	*scpA*	segregation and condensation protein A	-1.49	0.00	-1.84	0.02	-1.67	0.18	-1.40	0.02	1.10	0.66	-0.15	1.25	-1.54	0.11	-1.48	0.06	-1.51	0.03
SPO2502		beta-N-acetylhexosaminidase	-1.16	0.76	-1.26	0.52	-1.21	0.05	-1.23	0.75	-1.11	0.81	-1.17	0.06	1.60	0.20	1.00	0.96	1.30	0.30
SPO2503		hypothetical protein	-1.49	0.01	-1.54	0.07	-1.52	0.03	1.05	0.02	-1.43	0.01	-0.19	1.24	1.12	0.72	1.24	0.30	1.18	0.06
SPO2504	*argS*	arginyl-tRNA synthetase (EC:6.1.1.19)	1.54	0.73	1.05	0.85	1.30	0.25	3.81	0.29	-1.50	0.20	1.16	2.66	-1.33	0.19	-1.71	0.14	-1.52	0.19
SPO2505		deoxyguanosinetriphosphate triphosphohydrolase	-1.20	0.27	-1.34	0.40	-1.27	0.07	1.59	0.02	1.25	0.20	1.42	0.17	-1.13	0.58	-1.12	0.13	-1.13	0.00
SPO2506		Iron-sulfur cluster assembly family protein	-1.10	0.38	1.20	0.56	0.05	1.15	1.11	0.69	0.98	0.53	1.05	0.06	2.08	0.03	1.75	0.03	1.92	0.17
SPO2507		hypothetical protein	1.17	0.32	1.68	0.09	1.43	0.26	-4.17	0.01	5.26	0.00	0.55	4.72	1.12	0.27	1.98	0.02	1.55	0.43
SPO2508		hypothetical protein	1.35	0.79	4.72	0.02	3.04	1.69	-3.84	0.00	17.70	0.00	6.93	10.77	1.55	0.29	6.59	0.01	4.07	2.52
SPO2509	*xth*	exodeoxyribonuclease III (EC:3.1.11.2)	1.03	0.60	1.06	0.89	1.05	0.02	1.45	0.00	1.31	0.33	1.38	0.07	1.07	0.79	0.99	0.86	1.03	0.04
SPO2510	*nahG*	salicylate hydroxylase (EC:1.14.13.1)	1.22	0.93	2.70	0.03	1.96	0.74	1.54	0.73	-1.12	0.61	0.21	1.33	-1.13	0.70	-1.14	0.87	-1.14	0.01
SPO2511		dnaK suppressor protein	1.50	0.16	1.03	0.99	1.27	0.24	1.94	0.04	1.24	0.17	1.59	0.35	0.97	0.37	1.09	0.77	1.03	0.06
SPO2512		ATPase AAA	1.80	0.05	1.04	0.96	1.42	0.38	1.72	0.03	1.06	0.96	1.39	0.33	-1.43	0.04	-1.16	0.31	-1.30	0.14
SPO2513		hypothetical protein	-1.57	0.04	1.22	0.27	-0.18	1.40	-2.96	0.01	1.65	0.01	-0.66	2.31	-1.57	0.01	-1.56	0.00	-1.57	0.01
SPO2514		hypothetical protein	-1.22	0.54	1.24	0.28	0.01	1.23	1.46	0.16	-1.28	0.12	0.09	1.37	-1.26	0.13	-1.12	0.18	-1.19	0.07
SPO2515		hypothetical protein	-1.07	0.66	1.17	0.59	0.05	1.12	1.50	0.32	-1.01	0.95	0.25	1.26	1.26	0.67	-1.41	0.34	-0.08	1.34
SPO2516		hypothetical protein	-5.28	0.00	-2.43	0.06	-3.86	1.43	5.33	0.00	-1.15	0.10	2.09	3.24	2.48	0.04	2.04	0.08	2.26	0.22
SPO2517		M48 family peptidase	-1.63	0.24	-1.90	0.14	-1.77	0.14	-1.18	0.56	1.21	0.69	0.02	1.20	1.24	0.72	1.81	0.14	1.53	0.29
SPO2518		luciferase	-1.18	0.53	-1.48	0.06	-1.33	0.15	-1.37	0.26	-1.43	0.17	-1.40	0.03	-1.02	0.70	1.36	0.25	0.17	1.19
SPO2519		hypothetical protein	X	X	-1.14	0.30	N/A	N/A	3.65	0.00	-1.01	0.80	1.32	2.33	1.02	0.75	-1.79	0.01	-0.39	1.41
SPO2520		hypothetical protein	-1.11	0.26	1.26	0.36	0.08	1.19	1.48	0.08	-1.45	0.17	0.02	1.47	1.08	0.70	-1.53	0.02	-0.23	1.31
SPO2521		lipoprotein	2.40	0.67	1.24	0.10	1.82	0.58	-1.70	0.04	1.17	0.41	-0.27	1.44	-1.54	0.09	1.04	0.07	-0.25	1.29
SPO2522		hypothetical protein	9.39	0.00	2.35	0.05	5.87	3.52	1.56	0.16	1.35	0.17	1.46	0.11	-1.03	0.73	1.05	0.54	0.01	1.04
SPO2523	*glnE*	glutamate-ammonia ligase adenylyltransferase (EC:2.7.7.42)	7.33	0.04	2.80	0.04	5.07	2.27	4.14	0.07	1.23	0.60	2.69	1.46	1.10	0.82	-1.26	0.63	-0.08	1.18
SPO2524		prolyl-tRNA synthetase	-1.32	0.47	-1.08	0.79	-1.20	0.12	-1.86	0.04	-1.24	0.54	-1.55	0.31	1.03	0.91	2.21	0.09	1.62	0.59
SPO2525		hypothetical protein	1.37	0.69	1.34	0.53	1.36	0.02	1.91	0.02	1.35	0.48	1.63	0.28	1.62	0.04	1.83	0.37	1.73	0.11
SPO2526		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.02	X	X	X	N/A	N/A
SPO2527	*nylA*	6-aminohexanoate-cyclic-dimer hydrolase (EC:3.5.2.12)	1.27	0.67	1.22	0.50	1.25	0.03	-1.92	0.16	1.08	0.78	-0.42	1.50	-0.97	0.84	-1.32	0.22	-1.14	0.18
SPO2528		AMP-binding protein (EC:2.3.1.86)	1.29	0.19	-1.02	0.97	0.14	1.16	-3.66	0.00	-1.05	0.83	-2.36	1.31	-1.77	0.08	-1.88	0.16	-1.83	0.05
SPO2529		hypothetical protein	-0.96	0.70	-1.14	0.86	-1.05	0.09	-2.46	0.02	-1.64	0.19	-2.05	0.41	-1.28	0.25	-1.52	X	-1.40	0.12
SPO2530		branched-chain amino acid ABC transporter permease	-0.99	0.97	1.03	0.85	0.02	1.01	-1.30	0.87	-1.20	0.26	-1.25	0.05	1.07	0.81	1.36	0.09	1.22	0.15
SPO2531		branched-chain amino acid ABC transporter permease	-1.16	0.44	-1.40	0.09	-1.28	0.12	-2.49	0.08	-1.13	0.64	-1.81	0.68	-1.21	0.30	X	X	N/A	N/A
SPO2532		branched-chain amino acid ABC transporter ATP-binding protein	-1.21	0.47	-1.03	0.97	-1.12	0.09	-2.13	0.17	-1.17	X	-1.65	0.48	X	X	X	X	N/A	N/A
SPO2533		branched-chain amino acid ABC transporter ATP-binding protein	-1.17	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.17	X	X	X	N/A	N/A

SPO2534		branched-chain amino acid ABC transporter substrate-binding protein	-2.37	0.05	-1.20	0.47	-1.79	0.59	-7.94	0.20	-1.01	0.98	-4.48	3.47	-1.14	0.72	-1.29	0.71	-1.22	0.08
SPO2535		histone deacetylase/AcuC/AphA family protein	-1.36	0.44	-1.11	0.90	-1.24	0.13	-11.10	0.04	-1.32	0.76	-6.21	4.89	-1.05	0.98	1.04	X	-0.01	1.05
SPO2536		LuxR family transcriptional regulator	-1.41	0.28	-1.15	0.58	-1.28	0.13	-2.05	0.15	X	X	N/A	N/A	-1.31	0.07	X	X	N/A	N/A
SPO2537		hypothetical protein	-1.62	0.05	-1.25	0.48	-1.44	0.19	-1.96	0.06	1.14	0.63	-0.41	1.55	-1.54	0.14	-1.05	X	-1.30	0.25
SPO2538		acyl-CoA dehydrogenase	-1.53	0.07	1.02	0.87	-0.26	1.28	-1.79	0.63	-1.01	0.99	-1.40	0.39	-1.33	0.68	-1.13	0.91	-1.23	0.10
SPO2539		AMP-binding protein	-1.45	0.17	-1.10	0.37	-1.28	0.18	-1.94	0.03	-1.17	0.31	-1.56	0.39	-1.11	0.44	-1.05	0.70	-1.08	0.03
SPO2540		carbamoyl-phosphate synthase	-1.39	0.06	-1.25	0.07	-1.32	0.07	-1.87	0.03	-1.26	0.38	-1.57	0.31	-1.12	0.61	-1.12	0.94	-1.12	0.00
SPO2541		propionyl-CoA carboxylase	-2.13	0.00	-1.15	0.62	-1.64	0.49	-3.30	0.01	-1.54	0.16	-2.42	0.88	-1.15	0.49	-1.11	0.94	-1.13	0.02
SPO2542		biotin/lipoate binding domain-containing protein	-3.45	0.01	-1.25	0.16	-2.35	1.10	-7.01	0.00	-1.02	0.98	-4.02	3.00	-1.29	0.16	-1.93	0.07	-1.61	0.32
SPO2543		GntR family transcriptional regulator	1.17	0.81	1.03	0.66	1.10	0.07	1.28	0.19	1.05	0.72	1.17	0.12	1.45	0.01	1.05	0.45	1.25	0.20
SPO2544		amidohydrolase	-1.01	0.99	1.09	0.93	0.04	1.05	-1.42	0.93	-1.20	0.89	-1.31	0.11	1.18	0.86	1.53	0.77	1.36	0.18
SPO2545		TRAP dicarboxylate transporter subunit DctP	-1.44	0.24	-1.23	0.18	-1.34	0.11	-1.86	0.61	-1.47	0.07	-1.67	0.19	1.04	0.77	-1.06	0.90	-0.01	1.05
SPO2546		TRAP dicarboxylate transporter subunit DctQ	-1.73	0.25	-1.28	0.44	-1.51	0.23	-3.52	0.11	-0.95	0.87	-2.24	1.28	-1.32	0.40	-1.45	X	-1.39	0.06
SPO2547		TRAP dicarboxylate transporter subunit DctM	-1.56	0.09	-1.05	0.82	-1.31	0.25	-2.40	0.41	-1.20	X	-1.80	0.60	1.38	0.62	1.41	X	1.40	0.02
SPO2548		zinc-binding dehydrogenase oxidoreductase	-2.68	0.13	-1.29	0.03	-1.99	0.70	-3.15	0.00	-1.16	0.43	-2.16	1.00	-1.28	0.03	1.39	0.05	0.05	1.34
SPO2549		phosphotransferase	1.31	X	-1.14	0.71	0.09	1.23	-1.47	0.80	-1.41	0.17	-1.44	0.03	-1.37	0.16	-1.80	0.54	-1.59	0.22
SPO2550		GntR family transcriptional regulator	X	X	-1.15	0.31	N/A	N/A	2.68	0.03	1.06	0.68	1.87	0.81	-1.58	0.02	-1.96	0.06	-1.77	0.19
SPO2551		peptide/opine/nickel uptake ABC transporter ATP-binding protein	-1.08	0.96	-1.04	0.98	-1.06	0.02	1.16	0.90	1.16	0.93	1.16	0.00	-1.19	0.91	-1.24	0.94	-1.22	0.03
SPO2552		peptide/opine/nickel ABC transporter permease/ATP-binding protein	X	X	1.22	0.30	N/A	N/A	-1.11	0.17	-1.12	X	-1.12	0.01	-0.97	0.62	X	X	N/A	N/A
SPO2553		peptide/opine/nickel uptake ABC transporter permease	1.07	1.00	-1.01	1.00	0.03	1.04	1.11	0.96	-1.00	0.99	0.06	1.05	-1.02	1.00	1.33	0.65	0.16	1.18
SPO2554		peptide/opine/nickel uptake ABC transporter substrate-binding protein	-2.31	0.26	-1.18	0.90	-1.75	0.57	-3.16	0.26	-1.30	0.83	-2.23	0.93	1.19	0.88	1.91	0.65	1.55	0.36
SPO2555		hypothetical protein	X	X	-1.02	0.98	N/A	N/A	-1.43	0.88	1.17	0.31	-0.13	1.30	-1.36	0.33	1.14	X	-0.11	1.25
SPO2556		allantoate amidohydrolase	-1.97	X	-1.66	0.67	-1.82	0.16	-3.30	X	-1.07	X	-2.19	1.12	-1.58	0.68	1.59	X	0.01	1.59
SPO2559	*gnl*	gluconolactonase (EC:3.1.1.17)	-1.47	0.44	-1.09	0.78	-1.28	0.19	-1.34	0.68	1.89	0.12	0.28	1.62	1.20	0.32	1.11	0.76	1.16	0.04
SPO2560	*garR*	2-hydroxy-3-oxopropionate reductase (EC:1.1.1.60)	-1.04	0.39	-1.10	0.25	-1.07	0.03	1.06	0.41	1.98	0.01	1.52	0.46	1.18	0.10	1.12	0.15	1.15	0.03
SPO2561		hypothetical protein	-1.39	0.03	-1.00	0.98	-1.20	0.20	-1.31	0.08	2.06	0.05	0.38	1.69	1.30	0.33	-0.97	0.85	0.17	1.13
SPO2562	*fucA*	aldolase (EC:4.1.2.17)	-1.22	0.06	1.02	0.65	-0.10	1.12	-1.42	0.06	1.88	0.01	0.23	1.65	1.08	0.52	-1.00	0.66	0.04	1.04
SPO2563		hydroxypyruvate isomerase	-1.23	0.06	-1.13	0.33	-1.18	0.05	-1.52	0.08	2.11	0.02	0.30	1.82	1.04	0.85	-0.97	0.38	0.03	1.01
SPO2564		hypothetical protein	X	X	-1.22	0.79	N/A	N/A	-1.37	0.90	-1.11	0.72	-1.24	0.13	-1.15	0.73	1.09	X	-0.03	1.12
SPO2565		ribosome-associated GTPase	-1.11	0.92	1.09	0.87	-0.01	1.10	-1.32	0.85	-1.98	0.30	-1.65	0.33	-1.59	0.44	-1.76	0.38	-1.68	0.09
SPO2566		glyoxalase	-1.72	0.01	1.52	0.02	-0.10	1.62	1.41	0.03	-1.16	0.05	0.13	1.29	-1.39	0.06	-1.46	0.15	-1.43	0.04
SPO2567		hypothetical protein	0.92	0.02	-1.48	0.10	-0.28	1.20	1.24	0.53	1.37	0.13	1.31	0.07	-1.14	0.07	0.99	0.36	-0.07	1.07
SPO2568		RDD family protein	1.29	0.18	-1.07	0.38	0.11	1.18	2.05	0.01	-1.20	0.33	0.43	1.63	1.54	0.12	-1.12	0.21	0.21	1.33
SPO2569	*ate*	arginyl-tRNA-protein transferase (EC:2.3.2.8)	-1.31	0.57	1.02	0.93	-0.15	1.17	-1.30	0.53	1.28	0.11	-0.01	1.29	1.32	0.11	1.37	0.28	1.35	0.03
SPO2570		glyoxalase	0.99	0.63	-1.04	0.83	-0.03	1.01	1.07	0.62	1.15	0.65	1.11	0.04	1.54	0.07	1.03	0.34	1.29	0.25
SPO2571		TRAP C4-dicarboxylate transport system permease DctM	2.39	0.16	-1.17	0.34	0.61	1.78	3.47	0.05	1.94	0.03	2.71	0.77	1.40	0.37	1.89	0.04	1.65	0.25

SPO2572		hypothetical protein	2.05	0.56	-1.54	0.17	0.26	1.80	2.34	0.14	1.88	0.05	2.11	0.23	1.03	0.90	1.45	0.08	1.24	0.21
SPO2573		solute-binding family 7 protein	1.10	0.07	-3.16	0.01	-1.03	2.13	1.28	0.26	1.76	0.08	1.52	0.24	1.24	0.31	1.41	0.30	1.33	0.09
SPO2574		sensor histidine kinase (EC:2.7.3.-)	1.22	0.39	-1.26	0.07	-0.02	1.24	1.98	0.01	1.25	0.13	1.62	0.37	-1.35	0.19	-1.51	0.13	-1.43	0.08
SPO2575		LuxR family transcriptional regulator	1.07	1.00	-1.11	0.86	-0.02	1.09	1.92	0.69	-1.29	0.76	0.32	1.61	-1.06	0.88	-1.17	0.77	-1.12	0.05
SPO2576		TetR family transcriptional regulator	1.09	0.85	3.28	0.01	2.19	1.10	-1.61	0.43	-1.10	0.63	-1.36	0.26	1.75	0.05	3.34	0.01	2.55	0.80
SPO2577		hypothetical protein	-1.08	0.54	1.50	0.11	0.21	1.29	1.84	0.03	-2.07	0.01	-0.12	1.96	1.59	0.12	5.56	0.00	3.58	1.99
SPO2578	*ilvB*	acetolactate synthase 3 catalytic subunit	-1.17	0.25	1.23	0.20	0.03	1.20	2.76	0.05	1.61	0.01	2.19	0.57	-1.32	0.03	-1.28	0.16	-1.30	0.02
SPO2579	*ilvH*	acetolactate synthase 3 regulatory subunit (EC:2.2.1.6)	1.28	X	1.54	0.24	1.41	0.13	3.83	0.01	-1.21	0.06	1.31	2.52	-1.05	0.17	-1.58	0.04	-1.32	0.27
SPO2580		hypothetical protein	-2.20	0.16	1.73	0.04	-0.24	1.97	-3.26	0.00	2.91	0.01	-0.18	3.09	1.86	0.04	3.91	0.00	2.89	1.03
SPO2581		DNA-binding protein	-1.70	0.01	-1.16	0.39	-1.43	0.27	-1.34	0.16	-1.05	0.74	-1.20	0.15	-1.39	0.12	-1.78	0.06	-1.59	0.20
SPO2582		hypothetical protein	1.54	0.41	1.25	0.32	1.40	0.14	1.69	0.10	1.24	0.52	1.47	0.23	1.29	0.41	1.29	0.50	1.29	0.00
SPO2583		amidase (EC:3.5.1.4)	0.99	0.02	1.24	0.48	1.11	0.13	0.94	0.24	1.26	0.11	1.10	0.16	1.34	0.17	1.18	0.26	1.26	0.08
SPO2584		glyoxalase	1.16	0.82	-1.05	0.90	0.05	1.11	-1.07	0.97	1.22	0.62	0.08	1.15	1.21	0.57	-0.97	0.78	0.12	1.09
SPO2585	*prfB*	peptide chain release factor 2	-1.16	0.43	0.99	0.82	-0.09	1.07	4.00	0.01	-1.16	0.10	1.42	2.58	-1.23	0.06	-1.72	0.04	-1.48	0.24
SPO2586		type I secretion target repeat-containing protein	1.52	0.02	1.70	0.01	1.61	0.09	1.19	0.17	-1.54	0.13	-0.18	1.37	-1.38	0.02	X	X	N/A	N/A
SPO2587	*mrca*	penicillin-binding protein 1A	-1.57	0.17	-1.07	0.65	-1.32	0.25	2.30	0.08	-1.07	0.59	0.62	1.69	2.48	0.00	1.69	0.03	2.09	0.39
SPO2588		N-acetylmuramoyl-L-alanine amidase	-1.72	0.49	-1.05	0.86	-1.39	0.34	-1.11	0.78	-1.29	0.03	-1.20	0.09	1.14	0.18	-1.16	0.73	-0.01	1.15
SPO2589		class I and II aminotransferase	1.57	0.09	1.29	0.36	1.43	0.14	3.18	0.03	-1.22	0.45	0.98	2.20	1.14	0.67	-1.30	0.41	-0.08	1.22
SPO2590		M48 family peptidase	1.15	0.97	-1.07	0.28	0.04	1.11	1.02	0.13	1.58	0.21	1.30	0.28	1.34	0.28	1.58	0.29	1.46	0.12
SPO2591		hypothetical protein	2.00	0.03	-1.35	0.07	0.33	1.68	1.69	0.06	1.58	0.12	1.64	0.05	1.14	0.48	1.20	0.34	1.17	0.03
SPO2592		beta-lactamase	-1.13	X	1.13	0.84	0.00	1.13	2.98	0.21	1.03	0.95	2.01	0.98	1.43	0.56	1.12	0.37	1.28	0.16
SPO2593		hypothetical protein	-1.45	0.01	1.93	0.02	0.24	1.69	-3.71	0.01	2.01	0.09	-0.85	2.86	-1.28	0.52	X	X	N/A	N/A
SPO2594	*ispG*	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC:1.17.7.1)	1.21	0.50	-1.07	0.55	0.07	1.14	1.60	0.06	-1.48	0.06	0.06	1.54	1.22	0.15	1.42	0.11	1.32	0.10
SPO2595		hypothetical protein	1.29	X	1.52	0.74	1.41	0.12	-2.04	X	-1.36	X	-1.70	0.34	1.17	0.71	2.01	X	1.59	0.42
SPO2596	*hemA-1*	5-aminolevulinate synthase (EC:2.3.1.37)	3.05	0.00	1.75	0.07	2.40	0.65	4.82	0.01	-1.04	0.42	1.89	2.93	-1.04	0.69	0.93	0.46	-0.06	0.98
SPO2597		hypothetical protein	1.88	0.03	1.19	0.11	1.54	0.35	2.81	0.03	1.18	0.34	2.00	0.82	1.36	0.05	1.11	0.06	1.24	0.13
SPO2598		hypothetical protein	X	X	1.28	0.56	N/A	N/A	2.67	0.01	-1.04	0.88	0.82	1.86	-1.26	0.05	-2.06	0.19	-1.66	0.40
SPO2601		pirin	-1.74	0.36	-1.29	0.02	-1.52	0.22	-2.75	0.03	-1.22	0.22	-1.99	0.77	1.17	0.20	-1.05	0.75	0.06	1.11
SPO2602		RpiR family transcriptional regulator	-1.70	0.12	-1.25	0.22	-1.48	0.22	-3.00	0.03	-1.71	0.04	-2.36	0.64	-1.23	0.13	-1.58	0.08	-1.41	0.18
SPO2603		N-formylglutamate amidohydrolase	-1.51	0.07	-1.04	0.87	-1.28	0.24	-1.87	0.01	-1.81	0.04	-1.84	0.03	-1.16	0.16	-2.28	0.02	-1.72	0.56
SPO2604		hypothetical protein	-1.31	0.33	1.05	0.72	-0.13	1.18	-1.99	0.06	-1.73	0.49	-1.86	0.13	1.05	0.75	-1.14	0.93	-0.04	1.10
SPO2605		TRAP dicarboxylate transporter subunit DctM	-1.56	0.77	-1.50	0.19	-1.53	0.03	-2.34	0.11	-1.88	0.16	-2.11	0.23	-1.56	0.14	-1.61	0.09	-1.59	0.03
SPO2606		solute-binding family 7 protein	-1.29	0.15	-1.78	0.02	-1.54	0.25	-4.55	0.01	-1.93	0.04	-3.24	1.31	-1.03	0.56	0.96	0.33	-0.03	1.00
SPO2607		gamma-glutamylisopropylamide synthetase	1.34	0.27	-1.11	0.17	0.12	1.23	-2.26	0.00	-1.22	0.01	-1.74	0.52	-1.17	0.07	-1.41	0.16	-1.29	0.12
SPO2608		aldehyde dehydrogenase	1.95	0.10	-1.18	0.58	0.39	1.57	-1.61	0.02	-1.30	0.02	-1.46	0.16	-1.52	0.00	-1.45	0.03	-1.49	0.04
SPO2609		alcohol dehydrogenase	1.66	0.02	-1.22	0.21	0.22	1.44	-1.66	0.01	-1.21	0.01	-1.44	0.22	-1.45	0.10	-1.31	0.19	-1.38	0.07
SPO2610		hypothetical protein	-2.39	0.00	-1.71	0.03	-2.05	0.34	-1.94	0.00	-1.19	0.03	-1.57	0.38	-1.03	0.10	-1.33	0.02	-1.18	0.15
SPO2612		DNA-binding protein HU	-1.42	0.51	-1.78	0.06	-1.60	0.18	-2.29	0.02	1.10	0.71	-0.60	1.70	1.02	0.80	1.20	0.57	1.11	0.09

SPO2613	*lon*	ATP-dependent protease La (EC:3.4.21.53)	1.18	0.97	-1.60	0.19	-0.21	1.39	2.64	0.28	-1.21	0.42	0.72	1.93	2.10	0.05	2.26	0.11	2.18	0.08
SPO2614		hypothetical protein	-2.15	0.01	-1.84	0.01	-2.00	0.16	20.60	0.00	7.08	0.00	13.84	6.76	1.02	0.75	1.16	0.41	1.09	0.07
SPO2615		Oye family NADH-dependent flavin oxidoreductase	-1.30	0.80	-1.96	0.02	-1.63	0.33	6.46	0.17	5.36	0.01	5.91	0.55	1.71	0.14	1.98	0.09	1.85	0.14
SPO2616	*tgt*	queuine tRNA-ribosyltransferase (EC:2.4.2.29)	X	X	1.71	0.01	N/A	N/A	4.52	0.00	-1.70	0.01	1.41	3.11	-1.35	0.19	-2.54	0.01	-1.95	0.60
SPO2617		hypothetical protein	1.49	0.74	-1.08	0.75	0.21	1.29	0.88	0.75	1.42	0.36	1.15	0.27	1.47	0.34	1.46	0.31	1.47	0.01
SPO2618		hypothetical protein	1.39	0.02	-1.38	0.02	0.01	1.39	-1.30	0.06	1.30	0.13	0.00	1.30	-1.07	0.67	1.18	0.32	0.05	1.13
SPO2619		hypothetical protein	-1.13	0.15	-1.34	0.02	-1.24	0.11	1.18	0.41	1.31	0.14	1.25	0.07	1.00	0.83	1.17	0.62	1.09	0.09
SPO2620		iron-sulfur cluster assembly accessory protein	0.91	0.14	-1.60	0.03	-0.34	1.26	1.28	0.47	1.30	0.25	1.29	0.01	1.52	0.11	2.05	0.08	1.79	0.27
SPO2621	*tpiA*	triosephosphate isomerase (EC:5.3.1.1)	-0.99	0.98	1.22	0.51	0.11	1.11	2.23	0.48	-1.27	0.44	0.48	1.75	1.37	0.32	1.11	0.78	1.24	0.13
SPO2622		acetyltransferase	-1.21	0.58	-1.15	0.28	-1.18	0.03	1.13	0.15	1.43	0.27	1.28	0.15	1.14	0.23	-0.99	0.55	0.08	1.06
SPO2623		amino acid transporter LysE	-2.41	0.21	-1.13	0.77	-1.77	0.64	-2.67	0.24	-1.43	0.56	-2.05	0.62	1.18	0.79	-1.05	0.94	0.06	1.12
SPO2624		AsnC family transcriptional regulator	-1.38	0.22	1.12	0.05	-0.13	1.25	-0.94	0.33	-1.26	0.19	-1.10	0.16	1.18	0.44	-1.41	0.18	-0.12	1.30
SPO2625		hypothetical protein	-1.03	0.93	1.16	0.74	0.06	1.10	-1.28	0.84	1.11	0.86	-0.09	1.20	1.41	0.57	1.42	0.44	1.42	0.01
SPO2626		TRAP C4-dicarboxylate transport system permease DctM	-1.26	0.10	1.10	0.55	-0.08	1.18	9.23	0.00	1.44	0.03	5.34	3.90	2.44	0.01	2.47	0.04	2.46	0.02
SPO2627		TRAP dicarboxylate transporter subunit DctQ	-1.13	0.41	-2.13	0.00	-1.63	0.50	29.00	0.00	1.33	0.34	15.17	13.84	1.09	0.64	1.52	0.18	1.31	0.21
SPO2628		TRAP transporter solute receptor DctP family protein	-1.16	0.23	-3.48	0.02	-2.32	1.16	17.40	0.00	2.94	0.00	10.17	7.23	1.45	0.19	1.91	0.01	1.68	0.23
SPO2629		C4-dicarboxylate transport transcriptional regulator	-0.94	0.55	-1.08	0.43	-1.01	0.07	3.72	0.00	1.53	0.02	2.63	1.10	1.31	0.20	-1.25	0.37	0.03	1.28
SPO2630		C4-dicarboxylate transport sensor protein (EC:2.7.3.-)	-0.98	0.97	-1.14	0.37	-1.06	0.08	2.67	0.11	1.57	0.06	2.12	0.55	1.35	0.20	1.09	0.62	1.22	0.13
SPO2631		AsnC family transcriptional regulator	1.63	0.19	-1.72	0.03	-0.05	1.68	7.56	0.02	1.73	0.06	4.65	2.92	-1.13	0.48	-1.41	0.21	-1.27	0.14
SPO2632	*cobA-1*	uroporphyrin-III C-methyltransferase (EC:2.1.1.107)	-1.45	0.09	-2.30	0.01	-1.88	0.43	6.00	0.00	3.77	0.01	4.89	1.12	1.36	0.23	2.14	0.07	1.75	0.39
SPO2633		hypothetical protein	1.13	0.66	-3.37	0.03	-1.12	2.25	8.57	0.00	3.09	0.00	5.83	2.74	-1.64	0.07	-1.15	0.11	-1.40	0.24
SPO2634		sulfite reductase	-1.03	0.28	-2.09	0.02	-1.56	0.53	21.10	0.00	2.63	0.01	11.87	9.24	1.26	0.35	1.19	0.57	1.23	0.04
SPO2635	*cysH*	phosphoadenosine phosphosulfate reductase (EC:1.8.4.8)	1.40	0.45	-2.99	0.02	-0.80	2.20	23.00	0.00	2.89	0.01	12.95	10.06	-1.39	0.09	0.97	0.18	-0.21	1.18
SPO2636		hypothetical protein	1.14	0.41	-2.52	0.01	-0.69	1.83	34.30	0.03	3.54	0.03	18.92	15.38	0.98	0.73	1.07	0.59	1.03	0.04
SPO2637		ferredoxin-NADP reductase (EC:1.18.1.2)	-1.31	0.31	-2.45	0.03	-1.88	0.57	7.66	0.00	2.52	0.01	5.09	2.57	1.05	0.98	1.11	0.79	1.08	0.03
SPO2638	*infC*	translation initiation factor IF-3	1.23	0.90	1.24	0.38	1.24	0.01	2.98	0.13	1.29	0.09	2.14	0.85	1.45	0.13	1.14	0.88	1.30	0.16
SPO2639		molybdopterin biosynthesis protein	0.95	0.93	1.23	0.49	1.09	0.14	-1.80	0.73	1.53	0.36	-0.14	1.67	1.82	0.09	1.45	0.25	1.64	0.19
SPO2640		XdhC/CoxI family protein	-1.58	0.05	1.12	0.50	-0.23	1.35	-3.92	0.00	1.87	0.01	-1.03	2.90	1.34	0.18	1.68	0.20	1.51	0.17
SPO2641		hypothetical protein	X	X	-1.15	0.91	N/A	N/A	-1.11	X	1.07	X	-0.02	1.09	X	X	X	X	N/A	N/A
SPO2642		hypothetical protein	1.16	0.93	-1.44	0.55	-0.14	1.30	1.48	0.17	0.99	0.91	1.24	0.24	-1.35	0.43	2.24	0.05	0.45	1.80
SPO2643		hypothetical protein	1.13	0.40	1.16	0.63	1.15	0.02	-1.16	0.29	-1.02	X	-1.09	0.07	1.22	0.25	X	X	N/A	N/A
SPO2644		von Willebrand factor A	-1.05	0.53	2.20	0.01	0.58	1.63	-2.18	0.02	1.30	0.12	-0.44	1.74	1.47	0.07	-1.08	0.78	0.20	1.28
SPO2645		S2 family protease	-2.06	0.00	-1.09	0.63	-1.58	0.48	-5.52	0.00	1.24	0.09	-2.14	3.38	-1.02	0.96	-0.96	0.33	-0.99	0.03
SPO2646		hypothetical protein	1.09	0.58	2.44	0.01	1.77	0.68	-2.19	0.00	1.28	0.06	-0.46	1.74	1.36	0.05	1.29	0.07	1.33	0.04
SPO2647		hypothetical protein	-1.55	0.30	-1.61	0.37	-1.58	0.03	1.11	0.87	-1.12	0.56	-0.01	1.12	1.07	0.91	1.08	0.93	1.08	0.01
SPO2648		hypothetical protein	-1.71	0.05	-1.62	0.08	-1.67	0.04	1.02	0.77	-1.19	0.20	-0.09	1.11	-1.04	0.73	-1.05	0.70	-1.05	0.01
SPO2649		hypothetical protein	-1.67	0.05	-1.60	0.00	-1.64	0.03	1.02	0.68	-1.24	0.20	-0.11	1.13	-1.07	0.65	-1.19	0.07	-1.13	0.06

SPO2650		FkbM family methyltransferase	-1.31	0.49	-1.22	0.20	-1.27	0.05	1.14	0.85	-1.44	0.03	-0.15	1.29	1.30	0.06	-1.20	0.45	0.05	1.25
SPO2651		glycosyl transferase family protein	2.02	0.21	1.15	0.44	1.59	0.44	1.26	0.73	1.04	0.94	1.15	0.11	-1.11	0.75	-1.09	0.74	-1.10	0.01
SPO2652		hypothetical protein	1.53	0.60	-1.02	0.87	0.26	1.28	-1.93	0.30	1.04	1.00	-0.45	1.49	-2.30	0.04	-1.65	0.10	-1.98	0.33
SPO2653		dihydroorotase (EC:3.5.2.3)	1.80	0.02	1.12	0.54	1.46	0.34	2.44	0.02	-1.11	0.28	0.67	1.78	-1.79	0.04	-1.78	0.05	-1.79	0.01
SPO2654	*pyrE*	orotate phosphoribosyltransferase (EC:2.4.2.10)	1.55	0.19	1.86	0.17	1.71	0.16	2.73	0.03	-1.29	0.04	0.72	2.01	-1.52	0.01	-1.94	0.02	-1.73	0.21
SPO2655	*dnaB*	replicative DNA helicase (EC:3.6.1.-)	-1.50	0.57	0.99	0.84	-0.25	1.25	1.13	0.70	-1.12	0.21	0.00	1.13	1.38	0.30	1.38	0.29	1.38	0.00
SPO2656		LysR family transcriptional regulator	-1.44	0.72	-1.24	0.36	-1.34	0.10	-1.80	0.57	-1.10	0.63	-1.45	0.35	-1.09	0.55	1.06	0.82	-0.02	1.08
SPO2657		D-cysteine desulfhydrase (EC:4.4.1.15)	-1.56	X	-1.45	0.84	-1.51	0.06	-1.80	0.54	-1.29	0.87	-1.55	0.26	-1.41	0.71	-1.21	X	-1.31	0.10
SPO2658	*gltI*	glutamate/aspartate ABC transporter substrate-binding protein	-1.60	0.33	-2.80	0.04	-2.20	0.60	-1.64	0.38	-2.06	0.02	-1.85	0.21	-1.29	0.16	-0.98	0.55	-1.14	0.16
SPO2659	*gltJ*	glutamate/aspartate ABC transporter permease	-1.88	0.02	-2.00	0.00	-1.94	0.06	-2.15	0.04	-1.72	0.11	-1.94	0.21	-1.54	0.03	-1.24	0.46	-1.39	0.15
SPO2660	*gltK*	glutamate/aspartate ABC transporter permease	X	X	-1.37	0.41	N/A	N/A	1.42	0.11	-1.93	0.13	-0.26	1.68	-1.37	0.13	-1.46	0.22	-1.42	0.04
SPO2661	*gltL*	glutamate/aspartate ABC transporter ATP-binding protein	X	X	-1.20	0.60	N/A	N/A	-0.94	0.21	-1.30	0.60	-1.12	0.18	-1.12	0.43	-0.98	0.61	-1.05	0.07
SPO2662		aspartate racemase	X	X	-1.07	0.87	N/A	N/A	-1.77	0.12	-1.25	0.53	-1.51	0.26	-1.18	0.48	1.08	X	-0.05	1.13
SPO2663	*aspA*	aspartate ammonia-lyase (EC:4.3.1.1)	-1.52	0.67	1.17	0.75	-0.18	1.35	-1.48	0.75	-1.03	0.99	-1.26	0.23	-1.00	0.95	1.23	0.34	0.12	1.12
SPO2664		polar amino acid ABC transporter ATP-binding protein	-1.00	0.98	-1.00	1.00	-1.00	0.00	1.15	0.72	1.21	0.72	1.18	0.03	-1.52	0.27	-1.18	0.82	-1.35	0.17
SPO2665		polar amino acid ABC transporter permease	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.40	X	X	X	N/A	N/A
SPO2666		polar amino acid ABC transporter permease	-1.44	X	-1.20	0.88	-1.32	0.12	-2.27	0.74	-1.31	0.72	-1.79	0.48	-1.08	0.96	2.19	0.07	0.56	1.64
SPO2667		polar amino acid ABC transporter substrate-binding protein	X	X	-1.24	0.20	N/A	N/A	-1.59	0.39	-1.25	X	-1.42	0.17	-1.25	0.10	1.05	X	-0.10	1.15
SPO2668		LysR family transcriptional regulator	1.83	0.37	-0.99	0.79	0.42	1.41	-1.90	0.09	1.27	0.24	-0.32	1.59	1.18	0.37	-1.20	X	-0.01	1.19
SPO2669		2OG-Fe(II) oxygenase	-1.52	0.50	-1.09	0.47	-1.31	0.21	1.21	0.66	1.62	0.08	1.42	0.21	-1.44	0.09	1.05	0.94	-0.20	1.25
SPO2670	*alr*	alanine racemase (EC:5.1.1.1)	2.00	0.03	1.01	0.93	1.51	0.50	2.50	0.00	-1.35	0.25	0.58	1.93	-1.03	0.74	-1.31	0.03	-1.17	0.14
SPO2671		hypothetical protein	1.93	0.12	1.34	0.18	1.64	0.30	3.04	0.11	-1.33	0.30	0.86	2.19	1.04	0.89	-1.41	0.09	-0.19	1.23
SPO2672		ABC transporter ATP-binding protein	1.84	0.44	-1.03	0.89	0.41	1.44	2.74	0.22	0.97	0.89	1.85	0.89	-1.03	0.88	-1.30	0.59	-1.17	0.14
SPO2673		paraquat-inducible protein A	1.43	0.04	-1.11	0.72	0.16	1.27	1.36	0.07	1.75	0.05	1.56	0.19	-1.63	0.08	-1.53	0.11	-1.58	0.05
SPO2674	*radA*	DNA repair protein RadA	1.21	0.17	1.19	0.47	1.20	0.01	1.24	0.03	-1.05	0.25	0.10	1.15	1.02	0.93	-1.08	0.20	-0.03	1.05
SPO2675		colicin V production protein CvpA	-1.21	0.06	0.99	0.78	-0.11	1.10	1.58	0.08	-1.11	0.07	0.24	1.35	-1.39	0.02	-1.42	0.03	-1.41	0.02
SPO2676		hypothetical protein	1.65	0.52	2.02	0.02	1.84	0.18	-1.16	0.86	1.90	0.07	0.37	1.53	-1.32	0.30	-1.51	0.39	-1.42	0.10
SPO2677	*purF*	amidophosphoribosyltransferase (EC:2.4.2.14)	1.80	0.01	1.65	0.03	1.73	0.08	3.25	0.01	1.14	0.53	2.20	1.06	-1.08	0.67	-1.55	0.14	-1.32	0.24
SPO2678		hypothetical protein	1.46	0.23	1.41	0.33	1.44	0.03	1.55	0.34	-1.12	0.14	0.22	1.34	2.10	0.01	1.41	0.09	1.76	0.35
SPO2679		short chain dehydrogenase/reductase oxidoreductase	1.53	0.01	1.86	0.24	1.70	0.17	4.42	0.00	-1.44	0.17	1.49	2.93	1.07	0.20	-1.39	0.48	-0.16	1.23
SPO2680		hypothetical protein	1.84	0.04	0.99	0.34	1.41	0.43	3.48	0.00	-1.04	0.30	1.22	2.26	-1.43	0.62	-1.80	0.07	-1.62	0.19
SPO2681	*tatC*	twin-arginine translocation protein TatC	1.51	0.07	-1.08	0.46	0.22	1.30	2.31	0.02	-1.17	0.15	0.57	1.74	-1.13	0.05	-1.44	0.01	-1.29	0.16
SPO2682	*tatB*	twin-arginine translocation protein TatB	0.99	0.13	-1.47	0.07	-0.24	1.23	1.59	0.09	1.03	0.75	1.31	0.28	-1.40	0.07	-1.17	0.01	-1.29	0.12
SPO2683		twin arginine-targeting protein translocase	1.28	0.39	-1.38	0.27	-0.05	1.33	1.76	0.13	1.08	0.97	1.42	0.34	1.01	0.33	1.16	0.97	1.09	0.08
SPO2684		hypothetical protein	1.04	0.65	-1.07	0.74	-0.02	1.06	1.37	0.47	1.32	0.05	1.35	0.03	1.15	0.12	-1.09	0.45	0.03	1.12
SPO2685		hypothetical protein	1.06	1.00	1.09	0.90	1.08	0.02	2.44	0.62	1.21	0.80	1.83	0.62	-1.02	0.98	-1.11	0.92	-1.07	0.05
SPO2686		LysM/M23/M37 peptidase	-1.63	0.01	-1.10	0.41	-1.37	0.27	1.43	0.03	1.01	0.76	1.22	0.21	1.15	0.08	-1.26	0.01	-0.06	1.21

SPO2687	*pcm-2*	protein-L-isoaspartate O-methyltransferase (EC:2.1.1.77)	-2.13	0.01	-1.45	0.05	-1.79	0.34	-1.75	0.01	1.88	0.01	0.06	1.82	1.04	0.93	1.18	0.75	1.11	0.07
SPO2688	*surE*	stationary phase survival protein SurE (EC:3.1.3.2)	1.30	0.24	-1.18	0.37	0.06	1.24	1.76	0.00	-1.20	0.10	0.28	1.48	-1.43	0.03	-1.49	0.02	-1.46	0.03
SPO2689		iron ABC transporter ATP-binding protein	X	X	1.32	0.18	N/A	N/A	4.45	0.00	-1.44	0.21	1.51	2.95	-1.14	0.34	-1.94	0.14	-1.54	0.40
SPO2690		hypothetical protein	1.40	0.06	1.27	0.17	1.34	0.06	2.19	0.01	-1.16	0.02	0.52	1.68	-1.12	0.11	-1.75	0.02	-1.44	0.32
SPO2691		hypothetical protein	1.30	0.60	1.02	0.95	1.16	0.14	1.74	0.30	-1.09	0.58	0.33	1.42	1.57	0.10	1.11	0.36	1.34	0.23
SPO2692		short chain dehydrogenase/reductase oxidoreductase	1.38	0.65	-1.16	0.47	0.11	1.27	1.83	0.28	1.26	0.32	1.55	0.29	-1.12	0.43	0.98	0.72	-0.07	1.05
SPO2693		hypothetical protein	-1.03	0.95	1.02	0.95	-0.01	1.03	1.04	0.84	-1.12	0.50	-0.04	1.08	1.06	0.79	-1.10	0.14	-0.02	1.08
SPO2694		cytochrome c'	-1.13	0.03	-1.21	0.03	-1.17	0.04	-1.61	0.02	1.85	0.06	0.12	1.73	-1.16	0.46	-1.08	0.23	-1.12	0.04
SPO2695		peptide chain release factor 3	-1.26	0.32	-1.06	0.10	-1.16	0.10	3.91	0.00	-1.05	0.31	1.43	2.48	-2.38	0.00	-2.65	0.01	-2.52	0.14
SPO2696		beta-lactamase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2697		acyl-CoA synthetase	-1.19	0.91	-1.24	0.78	-1.22	0.03	-1.18	0.98	-1.15	0.51	-1.17	0.02	-1.11	0.73	1.34	X	0.12	1.23
SPO2698		acyl-CoA dehydrogenase	X	X	-1.19	0.53	N/A	N/A	-1.01	0.22	-0.98	0.79	-0.99	0.02	-1.11	0.53	X	X	N/A	N/A
SPO2699		opine/polyamine ABC transporter permease	X	X	-1.37	0.61	N/A	N/A	-1.37	0.85	-1.22	0.67	-1.30	0.08	1.74	0.03	3.26	X	2.50	0.76
SPO2700		opine/polyamine ABC transporter permease	1.17	0.34	-1.03	0.98	0.07	1.10	1.41	0.44	-1.41	0.72	0.00	1.41	1.79	0.39	1.59	0.61	1.69	0.10
SPO2701		opine/polyamine ABC transporter substrate-binding protein	1.41	0.30	-1.66	0.14	-0.13	1.54	-1.26	0.98	-1.01	0.97	-1.14	0.13	1.43	0.15	1.23	X	1.33	0.10
SPO2702		opine/polyamine ABC transporter ATP-binding protein	-1.40	0.46	-2.05	0.04	-1.73	0.33	5.39	0.03	-1.30	0.40	2.05	3.35	-1.17	0.17	1.11	X	-0.03	1.14
SPO2703		hypothetical protein	-1.64	0.14	X	X	N/A	N/A	5.38	0.08	X	X	N/A	N/A	1.17	X	X	X	N/A	N/A
SPO2704		AraC family transcriptional regulator	-1.60	0.04	-1.14	0.44	-1.37	0.23	-1.14	0.51	-1.01	0.97	-1.08	0.06	-1.25	0.16	-1.32	0.66	-1.29	0.04
SPO2705		3-hydroxyacyl-CoA dehydrogenase	2.93	0.00	1.17	0.59	2.05	0.88	1.24	0.06	1.17	0.29	1.21	0.04	-1.01	0.99	-1.04	0.88	-1.03	0.02
SPO2706	*caiD-1*	carnitinyl-CoA dehydratase	1.74	0.04	1.17	0.22	1.46	0.28	4.83	0.00	1.16	0.23	3.00	1.84	-1.12	0.22	-0.96	0.47	-1.04	0.08
SPO2707		luciferase	2.80	0.07	1.36	0.19	2.08	0.72	-1.34	0.83	1.41	0.02	0.03	1.38	1.04	0.62	-0.99	0.56	0.02	1.02
SPO2708		aldehyde dehydrogenase	2.80	0.27	1.14	0.48	1.97	0.83	-2.64	0.04	1.12	0.64	-0.76	1.88	-1.39	0.10	-1.17	0.83	-1.28	0.11
SPO2709		endoribonuclease L-PSP	1.76	0.88	1.54	0.71	1.65	0.11	1.12	0.98	1.12	0.91	1.12	0.00	1.40	0.73	2.80	X	2.10	0.70
SPO2710		3-oxoadipate enol-lactonase	1.79	0.06	1.40	0.04	1.60	0.19	-1.72	0.19	1.18	0.27	-0.27	1.45	1.34	0.10	-0.92	0.52	0.21	1.13
SPO2711		CaiB/BaiF family protein	3.72	0.00	1.12	0.56	2.42	1.30	1.12	0.15	1.22	0.16	1.17	0.05	-1.00	0.91	-1.00	0.55	-1.00	0.00
SPO2712		hypothetical protein	2.66	0.04	-1.11	0.73	0.78	1.89	-1.93	0.10	1.18	0.44	-0.38	1.56	-1.24	0.49	1.04	0.84	-0.10	1.14
SPO2713	*secA*	preprotein translocase subunit SecA	-1.40	X	1.03	0.52	-0.19	1.22	-2.06	0.12	1.67	0.04	-0.20	1.87	1.20	0.04	X	X	N/A	N/A
SPO2714		M50 family peptidase	-1.40	0.12	-1.05	0.92	-1.23	0.17	-2.10	0.02	1.50	0.11	-0.30	1.80	1.04	0.82	1.15	0.28	1.10	0.05
SPO2715		GAF domain-containing protein	-1.88	0.29	1.06	0.87	-0.41	1.47	-3.09	0.17	1.47	0.44	-0.81	2.28	1.29	0.61	1.32	0.52	1.31	0.02
SPO2716		type I secretion target repeat-containing protein	-1.54	0.28	1.48	0.04	-0.03	1.51	-1.95	0.15	-1.09	0.79	-1.52	0.43	1.79	0.04	1.37	0.09	1.58	0.21
SPO2717		protein SapC protein	-1.24	0.52	1.22	0.25	-0.01	1.23	-2.79	0.13	-1.28	0.20	-2.04	0.76	1.23	0.35	1.41	0.13	1.32	0.09
SPO2718		hypothetical protein	-1.06	1.00	1.47	0.41	0.21	1.27	-1.49	0.65	-0.98	0.94	-1.23	0.26	1.30	0.61	1.26	0.45	1.28	0.02
SPO2719		hypothetical protein	-1.81	0.29	1.03	0.75	-0.39	1.42	1.09	0.18	-1.18	0.63	-0.04	1.14	1.12	0.18	-1.25	0.09	-0.06	1.19
SPO2720		hypothetical protein	-1.91	0.82	-1.41	0.83	-1.66	0.25	-3.52	0.72	1.28	0.46	-1.12	2.40	-1.08	0.92	-0.90	0.65	-0.99	0.09
SPO2721		hypothetical protein	-4.13	0.00	-1.84	0.06	-2.99	1.15	-2.85	0.00	3.02	0.00	0.09	2.94	1.43	0.06	4.03	0.00	2.73	1.30
SPO2722		hypothetical protein	-3.02	0.01	-2.04	0.00	-2.53	0.49	-1.84	0.01	2.98	0.01	0.57	2.41	1.93	0.07	6.57	0.00	4.25	2.32
SPO2723		hypothetical protein	-2.58	0.02	-1.76	0.04	-2.17	0.41	-1.92	0.04	2.28	0.05	0.18	2.10	1.50	0.31	2.25	0.07	1.88	0.38
SPO2724		hypothetical protein	-2.17	0.03	-1.69	0.02	-1.93	0.24	-1.95	0.04	1.50	0.00	-0.23	1.73	1.05	0.65	1.45	0.04	1.25	0.20

SPO2725		hypothetical protein	1.50	X	-1.89	X	-0.20	1.70	1.74	0.02	X	X	N/A	N/A	-1.14	0.76	1.27	X	0.07	1.21
SPO2726		hypothetical protein	-1.23	0.77	-1.25	0.84	-1.24	0.01	-4.59	0.08	-1.00	1.00	-2.80	1.80	-0.98	0.90	2.07	0.58	0.55	1.52
SPO2729		hypothetical protein	-1.18	0.89	-1.18	0.76	-1.18	0.00	-2.49	0.68	-1.11	0.81	-1.80	0.69	-1.11	0.87	2.08	0.20	0.49	1.60
SPO2730		hypothetical protein	-1.04	0.80	-1.15	0.93	-1.10	0.05	1.55	0.16	-1.45	X	0.05	1.50	-1.05	0.99	X	X	N/A	N/A
SPO2731		ISSpo7, transposase	X	X	1.32	0.05	N/A	N/A	1.46	X	-1.41	0.09	0.03	1.44	-1.53	0.08	-3.11	0.11	-2.32	0.79
SPO2733	*hsdM*	type I restriction-modification system, M subunit (EC:2.1.1.72)	1.73	0.01	1.35	0.15	1.54	0.19	1.69	0.01	1.02	0.82	1.36	0.34	0.99	0.67	-1.16	0.10	-0.08	1.08
SPO2734	*hsdS*	type I restriction-modification system subunit S	1.84	0.13	1.23	0.34	1.54	0.31	1.80	0.34	-1.05	0.80	0.38	1.43	-1.12	0.57	-1.26	0.42	-1.19	0.07
SPO2735	*hsdR*	type I restriction-modification system, R subunit (EC:3.1.21.3)	1.63	0.64	1.56	0.15	1.60	0.03	1.06	0.96	1.13	0.44	1.10	0.03	1.23	0.16	-1.19	0.29	0.02	1.21
SPO2736		hypothetical protein	1.35	0.71	1.38	0.11	1.37	0.01	1.81	0.40	-1.00	0.99	0.41	1.41	-1.02	0.95	-1.61	0.09	-1.32	0.30
SPO2738		lipoprotein	1.20	0.99	-1.71	0.13	-0.26	1.46	1.09	0.07	1.18	0.31	1.14	0.04	1.14	0.17	1.26	0.48	1.20	0.06
SPO2739		D-alanyl-D-alanine carboxypeptidase (EC:3.4.16.4)	-1.16	0.76	0.98	0.55	-0.09	1.07	1.16	0.61	1.71	0.05	1.44	0.27	1.93	0.01	1.93	0.05	1.93	0.00
SPO2740	*tmk*	thymidylate kinase (EC:2.7.4.9)	1.08	0.59	-1.19	0.44	-0.05	1.14	1.28	0.06	1.02	0.47	1.15	0.13	1.62	0.12	1.08	0.21	1.35	0.27
SPO2741		DNA polymerase III subunit delta' (EC:2.7.7.7)	-1.08	0.69	-1.47	0.31	-1.28	0.20	1.05	0.93	-1.03	0.85	0.01	1.04	-1.41	0.24	-1.41	0.31	-1.41	0.00
SPO2742		TatD family hydrolase	1.14	0.51	-1.09	0.77	0.02	1.12	2.10	0.04	1.05	0.96	1.58	0.52	-1.54	0.15	-1.83	0.09	-1.69	0.15
SPO2743		hypothetical protein	-1.05	0.58	1.11	0.64	0.03	1.08	1.95	0.03	-1.05	0.74	0.45	1.50	-1.66	0.13	-3.00	0.01	-2.33	0.67
SPO2744		malonate transporter	1.81	0.01	1.14	0.18	1.48	0.33	3.23	0.00	-1.02	0.78	1.11	2.13	-1.27	0.02	-1.72	0.04	-1.50	0.22
SPO2745		hypothetical protein	-1.49	0.71	1.32	0.78	-0.09	1.41	-1.17	0.92	1.17	0.88	0.00	1.17	1.17	0.87	-0.97	0.92	0.10	1.07
SPO2746		hypothetical protein	1.06	0.21	-1.25	0.13	-0.10	1.16	0.84	0.03	1.55	0.05	1.19	0.36	1.62	0.10	2.82	0.01	2.22	0.60
SPO2747		diguanylate cyclase	-1.01	1.00	-1.05	0.76	-1.03	0.02	-1.87	0.35	1.07	0.76	-0.40	1.47	-1.27	0.42	-1.07	0.94	-1.17	0.10
SPO2748		hypothetical protein	1.27	0.12	1.40	0.09	1.34	0.06	-1.37	0.26	1.19	0.47	-0.09	1.28	-1.01	0.99	-1.49	0.11	-1.25	0.24
SPO2749		hypothetical protein	-1.02	0.41	-1.24	0.52	-1.13	0.11	1.02	0.50	1.08	0.47	1.05	0.03	1.04	0.76	-1.04	0.96	0.00	1.04
SPO2750		trimethylamine methyltransferase	4.96	0.03	2.83	0.01	3.90	1.07	-2.57	0.11	-1.12	0.63	-1.85	0.73	1.32	0.30	-1.17	0.70	0.08	1.25
SPO2751		HAD-superfamily hydrolase	1.93	0.84	1.58	0.34	1.76	0.18	2.25	0.76	-1.07	0.64	0.59	1.66	1.29	0.27	1.07	0.89	1.18	0.11
SPO2752		hypothetical protein	1.60	0.06	1.13	0.57	1.37	0.24	2.69	0.01	-1.14	0.04	0.78	1.92	-1.49	0.05	-2.09	0.08	-1.79	0.30
SPO2753		diguanylate cyclase,/response regulator	1.60	0.06	1.03	0.91	1.32	0.29	1.70	0.04	1.59	0.13	1.65	0.05	-1.20	0.29	2.18	0.08	0.49	1.69
SPO2754		hypothetical protein	1.34	0.76	1.48	0.30	1.41	0.07	1.38	0.72	1.05	0.91	1.22	0.17	1.48	0.21	-0.98	0.77	0.25	1.23
SPO2755		hypothetical protein	-1.23	0.30	-1.15	0.27	-1.19	0.04	1.97	0.01	1.06	0.89	1.52	0.46	-1.26	0.19	1.87	0.04	0.31	1.57
SPO2756		RNA polymerase sigma factor	1.13	0.74	1.40	0.43	1.27	0.14	-0.97	0.78	-1.02	0.95	-1.00	0.03	-1.10	0.65	-1.43	0.34	-1.27	0.16
SPO2757		EF hand domain-containing protein	-1.36	0.02	1.00	0.99	-0.18	1.18	-2.26	0.00	1.05	0.69	-0.61	1.66	-1.00	1.00	1.34	0.05	0.17	1.17
SPO2758		hypothetical protein	8.02	0.05	3.69	0.00	5.86	2.17	7.74	0.00	1.55	0.03	4.65	3.10	1.84	0.06	1.67	0.08	1.76	0.09
SPO2759		NUDIX family hydrolase	2.86	0.03	2.49	0.00	2.68	0.19	2.79	0.02	1.94	0.03	2.37	0.42	1.09	0.63	-1.00	0.95	0.05	1.04
SPO2760		metallo-beta-lactamase	-1.70	0.63	1.20	0.47	-0.25	1.45	1.21	0.66	1.12	0.21	1.17	0.04	1.04	0.97	1.05	0.90	1.05	0.01
SPO2761		pantothenate kinase (EC:2.7.1.33)	1.10	0.80	1.15	0.76	1.13	0.02	2.09	0.11	-1.08	0.79	0.51	1.59	-1.47	0.47	-1.83	0.23	-1.65	0.18
SPO2762		biotin--acetyl-CoA-carboxylase ligase (EC:6.3.4.15)	1.32	0.31	1.18	0.22	1.25	0.07	2.81	0.03	1.07	0.93	1.94	0.87	-1.10	0.62	-1.56	0.10	-1.33	0.23
SPO2763	*nuoN*	NADH dehydrogenase subunit N (EC:1.6.5.3)	2.08	0.01	1.04	0.92	1.56	0.52	4.02	0.02	-1.56	0.04	1.23	2.79	-1.09	0.54	-1.55	0.00	-1.32	0.23
SPO2764	*nuoM*	NADH dehydrogenase subunit M (EC:1.6.5.3)	1.68	0.05	1.11	0.66	1.40	0.29	3.08	0.02	-1.08	0.46	1.00	2.08	1.02	0.90	0.99	0.60	1.00	0.02
SPO2765	*nuoL*	NADH dehydrogenase subunit L (EC:1.6.99.5)	1.86	0.08	1.12	0.10	1.49	0.37	2.85	0.01	-1.35	0.03	0.75	2.10	-1.15	0.10	-1.59	0.01	-1.37	0.22
SPO2766	*nuoK*	NADH dehydrogenase subunit	2.17	0.07	1.19	0.61	1.68	0.49	3.36	0.02	-1.07	0.47	1.15	2.22	1.18	0.51	0.95	0.29	1.07	0.11

SPO2767	*nuoJ*	NADH dehydrogenase subunit J (EC:1.6.5.3)	1.24	0.44	-1.06	0.37	0.09	1.15	2.32	0.02	1.14	0.57	1.73	0.59	1.03	0.77	0.95	0.09	0.99	0.04
SPO2768		4-carboxymuconolactone decarboxylase	1.47	0.00	1.22	0.34	1.35	0.13	2.92	0.01	1.25	0.40	2.09	0.84	0.98	0.29	0.98	0.39	0.98	0.00
SPO2769		hypothetical protein	1.09	0.89	1.29	0.15	1.19	0.10	1.81	0.12	-1.17	0.52	0.32	1.49	-1.04	0.40	-1.29	0.03	-1.17	0.13
SPO2770	*nuoI*	NADH dehydrogenase subunit I (EC:1.6.5.3)	2.46	0.17	1.27	0.34	1.87	0.60	3.43	0.07	1.34	0.13	2.39	1.05	-1.12	0.42	-1.22	0.07	-1.17	0.05
SPO2771		hypothetical protein	2.16	0.13	-1.22	0.40	0.47	1.69	2.70	0.07	1.05	0.69	1.88	0.83	-1.52	0.04	-1.56	0.03	-1.54	0.02
SPO2772	*nuoH*	NADH dehydrogenase subunit H (EC:1.6.5.3)	2.42	0.05	1.02	0.97	1.72	0.70	3.30	0.05	1.04	0.85	2.17	1.13	-1.26	0.17	-1.47	0.13	-1.37	0.11
SPO2773		lipoprotein	1.22	0.98	1.93	0.01	1.58	0.36	1.29	0.95	1.14	0.71	1.22	0.08	-1.11	0.16	-1.44	0.06	-1.28	0.17
SPO2774	*nuoG*	NADH dehydrogenase subunit G (EC:1.6.5.3)	0.92	0.44	1.59	0.02	1.26	0.33	1.28	0.28	-1.07	0.54	0.11	1.18	1.02	0.90	-1.34	0.02	-0.16	1.18
SPO2775		hypothetical protein	1.14	0.70	1.03	0.92	1.09	0.05	1.97	0.09	0.99	0.65	1.48	0.49	-1.33	0.32	-1.73	0.01	-1.53	0.20
SPO2776		hypothetical protein	1.61	0.01	1.26	0.19	1.44	0.18	3.67	0.01	0.99	0.51	2.33	1.34	-1.16	0.19	-1.65	0.02	-1.41	0.25
SPO2777	*nuoF*	NADH dehydrogenase I subunit F (EC:1.6.99.5)	1.56	0.01	1.18	0.45	1.37	0.19	2.69	0.02	1.10	0.70	1.90	0.80	-1.23	0.10	-1.19	0.13	-1.21	0.02
SPO2778		hypothetical protein	1.10	0.81	1.07	0.82	1.09	0.02	1.93	0.02	-1.07	0.19	0.43	1.50	-1.56	0.03	-1.71	0.02	-1.64	0.08
SPO2779		hypothetical protein	-1.47	0.68	1.34	0.28	-0.06	1.41	0.92	0.22	1.50	0.11	1.21	0.29	-1.33	0.26	-1.28	0.06	-1.31	0.03
SPO2780	*nuoE*	NADH dehydrogenase subunit E (EC:1.6.5.3)	1.56	0.10	-1.11	0.14	0.23	1.34	2.63	0.01	-1.12	0.02	0.76	1.88	-1.10	0.41	0.98	0.44	-0.06	1.04
SPO2781		lipoprotein	1.25	0.39	1.28	0.55	1.27	0.02	1.84	0.03	1.20	0.14	1.52	0.32	1.10	0.17	-1.10	0.39	0.00	1.10
SPO2782	*nuoD*	NADH dehydrogenase subunit D (EC:1.6.5.3)	1.30	0.72	0.99	0.73	1.15	0.15	3.03	0.08	-1.13	0.46	0.95	2.08	-1.05	0.73	0.96	0.48	-0.05	1.01
SPO2783		hypothetical protein	-1.15	0.82	1.61	0.00	0.23	1.38	2.63	0.01	-1.49	0.02	0.57	2.06	1.65	0.00	0.97	0.40	1.31	0.34
SPO2784	*nuoC*	NADH dehydrogenase subunit C (EC:1.6.5.3)	1.30	0.22	1.23	0.27	1.27	0.04	3.04	0.01	-1.23	0.08	0.91	2.14	1.21	0.19	-1.25	0.09	-0.02	1.23
SPO2785	*nuoB*	NADH dehydrogenase subunit B (EC:1.6.5.3)	1.37	0.09	1.09	0.79	1.23	0.14	2.77	0.01	1.21	0.25	1.99	0.78	-1.07	0.96	1.05	0.40	-0.01	1.06
SPO2786	*nuoA*	NADH dehydrogenase subunit A (EC:1.6.5.3)	1.43	0.10	1.05	0.97	1.24	0.19	3.42	0.02	-1.09	0.10	1.17	2.26	1.21	0.26	0.92	0.20	1.07	0.14
SPO2787		enoyl-CoA hydratase (EC:4.2.1.17)	-1.04	0.14	1.22	0.50	0.09	1.13	-1.41	0.17	1.34	0.16	-0.03	1.38	-1.02	0.90	-1.00	1.00	-1.01	0.01
SPO2788	*mvaB*	hydroxymethylglutaryl-CoA lyase (EC:4.1.3.4)	1.10	0.50	1.37	0.07	1.24	0.14	-1.89	0.00	1.36	0.06	-0.27	1.63	1.07	0.56	1.01	0.93	1.04	0.03
SPO2789	*mccA*	methylcrotonyl-CoA carboxylase subunit alpha (EC:6.4.1.4)	1.23	0.46	1.17	0.11	1.20	0.03	-1.45	0.23	1.22	0.52	-0.12	1.34	1.23	0.14	1.11	0.27	1.17	0.06
SPO2790	*mccB*	methylcrotonyl-CoA carboxylase subunit beta (EC:6.4.1.4)	0.97	0.09	-1.12	0.44	-0.08	1.04	-2.51	0.00	1.10	0.33	-0.71	1.81	-1.16	0.13	-1.08	0.92	-1.12	0.04
SPO2791	*acsA*	acetyl-coenzyme A synthetase (EC:6.2.1.1)	-1.89	0.03	-1.23	0.35	-1.56	0.33	-2.20	0.07	-1.16	0.32	-1.68	0.52	-1.04	0.94	-1.31	0.60	-1.18	0.14
SPO2792	*ompW*	outer membrane protein OmpW	1.52	X	3.38	0.21	2.45	0.93	8.08	0.03	1.19	0.83	4.64	3.45	-0.98	0.94	1.82	X	0.42	1.40
SPO2793	*ivD*	isovaleryl-CoA dehydrogenase (EC:1.3.99.10)	1.26	0.58	-1.25	0.46	0.01	1.26	-1.96	0.12	1.16	0.52	-0.40	1.56	1.12	0.59	1.48	0.21	1.30	0.18
SPO2794		hypothetical protein	-2.36	0.25	-1.15	0.56	-1.76	0.61	-3.57	0.01	-0.99	0.90	-2.28	1.29	-1.06	0.89	1.76	0.04	0.35	1.41
SPO2795		aminotransferase	-2.20	0.17	1.23	0.73	-0.49	1.72	-1.34	0.42	1.27	0.60	-0.04	1.31	1.25	0.50	1.16	0.84	1.21	0.05
SPO2796	*gph-2*	phosphoglycolate phosphatase (EC:3.1.3.18)	1.37	0.79	1.60	0.17	1.49	0.12	2.22	0.54	-1.49	0.21	0.37	1.86	1.11	0.71	-1.30	0.28	-0.10	1.21
SPO2797	*glmU*	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase (EC:2.7.7.23)	1.03	0.82	-1.21	0.35	-0.09	1.12	3.75	0.00	-1.53	0.01	1.11	2.64	-1.29	0.05	-1.42	0.14	-1.36	0.06
SPO2798		hypothetical protein	1.54	0.07	-1.03	0.75	0.26	1.29	3.90	0.01	-1.09	0.27	1.41	2.50	0.99	0.83	-1.12	0.47	-0.07	1.05
SPO2799	*moaA*	molybdenum cofactor biosynthesis protein A	1.24	0.56	-1.59	0.23	-0.18	1.42	2.04	0.03	-1.12	0.51	0.46	1.58	-1.12	0.46	-1.12	0.69	-1.12	0.00
SPO2800	*kdtA*	3-deoxy-D-manno-octulosonic acid transferase (EC:2.-.-.-)	-0.95	0.40	-1.23	0.03	-1.09	0.14	3.50	0.01	1.02	1.00	2.26	1.24	-1.18	0.21	-1.66	0.04	-1.42	0.24
SPO2801	*lpcC*	lipopolysaccharide core biosynthesis mannosyltransferase (EC:2.4.1.-)	1.25	0.62	1.33	0.24	1.29	0.04	1.61	0.32	1.30	0.29	1.46	0.16	1.37	0.15	-1.05	0.95	0.16	1.21
SPO2802		bmp family protein	-3.77	0.00	-2.60	0.01	-3.19	0.58	-14.60	0.00	-2.11	0.01	-8.36	6.25	1.31	0.14	1.22	0.24	1.27	0.05

SPO2803		sugar ABC transporter ATP-binding protein	-4.18	0.00	-1.92	0.09	-3.05	1.13	-8.66	0.00	-1.47	0.17	-5.07	3.60	1.13	0.25	1.29	0.17	1.21	0.08
SPO2804		sugar ABC transporter permease	X	X	-1.69	0.23	N/A	N/A	-4.37	X	X	X	N/A	N/A	1.28	0.13	X	X	N/A	N/A
SPO2805		sugar ABC transporter permease	-2.61	0.02	-1.31	0.34	-1.96	0.65	-3.37	0.01	-1.27	0.38	-2.32	1.05	1.12	0.87	2.63	0.19	1.88	0.75
SPO2806		cytosine deaminase (EC:3.5.4.1)	-1.68	0.56	-1.12	0.61	-1.40	0.28	-1.87	0.35	1.08	0.70	-0.40	1.48	1.11	0.53	1.29	0.37	1.20	0.09
SPO2807		hypothetical protein	-1.22	0.42	1.23	0.33	0.01	1.23	-1.15	0.31	1.34	0.06	0.10	1.25	1.15	0.20	1.19	X	1.17	0.02
SPO2808		amidohydrolase	1.22	0.22	-1.49	0.05	-0.14	1.36	1.22	0.85	1.46	0.04	1.34	0.12	1.15	0.43	1.54	0.10	1.35	0.20
SPO2809		amidohydrolase	1.09	0.56	-1.57	0.09	-0.24	1.33	0.96	0.46	1.65	0.12	1.30	0.35	-1.04	0.79	1.46	0.32	0.21	1.25
SPO2810		amidohydrolase	1.07	0.78	-1.16	0.59	-0.04	1.12	1.32	0.05	2.17	0.00	1.75	0.43	1.02	0.94	1.10	0.33	1.06	0.04
SPO2811		amidohydrolase	-1.07	0.76	-1.61	0.04	-1.34	0.27	0.84	0.16	1.62	0.01	1.23	0.39	1.35	0.20	1.45	0.08	1.40	0.05
SPO2812	*argE-1*	acetylornithine deacetylase (EC:3.5.1.16)	1.19	0.29	1.08	0.50	1.14	0.05	1.21	0.34	1.45	0.06	1.33	0.12	1.28	0.04	1.32	0.15	1.30	0.02
SPO2813		peptide/nickel/opine uptake ABC transporter ATP-binding protein	-1.17	0.16	-1.03	0.50	-1.10	0.07	-1.37	0.02	1.25	0.12	-0.06	1.31	1.23	0.17	1.33	0.04	1.28	0.05
SPO2814		peptide/opine/nickel uptake ABC transporter substrate-binding protein	-2.25	0.00	-2.67	0.03	-2.46	0.21	-1.81	0.01	1.76	0.06	-0.03	1.79	1.65	0.07	3.36	0.02	2.51	0.86
SPO2815		peptide/nickel/opine uptake ABC transporter permease	-1.31	0.73	-1.39	0.19	-1.35	0.04	-1.38	0.13	2.21	0.03	0.42	1.80	-1.18	0.15	1.37	0.35	0.10	1.28
SPO2816		peptide/nickel/opine uptake ABC transporter permease	-1.63	0.34	1.60	0.49	-0.01	1.62	-1.13	0.68	1.41	0.57	0.14	1.27	2.62	0.15	1.70	0.53	2.16	0.46
SPO2817		hypothetical protein	-0.96	0.30	-3.60	0.01	-2.28	1.32	19.30	0.00	1.92	0.01	10.61	8.69	-1.38	0.13	1.10	0.82	-0.14	1.24
SPO2818		hypothetical protein	-1.88	0.19	1.20	0.33	-0.34	1.54	-1.20	0.78	-1.69	0.12	-1.45	0.25	1.35	0.11	-1.10	0.97	0.13	1.23
SPO2819	*pntB*	NAD(P) transhydrogenase subunit beta (EC:1.6.1.1)	1.80	0.23	1.67	0.02	1.74	0.07	1.82	0.22	1.35	0.16	1.59	0.24	-1.25	0.12	-1.45	0.03	-1.35	0.10
SPO2820	*pntA*	NAD(P) transhydrogenase subunit alpha (EC:1.6.1.2)	1.91	0.17	1.78	0.03	1.85	0.06	1.74	0.05	1.76	0.04	1.75	0.01	1.34	0.06	1.65	0.01	1.50	0.16
SPO2821		isoprenylcysteine carboxyl methyltransferase	2.06	0.01	1.20	0.16	1.63	0.43	5.36	0.01	1.24	0.02	3.30	2.06	-1.91	0.01	-2.05	0.03	-1.98	0.07
SPO2822		soxH protein-like protein	1.81	0.08	-1.25	0.77	0.28	1.53	1.20	0.18	1.41	0.56	1.31	0.11	-1.07	0.94	1.13	0.69	0.03	1.10
SPO2823	*bdh-2*	D-beta-hydroxybutyrate dehydrogenase (EC:1.1.1.30)	2.15	0.02	-1.39	0.07	0.38	1.77	-2.82	0.01	1.95	0.02	-0.44	2.39	1.29	0.23	3.27	0.01	2.28	0.99
SPO2824	*kynU*	kynureninase (EC:3.7.1.3)	1.35	0.81	1.32	0.66	1.34	0.02	1.12	0.81	-1.61	0.45	-0.25	1.37	-1.11	0.84	-1.19	0.83	-1.15	0.04
SPO2825		TetR family transcriptional regulator	-3.00	0.00	-1.48	0.01	-2.24	0.76	-1.57	0.04	-1.39	0.03	-1.48	0.09	1.37	0.03	1.61	0.02	1.49	0.12
SPO2826	*iorA*	isoquinoline 1-oxidoreductase subunit alpha (EC:1.3.99.16)	-1.70	0.70	-1.46	0.03	-1.58	0.12	-1.76	0.66	-1.10	0.50	-1.43	0.33	1.20	0.33	1.94	0.03	1.57	0.37
SPO2827		isoquinoline 1-oxidoreductase subunit beta	-2.21	0.03	-1.40	0.15	-1.81	0.41	-1.08	0.93	-1.23	0.30	-1.16	0.08	1.29	0.08	1.50	0.07	1.40	0.11
SPO2828		type I secretion target repeat-containing protein	1.05	0.74	1.02	0.79	1.04	0.02	-1.58	0.07	-1.13	0.32	-1.36	0.23	-1.99	0.01	-1.45	0.12	-1.72	0.27
SPO2829		dipeptidase domain-containing protein	-1.17	0.81	1.08	0.83	-0.04	1.13	1.18	0.57	1.06	0.82	1.12	0.06	-1.08	0.94	-1.22	0.79	-1.15	0.07
SPO2830		hypothetical protein	-2.35	0.00	-1.31	0.35	-1.83	0.52	-4.65	0.00	-1.04	0.93	-2.85	1.81	-1.43	0.35	1.91	0.25	0.24	1.67
SPO2831		oligopeptide ABC transporter ATP-binding protein	-1.03	X	-1.10	0.57	-1.07	0.04	-1.09	0.46	-0.98	0.72	-1.04	0.05	-1.04	0.90	X	X	N/A	N/A
SPO2832		dipeptide ABC transporter ATP-binding protein	1.41	X	1.18	X	1.30	0.12	-0.89	0.86	-1.10	X	-0.99	0.11	-1.02	0.94	X	X	N/A	N/A
SPO2833		dipeptide ABC transporter permease	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2834		dipeptide ABC transporter permease	X	X	-1.40	0.27	N/A	N/A	2.10	0.11	-1.04	0.98	0.53	1.57	-1.38	0.47	-1.05	0.49	-1.22	0.17
SPO2835		dipeptide ABC transporter substrate-binding protein	-1.74	X	-1.69	0.01	-1.72	0.03	3.32	0.01	1.12	0.13	2.22	1.10	-1.24	0.24	-1.28	0.50	-1.26	0.02
SPO2836		DNA-binding protein	-2.79	X	-1.32	0.08	-2.06	0.74	-0.94	0.64	-1.26	0.16	-1.10	0.16	1.35	0.10	-1.06	0.75	0.15	1.21
SPO2837		hypothetical protein	-2.67	0.00	-1.38	0.21	-2.03	0.64	-1.87	0.01	1.40	0.13	-0.24	1.64	1.32	0.09	1.07	0.81	1.20	0.13

SPO2838		hypothetical protein	1.96	0.77	-1.06	0.90	0.45	1.51	1.38	0.90	1.79	0.31	1.59	0.20	1.06	0.86	-1.13	0.82	-0.03	1.10
SPO2839	*glcB*	malate synthase G (EC:2.3.3.9)	2.69	0.00	-1.43	0.02	0.63	2.06	1.58	0.06	2.44	0.05	2.01	0.43	-1.11	0.33	-1.81	0.02	-1.46	0.35
SPO2840		diguanylate cyclase	-1.31	0.27	-1.30	0.64	-1.31	0.01	-2.25	0.04	1.23	0.71	-0.51	1.74	-1.06	0.38	1.38	0.11	0.16	1.22
SPO2841	*pepN*	aminopeptidase (EC:3.4.11.2)	1.36	0.08	1.17	0.07	1.27	0.10	1.20	0.16	1.03	0.93	1.12	0.09	1.13	0.18	1.59	0.01	1.36	0.23
SPO2842		short chain dehydrogenase/reductase oxidoreductase	1.44	0.11	1.07	0.42	1.26	0.19	2.13	0.01	1.31	0.06	1.72	0.41	-1.13	0.44	1.02	0.97	-0.05	1.08
SPO2843		hypothetical protein	-1.35	0.55	-1.20	0.55	-1.28	0.08	1.26	0.26	1.48	0.06	1.37	0.11	-1.13	0.18	1.35	0.20	0.11	1.24
SPO2844		hypothetical protein	-3.26	0.17	-1.35	0.36	-2.31	0.96	-5.43	0.07	1.14	0.69	-2.15	3.29	-1.09	0.85	1.89	0.26	0.40	1.49
SPO2845		hypothetical protein	1.30	0.54	1.40	0.42	1.35	0.05	-1.37	0.44	-1.15	0.68	-1.26	0.11	1.04	0.97	-1.17	0.30	-0.06	1.11
SPO2846		hypothetical protein	-1.51	0.18	1.13	0.38	-0.19	1.32	-1.83	0.25	-1.14	0.63	-1.49	0.35	-1.04	0.84	-1.02	X	-1.03	0.01
SPO2847	*gatB*	aspartyl/glutamyl-tRNA amidotransferase subunit B (EC:6.3.5.-)	1.36	0.88	1.68	0.15	1.52	0.16	2.23	0.35	-1.19	0.22	0.52	1.71	1.14	0.67	-1.12	0.40	0.01	1.13
SPO2848		hypothetical protein	-1.07	0.28	-1.78	0.02	-1.43	0.36	2.65	0.00	-1.22	0.08	0.72	1.94	-1.31	0.11	-1.22	0.04	-1.27	0.05
SPO2849		BolA protein, truncation	1.25	0.71	1.39	0.71	1.32	0.07	-1.35	0.10	1.11	0.93	-0.12	1.23	1.77	0.54	1.25	0.63	1.51	0.26
SPO2850		DnaJ domain-containing protein	-1.62	0.01	-1.47	0.03	-1.55	0.08	1.10	0.40	0.96	0.27	1.03	0.07	-1.24	0.00	-1.41	0.04	-1.33	0.09
SPO2851		hypothetical protein	-1.95	X	-1.10	0.94	-1.53	0.43	-1.22	0.97	-1.06	0.95	-1.14	0.08	1.24	0.83	1.27	0.72	1.26	0.02
SPO2852		CzcN domain-containing protein	X	X	-1.18	0.22	N/A	N/A	-0.92	0.03	-1.33	0.23	-1.13	0.20	-1.22	0.16	X	X	N/A	N/A
SPO2853		cobalt chelatase, CobS subunit (EC:6.6.1.2)	1.58	0.06	1.07	0.33	1.33	0.25	5.48	0.00	-1.16	0.11	2.16	3.32	1.20	0.21	0.97	0.09	1.09	0.11
SPO2854	*nucH*	thermonuclease (EC:3.1.31.1)	-1.55	0.07	1.12	0.59	-0.22	1.34	2.29	0.01	1.06	0.91	1.68	0.62	-1.20	0.21	-1.36	0.06	-1.28	0.08
SPO2855		cobalt chelatase large subunit	-2.00	0.01	1.19	0.34	-0.41	1.60	1.12	0.56	1.19	0.15	1.16	0.03	-1.05	0.64	-1.30	0.01	-1.18	0.13
SPO2856		hypothetical protein	-1.48	0.01	-1.27	0.34	-1.38	0.11	-1.43	0.08	1.40	0.11	-0.02	1.42	1.05	0.75	1.20	0.37	1.13	0.08
SPO2857		M24 family metallopeptidase	2.19	0.15	-1.31	0.31	0.44	1.75	2.64	0.12	1.26	0.22	1.95	0.69	-1.12	0.61	1.05	0.89	-0.04	1.09
SPO2858		hypothetical protein	2.97	0.05	1.70	0.06	2.34	0.64	2.41	0.02	1.45	0.03	1.93	0.48	1.87	0.02	1.19	0.19	1.53	0.34
SPO2859		3-hydroxyisobutyrate dehydrogenase	3.20	0.04	-1.16	0.36	1.02	2.18	-2.07	0.14	-1.04	0.92	-1.56	0.52	-0.98	0.71	-1.02	0.54	-1.00	0.02
SPO2860		LysR family transcriptional regulator	-2.13	X	-1.42	0.10	-1.78	0.36	-1.31	0.88	-1.62	0.37	-1.47	0.16	-1.11	0.49	-1.50	0.12	-1.31	0.19
SPO2861		hypothetical protein	1.33	0.63	1.25	0.48	1.29	0.04	1.29	0.73	1.15	0.41	1.22	0.07	-1.70	0.02	-1.91	0.00	-1.81	0.11
SPO2862	*cobW*	CobW	2.18	0.00	1.56	0.18	1.87	0.31	4.26	0.00	-1.11	0.16	1.58	2.69	-1.18	0.18	-1.68	0.11	-1.43	0.25
SPO2863	*cobN*	cobaltochelatase subunit CobN (EC:6.6.1.2)	1.27	0.69	1.36	0.08	1.32	0.05	-1.15	0.82	-1.06	0.23	-1.11	0.04	-1.12	0.29	-1.30	0.38	-1.21	0.09
SPO2864	*cobG*	CobG	1.74	0.01	1.13	0.64	1.44	0.31	3.74	0.00	1.12	0.17	2.43	1.31	-1.96	0.01	-2.50	0.00	-2.23	0.27
SPO2865	*cobH*	precorrin-8X methylmutase (EC:5.4.1.2)	1.15	0.95	1.58	0.03	1.37	0.22	1.21	0.84	-1.23	0.10	-0.01	1.22	-1.71	0.01	-2.21	0.02	-1.96	0.25
SPO2866	*cobI*	precorrin-2 C(20)-methyltransferase (EC:2.1.1.130)	1.89	0.17	1.43	0.14	1.66	0.23	2.68	0.06	-1.67	0.03	0.51	2.18	-1.46	0.03	-2.34	0.03	-1.90	0.44
SPO2867	*cobJ*	precorrin-3B C(17)-methyltransferase (EC:2.1.1.131)	1.06	0.87	1.50	0.25	1.28	0.22	4.92	0.17	-1.29	0.07	1.82	3.11	-1.28	0.07	-2.15	0.00	-1.72	0.44
SPO2868	*cobK*	cobalt-precorrin-6x reductase (EC:1.3.1.54)	-1.40	0.65	1.06	0.69	-0.17	1.23	-1.39	0.69	-1.22	0.24	-1.31	0.09	-1.37	0.11	-1.25	0.32	-1.31	0.06
SPO2869	*cobL*	precorrin-6Y C5,15-methyltransferase (EC:2.1.1.132)	1.65	0.88	1.48	0.45	1.57	0.09	2.49	0.72	-1.13	0.49	0.68	1.81	-1.04	0.79	-1.12	0.75	-1.08	0.04
SPO2870		cobalamin biosynthesis domain-containing protein	1.36	0.89	1.37	0.13	1.37	0.01	2.33	0.63	-1.10	0.53	0.62	1.72	-1.69	0.07	-2.25	0.05	-1.97	0.28
SPO2871	*cobM*	precorrin-4 C(11)-methyltransferase (EC:2.1.1.133)	1.73	0.06	1.61	0.03	1.67	0.06	2.78	0.00	-1.25	0.20	0.77	2.02	-1.21	0.17	-2.00	0.02	-1.61	0.40
SPO2872	*cobB*	cobyrinic acid a,c-diamide synthase	1.65	0.32	1.73	0.04	1.69	0.04	2.48	0.03	-1.49	0.02	0.50	1.99	-1.15	0.35	-2.20	0.01	-1.68	0.53
SPO2873	*cobA-2*	uroporphyrin-III C-methyltransferase (EC:2.1.1.107)	2.19	0.78	1.47	0.07	1.83	0.36	2.83	0.63	-1.24	0.43	0.80	2.04	-1.14	0.39	-1.71	0.12	-1.43	0.29
SPO2874	*cobF*	precorrin 6A synthase (EC:2.1.1.152)	1.27	0.18	1.57	0.04	1.42	0.15	2.18	0.02	-1.34	0.06	0.42	1.76	-1.18	0.11	-2.18	0.04	-1.68	0.50

SPO2875		hypothetical protein	1.59	0.04	1.08	0.92	1.34	0.26	1.09	0.01	1.53	0.08	1.31	0.22	1.35	0.20	2.21	0.08	1.78	0.43
SPO2876		hypothetical protein	2.04	0.22	1.54	0.29	1.79	0.25	1.13	0.58	2.68	0.01	1.91	0.78	1.29	0.37	1.66	0.10	1.48	0.18
SPO2877		hypothetical protein	2.60	0.01	1.33	0.34	1.97	0.64	2.32	0.04	1.60	0.02	1.96	0.36	1.14	0.03	1.25	0.20	1.20	0.06
SPO2878		hypothetical protein	1.67	0.02	1.42	0.03	1.55	0.13	3.53	0.00	-1.08	0.38	1.23	2.31	-1.11	0.28	-1.47	0.01	-1.29	0.18
SPO2879		LysR family transcriptional regulator	-1.54	0.01	-1.22	0.01	-1.38	0.16	-1.03	0.62	1.02	0.82	-0.01	1.03	1.09	0.59	-1.02	0.69	0.04	1.06
SPO2880		L-aspartate dehydrogenase (EC:1.4.1.21)	1.09	X	1.09	0.57	1.09	0.00	-1.32	0.96	1.14	0.70	-0.09	1.23	1.26	0.06	-1.16	0.91	0.05	1.21
SPO2881		xanthine dehydrogenase, large subunit	1.80	0.00	-1.10	0.86	0.35	1.45	-1.51	0.19	1.21	X	-0.15	1.36	-1.13	0.59	X	X	N/A	N/A
SPO2882		dihydrodipicolinate synthase	-1.26	0.73	-1.02	1.00	-1.14	0.12	-2.75	0.26	1.11	0.88	-0.82	1.93	-1.09	0.93	1.40	0.48	0.16	1.25
SPO2883		hypothetical protein	1.14	0.32	-1.02	0.87	0.06	1.08	1.69	0.02	1.16	0.21	1.43	0.27	1.16	0.40	-1.05	0.68	0.05	1.11
SPO2884		hypothetical protein	-1.09	0.78	-1.07	0.90	-1.08	0.01	-3.62	0.04	1.05	0.93	-1.29	2.34	-1.22	0.75	-0.98	0.78	-1.10	0.12
SPO2885		acetolactate synthase, catabolic	1.34	0.04	1.56	0.12	1.45	0.11	1.83	0.02	1.13	0.20	1.48	0.35	-1.58	0.00	-2.04	0.02	-1.81	0.23
SPO2886		CAIB/BAIF family protein	2.30	0.21	1.47	0.03	1.89	0.42	2.46	0.02	1.12	0.55	1.79	0.67	1.23	0.14	-1.13	0.20	0.05	1.18
SPO2887		hypothetical protein	1.42	0.06	-1.16	0.10	0.13	1.29	1.09	0.99	-1.44	0.08	-0.18	1.27	-1.81	0.02	-1.91	0.04	-1.86	0.05
SPO2888		hypothetical protein	1.44	0.23	1.04	0.92	1.24	0.20	2.39	0.03	-1.75	0.02	0.32	2.07	1.23	0.32	-1.50	0.04	-0.14	1.37
SPO2889	*mdoG*	glucan biosynthesis protein G	1.11	0.24	-1.24	0.38	-0.06	1.18	2.09	0.00	-1.54	0.01	0.28	1.82	-1.42	0.14	-1.53	0.02	-1.48	0.06
SPO2890		glucosyltransferase MdoH	1.76	0.14	1.32	0.19	1.54	0.22	2.24	0.01	1.04	0.92	1.64	0.60	1.92	0.01	2.15	0.02	2.04	0.12
SPO2891		hypothetical protein	1.00	0.97	1.56	0.33	1.28	0.28	2.00	0.77	-1.15	0.69	0.43	1.58	1.44	0.04	1.19	0.34	1.32	0.13
SPO2892		hypothetical protein	1.20	0.89	1.64	0.15	1.42	0.22	1.34	0.78	1.04	0.95	1.19	0.15	1.76	0.12	1.26	0.29	1.51	0.25
SPO2893	*phaA*	monovalent cation/H+ antiporter subunit A	1.08	0.78	-1.25	0.04	-0.09	1.17	1.66	0.18	1.09	0.81	1.38	0.29	1.34	0.14	1.78	0.10	1.56	0.22
SPO2894	*phaC*	monovalent cation/H+ antiporter subunit C	1.06	0.93	1.15	0.71	1.11	0.04	1.87	0.11	-1.10	0.29	0.39	1.49	1.51	0.08	1.22	0.55	1.37	0.15
SPO2895	*phaD*	monovalent cation/H+ antiporter subunit D	1.11	0.67	-1.16	0.28	-0.02	1.14	1.91	0.01	-1.10	0.18	0.41	1.51	1.33	0.02	1.22	0.23	1.28	0.06
SPO2896	*phaE*	monovalent cation/H+ antiporter subunit E	-1.13	0.46	-1.12	0.17	-1.13	0.00	1.26	0.76	1.16	0.57	1.21	0.05	1.38	0.01	1.60	0.06	1.49	0.11
SPO2897	*phaF*	monovalent cation/H+ antiporter subunit F	1.26	0.20	-1.22	0.29	0.02	1.24	1.65	0.08	1.40	0.02	1.53	0.13	-1.12	0.13	0.99	0.60	-0.07	1.05
SPO2898	*phaG*	monovalent cation/H+ antiporter subunit G	1.01	0.67	-1.55	0.13	-0.27	1.28	1.03	0.71	1.30	0.50	1.17	0.14	-1.23	0.38	1.43	0.31	0.10	1.33
SPO2899		selenide,water dikinase	-1.43	0.59	1.08	0.85	-0.18	1.26	1.36	0.33	1.19	0.45	1.28	0.09	1.37	0.32	1.30	0.49	1.34	0.04
SPO2900		tRNA 2-selenouridine synthase	1.10	0.29	-1.25	0.04	-0.08	1.18	3.63	0.00	-1.47	0.04	1.08	2.55	-2.02	0.00	-3.18	0.01	-2.60	0.58
SPO2901		hypothetical protein	-2.14	0.03	-1.14	0.65	-1.64	0.50	-1.75	0.05	1.40	0.05	-0.18	1.58	-1.26	0.08	-1.00	0.88	-1.13	0.13
SPO2902		glutathione S-transferase	-2.18	0.03	-1.52	0.01	-1.85	0.33	-2.34	0.04	1.13	0.30	-0.61	1.74	-1.12	0.39	-1.00	0.98	-1.06	0.06
SPO2903		TPR/sulfotransferase domain-containing protein	1.69	0.27	1.71	0.46	1.70	0.01	1.63	0.45	1.10	0.90	1.37	0.27	1.56	0.38	1.30	0.57	1.43	0.13
SPO2904		Ser/Thr protein phosphatase/nucleotidase	-1.34	0.05	-1.37	0.04	-1.36	0.02	-2.30	0.01	1.52	0.20	-0.39	1.91	2.11	0.02	3.20	0.01	2.66	0.55
SPO2905		hypothetical protein	1.24	0.70	-1.20	0.28	0.02	1.22	2.72	0.18	-1.14	0.48	0.79	1.93	1.03	0.98	-1.25	0.53	-0.11	1.14
SPO2906		hypothetical protein	1.13	0.89	-1.15	0.39	-0.01	1.14	2.66	0.03	-1.14	0.47	0.76	1.90	-1.06	0.73	-1.58	0.03	-1.32	0.26
SPO2907	*pyrD*	dihydroorotate dehydrogenase 2	1.20	0.06	-1.11	0.16	0.04	1.16	2.60	0.02	-1.41	0.01	0.60	2.01	-1.19	0.02	-1.87	0.02	-1.53	0.34
SPO2908	*arsC-1*	arsenate reductase (EC:1.20.4.1)	1.58	0.85	1.01	1.00	1.30	0.29	2.13	0.72	-1.13	0.76	0.50	1.63	1.21	0.79	-1.08	0.86	0.06	1.15
SPO2909	*dinF*	DNA-damage-inducible protein F	1.33	X	1.44	0.60	1.39	0.05	2.24	0.21	-1.13	0.80	0.56	1.69	-1.05	0.94	-1.20	0.89	-1.13	0.08
SPO2910		thioesterase	-1.19	0.55	1.09	0.44	-0.05	1.14	-1.15	0.59	-1.08	0.30	-1.12	0.03	-1.86	0.00	-1.29	0.24	-1.58	0.28
SPO2911		thioesterase	1.39	0.02	1.39	0.01	1.39	0.00	1.95	0.02	1.08	0.47	1.52	0.43	-1.19	0.07	-1.27	0.10	-1.23	0.04
SPO2912		MerR family transcriptional regulator	1.43	0.23	-1.16	0.45	0.14	1.30	1.79	0.07	1.42	0.07	1.61	0.18	1.06	0.95	1.34	0.14	1.20	0.14
SPO2913		hypothetical protein	1.19	0.94	1.28	0.62	1.24	0.05	0.89	0.63	1.30	0.47	1.09	0.21	1.03	0.95	-1.04	0.91	-0.01	1.04

SPO2914		MerR family transcriptional regulator	1.26	0.86	-1.73	0.14	-0.24	1.50	-2.14	0.20	1.32	0.27	-0.41	1.73	-1.06	0.52	2.50	0.07	0.72	1.78
SPO2915		acyl-CoA dehydrogenase	1.53	0.29	-1.47	0.17	0.03	1.50	-1.47	0.17	-1.11	0.25	-1.29	0.18	1.20	0.37	2.61	0.07	1.91	0.71
SPO2916		hypothetical protein	1.63	0.54	-1.40	0.35	0.12	1.52	-1.49	0.08	-1.08	0.55	-1.29	0.20	1.14	0.65	2.19	0.06	1.67	0.53
SPO2917		glutathione S-transferase	1.59	0.00	-2.01	0.02	-0.21	1.80	-3.17	0.01	1.27	0.20	-0.95	2.22	1.01	0.91	2.38	0.04	1.70	0.69
SPO2918		acetyl-CoA acetyltransferase (EC:2.3.1.9)	1.90	0.02	-1.66	0.04	0.12	1.78	-1.95	0.01	1.47	0.02	-0.24	1.71	1.10	0.60	2.65	0.01	1.88	0.78
SPO2919		hypothetical protein	2.26	0.00	-1.71	0.06	0.28	1.99	-2.11	0.00	1.63	0.02	-0.24	1.87	0.99	0.74	2.99	0.00	1.99	1.00
SPO2920	*fabJ-1*	fatty oxidation complex subunit alpha	1.95	0.09	-1.40	0.05	0.28	1.68	-1.46	0.12	-1.09	0.46	-1.28	0.19	1.93	0.02	3.44	0.01	2.69	0.75
SPO2921		hypothetical protein	2.02	0.07	3.84	0.00	2.93	0.91	-3.47	0.01	1.64	0.04	-0.92	2.56	1.14	0.22	-1.36	0.08	-0.11	1.25
SPO2922		hypothetical protein	1.05	0.36	1.17	0.20	1.11	0.06	1.59	0.01	1.48	0.06	1.54	0.06	1.42	0.04	1.16	0.08	1.29	0.13
SPO2923		hypothetical protein	2.30	0.04	1.38	0.11	1.84	0.46	-1.41	0.37	-1.07	0.76	-1.24	0.17	1.16	0.09	-0.98	0.46	0.09	1.07
SPO2924		hypothetical protein	1.08	0.93	-1.14	0.31	-0.03	1.11	1.21	0.07	1.20	0.19	1.21	0.01	1.01	0.95	-1.05	0.58	-0.02	1.03
SPO2925		hypothetical protein	X	X	-1.02	X	N/A	N/A	X	X	X	X	N/A	N/A	1.33	0.10	X	X	N/A	N/A
SPO2926	*upp*	uracil phosphoribosyltransferase (EC:2.4.2.9)	1.29	0.29	1.14	0.24	1.22	0.08	-1.39	0.02	1.00	0.66	-0.20	1.19	1.43	0.02	1.36	0.07	1.40	0.03
SPO2927	*add*	adenosine deaminase (EC:3.5.4.4)	1.03	0.95	-1.27	0.07	-0.12	1.15	-1.23	0.38	-1.62	0.08	-1.43	0.20	-1.11	0.32	-1.38	0.07	-1.25	0.13
SPO2928	*deoB*	phosphopentomutase (EC:5.4.2.7)	1.03	0.80	-1.05	0.69	-0.01	1.04	-1.12	0.68	-1.70	0.10	-1.41	0.29	1.17	0.37	1.04	0.94	1.11	0.06
SPO2929	*deoA*	thymidine phosphorylase (EC:2.4.2.4)	-1.39	0.31	-1.04	0.87	-1.22	0.18	-1.37	0.63	-1.48	0.24	-1.43	0.05	1.29	0.70	1.08	0.67	1.19	0.11
SPO2930	*cdd*	cytidine deaminase (EC:3.5.4.5)	-1.31	0.11	-1.08	0.60	-1.20	0.12	-1.34	0.08	-1.90	0.01	-1.62	0.28	1.02	0.89	-1.49	0.12	-0.24	1.26
SPO2931		hypothetical protein	1.27	0.33	-1.61	0.00	-0.17	1.44	1.16	0.39	1.31	0.16	1.24	0.08	-1.03	0.62	1.56	0.04	0.27	1.30
SPO2932		malic enzyme (EC:1.1.1.39)	2.94	0.00	1.78	0.04	2.36	0.58	8.67	0.00	1.52	0.05	5.10	3.58	1.18	0.19	1.73	0.03	1.46	0.27
SPO2933		hypothetical protein	-1.58	0.03	-1.24	0.40	-1.41	0.17	0.92	0.29	1.33	0.42	1.13	0.20	-1.22	0.19	1.30	0.31	0.04	1.26
SPO2934	*prpE*	propionate--CoA ligase (EC:6.2.1.17)	5.89	0.00	2.29	0.01	4.09	1.80	1.61	0.02	13.70	0.00	7.66	6.05	-1.22	0.06	-1.11	0.09	-1.17	0.05
SPO2935		hypothetical protein	1.74	0.00	-1.04	0.71	0.35	1.39	-2.76	0.00	1.47	0.05	-0.65	2.12	-1.38	0.12	-1.16	0.29	-1.27	0.11
SPO2936		hypothetical protein	1.81	0.00	1.06	0.75	1.44	0.38	-1.59	0.04	1.15	0.44	-0.22	1.37	1.27	0.03	1.23	0.55	1.25	0.02
SPO2937		SCO1/SenC family protein	1.72	0.09	1.23	0.27	1.48	0.24	-1.21	0.74	1.45	0.05	0.12	1.33	1.10	0.08	-1.29	0.16	-0.10	1.20
SPO2938		amidase (EC:3.5.1.4)	1.75	0.50	1.00	0.96	1.38	0.38	-2.32	0.26	1.73	0.16	-0.30	2.03	1.51	0.32	2.91	0.04	2.21	0.70
SPO2939	*ppnK*	inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23)	-1.00	0.91	1.23	0.13	0.12	1.12	1.85	0.00	1.72	0.05	1.79	0.07	-1.12	0.48	-1.33	0.28	-1.23	0.11
SPO2940	*glyA*	serine hydroxymethyltransferase (EC:2.1.2.1)	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO2941		hypothetical protein	-3.04	X	1.66	0.09	-0.69	2.35	-2.97	0.01	-1.43	0.56	-2.20	0.77	-1.27	0.14	-1.04	0.98	-1.16	0.12
SPO2942		hypothetical protein	1.16	0.97	0.99	0.97	1.08	0.08	1.36	0.93	1.03	1.00	1.20	0.17	1.42	0.64	1.82	0.56	1.62	0.20
SPO2943		alpha/beta hydrolase	-1.74	0.08	1.15	0.16	-0.30	1.45	-1.82	0.04	-1.29	0.05	-1.56	0.27	1.04	0.80	-2.06	0.04	-0.51	1.55
SPO2944		hypothetical protein	-1.04	0.61	-1.04	0.90	-1.04	0.00	-1.07	1.00	-1.08	0.74	-1.08	0.01	1.28	0.41	1.31	0.03	1.30	0.02
SPO2945		rhodanese-like domain-containing protein	1.19	0.31	-1.11	0.78	0.04	1.15	-1.76	0.05	-1.05	0.80	-1.41	0.36	1.14	0.44	1.13	0.51	1.14	0.01
SPO2946		monooxygenase domain-containing protein	3.33	0.04	-1.07	0.73	1.13	2.20	-2.74	0.04	1.20	0.31	-0.77	1.97	2.24	0.02	2.19	0.08	2.22	0.03
SPO2947		cupin	2.30	0.00	1.06	0.86	1.68	0.62	-6.48	0.00	1.34	0.47	-2.57	3.91	4.28	0.01	3.02	0.01	3.65	0.63
SPO2948		AraC family transcriptional regulator	-1.91	0.09	-1.18	0.36	-1.55	0.37	1.69	0.08	1.21	0.33	1.45	0.24	1.06	0.76	1.46	0.23	1.26	0.20
SPO2949		endoribonuclease L-PSP	1.43	0.21	1.60	0.03	1.52	0.09	1.59	0.12	-1.21	0.20	0.19	1.40	1.13	0.68	-1.34	0.12	-0.11	1.24
SPO2950		hypothetical protein	-1.04	0.26	-1.31	0.07	-1.18	0.14	-1.71	0.03	1.59	0.01	-0.06	1.65	-1.35	0.03	-1.09	0.81	-1.22	0.13
SPO2951		hypothetical protein	-1.51	0.06	1.30	0.15	-0.11	1.41	-2.92	0.01	1.89	0.02	-0.52	2.41	1.59	0.01	1.65	0.01	1.62	0.03
SPO2952		TrkA domain-containing protein	-1.11	0.80	1.22	0.10	0.05	1.17	1.23	0.40	1.10	0.21	1.17	0.06	1.14	0.08	-1.16	0.40	-0.01	1.15

SPO2953		Ser/Thr protein phosphatase	1.13	0.61	1.09	0.77	1.11	0.02	2.59	0.02	-1.29	0.15	0.65	1.94	1.10	0.26	-1.31	0.18	-0.11	1.21
SPO2954		5-formyltetrahydrofolate cyclo-ligase	1.23	0.78	1.55	0.26	1.39	0.16	1.30	0.65	-1.11	0.51	0.10	1.21	1.11	0.46	-1.29	0.59	-0.09	1.20
SPO2955	*mgtE*	magnesium transporter	1.34	0.08	1.28	0.06	1.31	0.03	-1.36	0.07	1.03	0.98	-0.17	1.20	1.08	0.73	-1.03	0.86	0.03	1.06
SPO2956		guanine deaminase	-1.29	0.08	1.00	0.97	-0.15	1.14	-1.40	0.09	-1.20	0.28	-1.30	0.10	-0.99	0.99	-1.16	0.54	-1.08	0.08
SPO2957		hydroxydechloroatrazine ethylaminohydrolase (EC:3.5.99.3)	1.37	0.35	1.33	0.27	1.35	0.02	1.79	0.06	2.48	0.02	2.14	0.35	1.48	0.07	-0.97	0.15	0.26	1.22
SPO2958		inositol monophosphatase	-1.31	0.59	1.12	0.47	-0.10	1.22	1.16	0.18	2.23	0.02	1.70	0.54	2.05	0.07	2.17	0.04	2.11	0.06
SPO2959		DNA-binding protein	-1.45	0.01	1.22	0.09	-0.12	1.34	0.76	0.00	2.49	0.00	1.63	0.86	2.22	0.00	3.27	0.00	2.75	0.53
SPO2960		zinc-binding dehydrogenase oxidoreductase	-1.21	0.83	-1.38	0.10	-1.30	0.09	1.33	0.25	-1.22	0.23	0.06	1.28	-1.66	0.02	-1.78	0.05	-1.72	0.06
SPO2961		LysR family transcriptional regulator	-1.22	0.04	-1.24	0.07	-1.23	0.01	1.16	0.04	-1.04	0.31	0.06	1.10	1.08	0.28	1.19	0.02	1.14	0.05
SPO2962		hypothetical protein	-3.65	0.03	-1.66	0.02	-2.66	1.00	4.22	0.01	1.65	0.02	2.94	1.29	1.16	0.10	2.09	0.01	1.63	0.47
SPO2963		hypothetical protein	1.27	0.99	-1.61	0.13	-0.17	1.44	1.29	0.66	-1.13	0.26	0.08	1.21	1.51	0.26	2.20	0.09	1.86	0.35
SPO2964		hypothetical protein	-1.43	0.03	1.34	0.20	-0.04	1.39	-1.65	0.03	1.64	0.21	-0.01	1.65	1.12	0.08	1.21	0.10	1.17	0.04
SPO2965	*rpmG*	50S ribosomal protein L33	-1.69	0.25	1.58	0.16	-0.05	1.64	2.66	0.01	1.11	0.74	1.89	0.78	-1.59	0.01	-2.21	0.01	-1.90	0.31
SPO2967		N-acetylmuramoyl-L-alanine amidase	1.21	0.64	-1.18	0.28	0.02	1.20	1.75	0.07	-1.15	0.11	0.30	1.45	1.03	0.93	-1.29	0.34	-0.13	1.16
SPO2968		hypothetical protein	0.90	0.02	-1.11	0.58	-0.10	1.01	1.27	0.84	1.11	0.93	1.19	0.08	1.31	0.01	1.23	0.83	1.27	0.04
SPO2969	*gatA*	aspartyl/glutamyl-tRNA amidotransferase subunit A (EC:6.3.5.-)	1.95	0.01	-1.11	0.33	0.42	1.53	3.74	0.00	-1.08	0.10	1.33	2.41	-1.53	0.00	-1.51	0.01	-1.52	0.01
SPO2970	*gatC*	aspartyl/glutamyl-tRNA amidotransferase subunit C (EC:6.3.5.-)	1.58	0.03	1.39	0.30	1.49	0.10	4.69	0.00	-1.06	0.43	1.82	2.88	-1.19	0.12	-1.72	0.01	-1.46	0.26
SPO2971		hypothetical protein	-1.38	0.19	1.02	0.94	-0.18	1.20	-1.40	0.67	-1.22	0.68	-1.31	0.09	1.24	0.56	1.45	0.33	1.35	0.11
SPO2972		hypothetical protein	X	X	1.21	0.25	N/A	N/A	X	X	X	X	N/A	N/A	1.99	0.17	X	X	N/A	N/A
SPO2974		hypothetical protein	1.65	0.02	1.13	0.07	1.39	0.26	2.03	0.01	-1.55	0.08	0.24	1.79	1.10	0.23	-0.95	0.26	0.08	1.03
SPO2975		hypothetical protein	1.03	0.98	-1.52	0.02	-0.25	1.28	1.71	0.06	-1.70	0.03	0.01	1.71	1.38	0.10	-1.04	0.69	0.17	1.21
SPO2976		metallo-beta-lactamase	-1.21	0.76	-1.37	0.16	-1.29	0.08	-2.20	0.05	1.30	0.08	-0.45	1.75	1.09	0.31	1.27	0.06	1.18	0.09
SPO2977		guanylate cyclase	-1.58	0.08	-1.13	0.64	-1.36	0.23	-2.55	0.03	1.32	0.37	-0.62	1.94	1.11	0.60	1.14	0.57	1.13	0.01
SPO2978		guanylate cyclase	-1.99	0.35	-1.13	0.75	-1.56	0.43	-1.96	0.52	1.27	0.62	-0.35	1.62	1.19	0.61	1.30	0.52	1.25	0.06
SPO2979		hypothetical protein	-1.37	0.27	1.20	0.14	-0.09	1.29	-1.94	0.06	1.16	0.16	-0.39	1.55	-1.22	0.38	-1.38	0.37	-1.30	0.08
SPO2980		peptidyl-arginine deiminase	-1.07	0.94	1.17	0.70	0.05	1.12	-1.39	0.17	1.17	0.38	-0.11	1.28	1.14	0.61	1.10	0.42	1.12	0.02
SPO2981		hypothetical protein	1.44	0.22	1.33	0.13	1.39	0.05	1.66	0.07	1.37	0.03	1.52	0.15	1.32	0.09	-1.10	0.94	0.11	1.21
SPO2982		hypothetical protein	2.59	0.00	2.01	0.05	2.30	0.29	2.85	0.00	1.13	0.21	1.99	0.86	1.05	0.57	-1.11	0.39	-0.03	1.08
SPO2983		cytidine and deoxycytidylate deaminase	0.96	0.85	1.89	0.60	1.42	0.47	0.93	0.82	1.32	0.86	1.13	0.19	1.18	0.89	1.23	0.83	1.21	0.03
SPO2984		RNA pseudouridylate synthase	-1.15	0.27	-1.12	0.33	-1.14	0.01	2.82	0.00	1.22	0.40	2.02	0.80	-1.80	0.09	-1.93	0.11	-1.87	0.06
SPO2985		hypothetical protein	1.11	0.79	-1.14	0.49	-0.01	1.13	1.21	0.15	1.05	0.96	1.13	0.08	-1.08	0.68	1.30	0.14	0.11	1.19
SPO2986		tellurite resistance protein	1.33	0.68	-1.20	0.12	0.07	1.27	1.35	0.65	1.13	0.73	1.24	0.11	1.15	0.42	1.26	0.44	1.21	0.06
SPO2987		lipoprotein	1.17	0.63	-1.49	0.04	-0.16	1.33	1.17	0.79	1.05	1.00	1.11	0.06	-1.38	0.07	-1.48	0.03	-1.43	0.05
SPO2988		hypothetical protein	1.58	0.17	-1.20	0.12	0.19	1.39	1.77	0.02	1.16	0.40	1.47	0.31	1.04	0.97	1.08	0.94	1.06	0.02
SPO2989		cytochrome b562	1.33	0.12	1.10	0.53	1.22	0.12	1.81	0.04	1.37	0.03	1.59	0.22	1.17	0.28	1.04	0.97	1.11	0.06
SPO2990		hypothetical protein	-1.06	0.54	1.03	0.85	-0.02	1.05	1.56	0.07	1.19	0.25	1.38	0.19	-1.55	0.03	-1.74	0.01	-1.65	0.10
SPO2991		nitroreductase	1.54	0.02	-1.47	0.08	0.04	1.51	1.58	0.02	1.19	0.28	1.39	0.20	-1.24	0.13	-1.40	0.12	-1.32	0.08
SPO2992	*dtd*	D-tyrosyl-tRNA(Tyr) deacylase (EC:3.1.-.-)	1.39	0.01	-1.24	0.09	0.08	1.32	2.05	0.02	-1.03	0.61	0.51	1.54	1.06	0.65	-1.14	0.49	-0.04	1.10

SPO2993		MOFRL family protein	1.55	0.63	-1.24	0.54	0.16	1.40	1.14	0.76	1.27	0.43	1.21	0.07	1.09	0.82	1.41	0.41	1.25	0.16
SPO2994		X-Pro dipeptidyl-peptidase	3.46	0.04	1.57	0.05	2.52	0.95	-1.76	0.19	-1.00	0.84	-1.38	0.38	-1.97	0.04	-2.29	0.05	-2.13	0.16
SPO2995		peptide/nickel/opine uptake ABC transporter substrate-binding protein	-1.32	0.04	-2.66	0.00	-1.99	0.67	-1.40	0.04	1.26	0.09	-0.07	1.33	1.27	0.41	2.13	0.05	1.70	0.43
SPO2996		peptide/nickel/opine uptake ABC transporter permease	-1.59	0.13	-2.12	0.01	-1.86	0.27	-1.38	0.20	1.14	0.67	-0.12	1.26	1.37	0.14	1.59	0.25	1.48	0.11
SPO2997		peptide/nickel/opine uptake ABC transporter permease	-1.51	0.49	-1.51	0.15	-1.51	0.00	-1.60	0.44	1.31	0.33	-0.15	1.46	1.47	0.08	1.62	0.03	1.55	0.08
SPO2998		peptide/nickel/opine uptake ABC transporter ATP-binding protein	-1.99	0.23	-1.36	0.39	-1.68	0.32	-1.48	0.27	1.42	0.15	-0.03	1.45	1.39	0.12	1.49	0.18	1.44	0.05
SPO2999		hypothetical protein	-1.35	0.39	1.05	0.86	-0.15	1.20	-1.10	0.68	-1.07	0.83	-1.09	0.02	-1.05	0.88	-1.13	0.93	-1.09	0.04
SPO3000		hypothetical protein	2.00	0.03	1.03	0.87	1.52	0.49	2.05	0.05	1.33	0.11	1.69	0.36	-1.13	0.47	1.43	0.27	0.15	1.28
SPO3001		hypothetical protein	1.00	0.88	-1.05	0.53	-0.03	1.02	-1.19	0.78	1.17	0.23	-0.01	1.18	1.31	0.19	1.68	0.11	1.50	0.18
SPO3002		lipase	-1.09	0.88	-1.36	0.22	-1.23	0.14	-1.93	0.52	1.50	0.15	-0.22	1.72	1.61	0.10	1.68	0.12	1.65	0.03
SPO3003		AMP-binding protein (EC:2.3.1.86)	-1.42	0.10	-1.86	0.17	-1.64	0.22	-4.22	0.06	1.47	0.34	-1.38	2.85	1.13	0.83	2.02	0.10	1.58	0.45
SPO3004		LysM domain/BON superfamily protein	-1.26	0.03	-2.53	0.08	-1.90	0.64	2.80	0.02	1.58	0.15	2.19	0.61	1.01	0.90	-1.99	0.10	-0.49	1.50
SPO3005		ABC transporter ATP-binding protein/permease	1.42	0.92	1.95	0.04	1.69	0.26	2.62	0.53	-1.31	0.09	0.66	1.97	1.19	0.40	1.33	0.44	1.26	0.07
SPO3008		hypothetical protein	1.32	0.34	1.06	0.36	1.19	0.13	-1.98	0.00	1.92	0.09	-0.03	1.95	1.17	0.45	-1.47	0.18	-0.15	1.32
SPO3009	*putR*	proline dehydrogenase	1.14	0.06	-1.02	0.93	0.06	1.08	-2.28	0.01	-1.19	0.31	-1.74	0.55	1.04	0.63	-1.91	0.04	-0.44	1.48
SPO3010	*putA*	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase (EC:1.5.1.12 1.5.99.8)	-1.08	0.36	1.29	0.24	0.11	1.19	-1.81	0.03	-1.39	0.04	-1.60	0.21	-1.11	0.84	-1.02	X	-1.07	0.05
SPO3011		rhomboid family protein	1.35	0.02	1.20	0.04	1.28	0.08	2.16	0.00	1.25	0.05	1.71	0.46	1.38	0.06	1.24	0.07	1.31	0.07
SPO3012		inositol monophosphatase	-1.15	0.87	1.54	0.26	0.20	1.35	1.64	0.68	-1.18	0.56	0.23	1.41	-1.65	0.04	-2.19	0.07	-1.92	0.27
SPO3013		L4BD family NADP-dependent oxidoreductase	-1.45	0.02	-1.13	0.77	-1.29	0.16	-1.56	0.26	1.93	0.21	0.19	1.75	1.05	0.93	1.42	0.49	1.24	0.19
SPO3014		hypothetical protein	-5.00	0.00	-1.27	0.01	-3.14	1.87	-12.00	0.00	1.21	0.14	-5.40	6.61	2.59	0.00	5.36	0.00	3.98	1.39
SPO3015	*metR*	transcriptional regulator MetR	-1.94	0.09	-1.36	0.11	-1.65	0.29	1.35	0.10	1.21	0.06	1.28	0.07	1.14	0.24	1.13	0.18	1.14	0.01
SPO3016	*metF*	5,10-methylenetetrahydrofolate reductase	-74.30	0.00	-22.40	0.02	-48.35	25.95	4.39	0.00	2.56	0.01	3.48	0.92	-1.50	0.03	1.14	0.99	-0.18	1.32
SPO3017		thioesterase	-1.34	0.70	-3.15	0.00	-2.25	0.90	9.78	0.00	1.80	0.02	5.79	3.99	-1.18	0.10	1.66	0.09	0.24	1.42
SPO3018		hypothetical protein	1.06	0.96	1.11	0.58	1.09	0.03	1.03	0.82	1.21	0.42	1.12	0.09	1.39	0.04	1.08	0.60	1.24	0.16
SPO3019		xanthine dehydrogenase, large subunit	1.02	0.49	1.23	0.12	1.13	0.11	0.95	0.59	1.31	0.15	1.13	0.18	1.65	0.01	1.53	0.09	1.59	0.06
SPO3020		LysR family transcriptional regulator	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3021		phytanoyl-CoA dioxygenase	3.15	0.03	-1.24	0.89	0.96	2.20	1.69	0.58	-1.20	0.85	0.25	1.45	-1.21	0.90	1.72	0.44	0.26	1.47
SPO3022	*valS*	valyl-tRNA synthetase (EC:6.1.1.9)	1.15	0.97	1.22	0.61	1.19	0.04	3.16	0.46	-1.35	0.07	0.91	2.26	-1.15	0.45	-1.20	0.37	-1.18	0.03
SPO3023		hypothetical protein	-1.72	0.04	-1.05	0.67	-1.39	0.34	-2.45	0.02	-1.02	0.82	-1.74	0.72	-1.19	0.35	-1.40	0.30	-1.30	0.11
SPO3024		adenylate cyclase	1.97	0.01	-1.26	0.07	0.36	1.62	-1.73	0.36	1.61	0.03	-0.06	1.67	-1.44	0.02	X	X	N/A	N/A
SPO3025		enoyl-CoA hydratase (EC:4.2.1.17)	1.94	0.03	1.17	0.65	1.56	0.39	-1.58	0.00	1.16	0.63	-0.21	1.37	1.37	0.21	2.60	0.14	1.99	0.62
SPO3026		strictosidine synthase	1.62	0.06	1.33	0.04	1.48	0.15	4.55	0.00	-1.41	0.03	1.57	2.98	-1.11	0.32	-1.62	0.04	-1.37	0.25
SPO3027		histidinol-phosphate aminotransferase (EC:2.6.1.9)	1.16	0.57	1.41	0.04	1.29	0.13	6.37	0.00	-1.15	0.29	2.61	3.76	1.19	0.09	-1.87	0.01	-0.34	1.53
SPO3028		hypothetical protein	-1.20	0.30	1.67	0.21	0.24	1.44	-1.23	0.85	-1.21	0.55	-1.22	0.01	1.32	0.09	-1.38	X	-0.03	1.35
SPO3029		serine--glyoxylate transaminase	1.50	0.32	1.18	0.39	1.34	0.16	1.30	0.27	1.07	0.59	1.19	0.12	1.42	0.05	2.30	0.03	1.86	0.44
SPO3030		efflux ABC transporter transmembrane ATP-binding protein	-1.19	0.27	-1.05	0.51	-1.12	0.07	1.47	0.06	-1.04	0.39	0.22	1.26	1.28	0.16	1.12	0.67	1.20	0.08
SPO3031	*eda-1*	2-dehydro-3-deoxyphosphooctonate aldolase	1.68	0.83	1.57	0.51	1.63	0.05	1.42	0.88	2.75	0.14	2.09	0.67	1.38	0.65	1.20	0.83	1.29	0.09

		(EC:4.1.2.14 4.1.3.16)																		
SPO3032	*edd*	phosphogluconate dehydratase (EC:4.2.1.12)	1.31	0.28	1.17	0.75	1.24	0.07	0.95	0.06	3.26	0.01	2.11	1.16	1.12	0.20	1.67	0.57	1.40	0.28
SPO3033	*zwf-2*	glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49)	1.10	0.86	1.29	0.34	1.20	0.10	0.84	0.41	2.95	0.03	1.90	1.05	-1.31	0.56	-1.21	0.63	-1.26	0.05
SPO3034		phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9)	-1.19	0.24	1.84	0.08	0.33	1.52	-1.37	0.30	1.05	0.83	-0.16	1.21	1.51	0.20	-1.33	0.47	0.09	1.42
SPO3035		aspartate kinase (EC:2.7.2.4)	1.10	0.72	1.68	0.07	1.39	0.29	4.03	0.02	1.00	0.68	2.52	1.52	-1.42	0.16	-1.93	0.01	-1.68	0.26
SPO3036		metallo-beta-lactamase	0.99	0.42	-1.42	0.10	-0.22	1.20	-1.97	0.03	1.13	0.49	-0.42	1.55	1.61	0.01	1.62	0.05	1.62	0.01
SPO3037		LysR family transcriptional regulator	-1.56	0.10	-1.40	0.00	-1.48	0.08	-0.99	0.34	1.25	0.03	0.13	1.12	-1.42	0.02	-1.70	0.02	-1.56	0.14
SPO3038		sensor histidine kinase/response regulator (EC:2.7.3.-)	-1.20	0.74	1.19	0.73	-0.01	1.20	-1.11	0.85	1.28	0.45	0.09	1.20	1.19	0.54	-1.12	0.97	0.03	1.16
SPO3039		polar amino acid ABC transporter substrate-binding protein	1.21	0.53	1.20	0.18	1.21	0.01	-1.29	0.36	1.42	0.13	0.06	1.36	1.08	0.60	-1.13	0.67	-0.02	1.11
SPO3040		polar amino acid ABC transporter substrate-binding protein	1.14	0.95	-1.12	0.95	0.01	1.13	-1.71	0.85	1.11	0.94	-0.30	1.41	-1.43	0.76	1.71	X	0.14	1.57
SPO3041		polar amino acid ABC transporter permease	-2.00	0.53	-1.14	0.81	-1.57	0.43	-1.20	1.00	1.08	0.89	-0.06	1.14	-1.33	0.73	1.32	0.32	-0.01	1.33
SPO3042		polar amino acid ABC transporter permease	X	X	-1.15	0.39	N/A	N/A	X	X	-1.07	X	N/A	N/A	1.08	0.14	1.21	X	1.15	0.06
SPO3043	*glnQ*	glutamine ABC transporter ATP-binding protein	-1.37	0.17	1.01	0.98	-0.18	1.19	-1.43	0.31	-1.25	0.56	-1.34	0.09	-1.34	0.48	-1.11	0.95	-1.23	0.12
SPO3044		LysR family transcriptional regulator	-1.06	X	-1.11	0.85	-1.09	0.03	-1.15	0.85	1.14	0.83	-0.01	1.15	-1.19	0.83	1.46	X	0.14	1.33
SPO3045		glutamine amidotransferase	-1.00	0.96	-1.04	0.90	-1.02	0.02	-0.97	0.67	-1.18	0.49	-1.07	0.11	-1.32	0.37	-1.58	0.22	-1.45	0.13
SPO3046		oligopeptide ABC transporter ATP-binding protein	-1.40	0.54	-1.79	0.00	-1.60	0.19	-2.26	0.02	1.29	0.14	-0.49	1.78	1.25	0.27	1.41	0.02	1.33	0.08
SPO3047		dipeptide ABC transporter permease	X	X	1.12	0.64	N/A	N/A	1.25	0.34	-1.30	X	-0.03	1.28	-1.17	0.60	-1.06	X	-1.12	0.05
SPO3048		dipeptide ABC transporter permease	1.13	X	-1.11	0.36	0.01	1.12	-1.45	0.81	1.24	0.46	-0.11	1.35	-1.28	0.19	X	X	N/A	N/A
SPO3049		dipeptide ABC transporter substrate-binding protein	1.14	0.96	-1.33	0.23	-0.10	1.24	-2.42	0.67	1.33	0.21	-0.55	1.88	-1.11	0.71	-1.03	0.60	-1.07	0.04
SPO3050		hypothetical protein	X	X	1.12	0.40	N/A	N/A	-0.88	0.10	-1.16	0.71	-1.02	0.14	-0.96	0.75	1.14	0.29	0.09	1.05
SPO3051		short chain dehydrogenase/reductase oxidoreductase	0.95	0.14	1.01	0.93	0.98	0.03	1.38	0.10	0.98	0.48	1.18	0.20	1.45	0.02	1.39	0.08	1.42	0.03
SPO3052		hypothetical protein	-1.22	0.22	-1.53	0.01	-1.38	0.16	1.36	0.16	1.10	0.80	1.23	0.13	1.09	0.73	1.19	0.57	1.14	0.05
SPO3053		NUDIX domain-containing protein	1.07	0.97	-1.20	0.72	-0.06	1.14	-1.20	0.73	-1.25	0.49	-1.23	0.03	1.42	0.43	1.47	0.38	1.45	0.03
SPO3054		hypothetical protein	1.30	0.05	-2.27	0.01	-0.49	1.79	-1.16	0.22	-1.18	0.15	-1.17	0.01	1.82	0.02	1.48	0.02	1.65	0.17
SPO3055		acetyltransferase	-1.56	0.14	1.30	0.05	-0.13	1.43	1.08	0.46	-1.45	0.04	-0.19	1.27	1.16	0.15	-1.29	0.17	-0.07	1.23
SPO3056		hypothetical protein	1.40	0.66	1.58	0.13	1.49	0.09	1.58	0.19	1.55	0.05	1.57	0.02	0.99	0.55	1.07	0.75	1.03	0.04
SPO3057		streptogramin acetyltransferase	2.10	0.04	1.44	0.27	1.77	0.33	2.27	0.02	1.46	0.06	1.87	0.41	-1.35	0.02	-1.28	0.17	-1.32	0.04
SPO3058		sulfate transporter family protein	0.97	0.91	1.83	0.13	1.40	0.43	2.64	0.63	1.20	0.59	1.92	0.72	-1.10	0.44	-1.58	0.39	-1.34	0.24
SPO3059		hypothetical protein	2.63	0.01	-1.14	0.50	0.75	1.89	1.83	0.00	1.08	0.28	1.46	0.38	-1.22	0.20	-1.10	0.91	-1.16	0.06
SPO3060	*mtaP*	5'-methylthioadenosine phosphorylase (EC:2.4.2.28)	1.63	0.00	1.49	0.03	1.56	0.07	1.64	0.01	1.53	0.04	1.59	0.05	-1.41	0.01	-1.25	0.39	-1.33	0.08
SPO3062		hypothetical protein	X	X	-1.34	X	N/A	N/A	X	X	-1.26	X	N/A	N/A	1.05	X	X	X	N/A	N/A
SPO3063		transmembrane efflux protein	1.22	0.78	1.21	0.60	1.22	0.01	1.94	0.07	1.27	0.25	1.61	0.34	1.20	0.22	1.03	0.79	1.12	0.09
SPO3064		hypothetical protein	-11.90	0.01	-1.16	0.39	-6.53	5.37	-1.55	0.02	1.05	0.77	-0.25	1.30	1.29	0.15	-0.99	0.82	0.15	1.14
SPO3065		hypothetical protein	-26.30	0.01	-3.92	0.08	-15.11	11.19	-9.57	0.00	-2.13	0.03	-5.85	3.72	1.33	0.08	1.64	0.07	1.49	0.16
SPO3066	*apt*	adenine phosphoribosyltransferase (EC:2.4.2.7)	-3.18	0.03	1.40	0.24	-0.89	2.29	-2.15	0.08	-1.59	0.12	-1.87	0.28	1.56	0.06	1.21	0.16	1.39	0.18
SPO3067		oxidoreductase, FAD-binding	1.31	0.65	-1.07	0.84	0.12	1.19	1.05	0.81	1.02	0.99	1.04	0.02	-1.09	0.80	-1.59	0.36	-1.34	0.25

SPO3068		hypothetical protein	-1.43	0.61	1.03	0.83	-0.20	1.23	-1.43	0.71	2.36	0.14	0.47	1.90	1.68	0.30	1.84	0.29	1.76	0.08
SPO3069		ribosomal-protein-alanine acetyltransferase	1.04	0.06	1.13	0.73	1.09	0.04	-2.54	0.00	1.01	0.95	-0.77	1.78	-1.14	0.41	1.16	0.68	0.01	1.15
SPO3070		M16 family peptidase	1.83	0.07	1.15	0.43	1.49	0.34	4.93	0.01	-1.14	0.35	1.90	3.04	-1.34	0.04	-1.65	0.10	-1.50	0.16
SPO3071	*thrC*	threonine synthase (EC:4.2.3.1)	1.17	0.10	1.00	0.60	1.09	0.09	3.98	0.00	-1.70	0.02	1.14	2.84	-1.85	0.02	-2.30	0.01	-2.08	0.22
SPO3072		SURF1 family protein	-0.98	0.93	1.39	0.08	0.21	1.18	3.97	0.03	-1.46	0.11	1.26	2.72	-1.25	0.27	-2.23	0.03	-1.74	0.49
SPO3073	*ctaE*	cytochrome c oxidase subunit III (EC:1.9.3.1)	2.48	0.01	1.17	0.18	1.83	0.66	2.82	0.00	1.20	0.24	2.01	0.81	-1.29	0.00	0.88	0.04	-0.21	1.08
SPO3074	*ctaG*	cytochrome C oxidase assembly protein	3.15	0.02	1.12	0.61	2.14	1.02	5.20	0.02	1.16	0.63	3.18	2.02	-1.96	0.01	-1.60	0.11	-1.78	0.18
SPO3075	*cyoE*	protoheme IX farnesyltransferase (EC:2.5.1.-)	4.94	0.06	1.50	0.05	3.22	1.72	13.10	0.00	0.98	0.26	7.04	6.06	1.08	0.53	0.95	0.03	1.02	0.06
SPO3076	*ctaC*	cytochrome c oxidase subunit II (EC:1.9.3.1)	4.28	0.03	2.03	0.08	3.16	1.13	8.56	0.01	1.11	0.80	4.84	3.73	1.20	0.13	1.63	0.13	1.42	0.21
SPO3077		TldD/PmbA family protein	1.04	0.97	-1.26	0.33	-0.11	1.15	2.13	0.01	0.99	0.65	1.56	0.57	1.52	0.02	1.41	0.46	1.47	0.06
SPO3078		DNA processing protein DprA	1.21	0.60	1.99	0.06	1.60	0.39	-3.63	0.00	3.76	0.01	0.06	3.70	-1.19	0.32	-1.21	0.76	-1.20	0.01
SPO3079	*topA*	DNA topoisomerase I (EC:5.99.1.2)	-1.18	0.71	-1.07	0.74	-1.13	0.05	3.92	0.08	-1.07	0.49	1.43	2.50	-1.26	0.37	-1.48	0.15	-1.37	0.11
SPO3080		TetR family transcriptional regulator	-1.23	0.62	1.25	0.44	0.01	1.24	1.96	0.62	-1.21	0.46	0.38	1.59	1.31	0.24	1.12	0.45	1.22	0.10
SPO3081		glyoxalase	-1.28	0.36	-1.36	0.29	-1.32	0.04	1.10	0.52	-2.01	0.04	-0.46	1.56	-1.40	0.03	-2.61	0.01	-2.01	0.61
SPO3082	*dxnG*	3-oxoadipate CoA-succinyl transferase subunit alpha (EC:2.8.3.6)	1.42	0.77	1.06	0.80	1.24	0.18	2.91	0.03	2.12	0.06	2.52	0.40	1.02	0.67	2.41	0.00	1.72	0.70
SPO3083	*dxnH*	3-oxoadipate CoA-succinyl transferase subunit beta (EC:2.8.3.6)	1.58	0.21	1.56	0.21	1.57	0.01	3.49	0.01	1.59	0.01	2.54	0.95	1.43	0.01	2.27	0.07	1.85	0.42
SPO3084		Slt family transglycosylase	-2.55	0.01	-1.13	0.48	-1.84	0.71	-3.04	0.00	1.07	0.66	-0.99	2.06	1.03	0.75	-1.20	0.58	-0.09	1.12
SPO3085		hypothetical protein	1.28	0.84	1.59	0.11	1.44	0.16	0.68	0.00	1.32	0.40	1.00	0.32	1.20	0.57	1.20	0.92	1.20	0.00
SPO3086		CpaB family protein	1.62	0.56	-1.19	0.38	0.22	1.41	-1.77	0.21	1.02	0.87	-0.38	1.40	-1.34	0.06	1.49	0.44	0.08	1.42
SPO3087		type II/III secretion system protein	-1.60	0.01	-1.12	0.29	-1.36	0.24	-2.56	0.00	-1.77	0.02	-2.17	0.40	-1.22	0.18	-1.38	0.14	-1.30	0.08
SPO3088		OmpA family protein	1.13	0.85	-1.23	0.17	-0.05	1.18	1.04	0.02	-1.47	0.02	-0.22	1.26	-1.63	0.02	-1.74	0.01	-1.69	0.06
SPO3089		ATPase	1.31	0.89	1.03	0.92	1.17	0.14	-3.21	0.01	0.99	0.74	-1.11	2.10	-1.98	0.02	-1.26	0.05	-1.62	0.36
SPO3090		type II/IV secretion system protein	1.76	0.50	1.16	0.30	1.46	0.30	-2.62	0.22	1.03	0.95	-0.80	1.83	-1.48	0.12	0.97	0.70	-0.25	1.23
SPO3091		TadC family type II/IV secretion system protein	1.73	0.66	1.27	0.61	1.50	0.23	-2.13	0.36	1.01	0.90	-0.56	1.57	-1.47	0.24	1.03	0.92	-0.22	1.25
SPO3092		TadC family type II/IV secretion system protein	1.62	0.51	1.20	0.55	1.41	0.21	-1.71	0.20	-1.03	0.87	-1.37	0.34	-1.21	0.56	-1.07	0.68	-1.14	0.07
SPO3093		hypothetical protein	-1.47	0.02	-1.57	0.15	-1.52	0.05	-2.65	0.01	1.09	0.90	-0.78	1.87	-1.70	0.03	1.09	0.81	-0.31	1.40
SPO3094		lipoprotein	-2.18	0.01	-2.10	0.08	-2.14	0.04	-2.41	0.01	-1.12	0.31	-1.77	0.65	-1.18	0.18	0.88	0.03	-0.15	1.03
SPO3095		hypothetical protein	-2.21	0.00	-1.61	0.14	-1.91	0.30	-1.89	0.01	-1.10	0.08	-1.50	0.39	-1.17	0.26	-1.62	0.03	-1.40	0.23
SPO3096		hypothetical protein	1.62	0.52	-1.02	0.45	0.30	1.32	-2.22	0.19	-1.12	0.36	-1.67	0.55	-1.80	0.09	-2.38	0.03	-2.09	0.29
SPO3097	*mmsB-2*	3-hydroxyisobutyrate dehydrogenase (EC:1.1.1.31)	1.05	0.81	-1.12	0.16	-0.04	1.09	-2.95	0.00	-1.17	0.12	-2.06	0.89	-2.46	0.00	-2.64	0.01	-2.55	0.09
SPO3098		DEAD/DEAH box helicase	-2.07	0.01	-1.37	0.23	-1.72	0.35	-2.68	0.00	1.13	0.28	-0.78	1.91	-1.39	0.16	1.15	0.26	-0.12	1.27
SPO3099		hypothetical protein	-1.32	0.25	1.23	0.27	-0.05	1.28	1.37	0.04	-1.35	0.08	0.01	1.36	1.22	0.26	-1.21	0.72	0.01	1.22
SPO3100		hypothetical protein	1.21	0.01	1.14	0.35	1.18	0.04	0.99	0.95	-1.41	0.09	-0.21	1.20	-1.01	0.44	-1.20	0.09	-1.11	0.10
SPO3101		bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3102		chorismate mutase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3103	*fhs-2*	formate--tetrahydrofolate ligase (EC:6.3.4.3)	12.00	0.00	2.10	0.04	7.05	4.95	1.10	0.63	-2.47	0.01	-0.69	1.79	-1.53	0.11	-1.77	0.25	-1.65	0.12
SPO3104		MOSC domain-containing protein	1.26	0.61	1.00	0.81	1.13	0.13	2.63	0.16	1.45	0.25	2.04	0.59	1.03	0.98	1.02	0.91	1.03	0.01

SPO3105	*ftsH*	ATP-dependent metalloprotease FtsH (EC:3.4.24.-)	1.44	0.05	-1.43	0.11	0.01	1.44	2.13	0.01	1.29	0.06	1.71	0.42	1.33	0.04	1.94	0.07	1.64	0.31
SPO3106		PP-loop family protein	-1.66	0.22	-1.07	0.77	-1.37	0.30	-1.85	0.20	-1.06	0.87	-1.46	0.40	1.50	0.05	-1.32	0.33	0.09	1.41
SPO3107		hypothetical protein	1.29	0.71	-1.45	0.10	-0.08	1.37	1.09	0.45	-1.14	0.18	-0.02	1.12	1.25	0.19	1.00	0.54	1.12	0.13
SPO3108	*pal*	peptidoglycan-associated lipoprotein	0.98	0.13	-1.81	0.16	-0.41	1.40	-1.47	0.01	-1.30	0.09	-1.39	0.09	-1.22	0.18	-1.40	0.00	-1.31	0.09
SPO3109	*tolB*	translocation protein TolB	1.38	0.08	-1.38	0.06	0.00	1.38	1.55	0.09	-1.23	0.00	0.16	1.39	-1.10	0.07	-1.15	0.04	-1.13	0.02
SPO3110		TonB domain-containing protein	1.13	0.70	-1.31	0.32	-0.09	1.22	0.98	0.71	-1.12	0.16	-0.07	1.05	-1.28	0.16	1.05	0.77	-0.12	1.17
SPO3111		biopolymer ExbD/TolR family transporter	-1.30	0.04	-1.26	0.19	-1.28	0.02	1.95	0.01	1.00	0.58	1.47	0.48	1.03	0.74	-1.45	0.04	-0.21	1.24
SPO3112	*tolQ*	proton transporter TolQ	1.02	0.68	1.09	0.72	1.06	0.04	2.21	0.04	0.99	0.27	1.60	0.61	1.57	0.01	1.24	0.14	1.41	0.17
SPO3113		hypothetical protein	-1.28	0.82	1.12	0.74	-0.08	1.20	-1.45	0.18	1.11	0.30	-0.17	1.28	1.09	0.47	-1.03	0.84	0.03	1.06
SPO3114		hypothetical protein	-1.28	0.43	1.39	0.67	0.05	1.34	1.94	0.08	-1.54	0.56	0.20	1.74	1.34	0.60	1.29	0.75	1.32	0.03
SPO3115	*ruvB*	Holliday junction DNA helicase RuvB (EC:3.1.22.4)	-1.28	0.67	1.19	0.43	-0.05	1.24	-1.23	0.78	-1.63	0.06	-1.43	0.20	1.48	0.16	1.20	0.51	1.34	0.14
SPO3116	*ruvA*	Holliday junction DNA helicase RuvA	-1.18	0.35	1.11	0.34	-0.03	1.15	1.46	0.16	-1.38	0.08	0.04	1.42	1.35	0.01	-1.06	0.60	0.15	1.21
SPO3117	*ruvC*	Holliday junction resolvase (EC:3.1.22.4)	-1.56	0.06	1.03	0.59	-0.27	1.30	-1.56	0.16	-1.89	0.04	-1.73	0.17	1.16	0.14	-1.00	0.48	0.08	1.08
SPO3118		hypothetical protein	7.25	0.00	2.56	0.01	4.91	2.35	7.21	0.00	1.48	0.05	4.35	2.87	-1.71	0.03	-2.39	0.14	-2.05	0.34
SPO3119		hypothetical protein	2.20	0.02	1.60	0.02	1.90	0.30	-2.93	0.01	1.47	0.06	-0.73	2.20	-1.05	0.41	-1.48	0.10	-1.27	0.21
SPO3120		50S ribosomal protein L11 methyltransferase	-1.41	0.01	1.46	0.02	0.03	1.44	-1.08	0.43	-1.41	0.03	-1.25	0.16	-1.11	0.24	-1.46	0.20	-1.29	0.17
SPO3121		MATE efflux family protein	X	X	1.30	0.02	N/A	N/A	2.39	0.01	-1.46	0.09	0.47	1.93	1.10	0.52	-2.02	0.15	-0.46	1.56
SPO3122		hypothetical protein	-1.19	0.68	1.09	0.69	-0.05	1.14	1.61	0.10	-1.66	0.03	-0.02	1.64	-1.34	0.06	-1.18	0.74	-1.26	0.08
SPO3123		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3124		hypothetical protein	1.33	0.06	-1.08	0.54	0.13	1.21	1.14	0.39	-1.08	0.73	0.03	1.11	-1.01	0.88	-1.61	0.02	-1.31	0.30
SPO3125		ECF subfamily RNA polymerase sigma factor	-1.42	0.87	-1.06	0.89	-1.24	0.18	-1.89	0.78	1.09	0.65	-0.40	1.49	1.34	0.05	1.31	0.23	1.33	0.02
SPO3126		sigma factor regulator PrtR	-1.07	0.87	-1.05	0.90	-1.06	0.01	-1.01	0.24	1.11	0.44	0.05	1.06	1.42	0.06	1.23	0.62	1.33	0.10
SPO3127	*priA*	primosome assembly protein PriA	-1.07	0.88	-1.04	0.92	-1.06	0.02	-1.75	0.30	-1.29	0.23	-1.52	0.23	-1.36	0.07	-1.28	0.68	-1.32	0.04
SPO3128	*fsaB*	translaldolase (EC:2.2.1.2)	1.34	0.03	1.29	0.05	1.32	0.03	4.57	0.01	-1.60	0.07	1.49	3.09	-1.20	0.14	-1.65	0.07	-1.43	0.23
SPO3129		hypothetical protein	-1.74	0.29	-1.07	0.17	-1.41	0.34	0.91	0.74	-1.11	0.25	-0.10	1.01	1.19	0.28	-1.30	0.11	-0.06	1.25
SPO3130	*xerC*	site-specific tyrosine recombinase XerC	-1.40	0.20	-1.14	0.31	-1.27	0.13	1.27	0.23	-1.35	0.08	-0.04	1.31	1.10	0.65	-2.01	0.02	-0.46	1.56
SPO3131	*pcs*	phosphatidylcholine synthase (EC:2.7.8.24)	-1.09	0.71	-1.07	0.76	-1.08	0.01	2.45	0.02	1.05	0.95	1.75	0.70	-1.39	0.17	-1.35	0.13	-1.37	0.02
SPO3132		hypothetical protein	-1.10	0.90	1.04	0.94	-0.03	1.07	1.25	0.54	-0.98	0.97	0.14	1.11	1.24	0.79	1.23	0.09	1.24	0.01
SPO3133		hypothetical protein	1.07	0.93	1.09	0.09	1.08	0.01	1.39	0.72	1.64	0.03	1.52	0.13	1.36	0.02	1.42	0.13	1.39	0.03
SPO3134	*ogt*	methylated-DNA--protein-cysteine methyltransferase (EC:2.1.1.63)	-1.45	0.10	-1.12	0.72	-1.29	0.16	-1.62	0.11	1.10	0.66	-0.26	1.36	1.24	0.07	1.87	0.25	1.56	0.31
SPO3135		T4 family peptidase	1.40	X	1.51	0.22	1.46	0.06	3.34	0.00	-1.34	0.08	1.00	2.34	-1.06	0.52	-2.07	0.03	-1.57	0.51
SPO3136	*ileS*	isoleucyl-tRNA synthetase (EC:6.1.1.5)	1.26	0.27	1.40	0.12	1.33	0.07	4.27	0.02	-2.34	0.02	0.97	3.31	-1.06	0.56	-1.95	0.06	-1.51	0.45
SPO3137		hypothetical protein	1.20	0.13	-1.28	0.50	-0.04	1.24	2.54	0.01	-1.56	0.12	0.49	2.05	-1.60	0.13	-2.48	0.00	-2.04	0.44
SPO3138		hypothetical protein	-1.16	0.88	1.82	0.46	0.33	1.49	1.37	0.77	-1.05	0.93	0.16	1.21	1.11	0.69	1.38	X	1.25	0.13
SPO3139		hypothetical protein	-1.72	0.29	-1.30	0.08	-1.51	0.21	-3.10	0.03	1.05	1.00	-1.03	2.08	-1.52	0.32	2.05	0.14	0.27	1.79
SPO3140		hypothetical protein	-1.16	0.30	-1.31	0.82	-1.24	0.08	1.08	0.02	-1.39	0.02	-0.16	1.24	1.90	0.01	1.35	0.06	1.63	0.28
SPO3141		acetyltransferase	-1.27	0.68	-1.61	0.12	-1.44	0.17	-1.23	0.76	-1.38	0.04	-1.31	0.08	1.57	0.09	1.27	0.22	1.42	0.15
SPO3142		hypothetical protein	1.33	0.18	-1.83	0.04	-0.25	1.58	1.65	0.03	-1.26	0.17	0.20	1.46	1.34	0.09	1.26	0.07	1.30	0.04

SPO3143	*truA*	tRNA pseudouridine synthase A (EC:5.4.99.12)	-1.52	X	1.10	0.59	-0.21	1.31	3.83	0.02	-1.29	0.15	1.27	2.56	-1.53	0.05	-2.47	0.01	-2.00	0.47
SPO3144		hypothetical protein	-2.69	0.25	-1.05	0.81	-1.87	0.82	-1.77	0.15	1.13	0.46	-0.32	1.45	1.60	0.03	1.82	0.14	1.71	0.11
SPO3145		GumN family protein	1.15	0.62	0.99	0.86	1.07	0.08	1.21	0.09	-1.25	0.09	-0.02	1.23	1.15	0.32	1.34	0.08	1.25	0.10
SPO3146		GumN family protein	1.88	0.01	-1.05	0.60	0.42	1.47	2.30	0.00	-1.26	0.12	0.52	1.78	-1.27	0.06	-1.36	0.02	-1.32	0.05
SPO3147	*ppaC*	manganese-dependent inorganic pyrophosphatase (EC:3.6.1.1)	2.62	0.00	2.15	0.01	2.39	0.24	7.22	0.00	-1.22	0.05	3.00	4.22	1.06	0.65	-1.43	0.12	-0.19	1.25
SPO3148		hypothetical protein	-0.96	0.80	1.14	0.37	0.09	1.05	1.50	0.20	-1.09	0.69	0.21	1.30	1.42	0.23	-1.25	0.51	0.09	1.34
SPO3149		hypothetical protein	-1.44	1.00	-1.36	0.74	-1.40	0.04	-1.38	0.54	-1.00	0.98	-1.19	0.19	-1.32	0.06	-1.19	0.83	-1.26	0.07
SPO3150		AraC family transcriptional regulator	1.16	1.00	1.01	0.97	1.09	0.08	0.98	1.00	-1.17	0.86	-0.10	1.07	-1.06	0.94	1.10	0.80	0.02	1.08
SPO3151		HAD family hydrolase	1.11	0.23	-1.18	0.21	-0.03	1.15	2.93	0.01	-1.61	0.01	0.66	2.27	-1.88	0.01	-2.33	0.03	-2.11	0.23
SPO3152		acyl dehydratase MaoC	-3.74	0.00	1.23	0.40	-1.26	2.49	-2.70	0.01	-1.25	0.17	-1.98	0.73	-1.10	0.30	-1.51	0.05	-1.31	0.20
SPO3153		monooxygenase	-2.22	0.08	-1.39	0.05	-1.81	0.42	-5.22	0.00	-1.08	0.64	-3.15	2.07	-1.25	0.10	1.91	0.01	0.33	1.58
SPO3154	*ribF*	riboflavin biosynthesis protein RibF (EC:2.7.1.26 2.7.7.2)	1.29	0.25	1.23	0.18	1.26	0.03	3.87	0.00	-1.39	0.20	1.24	2.63	-1.16	0.14	-2.59	0.02	-1.88	0.72
SPO3155		hypothetical protein	-1.03	0.88	1.27	0.05	0.12	1.15	1.41	0.02	-1.11	0.15	0.15	1.26	-1.31	0.03	-2.15	0.01	-1.73	0.42
SPO3156		L-threonine aldolase	2.28	0.07	1.22	0.52	1.75	0.53	2.89	0.06	-1.19	0.20	0.85	2.04	-1.26	0.48	-1.45	0.30	-1.36	0.10
SPO3157		alpha/beta hydrolase	1.72	0.20	1.23	0.30	1.48	0.24	3.36	0.05	1.19	0.41	2.28	1.09	1.31	0.29	1.01	0.80	1.16	0.15
SPO3158	*nahD*	2-hydroxychromene-2-carboxylate isomerase	1.80	0.07	1.11	0.44	1.46	0.35	2.81	0.02	1.00	0.66	1.90	0.91	-1.14	0.37	-1.39	0.00	-1.27	0.13
SPO3159	*prs*	ribose-phosphate pyrophosphokinase (EC:2.7.6.1)	1.83	0.28	1.64	0.22	1.74	0.10	1.74	0.27	-1.13	0.62	0.31	1.44	-1.29	0.35	-1.55	0.28	-1.42	0.13
SPO3160		hypothetical protein	1.15	0.24	1.37	0.10	1.26	0.11	1.30	0.23	-1.29	0.14	0.01	1.30	1.16	0.39	-1.02	0.77	0.07	1.09
SPO3161	*atpC*	ATP synthase F0F1 subunit epsilon (EC:3.6.3.14)	2.05	0.01	2.12	0.02	2.09	0.04	9.45	0.00	-1.69	0.06	3.88	5.57	1.61	0.04	-1.30	0.05	0.16	1.46
SPO3162	*atpD*	ATP synthase F0F1 subunit beta (EC:3.6.3.14)	2.01	0.02	1.09	0.74	1.55	0.46	6.51	0.00	-1.36	0.06	2.58	3.94	1.07	0.90	-1.29	0.06	-0.11	1.18
SPO3163	*atpG*	ATP synthase F0F1 subunit gamma (EC:3.6.3.14)	2.17	0.10	0.96	0.68	1.57	0.60	6.44	0.01	-1.49	0.07	2.48	3.97	-1.49	0.02	-1.73	0.10	-1.61	0.12
SPO3164	*atpA*	ATP synthase F0F1 subunit alpha (EC:3.6.3.14)	1.78	0.02	0.99	0.70	1.38	0.40	5.33	0.00	-1.26	0.03	2.04	3.30	-1.10	0.23	-1.39	0.07	-1.25	0.14
SPO3165	*atpH*	ATP synthase subunit delta (EC:3.6.3.14)	1.58	0.04	1.04	1.00	1.31	0.27	5.60	0.01	-1.63	0.13	1.99	3.62	-1.62	0.02	-2.51	0.06	-2.07	0.44
SPO3166		hypothetical protein	0.96	0.66	1.30	0.61	1.13	0.17	-1.94	0.05	1.90	0.01	-0.02	1.92	1.44	0.10	2.16	0.26	1.80	0.36
SPO3167		hypothetical protein	-1.61	0.01	1.05	0.77	-0.28	1.33	-2.27	0.00	-1.20	0.35	-1.74	0.54	1.04	0.74	1.53	0.05	1.29	0.24
SPO3168		hydroxyacylglutathione hydrolase	-1.18	0.01	-1.32	0.14	-1.25	0.07	-1.43	0.01	1.41	0.20	-0.01	1.42	-1.49	0.01	0.98	0.30	-0.26	1.24
SPO3169	*clpA*	ATP-dependent Clp protease ATP-binding subunit ClpA	1.02	0.01	-1.39	0.02	-0.19	1.21	-1.61	0.00	1.22	0.63	-0.20	1.42	1.06	0.86	1.84	0.01	1.45	0.39
SPO3170		M24/M37 family peptidase	-1.17	0.56	-1.24	0.01	-1.21	0.04	-1.74	0.10	1.04	0.87	-0.35	1.39	1.44	0.01	1.85	0.01	1.65	0.21
SPO3171		hypothetical protein	0.99	0.37	-1.11	0.61	-0.06	1.05	1.14	0.96	1.20	0.18	1.17	0.03	1.15	0.55	2.10	0.03	1.63	0.48
SPO3172		hypothetical protein	-1.50	0.39	1.25	0.40	-0.13	1.38	-1.30	0.08	1.12	0.06	-0.09	1.21	1.50	0.20	1.40	0.18	1.45	0.05
SPO3173		cation transport protein ChaC	-1.16	0.93	1.12	0.73	-0.02	1.14	1.37	0.87	-1.32	0.54	0.03	1.35	-1.04	0.78	-1.42	0.59	-1.23	0.19
SPO3174		hypothetical protein	-1.36	0.57	-1.19	0.41	-1.28	0.09	-2.05	0.20	-1.37	0.19	-1.71	0.34	1.33	0.25	2.45	0.02	1.89	0.56
SPO3175		hypothetical protein	1.13	0.76	1.00	0.68	1.06	0.07	1.21	0.32	-1.11	0.25	0.05	1.16	-1.49	0.06	-1.47	0.05	-1.48	0.01
SPO3176		cyclohexadienyl dehydrogenase (EC:1.3.1.12)	1.48	0.01	1.37	0.00	1.43	0.05	-1.43	0.01	-1.35	0.07	-1.39	0.04	-1.25	0.17	-1.90	0.05	-1.58	0.33
SPO3177	*hisC*	histidinol-phosphate aminotransferase (EC:2.6.1.9)	-1.26	0.16	1.02	0.99	-0.12	1.14	-1.22	0.53	-1.35	0.50	-1.29	0.07	-1.13	0.80	1.22	0.84	0.05	1.18
SPO3178		hypothetical protein	1.25	0.39	-1.18	0.69	0.04	1.22	-2.07	0.03	-1.38	0.16	-1.73	0.35	-1.13	0.92	1.68	0.06	0.28	1.41
SPO3179		AsnC family transcriptional regulator	1.33	0.11	1.46	0.01	1.40	0.06	-2.03	0.04	-1.70	0.06	-1.87	0.17	-1.56	0.07	-2.99	0.09	-2.28	0.71
SPO3180	*rpiB*	ribose 5-phosphate isomerase B (EC:5.3.1.6)	1.25	0.40	1.58	0.18	1.42	0.17	2.99	0.01	-1.61	0.04	0.69	2.30	-1.40	0.08	-2.52	0.00	-1.96	0.56

SPO3181	*rpsD*	30S ribosomal protein S4	-2.09	0.04	1.46	0.07	-0.32	1.78	2.37	0.01	-1.52	0.08	0.43	1.95	1.06	0.83	-1.54	0.05	-0.24	1.30
SPO3182		hypothetical protein	-2.11	0.00	-1.09	0.61	-1.60	0.51	-1.42	0.03	-2.04	0.02	-1.73	0.31	-1.53	0.15	-2.06	0.02	-1.80	0.27
SPO3183		molybdopterin-binding oxidoreductase	-1.10	0.33	1.07	0.39	-0.02	1.09	-2.30	0.02	-1.49	0.07	-1.90	0.41	-1.17	0.66	1.52	0.23	0.18	1.35
SPO3184		acetyltransferase	2.16	0.08	1.04	0.90	1.60	0.56	-1.00	0.56	1.18	0.55	0.09	1.09	-1.15	0.56	-0.93	0.56	-1.04	0.11
SPO3185		GntR family transcriptional regulator	-1.85	0.04	-1.10	0.24	-1.48	0.38	-1.97	0.04	-1.04	0.78	-1.51	0.47	-1.29	0.20	1.45	0.09	0.08	1.37
SPO3186	*opuD*	glycine betaine transporter	-1.47	0.10	-1.44	0.15	-1.46	0.02	-2.56	0.02	1.47	0.03	-0.55	2.02	1.51	0.02	1.79	0.06	1.65	0.14
SPO3187	*comC*	(2R)-3-sulfolactate dehydrogenase	-1.75	0.23	-1.53	0.19	-1.64	0.11	-1.48	0.64	1.51	0.37	0.02	1.50	-1.00	0.96	-0.94	0.41	-0.97	0.03
SPO3188		hypothetical protein	1.25	0.94	-1.27	0.55	-0.01	1.26	1.57	0.81	1.18	0.21	1.38	0.20	1.03	0.94	1.54	0.33	1.29	0.25
SPO3189		hypothetical protein	-1.69	0.57	-1.25	0.19	-1.47	0.22	-1.66	0.70	1.42	0.05	-0.12	1.54	-0.98	0.74	1.23	0.37	0.13	1.10
SPO3190		renal dipeptidase	-2.17	0.02	-1.54	0.06	-1.86	0.32	-1.50	0.15	1.54	0.07	0.02	1.52	1.07	0.64	-0.92	0.42	0.07	1.00
SPO3191		aldehyde dehydrogenase	-2.06	0.17	-1.41	0.05	-1.74	0.33	-1.55	0.44	1.08	0.63	-0.24	1.32	-1.06	0.77	-0.98	0.72	-1.02	0.04
SPO3192		LysR family transcriptional regulator	-3.99	0.01	-1.54	0.07	-2.77	1.23	-1.21	0.84	1.18	0.10	-0.02	1.20	-1.07	0.75	-1.24	0.41	-1.16	0.09
SPO3193		hypothetical protein	-1.09	0.26	1.08	0.69	-0.01	1.09	1.08	0.86	2.12	0.01	1.60	0.52	1.57	0.18	2.86	0.04	2.22	0.65
SPO3194		ribonucleoside-diphosphate reductase	1.78	0.32	1.32	0.14	1.55	0.23	3.11	0.09	-1.18	0.55	0.97	2.15	1.29	0.55	-1.15	0.61	0.07	1.22
SPO3195		histone deacetylase	1.40	0.50	1.32	0.16	1.36	0.04	-1.13	0.81	1.31	0.09	0.09	1.22	1.11	0.68	1.08	0.48	1.10	0.02
SPO3196	*recO*	DNA repair protein RecO	1.07	0.79	-1.11	0.28	-0.02	1.09	-1.06	0.76	1.36	0.10	0.15	1.21	1.04	0.76	1.84	0.01	1.44	0.40
SPO3197		hypothetical protein	1.00	0.61	1.63	0.13	1.31	0.32	1.06	0.93	-1.33	0.55	-0.14	1.20	1.35	0.41	-1.06	0.95	0.15	1.21
SPO3198	*rnc*	ribonuclease III (EC:3.1.26.3)	1.52	0.21	1.24	0.33	1.38	0.14	4.14	0.00	-1.28	0.01	1.43	2.71	1.26	0.05	-1.38	0.04	-0.06	1.32
SPO3199	*lepB*	signal peptidase I (EC:3.4.21.89)	2.43	0.05	1.04	0.92	1.74	0.70	5.31	0.03	-1.06	0.60	2.13	3.19	-1.03	0.67	-1.16	0.37	-1.10	0.06
SPO3200	*acpS*	4'-phosphopantetheinyl transferase (EC:2.7.8.7)	1.64	0.01	1.02	0.75	1.33	0.31	2.64	0.00	1.21	0.25	1.93	0.72	-1.37	0.05	1.17	0.77	-0.10	1.27
SPO3201	*pdxJ*	pyridoxine 5'-phosphate synthase	1.54	0.02	1.14	0.36	1.34	0.20	2.62	0.03	1.35	0.00	1.99	0.64	1.03	0.70	1.44	0.04	1.24	0.21
SPO3202		hypothetical protein	-1.21	0.11	1.13	0.42	-0.04	1.17	1.91	0.02	1.13	0.57	1.52	0.39	-1.46	0.04	-1.36	0.13	-1.41	0.05
SPO3203		guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.09	0.71	1.11	0.66	1.10	0.01	2.38	0.01	1.29	0.07	1.84	0.55	0.99	0.34	0.98	0.29	0.98	0.01
SPO3204	*rpoZ*	DNA-directed RNA polymerase subunit omega (EC:2.7.7.6)	1.27	0.10	-1.47	0.04	-0.10	1.37	4.17	0.00	1.37	0.30	2.77	1.40	-1.36	0.17	0.89	0.23	-0.24	1.12
SPO3205	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC:2.7.6.3)	-1.41	0.12	-1.17	0.45	-1.29	0.12	1.13	0.25	-1.12	0.10	0.00	1.13	-1.57	0.03	-1.55	0.04	-1.56	0.01
SPO3206		hypothetical protein	-1.47	0.49	0.99	0.90	-0.24	1.23	2.26	0.06	0.98	0.70	1.62	0.64	1.44	0.31	1.46	0.37	1.45	0.01
SPO3207	*ispH*	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC:1.17.1.2)	-1.42	0.36	1.01	0.89	-0.21	1.22	1.72	0.22	-1.19	0.23	0.27	1.46	1.31	0.28	1.25	0.33	1.28	0.03
SPO3208		glutathione S-transferase	-1.31	0.09	-1.13	0.04	-1.22	0.09	2.21	0.02	-1.59	0.02	0.31	1.90	-1.05	0.54	-1.52	0.03	-1.29	0.23
SPO3209		amino acid transporter LysE	-1.05	0.16	1.03	0.95	-0.01	1.04	1.10	0.10	1.10	0.75	1.10	0.00	1.03	0.93	1.28	0.37	1.16	0.13
SPO3210		hypothetical protein	1.01	0.97	1.07	0.85	1.04	0.03	1.41	0.17	1.01	0.72	1.21	0.20	1.58	0.05	1.38	0.44	1.48	0.10
SPO3211		hypothetical protein	-1.32	0.76	1.23	0.33	-0.05	1.28	1.61	0.14	1.07	0.75	1.34	0.27	-1.12	0.42	-1.10	0.70	-1.11	0.01
SPO3212	*rnhA*	ribonuclease H	-1.63	0.03	1.41	0.05	-0.11	1.52	-1.05	0.84	-1.45	0.09	-1.25	0.20	-1.03	0.61	-1.43	0.10	-1.23	0.20
SPO3213		hypothetical protein	-1.54	0.01	-1.40	0.21	-1.47	0.07	-2.05	0.02	1.09	0.67	-0.48	1.57	1.03	0.94	2.61	0.06	1.82	0.79
SPO3214		hypothetical protein	1.39	0.15	1.26	0.25	1.33	0.06	1.86	0.07	-1.03	0.71	0.42	1.45	1.40	0.03	1.05	0.87	1.23	0.17
SPO3215		hypothetical protein	1.27	0.86	-1.05	0.69	0.11	1.16	1.63	0.13	1.13	0.38	1.38	0.25	1.02	0.93	-1.27	0.12	-0.13	1.15
SPO3216	*fmt*	methionyl-tRNA formyltransferase (EC:2.1.2.9)	1.02	0.90	0.99	0.95	1.00	0.02	1.19	0.20	-1.22	0.44	-0.02	1.21	1.33	0.12	1.57	0.30	1.45	0.12
SPO3217	*def-1*	peptide deformylase (EC:3.5.1.88)	1.47	0.09	-1.09	0.48	0.19	1.28	2.66	0.01	-1.08	0.26	0.79	1.87	1.18	0.21	-1.16	0.14	0.01	1.17

SPO3218	*def-2*	peptide deformylase (EC:3.5.1.88)	1.45	0.03	0.99	0.92	1.22	0.23	3.36	0.00	-1.18	0.24	1.09	2.27	-1.02	0.45	-1.39	0.04	-1.21	0.18
SPO3219	*def-3*	peptide deformylase (EC:3.5.1.88)	-1.06	0.45	-1.42	0.08	-1.24	0.18	1.90	0.02	-1.58	0.02	0.16	1.74	-1.18	0.17	-1.52	0.04	-1.35	0.17
SPO3220		class I and II aminotransferase	1.42	0.03	-1.17	0.02	0.13	1.30	2.76	0.01	1.60	0.04	2.18	0.58	0.98	0.55	1.59	0.02	1.28	0.31
SPO3221		hypothetical protein	0.95	0.08	1.21	0.04	1.08	0.13	-2.70	0.00	1.25	0.17	-0.73	1.98	1.72	0.00	1.88	0.01	1.80	0.08
SPO3222		hypothetical protein	-1.59	0.81	-1.53	0.36	-1.56	0.03	-1.50	0.84	1.07	0.83	-0.22	1.29	-1.52	0.21	-1.58	0.09	-1.55	0.03
SPO3223		response regulator	-1.82	0.08	1.51	0.01	-0.16	1.67	-2.16	0.02	1.72	0.04	-0.22	1.94	1.07	0.33	1.11	0.09	1.09	0.02
SPO3224	*cobC*	cobalamin biosynthetic protein CobC	-1.08	0.93	1.23	0.50	0.08	1.16	1.78	0.67	-1.21	0.30	0.29	1.50	-1.18	0.40	-1.54	0.25	-1.36	0.18
SPO3225	*cobD*	cobalamin biosynthesis protein	1.52	0.08	1.27	0.04	1.40	0.13	1.69	0.00	-1.06	0.63	0.32	1.38	-1.31	0.08	-1.58	0.16	-1.45	0.14
SPO3226		hypothetical protein	-1.66	0.04	-1.35	0.20	-1.51	0.16	2.15	0.03	-1.76	0.03	0.20	1.96	1.07	0.61	-1.16	0.23	-0.04	1.12
SPO3227		hypothetical protein	-1.66	0.42	-1.19	0.73	-1.43	0.24	-1.88	0.08	1.27	0.81	-0.31	1.58	1.09	0.71	2.25	0.10	1.67	0.58
SPO3228		SMC protein	-1.85	0.04	1.39	0.20	-0.23	1.62	-1.26	0.44	1.37	0.08	0.06	1.32	1.78	0.03	1.37	0.09	1.58	0.20
SPO3229		lipoprotein	1.49	0.41	X	X	N/A	N/A	-2.43	0.07	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3230		class I and II aminotransferase	1.77	0.75	-1.38	0.66	0.20	1.58	1.20	0.91	-1.27	0.51	-0.04	1.24	-1.30	0.55	-1.18	0.87	-1.24	0.06
SPO3231	*pdhR*	pyruvate dehydrogenase complex repressor	1.10	0.98	-1.32	0.42	-0.11	1.21	1.66	0.44	1.58	0.27	1.62	0.04	1.03	0.99	1.45	0.56	1.24	0.21
SPO3232		hypothetical protein	-1.11	0.44	1.23	0.47	0.06	1.17	1.34	0.33	1.61	0.10	1.48	0.14	1.42	0.10	1.21	0.50	1.32	0.11
SPO3233	*atpF*	ATP synthase F0F1 subunit B (EC:3.6.3.14)	2.45	0.01	1.32	0.25	1.89	0.57	11.70	0.00	-1.64	0.02	5.03	6.67	1.65	0.04	0.94	0.26	1.30	0.35
SPO3234		ATP synthase F0F1 subunit B' (EC:3.6.3.14)	2.83	0.02	1.19	0.29	2.01	0.82	13.60	0.00	-1.24	0.09	6.18	7.42	1.08	0.90	-1.37	0.12	-0.15	1.23
SPO3235	*atpE*	ATP synthase F0F1 subunit C (EC:3.6.3.14)	3.36	0.01	1.90	0.00	2.63	0.73	11.40	0.00	-1.29	0.11	5.06	6.35	1.42	0.18	0.92	0.21	1.17	0.25
SPO3236	*atpB*	ATP synthase F0F1 subunit A (EC:3.6.3.14)	2.21	0.01	-1.04	0.83	0.59	1.63	9.39	0.00	-1.50	0.04	3.95	5.45	-1.52	0.00	-1.35	0.14	-1.44	0.09
SPO3237	*atpI*	ATP synthase F0 subunit I (EC:3.6.3.14)	1.09	0.80	0.98	0.65	1.03	0.06	7.24	0.02	-1.52	0.01	2.86	4.38	-1.64	0.01	-1.66	0.10	-1.65	0.01
SPO3238		ArsR family transcriptional regulator	-1.68	0.02	-1.38	0.08	-1.53	0.15	1.14	0.03	1.18	0.42	1.16	0.02	-1.40	0.22	-1.05	0.81	-1.23	0.17
SPO3239		hypothetical protein	1.26	0.90	-1.13	0.85	0.07	1.20	2.31	0.63	1.04	0.96	1.68	0.64	1.45	0.41	1.30	0.63	1.38	0.08
SPO3240		LysR family transcriptional regulator	1.22	0.70	-1.02	0.95	0.10	1.12	2.10	0.14	-1.19	0.59	0.46	1.65	1.60	0.28	1.13	0.72	1.37	0.24
SPO3241		Asp/Glu/Hydantoin racemase	1.19	0.60	-1.06	0.36	0.06	1.13	1.00	0.52	1.32	0.04	1.16	0.16	1.02	0.97	1.14	0.11	1.08	0.06
SPO3242		prolyl-tRNA synthetase	2.66	0.05	1.24	0.24	1.95	0.71	4.26	0.03	-1.37	0.04	1.45	2.82	-1.00	0.91	-1.77	0.05	-1.38	0.39
SPO3243	*nadA*	quinolinate synthetase	1.26	0.67	-1.91	0.07	-0.33	1.59	3.65	0.08	-1.39	0.06	1.13	2.52	-1.16	0.44	-1.20	0.07	-1.18	0.02
SPO3244		L-aspartate oxidase (EC:1.4.3.16)	1.58	0.85	-1.73	0.21	-0.08	1.66	2.45	0.64	1.16	0.78	1.81	0.65	-1.52	0.12	-1.26	0.25	-1.39	0.13
SPO3245	*nadC*	nicotinate-nucleotide pyrophosphorylase (EC:2.4.2.19)	1.94	0.17	-1.53	0.01	0.21	1.74	6.42	0.04	-1.12	0.34	2.65	3.77	0.99	0.78	0.93	0.14	0.96	0.03
SPO3246	*ffh*	signal recognition particle protein	-1.14	0.67	1.17	0.08	0.02	1.16	1.98	0.01	-2.94	0.01	-0.48	2.46	-1.19	0.23	-1.15	0.43	-1.17	0.02
SPO3247		acetyltransferase	-1.06	0.46	1.59	0.01	0.27	1.33	2.87	0.00	-2.00	0.01	0.44	2.44	-1.11	0.50	-2.02	0.01	-1.57	0.46
SPO3248		acetyltransferase	-1.38	0.72	1.13	0.70	-0.13	1.26	2.26	0.35	-2.60	0.10	-0.17	2.43	-1.65	0.26	-1.77	0.04	-1.71	0.06
SPO3249		acetyltransferase	-1.38	X	1.28	0.06	-0.05	1.33	2.38	0.00	-2.62	0.00	-0.12	2.50	-1.32	0.03	-2.07	0.01	-1.70	0.38
SPO3250		acetyltransferase	-1.31	X	1.17	0.75	-0.07	1.24	1.23	0.84	-2.67	0.17	-0.72	1.95	-1.49	0.50	-2.10	0.23	-1.80	0.31
SPO3251		hypothetical protein	-1.30	0.01	0.99	0.09	-0.15	1.15	-1.59	0.03	-2.45	0.01	-2.02	0.43	-1.81	0.04	-1.64	0.05	-1.73	0.09
SPO3252		chorismate mutase (EC:5.4.99.5)	1.06	1.00	-1.19	0.35	-0.06	1.13	1.78	0.03	-2.83	0.01	-0.53	2.31	-2.59	0.00	-3.69	0.01	-3.14	0.55
SPO3253	*rpsP*	30S ribosomal protein S16	1.04	0.79	1.15	0.06	1.10	0.05	2.32	0.03	-3.18	0.01	-0.43	2.75	1.09	0.60	-1.45	0.01	-0.18	1.27
SPO3254	*bluB*	cobalamin biosynthesis protein BluB	-1.09	0.76	1.17	0.38	0.04	1.13	1.94	0.01	-2.46	0.07	-0.26	2.20	-1.05	0.68	-1.33	0.60	-1.19	0.14
SPO3255	*rimM*	16S rRNA-processing protein RimM	1.07	0.60	1.48	0.44	1.28	0.21	2.45	0.08	-1.51	0.49	0.47	1.98	1.10	0.88	-1.78	0.42	-0.34	1.44
SPO3256	*rpmE*	50S ribosomal protein L31	-1.42	0.32	1.48	0.01	0.03	1.45	5.13	0.00	-1.14	0.29	2.00	3.14	-1.16	0.14	-1.81	0.01	-1.49	0.33

SPO3257	*rplS*	50S ribosomal protein L19	-1.42	0.04	-1.42	0.18	-1.42	0.00	5.94	0.00	-1.33	0.06	2.31	3.64	-1.52	0.04	-2.30	0.02	-1.91	0.39
SPO3258		glycosyl hydrolase	1.09	0.83	-1.63	0.01	-0.27	1.36	4.76	0.05	-1.21	0.27	1.78	2.99	1.34	0.07	1.30	0.05	1.32	0.02
SPO3259	*trmD*	tRNA (guanine-N(1)-)-methyltransferase	-1.08	0.48	-1.30	0.09	-1.19	0.11	2.35	0.00	-1.11	0.17	0.62	1.73	-1.06	0.34	1.11	0.55	0.03	1.09
SPO3260		methyltransferase-like protein	-1.39	0.61	1.07	0.44	-0.16	1.23	-1.36	0.78	-1.13	0.56	-1.25	0.12	1.09	0.70	-1.22	0.19	-0.06	1.16
SPO3261		glutathione S-transferase	-1.20	0.05	-1.45	0.25	-1.33	0.13	-1.48	0.04	-2.76	0.00	-2.12	0.64	-1.12	0.21	-1.44	0.09	-1.28	0.16
SPO3262		MarR family transcriptional regulator	-1.41	0.32	-1.32	0.51	-1.37	0.04	-2.75	0.03	-1.09	0.30	-1.92	0.83	-1.24	0.33	-1.20	0.51	-1.22	0.02
SPO3263		hypothetical protein	-1.16	0.76	-1.23	0.75	-1.20	0.04	-1.03	0.50	-1.29	0.77	-1.16	0.13	1.07	0.83	-0.94	0.44	0.07	1.00
SPO3270		sulfite oxidase subunit YedZ	X	X	1.52	0.03	N/A	N/A	1.27	X	-1.18	X	0.05	1.23	1.65	0.26	X	X	N/A	N/A
SPO3271		sulfite oxidase subunit YedY	1.26	0.40	1.45	0.13	1.36	0.10	1.07	0.76	1.29	0.26	1.18	0.11	1.25	0.30	-1.27	0.57	-0.01	1.26
SPO3272		glutamate synthase	-1.08	0.09	1.04	0.92	-0.02	1.06	-1.21	0.15	1.61	0.01	0.20	1.41	1.66	0.01	1.71	0.14	1.69	0.03
SPO3273		hypothetical protein	-1.75	0.09	-1.03	0.85	-1.39	0.36	-1.96	0.24	-1.20	0.20	-1.58	0.38	1.11	0.52	1.11	0.62	1.11	0.00
SPO3274		hypothetical protein	2.37	0.00	-1.31	0.46	0.53	1.84	-2.61	0.02	-1.00	0.92	-1.81	0.81	-1.15	0.57	-1.56	0.07	-1.36	0.21
SPO3275		hypothetical protein	-1.98	0.01	-1.00	0.85	-1.49	0.49	3.12	0.33	1.43	0.07	2.28	0.85	1.49	0.02	-1.08	0.79	0.21	1.29
SPO3276	*clpB*	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.04	0.40	-2.24	0.03	-0.60	1.64	1.38	0.16	-1.80	0.02	-0.21	1.59	1.55	0.09	1.34	0.09	1.45	0.11
SPO3277		hypothetical protein	1.52	0.13	-1.11	0.55	0.21	1.32	1.25	0.27	1.43	0.12	1.34	0.09	-1.30	0.04	-1.56	0.03	-1.43	0.13
SPO3278	*pyrF*	orotidine 5'-phosphate decarboxylase (EC:4.1.1.23)	1.43	0.28	-1.12	0.27	0.16	1.28	4.24	0.01	-1.36	0.18	1.44	2.80	-1.31	0.02	-1.54	0.11	-1.43	0.12
SPO3279		NUDIX domain-containing protein	1.18	0.57	-1.11	0.61	0.03	1.15	1.92	0.04	-1.18	0.37	0.37	1.55	1.21	0.13	-0.99	0.75	0.11	1.10
SPO3280		DNA polymerase IV (EC:2.7.7.7)	1.02	0.78	1.43	0.12	1.23	0.20	1.53	0.16	-1.31	0.21	0.11	1.42	1.52	0.02	-1.31	0.07	0.11	1.42
SPO3281		DinB family protein	1.97	0.00	1.10	0.63	1.54	0.44	2.17	0.01	-0.99	0.95	0.59	1.58	-1.82	0.02	-1.86	0.03	-1.84	0.02
SPO3282		N-formylglutamate amidohydrolase	-1.45	0.04	1.06	0.57	-0.20	1.26	-1.38	0.10	-1.30	0.22	-1.34	0.04	2.09	0.01	1.30	0.06	1.70	0.40
SPO3284	*rpmJ*	50S ribosomal protein L36	-1.30	0.04	1.41	0.15	0.05	1.36	8.20	0.00	-1.37	0.13	3.42	4.79	-1.19	0.30	-2.50	0.01	-1.85	0.66
SPO3285		hypothetical protein	1.84	0.07	1.50	0.28	1.67	0.17	-1.87	0.09	-1.13	0.68	-1.50	0.37	1.04	0.83	-1.27	0.32	-0.12	1.16
SPO3286	*atsA*	arylsulfatase (EC:3.1.6.1)	3.36	0.15	1.23	0.20	2.30	1.07	-1.69	0.44	1.33	0.28	-0.18	1.51	1.13	0.32	1.30	0.38	1.22	0.09
SPO3287		ferric iron ABC transporter substrate-binding protein	1.41	0.08	1.96	0.32	1.69	0.27	2.26	0.05	1.23	0.49	1.75	0.52	-1.54	0.20	-1.78	X	-1.66	0.12
SPO3288		ferric iron ABC transporter permease	-1.30	0.09	1.09	0.82	-0.11	1.20	-1.06	0.79	1.02	0.97	-0.02	1.04	-1.43	0.17	-1.03	0.97	-1.23	0.20
SPO3289		phenylacetate-CoA ligase	1.07	0.91	-1.09	0.52	-0.01	1.08	-1.59	0.23	1.18	0.51	-0.21	1.39	-1.16	0.33	1.08	0.44	-0.04	1.12
SPO3290		branched-chain amino acid ABC transporter ATP-binding protein	-1.10	0.21	-1.06	0.83	-1.08	0.02	-2.91	0.06	1.49	0.19	-0.71	2.20	1.28	0.43	1.31	0.39	1.30	0.02
SPO3291		branched chain amino acid ABC transporter substrate-binding protein	-1.90	0.01	-1.41	0.00	-1.66	0.25	-6.52	0.00	1.49	0.06	-2.52	4.01	1.25	0.24	2.60	0.03	1.93	0.68
SPO3292		branched-chain amino acid ABC transporter permease	-1.24	0.72	1.07	0.86	-0.09	1.16	-1.46	0.67	1.02	0.98	-0.22	1.24	-1.03	0.90	1.11	0.66	0.04	1.07
SPO3293		hypothetical protein	-1.48	0.63	1.32	0.01	-0.08	1.40	-2.96	0.03	1.04	0.56	-0.96	2.00	-1.26	0.21	-1.20	0.26	-1.23	0.03
SPO3294		branched-chain amino acid ABC transporter permease	-2.06	0.00	1.13	0.77	-0.47	1.60	-4.14	0.00	-1.15	0.52	-2.65	1.50	-1.12	0.09	1.22	0.43	0.05	1.17
SPO3295		branched-chain amino acid ABC transporter ATP-binding protein	-1.48	0.07	1.16	0.58	-0.16	1.32	-3.43	0.03	1.19	0.69	-1.12	2.31	-1.16	0.77	1.13	0.70	-0.02	1.15
SPO3296		AMP-binding protein	-1.94	0.55	1.03	0.94	-0.46	1.49	-4.03	0.29	1.39	0.46	-1.32	2.71	1.11	0.76	1.19	0.64	1.15	0.04
SPO3297		sensory box histidine kinase/response regulator	2.53	0.00	1.43	0.19	1.98	0.55	1.65	0.03	1.14	0.12	1.40	0.26	1.17	0.48	-1.10	0.52	0.03	1.14
SPO3298		DNA-binding response regulator	4.80	0.00	1.39	0.50	3.10	1.71	2.90	0.03	1.11	0.80	2.01	0.90	1.11	0.54	1.38	0.52	1.25	0.13
SPO3299		TetR family transcriptional regulator	X	X	1.21	0.09	N/A	N/A	-0.89	0.14	-1.92	0.07	-1.40	0.52	1.53	0.02	-1.36	0.18	0.09	1.45

SPO3300		hypothetical protein	-1.54	0.09	-1.04	0.51	-1.29	0.25	-1.17	0.67	-1.25	0.25	-1.21	0.04	1.23	0.17	-1.03	0.90	0.10	1.13
SPO3301		LysR family transcriptional regulator	-1.29	0.74	-1.34	0.50	-1.32	0.03	1.89	0.43	-1.06	0.70	0.42	1.48	1.10	0.38	1.19	0.35	1.15	0.04
SPO3302		hypothetical protein	X	X	-1.02	0.92	N/A	N/A	-1.46	0.21	1.15	0.42	-0.16	1.31	-1.14	0.79	X	X	N/A	N/A
SPO3303		GDSL-like lipase/acylhydrolase	1.96	0.03	1.54	0.05	1.75	0.21	-1.85	0.03	-1.15	0.14	-1.50	0.35	1.14	0.21	-1.15	0.29	-0.01	1.15
SPO3304		allantoate amidohydrolase	2.07	0.52	-1.29	0.11	0.39	1.68	1.38	0.12	-1.23	0.42	0.08	1.31	1.29	0.32	1.37	0.39	1.33	0.04
SPO3305		phosphoglycerate mutase	-1.07	0.90	1.10	0.58	0.02	1.09	2.92	0.11	-1.11	0.37	0.91	2.02	-1.50	0.09	-1.97	0.02	-1.74	0.24
SPO3306		glutathione S-transferase	-1.38	0.06	-1.09	0.59	-1.24	0.15	1.76	0.08	0.99	0.58	1.37	0.39	-2.04	0.01	-1.84	0.01	-1.94	0.10
SPO3307		saccharopine dehydrogenase	1.52	0.02	1.18	0.06	1.35	0.17	2.02	0.01	-1.14	0.18	0.44	1.58	-1.45	0.10	-1.22	0.09	-1.34	0.12
SPO3308		hypothetical protein	2.06	0.02	1.05	0.89	1.56	0.50	2.54	0.00	0.99	0.43	1.76	0.78	-2.20	0.58	-1.86	0.01	-2.03	0.17
SPO3309		saccharopine dehydrogenase	1.51	0.47	-1.07	0.59	0.22	1.29	1.51	0.65	-1.10	0.41	0.21	1.31	-1.87	0.03	-1.52	0.10	-1.70	0.18
SPO3310		hypothetical protein	-2.38	0.03	1.71	0.02	-0.34	2.05	1.13	0.68	1.06	0.71	1.10	0.03	1.20	0.19	-1.29	0.16	-0.05	1.25
SPO3311		ADA regulatory protein	-1.49	0.02	-1.23	0.16	-1.36	0.13	-1.76	0.03	1.23	0.59	-0.27	1.50	-1.25	0.02	-1.38	0.03	-1.32	0.06
SPO3312		hypothetical protein	1.13	0.23	1.05	0.43	1.09	0.04	-1.17	0.94	1.37	0.05	0.10	1.27	1.27	0.20	-1.03	0.70	0.12	1.15
SPO3313		DNA-binding protein	-1.93	0.07	-1.28	0.28	-1.61	0.33	-1.52	0.24	-1.10	0.59	-1.31	0.21	-1.49	0.10	2.05	0.17	0.28	1.77
SPO3314	*ilvD*	dihydroxy-acid dehydratase (EC:4.2.1.9)	-2.58	0.51	1.06	0.77	-0.76	1.82	-1.92	0.53	-1.56	0.09	-1.74	0.18	1.09	0.70	0.96	0.74	1.02	0.07
SPO3315		LysR family transcriptional regulator	0.91	0.86	-1.14	0.79	-0.11	1.03	-2.13	0.54	-1.05	0.91	-1.59	0.54	1.24	0.61	2.01	0.34	1.63	0.38
SPO3316		hypothetical protein	-1.85	0.57	1.40	0.54	-0.23	1.63	-1.26	0.97	3.91	0.16	1.33	2.59	-1.08	0.95	1.34	0.65	0.13	1.21
SPO3317		transcriptional regulator	-1.23	0.05	-1.12	0.71	-1.18	0.05	1.57	0.01	1.05	0.78	1.31	0.26	-1.18	0.34	-1.46	0.09	-1.32	0.14
SPO3318		hypothetical protein	1.62	0.05	-1.15	0.14	0.24	1.39	1.15	0.59	-1.28	0.12	-0.07	1.22	-1.34	0.05	-1.51	0.03	-1.43	0.09
SPO3319		EpsK domain-containing protein	-1.62	0.52	-1.37	0.21	-1.50	0.13	1.77	0.37	-1.15	0.36	0.31	1.46	-1.12	0.44	-1.17	0.63	-1.15	0.02
SPO3320		hypothetical protein	1.48	0.52	1.18	0.60	1.33	0.15	1.11	0.91	-1.05	0.64	0.03	1.08	1.48	0.02	1.41	0.14	1.45	0.04
SPO3321		hypothetical protein	1.93	0.01	-1.26	0.49	0.34	1.60	1.28	0.15	1.15	0.17	1.22	0.07	-1.39	0.02	-1.11	0.25	-1.25	0.14
SPO3322		hypothetical protein	1.57	0.01	-1.07	0.21	0.25	1.32	1.16	0.61	-1.06	0.40	0.05	1.11	1.35	0.05	1.21	0.42	1.28	0.07
SPO3323		hypothetical protein	1.49	0.41	-1.34	0.09	0.08	1.42	1.11	1.00	1.09	0.76	1.10	0.01	1.39	0.19	1.72	0.06	1.56	0.17
SPO3324		hypothetical protein	-1.24	0.09	-1.27	0.34	-1.26	0.02	1.36	0.28	1.03	0.91	1.20	0.17	1.56	0.13	1.65	0.01	1.61	0.04
SPO3325		hypothetical protein	1.35	0.59	-1.20	0.16	0.08	1.28	1.57	0.21	1.39	0.05	1.48	0.09	1.58	0.09	2.20	0.04	1.89	0.31
SPO3326		hypothetical protein	-1.45	0.02	1.34	0.08	-0.05	1.40	-1.21	0.05	1.03	0.88	-0.09	1.12	1.49	0.27	1.05	0.65	1.27	0.22
SPO3327		creatinase (EC:3.5.3.3)	1.73	0.74	1.45	0.38	1.59	0.14	1.26	0.83	-0.99	0.97	0.14	1.13	1.09	0.82	-1.18	0.91	-0.04	1.14
SPO3328	*gabD-2*	succinate-semialdehyde dehydrogenase (EC:1.2.1.16)	1.10	0.95	1.04	0.94	1.07	0.03	-1.14	0.16	1.20	0.32	0.03	1.17	1.04	0.93	1.02	0.96	1.03	0.01
SPO3329		globin domain-containing protein	1.61	0.02	1.66	0.05	1.64	0.02	-6.40	0.00	1.63	0.09	-2.39	4.02	-1.00	0.37	X	X	N/A	N/A
SPO3330	*rnr*	ribonuclease R (EC:3.1.-.-)	1.58	X	1.17	0.25	1.38	0.21	2.56	0.03	-1.35	0.09	0.61	1.96	-1.16	0.05	-1.68	0.02	-1.42	0.26
SPO3331		hypothetical protein	1.11	1.00	1.03	0.97	1.07	0.04	1.11	0.99	1.03	0.96	1.07	0.04	-1.01	0.99	1.62	0.45	0.31	1.32
SPO3332	*dapE*	succinyl-diaminopimelate desuccinylase (EC:3.5.1.18)	-1.81	0.01	1.27	0.66	-0.27	1.54	-1.16	0.33	-1.63	0.24	-1.40	0.23	1.84	0.01	1.37	0.04	1.61	0.24
SPO3333		hypothetical protein	-2.35	0.14	-1.72	0.07	-2.04	0.31	-2.88	0.14	-1.58	0.06	-2.23	0.65	-1.35	0.28	-1.56	0.13	-1.46	0.11
SPO3334		hypothetical protein	-2.21	0.04	-1.59	0.07	-1.90	0.31	-2.49	0.09	-1.74	0.03	-2.12	0.37	-1.23	0.21	-1.14	0.36	-1.19	0.05
SPO3335		glutamine ABC transporter substrate-binding protein	X	X	1.66	0.02	N/A	N/A	1.88	0.04	-1.16	0.27	0.36	1.52	-1.14	0.38	-1.46	0.07	-1.30	0.16
SPO3336		hypothetical protein	-1.38	0.02	1.40	0.46	0.01	1.39	-1.17	0.27	-1.18	0.11	-1.18	0.01	1.23	0.14	1.24	0.42	1.24	0.01
SPO3337	*dapD*	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase (EC:2.3.1.117)	1.97	0.34	1.35	0.09	1.66	0.31	3.10	0.02	1.07	0.91	2.09	1.02	1.02	0.81	1.17	0.23	1.10	0.08

SPO3338	*bioB*	biotin synthase (EC:2.8.1.6)	-1.05	X	1.01	0.98	-0.02	1.03	-1.19	0.90	1.40	0.71	0.11	1.30	-1.00	0.97	-1.16	0.90	-1.08	0.08
SPO3339		bioY family protein	1.07	0.61	1.10	0.73	1.09	0.02	1.30	0.11	1.09	0.65	1.20	0.11	-1.10	0.71	1.11	0.63	0.01	1.11
SPO3340		GntR family transcriptional regulator	1.24	X	-1.17	0.09	0.04	1.21	1.99	0.02	-1.10	0.50	0.45	1.55	1.27	0.06	-1.16	0.60	0.06	1.22
SPO3341		threonine dehydratase (EC:4.3.1.19)	-1.06	0.59	1.10	0.63	0.02	1.08	2.04	0.05	1.29	0.21	1.67	0.38	-1.12	0.65	-1.13	0.70	-1.13	0.00
SPO3342		decarboxylase	1.25	0.05	1.37	0.22	1.31	0.06	2.21	0.00	-1.36	0.07	0.43	1.79	1.09	0.34	-1.49	0.12	-0.20	1.29
SPO3343		hypothetical protein	-1.59	0.75	-1.01	1.00	-1.30	0.29	-4.18	0.28	-1.14	0.94	-2.66	1.52	-1.09	0.97	1.69	X	0.30	1.39
SPO3344		cystathionine gamma-lyase (EC:4.4.1.1)	-1.26	0.17	1.08	0.61	-0.09	1.17	-1.61	0.04	-1.02	0.54	-1.32	0.30	-1.18	0.18	1.24	0.35	0.03	1.21
SPO3345		hypothetical protein	1.53	0.12	1.59	0.08	1.56	0.03	-1.80	0.03	1.22	0.19	-0.29	1.51	1.56	0.05	1.45	0.03	1.51	0.06
SPO3346		radical SAM protein	-1.08	0.46	-1.02	0.28	-1.05	0.03	2.56	0.01	-1.85	0.10	0.36	2.21	-1.23	0.17	-1.41	0.04	-1.32	0.09
SPO3347		hypothetical protein	-1.37	0.44	-1.18	0.64	-1.28	0.10	1.75	0.49	1.22	0.71	1.49	0.27	1.29	0.42	1.12	0.93	1.21	0.09
SPO3348		hypothetical protein	-1.25	0.15	-1.13	0.30	-1.19	0.06	2.30	0.03	1.43	0.29	1.87	0.44	1.54	0.08	1.30	0.24	1.42	0.12
SPO3349		L-asparaginase	1.09	0.10	-1.47	0.01	-0.19	1.28	2.38	0.00	1.04	0.93	1.71	0.67	-1.32	0.01	-1.28	0.11	-1.30	0.02
SPO3350		hypothetical protein	-1.78	0.16	1.05	0.92	-0.37	1.42	-1.39	0.13	1.14	0.75	-0.13	1.27	1.41	0.33	1.24	0.59	1.33	0.09
SPO3351		Aha1 domain-containing protein	-1.52	0.04	-1.04	0.28	-1.28	0.24	-1.58	0.06	1.39	0.02	-0.10	1.49	1.05	0.84	1.01	0.71	1.03	0.02
SPO3352		ArsR family transcriptional regulator	-2.80	0.47	-1.19	0.57	-2.00	0.81	-2.36	0.59	-1.42	0.40	-1.89	0.47	-1.18	0.63	-1.49	0.37	-1.34	0.16
SPO3353	*serB-2*	phosphoserine phosphatase (EC:3.1.3.3)	-1.05	0.62	1.69	0.15	0.32	1.37	2.37	0.05	-1.37	0.45	0.50	1.87	1.07	0.89	1.04	0.96	1.06	0.02
SPO3354		phosphoserine aminotransferase (EC:2.6.1.52)	1.19	1.00	0.97	0.29	1.08	0.11	2.64	0.11	-1.13	0.58	0.76	1.89	-1.09	0.58	1.11	0.85	0.01	1.10
SPO3355	*serA*	D-3-phosphoglycerate dehydrogenase (EC:1.1.1.95)	-1.12	0.67	1.50	0.20	0.19	1.31	2.80	0.13	-1.24	0.58	0.78	2.02	-1.68	0.31	-1.57	0.40	-1.63	0.05
SPO3356		hypothetical protein	-2.59	0.14	-1.00	0.97	-1.79	0.80	-1.78	0.33	-1.13	0.80	-1.46	0.32	1.08	0.69	-0.93	0.32	0.08	1.01
SPO3357		LysR family transcriptional regulator	-1.50	0.09	-1.11	0.33	-1.31	0.19	-2.03	0.07	-1.57	0.09	-1.80	0.23	-1.25	0.25	-1.21	0.37	-1.23	0.02
SPO3358		serine/threonine protein phosphatase	-1.16	0.33	1.25	0.12	0.05	1.21	1.45	0.04	-1.62	0.01	-0.09	1.54	-1.37	0.22	-1.75	0.06	-1.56	0.19
SPO3359	*tdh*	L-threonine 3-dehydrogenase (EC:1.1.1.103)	-1.03	0.93	-1.17	0.27	-1.10	0.07	23.70	0.00	1.19	0.32	12.45	11.26	1.08	0.38	1.19	0.40	1.14	0.05
SPO3360	*kbl*	2-amino-3-ketobutyrate CoA ligase (EC:2.3.1.29)	-1.23	0.57	-1.56	0.03	-1.40	0.17	17.20	0.00	1.04	0.73	9.12	8.08	-1.56	0.09	-1.15	0.31	-1.36	0.21
SPO3361		RmuC domain-containing protein	1.21	0.09	-1.38	0.05	-0.09	1.30	1.02	0.50	-1.16	0.31	-0.07	1.09	1.07	0.50	1.19	0.15	1.13	0.06
SPO3362	*mutL*	DNA mismatch repair protein	1.75	0.17	-1.10	0.17	0.33	1.43	1.89	0.11	1.15	0.05	1.52	0.37	-1.00	0.93	1.18	0.33	0.09	1.09
SPO3363		zinc/manganese/iron ABC transporter permease	2.56	0.00	1.15	0.48	1.86	0.71	1.13	0.89	-2.63	0.02	-0.75	1.88	1.31	0.16	-1.42	0.19	-0.05	1.37
SPO3364		zinc/manganese/iron ABC transporter permease	2.35	0.32	1.21	0.56	1.78	0.57	1.28	0.97	-1.92	0.12	-0.32	1.60	1.28	0.41	-1.12	0.68	0.08	1.20
SPO3365		zinc/manganese/iron ABC transporter ATP-binding protein	2.96	0.11	-1.16	0.34	0.90	2.06	1.14	0.37	-1.86	0.02	-0.36	1.50	-1.06	0.67	-1.74	0.01	-1.40	0.34
SPO3366		zinc/manganese/iron ABC transporter substrate-binding protein	2.76	0.01	-1.21	0.06	0.78	1.99	1.17	0.03	-2.18	0.02	-0.51	1.68	-1.01	0.89	-1.23	0.04	-1.12	0.11
SPO3367	*deoC*	deoxyribose-phosphate aldolase (EC:4.1.2.4)	-1.23	0.01	-1.55	0.02	-1.39	0.16	-1.33	0.04	-1.08	0.27	-1.21	0.13	-1.12	0.18	-1.09	0.63	-1.11	0.02
SPO3368		aldehyde dehydrogenase	0.96	0.48	-1.23	0.08	-0.13	1.10	-1.28	0.19	-1.20	0.28	-1.24	0.04	-1.01	0.88	-1.28	0.17	-1.15	0.14
SPO3369		short chain dehydrogenase	1.07	0.79	-1.04	0.92	0.02	1.06	-2.91	0.01	-1.15	0.38	-2.03	0.88	1.29	0.15	2.85	0.01	2.07	0.78
SPO3370		M16 family peptidase	-1.13	0.01	-1.32	0.04	-1.23	0.10	2.06	0.01	1.13	0.49	1.60	0.47	1.29	0.22	1.34	0.08	1.32	0.03
SPO3371		M16 family peptidase	1.56	0.17	-1.46	0.23	0.05	1.51	3.92	0.02	1.15	0.67	2.54	1.39	1.13	0.82	1.41	0.31	1.27	0.14
SPO3372		hypothetical protein	0.99	0.68	1.14	0.34	1.06	0.08	1.28	0.22	-1.06	0.53	0.11	1.17	-1.21	0.16	-1.37	0.13	-1.29	0.08
SPO3373	*lspA*	lipoprotein signal peptidase (EC:3.4.23.36)	1.82	0.03	1.71	0.07	1.77	0.06	3.54	0.00	-1.28	0.23	1.13	2.41	-1.20	0.04	-2.47	0.00	-1.84	0.64
SPO3374	*purH*	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (EC:2.1.2.3	-1.19	0.17	1.90	0.00	0.36	1.55	1.63	0.01	-1.15	0.20	0.24	1.39	1.06	0.81	-1.16	0.10	-0.05	1.11

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SPO3375		hypothetical protein	-1.58	0.01	-1.40	0.01	-1.49	0.09	-1.30	0.15	-1.06	0.44	-1.18	0.12	-1.20	0.03	-2.07	0.00	-1.64	0.44
SPO3376		ribosomal RNA small subunit methyltransferase B	-2.28	0.23	-1.27	0.62	-1.78	0.51	-2.24	0.03	-1.10	0.86	-1.67	0.57	-1.10	0.57	1.47	0.43	0.19	1.29
SPO3377		hypothetical protein	1.56	0.58	1.82	0.05	1.69	0.13	1.22	0.34	1.44	0.15	1.33	0.11	1.23	0.42	1.26	0.63	1.25	0.02
SPO3378		benzoate transporter	1.28	0.93	1.45	0.01	1.37	0.09	1.19	0.97	1.09	0.18	1.14	0.05	1.63	0.04	-0.96	0.43	0.34	1.29
SPO3379		LysR family transcriptional regulator	1.04	0.98	-1.13	0.87	-0.04	1.09	1.07	1.00	-1.02	0.96	0.03	1.05	1.29	0.19	1.78	0.53	1.54	0.25
SPO3380		gamma-butyrobetaine hydroxylase	3.40	0.14	1.06	0.38	2.23	1.17	-1.12	0.18	-1.05	0.78	-1.09	0.04	-1.31	0.18	-1.88	0.04	-1.60	0.29
SPO3381		hypothetical protein	-1.31	0.11	1.08	0.25	-0.12	1.20	8.50	0.01	-1.23	0.34	3.64	4.87	1.18	0.23	-1.50	0.24	-0.16	1.34
SPO3382		aldehyde dehydrogenase	1.20	0.18	1.31	0.09	1.26	0.06	1.74	0.00	-1.29	0.18	0.23	1.52	1.07	0.59	1.27	0.05	1.17	0.10
SPO3383		thiol-specific antioxidant protein	2.17	0.01	1.21	0.47	1.69	0.48	2.94	0.01	1.56	0.02	2.25	0.69	1.28	0.18	1.70	0.09	1.49	0.21
SPO3384		FkbM family methyltransferase	1.07	0.91	1.33	0.15	1.20	0.13	0.94	0.56	1.03	0.93	0.98	0.05	1.25	0.32	1.59	0.09	1.42	0.17
SPO3385		glycosyl transferase family protein	-1.43	0.22	1.20	0.12	-0.12	1.32	1.42	0.04	-1.54	0.57	-0.06	1.48	1.41	0.20	-1.43	0.06	-0.01	1.42
SPO3386		hypothetical protein	1.42	0.17	-1.15	0.71	0.14	1.29	-1.33	0.73	-1.12	0.24	-1.23	0.11	-1.26	0.11	-1.15	0.96	-1.21	0.06
SPO3387		hypothetical protein	1.41	0.36	-1.11	0.82	0.15	1.26	-1.03	0.75	-1.20	0.49	-1.12	0.09	1.21	0.50	-1.24	0.64	-0.02	1.23
SPO3388		TetR family transcriptional regulator	1.25	0.36	-1.03	0.93	0.11	1.14	-1.08	0.80	-1.33	0.36	-1.21	0.13	1.14	0.53	-1.54	0.35	-0.20	1.34
SPO3389	*pnp*	polynucleotide phosphorylase (EC:2.7.7.8)	-1.20	0.80	1.55	0.31	0.18	1.38	3.88	0.25	-1.51	0.15	1.19	2.70	1.20	0.61	-1.22	0.43	-0.01	1.21
SPO3390		hypothetical protein	-7.48	0.06	-2.43	0.04	-4.96	2.53	0.87	0.20	-1.10	0.20	-0.11	0.99	-1.25	0.12	1.33	0.37	0.04	1.29
SPO3391		alpha-1,2-fucosyltransferase	-1.57	0.20	1.11	0.08	-0.23	1.34	1.60	0.07	-1.07	0.40	0.27	1.34	1.12	0.64	-1.45	0.10	-0.17	1.29
SPO3392	*rluA*	ribosomal large subunit pseudouridine synthase A (EC:4.2.1.70)	X	X	-1.06	0.79	N/A	N/A	2.46	0.00	-1.49	0.15	0.49	1.98	-1.40	0.14	-1.12	0.79	-1.26	0.14
SPO3393		hypothetical protein	2.19	0.01	1.06	0.75	1.63	0.57	-1.56	0.02	1.64	0.09	0.04	1.60	1.35	0.02	2.06	0.08	1.71	0.36
SPO3394		GDSL-like lipase/acylhydrolase	1.20	0.65	-1.08	0.88	0.06	1.14	2.56	0.32	1.38	0.58	1.97	0.59	1.40	0.22	2.30	0.05	1.85	0.45
SPO3395	*rarD-2*	protein RarD	1.23	X	1.41	0.02	1.32	0.09	2.47	0.00	-1.10	0.53	0.69	1.79	1.21	0.17	-1.53	0.15	-0.16	1.37
SPO3396		FAD-dependent oxidoreductase	5.46	0.00	1.89	0.13	3.68	1.79	-1.12	0.72	-1.02	0.85	-1.07	0.05	1.09	0.42	1.12	0.23	1.11	0.02
SPO3397		AraC family transcriptional regulator	4.67	0.23	1.28	0.72	2.98	1.70	-1.10	0.99	-1.38	0.47	-1.24	0.14	-1.43	0.42	-1.05	0.96	-1.24	0.19
SPO3398		homocysteine S-methyltransferase	6.35	0.00	1.57	0.17	3.96	2.39	-1.40	0.58	-1.06	0.81	-1.23	0.17	-1.33	0.20	-1.32	0.36	-1.33	0.01
SPO3399		alcohol dehydrogenase (EC:1.1.1.1)	2.31	0.11	1.15	0.74	1.73	0.58	-1.45	0.32	-1.43	0.31	-1.44	0.01	-1.62	0.14	-1.54	0.15	-1.58	0.04
SPO3400		glycine cleavage system protein T	6.07	0.10	1.65	0.01	3.86	2.21	-1.06	0.97	-2.07	0.04	-1.57	0.51	1.10	0.25	-1.29	0.32	-0.10	1.20
SPO3401		hypothetical protein	1.35	0.09	1.40	0.00	1.38	0.02	-2.35	0.00	-1.48	0.08	-1.92	0.44	-1.55	0.08	-1.37	0.26	-1.46	0.09
SPO3402		amino acid transporter LysE	4.96	0.00	1.47	0.17	3.22	1.75	-1.36	0.89	-1.36	X	-1.36	0.00	-1.17	0.37	-1.15	1.00	-1.16	0.01
SPO3403		DNA-binding protein	3.95	0.01	1.44	0.03	2.70	1.26	-2.11	0.02	-1.65	0.01	-1.88	0.23	-1.28	0.10	-1.57	0.04	-1.43	0.14
SPO3404		hypothetical protein	X	X	1.17	0.20	N/A	N/A	3.96	0.01	-1.50	0.08	1.23	2.73	-1.02	0.97	-1.70	0.24	-1.36	0.34
SPO3405		hypothetical protein	1.40	0.89	1.35	0.32	1.38	0.02	2.35	0.56	-1.14	0.63	0.61	1.75	1.02	0.98	-1.07	0.92	-0.03	1.05
SPO3406		TetR family transcriptional regulator	-1.00	0.95	1.22	0.36	0.11	1.11	1.14	0.13	-1.08	0.30	0.03	1.11	1.12	0.11	1.12	0.41	1.12	0.00
SPO3407		hypothetical protein	X	X	1.27	0.36	N/A	N/A	-0.96	0.10	-1.29	0.19	-1.13	0.16	-1.05	0.40	-1.21	0.82	-1.13	0.08
SPO3408		acetyl-CoA C-acetyltransferase	3.83	0.07	2.75	0.02	3.29	0.54	2.38	0.18	1.37	0.01	1.88	0.51	1.92	0.09	1.61	0.10	1.77	0.16
SPO3409		anti-anti-sigma factor	1.15	0.84	2.43	0.01	1.79	0.64	-7.68	0.01	4.54	0.00	-1.57	6.11	-1.24	0.43	X	X	N/A	N/A
SPO3410		anti-sigma B factor	1.43	0.03	1.86	0.03	1.65	0.22	-4.24	0.00	3.14	0.01	-0.55	3.69	-0.95	0.66	X	X	N/A	N/A
SPO3411		gamma-glutamyltranspeptidase	1.81	0.01	1.27	0.49	1.54	0.27	2.00	0.00	1.11	0.55	1.56	0.44	1.34	0.11	-0.99	0.76	0.18	1.16
SPO3412		hypothetical protein	1.22	0.67	1.38	0.01	1.30	0.08	-2.25	0.02	1.82	0.01	-0.22	2.04	-1.38	0.00	-1.67	0.28	-1.53	0.15

SPO3413		auxin efflux carrier family protein	-1.05	0.96	1.01	0.99	-0.02	1.03	1.52	0.06	-1.25	0.05	0.14	1.39	-1.19	0.02	-1.39	0.58	-1.29	0.10
SPO3414		lipoprotein	-1.27	0.02	-1.23	0.38	-1.25	0.02	-1.78	0.00	-1.10	0.29	-1.44	0.34	1.10	0.70	1.14	0.47	1.12	0.02
SPO3415		outer membrane lipoprotein carrier protein LolA	-1.22	0.00	-1.90	0.07	-1.56	0.34	1.51	0.01	1.10	0.50	1.31	0.20	1.40	0.01	1.84	0.09	1.62	0.22
SPO3416		DNA translocase FtsK	0.94	0.69	-1.27	0.33	-0.16	1.11	0.84	0.41	-1.19	0.41	-0.18	1.02	1.15	0.43	-1.26	0.37	-0.06	1.21
SPO3417		class I and II aminotransferase	-1.79	0.03	-1.18	0.67	-1.49	0.31	-1.63	0.29	-1.43	0.41	-1.53	0.10	1.08	0.89	-1.13	0.76	-0.02	1.11
SPO3418		amidase	1.69	0.05	1.29	0.05	1.49	0.20	1.33	0.32	1.24	0.13	1.29	0.05	1.16	0.18	1.21	0.19	1.19	0.03
SPO3419		UbiH/UbiF/VisC/COQ6 family ubiquinone biosynthesis hydroxylase	1.67	0.12	1.72	0.05	1.70	0.03	1.75	0.02	1.06	0.89	1.41	0.35	-1.05	0.73	1.48	0.54	0.22	1.27
SPO3420		hypothetical protein	1.25	0.10	-1.08	0.65	0.09	1.17	1.32	0.02	1.24	0.30	1.28	0.04	-1.07	0.71	-1.13	0.96	-1.10	0.03
SPO3421		hypothetical protein	-1.07	0.87	1.15	0.39	0.04	1.11	1.10	0.44	-1.05	0.69	0.03	1.08	1.20	0.06	1.24	0.05	1.22	0.02
SPO3422		ATP-dependent protease La	1.05	0.82	-1.10	0.64	-0.03	1.08	1.12	0.82	-1.12	0.15	0.00	1.12	-1.07	0.51	-1.16	0.12	-1.12	0.04
SPO3423		thioredoxin	1.52	0.06	-1.29	0.23	0.12	1.41	1.92	0.00	-1.16	0.20	0.38	1.54	-1.07	0.04	0.99	0.40	-0.04	1.03
SPO3424		hypothetical protein	-2.25	0.13	-1.14	0.71	-1.70	0.56	-1.65	0.10	1.10	0.85	-0.28	1.38	1.11	0.72	1.99	0.14	1.55	0.44
SPO3425		exodeoxyribonuclease III	1.63	0.01	1.15	0.51	1.39	0.24	4.22	0.00	0.96	0.19	2.59	1.63	-1.14	0.56	-1.34	0.11	-1.24	0.10
SPO3426		DNA-binding response regulator	-1.25	0.08	-1.31	0.04	-1.28	0.03	-1.75	0.01	1.19	0.38	-0.28	1.47	-1.29	0.02	-1.18	0.07	-1.24	0.06
SPO3427	*ribBA*	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC:3.5.4.25)	-2.84	0.00	-1.04	0.78	-1.94	0.90	-1.50	0.06	-1.07	0.66	-1.29	0.21	1.19	0.15	1.06	0.50	1.13	0.06
SPO3428		hypothetical protein	-1.77	0.44	-1.06	0.85	-1.42	0.36	-1.22	0.72	-1.28	0.27	-1.25	0.03	-1.00	0.99	1.08	0.60	0.04	1.04
SPO3429		alanine racemase	1.17	0.79	-1.11	0.79	0.03	1.14	1.28	0.39	-1.11	0.64	0.09	1.20	-1.15	0.65	1.18	0.87	0.02	1.17
SPO3430		porin	1.70	0.66	1.33	0.51	1.52	0.18	2.19	0.38	-1.76	0.09	0.22	1.98	1.28	0.34	1.22	0.93	1.25	0.03
SPO3431		hypothetical protein	1.55	0.02	-1.05	0.68	0.25	1.30	2.69	0.00	-1.20	0.27	0.75	1.95	1.01	0.72	0.96	0.23	0.99	0.02
SPO3432	*leuS*	leucyl-tRNA synthetase (EC:6.1.1.4)	1.09	0.29	1.14	0.33	1.12	0.02	3.35	0.01	-1.47	0.03	0.94	2.41	-1.44	0.02	-2.09	0.02	-1.77	0.33
SPO3433		lipoprotein	-1.54	0.33	1.02	0.98	-0.26	1.28	1.06	0.96	1.20	0.70	1.13	0.07	1.04	0.96	-1.26	0.26	-0.11	1.15
SPO3434		hypothetical protein	-1.24	0.09	1.30	0.16	0.03	1.27	1.01	0.63	1.17	0.35	1.09	0.08	1.36	0.10	-1.00	0.93	0.18	1.18
SPO3435		glutathione S-transferase	2.09	0.42	1.32	0.19	1.71	0.38	1.31	0.79	1.44	0.36	1.38	0.06	1.29	0.48	1.40	0.20	1.35	0.05
SPO3436		hypothetical protein	X	X	1.36	0.04	N/A	N/A	2.44	0.00	-1.19	0.34	0.63	1.82	1.08	0.29	-1.94	0.01	-0.43	1.51
SPO3437		mechanosensitive ion channel protein MscS	-1.07	0.89	1.15	0.49	0.04	1.11	2.89	0.02	-1.15	0.50	0.87	2.02	-1.43	0.12	-2.12	0.03	-1.78	0.35
SPO3438		hypothetical protein	-1.06	0.90	-1.19	0.86	-1.13	0.06	-1.65	0.59	1.06	0.94	-0.30	1.36	1.12	0.85	1.39	0.61	1.26	0.14
SPO3439		enoyl-CoA hydratase	1.25	0.68	1.11	0.52	1.18	0.07	2.05	0.12	-1.02	0.78	0.52	1.54	1.18	0.22	-1.22	0.16	-0.02	1.20
SPO3440		20-beta-hydroxysteroid dehydrogenase	1.34	0.79	1.08	0.84	1.21	0.13	1.52	0.04	1.18	0.17	1.35	0.17	1.03	0.89	-1.17	0.06	-0.07	1.10
SPO3441		hypothetical protein	0.96	0.02	-1.05	0.27	-0.05	1.01	1.98	0.06	1.45	0.12	1.72	0.27	1.24	0.19	1.74	0.08	1.49	0.25
SPO3442		hypothetical protein	1.19	0.14	1.25	0.27	1.22	0.03	2.86	0.02	-1.18	0.15	0.84	2.02	1.30	0.23	-1.02	0.82	0.14	1.16
SPO3443		inositol monophosphatase	1.19	0.92	-1.04	0.87	0.08	1.12	1.70	0.65	1.25	0.18	1.48	0.22	1.08	0.72	-1.15	0.31	-0.03	1.12
SPO3444		3-deoxy-D-manno-octulosonic-acid transferase	-1.40	0.53	1.08	0.70	-0.16	1.24	1.34	0.58	-1.18	0.31	0.08	1.26	1.32	0.41	-1.17	0.54	0.08	1.25
SPO3445	*lpxK*	tetraacyldisaccharide 4'-kinase (EC:2.7.1.130)	-1.80	0.10	1.33	0.10	-0.24	1.57	8.27	0.00	1.02	0.85	4.65	3.63	1.13	0.44	-1.62	0.00	-0.25	1.38
SPO3446		DsbA family thiol:disulfide interchange protein	1.64	0.01	-1.14	0.19	0.25	1.39	1.45	0.13	-1.08	0.50	0.19	1.27	1.32	0.07	1.68	0.01	1.50	0.18
SPO3447		hypothetical protein	-1.06	0.30	1.31	0.17	0.13	1.19	1.00	0.95	-1.09	0.07	-0.05	1.05	-1.10	0.05	-1.37	0.14	-1.24	0.14
SPO3448	*mutY*	A/G-specific adenine glycosylase (EC:3.2.2.-)	1.18	0.31	-1.25	0.01	-0.04	1.22	1.37	0.06	1.02	0.88	1.20	0.18	-1.59	0.02	-1.85	0.06	-1.72	0.13
SPO3449		fatty acid desaturase	3.65	0.05	1.41	0.35	2.53	1.12	1.17	0.81	1.26	0.56	1.22	0.05	-1.12	0.59	1.06	0.91	-0.03	1.09
SPO3450		guanylate cyclase	-1.10	0.85	-1.47	0.28	-1.29	0.18	1.62	0.17	-1.16	0.25	0.23	1.39	1.62	0.02	1.91	0.01	1.77	0.15

SPO3451		modification methylase	1.19	0.94	-1.27	0.36	-0.04	1.23	-1.83	0.07	-1.33	0.19	-1.58	0.25	-1.04	0.77	-1.20	0.08	-1.12	0.08
SPO3452	*rnhB*	ribonuclease HII (EC:3.1.26.4)	-1.16	0.17	-1.44	0.06	-1.30	0.14	1.25	0.02	1.13	0.28	1.19	0.06	-1.87	0.01	-2.66	0.02	-2.27	0.40
SPO3453		hypothetical protein	0.99	0.05	-1.07	0.60	-0.04	1.03	-1.58	0.03	1.06	0.84	-0.26	1.32	1.05	0.72	-1.15	0.66	-0.05	1.10
SPO3454		hypothetical protein	-1.29	0.11	1.02	0.93	-0.14	1.16	-1.20	0.67	-1.00	0.93	-1.10	0.10	-1.03	0.46	-1.08	0.92	-1.06	0.03
SPO3455		guanylate cyclase	1.40	0.77	-1.36	0.17	0.02	1.38	-1.24	0.28	-1.06	0.42	-1.15	0.09	1.49	0.23	1.59	0.04	1.54	0.05
SPO3456		flagellar protein	1.40	0.32	1.09	0.90	1.25	0.15	-1.55	0.49	-1.14	0.85	-1.35	0.21	-1.08	0.94	1.29	0.84	0.11	1.19
SPO3457	*flbT*	flagellar biosynthesis repressor FlbT	3.02	0.05	1.56	0.07	2.29	0.73	-1.70	0.42	2.66	0.01	0.48	2.18	-1.13	0.74	-0.95	0.63	-1.04	0.09
SPO3458	*flaF*	flagellar biosynthesis regulatory protein FlaF	3.71	0.05	1.86	0.02	2.79	0.93	-1.42	0.86	4.64	0.01	1.61	3.03	-1.25	0.19	X	X	N/A	N/A
SPO3459		flagellin protein	2.16	0.21	2.62	0.01	2.39	0.23	-2.39	0.28	4.71	0.00	1.16	3.55	-1.12	0.70	-1.11	0.91	-1.12	0.01
SPO3460		hypothetical protein	1.41	0.20	1.09	0.71	1.25	0.16	-7.15	0.00	2.85	0.04	-2.15	5.00	-1.47	0.12	1.16	0.38	-0.16	1.32
SPO3461	*flgJ*	flagellar protein FlgJ	1.79	0.67	1.27	0.52	1.53	0.26	-10.80	0.00	2.47	0.08	-4.17	6.64	-1.24	0.78	1.52	0.50	0.14	1.38
SPO3462		flagellar hook-length control protein	1.45	0.04	1.23	0.57	1.34	0.11	-3.65	0.01	2.19	0.05	-0.73	2.92	-1.66	0.26	-1.44	0.26	-1.55	0.11
SPO3463	*flgD*	flagellar basal body rod modification protein	1.46	0.44	-1.08	0.79	0.19	1.27	-1.99	0.15	1.09	0.87	-0.45	1.54	-1.03	0.97	1.23	0.52	0.10	1.13
SPO3464		hypothetical protein	-1.22	0.37	-1.05	0.87	-1.14	0.09	1.57	0.05	-1.02	0.89	0.28	1.30	-1.24	0.29	-1.51	0.17	-1.38	0.14
SPO3465		hypothetical protein	-1.29	0.20	-1.14	0.76	-1.22	0.08	-1.63	0.25	-1.16	0.24	-1.40	0.23	-1.24	0.13	1.63	0.14	0.20	1.44
SPO3466	*potI*	putrescine ABC transporter permease	1.56	0.48	1.58	0.37	1.57	0.01	1.44	0.45	1.27	0.62	1.36	0.09	2.05	0.20	1.61	0.28	1.83	0.22
SPO3467	*potH*	putrescine ABC transporter permease	1.55	0.64	1.30	0.40	1.43	0.13	-1.20	0.53	1.45	0.10	0.13	1.33	1.05	0.67	1.08	0.52	1.07	0.02
SPO3468	*potG*	putrescine ABC transporter ATP-binding protein	1.36	0.57	1.02	0.98	1.19	0.17	-1.30	0.25	1.23	0.56	-0.04	1.27	1.02	0.99	1.39	0.34	1.21	0.18
SPO3469	*potF*	putrescine ABC transporter substrate-binding protein	-2.08	0.17	-1.77	0.03	-1.93	0.16	-3.21	0.00	1.59	0.08	-0.81	2.40	1.00	0.67	2.06	0.02	1.53	0.53
SPO3470		GntR family transcriptional regulator	-1.41	0.33	-1.02	0.16	-1.22	0.20	-1.34	0.16	-1.27	0.03	-1.31	0.04	-1.10	0.32	-1.09	0.41	-1.10	0.01
SPO3471		aminotransferase	2.18	0.19	1.36	0.47	1.77	0.41	1.22	0.58	-1.49	0.34	-0.14	1.36	1.01	0.96	-1.06	0.79	-0.03	1.04
SPO3472		polyamine ABC transporter ATP-binding protein	-1.41	0.15	-1.97	0.25	-1.69	0.28	1.27	0.35	-1.48	0.04	-0.11	1.38	-1.24	0.02	-1.20	0.08	-1.22	0.02
SPO3473		polyamine ABC transporter substrate-binding protein	-2.11	0.00	-2.44	0.05	-2.28	0.17	-1.49	0.02	-1.28	0.03	-1.39	0.11	1.40	0.04	1.49	0.21	1.45	0.05
SPO3474		polyamine ABC transporter permease	1.00	0.61	-1.59	0.06	-0.30	1.30	1.14	0.87	1.00	0.70	1.07	0.07	1.05	1.00	1.45	0.23	1.25	0.20
SPO3475		polyamine ABC transporter permease	1.04	0.69	-1.22	0.34	-0.09	1.13	1.60	0.36	-1.15	0.23	0.23	1.38	1.49	0.29	1.87	0.04	1.68	0.19
SPO3476		hypothetical protein	1.83	0.27	1.31	0.26	1.57	0.26	-2.06	0.13	1.34	0.10	-0.36	1.70	1.66	0.01	-1.01	0.49	0.33	1.34
SPO3477		hypothetical protein	-1.54	0.21	1.23	0.07	-0.16	1.39	1.45	0.10	1.07	0.52	1.26	0.19	1.19	0.29	-1.25	0.49	-0.03	1.22
SPO3478	*glcD*	glycolate oxidase subunit GlcD	-1.03	0.93	1.07	0.87	0.02	1.05	-1.30	0.82	4.70	0.10	1.70	3.00	-0.98	0.93	-0.98	0.79	-0.98	0.00
SPO3479	*glcE*	glycolate oxidase subunit GlcE	1.27	0.46	1.34	0.17	1.31	0.04	1.02	0.24	6.05	0.01	3.54	2.52	-0.99	0.86	-1.37	0.26	-1.18	0.19
SPO3480	*glcF*	glycolate oxidase, iron-sulfur subunit	1.89	0.03	1.22	0.48	1.56	0.34	1.34	0.07	5.28	0.00	3.31	1.97	-0.98	0.79	-1.31	0.62	-1.14	0.17
SPO3481		hypothetical protein	1.20	X	1.06	0.73	1.13	0.07	1.70	0.05	-1.08	0.64	0.31	1.39	1.21	0.08	1.15	0.51	1.18	0.03
SPO3482		serine protease	1.11	0.83	1.37	0.04	1.24	0.13	-1.90	0.06	-1.03	0.87	-1.47	0.44	-1.18	0.17	1.16	0.68	-0.01	1.17
SPO3483		hypothetical protein	-1.08	0.33	1.30	0.23	0.11	1.19	-1.72	0.19	1.18	0.15	-0.27	1.45	-1.35	0.30	-1.17	0.82	-1.26	0.09
SPO3484		heat shock protein 20	-2.10	0.44	-2.90	0.28	-2.50	0.40	0.84	0.64	-1.11	0.79	-0.13	0.98	1.57	0.52	2.44	0.45	2.01	0.44
SPO3485		hypothetical protein	1.06	0.88	-1.07	0.80	-0.01	1.07	-1.50	0.13	1.20	0.03	-0.15	1.35	1.26	0.08	1.21	0.10	1.24	0.03
SPO3486		hypothetical protein	1.03	0.98	-1.18	0.79	-0.08	1.11	-1.36	0.22	-1.37	0.14	-1.37	0.01	1.10	0.07	2.02	0.10	1.56	0.46
SPO3487		hypothetical protein	-1.09	0.49	-1.22	0.31	-1.16	0.06	-1.10	0.38	-1.24	X	-1.17	0.07	-1.01	0.87	-1.38	X	-1.20	0.19
SPO3488		peptidoglycan binding domain-containing protein	-1.34	0.03	-1.23	0.23	-1.29	0.06	0.95	0.32	-1.10	0.55	-0.07	1.03	1.28	0.28	1.01	0.87	1.15	0.14

SPO3489	*pheT*	phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20)	1.74	0.01	1.67	0.07	1.71	0.04	2.83	0.00	-1.14	0.38	0.85	1.99	1.18	0.16	-1.36	0.07	-0.09	1.27
SPO3490		LysR family transcriptional regulator	X	X	-1.05	0.93	N/A	N/A	-1.24	0.70	-1.11	0.49	-1.18	0.06	1.27	0.11	1.13	0.19	1.20	0.07
SPO3491		UbiE/COQ5 family methlytransferase	-1.44	0.03	-1.33	0.10	-1.39	0.05	-1.32	0.10	1.12	0.34	-0.10	1.22	-1.15	0.17	-1.09	0.81	-1.12	0.03
SPO3492		hypothetical protein	-1.07	0.33	-1.11	0.53	-1.09	0.02	2.03	0.03	1.48	0.03	1.76	0.28	1.40	0.03	1.36	0.16	1.38	0.02
SPO3493		transporter	1.09	0.66	1.12	0.46	1.11	0.02	-0.98	0.20	-1.02	0.95	-1.00	0.02	1.15	0.35	1.30	0.04	1.23	0.08
SPO3494		glutathione S-transferase	1.06	0.20	-2.38	0.02	-0.66	1.72	-1.24	0.01	1.09	0.63	-0.08	1.17	1.35	0.36	1.86	0.04	1.61	0.26
SPO3495	*mscL*	large conductance mechanosensitive channel protein	-1.45	0.02	-2.13	0.05	-1.79	0.34	0.87	0.04	-1.19	0.07	-0.16	1.03	1.12	0.11	1.56	0.12	1.34	0.22
SPO3496		mechanosensitive ion channel protein MscS	1.53	0.06	-1.94	0.01	-0.21	1.74	2.10	0.03	-1.40	0.01	0.35	1.75	-1.04	0.55	1.10	0.83	0.03	1.07
SPO3498	*tuf-2*	elongation factor Tu (EC:3.6.5.3)	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3499	*fusA*	elongation factor G	2.36	0.08	-1.40	0.21	0.48	1.88	9.93	0.01	-1.34	0.06	4.30	5.64	-1.59	0.11	-1.93	0.08	-1.76	0.17
SPO3500	*rpsG*	30S ribosomal protein S7	1.51	0.19	-1.67	0.09	-0.08	1.59	6.86	0.00	-1.99	0.15	2.44	4.43	-2.59	0.00	-3.02	0.01	-2.81	0.22
SPO3501	*rpsL*	30S ribosomal protein S12	1.70	0.03	-1.36	0.17	0.17	1.53	7.08	0.00	-1.08	0.21	3.00	4.08	-1.60	0.05	-2.57	0.01	-2.09	0.49
SPO3502		hypothetical protein	1.02	0.93	-1.09	0.59	-0.04	1.06	1.06	0.95	1.27	0.35	1.17	0.11	-1.01	0.94	-1.05	0.66	-1.03	0.02
SPO3503		hypothetical protein	1.04	0.66	1.03	0.84	1.04	0.01	1.09	0.19	1.37	0.11	1.23	0.14	-1.18	0.17	-1.19	0.34	-1.19	0.01
SPO3504		hypothetical protein	-0.98	0.62	1.20	0.42	0.11	1.09	2.27	0.02	-1.30	0.10	0.49	1.79	-1.01	0.79	-1.08	0.83	-1.05	0.04
SPO3505		hypothetical protein	1.07	0.57	-1.16	0.02	-0.04	1.12	1.38	0.21	-1.19	0.43	0.10	1.29	-1.00	0.99	1.17	0.13	0.09	1.09
SPO3506		DNA-binding protein	-1.45	0.04	-1.06	0.65	-1.26	0.20	-1.59	0.06	1.68	0.02	0.04	1.64	1.11	0.51	1.22	0.08	1.17	0.05
SPO3507	*rpoC*	DNA-directed RNA polymerase subunit beta' (EC:2.7.7.6)	-1.17	0.60	1.43	0.10	0.13	1.30	2.86	0.09	-1.48	0.03	0.69	2.17	1.47	0.16	1.25	0.28	1.36	0.11
SPO3508	*rpoB*	DNA-directed RNA polymerase subunit beta (EC:2.7.7.6)	1.47	0.38	-1.25	0.48	0.11	1.36	4.58	0.04	-1.15	0.15	1.72	2.87	-1.51	0.01	-1.68	0.01	-1.60	0.09
SPO3509	*rplL*	50S ribosomal protein L7/L12	-1.83	0.02	2.19	0.06	0.18	2.01	5.97	0.00	-6.38	0.00	-0.21	6.18	1.46	0.02	-3.47	0.00	-1.01	2.47
SPO3510	*rplJ*	50S ribosomal protein L10	-2.35	0.01	-1.47	0.10	-1.91	0.44	6.97	0.00	-4.81	0.00	1.08	5.89	-1.61	0.04	-4.23	0.00	-2.92	1.31
SPO3511		hypothetical protein	-1.34	0.04	1.35	0.09	0.01	1.35	1.09	0.25	1.14	0.08	1.12	0.02	1.43	0.04	-1.15	0.29	0.14	1.29
SPO3512		hypothetical protein	-1.23	0.03	-1.22	0.40	-1.23	0.01	1.30	0.10	1.34	0.08	1.32	0.02	1.21	0.22	1.51	0.08	1.36	0.15
SPO3513	*rplA*	50S ribosomal protein L1	-1.58	0.05	1.90	0.05	0.16	1.74	3.05	0.05	-4.39	0.01	-0.67	3.72	1.05	0.97	-2.45	0.03	-0.70	1.75
SPO3514	*rplK*	50S ribosomal protein L11	1.15	0.87	-1.08	0.12	0.03	1.12	10.10	0.00	-3.66	0.02	3.22	6.88	-1.28	0.01	-2.29	0.03	-1.79	0.51
SPO3515		hypothetical protein	X	X	1.28	0.75	N/A	N/A	-1.31	X	-1.15	0.93	-1.23	0.08	-1.20	X	1.90	X	0.35	1.55
SPO3516	*nusG*	transcription termination/antitermination factor NusG	-1.30	0.61	1.26	0.33	-0.02	1.28	3.97	0.02	-1.78	0.02	1.10	2.88	-1.29	0.10	-1.81	0.07	-1.55	0.26
SPO3517	*secE*	preprotein translocase subunit SecE	-1.37	0.01	-1.03	0.73	-1.20	0.17	1.54	0.03	-1.40	0.02	0.07	1.47	-1.03	0.71	1.04	0.69	0.01	1.04
SPO3518		hypothetical protein	-1.06	0.25	1.45	0.18	0.20	1.26	-1.23	0.14	1.52	0.10	0.15	1.38	1.57	0.02	1.24	0.30	1.41	0.17
SPO3519	*ccoS*	cbb3-type cytochrome oxidase maturation protein	1.03	0.22	1.28	0.43	1.16	0.13	0.97	0.36	1.31	0.23	1.14	0.17	1.74	0.06	2.05	0.07	1.90	0.16
SPO3520		copper-translocating P-type ATPase (EC:3.6.3.4)	2.31	0.01	1.77	0.01	2.04	0.27	3.36	0.00	-1.13	0.45	1.12	2.25	1.19	0.18	-1.11	0.12	0.04	1.15
SPO3521		fixH protein	3.52	0.02	1.58	0.06	2.55	0.97	7.86	0.00	-1.20	0.19	3.33	4.53	1.71	0.08	1.71	0.05	1.71	0.00
SPO3522		iron-sulfur-binding protein RdxA/RdxB/FixG family	1.56	0.50	1.61	0.03	1.59	0.03	3.51	0.02	1.03	0.84	2.27	1.24	1.34	0.18	1.85	0.04	1.60	0.26
SPO3523	*ccoP-1*	cytochrome c oxidase, cbb3-type subunit III (EC:1.9.3.1)	2.24	0.01	2.10	0.02	2.17	0.07	8.51	0.00	-1.08	0.22	3.72	4.80	2.09	0.00	1.37	0.03	1.73	0.36
SPO3524	*ccoQ-1*	cytochrome c oxidase, cbb3-type subunit IV (EC:1.9.3.1)	2.11	0.00	1.34	0.07	1.73	0.38	7.30	0.00	1.01	0.63	4.16	3.15	1.02	0.29	1.04	0.58	1.03	0.01
SPO3525	*ccoO-1*	cbb3-type cytochrome c oxidase subunit II	2.14	0.07	1.30	0.31	1.72	0.42	6.96	0.00	1.17	0.17	4.07	2.90	-1.18	0.09	-1.14	0.35	-1.16	0.02

		(EC:1.9.3.1)																		
SPO3526	*ccoN-1*	cbb3-type cytochrome c oxidase subunit I (EC:1.9.3.1)	2.27	0.19	1.62	0.30	1.95	0.33	9.29	0.01	-1.10	0.49	4.10	5.20	1.15	0.52	0.98	0.50	1.07	0.08
SPO3527		universal stress protein family protein	1.86	0.01	1.42	0.02	1.64	0.22	3.34	0.01	-1.29	0.06	1.03	2.32	1.92	0.00	1.64	0.12	1.78	0.14
SPO3528		hypothetical protein	0.87	0.04	1.09	0.74	0.98	0.11	-2.37	0.01	1.41	0.12	-0.48	1.89	1.19	0.56	1.11	0.73	1.15	0.04
SPO3529	*glyA-3*	serine hydroxymethyltransferase (EC:2.1.2.1)	1.54	0.02	-1.31	0.29	0.12	1.43	-3.40	0.01	-1.83	0.08	-2.62	0.78	1.14	0.32	1.12	0.21	1.13	0.01
SPO3530		LysR family transcriptional regulator	-1.14	0.66	-1.08	0.41	-1.11	0.03	-1.39	0.51	-1.20	0.54	-1.30	0.10	1.21	0.66	1.67	0.09	1.44	0.23
SPO3531	*fnrL*	transcriptional activator protein FnrL	2.86	0.00	3.01	0.00	2.94	0.07	2.30	0.00	1.61	0.04	1.96	0.34	1.56	0.01	1.23	0.05	1.40	0.17
SPO3532	*hemN*	coproporphyrinogen III oxidase (EC:1.-.-.-)	1.12	0.32	1.33	0.02	1.23	0.11	6.46	0.01	1.01	0.94	3.74	2.73	1.44	0.01	-1.10	0.34	0.17	1.27
SPO3533	*fusA*	elongation factor G	-1.34	0.12	1.08	0.44	-0.13	1.21	-2.93	0.01	2.16	0.00	-0.39	2.55	2.41	0.02	2.50	0.00	2.46	0.04
SPO3534	*yejF*	oligopeptide/dipeptide ABC transporter ATP-binding protein	-1.41	0.04	-1.01	0.88	-1.21	0.20	-1.17	0.14	-1.31	0.12	-1.24	0.07	1.09	0.24	-1.10	0.48	-0.01	1.10
SPO3535	*yejE*	oligopeptide/dipeptide ABC transporter permease	-0.94	0.44	-1.07	0.57	-1.00	0.07	2.82	0.00	-1.23	0.19	0.80	2.03	1.23	0.26	-1.11	0.70	0.06	1.17
SPO3536	*yejB*	oligopeptide/dipeptide ABC transporter permease	-1.16	0.66	1.06	0.88	-0.05	1.11	2.66	0.19	-1.03	0.86	0.82	1.85	1.18	0.46	-1.09	0.79	0.04	1.14
SPO3537	*yejA*	oligopeptide/dipeptide ABC transporter substrate-binding protein	1.27	0.61	-1.08	0.78	0.10	1.18	2.58	0.11	1.15	0.48	1.87	0.72	1.42	0.14	1.47	0.30	1.45	0.03
SPO3538	*cycM*	cytochrome c552	2.95	0.05	1.60	0.06	2.28	0.67	6.92	0.02	1.14	0.73	4.03	2.89	-1.04	0.68	-1.15	0.23	-1.10	0.05
SPO3539		prephenate dehydratase (EC:4.2.1.51)	-1.10	0.50	1.25	0.63	0.08	1.18	4.13	0.00	-1.68	0.01	1.23	2.91	-1.33	0.13	-2.44	0.04	-1.89	0.56
SPO3540		hypothetical protein	-1.03	X	1.55	0.10	0.26	1.29	4.85	0.08	-1.64	0.15	1.61	3.25	-1.02	0.98	-2.72	0.03	-1.87	0.85
SPO3541		NUDIX family hydrolase	1.93	0.00	1.07	0.66	1.50	0.43	2.58	0.02	-1.49	0.32	0.55	2.04	-1.09	0.26	-1.40	0.23	-1.25	0.15
SPO3542		2`,3`-cyclic-nucleotide 2`-phosphodiesterase	1.31	0.20	1.85	0.02	1.58	0.27	1.46	0.02	2.66	0.06	2.06	0.60	-1.05	0.72	-1.34	0.13	-1.20	0.15
SPO3543		hypothetical protein	-1.40	0.33	-1.28	0.16	-1.34	0.06	-1.29	0.96	-1.53	0.19	-1.41	0.12	1.17	0.22	1.73	0.01	1.45	0.28
SPO3544		hypothetical protein	-1.57	0.28	-1.30	0.39	-1.44	0.14	-2.73	0.03	-1.39	0.39	-2.06	0.67	-1.15	0.76	1.25	X	0.05	1.20
SPO3545		TetR family transcriptional regulator	-1.26	0.79	-1.21	0.78	-1.24	0.03	-1.53	0.72	-1.20	0.62	-1.37	0.17	-1.05	0.86	1.44	0.57	0.20	1.25
SPO3546		zinc metallopeptidase	-1.02	0.95	1.07	0.70	0.03	1.05	0.91	0.69	1.45	0.01	1.18	0.27	-1.24	0.40	-1.06	0.57	-1.15	0.09
SPO3547		hypothetical protein	2.49	0.12	2.21	0.03	2.35	0.14	2.66	0.02	3.20	0.02	2.93	0.27	1.35	0.50	1.21	0.53	1.28	0.07
SPO3548		hypothetical protein	-1.58	0.75	1.13	0.85	-0.23	1.36	-1.39	0.79	1.58	0.52	0.10	1.49	1.76	0.31	1.51	0.43	1.64	0.13
SPO3549		hypothetical protein	1.27	0.06	1.23	0.07	1.25	0.02	-1.04	0.30	1.10	0.45	0.03	1.07	-1.26	0.06	-1.26	0.45	-1.26	0.00
SPO3550	*dnaX*	DNA polymerase III subunits gamma and tau (EC:2.7.7.7)	-1.41	0.01	-1.02	0.87	-1.22	0.20	1.31	0.12	1.07	0.78	1.19	0.12	1.33	0.28	1.18	0.44	1.26	0.08
SPO3551		acetyltransferase	-1.02	0.97	1.16	0.43	0.07	1.09	1.21	0.11	-1.50	0.24	-0.15	1.36	-1.39	0.20	-1.36	0.68	-1.38	0.01
SPO3552		oxidoreductase, FAD-binding	1.26	0.04	1.06	0.76	1.16	0.10	2.12	0.00	-1.50	0.05	0.31	1.81	-1.15	0.45	-1.80	0.04	-1.48	0.33
SPO3553		hypothetical protein	-1.15	0.40	1.45	0.03	0.15	1.30	5.06	0.00	-1.45	0.03	1.81	3.26	-1.22	0.08	-1.67	0.04	-1.45	0.23
SPO3554		hypothetical protein	1.30	0.09	1.13	0.56	1.22	0.09	1.59	0.02	-1.33	0.34	0.13	1.46	-1.21	0.50	1.07	0.87	-0.07	1.14
SPO3555		Slt family transglycosylase	-1.20	0.16	-1.57	0.01	-1.39	0.19	1.38	0.14	1.17	0.48	1.28	0.11	1.71	0.05	1.50	0.02	1.61	0.11
SPO3556	*dapA*	dihydrodipicolinate synthase (EC:4.2.1.52)	-1.07	0.83	1.64	0.10	0.29	1.36	2.68	0.06	-1.19	0.26	0.75	1.94	1.01	0.94	-1.29	0.10	-0.14	1.15
SPO3557		dimethyl sulfoxide reductase subunit C	-1.30	0.66	1.81	0.19	0.26	1.56	-3.09	0.07	-1.35	0.30	-2.22	0.87	1.44	0.29	-1.03	X	0.21	1.24
SPO3558		(Fe-S)-binding protein	-1.72	0.01	1.45	0.18	-0.14	1.59	-7.75	0.00	-1.19	0.75	-4.47	3.28	1.55	0.02	1.16	0.62	1.36	0.20
SPO3559		molybdopterin-binding oxidoreductase	-1.44	0.08	1.92	0.00	0.24	1.68	-6.55	0.01	-1.32	0.12	-3.94	2.62	1.24	0.08	1.24	X	1.24	0.00
SPO3560	*pta*	phosphate acetyltransferase (EC:2.3.1.8)	-1.16	0.66	-1.30	0.14	-1.23	0.07	-1.54	0.30	X	X	N/A	N/A	-1.33	0.12	X	X	N/A	N/A
SPO3561	*xsc*	sulfoacetaldehyde acetyltransferase (EC:2.3.3.15)	1.37	0.88	-1.00	1.00	0.19	1.19	-1.11	0.98	-1.46	0.36	-1.29	0.17	1.30	0.50	1.61	0.33	1.46	0.16
SPO3562	*tauR*	taurine transcriptional regulator	-1.97	0.00	-1.34	0.54	-1.66	0.32	-2.13	0.01	-1.40	0.46	-1.77	0.37	1.04	0.42	-0.98	0.76	0.03	1.01

SPO3563		ArsR family transcriptional regulator	1.13	0.09	-1.04	0.80	0.04	1.09	-1.06	0.61	-1.38	0.08	-1.22	0.16	-1.24	0.11	-1.16	0.48	-1.20	0.04
SPO3564		permease	0.95	0.37	1.02	0.91	0.98	0.04	0.93	0.27	-1.65	0.12	-0.36	1.29	1.20	0.05	1.59	0.02	1.40	0.20
SPO3565		hypothetical protein	-1.79	0.63	-1.15	0.63	-1.47	0.32	0.87	0.83	-1.06	0.73	-0.10	0.96	1.04	1.00	0.95	0.71	1.00	0.05
SPO3566		hypothetical protein	-1.16	0.10	-1.82	0.11	-1.49	0.33	3.98	0.00	-1.09	0.21	1.45	2.54	-1.55	0.00	-1.39	0.15	-1.47	0.08
SPO3567		ribonuclease T2 family protein	-1.37	0.51	1.39	0.27	0.01	1.38	1.65	0.22	1.18	0.55	1.42	0.23	1.39	0.21	1.08	0.73	1.24	0.16
SPO3568		hypothetical protein	1.02	0.54	1.11	0.73	1.07	0.05	-1.27	0.15	1.00	0.40	-0.14	1.14	1.19	0.06	1.14	0.56	1.17	0.03
SPO3569	*recR*	recombination protein RecR	1.37	0.20	1.09	0.64	1.23	0.14	1.82	0.01	-1.67	0.01	0.08	1.75	-1.04	0.26	-1.20	0.13	-1.12	0.08
SPO3570		hypothetical protein	1.05	0.09	1.22	0.40	1.14	0.09	0.79	0.00	-1.52	0.02	-0.37	1.15	-1.13	0.66	-1.43	0.04	-1.28	0.15
SPO3571		AraC family transcriptional regulator	X	X	1.06	0.35	N/A	N/A	2.06	0.01	-1.50	0.09	0.28	1.78	-1.07	0.79	-1.32	X	-1.20	0.13
SPO3572		isochorismatase	-2.21	0.39	-1.34	0.62	-1.78	0.44	-3.48	0.21	-1.50	0.34	-2.49	0.99	-1.09	0.89	1.38	0.52	0.15	1.24
SPO3573		NADPH-dependent FMN reductase domain-containing protein	-1.43	0.75	-1.92	0.12	-1.68	0.25	1.67	0.00	-1.32	0.02	0.18	1.50	1.06	0.88	1.11	0.96	1.09	0.03
SPO3574		short chain dehydrogenase	1.19	0.51	-1.44	0.20	-0.13	1.32	-1.88	0.00	1.31	0.29	-0.29	1.60	-1.00	0.81	-1.25	0.20	-1.12	0.13
SPO3575		MerR family transcriptional regulator	-1.88	0.18	-1.49	0.31	-1.69	0.19	-1.53	0.55	-1.36	0.12	-1.45	0.09	1.39	0.09	1.22	0.55	1.31	0.09
SPO3576		OmpA domain-containing protein	0.89	0.34	-2.02	0.06	-0.57	1.45	2.22	0.10	1.23	0.42	1.73	0.50	1.28	0.41	1.16	0.84	1.22	0.06
SPO3577		hypothetical protein	2.15	0.02	-1.02	0.95	0.57	1.59	-1.27	0.63	1.05	0.55	-0.11	1.16	-1.08	0.78	-0.92	0.16	-1.00	0.08
SPO3578		ADA regulatory protein	-1.20	0.15	-1.02	0.89	-1.11	0.09	-1.32	0.10	1.24	0.60	-0.04	1.28	1.20	0.23	1.27	0.57	1.24	0.04
SPO3579		MarR family transcriptional regulator	1.32	0.04	1.02	0.79	1.17	0.15	1.45	0.00	-1.16	0.25	0.15	1.31	1.30	0.11	-1.08	0.67	0.11	1.19
SPO3580		isochorismatase	-1.26	0.07	1.07	0.68	-0.10	1.17	3.37	0.00	-1.07	0.62	1.15	2.22	1.33	0.09	1.13	0.28	1.23	0.10
SPO3581	*nth*	endonuclease III (EC:4.2.99.18)	-1.01	0.86	-1.05	0.63	-1.03	0.02	2.60	0.02	0.99	0.59	1.79	0.81	-1.48	0.06	-1.43	0.08	-1.46	0.03
SPO3582		PfkB family kinase	-1.03	0.70	1.10	0.49	0.04	1.07	1.03	0.93	-1.74	0.02	-0.36	1.39	1.16	0.45	-1.26	0.11	-0.05	1.21
SPO3583	*pecS*	transcriptional regulator PecS	-1.43	0.18	-1.06	0.54	-1.25	0.18	-1.59	0.18	-1.01	0.82	-1.30	0.29	-1.09	0.21	-1.05	0.70	-1.07	0.02
SPO3584		drug/metabolite transporter family membrane protein	X	X	1.04	0.60	N/A	N/A	1.99	0.02	-1.56	0.05	0.22	1.78	1.13	0.27	-0.96	0.34	0.08	1.05
SPO3585		NUDIX family hydrolase NudH subfamily hydrolase	1.30	0.69	1.18	0.32	1.24	0.06	1.86	0.15	-1.08	0.51	0.39	1.47	-1.18	0.04	-1.55	0.01	-1.37	0.19
SPO3586	*fadH*	2,4-dienoyl-CoA reductase (EC:1.3.1.34)	1.28	0.83	-1.01	0.95	0.14	1.15	-1.67	0.10	1.16	0.76	-0.26	1.42	1.48	0.37	3.12	0.13	2.30	0.82
SPO3587		hypothetical protein	-1.69	0.00	1.11	0.46	-0.29	1.40	-1.53	0.02	-1.09	0.82	-1.31	0.22	1.58	0.01	1.58	0.01	1.58	0.00
SPO3588		hypothetical protein	1.20	X	-1.05	0.81	0.08	1.13	-2.08	0.07	-1.45	X	-1.77	0.31	-0.94	0.53	X	X	N/A	N/A
SPO3589		hypothetical protein	2.89	0.00	1.06	0.48	1.98	0.92	-1.19	0.37	-1.52	0.11	-1.36	0.16	1.15	0.30	1.35	0.08	1.25	0.10
SPO3590		hypothetical protein	1.80	0.23	1.01	0.98	1.41	0.40	-4.29	0.03	1.42	0.31	-1.44	2.86	-1.26	0.30	1.04	0.98	-0.11	1.15
SPO3591		auxin efflux carrier family protein	1.35	0.17	1.37	0.03	1.36	0.01	1.14	0.19	-1.21	0.29	-0.04	1.18	1.41	0.02	-1.28	0.33	0.06	1.35
SPO3592		LysR family transcriptional regulator	1.08	0.88	1.18	0.45	1.13	0.05	-2.44	0.09	-1.09	0.42	-1.77	0.68	-1.95	0.03	-1.51	0.05	-1.73	0.22
SPO3593		sulfatase	1.63	0.31	-1.18	0.57	0.23	1.41	1.51	0.49	1.43	0.38	1.47	0.04	1.10	0.83	1.40	0.44	1.25	0.15
SPO3594	*pheS*	phenylalanyl-tRNA synthetase subunit alpha (EC:6.1.1.20)	1.47	0.53	1.31	0.67	1.39	0.08	4.49	0.09	-1.40	0.42	1.55	2.95	-1.06	0.80	-1.57	0.35	-1.32	0.26
SPO3595		AraC family transcriptional regulator	X	X	-1.33	0.10	N/A	N/A	2.14	0.01	-1.00	0.89	0.57	1.57	1.04	0.52	-1.21	0.57	-0.09	1.13
SPO3596		pyridoxamine 5'-phosphate oxidase	1.29	0.16	1.03	0.96	1.16	0.13	1.52	0.09	-1.10	0.80	0.21	1.31	1.10	0.82	-1.13	0.88	-0.01	1.12
SPO3597		amine oxidase	-1.55	0.53	1.35	0.40	-0.10	1.45	-1.99	0.33	1.21	0.18	-0.39	1.60	1.63	0.03	-1.02	0.66	0.31	1.33
SPO3598	*rplT*	50S ribosomal protein L20	-1.12	0.02	1.11	0.68	-0.01	1.12	3.53	0.00	-1.38	0.20	1.08	2.46	-1.50	0.05	-1.91	0.04	-1.71	0.20
SPO3599	*rpmI*	50S ribosomal protein L35	-1.13	0.01	-1.28	0.12	-1.21	0.08	3.35	0.00	-1.33	0.07	1.01	2.34	-1.98	0.04	-1.97	0.08	-1.98	0.01
SPO3600	*pyk*	pyruvate kinase (EC:2.7.1.40)	1.46	0.42	2.00	0.04	1.73	0.27	1.48	0.20	5.01	0.01	3.25	1.77	-1.85	0.03	-3.14	0.01	-2.50	0.64

SPO3601		N-formylglutamate amidohydrolase	-1.40	0.06	-1.13	0.55	-1.27	0.14	1.68	0.03	-1.19	0.31	0.25	1.44	-1.59	0.01	-2.13	0.00	-1.86	0.27
SPO3602		hypothetical protein	1.38	0.04	-1.13	0.48	0.13	1.26	0.89	0.17	1.00	0.35	0.94	0.05	-1.32	0.05	-1.28	0.07	-1.30	0.02
SPO3603		thioesterase	1.21	0.54	-1.21	0.68	0.00	1.21	1.01	0.04	-1.16	0.70	-0.08	1.09	-1.07	0.57	1.40	0.52	0.17	1.24
SPO3604		D-amino acid aminotransferase	4.07	0.04	1.20	0.51	2.64	1.44	6.01	0.05	-1.62	0.06	2.20	3.82	1.18	0.24	1.23	0.66	1.21	0.03
SPO3605		hypothetical protein	3.43	0.15	1.58	0.01	2.51	0.93	7.22	0.01	-1.87	0.02	2.68	4.55	-1.40	0.08	-1.22	0.11	-1.31	0.09
SPO3606		mandelate racemase	1.86	0.08	1.98	0.02	1.92	0.06	3.19	0.01	-2.11	0.04	0.54	2.65	1.78	0.11	1.45	0.02	1.62	0.17
SPO3607		hypothetical protein	1.33	0.86	-1.09	0.97	0.12	1.21	-1.73	0.82	-1.06	0.97	-1.40	0.34	1.03	0.99	1.31	X	1.17	0.14
SPO3608	*mclA*	malyl-CoA lyase (EC:4.1.3.24)	-1.91	0.00	-1.18	0.10	-1.55	0.37	-1.34	0.02	-1.11	0.15	-1.23	0.12	-1.05	0.63	1.13	0.67	0.04	1.09
SPO3609	*linC-2*	short chain dehydrogenase (EC:1.1.1.-)	X	X	1.04	0.77	N/A	N/A	1.64	0.01	-1.05	0.91	0.30	1.35	1.28	0.12	1.07	X	1.18	0.11
SPO3610		hypothetical protein	1.06	1.00	1.21	0.75	1.14	0.08	1.49	0.63	-1.11	0.86	0.19	1.30	1.26	0.73	-0.95	0.89	0.16	1.10
SPO3611		hypothetical protein	-2.14	0.08	-1.16	0.75	-1.65	0.49	-2.94	0.06	-1.08	0.78	-2.01	0.93	1.25	0.50	1.54	0.24	1.40	0.14
SPO3612		AsnC family transcriptional regulator	1.61	0.05	-1.10	0.71	0.26	1.36	-1.08	0.31	-1.78	0.07	-1.43	0.35	1.17	0.07	-1.09	0.95	0.04	1.13
SPO3613		amino acid transporter LysE	2.73	X	2.34	0.07	2.54	0.20	6.17	0.03	-1.61	0.18	2.28	3.89	-1.04	0.99	-1.64	X	-1.34	0.30
SPO3614		hypothetical protein	-1.00	0.63	4.70	0.02	1.85	2.85	-1.19	0.91	1.19	0.55	0.00	1.19	-1.58	0.06	3.04	0.02	0.73	2.31
SPO3615		AraC family transcriptional regulator	1.29	0.80	16.00	0.00	8.65	7.36	-1.45	0.23	-1.03	0.61	-1.24	0.21	1.05	0.64	25.30	0.00	13.18	12.13
SPO3616	*accA*	acetyl-CoA carboxylase carboxyltransferase subunit alpha (EC:6.4.1.2)	1.48	0.34	1.21	0.18	1.35	0.14	3.26	0.02	-1.21	0.16	1.03	2.24	-1.09	0.14	-1.17	0.14	-1.13	0.04
SPO3617		peptidoglycan-binding protein	0.95	0.13	-1.56	0.27	-0.31	1.25	1.09	0.39	-1.11	0.10	-0.01	1.10	1.35	0.01	1.37	0.26	1.36	0.01
SPO3618		sulfonate ABC transporter permease	1.77	0.65	-1.15	0.71	0.31	1.46	1.57	0.65	-1.03	0.90	0.27	1.30	1.34	0.42	1.06	0.80	1.20	0.14
SPO3619		sulfonate ABC transporter ATP-binding protein	1.30	0.20	-1.07	0.75	0.12	1.19	0.95	0.56	1.50	0.03	1.23	0.27	1.64	0.02	1.46	0.09	1.55	0.09
SPO3620		sulfonate ABC transporter substrate-binding protein	1.37	0.24	-1.11	0.51	0.13	1.24	-1.25	0.25	1.60	0.18	0.18	1.43	1.83	0.18	1.93	0.03	1.88	0.05
SPO3621		GntR family transcriptional regulator	1.08	0.52	1.21	0.46	1.15	0.06	1.08	0.40	1.20	0.18	1.14	0.06	-1.27	0.03	-1.30	0.06	-1.29	0.02
SPO3622		hypothetical protein	-1.17	0.30	1.10	0.19	-0.03	1.14	3.12	0.01	-1.15	0.08	0.99	2.14	-1.37	0.02	-1.94	0.01	-1.66	0.29
SPO3623		hypothetical protein	1.27	0.07	1.42	0.10	1.35	0.08	6.31	0.00	-1.60	0.01	2.36	3.96	-1.25	0.22	-2.20	0.02	-1.73	0.48
SPO3625	*cspA*	cold shock protein CspA	-1.74	0.00	1.33	0.09	-0.21	1.54	1.45	0.13	-1.07	0.21	0.19	1.26	1.30	0.01	-1.12	0.17	0.09	1.21
SPO3626	*gshA*	glutamate--cysteine ligase (EC:6.3.2.2)	1.71	0.43	1.15	0.75	1.43	0.28	3.21	0.08	1.11	0.89	2.16	1.05	-1.05	0.75	-1.28	0.42	-1.17	0.12
SPO3627		hypothetical protein	1.22	0.96	-1.13	0.62	0.05	1.18	1.98	0.73	-1.05	0.73	0.47	1.52	1.35	0.32	1.61	0.23	1.48	0.13
SPO3628		acetyltransferase	1.04	0.81	-1.08	0.34	-0.02	1.06	2.01	0.02	-1.81	0.02	0.10	1.91	1.26	0.08	-1.04	0.66	0.11	1.15
SPO3629		16S ribosomal RNA methyltransferase RsmE	1.05	0.79	-1.17	0.47	-0.06	1.11	1.89	0.03	-1.18	0.25	0.36	1.54	1.05	0.49	-1.14	0.20	-0.04	1.10
SPO3630	*ubiA*	4-hydroxybenzoate polyprenyltransferase (EC:2.5.1.-)	2.69	0.03	1.56	0.04	2.13	0.57	2.86	0.01	-1.20	0.15	0.83	2.03	1.22	0.34	-1.23	0.04	-0.01	1.23
SPO3631		OmpA domain-containing protein	1.19	0.78	-1.41	0.14	-0.11	1.30	2.18	0.13	1.14	0.73	1.66	0.52	-1.07	0.57	1.22	0.64	0.08	1.15
SPO3632		hypothetical protein	1.54	0.02	-1.07	0.48	0.24	1.31	2.84	0.02	-1.07	0.44	0.89	1.96	1.36	0.06	1.16	0.17	1.26	0.10
SPO3633		molybdopterin converting factor subunit 2	-1.11	0.63	1.75	0.08	0.32	1.43	-1.29	0.60	-1.05	0.75	-1.17	0.12	-1.04	0.91	-1.24	0.44	-1.14	0.10
SPO3634	*moaD*	molybdopterin converting factor subunit 1	1.09	0.99	1.88	0.06	1.49	0.40	1.33	0.89	1.03	0.98	1.18	0.15	1.61	0.11	1.43	0.28	1.52	0.09
SPO3635	*pgsA*	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC:2.7.8.5)	1.04	0.97	1.37	0.27	1.21	0.17	1.71	0.01	-1.04	0.13	0.34	1.38	1.24	0.32	-1.08	0.18	0.08	1.16
SPO3636		beta-lactamase	1.24	0.81	-1.50	0.08	-0.13	1.37	-1.82	0.07	1.96	0.03	0.07	1.89	1.41	0.04	1.41	0.02	1.41	0.00
SPO3637	*uvrC*	excinuclease ABC subunit C	1.08	0.29	-1.37	0.06	-0.15	1.23	1.07	0.21	-1.33	0.06	-0.13	1.20	-1.03	0.44	1.18	0.34	0.08	1.11
SPO3638		short chain dehydrogenase	1.54	0.09	-1.24	0.13	0.15	1.39	2.47	0.11	-1.09	0.55	0.69	1.78	1.16	0.42	1.14	0.58	1.15	0.01
SPO3639		K+-dependent Na+/Ca+ exchanger-like protein	1.16	0.74	-1.13	0.77	0.02	1.15	2.36	0.11	-1.62	0.26	0.37	1.99	1.19	0.74	1.18	0.81	1.19	0.01

SPO3640		S49 family peptidase	-1.46	0.26	-1.42	0.39	-1.44	0.02	1.55	0.12	-1.40	0.22	0.08	1.48	1.21	0.38	1.60	0.16	1.41	0.20
SPO3641		ABC transporter permease	1.18	0.86	1.04	0.94	1.11	0.07	1.77	0.07	1.24	0.45	1.51	0.27	1.04	0.94	-1.07	0.73	-0.02	1.06
SPO3642		ABC transporter ATP-binding protein	1.22	0.83	1.08	0.48	1.15	0.07	1.68	0.07	-1.02	0.59	0.33	1.35	-1.04	0.62	-1.21	0.19	-1.13	0.09
SPO3643		hypothetical protein	-1.03	0.98	1.40	0.07	0.19	1.22	1.58	0.16	-1.19	0.56	0.20	1.39	1.74	0.01	-0.99	0.94	0.38	1.36
SPO3644		hypothetical protein	X	X	-1.40	0.22	N/A	N/A	-0.87	0.01	-1.56	0.06	-1.22	0.34	-1.40	0.28	X	X	N/A	N/A
SPO3645		transcriptional regulator	-0.99	0.93	-1.22	0.14	-1.11	0.11	-1.25	0.15	1.06	0.59	-0.10	1.16	1.37	0.08	1.28	0.05	1.33	0.05
SPO3646		enoyl-CoA hydratase (EC:4.2.1.17)	1.30	0.23	-1.10	0.73	0.10	1.20	-4.28	0.01	1.70	0.04	-1.29	2.99	1.06	0.70	2.55	0.03	1.81	0.75
SPO3647		CAIB/BAIF family protein	2.92	0.01	1.99	0.02	2.46	0.47	-1.63	0.10	1.81	0.04	0.09	1.72	-1.06	0.72	2.30	0.13	0.62	1.68
SPO3648	*hemE*	uroporphyrinogen decarboxylase (EC:4.1.1.37)	2.14	0.48	3.30	0.03	2.72	0.58	3.14	0.25	1.36	0.27	2.25	0.89	-1.03	0.85	-1.46	0.01	-1.25	0.21
SPO3649	*hemC*	porphobilinogen deaminase (EC:2.5.1.61)	1.41	0.71	1.62	0.10	1.52	0.11	2.69	0.26	1.10	0.84	1.90	0.80	-1.46	0.21	-1.06	0.47	-1.26	0.20
SPO3650		guanylate cyclase	-1.48	0.02	-1.15	0.17	-1.32	0.17	-2.12	0.02	1.26	0.16	-0.43	1.69	-1.11	0.22	1.56	0.02	0.23	1.34
SPO3651		fatty acid desaturase	0.98	0.01	-1.18	0.57	-0.10	1.08	-17.70	0.00	1.46	0.07	-8.12	9.58	-0.98	0.55	3.50	0.00	1.26	2.24
SPO3652		hypothetical protein	1.58	0.17	1.29	0.51	1.44	0.15	-1.40	0.04	1.20	0.62	-0.10	1.30	1.08	0.77	1.26	0.62	1.17	0.09
SPO3653	*hemF*	coproporphyrinogen III oxidase (EC:1.3.3.3)	1.42	0.04	1.51	0.01	1.47	0.05	1.82	0.03	1.07	0.44	1.45	0.38	1.24	0.08	-1.28	0.03	-0.02	1.26
SPO3654		7-alpha-hydroxysteroid dehydrogenase	1.51	0.79	-1.03	0.83	0.24	1.27	1.94	0.63	1.07	0.94	1.51	0.44	0.99	0.87	1.02	0.95	1.01	0.01
SPO3655		methyltransferase	-1.34	0.21	1.13	0.66	-0.11	1.24	-1.12	0.71	-1.11	0.51	-1.12	0.01	1.10	0.21	1.09	0.62	1.10	0.01
SPO3656	*clpS*	ATP-dependent Clp protease, adaptor protein ClpS	0.98	0.13	1.16	0.48	1.07	0.09	1.38	0.14	1.26	0.07	1.32	0.06	-1.23	0.30	-1.08	0.48	-1.16	0.08
SPO3657		HAD superfamily hydrolase	-1.68	0.45	-1.22	0.26	-1.45	0.23	-1.79	0.52	1.30	0.45	-0.25	1.55	-1.08	0.79	1.30	0.25	0.11	1.19
SPO3658		D-alanyl-D-alanine carboxypeptidase	0.96	0.78	-1.82	0.07	-0.43	1.39	0.79	0.02	0.97	0.12	0.88	0.09	1.09	0.75	1.03	0.37	1.06	0.03
SPO3659		LamB/YcsF family protein	-1.14	0.07	-1.02	0.78	-1.08	0.06	1.11	0.16	1.26	0.19	1.19	0.08	-1.06	0.63	-1.02	0.80	-1.04	0.02
SPO3660		urea amidolyase	1.29	X	-1.19	0.31	0.05	1.24	3.40	0.01	1.97	0.03	2.69	0.72	-1.48	0.02	-1.86	0.09	-1.67	0.19
SPO3661		allophanate hydrolase	-1.04	1.00	-1.17	0.27	-1.11	0.06	2.53	0.00	2.10	0.04	2.32	0.22	-1.29	0.08	-2.12	0.02	-1.71	0.42
SPO3662		hypothetical protein	-1.24	0.08	-1.63	0.04	-1.44	0.19	2.33	0.01	4.35	0.00	3.34	1.01	-1.17	0.40	-1.13	0.97	-1.15	0.02
SPO3663		TRAP dicarboxylate transporter subunit DctM	-1.37	0.60	-2.12	0.05	-1.75	0.38	1.72	0.41	3.09	0.03	2.41	0.69	1.03	0.92	1.06	0.56	1.05	0.02
SPO3664		hypothetical protein	-1.31	0.02	-3.25	0.00	-2.28	0.97	1.99	0.02	3.67	0.00	2.83	0.84	-1.22	0.14	1.15	0.27	-0.04	1.19
SPO3665		solute-binding family 7 protein	-2.26	0.01	-2.94	0.04	-2.60	0.34	1.04	0.23	3.47	0.01	2.26	1.22	1.41	0.02	2.12	0.01	1.77	0.35
SPO3666		oxidoreductase, FAD-binding	1.05	0.55	-2.00	0.24	-0.48	1.53	2.49	0.00	4.17	0.00	3.33	0.84	-1.39	0.37	-1.21	0.83	-1.30	0.09
SPO3667	*catB*	muconate cycloisomerase I (EC:5.5.1.1)	1.50	0.01	1.05	0.74	1.28	0.23	-1.58	0.53	-1.04	0.97	-1.31	0.27	1.07	0.40	1.32	0.26	1.20	0.13
SPO3668		LysR family transcriptional regulator	-1.44	0.47	-1.16	0.79	-1.30	0.14	-1.27	0.88	-1.40	0.51	-1.34	0.06	-1.15	0.80	-1.23	0.87	-1.19	0.04
SPO3670		hypothetical protein	X	X	-1.41	0.57	N/A	N/A	-1.16	X	-1.03	1.00	-1.10	0.06	-1.71	0.17	1.19	0.48	-0.26	1.45
SPO3671		muticopper oxidase domain-containing protein	1.44	0.04	-1.34	0.04	0.05	1.39	-1.73	0.02	1.87	0.01	0.07	1.80	-1.17	0.38	1.41	0.04	0.12	1.29
SPO3672		hypothetical protein	1.30	0.72	1.10	0.87	1.20	0.10	-1.45	0.40	2.12	0.20	0.34	1.79	1.14	0.68	1.75	0.37	1.45	0.31
SPO3673		type I secretion target repeat-containing protein	1.67	0.39	1.20	0.43	1.44	0.23	3.28	0.12	1.26	0.22	2.27	1.01	0.97	0.65	1.07	0.67	1.02	0.05
SPO3674		ISSpo7, transposase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPO3675		hypothetical protein	X	X	1.21	0.07	N/A	N/A	4.71	0.13	-1.36	0.22	1.68	3.04	-1.75	0.20	-2.95	0.07	-2.35	0.60
SPO3676	*argE-2*	acetylornithine deacetylase (EC:3.5.1.16)	1.60	0.03	1.33	0.04	1.47	0.14	-1.02	0.36	1.09	0.64	0.04	1.06	1.31	0.11	X	X	N/A	N/A
SPO3677		LysR family transcriptional regulator	1.14	0.29	1.02	0.58	1.08	0.06	-1.43	0.05	1.20	0.20	-0.12	1.32	-1.11	0.71	-1.31	0.05	-1.21	0.10
SPO3678		Rieske (2Fe-2S) domain-containing protein	1.01	0.97	1.07	0.84	1.04	0.03	-1.66	0.26	1.04	0.92	-0.31	1.35	1.11	0.68	-1.01	0.92	0.05	1.06
SPO3679		hypothetical protein	1.09	0.93	1.06	0.41	1.08	0.02	-2.08	0.01	-1.05	0.59	-1.57	0.52	-1.11	0.43	1.02	0.91	-0.05	1.07

SPO3680		endoribonuclease L-PSP	1.28	0.39	1.31	0.02	1.30	0.02	-2.11	0.03	1.07	0.73	-0.52	1.59	1.24	0.34	1.43	0.02	1.34	0.10
SPO3681		Rieske (2Fe-2S) domain-containing protein	1.14	0.99	-1.07	0.79	0.03	1.11	-2.83	0.01	1.16	0.47	-0.84	2.00	-1.17	0.34	1.28	0.23	0.06	1.23
SPO3682		hypothetical protein	-1.69	0.13	-1.41	0.55	-1.55	0.14	-1.64	0.52	-1.99	0.10	-1.82	0.18	-1.04	0.89	-1.23	0.48	-1.14	0.10
SPO3684		LacI family transcriptional regulator	1.58	0.02	1.10	0.80	1.34	0.24	0.98	0.07	1.91	0.02	1.45	0.46	-1.10	0.58	-1.41	0.05	-1.26	0.16
SPO3685		hypothetical protein	-1.48	0.00	1.19	0.27	-0.15	1.34	-3.09	0.00	1.55	0.05	-0.77	2.32	1.04	0.61	-1.25	0.32	-0.11	1.15
SPO3686		HpcH/HpaI aldolase	1.66	0.01	1.12	0.44	1.39	0.27	1.26	0.04	-1.05	0.41	0.11	1.16	1.24	0.15	1.07	0.54	1.16	0.09
SPO3687		decarboxylase, pyridoxal-dependent	1.24	0.20	-1.05	0.60	0.10	1.15	-1.35	0.35	1.30	0.06	-0.03	1.33	1.14	0.16	1.30	0.02	1.22	0.08
SPO3688		extradiol ring-cleavage dioxygenase	0.99	0.90	-1.08	0.78	-0.05	1.03	-1.11	0.93	1.27	0.51	0.08	1.19	1.20	0.54	1.23	0.50	1.22	0.02
SPO3689		MarR family transcriptional regulator	-1.56	0.00	1.07	0.78	-0.25	1.32	-1.22	0.16	1.05	0.87	-0.09	1.14	1.05	0.85	1.19	0.16	1.12	0.07
SPO3690	*gtdA-1*	gentisate 1,2-dioxygenase (EC:1.13.11.4)	0.89	0.03	-1.69	0.02	-0.40	1.29	-1.49	0.04	1.93	0.01	0.22	1.71	-1.07	0.60	1.35	0.36	0.14	1.21
SPO3691		fumarylacetoacetate hydrolase	-1.11	0.16	-1.19	0.43	-1.15	0.04	-1.27	0.09	1.47	0.15	0.10	1.37	1.18	0.08	1.22	0.29	1.20	0.02
SPO3692		salicylate hydroxylase (EC:1.14.13.1)	-1.20	0.05	-1.62	0.03	-1.41	0.21	-1.70	0.06	1.57	0.03	-0.06	1.64	1.03	0.97	1.14	0.14	1.09	0.05
SPO3693		TRAP dicarboxylate transporter subunit DctP	1.10	0.52	-2.43	0.00	-0.67	1.77	-8.91	0.00	1.81	0.05	-3.55	5.36	1.56	0.01	2.54	0.02	2.05	0.49
SPO3694		hypothetical protein	1.12	0.96	-1.45	0.35	-0.17	1.29	-2.59	0.01	1.62	0.32	-0.49	2.11	1.38	0.33	1.45	0.22	1.42	0.04
SPO3695		TRAP dicarboxylate transporter subunit DctM	-1.09	0.72	-1.36	0.57	-1.23	0.14	-1.23	0.72	1.42	0.26	0.10	1.33	1.53	0.14	1.70	0.24	1.62	0.09
SPO3696	*fcs*	feruloyl-CoA synthase	1.13	0.82	-1.70	0.42	-0.29	1.42	-2.99	0.07	1.55	0.26	-0.72	2.27	1.22	0.21	1.77	0.16	1.50	0.27
SPO3697	*badA-1*	benzoate-coenzyme A ligase (EC:6.2.1.25)	1.06	0.72	-1.44	0.37	-0.19	1.25	-4.32	0.01	1.96	0.07	-1.18	3.14	1.19	0.47	1.37	0.35	1.28	0.09
SPO3698		hydrolase	1.14	0.88	-1.57	0.44	-0.22	1.36	-4.21	0.04	1.62	0.19	-1.30	2.92	1.03	0.94	1.43	0.26	1.23	0.20
SPO3699		hypothetical protein	1.09	0.91	-1.77	0.14	-0.34	1.43	-2.77	0.03	1.43	0.13	-0.67	2.10	-1.05	0.95	-1.03	0.84	-1.04	0.01
SPO3700		benzoyl-CoA-dihydrodiol lyase (EC:4.2.1.17)	1.36	0.00	-1.57	0.41	-0.11	1.47	-3.39	0.00	1.37	0.31	-1.01	2.38	-1.10	0.17	-1.02	0.98	-1.06	0.04
SPO3701	*boxB*	benzoyl-CoA oxygenase subunit B	1.34	0.74	-1.47	0.58	-0.06	1.41	-2.67	0.23	1.67	0.26	-0.50	2.17	-1.08	0.64	1.27	0.56	0.10	1.18
SPO3702		hypothetical protein	1.68	0.34	1.02	0.99	1.35	0.33	-3.17	0.04	2.67	0.03	-0.25	2.92	1.03	0.99	1.06	0.95	1.05	0.02
SPO3703	*boxA*	benzoyl-CoA oxygenase, A subunit	1.27	0.63	-1.39	0.05	-0.06	1.33	-1.97	0.01	1.43	0.22	-0.27	1.70	-1.09	0.33	2.34	0.03	0.63	1.72
SPO3704		anaerobic benzoate catabolism transcriptional regulator	-1.86	0.02	-1.32	0.22	-1.59	0.27	-1.99	0.03	-1.11	0.61	-1.55	0.44	1.15	0.58	1.40	0.13	1.28	0.13
SPO3705		branched-chain amino acid ABC transporter substrate-binding protein	-1.76	0.00	-1.57	0.08	-1.67	0.10	-11.30	0.01	5.37	0.02	-2.97	8.34	1.19	0.36	2.01	0.02	1.60	0.41
SPO3706		branched-chain amino acid ABC transporter ATP-binding protein	-1.05	0.19	-1.34	0.45	-1.20	0.15	-3.29	0.02	4.26	0.00	0.49	3.78	-0.99	0.66	1.12	0.25	0.07	1.05
SPO3707		branched-chain amino acid ABC transporter ATP-binding protein	1.06	0.98	-1.28	0.34	-0.11	1.17	-1.20	0.49	3.54	0.01	1.17	2.37	-1.03	0.90	1.14	0.04	0.05	1.09
SPO3708		branched-chain amino acid ABC transporter permease	1.19	0.86	1.20	0.01	1.20	0.01	-2.14	0.13	2.95	0.14	0.41	2.55	1.38	0.07	-0.95	0.24	0.21	1.17
SPO3709		branched-chain amino acid ABC transporter permease	1.11	0.98	1.06	0.90	1.09	0.03	-1.38	0.84	2.03	0.13	0.33	1.71	1.19	0.66	1.27	0.36	1.23	0.04
SPO3710		hypothetical protein	1.08	0.19	-1.09	0.57	-0.01	1.09	-1.33	0.10	1.28	0.08	-0.03	1.31	-1.07	0.68	-0.97	0.24	-1.02	0.05
SPO3711		hypothetical protein	-1.37	0.05	1.09	0.65	-0.14	1.23	-1.49	0.19	-1.11	0.49	-1.30	0.19	-1.12	0.48	-1.14	0.62	-1.13	0.01
SPO3712	*asd*	aspartate-semialdehyde dehydrogenase (EC:1.2.1.11)	1.03	0.95	1.13	0.69	1.08	0.05	6.31	0.04	-1.30	0.14	2.51	3.81	-1.32	0.30	-1.88	0.06	-1.60	0.28
SPO3713		hypothetical protein	-1.42	0.06	1.04	0.89	-0.19	1.23	2.05	0.06	1.00	0.46	1.52	0.53	2.18	0.00	2.14	0.01	2.16	0.02
SPO3714		hypothetical protein	1.59	0.09	1.90	0.02	1.75	0.16	-0.91	0.09	-1.01	0.98	-0.96	0.05	-1.26	0.11	-1.83	0.08	-1.55	0.29
SPO3715		carbonic anhydrase	2.21	0.47	1.35	0.18	1.78	0.43	2.52	0.36	-1.16	0.38	0.68	1.84	1.04	0.97	-1.33	0.19	-0.15	1.19
SPO3716		hypothetical protein	X	X	1.35	0.31	N/A	N/A	X	X	-1.20	0.71	N/A	N/A	-1.06	0.97	-1.17	X	-1.12	0.05

SPO3717		cytosol aminopeptidase	1.19	0.45	1.20	0.10	1.20	0.01	1.45	0.09	1.35	0.09	1.40	0.05	1.47	0.28	1.30	0.10	1.39	0.09
SPO3718		NLP/P60 family protein	1.26	0.18	1.19	0.03	1.23	0.04	1.51	0.05	1.29	0.02	1.40	0.11	1.38	0.02	1.46	0.30	1.42	0.04
SPO3719		thiosulfate sulfurtransferase	2.17	0.01	-1.04	0.80	0.57	1.61	2.23	0.06	1.00	0.50	1.61	0.62	-1.17	0.38	0.95	0.13	-0.11	1.06
SPO3720	*tyrB*	aromatic amino acid aminotransferase (EC:2.6.1.57)	3.12	0.00	1.45	0.03	2.29	0.84	3.51	0.00	-1.11	0.17	1.20	2.31	1.17	0.20	-1.19	0.04	-0.01	1.18
SPO3721		hypothetical protein	X	X	1.60	0.00	N/A	N/A	1.57	X	-1.28	0.24	0.15	1.43	-1.00	0.52	-1.18	0.86	-1.09	0.09
SPO3722		Rrf2 family protein	-0.97	0.43	1.01	0.66	0.02	0.99	-1.09	0.36	-1.03	0.81	-1.06	0.03	-1.59	0.03	-1.43	0.15	-1.51	0.08
SPO3723	*amt-2*	ammonium transporter	-2.15	0.11	-1.12	0.89	-1.64	0.52	-1.84	0.48	1.10	0.84	-0.37	1.47	-1.14	0.64	1.12	0.63	-0.01	1.13
SPO3724	*glnB-2*	nitrogen regulatory protein P-II	X	X	-1.13	0.54	N/A	N/A	-1.62	0.22	-0.97	0.78	-1.30	0.32	-1.16	0.56	-0.95	0.69	-1.05	0.11
SPO3725		1A family penicillin-binding protein	-1.30	0.25	1.03	0.96	-0.14	1.17	1.16	0.71	-1.04	0.74	0.06	1.10	1.16	0.58	1.01	0.93	1.09	0.08
SPO3726		toluene tolerance family protein	1.18	0.74	-1.58	0.02	-0.20	1.38	2.56	0.23	-1.14	0.27	0.71	1.85	1.18	0.44	1.53	0.12	1.36	0.18
SPO3727		VacJ lipoprotein	1.13	0.95	-1.55	0.09	-0.21	1.34	2.41	0.01	1.12	0.78	1.77	0.65	-1.31	0.18	0.98	0.54	-0.16	1.15
SPO3728		type I secretion system ATPase	1.20	0.87	-1.09	0.68	0.05	1.15	2.53	0.08	1.17	0.35	1.85	0.68	1.78	0.06	2.38	0.03	2.08	0.30
SPO3729		HlyD family type I secretion membrane fusion protein	1.35	0.67	0.99	0.81	1.17	0.18	2.62	0.32	1.17	0.56	1.90	0.73	1.77	0.12	1.59	0.08	1.68	0.09
SPO3730		endoribonuclease L-PSP	1.32	0.73	1.00	0.92	1.16	0.16	2.41	0.22	1.01	0.80	1.71	0.70	1.17	0.39	1.44	0.19	1.31	0.14
SPO3731		glycerophosphoryl diester phosphodiesterase	2.01	0.04	1.06	0.87	1.54	0.47	3.75	0.01	1.31	0.14	2.53	1.22	1.04	0.77	1.08	0.72	1.06	0.02
SPO3732		hypothetical protein	1.20	0.83	-1.45	0.06	-0.13	1.33	1.71	0.38	-1.23	0.22	0.24	1.47	1.38	0.13	1.33	0.20	1.36	0.02
SPO3733	*phhB*	pterin-4-alpha-carbinolamine dehydratase (EC:4.2.1.96)	-1.20	0.13	1.25	0.36	0.03	1.23	-1.13	0.37	1.26	0.19	0.07	1.20	2.06	0.00	1.32	0.12	1.69	0.37
SPO3734		MerR family transcriptional regulator	-1.76	0.03	1.04	0.59	-0.36	1.40	-1.42	0.44	-1.28	0.36	-1.35	0.07	1.19	0.28	1.14	0.12	1.17	0.03
SPO3735		major facilitator family protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.15	X	X	X	N/A	N/A
SPO3736		anti-oxidant AhpCTSA family protein	1.88	0.25	1.12	0.78	1.50	0.38	1.43	0.40	1.06	0.99	1.25	0.18	-1.06	0.17	1.00	0.82	-0.03	1.03
SPO3737		pyridine nucleotide-disulfide oxidoreductase	1.22	0.20	1.03	0.89	1.13	0.10	1.34	0.11	-1.09	0.27	0.13	1.22	-1.08	0.57	-1.30	0.21	-1.19	0.11
SPO3738		methyltransferase	1.81	0.00	-1.01	0.90	0.40	1.41	2.24	0.00	-1.14	0.17	0.55	1.69	1.05	0.83	-1.27	0.22	-0.11	1.16
SPO3739		hydantoinase/oxoprolinase	1.44	0.32	1.37	0.50	1.41	0.03	-2.03	0.07	-1.04	0.70	-1.54	0.50	-1.34	0.06	1.10	0.47	-0.12	1.22
SPO3740	*msrA-2*	methionine sulfoxide reductase A (EC:1.8.4.11)	2.00	0.00	1.37	0.02	1.69	0.31	-1.31	0.01	1.38	0.06	0.03	1.35	1.27	0.08	1.05	0.64	1.16	0.11
SPO3741	*msrB*	methionine sulfoxide reductase B (EC:1.8.4.11)	2.27	0.02	1.28	0.35	1.78	0.50	0.91	0.14	1.65	0.03	1.28	0.37	1.19	0.43	1.08	0.95	1.14	0.05
SPO3742		glutathione peroxidase	2.18	0.01	1.10	0.48	1.64	0.54	-2.68	0.00	-1.05	0.92	-1.87	0.81	-0.97	0.65	-1.17	0.91	-1.07	0.10
SPO3743		hypothetical protein	1.76	0.11	1.50	0.20	1.63	0.13	2.40	0.02	-0.99	0.97	0.70	1.70	-1.09	0.57	-1.25	0.18	-1.17	0.08
SPO3744	*hup*	DNA-binding protein HU	1.04	0.53	0.97	0.79	1.00	0.04	2.24	0.41	-1.26	0.42	0.49	1.75	1.19	0.80	0.98	0.66	1.08	0.11
SPO3745	*amn*	AMP nucleosidase (EC:3.2.2.4)	1.22	0.12	-1.54	0.19	-0.16	1.38	3.45	0.01	-1.19	0.11	1.13	2.32	-1.23	0.02	-1.26	0.02	-1.25	0.02
SPO3746	*ade*	adenine deaminase (EC:3.5.4.2)	-1.15	0.71	-1.84	0.00	-1.50	0.35	1.87	0.08	1.21	0.35	1.54	0.33	-1.41	0.17	1.00	0.26	-0.21	1.20
SPO3747		hypothetical protein	1.10	0.49	1.07	0.71	1.09	0.02	-1.22	0.20	1.28	0.19	0.03	1.25	1.04	0.78	-1.07	0.96	-0.02	1.06
SPO3748		LysR family transcriptional regulator	-3.14	0.04	-1.37	0.56	-2.26	0.89	-7.31	0.02	-1.15	0.64	-4.23	3.08	-1.10	0.77	2.08	0.18	0.49	1.59
SPO3749		hypothetical protein	10.20	0.00	3.57	0.02	6.89	3.32	-1.56	0.09	1.01	0.98	-0.28	1.29	1.33	0.35	1.44	0.38	1.39	0.05
SPO3750		hypothetical protein	14.60	0.00	4.58	0.00	9.59	5.01	-1.03	0.08	1.20	0.15	0.09	1.12	-1.41	0.10	-1.38	0.13	-1.40	0.02
SPO3751	*exsB*	exoenzyme S synthesis protein B	X	X	1.07	0.59	N/A	N/A	-0.97	0.27	-7.34	0.00	-4.16	3.18	-5.55	0.01	-6.32	0.00	-5.94	0.39
SPO3752		radical SAM domain-containing protein	X	X	1.26	0.10	N/A	N/A	X	X	-8.54	0.00	N/A	N/A	-6.48	0.00	-11.30	0.00	-8.89	2.41
SPO3753		7-cyano-7-deazaguanine reductase	X	X	1.70	0.04	N/A	N/A	2.25	0.01	-5.44	0.01	-1.60	3.85	-3.39	0.01	-5.05	0.01	-4.22	0.83
SPO3754		hypothetical protein	-1.19	0.03	-1.08	0.51	-1.14	0.05	-2.62	0.00	1.75	0.05	-0.44	2.19	1.22	0.25	1.20	0.24	1.21	0.01

SPO3755		hypothetical protein	1.90	0.26	1.50	0.21	1.70	0.20	2.08	0.02	1.15	0.07	1.62	0.47	1.10	0.45	1.12	0.50	1.11	0.01
SPO3756		OmpA domain-containing protein	2.14	0.02	1.43	0.16	1.79	0.35	1.46	0.05	1.14	0.62	1.30	0.16	1.47	0.24	1.50	0.21	1.49	0.02
SPO3757		alkylhydroperoxidase	3.43	0.01	1.04	0.95	2.24	1.20	1.36	0.15	1.84	0.05	1.60	0.24	1.14	0.52	1.46	0.04	1.30	0.16
SPO3758		acetyltransferase	2.61	0.02	1.36	0.13	1.99	0.63	0.98	0.30	2.18	0.00	1.58	0.60	-1.11	0.07	1.41	0.26	0.15	1.26
SPO3759		molybdenum cofactor biosynthesis domain-containing protein	1.20	0.68	1.22	0.44	1.21	0.01	2.01	0.03	-1.35	0.12	0.33	1.68	1.16	0.15	-1.25	0.02	-0.05	1.21
SPO3760	*sfsA*	sugar fermentation stimulation protein A	-2.74	X	-1.21	0.08	-1.98	0.77	-1.87	0.14	-1.35	0.05	-1.61	0.26	-1.39	0.17	-1.48	0.00	-1.44	0.05
SPO3761	*map*	methionine aminopeptidase (EC:3.4.11.18)	1.09	1.00	1.08	0.42	1.09	0.01	2.36	0.02	1.05	0.95	1.71	0.65	-1.04	0.11	1.01	0.63	-0.02	1.03
SPO3762		HAD family hydrolase	3.14	0.03	-1.13	0.05	1.01	2.14	2.92	0.03	-1.76	0.06	0.58	2.34	-1.10	0.39	-2.08	0.01	-1.59	0.49
SPO3763		(Fe-S)-binding protein	-1.32	0.12	-1.02	0.82	-1.17	0.15	1.82	0.03	-1.50	0.03	0.16	1.66	1.30	0.03	-1.10	0.40	0.10	1.20
SPO3764		glutathione S-transferase	-1.11	0.33	1.14	0.44	0.01	1.13	2.33	0.01	-1.14	0.15	0.60	1.74	1.45	0.01	1.06	0.86	1.26	0.20
SPO3765		hypothetical protein	1.78	0.46	-1.14	0.16	0.32	1.46	1.26	0.97	1.04	0.98	1.15	0.11	1.10	0.82	2.24	0.13	1.67	0.57
SPO3766	*mtgA*	monofunctional biosynthetic peptidoglycan transglycosylase (EC:2.4.2.-)	-1.43	0.06	-1.34	0.30	-1.39	0.04	1.12	0.45	-1.12	0.39	0.00	1.12	1.08	0.78	-1.24	0.42	-0.08	1.16
SPO3767		hypothetical protein	-2.34	0.04	-2.43	0.00	-2.39	0.05	-2.16	0.02	-1.84	0.04	-2.00	0.16	-1.06	0.45	-1.98	0.24	-1.52	0.46
SPO3768	*gltB*	glutamate synthase, large subunit (EC:1.4.1.13)	2.22	0.02	3.30	0.00	2.76	0.54	7.10	0.00	3.14	0.01	5.12	1.98	-1.36	0.12	-2.49	0.00	-1.93	0.57
SPO3769		hypothetical protein	2.21	0.58	1.92	0.30	2.07	0.15	4.95	0.29	1.92	0.30	3.44	1.52	-1.63	0.30	-1.51	0.57	-1.57	0.06
SPO3770	*gltD*	oxidoreductase (EC:1.4.1.13)	2.81	0.06	2.39	0.06	2.60	0.21	5.01	0.02	3.27	0.00	4.14	0.87	-1.06	0.68	-1.59	0.24	-1.33	0.27
SPO3771		UDP pyrophosphate phosphatase	1.83	0.58	1.36	0.73	1.60	0.24	4.35	0.21	-1.20	0.79	1.58	2.78	-1.02	0.97	-1.26	0.78	-1.14	0.12
SPO3772		NADH ubiquinone oxidoreductase	3.89	0.00	1.72	0.02	2.81	1.09	3.23	0.00	-1.09	0.50	1.07	2.16	1.13	0.62	-1.10	0.29	0.01	1.12
SPO3774		oligopeptide/dipeptide ABC transporter substrate-binding protein	-3.83	0.21	-2.23	0.15	-3.03	0.80	0.88	0.46	1.08	0.83	0.98	0.10	1.08	0.88	1.34	0.40	1.21	0.13
SPO3775		oligopeptide/dipeptide ABC transporter permease	-1.44	0.70	-1.44	0.32	-1.44	0.00	1.12	0.84	-1.04	0.74	0.04	1.08	-1.01	0.87	1.02	0.97	0.01	1.02
SPO3776		oligopeptide/dipeptide ABC transporter permease	-1.36	0.73	-1.41	0.39	-1.39	0.02	1.59	0.38	-1.08	0.81	0.26	1.34	-1.18	0.70	-1.26	0.57	-1.22	0.04
SPO3777		oligopeptide/dipeptide ABC transporter ATP-binding protein	-1.29	0.24	-1.47	0.23	-1.38	0.09	1.58	0.08	-1.02	0.72	0.28	1.30	-1.43	0.04	-1.27	0.17	-1.35	0.08
SPO3778		oligopeptide/dipeptide ABC transporter ATP-binding protein	-1.27	0.02	-1.44	0.00	-1.36	0.09	1.16	0.28	1.05	0.91	1.11	0.05	-1.25	0.32	1.02	0.87	-0.12	1.14
SPO3779		LysR family transcriptional regulator	-1.42	0.85	-1.21	0.69	-1.32	0.11	-1.06	0.93	-1.43	0.48	-1.25	0.18	1.18	0.74	-1.06	0.96	0.06	1.12
SPO3780		hypothetical protein	-1.04	0.37	1.13	0.32	0.04	1.09	1.80	0.02	-1.03	0.61	0.39	1.42	1.41	0.02	-1.04	0.52	0.19	1.23
SPO3781		hypothetical protein	-1.78	0.37	1.06	0.88	-0.36	1.42	2.15	0.45	-1.21	0.55	0.47	1.68	-1.09	0.93	-1.32	0.65	-1.21	0.12
SPO3782		hypothetical protein	1.31	0.90	1.08	0.79	1.20	0.12	-1.15	0.96	-1.43	0.35	-1.29	0.14	-1.15	0.65	1.18	0.68	0.02	1.17
SPO3783		sugar ABC transporter ATP-binding protein	1.72	0.11	-1.06	0.74	0.33	1.39	-1.11	0.50	-0.98	0.79	-1.05	0.07	-1.09	0.71	-1.19	0.88	-1.14	0.05
SPO3784		sugar ABC transporter ATP-binding protein	2.23	0.19	-1.08	0.80	0.58	1.66	-1.14	0.83	1.26	0.12	0.06	1.20	-1.24	0.49	-1.74	X	-1.49	0.25
SPO3785		sugar ABC transporter permease	1.73	X	-1.06	0.92	0.34	1.40	-1.79	0.55	-0.97	0.82	-1.38	0.41	-1.16	0.72	-1.69	X	-1.43	0.27
SPO3786		sugar ABC transporter permease	1.34	0.12	-1.25	0.30	0.05	1.30	-2.48	0.04	1.25	0.17	-0.62	1.87	-1.18	0.58	-1.25	0.39	-1.22	0.04
SPO3787		sugar ABC transporter substrate-binding protein	1.77	0.29	-1.05	0.94	0.36	1.41	-5.62	0.04	1.53	0.16	-2.05	3.58	-1.14	0.44	X	X	N/A	N/A
SPO3788	*acoR*	acetoin catabolism regulatory protein	1.12	0.77	-2.03	0.50	-0.46	1.58	-4.82	0.10	1.70	0.26	-1.56	3.26	1.15	0.71	1.37	X	1.26	0.11
SPO3789		alkylhydroperoxidase	2.92	0.07	-1.15	0.71	0.89	2.04	-2.27	0.03	X	X	N/A	N/A	-1.12	0.70	X	X	N/A	N/A
SPO3790	*acoC*	branched-chain alpha-keto acid dehydrogenase E2 subunit (EC:2.3.1.12)	2.13	0.45	-1.30	0.76	0.42	1.72	-4.28	0.30	1.72	0.13	-1.28	3.00	-0.97	0.88	1.25	0.67	0.14	1.11
SPO3791	*acoB*	acetoin dehydrogenase complex, E1 component subunit beta (EC:1.1.1.-)	3.20	0.05	-1.67	0.01	0.77	2.44	-8.30	0.00	1.77	0.04	-3.27	5.04	-1.22	0.28	-1.19	X	-1.21	0.02

SPO3792	*acoA*	acetoin dehydrogenase complex, E1 component subunit alpha (EC:1.1.1.-)	2.92	0.02	-1.69	0.00	0.62	2.31	-14.90	0.00	2.12	0.02	-6.39	8.51	-1.78	0.05	X	X	N/A	N/A
SPO3793	*acoX*	acetoin catabolism protein X	1.75	0.02	-1.78	X	-0.02	1.77	-4.43	0.06	X	X	N/A	N/A	-1.83	X	X	X	N/A	N/A
SPO3794		hypothetical protein	-1.62	0.14	-1.32	0.09	-1.47	0.15	-4.14	0.00	-1.26	0.57	-2.70	1.44	-1.43	0.49	2.26	0.03	0.42	1.85
SPO3795	*rpoN*	RNA polymerase sigma-54 factor	1.36	0.18	-1.02	0.97	0.17	1.19	-1.43	0.63	1.15	0.65	-0.14	1.29	-1.00	0.99	-1.28	0.70	-1.14	0.14
SPO3802		hypothetical protein	-1.33	0.62	-1.04	0.94	-1.19	0.15	-1.79	0.54	1.19	0.76	-0.30	1.49	1.34	0.53	1.19	0.60	1.27	0.08
SPO3803		AraC family transcriptional regulator	X	X	-1.02	0.99	N/A	N/A	-1.18	0.85	1.05	0.64	-0.06	1.12	1.08	0.67	-1.27	0.42	-0.10	1.18
SPO3804	*dmdC*	3-methylmercaptopropionyl-CoA dehydrogenase	4.36	0.09	4.75	0.01	4.56	0.20	1.23	0.82	1.44	0.15	1.34	0.11	1.22	0.18	1.35	0.13	1.29	0.07
SPO3805	*dmdD*	methylthioacryloyl-CoA hydratase (EC:4.2.1.17)	6.53	0.00	3.96	0.01	5.25	1.29	1.81	0.07	1.74	0.03	1.78	0.04	-1.08	0.40	1.32	0.39	0.12	1.20
SPO3806	*smpB*	SsrA-binding protein	-1.00	0.76	-1.33	0.17	-1.16	0.17	2.23	0.00	-1.20	0.28	0.52	1.72	-1.19	0.29	-1.30	0.00	-1.25	0.06
SPO3807		hypothetical protein	-1.89	0.28	-1.03	0.86	-1.46	0.43	-2.98	0.02	1.49	0.10	-0.75	2.24	1.41	0.01	1.40	0.14	1.41	0.01
SPO3808		hypothetical protein	0.97	0.80	1.01	0.99	0.99	0.02	-1.33	0.43	-1.05	0.98	-1.19	0.14	1.35	0.79	1.53	0.87	1.44	0.09
SPO3809		ArsR family transcriptional regulator	1.05	1.00	-1.04	0.96	0.01	1.05	1.25	0.92	1.10	0.89	1.18	0.08	1.40	0.63	1.92	0.40	1.66	0.26
SPO3810	*gpmI*	phosphoglyceromutase (EC:5.4.2.1)	-1.24	0.83	-1.18	0.59	-1.21	0.03	1.99	0.47	-1.51	0.20	0.24	1.75	-1.61	0.13	-1.28	0.31	-1.45	0.17
SPO3811		hypothetical protein	-1.28	0.37	1.04	0.72	-0.12	1.16	2.37	0.11	-1.67	0.00	0.35	2.02	-1.17	0.25	-1.07	0.54	-1.12	0.05
SPO3812		carboxyl-terminal protease	-1.22	0.54	-1.07	0.76	-1.15	0.08	1.18	1.00	-1.08	0.62	0.05	1.13	1.27	0.33	1.54	0.07	1.41	0.14
SPO3813		hypothetical protein	0.98	0.11	1.14	0.30	1.06	0.08	1.02	0.98	-1.32	0.07	-0.15	1.17	1.26	0.03	-1.45	0.08	-0.10	1.36
SPO3814		hypothetical protein	-1.41	0.01	-1.13	0.39	-1.27	0.14	-1.48	0.04	-1.09	0.17	-1.29	0.19	-1.32	0.05	-1.40	0.02	-1.36	0.04
SPO3815		ABC transporter permease	1.12	0.72	1.00	0.99	1.06	0.06	1.57	0.08	1.07	0.31	1.32	0.25	-1.07	0.65	1.11	0.32	0.02	1.09
SPO3816		CAAX amino terminal protease	1.29	0.02	1.01	0.84	1.15	0.14	2.00	0.01	-1.11	0.59	0.45	1.56	1.18	0.21	-0.94	0.45	0.12	1.06
SPO3817	*accD*	acetyl-CoA carboxylase, carboxyl transferase subunit beta (EC:6.4.1.2)	1.15	0.86	-1.77	0.10	-0.31	1.46	2.29	0.06	1.18	0.39	1.74	0.56	-1.27	0.06	1.03	0.03	-0.12	1.15
SPO3818	*folC*	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	1.47	0.03	-1.33	0.02	0.07	1.40	3.83	0.01	-1.23	0.13	1.30	2.53	-1.50	0.07	-1.99	0.00	-1.75	0.25
SPO3819		AFG1 family ATPase	1.45	0.12	1.27	0.18	1.36	0.09	2.14	0.04	-1.67	0.05	0.24	1.91	-1.12	0.08	-1.91	0.02	-1.52	0.39
SPO3820		major facilitator superfamily transporter	1.42	0.67	1.55	0.32	1.49	0.07	3.97	0.16	-1.01	0.91	1.48	2.49	-1.01	0.93	-1.11	0.84	-1.06	0.05
SPO3821		ornithine cyclodeaminase/mu-crystallin family protein	1.00	0.75	-1.20	0.38	-0.10	1.10	1.40	0.51	1.16	0.06	1.28	0.12	-1.13	0.55	-1.22	0.24	-1.18	0.05
SPO3822		HAD-superfamily hydrolase	-1.01	0.44	-1.11	0.28	-1.06	0.05	1.97	0.05	-1.10	0.52	0.44	1.54	-1.10	0.53	-1.18	0.16	-1.14	0.04
SPO3823	*rplW*	50S ribosomal protein L23	1.07	0.82	1.61	0.13	1.34	0.27	14.10	0.01	-2.10	0.02	6.00	8.10	-1.11	0.09	-3.29	0.00	-2.20	1.09
SPO3824	*rplD*	50S ribosomal protein L4	-1.35	0.01	-1.12	0.13	-1.24	0.12	9.01	0.00	-2.02	0.01	3.50	5.52	-1.04	0.57	-2.29	0.01	-1.67	0.63
SPO3825	*rplC*	50S ribosomal protein L3	-1.61	0.01	-1.44	0.08	-1.53	0.09	9.32	0.00	-1.33	0.02	4.00	5.33	-1.43	0.10	-2.39	0.00	-1.91	0.48
SPO3826	*rpsJ*	30S ribosomal protein S10	-1.39	0.01	-1.57	0.01	-1.48	0.09	9.22	0.00	-1.71	0.00	3.76	5.47	-1.44	0.01	-2.58	0.01	-2.01	0.57
SPO3827		YaiI/YqxD family protein	1.07	0.98	1.07	0.90	1.07	0.00	1.27	0.92	-1.04	0.95	0.12	1.16	1.08	0.91	1.22	0.84	1.15	0.07
SPO3828	*sthA*	soluble pyridine nucleotide transhydrogenase (EC:1.6.1.1)	1.40	0.53	1.17	0.53	1.29	0.12	2.40	0.14	-1.10	0.60	0.65	1.75	1.02	0.93	-1.24	0.33	-0.11	1.13
SPO3829		S-formylglutathione hydrolase	1.62	0.00	-1.08	0.71	0.27	1.35	2.64	0.01	-1.15	0.09	0.75	1.90	-1.41	0.07	-1.58	0.07	-1.50	0.09
SPO3830	*pepT*	peptidase T (EC:3.4.11.4)	2.41	0.01	1.05	0.70	1.73	0.68	2.57	0.01	1.18	0.41	1.88	0.70	1.25	0.11	1.32	0.09	1.29	0.04
SPO3831		alpha/beta hydrolase	1.80	0.32	-1.27	0.02	0.27	1.54	2.22	0.01	1.36	0.04	1.79	0.43	-1.22	0.06	-1.14	0.23	-1.18	0.04
SPO3832		ornithine cyclodeaminase/mu-crystallin family protein	-0.98	0.70	1.02	0.95	0.02	1.00	1.37	0.07	1.24	0.14	1.31	0.07	-1.02	0.62	1.23	0.79	0.11	1.13
SPO3833		DEAD/DEAH box helicase	X	X	1.62	0.38	N/A	N/A	7.51	0.00	-1.19	0.10	3.16	4.35	-1.93	0.01	-2.30	0.04	-2.12	0.19
SPO3834	*dapB*	dihydrodipicolinate reductase (EC:1.3.1.26)	-1.06	0.98	1.40	0.46	0.17	1.23	2.63	0.01	-1.57	0.02	0.53	2.10	1.30	0.14	-1.24	0.53	0.03	1.27

SPO3835	*rbfA*	ribosome-binding factor A	-1.23	0.06	-1.17	0.56	-1.20	0.03	1.66	0.01	-1.14	0.04	0.26	1.40	1.42	0.01	1.20	0.51	1.31	0.11
SPO3836		hypothetical protein	-1.11	0.35	-1.15	0.24	-1.13	0.02	1.79	0.02	-1.19	0.25	0.30	1.49	1.41	0.03	-1.06	0.58	0.18	1.24
SPO3837	*truB*	tRNA pseudouridine synthase B (EC:4.2.1.70)	-1.38	0.62	1.27	0.06	-0.05	1.33	1.87	0.18	-1.80	0.15	0.04	1.84	-1.07	0.74	-1.28	0.48	-1.18	0.11
SPO3838		hypothetical protein	-1.12	0.88	-1.15	0.21	-1.14	0.01	2.81	0.15	-1.28	0.15	0.77	2.05	-1.21	0.21	-1.56	0.07	-1.39	0.18
SPO3839		type I secretion target repeat-containing protein	1.02	0.85	-1.06	0.71	-0.02	1.04	-2.56	0.02	-1.13	0.36	-1.85	0.72	-1.02	0.85	1.44	0.07	0.21	1.23
SPO3840	*rpsO*	30S ribosomal protein S15	-1.17	0.70	1.18	0.09	0.01	1.18	11.40	0.03	-2.44	0.01	4.48	6.92	-1.20	0.34	-1.73	0.01	-1.47	0.27
SPO3841		TetR family transcriptional regulator	-1.42	0.00	-1.20	0.40	-1.31	0.11	-1.65	0.01	1.31	0.23	-0.17	1.48	1.60	0.05	1.91	0.05	1.76	0.16
SPO3842		hypothetical protein	-1.17	0.05	1.66	0.09	0.25	1.42	-1.45	0.07	1.28	0.05	-0.09	1.37	1.26	0.02	1.27	0.08	1.27	0.01
SPO3843		malonate transporter	1.28	0.25	1.29	0.11	1.29	0.01	1.79	0.06	1.48	0.03	1.64	0.16	1.23	0.11	-1.39	0.03	-0.08	1.31
SPO3844	*polA*	DNA polymerase I (EC:2.7.7.7)	1.07	0.92	1.33	0.44	1.20	0.13	1.52	0.40	-1.19	0.36	0.17	1.36	1.07	0.82	-1.34	0.36	-0.14	1.21
SPO3845		hypothetical protein	1.64	0.05	1.57	0.02	1.61	0.03	3.01	0.01	-1.30	0.03	0.86	2.16	-1.10	0.03	-1.68	0.03	-1.39	0.29
SPO3846		hypothetical protein	1.98	0.03	1.16	0.11	1.57	0.41	2.02	0.03	0.98	0.32	1.50	0.52	1.03	0.88	-1.17	0.19	-0.07	1.10
SPO3847		ABC transporter ATP-binding protein	-1.13	0.12	1.13	0.64	0.00	1.13	1.34	0.01	-1.42	0.05	-0.04	1.38	-1.26	0.04	-1.58	0.03	-1.42	0.16
SPO3848		sterol desaturase	-1.22	0.15	-1.05	0.61	-1.14	0.09	-1.97	0.02	1.44	0.06	-0.27	1.71	-1.06	0.45	1.23	0.13	0.09	1.15
SPO3849		hypothetical protein	-0.94	0.35	1.17	0.10	0.12	1.06	-1.12	0.45	1.45	0.19	0.17	1.29	-1.02	0.91	X	X	N/A	N/A
SPO3850		glutathione-dependent formaldehyde dehydrogenase (EC:1.1.1.284)	3.57	0.17	1.18	0.83	2.38	1.20	1.03	0.92	1.38	0.65	1.21	0.17	1.20	0.79	1.30	0.74	1.25	0.05
SPO3851		HemY domain-containing protein	2.35	0.05	1.93	0.00	2.14	0.21	1.96	0.07	1.68	0.03	1.82	0.14	1.11	0.40	1.66	0.04	1.39	0.28
SPO3852		hypothetical protein	2.17	0.13	2.14	0.07	2.16	0.01	2.23	0.05	1.32	0.16	1.78	0.46	1.63	0.01	1.76	0.07	1.70	0.07
SPO3853		uroporphyrinogen-III synthase	1.04	0.79	-1.18	0.04	-0.07	1.11	1.28	0.08	1.09	0.56	1.19	0.10	1.05	0.43	-1.16	0.48	-0.05	1.11
SPO3854		DNA-binding/iron metalloprotein/AP endonuclease	-1.40	0.02	1.06	0.90	-0.17	1.23	1.56	0.00	-1.60	0.07	-0.02	1.58	1.16	0.52	-1.31	0.48	-0.08	1.24
SPO3855	*gpsA*	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase (EC:1.1.1.94)	1.23	0.72	-1.14	0.29	0.05	1.19	2.02	0.01	0.97	0.46	1.49	0.53	-1.34	0.20	-1.37	0.11	-1.36	0.02
SPO3856		hypothetical protein	1.59	0.80	1.10	0.47	1.35	0.24	1.56	0.75	1.13	0.87	1.35	0.22	1.78	0.29	1.55	0.56	1.67	0.12
SPO3857		hypothetical protein	1.33	0.14	1.38	0.43	1.36	0.02	1.29	0.16	-1.18	0.26	0.06	1.24	1.46	0.15	-1.17	0.40	0.15	1.32
SPO3858		hypothetical protein	1.42	0.02	0.99	0.80	1.21	0.22	0.84	0.07	1.18	0.24	1.01	0.17	1.59	0.06	1.99	0.01	1.79	0.20
SPO3859		hypothetical protein	0.98	0.39	-1.38	0.25	-0.20	1.18	-1.39	0.08	1.47	0.07	0.04	1.43	1.05	0.94	-1.11	0.16	-0.03	1.08
SPO3860		hypothetical protein	1.11	0.66	1.18	0.07	1.15	0.03	-3.17	0.00	1.92	0.01	-0.63	2.55	1.18	0.20	1.42	0.30	1.30	0.12
SPO3861	*ahcY*	S-adenosyl-L-homocysteine hydrolase (EC:3.3.1.1)	1.17	0.91	1.15	0.80	1.16	0.01	4.34	0.03	-1.08	0.71	1.63	2.71	-1.18	0.68	-1.31	0.54	-1.25	0.07
SPO3862		lipoprotein	-3.76	0.29	-1.38	0.81	-2.57	1.19	-5.05	0.16	1.08	0.94	-1.99	3.07	-1.13	0.88	1.45	0.76	0.16	1.29
SPO3863		HD domain-containing protein	-1.35	0.34	-1.09	0.72	-1.22	0.13	2.01	0.52	-1.12	0.27	0.45	1.57	-1.10	0.53	-1.17	0.40	-1.14	0.03
SPO3864		hypothetical protein	-1.66	0.00	1.02	0.99	-0.32	1.34	0.89	0.27	1.01	0.83	0.95	0.06	1.53	0.01	1.36	0.16	1.45	0.09
SPO3865	*regA*	photosynthetic apparatus regulatory protein RegA	-1.19	0.04	-1.03	0.57	-1.11	0.08	1.08	0.24	1.18	0.23	1.13	0.05	1.09	0.80	1.02	0.36	1.06	0.04
SPO3866	*senC*	regulatory protein SenC	3.95	0.00	1.88	0.04	2.92	1.04	5.19	0.00	0.99	0.82	3.09	2.10	-1.22	0.05	-1.41	0.04	-1.32	0.10
SPO3867	*regB*	sensor histidine kinase RegB (EC:2.7.3.-)	-1.03	0.83	-1.16	0.66	-1.10	0.06	1.39	0.06	-1.41	0.04	-0.01	1.40	-1.11	0.52	-1.46	0.12	-1.29	0.17
SPO3868		hypothetical protein	1.38	0.53	2.43	0.01	1.91	0.53	-4.87	0.02	2.73	0.01	-1.07	3.80	-0.98	0.93	1.46	0.07	0.24	1.22
SPO3869		hypothetical protein	1.12	0.71	-1.11	0.43	0.01	1.12	1.65	0.10	1.34	0.28	1.50	0.16	-1.18	0.46	-1.11	0.46	-1.15	0.03
SPO3870		hypothetical protein	1.13	0.41	-1.01	0.95	0.06	1.07	1.83	0.05	-1.06	0.50	0.39	1.45	-0.99	0.86	-1.15	0.51	-1.07	0.08
SPO3871		nucleotidyltransferase	1.92	0.05	1.05	0.86	1.49	0.44	2.86	0.02	1.18	0.24	2.02	0.84	1.16	0.39	-1.20	0.60	-0.02	1.18
SPO3872		hypothetical protein	1.86	0.00	1.10	0.30	1.48	0.38	2.66	0.00	-1.01	0.52	0.83	1.84	1.02	0.68	-0.99	0.68	0.02	1.00

SPO3873	*uvrD*	ATP-dependent DNA helicase UvrD	-1.60	0.16	-1.32	0.49	-1.46	0.14	-1.96	0.04	1.16	0.55	-0.40	1.56	-1.15	0.28	1.87	0.38	0.36	1.51
SPO3874	*trx*	thioredoxin	1.79	0.08	1.27	0.35	1.53	0.26	2.07	0.01	-1.09	0.38	0.49	1.58	1.40	0.10	1.35	0.04	1.38	0.02
SPO3875		hypothetical protein	1.03	0.93	-1.07	0.66	-0.02	1.05	1.30	0.08	1.12	0.58	1.21	0.09	-1.19	0.10	-1.60	0.08	-1.40	0.21
SPO3876		hypothetical protein	1.16	0.61	-1.02	0.92	0.07	1.09	1.33	0.21	1.09	0.56	1.21	0.12	-0.99	0.92	-0.98	0.83	-0.98	0.01
SPO3877		transcriptional regulator/arsenate reductase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	1.16	0.40	X	X	N/A	N/A
SPO3878	*gap-4*	glyceraldehyde-3-phosphate dehydrogenase, type I (EC:1.2.1.-)	1.44	X	1.28	0.24	1.36	0.08	1.62	0.01	1.21	0.56	1.42	0.21	-1.01	0.88	-1.23	0.53	-1.12	0.11
SPO3879		hypothetical protein	1.08	0.90	-1.22	0.64	-0.07	1.15	0.84	0.29	-1.04	0.92	-0.10	0.94	-1.33	0.48	1.37	0.43	0.02	1.35
SPO3880	*hslV*	ATP-dependent protease peptidase subunit (EC:3.4.25.1)	1.36	0.05	1.19	0.63	1.28	0.09	3.12	0.01	-1.17	0.41	0.98	2.15	1.07	0.88	-1.56	0.32	-0.25	1.32
SPO3881		twin-arginine translocation pathway signal sequence domain-containing protein	1.63	0.01	-1.27	0.40	0.18	1.45	-1.09	0.75	1.20	0.08	0.05	1.15	-1.55	0.02	-1.91	0.01	-1.73	0.18
SPO3882	*hslU*	ATP-dependent protease ATP-binding subunit HslU	1.08	0.54	-1.51	0.15	-0.22	1.30	5.54	0.01	-1.26	0.01	2.14	3.40	1.14	0.27	1.15	0.63	1.15	0.01
SPO3883		lipoprotein	1.10	0.51	-1.12	0.65	-0.01	1.11	3.25	0.02	-1.06	0.58	1.10	2.16	1.28	0.44	1.15	0.37	1.22	0.07
SPO3884		smr domain-containing protein	-1.19	0.47	-1.16	0.03	-1.18	0.02	1.54	0.03	-1.09	0.49	0.23	1.32	-1.02	0.87	1.14	0.38	0.06	1.08
SPO3885		MltA/3D domain-containing protein	-1.32	0.77	-1.19	0.64	-1.26	0.07	1.89	0.67	-1.10	0.75	0.40	1.50	1.22	0.48	1.16	0.80	1.19	0.03
SPO3886		Tim44 family protein	1.19	0.94	-1.05	0.66	0.07	1.12	2.08	0.05	-1.10	0.24	0.49	1.59	1.65	0.06	2.28	0.01	1.97	0.32
SPO3887	*fxsA*	FxsA protein	1.06	0.91	-1.68	0.03	-0.31	1.37	1.50	0.26	-1.32	0.43	0.09	1.41	1.53	0.16	1.84	0.00	1.69	0.16
SPO3888	*secB*	preprotein translocase subunit SecB	1.57	0.01	-1.53	0.10	0.02	1.55	2.94	0.00	-1.20	0.05	0.87	2.07	0.97	0.61	1.06	0.56	1.01	0.05
SPO3889	*dnaQ*	DNA polymerase III subunit epsilon (EC:2.7.7.7)	-1.22	0.35	1.06	0.64	-0.08	1.14	1.00	0.91	-1.23	0.16	-0.12	1.11	1.06	0.79	-1.08	0.86	-0.01	1.07
SPO3890	*coaE*	dephospho-CoA kinase (EC:2.7.1.24)	1.37	0.01	1.17	0.33	1.27	0.10	1.83	0.00	1.06	0.71	1.45	0.39	-1.35	0.05	-1.81	0.04	-1.58	0.23
SPO3891	*aroE*	shikimate 5-dehydrogenase (EC:1.1.1.25)	1.27	0.74	1.30	0.05	1.29	0.02	2.06	0.01	-1.30	0.17	0.38	1.68	1.28	0.21	-1.25	0.13	0.02	1.27
SPO3892	*maf-1*	hypothetical protein	-1.42	0.16	1.20	0.38	-0.11	1.31	-0.99	0.52	-1.30	0.25	-1.15	0.16	-1.04	0.64	-1.06	0.85	-1.05	0.01
SPO3893		hypothetical protein	1.22	0.35	1.08	0.76	1.15	0.07	2.73	0.00	-1.23	0.10	0.75	1.98	1.35	0.06	1.59	0.34	1.47	0.12
SPO3894	*rho*	transcription termination factor Rho	-1.24	0.56	1.21	0.48	-0.02	1.23	6.05	0.02	-2.11	0.00	1.97	4.08	1.22	0.05	-1.42	0.16	-0.10	1.32
SPO3895	*trmE*	tRNA modification GTPase TrmE	-1.21	0.81	1.31	0.13	0.05	1.26	-1.51	0.12	-1.10	0.22	-1.31	0.20	-1.19	0.33	-1.66	0.02	-1.43	0.24
SPO3896		TetR family transcriptional regulator	1.16	0.89	-1.49	0.17	-0.17	1.33	0.95	0.65	1.11	0.32	1.03	0.08	-1.22	0.28	-1.23	0.25	-1.23	0.01
SPO3897		resolvase site-specific recombinase	-1.08	0.87	-1.38	0.31	-1.23	0.15	-0.97	0.22	-1.47	0.36	-1.22	0.25	-1.32	0.62	1.27	0.53	-0.03	1.30
SPO3898		DNA-binding protein	10.80	0.01	-1.19	0.03	4.81	6.00	1.00	0.98	-1.13	0.09	-0.06	1.07	-1.06	0.73	-1.22	0.13	-1.14	0.08
SPO3899		hypothetical protein	1.48	0.13	-1.20	0.41	0.14	1.34	1.51	0.05	1.14	0.25	1.33	0.19	-1.55	0.10	-1.70	0.10	-1.63	0.08
SPO3900		thermonuclease	1.65	0.07	1.40	0.22	1.53	0.13	-1.42	0.12	1.07	0.83	-0.18	1.25	1.14	0.58	-1.23	0.52	-0.05	1.19
SPO3901		carbon monoxide dehydrogenase G protein	1.63	0.89	1.31	0.42	1.47	0.16	2.28	0.77	-1.39	0.63	0.45	1.84	1.10	0.77	-1.09	0.97	0.01	1.10
SPO3902		transglycosylase domain-containing protein	-1.48	0.14	-1.25	0.47	-1.37	0.12	-1.82	0.03	1.61	0.10	-0.11	1.72	-1.06	0.76	1.10	0.44	0.02	1.08
SPO3903		6-pyruvoyl tetrahydrobiopterin synthase	-1.71	X	1.26	0.10	-0.23	1.49	-1.82	0.39	-5.41	0.00	-3.62	1.80	-4.41	0.01	-3.61	0.01	-4.01	0.40
SPOA0001		hypothetical protein	-1.20	0.10	1.04	0.88	-0.08	1.12	1.27	0.05	1.38	0.02	1.33	0.05	-1.31	0.12	-1.25	0.13	-1.28	0.03
SPOA0002	*miaB*	(dimethylallyl)adenosine tRNA methylthiotransferase	1.05	X	1.28	0.04	1.17	0.12	4.06	0.01	-1.09	0.38	1.49	2.58	-1.40	0.06	-1.73	0.02	-1.57	0.17
SPOA0003		hypothetical protein	2.07	0.05	1.30	0.06	1.69	0.38	-1.83	0.03	1.53	0.06	-0.15	1.68	1.31	0.25	1.22	0.19	1.27	0.05
SPOA0004		OmpA family protein	2.26	0.01	1.41	0.08	1.84	0.43	-2.12	0.01	1.76	0.06	-0.18	1.94	1.48	0.08	1.85	0.03	1.67	0.18
SPOA0005		lipoprotein	2.34	0.01	2.04	0.04	2.19	0.15	-2.28	0.00	1.53	0.02	-0.38	1.91	1.11	0.89	-1.06	0.55	0.03	1.09
SPOA0006		PhoH family protein	2.95	0.14	1.49	0.15	2.22	0.73	0.93	0.29	1.60	0.17	1.27	0.33	2.08	0.06	2.38	0.06	2.23	0.15

SPOA0007		hypothetical protein	1.46	0.32	1.62	0.21	1.54	0.08	0.91	0.62	1.40	0.12	1.16	0.24	1.22	0.08	1.26	0.69	1.24	0.02
SPOA0008		hypothetical protein	1.58	0.71	1.16	0.19	1.37	0.21	-1.08	0.74	1.49	0.03	0.21	1.29	-1.30	0.07	-1.43	0.01	-1.37	0.06
SPOA0009		hemolysin	-2.04	0.00	1.43	0.16	-0.31	1.74	1.15	0.09	-1.14	0.15	0.01	1.15	2.03	0.01	1.58	0.05	1.81	0.22
SPOA0010	*cutE*	apolipoprotein N-acyltransferase (EC:2.3.1.-)	-1.16	0.72	-1.10	0.46	-1.13	0.03	2.01	0.08	-1.34	0.07	0.34	1.68	1.11	0.41	-1.13	0.36	-0.01	1.12
SPOA0011	*metK*	S-adenosylmethionine synthetase (EC:2.5.1.6)	1.25	0.26	-1.22	0.35	0.02	1.24	5.46	0.00	1.21	0.21	3.34	2.13	-1.20	0.17	1.10	0.88	-0.05	1.15
SPOA0012		DNA topology modulation kinase FlaR	-1.81	0.04	1.20	0.46	-0.31	1.51	1.08	0.66	-1.12	0.69	-0.02	1.10	-1.17	0.37	-1.20	0.91	-1.19	0.02
SPOA0013		hypothetical protein	-1.34	0.16	1.21	0.25	-0.07	1.28	-1.23	0.25	1.33	0.26	0.05	1.28	1.60	0.03	1.19	0.20	1.40	0.21
SPOA0014	*trmB*	tRNA (guanine-N(7)-)-methyltransferase (EC:2.1.1.33)	-1.88	0.33	1.01	0.88	-0.44	1.45	1.95	0.10	-1.17	0.28	0.39	1.56	-1.25	0.30	1.06	0.96	-0.10	1.16
SPOA0015	*aroA*	3-phosphoshikimate 1-carboxyvinyltransferase (EC:2.5.1.19)	1.69	0.02	1.27	0.10	1.48	0.21	4.03	0.00	-1.28	0.07	1.38	2.66	-1.21	0.08	-1.41	0.05	-1.31	0.10
SPOA0017	*cmk*	cytidylate kinase (EC:2.7.4.14)	1.52	0.07	1.63	0.17	1.58	0.05	3.87	0.01	-1.45	0.03	1.21	2.66	1.15	0.13	-1.47	0.00	-0.16	1.31
SPOA0018		hypothetical protein	-1.28	0.68	-1.01	0.98	-1.15	0.14	-1.59	0.61	1.92	0.19	0.17	1.76	-1.08	0.80	1.30	0.56	0.11	1.19
SPOA0019		hypothetical protein	1.26	0.38	-1.02	0.92	0.12	1.14	-1.41	0.30	1.83	0.03	0.21	1.62	-1.13	0.31	-1.54	0.07	-1.34	0.20
SPOA0020		alanine racemase	-1.83	0.14	-1.34	0.21	-1.59	0.25	-3.80	0.00	1.34	0.16	-1.23	2.57	-1.92	0.15	1.38	0.22	-0.27	1.65
SPOA0021		oxidoreductase, FAD-binding	-1.12	0.58	-1.09	0.74	-1.11	0.02	-1.42	0.43	1.73	0.15	0.16	1.58	-1.15	0.59	-1.61	0.04	-1.38	0.23
SPOA0022		cytochrome c5	-1.25	0.25	-1.16	0.22	-1.21	0.05	-2.73	0.03	1.97	0.02	-0.38	2.35	-1.25	0.03	-1.35	0.02	-1.30	0.05
SPOA0023		TetR family transcriptional regulator	-1.48	0.14	-1.15	0.26	-1.32	0.17	-2.47	0.07	1.90	0.09	-0.29	2.19	-1.43	0.18	-1.91	0.02	-1.67	0.24
SPOA0024		2-oxo-hepta-3-ene-1,7-dioic acid hydratase	2.85	0.24	1.80	0.12	2.33	0.53	1.50	0.10	-1.08	0.51	0.21	1.29	-1.02	0.76	-1.25	0.31	-1.14	0.12
SPOA0025		fumarylacetoacetate hydrolase family protein	2.65	0.00	1.67	0.05	2.16	0.49	1.29	0.22	1.47	0.01	1.38	0.09	1.00	0.86	-1.10	0.33	-0.05	1.05
SPOA0026	*hpcB*	3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC:1.13.11.15)	2.23	0.33	2.22	0.01	2.23	0.00	1.16	0.90	1.42	0.03	1.29	0.13	1.10	0.66	1.17	0.54	1.14	0.03
SPOA0027	*hpcC*	5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase (EC:1.2.1.60)	1.57	0.04	1.10	0.63	1.34	0.24	-1.78	0.04	-1.20	0.14	-1.49	0.29	-1.43	0.07	-1.35	0.14	-1.39	0.04
SPOA0028	*nqrA*	Na(+)-translocating NADH-quinone reductase subunit A (EC:1.6.5.-)	1.37	0.62	1.82	0.29	1.60	0.22	6.09	0.11	-1.61	0.35	2.24	3.85	1.10	0.88	-1.33	0.54	-0.12	1.22
SPOA0029	*nqrB*	Na(+)-translocating NADH-quinone reductase subunit B (EC:1.6.5.-)	1.27	0.34	1.24	0.32	1.26	0.02	4.67	0.03	-1.50	0.06	1.59	3.09	-1.15	0.11	-1.22	0.06	-1.19	0.04
SPOA0030	*nqrC*	Na(+)-translocating NADH-quinone reductase subunit C (EC:1.6.5.-)	-1.21	0.41	1.46	0.02	0.13	1.34	1.29	0.32	-1.53	0.05	-0.12	1.41	-1.13	0.29	-1.41	0.12	-1.27	0.14
SPOA0031	*nqrD*	Na(+)-translocating NADH-quinone reductase subunit D (EC:1.6.5.-)	1.51	0.63	1.20	0.65	1.36	0.16	5.86	0.09	-1.41	0.04	2.23	3.64	-1.12	0.29	-1.37	0.09	-1.25	0.13
SPOA0032	*nqrE*	Na(+)-translocating NADH-quinone reductase subunit E (EC:1.6.5.-)	1.27	0.76	1.44	0.33	1.36	0.09	2.82	0.18	-1.20	0.24	0.81	2.01	1.06	0.95	0.94	0.38	1.00	0.06
SPOA0033	*nqrF*	Na(+)-translocating NADH-quinone reductase subunit F (EC:1.6.5.-)	1.31	0.53	1.57	0.29	1.44	0.13	4.11	0.10	-1.34	0.49	1.39	2.73	0.99	0.95	-1.27	0.63	-0.14	1.13
SPOA0034		CBS domain-containing protein	1.50	0.00	1.38	0.29	1.44	0.06	-1.83	0.00	1.93	0.01	0.05	1.88	1.25	0.44	1.56	0.04	1.41	0.16
SPOA0035		hypothetical protein	-1.05	0.98	1.31	0.32	0.13	1.18	1.80	0.02	-1.43	0.06	0.19	1.62	1.20	0.09	-1.56	0.03	-0.18	1.38
SPOA0036	*apbE*	thiamin biosynthesis lipoprotein ApbE	1.18	0.13	1.37	0.14	1.28	0.10	5.37	0.00	-1.33	0.03	2.02	3.35	1.04	0.93	-1.16	0.27	-0.06	1.10
SPOA0037		hypothetical protein	1.54	0.61	1.63	0.04	1.59	0.04	2.54	0.04	-1.26	0.25	0.64	1.90	2.13	0.06	2.38	0.08	2.26	0.13
SPOA0038		LuxR family transcriptional regulator	1.46	0.71	1.14	0.82	1.30	0.16	-2.51	0.30	1.31	0.71	-0.60	1.91	-1.04	0.94	1.64	0.41	0.30	1.34
SPOA0039		hypothetical protein	0.98	0.09	1.09	0.45	1.03	0.06	0.93	0.09	1.72	0.04	1.33	0.39	1.52	0.05	1.91	0.05	1.72	0.20
SPOA0040		crcB family protein	X	X	1.28	0.15	N/A	N/A	1.80	0.00	-0.98	0.80	0.41	1.39	-1.26	0.50	-1.40	X	-1.33	0.07
SPOA0041		crcB family protein	X	X	1.18	0.16	N/A	N/A	2.73	0.01	-1.16	0.25	0.79	1.95	-1.73	0.02	-2.51	0.02	-2.12	0.39
SPOA0042		hypothetical protein	1.21	0.95	1.49	0.64	1.35	0.14	-1.49	0.86	1.32	0.78	-0.09	1.41	-1.07	0.93	-1.32	0.75	-1.20	0.13

SPOA0043	*pcaG*	protocatechuate 3,4-dioxygenase alpha subunit (EC:1.13.11.3)	1.34	0.71	-1.18	0.23	0.08	1.26	-2.24	0.04	1.60	0.02	-0.32	1.92	-1.45	0.05	-1.07	0.42	-1.26	0.19
SPOA0044	*pcaH*	protocatechuate 3,4-dioxygenase subunit beta (EC:1.13.11.3)	-1.25	0.22	-1.12	0.26	-1.19	0.06	-2.83	0.01	1.27	0.13	-0.78	2.05	-1.13	0.07	-1.35	0.06	-1.24	0.11
SPOA0045	*pcaC*	4-carboxymuconolactone decarboxylase (EC:4.1.1.44)	-1.24	0.52	-1.14	0.68	-1.19	0.05	-1.83	0.52	1.47	0.03	-0.18	1.65	-1.01	0.88	1.02	0.76	0.01	1.02
SPOA0046	*pobA*	4-hydroxybenzoate 3-monooxygenase (EC:1.14.13.2)	-1.48	0.71	-1.25	0.50	-1.37	0.12	-2.84	0.04	-1.44	0.08	-2.14	0.70	-1.19	0.37	-1.43	0.23	-1.31	0.12
SPOA0047	*pcaQ*	pca operon transcriptional activator PcaQ	X	X	-1.01	0.98	N/A	N/A	1.54	0.02	-1.62	0.01	-0.04	1.58	1.17	0.19	1.29	X	1.23	0.06
SPOA0048		hypothetical protein	-2.40	0.09	-1.38	0.44	-1.89	0.51	3.62	0.01	1.11	0.82	2.37	1.26	-0.99	0.92	1.42	0.35	0.22	1.20
SPOA0049	*nosR*	nitrous-oxide reductase transcriptional activator NosR	1.00	X	-0.99	0.83	0.00	1.00	1.45	0.81	X	X	N/A	N/A	-1.15	X	X	X	N/A	N/A
SPOA0050	*nosZ*	nitrous-oxide reductase (EC:1.7.99.6)	-1.33	X	-1.30	0.74	-1.32	0.02	-1.15	0.99	-1.48	0.84	-1.32	0.17	-1.04	0.99	1.20	0.88	0.08	1.12
SPOA0051	*nosD*	nitrous oxide maturation protein NosD	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0052	*nosF*	ABC transporter, ATP-binding protein NosF	-1.08	0.72	-1.34	0.48	-1.21	0.13	-2.05	0.03	-1.44	0.16	-1.75	0.31	-1.03	0.98	1.88	0.10	0.43	1.46
SPOA0053	*nosY*	nitrous oxide maturation protein NosY	1.84	0.12	-1.11	0.59	0.37	1.48	2.15	0.05	-1.15	0.61	0.50	1.65	-1.04	0.98	-1.44	X	-1.24	0.20
SPOA0054	*nosL*	nitrous oxide reductase accessory protein	X	X	1.09	0.39	N/A	N/A	-0.95	0.24	X	X	N/A	N/A	-1.03	0.90	X	X	N/A	N/A
SPOA0055		cytochrome c family protein	1.26	0.28	-1.21	0.10	0.03	1.24	-1.47	0.13	1.23	0.20	-0.12	1.35	-1.23	0.09	-1.21	0.61	-1.22	0.01
SPOA0056		DNA-binding protein	-1.15	0.03	-2.89	0.00	-2.02	0.87	-4.06	0.00	-1.40	0.12	-2.73	1.33	-1.15	0.34	1.06	0.52	-0.04	1.11
SPOA0057	*gcvT*	glycine cleavage system T protein (EC:2.1.2.10)	-1.61	0.23	-5.58	0.01	-3.60	1.99	1.44	0.54	1.32	0.28	1.38	0.06	-1.68	0.09	-1.49	0.11	-1.59	0.10
SPOA0058	*gcvH-2*	glycine cleavage system protein H	-1.43	0.01	-5.32	0.00	-3.38	1.95	1.27	0.12	0.98	0.33	1.12	0.15	-2.63	0.06	-2.77	0.01	-2.70	0.07
SPOA0059	*gcvP*	glycine dehydrogenase (EC:1.4.4.2)	1.19	0.62	-2.26	0.01	-0.54	1.73	1.49	0.07	1.23	0.31	1.36	0.13	1.16	0.11	1.13	0.64	1.15	0.02
SPOA0060		AraC family transcriptional regulator	1.60	0.75	-1.78	0.07	-0.09	1.69	2.49	0.55	1.34	0.05	1.92	0.58	-1.26	0.17	-1.39	0.46	-1.33	0.06
SPOA0061	*katG*	catalase/peroxidase HPI (EC:1.11.1.6)	-1.67	0.01	0.99	0.65	-0.34	1.33	1.38	0.45	3.81	0.00	2.60	1.22	1.24	0.09	2.92	0.00	2.08	0.84
SPOA0062		aspartate racemase (EC:5.1.1.13)	1.18	0.45	-1.12	0.18	0.03	1.15	1.35	0.37	-1.06	0.83	0.15	1.21	-1.00	0.96	1.19	0.40	0.10	1.10
SPOA0063		FAD-dependent oxidoreductase	1.10	0.72	-1.15	0.38	-0.02	1.13	-2.04	0.05	1.42	0.02	-0.31	1.73	-1.18	0.17	-1.14	0.85	-1.16	0.02
SPOA0064		NG,NG-dimethylarginine dimethylaminohydrolase	-1.16	0.37	-1.24	0.57	-1.20	0.04	-1.45	0.41	-1.20	0.50	-1.33	0.13	-1.32	0.38	X	X	N/A	N/A
SPOA0065		hypothetical protein	-1.95	0.08	-1.30	0.10	-1.63	0.33	-2.06	0.12	-1.42	0.02	-1.74	0.32	-1.69	0.03	-2.69	0.01	-2.19	0.50
SPOA0066		aspartate aminotransferase	-2.00	0.02	1.18	0.17	-0.41	1.59	-1.65	0.04	-1.38	0.13	-1.52	0.14	1.22	0.19	-1.28	0.23	-0.03	1.25
SPOA0067		TetR family transcriptional regulator	-2.63	0.02	-1.20	0.57	-1.92	0.72	-3.00	0.03	-1.08	0.91	-2.04	0.96	-1.49	0.16	1.40	0.55	-0.05	1.45
SPOA0068		polar amino acid ABC transporter ATP-binding protein	-2.79	0.00	-1.46	0.08	-2.13	0.67	-4.53	0.01	-1.33	0.20	-2.93	1.60	-1.49	0.04	-1.46	0.14	-1.48	0.02
SPOA0069		polar amino acid ABC transporter periplasmic substrate-binding protein	-5.54	0.08	-1.89	0.07	-3.72	1.83	-6.93	0.01	-1.43	0.10	-4.18	2.75	-1.06	0.77	-1.08	0.55	-1.07	0.01
SPOA0070		polar amino acid ABC transporter permease	X	X	-1.32	0.27	N/A	N/A	-1.65	X	-1.88	X	-1.77	0.12	-1.03	0.83	-1.34	X	-1.19	0.16
SPOA0071		polar amino acid ABC transporter permease	-1.42	0.08	-1.05	0.96	-1.24	0.19	1.23	0.30	X	X	N/A	N/A	-0.98	0.54	X	X	N/A	N/A
SPOA0072		hypothetical protein	1.12	0.65	-1.35	0.09	-0.12	1.24	2.86	0.02	1.47	0.04	2.17	0.70	-2.32	0.02	-1.83	0.00	-2.08	0.24
SPOA0073	*arsC-2*	arsenate reductase (EC:1.20.4.1)	3.65	0.40	1.05	0.88	2.35	1.30	2.10	0.08	1.04	0.93	1.57	0.53	-1.46	0.08	-1.80	0.01	-1.63	0.17
SPOA0074		hypothetical protein	2.40	0.00	1.21	0.37	1.81	0.60	1.00	0.27	1.06	0.96	1.03	0.03	-1.10	0.15	0.97	0.62	-0.06	1.04
SPOA0075		hypothetical protein	3.07	0.01	1.08	0.85	2.08	0.99	1.29	0.28	1.11	0.77	1.20	0.09	-1.07	0.50	-1.06	0.72	-1.07	0.01
SPOA0076		carbon-nitrogen family hydrolase	2.59	0.02	1.18	0.07	1.89	0.71	2.01	0.01	-1.05	0.84	0.48	1.53	-1.06	0.86	-1.21	0.32	-1.14	0.08
SPOA0077	*infA*	translation initiation factor IF-1	1.13	0.56	-1.40	0.03	-0.14	1.27	2.74	0.00	0.96	0.28	1.85	0.89	-1.15	0.12	-1.40	0.03	-1.28	0.13
SPOA0078	*maf-2*	maf protein	-1.21	0.81	-1.36	0.01	-1.29	0.08	1.20	0.17	1.01	0.71	1.11	0.10	-1.37	0.06	-1.43	0.12	-1.40	0.03

SPOA0079		ribonuclease	-0.96	0.75	-1.28	0.34	-1.12	0.16	1.98	0.39	-1.09	0.61	0.45	1.54	-1.27	0.18	-1.55	0.17	-1.41	0.14
SPOA0081		hypothetical protein	-1.25	0.48	1.11	0.75	-0.07	1.18	-1.29	0.53	1.74	0.22	0.23	1.52	-1.03	0.96	1.15	0.69	0.06	1.09
SPOA0082		hypothetical protein	1.10	0.58	-1.23	0.07	-0.06	1.17	1.54	0.06	1.59	0.06	1.57	0.03	-1.07	0.61	1.20	0.10	0.06	1.14
SPOA0083		hypothetical protein	1.03	0.90	-1.30	0.41	-0.14	1.17	-1.40	0.38	1.35	0.34	-0.02	1.38	1.06	0.89	1.11	0.76	1.09	0.03
SPOA0084		hypothetical protein	-2.70	0.20	-1.13	0.21	-1.92	0.79	-3.33	0.04	-1.09	0.78	-2.21	1.12	-1.12	0.82	1.54	0.05	0.21	1.33
SPOA0085		DNA-binding protein	-2.16	X	1.44	0.08	-0.36	1.80	-1.19	0.82	-1.10	0.75	-1.15	0.04	-2.15	0.02	-1.92	0.11	-2.04	0.12
SPOA0086		hypothetical protein	X	X	-1.34	0.04	N/A	N/A	-1.15	0.68	-1.01	0.71	-1.08	0.07	-1.08	0.60	X	X	N/A	N/A
SPOA0087		phage integrase family site specific recombinase	-1.77	0.00	-1.20	0.09	-1.49	0.29	-1.82	0.00	1.02	0.87	-0.40	1.42	-1.14	0.30	-0.99	0.75	-1.07	0.07
SPOA0088		hypothetical protein	1.68	0.48	1.14	0.73	1.41	0.27	1.14	0.93	1.68	0.26	1.41	0.27	1.30	0.36	-1.16	0.52	0.07	1.23
SPOA0089		hypothetical protein	X	X	X	X	N/A	N/A	-1.39	0.96	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0090		ISSpo7, transposase	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0091		IS3 family transposase orfA	-1.06	0.93	-1.22	0.79	-1.14	0.08	-2.22	0.67	1.23	0.76	-0.50	1.73	-1.19	0.80	1.21	0.72	0.01	1.20
SPOA0093		FAD binding domain-containing protein	1.98	0.22	-1.31	0.39	0.34	1.65	1.52	0.22	-1.08	0.42	0.22	1.30	1.02	0.93	1.27	0.27	1.15	0.12
SPOA0094		hypothetical protein	1.50	0.08	1.06	0.36	1.28	0.22	1.32	0.11	-1.02	0.67	0.15	1.17	1.49	0.11	1.28	0.07	1.39	0.11
SPOA0095		hypothetical protein	1.47	0.60	-1.15	0.82	0.16	1.31	1.66	0.51	-1.51	0.45	0.08	1.59	1.26	0.62	1.28	0.56	1.27	0.01
SPOA0096		histone deacetylase/AcuC/AphA family protein	1.16	0.10	1.04	0.45	1.10	0.06	-1.25	0.71	1.23	0.08	-0.01	1.24	-1.25	0.06	-1.55	X	-1.40	0.15
SPOA0097		branched-chain amino acid ABC transporter, permease protein	1.46	0.92	1.07	0.94	1.27	0.19	1.66	0.88	-1.02	0.99	0.32	1.34	1.22	0.80	2.05	X	1.64	0.42
SPOA0098		branched-chain amino acid ABC transporter, permease protein	1.24	0.88	-0.97	0.38	0.13	1.11	1.02	0.96	X	X	N/A	N/A	1.13	0.45	X	X	N/A	N/A
SPOA0099		branched-chain amino acid ABC transporter, ATP-binding protein	X	X	-1.40	0.08	N/A	N/A	-2.64	0.11	-1.46	0.29	-2.05	0.59	1.08	0.73	2.50	0.04	1.79	0.71
SPOA0100		branched-chain amino acid ABC transporter, ATP-binding protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.13	X	X	X	N/A	N/A
SPOA0101		branched-chain amino acid ABC transporter, periplasmic branched-chain amino acid-binding protein	-1.38	X	-1.18	0.82	-1.28	0.10	-2.40	0.21	-1.24	X	-1.82	0.58	-1.04	0.98	X	X	N/A	N/A
SPOA0102		LuxR family transcriptional regulator	-1.19	0.62	-1.26	0.57	-1.23	0.04	-2.05	0.21	1.03	0.91	-0.51	1.54	1.02	0.94	1.14	0.65	1.08	0.06
SPOA0103		hypothetical protein	0.98	0.08	-1.33	0.07	-0.18	1.15	-2.84	0.00	1.10	0.39	-0.87	1.97	-1.22	0.43	-1.22	0.60	-1.22	0.00
SPOA0104		aldehyde dehydrogenase	-1.87	0.03	-1.08	0.73	-1.48	0.40	-2.31	0.02	-1.05	0.89	-1.68	0.63	1.32	0.49	2.41	0.06	1.87	0.54
SPOA0105		transcriptional regulator	-1.30	0.09	1.04	0.46	-0.13	1.17	-1.02	0.13	-1.36	0.05	-1.19	0.17	-1.17	0.17	-1.52	0.07	-1.35	0.18
SPOA0106		hypothetical protein	-1.77	0.68	-1.02	0.95	-1.40	0.38	-1.17	0.91	1.10	0.91	-0.03	1.14	-1.05	0.93	1.25	0.77	0.10	1.15
SPOA0107		LysR family transcriptional regulator	-1.33	0.73	-1.31	0.66	-1.32	0.01	-0.93	0.71	-1.48	0.67	-1.21	0.27	1.37	0.68	-1.25	0.91	0.06	1.31
SPOA0108		hypothetical protein	-1.53	X	-1.68	0.25	-1.61	0.08	-1.48	0.90	-1.20	0.82	-1.34	0.14	-1.34	0.72	-0.93	0.55	-1.14	0.21
SPOA0109		hypothetical protein	2.94	0.01	1.44	0.04	2.19	0.75	2.49	0.06	1.08	0.35	1.79	0.71	-1.41	0.03	-1.49	0.08	-1.45	0.04
SPOA0110		indolepyruvate oxidoreductase subunit B (EC:1.2.7.8)	-1.39	0.56	-1.17	0.74	-1.28	0.11	-2.02	0.36	-1.25	0.66	-1.64	0.39	-1.42	0.45	-1.28	0.60	-1.35	0.07
SPOA0111		indolepyruvate oxidoreductase, IorA subunit	-1.56	0.21	-1.22	0.61	-1.39	0.17	-2.14	0.13	-1.25	0.13	-1.70	0.45	-1.55	0.20	-0.97	0.88	-1.26	0.29
SPOA0112	*feaB*	phenylacetaldehyde dehydrogenase (EC:1.2.1.39)	-1.00	0.99	-1.26	0.51	-1.13	0.13	-1.55	0.82	-1.24	0.35	-1.40	0.16	-1.48	0.14	-1.17	0.88	-1.33	0.15
SPOA0113		hypothetical protein	-1.51	0.52	-1.13	0.86	-1.32	0.19	-2.26	0.27	-1.17	0.73	-1.72	0.55	-1.09	0.81	1.22	X	0.06	1.16
SPOA0114		nitrilase family protein	-1.22	0.57	-1.34	0.32	-1.28	0.06	-1.93	0.28	-1.46	0.31	-1.70	0.24	-1.43	0.18	-1.24	0.67	-1.34	0.10
SPOA0115	*gtdA-2*	gentisate 1,2-dioxygenase (EC:1.13.11.4)	-1.67	0.07	-1.63	0.08	-1.65	0.02	-2.78	0.01	-1.03	0.83	-1.91	0.88	-1.55	0.04	-1.06	0.97	-1.31	0.24
SPOA0116		fumarylacetoacetate hydrolase family protein	-2.10	0.01	-1.61	0.02	-1.86	0.25	-3.02	0.02	-1.04	0.72	-2.03	0.99	-1.65	0.08	-1.55	0.11	-1.60	0.05

SPOA0117		Asp/Glu/hydantoin racemase family protein	-1.39	0.25	-1.29	0.05	-1.34	0.05	-2.31	0.04	-1.03	0.89	-1.67	0.64	1.06	0.66	-0.91	0.26	0.08	0.98
SPOA0118		hypothetical protein	-1.54	0.21	-1.46	0.66	-1.50	0.04	-3.30	0.05	1.06	0.96	-1.12	2.18	-1.26	0.75	-1.03	0.97	-1.15	0.12
SPOA0119		hypothetical protein	-1.96	0.24	-1.54	0.08	-1.75	0.21	-2.82	0.11	-1.15	0.70	-1.99	0.84	-1.10	0.44	-1.23	0.63	-1.17	0.06
SPOA0120		hypothetical protein	-3.45	0.05	-1.56	0.05	-2.51	0.95	-5.09	0.03	-1.48	0.07	-3.29	1.81	-1.21	0.13	-1.39	0.13	-1.30	0.09
SPOA0121		sulfatase family protein	-1.18	0.92	-1.00	0.98	-1.09	0.09	-1.46	0.86	-0.98	0.81	-1.22	0.24	-1.02	0.96	-1.04	0.77	-1.03	0.01
SPOA0122		ISSpo9, transposase	-1.90	0.15	-1.60	0.18	-1.75	0.15	-1.71	0.12	-1.26	0.16	-1.49	0.23	-1.32	0.82	1.77	0.04	0.23	1.55
SPOA0123		hypothetical protein	-1.78	0.27	1.05	0.93	-0.37	1.42	0.87	0.44	1.28	0.70	1.07	0.21	1.43	0.47	1.55	0.40	1.49	0.06
SPOA0124		hypothetical protein	1.24	0.43	-1.09	0.82	0.08	1.17	1.03	0.93	1.26	0.53	1.15	0.12	1.21	0.63	1.16	0.63	1.19	0.03
SPOA0125		hypothetical protein	1.11	0.90	-1.25	0.09	-0.07	1.18	-1.36	0.22	1.36	0.18	0.00	1.36	-1.13	0.38	-1.03	0.80	-1.08	0.05
SPOA0126		short chain dehydrogenase/reductase family oxidoreductase	-1.15	0.94	-1.08	0.91	-1.12	0.03	-1.65	0.84	1.16	0.49	-0.25	1.41	-1.04	0.96	1.25	0.84	0.11	1.15
SPOA0127		cyclase	1.07	0.88	-1.18	0.38	-0.05	1.13	-1.75	0.26	-1.24	0.45	-1.50	0.26	-1.44	0.16	-1.53	0.24	-1.49	0.05
SPOA0128		short chain dehydrogenase/reductase family oxidoreductase	1.82	0.28	-1.26	0.66	0.28	1.54	1.15	0.73	-1.19	0.86	-0.02	1.17	-1.31	0.77	1.40	0.20	0.04	1.36
SPOA0129		hypothetical protein	X	X	-1.17	0.70	N/A	N/A	X	X	X	X	N/A	N/A	-1.88	X	X	X	N/A	N/A
SPOA0130		AMP-binding protein	-1.24	0.18	-1.09	0.80	-1.17	0.08	-1.24	0.79	-1.39	0.21	-1.32	0.08	-1.12	0.66	-0.99	0.77	-1.06	0.06
SPOA0131		aromatic 1,2-dioxygenase, beta subunit	X	X	-1.10	0.41	N/A	N/A	-0.97	0.43	-1.21	X	-1.09	0.12	-1.44	0.17	-1.19	X	-1.32	0.13
SPOA0132		aromatic 1,2-dioxygenase, alpha subunit	-1.06	0.92	-1.13	0.83	-1.10	0.03	-2.48	0.28	-1.17	0.76	-1.83	0.66	-1.11	0.81	1.17	0.25	0.03	1.14
SPOA0133		oxidoreductase	X	X	-1.47	0.15	N/A	N/A	X	X	X	X	N/A	N/A	-1.24	0.12	X	X	N/A	N/A
SPOA0134		ISSpo7, transposase	X	X	1.33	0.01	N/A	N/A	X	X	-1.22	0.05	N/A	N/A	-1.42	0.06	-2.25	X	-1.84	0.42
SPOA0136		hypothetical protein	1.69	0.04	-1.39	0.14	0.15	1.54	2.21	0.03	1.28	0.20	1.75	0.47	1.01	0.84	1.29	0.21	1.15	0.14
SPOA0137	*murA*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC:2.5.1.7)	1.21	0.43	-1.19	0.25	0.01	1.20	1.82	0.09	1.06	0.98	1.44	0.38	-1.08	0.96	1.03	0.64	-0.03	1.06
SPOA0138		hypothetical protein	1.52	0.05	1.06	0.82	1.29	0.23	2.85	0.03	-1.35	0.04	0.75	2.10	1.33	0.03	-1.17	0.58	0.08	1.25
SPOA0139		acetyltransferase	1.54	0.87	-1.04	0.96	0.25	1.29	2.22	0.73	-1.06	0.93	0.58	1.64	1.30	0.75	-1.07	0.95	0.12	1.19
SPOA0140	*glmS*	glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (EC:2.6.1.16)	2.59	0.06	-1.03	0.94	0.78	1.81	-1.86	0.25	-1.96	0.27	-1.91	0.05	-1.05	0.90	1.34	0.66	0.15	1.20
SPOA0141		hypothetical protein	-2.23	0.00	-1.37	0.08	-1.80	0.43	-2.18	0.00	-1.21	0.37	-1.70	0.49	1.42	0.05	1.23	0.12	1.33	0.10
SPOA0142		hypothetical protein	-1.01	0.97	-1.43	0.04	-1.22	0.21	1.24	0.17	-1.17	0.09	0.04	1.21	1.28	0.07	1.13	0.73	1.21	0.08
SPOA0143		IclR family transcriptional regulator	-2.55	0.08	1.06	0.78	-0.75	1.81	-3.36	0.01	-1.87	0.02	-2.62	0.74	-1.18	0.06	-1.36	0.22	-1.27	0.09
SPOA0144		serine--glyoxylate transaminase	-1.01	0.88	-1.19	0.38	-1.10	0.09	-2.37	0.00	-1.20	0.59	-1.79	0.59	-1.13	0.24	-0.90	0.08	-1.01	0.12
SPOA0145		pyridoxal-phosphate dependent enzyme	1.07	0.92	-1.15	0.48	-0.04	1.11	-3.52	0.02	1.07	0.67	-1.23	2.30	-1.28	0.03	-1.09	0.95	-1.19	0.10
SPOA0146		threonine aldolase (EC:4.1.2.5)	-1.11	0.78	-1.16	0.80	-1.14	0.02	-1.81	0.43	1.15	0.80	-0.33	1.48	-1.22	0.69	1.12	0.77	-0.05	1.17
SPOA0147		ornithine cyclodeaminase/mu-crystallin family protein	-1.49	0.01	-1.14	0.38	-1.32	0.18	-2.09	0.07	-1.11	0.23	-1.60	0.49	-0.97	0.43	-0.94	0.11	-0.96	0.02
SPOA0148		major facilitator transporter	X	X	-1.22	0.73	N/A	N/A	-2.48	0.09	-1.49	0.43	-1.99	0.50	1.08	0.78	1.34	0.56	1.21	0.13
SPOA0149		GntR family transcriptional regulator	-1.92	0.37	-1.25	0.18	-1.59	0.34	-1.79	0.20	-1.31	0.05	-1.55	0.24	-1.36	0.15	-1.39	0.15	-1.38	0.01
SPOA0150		AraC family transcriptional regulator	X	X	-0.98	0.73	N/A	N/A	1.35	0.24	X	X	N/A	N/A	-0.98	0.53	X	X	N/A	N/A
SPOA0151		cytochrome c family protein	X	X	X	X	N/A	N/A	-1.18	0.28	X	X	N/A	N/A	1.14	0.23	X	X	N/A	N/A
SPOA0152		di-haem cytochrome c peroxidase family protein	X	X	-1.38	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0153		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0154		hypothetical protein	-1.41	0.78	-1.16	0.81	-1.29	0.13	-1.07	0.95	-1.01	0.99	-1.04	0.03	-1.23	0.76	1.53	0.56	0.15	1.38

SPOA0155		type I secretion target repeat-containing protein	X	X	2.39	0.00	N/A	N/A	2.79	0.10	-1.44	0.10	0.68	2.12	1.36	0.11	X	X	N/A	N/A
SPOA0156		hypothetical protein	-1.26	0.74	-1.15	0.48	-1.21	0.06	1.52	0.45	1.19	0.55	1.36	0.16	1.11	0.42	1.20	0.46	1.16	0.04
SPOA0157		sulfite exporter, CuyZ	-1.82	0.82	-1.07	0.95	-1.45	0.38	-1.26	0.95	-1.38	0.69	-1.32	0.06	-1.00	0.99	1.44	0.57	0.22	1.22
SPOA0158	*cuyA*	L-cysteate sulfo-lyase (EC:4.4.1.15)	1.46	0.14	1.13	0.27	1.30	0.16	-1.52	0.15	-1.12	0.33	-1.32	0.20	-1.09	0.15	-1.19	0.29	-1.14	0.05
SPOA0159	*cuyR*	transcriptional regulator CuyR	-1.31	0.50	-0.99	0.83	-1.15	0.16	-1.37	0.90	-1.29	0.52	-1.33	0.04	1.07	0.52	-1.13	0.98	-0.03	1.10
SPOA0160		TRAP dicarboxylate transporter, DctM subunit	X	X	1.35	0.27	N/A	N/A	-1.34	0.89	-1.35	0.43	-1.35	0.01	-1.28	0.53	-1.46	X	-1.37	0.09
SPOA0161		TRAP dicarboxylate transporter, DctQ subunit	-2.06	X	-1.27	0.81	-1.67	0.39	-1.86	0.73	-1.55	0.80	-1.71	0.16	-1.52	0.72	-0.96	0.93	-1.24	0.28
SPOA0162		TRAP dicarboxylate family transporter DctP subunit	-2.49	0.25	-1.01	0.98	-1.75	0.74	-4.53	0.11	-1.21	0.55	-2.87	1.66	-1.00	0.94	1.69	0.04	0.35	1.35
SPOA0163	*mvaA*	hydroxymethylglutaryl-CoA reductase, degradative (EC:1.1.1.88)	X	X	X	X	N/A	N/A	-1.61	0.23	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0164		GntR family transcriptional regulator	-1.03	0.97	1.13	0.64	0.05	1.08	-1.35	0.93	-1.44	0.17	-1.40	0.04	-1.03	0.99	X	X	N/A	N/A
SPOA0165		LysR family transcriptional regulator	-2.09	0.33	-0.99	0.96	-1.54	0.55	-2.68	0.16	-1.38	0.66	-2.03	0.65	1.22	0.75	-0.97	0.82	0.13	1.09
SPOA0166		TRAP transporter solute receptor TAXI family protein	-1.85	0.48	-1.79	0.62	-1.82	0.03	-1.87	0.68	-1.35	0.77	-1.61	0.26	-1.48	0.63	1.21	0.88	-0.14	1.35
SPOA0167		TRAP transporter, 4TM/12TM fusion protein	X	X	-1.27	0.36	N/A	N/A	-1.24	0.64	-1.58	0.23	-1.41	0.17	1.11	0.74	1.21	0.19	1.16	0.05
SPOA0168		oxidoreductase, FAD-binding	-2.28	0.02	-1.07	0.79	-1.68	0.61	-3.13	0.01	1.52	0.04	-0.81	2.33	-1.01	0.88	-0.93	0.38	-0.97	0.04
SPOA0169		MOSC domain-containing protein	-1.35	0.36	-1.20	0.31	-1.28	0.08	-1.23	0.58	-1.20	0.41	-1.22	0.02	1.03	0.97	-1.18	0.37	-0.08	1.11
SPOA0170		MarR family transcriptional regulator	-1.99	0.04	-1.36	0.02	-1.68	0.32	-1.53	0.10	-1.12	0.29	-1.33	0.20	-1.34	0.17	-1.61	0.03	-1.48	0.14
SPOA0171		hypothetical protein	-1.60	0.62	-1.30	0.22	-1.45	0.15	-1.04	0.92	-1.82	0.05	-1.43	0.39	-1.17	0.29	-1.43	0.11	-1.30	0.13
SPOA0172		hypothetical protein	-1.79	0.01	-1.38	0.23	-1.59	0.20	-3.50	0.00	-1.07	0.74	-2.29	1.22	1.04	0.93	2.09	0.09	1.57	0.53
SPOA0173		hypothetical protein	-1.23	0.59	-1.22	0.18	-1.23	0.01	-1.95	0.02	-1.14	0.50	-1.55	0.41	-1.12	0.45	-1.44	0.14	-1.28	0.16
SPOA0174		MOSC domain-containing protein	-1.09	0.41	-1.05	0.85	-1.07	0.02	-1.70	0.11	1.07	0.24	-0.32	1.39	-1.36	0.05	-1.42	0.05	-1.39	0.03
SPOA0175		oxidoreductase	1.06	0.53	-1.03	0.94	0.02	1.05	-1.39	0.41	-1.11	0.69	-1.25	0.14	-1.27	0.36	-1.64	0.16	-1.46	0.18
SPOA0176		hypothetical protein	-2.32	0.04	-1.06	0.93	-1.69	0.63	-3.89	0.01	1.07	0.75	-1.41	2.48	-1.49	0.23	-1.18	0.81	-1.34	0.16
SPOA0177		hydrogen peroxide-inducible genes activator	X	X	-1.38	X	N/A	N/A	-1.34	X	-1.19	X	-1.27	0.08	1.42	X	2.49	X	1.96	0.53
SPOA0180		cytochrome c family protein	-1.06	0.97	1.38	0.07	0.16	1.22	-0.98	0.40	-1.02	0.96	-1.00	0.02	1.05	0.53	-1.70	X	-0.33	1.38
SPOA0181		FNT family protein	X	X	-1.00	0.93	N/A	N/A	2.43	X	-1.09	0.91	0.67	1.76	-1.32	0.51	X	X	N/A	N/A
SPOA0182		hypothetical protein	X	X	1.12	0.59	N/A	N/A	-2.02	0.08	-1.21	0.61	-1.62	0.41	-1.22	0.23	-1.35	X	-1.29	0.07
SPOA0183		SCO1/SenC family protein	-1.97	0.38	-1.12	0.50	-1.55	0.43	-2.38	0.04	-1.50	0.41	-1.94	0.44	1.08	0.75	1.23	0.23	1.16	0.08
SPOA0184		heme-copper respiratory oxidase family	1.10	0.77	1.17	0.47	1.14	0.03	-1.01	0.47	-1.34	0.25	-1.18	0.17	-1.23	0.53	-1.21	0.81	-1.22	0.01
SPOA0185		cytochrome c oxidase,ba3-type, subunit I	X	X	-1.01	0.97	N/A	N/A	-0.89	0.40	-1.50	0.61	-1.19	0.31	-1.60	0.06	-1.17	X	-1.39	0.22
SPOA0186		Rrf2 family protein	-1.38	0.24	-1.47	0.02	-1.43	0.05	1.46	0.01	1.23	0.07	1.35	0.12	-1.07	0.19	-1.40	0.11	-1.24	0.17
SPOA0187	*ccoP-2*	cytochrome c oxidase, cbb3-type, subunit III (EC:1.9.3.1)	X	X	1.10	0.81	N/A	N/A	1.37	X	-1.18	0.49	0.10	1.28	-1.16	0.77	1.63	X	0.24	1.40
SPOA0188	*ccoQ-2*	cytochrome c oxidase, cbb3-type, subunit IV (EC:1.9.3.1)	-3.40	0.19	-1.41	0.16	-2.41	1.00	-6.39	0.01	-1.30	0.44	-3.85	2.55	-1.62	0.05	1.30	0.51	-0.16	1.46
SPOA0189	*ccoO-2*	cytochrome c oxidase, cbb3-type, subunit II (EC:1.9.3.1)	-1.39	0.81	-1.07	0.96	-1.23	0.16	1.32	0.85	-1.01	0.99	0.16	1.17	-1.17	0.87	1.15	0.89	-0.01	1.16
SPOA0190	*ccoN-2*	cytochrome c oxidase, cbb3-type, subunit I (EC:1.9.3.1)	X	X	1.29	0.32	N/A	N/A	1.31	0.04	-1.23	X	0.04	1.27	-1.22	0.20	X	X	N/A	N/A
SPOA0191		hypothetical protein	1.07	X	1.58	0.04	1.33	0.25	1.52	0.52	-1.35	0.41	0.09	1.44	1.31	0.35	-1.05	0.77	0.13	1.18
SPOA0192		hypothetical protein	-1.86	0.06	1.32	0.33	-0.27	1.59	-2.11	0.04	-1.22	0.49	-1.67	0.45	-1.41	0.02	-1.09	0.93	-1.25	0.16

SPOA0193	*cycJ*	cytochrome c-type biogenesis protein CcmE	-1.76	0.33	-1.31	0.15	-1.54	0.22	-1.86	0.38	-1.05	0.92	-1.46	0.41	-1.21	0.62	1.90	0.21	0.35	1.56
SPOA0194	*hemA-2*	5-aminolevulinate synthase (EC:2.3.1.37)	1.47	0.49	-1.01	1.00	0.23	1.24	-0.93	0.52	-1.06	0.87	-0.99	0.07	1.09	0.65	-1.02	0.82	0.04	1.06
SPOA0195		hypothetical protein	1.14	0.71	-1.26	0.33	-0.06	1.20	-1.29	0.25	-1.34	0.49	-1.32	0.03	1.17	0.28	3.23	0.03	2.20	1.03
SPOA0196	*cycL*	cytochrome c-type biogenesis protein CycL	X	X	1.18	0.34	N/A	N/A	-1.15	0.44	-1.10	X	-1.13	0.02	1.32	0.16	X	X	N/A	N/A
SPOA0197	*dsbE*	thiol:disulfide interchange protein DsbE	-1.49	0.16	-1.53	0.16	-1.51	0.02	-1.36	0.26	-1.45	0.40	-1.41	0.04	-1.16	0.50	2.34	0.16	0.59	1.75
SPOA0198	*cycK*	cytochrome c-type biogenesis protein Cyc	-1.38	X	-1.03	0.99	-1.21	0.17	-1.43	0.93	1.28	X	-0.08	1.36	-1.05	0.99	-1.10	X	-1.08	0.03
SPOA0199		GntR family transcriptional regulator	X	X	-1.08	0.62	N/A	N/A	-0.96	0.12	X	X	N/A	N/A	-0.97	0.64	X	X	N/A	N/A
SPOA0200		hypothetical protein	-2.15	X	-1.13	0.87	-1.64	0.51	-1.82	0.79	-1.20	0.81	-1.51	0.31	-1.01	0.95	1.56	X	0.28	1.29
SPOA0201		hydroxylamine oxidoreductase (EC:1.7.3.4)	-1.95	X	1.18	0.59	-0.39	1.57	-2.00	0.59	1.06	X	-0.47	1.53	1.46	0.06	X	X	N/A	N/A
SPOA0202	*hisD*	histidinol dehydrogenase (EC:1.1.1.23)	-1.03	0.98	1.01	0.99	-0.01	1.02	3.50	0.01	-1.84	0.05	0.83	2.67	-1.40	0.03	-2.18	0.00	-1.79	0.39
SPOA0203		hypothetical protein	-1.40	0.23	1.12	0.76	-0.14	1.26	-1.59	0.30	1.13	0.80	-0.23	1.36	1.52	0.35	1.34	0.49	1.43	0.09
SPOA0204		hypothetical protein	-1.09	0.90	-1.26	0.15	-1.18	0.09	-1.50	0.11	1.18	0.29	-0.16	1.34	1.23	0.33	1.43	0.05	1.33	0.10
SPOA0205		serine protease	0.99	0.73	-1.01	0.69	-0.01	1.00	0.87	0.26	1.20	0.19	1.03	0.17	1.77	0.02	1.37	0.09	1.57	0.20
SPOA0206		Crp/Fnr family transcriptional regulator	-1.34	0.22	-1.21	0.19	-1.28	0.07	1.08	0.67	1.15	0.36	1.12	0.03	1.03	0.95	1.87	0.01	1.45	0.42
SPOA0207		guanylate cyclase	-1.18	0.19	1.02	0.81	-0.08	1.10	1.12	0.36	-1.06	0.56	0.03	1.09	1.47	0.02	1.03	0.81	1.25	0.22
SPOA0208		oxidoreductase, FAD-binding	-1.52	0.10	1.02	0.94	-0.25	1.27	0.93	0.13	1.28	0.35	1.10	0.18	1.69	0.10	2.02	0.10	1.86	0.17
SPOA0209		oxidoreductase, FAD-binding	-2.28	0.04	-1.17	0.29	-1.73	0.56	-2.06	0.02	-1.04	0.55	-1.55	0.51	-1.13	0.72	2.24	0.03	0.56	1.69
SPOA0210		hypothetical protein	-1.40	0.49	-1.01	0.98	-1.21	0.19	-1.64	0.48	-2.27	0.08	-1.96	0.31	1.40	0.16	-1.08	0.62	0.16	1.24
SPOA0211		Na/Pi-cotransporter family protein	1.09	0.07	1.21	0.03	1.15	0.06	1.51	0.01	-1.52	0.02	-0.01	1.52	-1.03	0.34	-1.20	0.15	-1.12	0.09
SPOA0212		nitric oxide reductase F protein	-1.14	0.88	-1.20	0.83	-1.17	0.03	-1.08	0.99	-1.17	0.30	-1.13	0.04	-1.16	0.78	1.88	X	0.36	1.52
SPOA0213		nitric oxide reductase E protein	X	X	-1.16	0.19	N/A	N/A	-2.26	0.04	1.38	0.31	-0.44	1.82	-1.41	0.20	1.59	0.27	0.09	1.50
SPOA0214	*norD*	nitric oxide reductase D protein	X	X	-1.51	X	N/A	N/A	X	X	X	X	N/A	N/A	1.06	X	X	X	N/A	N/A
SPOA0215	*norQ*	nitric oxide reductase Q protein	-2.34	0.05	-1.40	0.15	-1.87	0.47	-2.93	0.00	-1.51	0.12	-2.22	0.71	-1.51	0.09	1.26	0.45	-0.13	1.39
SPOA0216	*norB*	nitric oxide reductase, large subunit (EC:1.7.99.7)	1.34	X	-1.08	0.77	0.13	1.21	-1.06	0.61	-1.08	X	-1.07	0.01	1.14	0.70	X	X	N/A	N/A
SPOA0217	*norC*	nitric oxide reductase, small subunit (EC:1.7.99.7)	X	X	1.17	0.21	N/A	N/A	X	X	1.22	X	N/A	N/A	-1.07	0.73	X	X	N/A	N/A
SPOA0218		magnesium transporter CorA family protein	-1.17	0.37	1.13	0.31	-0.02	1.15	-1.80	0.38	1.67	0.07	-0.07	1.74	1.49	0.04	1.57	0.06	1.53	0.04
SPOA0219		NnrS	X	X	-1.00	0.91	N/A	N/A	-1.05	0.22	-1.47	0.15	-1.26	0.21	1.07	0.50	-1.10	0.86	-0.02	1.09
SPOA0220	*nirS*	cytochrome cd1 nitrite reductase (EC:1.7.2.1)	1.14	0.97	1.05	0.78	1.10	0.04	-1.93	0.82	-1.41	X	-1.67	0.26	1.23	0.13	-1.02	X	0.11	1.13
SPOA0221	*nirE*	nitrite reductase heme biosynthesis E protein	X	X	-1.23	0.45	N/A	N/A	-2.09	0.04	X	X	N/A	N/A	1.18	0.15	1.42	X	1.30	0.12
SPOA0222	*nirC*	cytochrome c55X	1.17	0.91	-1.08	0.90	0.04	1.13	-1.13	0.92	-1.12	0.86	-1.13	0.00	1.11	0.83	1.45	0.38	1.28	0.17
SPOA0223	*nirF*	cytochrome cd1 nitrite reductase (EC:1.7.2.1)	-2.23	0.02	-1.14	0.66	-1.69	0.55	-2.55	0.07	-1.05	0.88	-1.80	0.75	-1.35	0.08	1.25	0.35	-0.05	1.30
SPOA0224		nitrite reductase heme biosynthesis D/L protein	1.57	0.02	-1.23	0.83	0.17	1.40	-8.53	0.00	-0.97	0.62	-4.75	3.78	-1.20	0.24	-1.47	X	-1.34	0.14
SPOA0225	*nirG*	nitrite reductase heme biosynthesis G protein	X	X	-1.10	X	N/A	N/A	-0.99	0.07	X	X	N/A	N/A	-1.48	0.04	X	X	N/A	N/A
SPOA0226	*nirH*	nitrite reductase heme biosynthesis H protein	-1.24	0.34	-1.12	0.66	-1.18	0.06	-1.79	0.30	1.01	X	-0.39	1.40	-0.98	0.78	X	X	N/A	N/A
SPOA0227	*nirJ*	nitrite reductase heme biosynthesis J protein	-1.19	0.73	-1.46	0.54	-1.33	0.14	-1.61	0.73	-1.02	1.00	-1.32	0.30	-1.16	0.85	1.32	0.72	0.08	1.24
SPOA0228	*nirN*	nitrite reductase protein N (EC:1.7.2.1)	X	X	-1.76	X	N/A	N/A	-4.95	0.01	1.20	X	-1.88	3.08	-1.24	X	X	X	N/A	N/A
SPOA0229		hypothetical protein	1.73	0.25	1.17	0.07	1.45	0.28	1.97	0.02	-0.95	0.61	0.51	1.46	-1.02	0.98	X	X	N/A	N/A
SPOA0230		LysR family transcriptional regulator	-1.60	0.15	-1.25	0.19	-1.43	0.18	-0.99	0.63	-1.39	0.23	-1.19	0.20	1.31	0.31	-0.94	0.60	0.19	1.12
SPOA0231		glycine betaine/proline ABC transporter, periplasmic substrate-binding protein	0.98	0.88	-1.31	0.48	-0.16	1.15	-3.17	0.18	1.68	0.31	-0.75	2.43	-1.04	0.94	1.26	0.58	0.11	1.15

SPOA0232	*opuAA*	glycine betaine/proline ABC transporter, ATP-binding protein (EC:3.6.3.32)	-1.08	0.97	-1.08	0.96	-1.08	0.00	-1.68	0.83	-1.01	1.00	-1.35	0.34	1.22	0.71	1.81	0.79	1.52	0.29
SPOA0233		glycine betaine/proline ABC transporter, permease protein	X	X	-1.07	0.84	N/A	N/A	-0.87	0.43	-1.02	0.95	-0.95	0.07	1.07	0.66	X	X	N/A	N/A
SPOA0234		agmatinase	1.26	0.82	-1.01	0.99	0.13	1.14	-1.45	0.78	1.14	0.82	-0.16	1.30	-1.13	0.81	-1.09	0.99	-1.11	0.02
SPOA0235	*speB-4*	agmatinase (EC:3.5.3.11)	-1.05	0.38	1.18	0.12	0.06	1.12	-1.57	0.05	-1.11	0.47	-1.34	0.23	-1.03	0.84	1.54	0.24	0.26	1.29
SPOA0236	*dctB*	C4-dicarboxylate transport sensor protein dctB (EC:2.7.3.-)	-2.47	0.10	-1.18	0.64	-1.83	0.65	-1.95	0.10	-1.15	0.51	-1.55	0.40	-1.09	0.54	1.06	0.20	-0.02	1.08
SPOA0237	*dctD-2*	C4-dicarboxylate transport transcriptional regulatory protein DctD	1.10	0.43	1.14	0.72	1.12	0.02	1.32	0.20	-1.68	0.08	-0.18	1.50	1.22	0.04	-1.03	0.87	0.10	1.13
SPOA0238		TRAP dicarboxylate transporter, DctP subunit	-1.37	0.01	-1.88	0.03	-1.63	0.26	-4.86	0.00	1.69	0.06	-1.59	3.28	1.63	0.04	2.23	0.01	1.93	0.30
SPOA0239		TRAP dicarboxylate transporter, DctQ subunit	-1.10	0.53	-1.82	0.02	-1.46	0.36	-1.21	0.17	1.65	0.07	0.22	1.43	1.40	0.10	1.55	0.08	1.48	0.08
SPOA0240		TRAP transporter, DctM subunit	-1.43	0.06	-1.47	0.03	-1.45	0.02	-1.54	0.04	1.63	0.04	0.04	1.59	1.44	0.02	1.17	0.31	1.31	0.14
SPOA0241		gluconolactonase	-1.84	0.15	-1.12	0.81	-1.48	0.36	-2.11	0.17	-1.31	0.55	-1.71	0.40	-1.00	0.96	-1.21	0.87	-1.10	0.11
SPOA0242		LacI family transcription regulator	-1.44	0.15	-1.14	0.80	-1.29	0.15	-1.34	0.16	-1.01	0.94	-1.18	0.17	-1.22	0.65	-1.30	0.49	-1.26	0.04
SPOA0243		aldehyde dehydrogenase	-1.01	0.96	1.00	0.98	-0.01	1.01	-1.19	0.84	-1.26	0.60	-1.23	0.04	-1.16	0.73	-1.10	0.95	-1.13	0.03
SPOA0244		dihydrodipicolinate synthase family protein	1.12	0.36	-1.06	0.54	0.03	1.09	-1.17	0.75	-1.06	0.69	-1.12	0.05	-1.51	0.01	-1.64	0.03	-1.58	0.06
SPOA0245		galactonate dehydratase	-0.97	0.85	-1.46	0.04	-1.22	0.24	-1.39	0.53	-1.70	0.04	-1.55	0.16	1.03	0.94	2.19	0.03	1.61	0.58
SPOA0246	*pdxA*	4-hydroxythreonine-4-phosphate dehydrogenase (EC:1.1.1.262)	-1.20	0.65	-1.23	0.26	-1.22	0.02	-2.58	0.06	-1.42	0.09	-2.00	0.58	-1.78	0.04	-1.96	0.29	-1.87	0.09
SPOA0247		hypothetical protein	X	X	-1.16	0.38	N/A	N/A	-1.44	X	-1.18	X	-1.31	0.13	-1.74	0.03	X	X	N/A	N/A
SPOA0248		hypothetical protein	-1.25	0.28	-1.31	0.09	-1.28	0.03	-1.61	0.22	-1.41	0.13	-1.51	0.10	-1.23	0.25	X	X	N/A	N/A
SPOA0249		TRAP dicarboxylate transporter, DctP subunit	-1.22	0.50	-1.92	0.17	-1.57	0.35	-2.40	0.04	1.14	0.40	-0.63	1.77	-1.14	0.71	-1.01	0.59	-1.08	0.06
SPOA0250		TRAP dicarboxylate transporter, DctM subunit	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	-1.42	0.26	X	X	N/A	N/A
SPOA0251		TRAP dicarboxylate transporter, DctQ subunit	-1.21	0.83	-1.21	0.68	-1.21	0.00	-1.65	0.68	-1.16	0.81	-1.41	0.25	1.08	0.72	1.31	0.60	1.20	0.12
SPOA0252		LacI family transcription regulator	-1.26	0.03	-1.15	0.28	-1.21	0.06	-2.21	0.02	-1.02	0.65	-1.62	0.60	-1.33	0.00	-1.19	0.53	-1.26	0.07
SPOA0253		ribose ABC transporter, periplasmic ribose-binding protein	-3.01	X	-1.66	0.66	-2.34	0.68	-2.11	0.68	-1.08	0.94	-1.60	0.52	-0.97	0.92	1.35	X	0.19	1.16
SPOA0254	*rbsC-1*	ribose ABC transporter, permease protein	X	X	-1.47	0.31	N/A	N/A	-1.81	0.56	-1.31	0.33	-1.56	0.25	1.23	0.22	-1.19	X	0.02	1.21
SPOA0255		sugar ABC transporter, ATP binding protein	X	X	-2.49	0.11	N/A	N/A	-2.30	0.10	-1.08	0.85	-1.69	0.61	-1.19	0.63	1.18	0.32	-0.01	1.19
SPOA0256		ribose ABC transporter, periplasmic ribose-binding protein	-1.35	0.61	-1.94	0.36	-1.65	0.30	-6.26	0.08	1.09	0.84	-2.59	3.68	-1.02	0.98	1.08	0.80	0.03	1.05
SPOA0257	*rbsC-2*	ribose ABC transporter, permease protein	-1.17	0.81	-1.45	0.38	-1.31	0.14	-4.33	0.25	-1.33	0.61	-2.83	1.50	-1.16	0.71	-1.16	0.88	-1.16	0.00
SPOA0258	*rbsA*	ribose ABC transporter, ATP-binding protein	-1.26	0.82	-1.30	0.54	-1.28	0.02	-3.61	0.50	-0.98	0.95	-2.30	1.31	-1.37	0.51	1.39	0.47	0.01	1.38
SPOA0259		LacI family transcription regulator	-1.47	0.19	-1.33	0.10	-1.40	0.07	-2.56	0.02	-1.20	0.44	-1.88	0.68	-1.18	0.43	-1.28	0.30	-1.23	0.05
SPOA0260		aldehyde dehydrogenase	-0.95	1.00	-1.35	0.07	-1.15	0.20	1.31	0.11	-1.35	0.16	-0.02	1.33	1.05	0.77	1.31	0.34	1.18	0.13
SPOA0261		GntR family transcriptional regulator	-1.63	0.54	1.16	0.72	-0.24	1.40	-1.10	0.91	-1.12	0.79	-1.11	0.01	1.32	0.54	-1.07	0.93	0.13	1.20
SPOA0262		oxidoreductase, FAD-binding	X	X	-1.19	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0263		TRAP transporter, DctM subunit	X	X	-1.15	0.21	N/A	N/A	-1.82	0.12	-1.39	0.09	-1.61	0.22	-1.36	0.08	-1.74	0.08	-1.55	0.19
SPOA0264		TRAP transporter DctQ family protein	-1.86	X	-1.34	0.83	-1.60	0.26	-1.09	0.98	-1.26	0.91	-1.18	0.09	1.21	0.85	1.94	X	1.58	0.37
SPOA0265		TRAP transporter DctP family protein	1.01	0.97	-1.59	0.16	-0.29	1.30	-1.77	0.66	-1.32	0.45	-1.55	0.23	-1.07	0.90	-0.97	0.85	-1.02	0.05
SPOA0266		proline racemase	-1.12	0.95	-1.35	0.25	-1.24	0.12	-2.48	0.48	-1.36	0.59	-1.92	0.56	-1.34	0.39	1.36	X	0.01	1.35
SPOA0267		dihydroxydipicolinate synthase family protein	1.03	X	-1.16	0.67	-0.06	1.10	1.28	0.58	-1.53	0.14	-0.13	1.41	-1.36	0.29	X	X	N/A	N/A

SPOA0268		IclR family transcriptional regulator	9.05	0.33	2.09	0.17	5.57	3.48	-1.88	0.09	-1.23	0.66	-1.56	0.33	-1.56	0.16	-1.23	0.84	-1.40	0.17
SPOA0269		hypothetical protein	11.00	0.02	1.36	0.45	6.18	4.82	-4.36	0.10	1.24	0.69	-1.56	2.80	1.05	0.88	1.15	0.70	1.10	0.05
SPOA0270		hypothetical protein	6.90	0.02	-1.04	0.96	2.93	3.97	-2.40	0.20	1.05	0.96	-0.68	1.73	-1.14	0.87	1.67	0.55	0.27	1.41
SPOA0271		methylamine utilization protein MauG	14.00	0.01	1.82	0.04	7.91	6.09	-1.96	0.14	-0.95	0.39	-1.46	0.50	-1.43	0.08	-1.30	X	-1.37	0.06
SPOA0272		glutathione-dependent formaldehyde dehydrogenase	3.96	0.15	1.28	0.67	2.62	1.34	0.99	0.88	1.40	0.59	1.20	0.20	1.05	0.97	1.09	0.97	1.07	0.02
SPOA0273		DNA-binding protein	-1.27	0.26	-1.56	0.04	-1.42	0.14	9.33	0.00	-1.85	0.03	3.74	5.59	1.06	0.49	-1.62	0.04	-0.28	1.34
SPOA0274	*gabT*	4-aminobutyrate aminotransferase (EC:2.6.1.19)	2.27	0.17	1.66	0.24	1.97	0.31	-1.09	0.79	-1.39	0.64	-1.24	0.15	-1.28	0.74	1.52	X	0.12	1.40
SPOA0275	*gabD-3*	succinate-semialdehyde dehydrogenase (EC:1.2.1.16)	-1.56	X	1.32	0.03	-0.12	1.44	-3.24	0.04	-1.53	0.14	-2.39	0.86	-1.25	0.27	-1.37	0.61	-1.31	0.06
SPOA0276	*cscK*	fructokinase (EC:2.7.1.4)	-1.37	0.31	1.08	0.54	-0.15	1.23	-1.07	0.50	1.53	0.08	0.23	1.30	1.07	0.67	1.32	0.01	1.20	0.13
SPOA0277		alpha/beta hydrolase	X	X	-1.27	0.60	N/A	N/A	-1.49	0.62	-1.34	0.35	-1.42	0.08	-1.27	0.39	1.13	0.39	-0.07	1.20
SPOA0278		TRAP dicarboxylate transporter, DctM subunit	1.28	0.71	-1.00	0.96	0.14	1.14	-1.27	0.99	-1.04	1.00	-1.16	0.12	1.20	0.73	1.23	X	1.22	0.02
SPOA0279		TRAP dicarboxylate transporter, DctQ subunit	-1.99	0.23	1.13	0.17	-0.43	1.56	-3.03	0.04	X	X	N/A	N/A	1.67	0.13	X	X	N/A	N/A
SPOA0280		TRAP dicarboxylate transporter, DctP subunit	-4.06	0.02	-1.33	0.12	-2.70	1.37	-6.94	0.01	-1.06	0.85	-4.00	2.94	1.06	0.71	1.22	0.47	1.14	0.08
SPOA0281		LysR family transcriptional regulator	-1.68	0.02	1.06	0.73	-0.31	1.37	-2.37	0.06	-1.43	0.24	-1.90	0.47	1.25	0.60	-0.89	0.73	0.18	1.07
SPOA0282		malonyl-CoA synthase	-1.03	0.77	1.51	0.13	0.24	1.27	1.64	0.32	1.06	0.54	1.35	0.29	1.14	0.06	-1.21	0.12	-0.04	1.18
SPOA0283		GMC family oxidoreductase	7.77	0.00	-1.17	X	3.30	4.47	-1.17	0.15	X	X	N/A	N/A	-1.09	0.74	X	X	N/A	N/A
SPOA0284		LysR family transcriptional regulator	-1.55	X	1.17	0.70	-0.19	1.36	-1.03	0.91	-1.44	0.59	-1.24	0.21	1.08	0.82	-1.18	0.95	-0.05	1.13
SPOA0285	*caiD-2*	carnitinyl-CoA dehydratase	8.93	0.00	1.55	0.01	5.24	3.69	-1.06	0.83	1.24	0.27	0.09	1.15	1.19	0.05	-1.04	0.98	0.08	1.12
SPOA0286		ThiJ/PfpI family protein	6.36	0.00	1.19	0.24	3.78	2.59	1.01	0.50	1.10	0.23	1.06	0.05	-1.06	0.13	-1.02	1.00	-1.04	0.02
SPOA0287		acyl-CoA synthetase	35.90	0.00	X	X	N/A	N/A	-1.02	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0288	*acdA-3*	acyl-CoA dehydrogenase (EC:1.3.99.3)	15.00	0.22	1.47	0.79	8.24	6.77	-3.62	0.53	-1.08	0.97	-2.35	1.27	-1.32	0.88	1.98	0.70	0.33	1.65
SPOA0289		AraC family transcriptional regulator	-2.38	0.06	-1.25	0.38	-1.82	0.57	2.74	0.04	-1.21	0.16	0.77	1.98	-1.29	0.21	1.53	0.09	0.12	1.41
SPOA0290		hypothetical protein	1.53	0.90	1.08	0.83	1.31	0.22	1.81	0.77	1.06	0.83	1.44	0.38	1.32	0.38	1.33	0.48	1.33	0.01
SPOA0291		branched-chain amino acid aminotransferase	-1.01	0.59	1.26	0.26	0.13	1.14	1.45	0.04	-1.11	0.29	0.17	1.28	1.23	0.19	1.16	0.16	1.20	0.04
SPOA0292	*psd*	phosphatidylserine decarboxylase (EC:4.1.1.65)	2.06	0.00	1.18	0.21	1.62	0.44	4.38	0.00	-1.80	0.01	1.29	3.09	-1.31	0.08	-1.97	0.02	-1.64	0.33
SPOA0293	*pssA*	CDP-diacylglycerol--serine O-phosphatidyltransferase (EC:2.7.8.8)	X	X	1.45	0.08	N/A	N/A	3.67	0.01	-1.85	0.04	0.91	2.76	-1.54	0.03	-3.19	0.01	-2.37	0.82
SPOA0294	*pmtA*	phosphatidylethanolamine N-methyltransferase (EC:2.1.1.17)	2.39	0.06	1.11	0.69	1.75	0.64	3.50	0.01	-1.25	0.15	1.13	2.38	-1.50	0.02	-1.78	0.13	-1.64	0.14
SPOA0295		hydantoin racemase (EC:5.1.99.-)	-3.87	0.02	-1.14	0.86	-2.51	1.37	-8.33	0.02	-1.33	0.19	-4.83	3.50	-1.16	0.86	1.23	0.70	0.04	1.20
SPOA0296	*livF-2*	branched-chain amino acid ABC transporter, ATP-binding protein	-3.20	0.13	-1.16	0.88	-2.18	1.02	-7.58	0.09	-1.34	0.69	-4.46	3.12	-1.18	0.85	1.06	0.92	-0.06	1.12
SPOA0297	*livG*	branched-chain amino acid ABC transporter, ATP-binding protein	-3.44	0.10	-1.01	0.99	-2.23	1.22	-8.63	0.06	-1.23	0.11	-4.93	3.70	-1.16	0.35	-1.28	X	-1.22	0.06
SPOA0298		branched-chain amino acid ABC transporter, permease protein	-4.10	0.08	-1.18	0.53	-2.64	1.46	-12.50	0.02	-1.18	0.62	-6.84	5.66	-1.19	0.72	-1.30	X	-1.25	0.06
SPOA0299		branched-chain amino acid ABC transporter, permease protein	-4.57	0.02	1.05	0.25	-1.76	2.81	-10.50	0.00	X	X	N/A	N/A	-1.12	0.73	X	X	N/A	N/A
SPOA0300		branched-chain amino acid ABC transporter, periplasmic branched-chain amino acid-binding protein	-8.77	0.00	-1.22	0.21	-5.00	3.78	-26.30	0.01	-1.21	0.59	-13.76	12.55	1.17	0.51	-1.06	0.96	0.05	1.12
SPOA0301		GntR family transcriptional regulator	-2.02	0.04	1.02	0.88	-0.50	1.52	-1.70	0.06	1.08	0.54	-0.31	1.39	-1.66	0.00	-1.98	0.06	-1.82	0.16
SPOA0302		phage integrase family site specific recombinase	X	X	-1.11	0.60	N/A	N/A	-1.41	0.97	-0.99	0.29	-1.20	0.21	-0.99	0.30	X	X	N/A	N/A

SPOA0303		replication protein	1.30	0.18	-1.20	0.69	0.05	1.25	1.32	0.12	-1.20	0.73	0.06	1.26	-1.21	0.21	1.15	0.68	-0.03	1.18
SPOA0304	*repA*	replication protein	1.40	0.26	-1.19	0.10	0.11	1.30	1.38	0.03	-1.35	0.03	0.01	1.37	-1.15	0.31	-1.45	0.24	-1.30	0.15
SPOA0305		hypothetical protein	1.04	0.96	-1.07	0.77	-0.02	1.06	1.40	0.39	-1.07	0.68	0.17	1.24	1.31	0.04	-1.06	0.56	0.13	1.19
SPOA0306		S1 RNA-binding domain-containing protein	1.27	0.30	1.00	0.96	1.14	0.14	2.13	0.01	-1.13	0.26	0.50	1.63	-1.09	0.08	-1.13	0.67	-1.11	0.02
SPOA0309		sulphoacetaldehyde acetyltransferase	1.21	0.40	-1.09	0.28	0.06	1.15	-1.24	0.81	1.07	0.45	-0.09	1.16	-1.71	0.04	-1.34	0.38	-1.53	0.19
SPOA0310		glycine cleavage system protein T	-1.16	0.73	-1.09	0.54	-1.13	0.03	-1.15	0.62	-1.18	0.21	-1.17	0.02	-1.41	0.02	-1.23	0.41	-1.32	0.09
SPOA0311		FAD-dependent oxidoreductase	-2.81	X	-1.17	0.86	-1.99	0.82	-1.49	0.87	-1.42	X	-1.46	0.04	1.34	0.56	1.22	X	1.28	0.06
SPOA0312		glutamate-1-semialdehyde 2,1-aminomutase	X	X	-1.02	0.98	N/A	N/A	-1.41	0.89	-1.12	0.83	-1.27	0.14	-1.20	0.61	1.01	X	-0.10	1.11
SPOA0313		trimethylamine methyltransferase family protein	-1.68	X	-1.14	0.72	-1.41	0.27	-1.43	0.85	-1.24	0.46	-1.34	0.10	1.33	0.28	1.26	0.21	1.30	0.04
SPOA0314		LysR family transcriptional regulator	-1.11	0.79	1.01	0.98	-0.05	1.06	-1.31	0.91	-1.12	0.76	-1.22	0.10	-0.98	0.88	1.27	0.79	0.14	1.13
SPOA0315	*icd*	isocitrate dehydrogenase, NADP-dependent (EC:1.1.1.42)	4.68	0.00	2.12	0.05	3.40	1.28	4.28	0.01	2.33	0.01	3.31	0.98	1.14	0.60	-1.25	0.10	-0.06	1.20
SPOA0316		amidohydrolase	2.02	0.02	1.12	0.57	1.57	0.45	-3.73	0.00	1.58	0.01	-1.08	2.66	-1.13	0.28	1.26	0.23	0.07	1.20
SPOA0317		AsnC family transcriptional regulator	1.71	0.75	-1.11	0.38	0.30	1.41	-2.68	0.50	1.07	0.81	-0.81	1.88	-1.51	0.19	-1.09	0.76	-1.30	0.21
SPOA0318	*megL*	methionine gamma-lyase (EC:4.4.1.11)	1.10	0.99	-1.32	0.66	-0.11	1.21	-1.30	0.81	-1.00	1.00	-1.15	0.15	6.50	0.04	59.60	0.02	33.05	26.55
SPOA0319		transketolase	1.39	0.64	-1.01	0.99	0.19	1.20	-1.60	0.67	-1.08	0.93	-1.34	0.26	3.83	0.12	36.90	0.01	20.37	16.54
SPOA0320	*hpcD*	5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC:5.3.3.10)	-1.30	0.06	-1.07	0.95	-1.19	0.12	-1.38	0.41	1.11	0.35	-0.14	1.25	1.08	0.33	2.94	0.07	2.01	0.93
SPOA0321		glyoxalase family protein	-1.37	0.49	-1.25	0.19	-1.31	0.06	-1.53	0.13	1.15	0.46	-0.19	1.34	-1.03	0.98	1.33	X	0.15	1.18
SPOA0322		hypothetical protein	-1.44	0.15	1.35	0.07	-0.04	1.40	-1.16	0.82	-1.66	0.05	-1.41	0.25	1.02	0.61	-1.95	0.03	-0.47	1.49
SPOA0323		cyclic nucleotide-binding protein	1.02	0.96	1.38	0.22	1.20	0.18	1.47	0.62	-1.12	0.51	0.18	1.30	1.10	0.58	1.06	0.66	1.08	0.02
SPOA0324		hypothetical protein	-1.13	0.06	1.54	0.05	0.21	1.34	-1.14	0.55	-1.14	0.39	-1.14	0.00	1.10	0.36	-1.28	0.21	-0.09	1.19
SPOA0325		2-nitropropane dioxygenase	2.05	0.21	4.04	0.00	3.05	1.00	-1.60	0.04	1.43	0.02	-0.09	1.52	-1.56	0.04	1.18	0.04	-0.19	1.37
SPOA0326		LysR family transcriptional regulator	1.68	0.01	1.51	0.02	1.60	0.09	-1.47	0.03	1.09	0.29	-0.19	1.28	1.20	0.40	1.33	0.24	1.27	0.07
SPOA0327		rzcC protein	-1.70	0.14	-1.03	0.81	-1.37	0.34	-1.17	0.86	1.10	0.84	-0.03	1.14	1.21	0.45	1.08	0.85	1.15	0.06
SPOA0328		hypothetical protein	X	X	-1.26	0.09	N/A	N/A	-0.85	0.09	-1.06	0.74	-0.95	0.11	-1.04	0.80	-1.19	0.68	-1.12	0.08
SPOA0329	*mgsA*	methylglyoxal synthase (EC:4.2.3.3)	-1.14	0.48	-1.37	0.10	-1.26	0.12	-1.39	0.54	-1.54	0.14	-1.47	0.08	-1.41	0.24	-1.02	0.81	-1.22	0.20
SPOA0330	*eda-2*	2-dehydro-3-deoxyphosphogluconate aldolase (EC:4.1.2.14 4.1.3.16)	-2.30	0.02	-1.51	0.46	-1.91	0.40	-3.27	0.00	-1.36	0.35	-2.32	0.96	-1.30	0.20	1.16	0.65	-0.07	1.23
SPOA0331		2-dehydro-3-deoxygluconokinase	-0.98	0.73	-1.25	0.66	-1.12	0.13	-1.14	0.76	-1.82	0.20	-1.48	0.34	-1.45	0.40	-1.05	0.84	-1.25	0.20
SPOA0332		dihydroxy-acid dehydratase (EC:4.2.1.9)	-1.70	X	-1.46	0.60	-1.58	0.12	-1.67	0.71	-1.90	0.38	-1.79	0.12	-1.29	0.63	1.09	0.71	-0.10	1.19
SPOA0333		TRAP dicarboxylate transporter, DctM subunit	-1.56	0.81	-1.62	0.68	-1.59	0.03	-2.05	0.75	-1.31	0.82	-1.68	0.37	-1.32	0.81	1.69	0.63	0.19	1.51
SPOA0334		TRAP dicarboxylate family transporter DctQ subunit	-1.35	0.03	-1.93	0.04	-1.64	0.29	-2.02	0.16	-2.27	0.03	-2.15	0.13	-1.33	0.13	-1.36	0.13	-1.35	0.02
SPOA0335		TRAP dicarboxylate family transporter DctP subunit	-1.53	0.03	-2.16	0.09	-1.85	0.31	-3.91	0.04	-1.56	0.05	-2.74	1.18	-1.19	0.24	-1.10	0.71	-1.15	0.04
SPOA0336		LacI family transcription regulator	-1.53	0.63	-1.86	0.13	-1.70	0.17	-2.61	0.44	-2.64	0.10	-2.63	0.02	-1.24	0.48	1.08	0.83	-0.08	1.16
SPOA0337		hypothetical protein	-1.70	0.04	-1.58	0.18	-1.64	0.06	-2.18	0.05	-1.33	0.17	-1.76	0.43	-1.47	0.01	-0.97	0.49	-1.22	0.25
SPOA0338		LysR family transcriptional regulator	1.12	0.91	-1.42	0.55	-0.15	1.27	1.29	0.38	-1.98	X	-0.35	1.64	1.37	0.36	-1.14	0.98	0.12	1.26
SPOA0339		HAD family hydrolase	3.23	0.09	-6.80	0.01	-1.79	5.02	5.81	0.02	-177.00	0.00	-85.60	91.41	1.80	0.07	1.98	0.19	1.89	0.09
SPOA0340		tautomerase	2.81	0.00	-6.74	0.01	-1.97	4.78	4.79	0.00	-118.00	0.00	-56.61	61.40	1.68	0.00	1.72	0.21	1.70	0.02
SPOA0341		hypothetical protein	1.64	0.06	-8.35	0.02	-3.36	5.00	2.93	0.00	-144.00	0.00	-70.54	73.47	1.13	0.85	1.74	0.14	1.44	0.31

SPOA0342		hypothetical protein	1.39	0.75	-9.09	0.02	-3.85	5.24	3.93	0.01	-137.00	0.01	-66.54	70.47	1.22	0.73	1.88	0.28	1.55	0.33
SPOA0343		hypothetical protein	1.63	0.54	-9.67	0.01	-4.02	5.65	3.51	0.02	-179.00	0.00	-87.75	91.26	1.13	0.77	1.77	0.12	1.45	0.32
SPOA0344		LysR family transcriptional regulator	-1.31	0.44	-1.39	0.11	-1.35	0.04	-1.07	0.98	1.19	0.20	0.06	1.13	-1.45	0.02	-1.01	0.94	-1.23	0.22
SPOA0345		aldo/keto reductase	1.99	0.16	-4.87	0.01	-1.44	3.43	2.34	0.01	-158.00	0.00	-77.83	80.17	1.69	0.29	2.39	0.07	2.04	0.35
SPOA0346		carboxymuconolactone decarboxylase family protein	1.95	0.07	-5.10	0.00	-1.58	3.53	2.39	0.01	-120.00	0.00	-58.81	61.20	1.46	0.09	1.87	0.03	1.67	0.21
SPOA0347		hypothetical protein	2.60	0.04	-4.37	0.01	-0.89	3.49	3.39	0.00	-111.00	0.00	-53.81	57.20	2.27	0.06	2.29	0.01	2.28	0.01
SPOA0348		hypothetical protein	1.87	0.02	-4.78	0.00	-1.46	3.33	3.19	0.01	-8.88	0.00	-2.85	6.04	1.05	0.96	1.42	0.02	1.24	0.19
SPOA0349		hypothetical protein	-1.69	0.01	1.44	0.03	-0.13	1.57	1.37	0.07	-0.99	0.86	0.19	1.18	-1.48	0.17	-2.11	0.02	-1.80	0.32
SPOA0350		hypothetical protein	X	X	1.05	X	N/A	N/A	1.47	0.03	1.35	X	1.41	0.06	-1.40	0.20	X	X	N/A	N/A
SPOA0351		hypothetical protein	-1.96	0.61	-1.09	0.86	-1.53	0.44	-2.50	0.25	-1.22	0.62	-1.86	0.64	-1.00	0.98	1.85	0.40	0.43	1.43
SPOA0352		hypothetical protein	1.13	0.67	1.12	0.44	1.13	0.00	-1.14	0.98	1.40	0.26	0.13	1.27	1.05	0.81	-0.92	0.54	0.07	0.98
SPOA0353		aldehyde dehydrogenase	-0.98	0.51	-1.51	0.36	-1.24	0.27	-1.45	0.24	-1.09	0.88	-1.27	0.18	-1.13	0.49	1.32	0.46	0.10	1.23
SPOA0354		aminotransferase, class III	-1.32	0.09	-1.42	0.02	-1.37	0.05	-2.12	0.03	-1.12	0.65	-1.62	0.50	-1.12	0.67	1.35	0.19	0.12	1.24
SPOA0355		hypothetical protein	-1.05	0.12	-1.44	0.03	-1.25	0.19	-1.53	0.01	1.20	0.14	-0.17	1.37	1.16	0.66	-0.95	0.37	0.11	1.05
SPOA0356		hypothetical protein	-1.07	0.84	-1.21	0.17	-1.14	0.07	-1.09	0.67	-1.09	0.58	-1.09	0.00	1.22	0.15	1.36	0.03	1.29	0.07
SPOA0357		DNA-binding response regulator	-1.94	0.04	-1.43	0.41	-1.69	0.25	-1.96	0.01	1.11	0.72	-0.43	1.54	1.03	0.99	2.46	0.18	1.75	0.72
SPOA0358		sensor histidine kinase (EC:2.7.3.-)	-1.03	0.98	-1.19	0.12	-1.11	0.08	1.24	0.19	1.08	0.48	1.16	0.08	1.07	0.42	-0.91	0.21	0.08	0.99
SPOA0359		cytochrome c family protein	1.11	0.38	-1.08	0.66	0.02	1.10	-1.01	0.32	1.13	0.44	0.06	1.07	1.17	0.26	-0.92	0.20	0.12	1.05
SPOA0360		multicopper oxidase	-1.07	0.96	-1.06	0.96	-1.07	0.01	1.10	0.88	-1.09	0.95	0.01	1.10	-1.21	0.89	1.88	0.62	0.34	1.55
SPOA0361		cytochrome c family protein	1.21	0.21	-1.05	0.63	0.08	1.13	-1.30	0.44	1.22	0.17	-0.04	1.26	-1.09	0.63	-1.06	0.61	-1.08	0.02
SPOA0362		hypothetical protein	1.41	0.89	-1.12	0.89	0.15	1.27	0.97	0.98	1.16	0.77	1.07	0.09	1.25	0.28	1.40	0.43	1.33	0.08
SPOA0363		hypothetical protein	1.15	X	-1.49	0.10	-0.17	1.32	1.37	0.43	-1.06	X	0.16	1.22	1.10	0.26	1.50	X	1.30	0.20
SPOA0364		hypothetical protein	2.13	0.04	-1.62	0.01	0.26	1.88	-1.02	0.22	-1.11	0.50	-1.07	0.05	-1.24	0.08	-0.95	0.20	-1.10	0.14
SPOA0365		copper-translocating P-type ATPase (EC:3.6.3.4)	-0.94	0.77	1.01	0.85	0.04	0.97	-1.23	0.83	-1.22	0.66	-1.23	0.01	1.29	0.52	1.95	0.25	1.62	0.33
SPOA0366		amino acid permease	-1.01	0.99	-1.20	0.95	-1.11	0.10	-1.12	0.98	-1.45	X	-1.29	0.16	-1.02	0.99	2.27	X	0.63	1.65
SPOA0367		ABC transporter, permease protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0368		hypothetical protein	-1.10	0.16	-1.48	0.01	-1.29	0.19	-1.32	0.17	-1.23	0.15	-1.28	0.05	-1.21	0.53	-1.17	0.19	-1.19	0.02
SPOA0369	*copB*	copper resistance protein B	1.08	0.85	-1.37	0.22	-0.15	1.23	-2.35	0.02	1.13	0.74	-0.61	1.74	-1.40	0.14	1.81	0.23	0.21	1.61
SPOA0370	*copA*	copper resistance protein A	X	X	-1.11	0.87	N/A	N/A	-1.36	0.83	-1.10	X	-1.23	0.13	1.73	0.02	X	X	N/A	N/A
SPOA0371		hypothetical protein	1.43	0.60	1.09	0.71	1.26	0.17	1.44	0.12	1.05	0.83	1.25	0.19	1.04	0.66	-1.37	0.33	-0.17	1.21
SPOA0372		TRAP dicarboxylate transporter, DctQ subunit	-1.51	0.86	-1.10	0.96	-1.31	0.20	-2.03	0.70	1.10	0.98	-0.47	1.57	1.06	0.94	1.47	0.90	1.27	0.20
SPOA0373		TRAP dicarboxylate transporter, DctM subunit	-1.45	0.47	-1.21	0.88	-1.33	0.12	-1.67	0.43	-1.31	X	-1.49	0.18	1.53	0.45	1.43	X	1.48	0.05
SPOA0374		TRAP dicarboxylate transporter, DctP subunit	X	X	-1.57	0.46	N/A	N/A	-1.12	0.28	-1.06	0.97	-1.09	0.03	-0.96	0.79	1.02	X	0.03	0.99
SPOA0375		GntR family transcriptional regulator	1.44	0.34	1.18	0.42	1.31	0.13	-1.06	0.12	X	X	N/A	N/A	1.17	0.65	X	X	N/A	N/A
SPOA0376		epoxide hydrolase	-1.42	0.79	-1.41	0.77	-1.42	0.01	-1.61	0.83	-1.27	0.86	-1.44	0.17	-1.11	0.95	1.52	0.73	0.21	1.32
SPOA0377		aldehyde dehydrogenase	-1.64	X	1.08	0.86	-0.28	1.36	-1.12	0.90	-1.02	0.99	-1.07	0.05	1.29	0.59	2.44	X	1.87	0.58
SPOA0378		mandelate racemase	-1.17	0.76	1.12	X	-0.02	1.15	-2.19	0.16	X	X	N/A	N/A	1.15	0.50	X	X	N/A	N/A
SPOA0379		GntR family transcriptional regulator	-1.91	0.08	-1.46	0.06	-1.69	0.22	-1.55	0.25	-1.22	0.60	-1.39	0.17	-1.02	0.94	-1.23	0.67	-1.13	0.11
SPOA0380		hypothetical protein	-1.35	0.49	-1.41	0.33	-1.38	0.03	-2.65	0.13	-1.15	0.78	-1.90	0.75	-1.14	0.72	-1.09	0.86	-1.12	0.02

SPOA0381		spermidine/putrescine ABC transporter, periplasmic substrate-binding protein	-1.41	0.04	-1.74	0.02	-1.58	0.17	-2.06	0.41	-1.05	0.41	-1.56	0.50	1.29	0.08	1.22	0.24	1.26	0.04
SPOA0382		spermidine/putrescine ABC transporter, ATP-binding protein	-1.36	0.53	-1.22	0.73	-1.29	0.07	-1.86	0.48	-1.37	0.48	-1.62	0.24	1.34	0.44	1.16	0.66	1.25	0.09
SPOA0383		spermidine/putrescine ABC transporter, permease protein	-1.09	0.91	-1.06	0.92	-1.08	0.02	-1.43	0.84	-1.83	0.38	-1.63	0.20	1.40	0.50	1.44	0.57	1.42	0.02
SPOA0384		spermidine/putrescine ABC transporter, permease protein	1.00	0.98	-1.32	0.80	-0.16	1.16	1.07	0.92	-1.13	0.91	-0.03	1.10	1.17	0.88	1.34	0.79	1.26	0.09
SPOA0385		hypothetical protein	1.13	0.86	-1.27	0.53	-0.07	1.20	-1.58	0.67	-1.17	0.60	-1.38	0.21	-1.16	0.56	-1.14	0.95	-1.15	0.01
SPOA0386		GMC family oxidoreductase	1.14	0.68	-1.06	0.91	0.04	1.10	-1.26	0.96	1.14	0.58	-0.06	1.20	1.30	0.51	-1.60	X	-0.15	1.45
SPOA0387		LysR family transcriptional regulator	-1.76	0.46	-1.45	0.27	-1.61	0.16	-1.82	0.53	-1.42	0.19	-1.62	0.20	1.07	0.76	1.15	0.43	1.11	0.04
SPOA0388		acetyl-CoA synthetase	-1.15	0.82	-1.43	0.41	-1.29	0.14	-2.00	0.36	-1.37	0.08	-1.69	0.31	-1.04	0.97	2.34	0.15	0.65	1.69
SPOA0389		MerR family transcriptional regulator	-1.34	0.02	1.15	0.32	-0.10	1.25	-1.42	0.19	1.20	0.24	-0.11	1.31	1.24	0.24	-0.98	0.56	0.13	1.11
SPOA0390		phosphonate monoester hydrolase	1.50	0.11	1.00	0.98	1.25	0.25	1.60	0.02	1.07	0.87	1.34	0.27	-1.71	0.02	-1.77	0.06	-1.74	0.03
SPOA0391		cyclic nucleotide-binding protein	1.41	0.84	-1.08	0.86	0.17	1.25	1.40	0.68	-1.34	0.36	0.03	1.37	-1.06	0.90	1.40	0.49	0.17	1.23
SPOA0392		RNA polymerase sigma-70 factor	-1.02	0.55	-0.99	0.78	-1.01	0.01	-3.33	0.02	1.92	0.01	-0.71	2.63	-1.37	0.02	X	X	N/A	N/A
SPOA0393		R body protein RebB-like protein	1.56	0.16	1.17	0.58	1.37	0.20	-4.74	0.00	1.88	0.12	-1.43	3.31	-1.29	0.57	1.24	0.13	-0.03	1.27
SPOA0394		hypothetical protein	X	X	1.11	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0395		hypothetical protein	2.22	0.10	-1.00	0.98	0.61	1.61	-3.10	0.06	1.66	0.22	-0.72	2.38	-1.40	0.45	1.19	0.63	-0.11	1.30
SPOA0396		hypothetical protein	2.56	0.00	1.69	0.06	2.13	0.44	-3.46	0.00	2.11	0.02	-0.68	2.79	-1.01	0.91	-1.10	0.84	-1.06	0.05
SPOA0397		hypothetical protein	1.94	0.00	1.06	0.86	1.50	0.44	-4.71	0.00	2.36	0.05	-1.18	3.54	-1.79	0.02	-1.72	0.54	-1.76	0.04
SPOA0398		R body protein RebB-like protein	1.80	0.00	1.37	0.22	1.59	0.22	-6.80	0.00	3.18	0.02	-1.81	4.99	-1.26	0.31	-1.37	0.11	-1.32	0.06
SPOA0399		R body protein RebB-like protein	1.67	0.04	1.98	0.08	1.83	0.16	-5.36	0.00	3.19	0.02	-1.09	4.28	1.22	0.43	-1.49	0.09	-0.14	1.36
SPOA0400		endoribonuclease L-PSP	1.05	0.92	-1.10	0.72	-0.03	1.08	-2.71	0.01	1.26	0.19	-0.73	1.99	1.12	0.16	1.06	0.45	1.09	0.03
SPOA0401	*badA-2*	benzoate-coenzyme A ligase (EC:6.2.1.25)	-1.26	0.15	-2.25	0.14	-1.76	0.50	-5.13	0.00	1.13	0.65	-2.00	3.13	-1.52	0.09	-1.04	0.93	-1.28	0.24
SPOA0402		cupin	-1.19	0.31	-1.61	0.25	-1.40	0.21	-2.99	0.29	1.42	0.06	-0.79	2.21	1.19	0.34	1.46	0.06	1.33	0.14
SPOA0403		acyl-CoA dehydrogenase	1.24	0.51	-1.26	0.74	-0.01	1.25	-1.85	0.28	-1.18	0.77	-1.52	0.33	-1.02	0.97	-1.15	0.86	-1.09	0.06
SPOA0404		enoyl-CoA hydratase (EC:4.2.1.17)	1.52	0.02	1.04	0.83	1.28	0.24	-1.51	0.18	1.09	0.57	-0.21	1.30	-1.02	0.86	-1.07	0.70	-1.05	0.03
SPOA0405		MarR family transcriptional regulator	-1.67	0.40	-1.26	0.31	-1.47	0.21	-1.80	0.50	-1.01	0.84	-1.41	0.40	-1.24	0.10	1.04	0.75	-0.10	1.14
SPOA0406		D-beta-hydroxybutyrate dehydrogenase	1.07	0.34	-1.10	0.30	-0.02	1.09	-2.10	0.02	-1.42	0.02	-1.76	0.34	-1.10	0.33	-1.13	0.98	-1.12	0.01
SPOA0407		salicylyl-CoA 5-hydroxylase (EC:1.14.13.40)	1.25	0.47	-1.14	0.26	0.06	1.20	-2.13	0.03	-1.45	0.07	-1.79	0.34	-1.12	0.22	-1.01	0.54	-1.07	0.06
SPOA0408		hypothetical protein	1.43	0.22	1.26	0.27	1.35	0.09	-1.59	0.38	-1.11	0.80	-1.35	0.24	-1.01	0.99	-1.33	0.26	-1.17	0.16
SPOA0409		tryptophan 2,3-dioxygenase	1.73	0.07	1.17	0.29	1.45	0.28	-1.27	0.64	-1.10	0.11	-1.19	0.09	-1.29	0.19	-1.42	0.14	-1.36	0.06
SPOA0410		hypothetical protein	-1.76	0.00	-1.62	0.24	-1.69	0.07	0.68	0.00	1.41	0.09	1.05	0.36	0.95	0.10	1.56	0.25	1.26	0.31
SPOA0411		hypothetical protein	-1.15	0.13	1.20	0.25	0.03	1.18	-1.13	0.53	-1.49	0.19	-1.31	0.18	1.11	0.25	-0.96	0.46	0.07	1.04
SPOA0412		xanthine dehydrogenase family protein, medium subunit	2.92	0.01	1.35	0.04	2.14	0.79	2.45	0.01	1.40	0.00	1.93	0.53	1.27	0.18	1.48	0.05	1.38	0.11
SPOA0413		xanthine dehydrogenase family protein, small subunit	3.16	0.44	1.25	0.34	2.21	0.96	1.17	0.98	1.61	0.04	1.39	0.22	1.10	0.86	1.52	0.28	1.31	0.21
SPOA0414		xanthine dehydrogenase family protein, large subunit	4.06	0.01	1.85	0.05	2.96	1.11	1.37	0.31	1.47	0.18	1.42	0.05	2.11	0.04	1.92	0.14	2.02	0.10
SPOA0415		hypothetical protein	3.06	0.21	1.55	0.28	2.31	0.75	2.76	0.36	1.00	0.91	1.88	0.88	1.79	0.16	1.37	0.24	1.58	0.21
SPOA0416		hypothetical protein	1.68	0.06	1.24	0.42	1.46	0.22	-1.61	0.30	-1.08	0.57	-1.35	0.27	-1.28	0.11	-1.31	0.12	-1.30	0.02

SPOA0417		GntR family transcriptional regulator	-1.72	0.20	-1.17	0.28	-1.45	0.28	-2.35	0.21	-1.48	0.06	-1.92	0.44	-1.48	0.11	-1.70	0.04	-1.59	0.11
SPOA0418		acetolactate synthase, large subunit	-1.07	0.88	-1.15	0.45	-1.11	0.04	1.11	0.76	-1.66	0.06	-0.28	1.39	-1.15	0.36	-1.34	0.64	-1.25	0.10
SPOA0419		PhzF family phenazine biosynthesis protein	1.69	0.03	-1.55	0.03	0.07	1.62	-1.86	0.03	1.05	0.78	-0.41	1.46	-1.25	0.28	1.20	0.18	-0.03	1.23
SPOA0420		hypothetical protein	1.84	0.16	-1.52	0.05	0.16	1.68	-1.46	0.44	-1.04	0.75	-1.25	0.21	1.18	0.21	1.83	0.06	1.51	0.33
SPOA0421		pyridoxamine 5'-phosphate oxidase family protein	-1.64	0.39	-1.33	0.53	-1.49	0.16	-2.02	0.68	1.07	0.68	-0.48	1.55	-1.54	0.17	1.09	0.51	-0.23	1.32
SPOA0422		hypothetical protein	1.20	0.44	-1.30	0.25	-0.05	1.25	-1.35	0.63	-1.03	0.90	-1.19	0.16	-1.53	0.13	-1.42	0.64	-1.48	0.06
SPOA0423		TetR family transcriptional regulator	0.97	0.32	-1.24	0.30	-0.13	1.11	1.47	0.08	1.22	0.02	1.35	0.13	1.03	0.94	1.13	0.47	1.08	0.05
SPOA0424	*fabJ-2*	fatty oxidation complex, alpha subunit	1.59	0.06	-1.00	0.96	0.30	1.30	-1.71	0.04	1.40	0.17	-0.16	1.56	1.26	0.03	1.69	0.03	1.48	0.21
SPOA0425		acetyl-CoA acetyltransferase (EC:2.3.1.9)	1.51	0.72	1.07	0.82	1.29	0.22	-1.93	0.03	1.32	0.14	-0.31	1.63	1.55	0.06	2.15	0.05	1.85	0.30
SPOA0426		AraC family transcriptional regulator	1.07	0.28	-1.08	0.32	-0.01	1.08	1.64	0.05	-1.56	0.07	0.04	1.60	-1.09	0.45	-1.32	0.09	-1.21	0.12
SPOA0427		ArsR family transcriptional regulator	-1.16	0.02	-1.33	0.17	-1.25	0.09	-1.19	0.03	1.15	0.44	-0.02	1.17	1.47	0.01	1.03	0.89	1.25	0.22
SPOA0428		mandelate racemase	7.01	0.07	1.26	0.23	4.14	2.88	1.25	0.70	1.44	0.12	1.35	0.10	1.28	0.28	1.44	0.07	1.36	0.08
SPOA0429		hypothetical protein	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A	X	X	X	X	N/A	N/A
SPOA0430		zinc-binding dehydrogenase family oxidoreductase	2.33	0.01	2.83	0.01	2.58	0.25	-1.14	0.12	2.35	0.00	0.61	1.75	1.06	0.56	1.72	0.05	1.39	0.33
SPOA0431		tetracycline resistance protein	1.12	X	1.05	0.58	1.09	0.04	3.05	0.00	-1.34	0.04	0.86	2.20	-1.12	0.19	1.12	0.49	0.00	1.12
SPOA0432	*pcaB*	3-carboxy-cis,cis-muconate cycloisomerase (EC:5.5.1.2)	1.64	0.02	1.40	0.03	1.52	0.12	2.38	0.02	1.09	0.84	1.74	0.65	1.43	0.29	-1.35	0.03	0.04	1.39
SPOA0433		esterase	1.58	0.30	1.07	0.89	1.33	0.25	1.16	0.99	1.49	0.26	1.33	0.16	1.23	0.46	0.95	0.50	1.09	0.14
SPOA0434	*catD*	3-oxoadipate enol-lactone hydrolase (EC:3.1.1.24)	0.99	0.01	1.40	0.15	1.20	0.20	1.43	0.20	1.10	0.91	1.27	0.16	2.07	0.01	1.07	0.50	1.57	0.50
SPOA0435		pyridoxal-phosphate dependent enzyme	1.87	0.57	1.56	0.04	1.72	0.16	1.52	0.16	1.35	0.24	1.44	0.09	1.37	0.09	-1.01	0.96	0.18	1.19
SPOA0436		alpha/beta hydrolase	1.24	0.74	-1.15	0.11	0.05	1.20	-1.72	0.19	1.24	0.55	-0.24	1.48	-1.38	0.15	1.70	0.17	0.16	1.54
SPOA0437	*dehII*	haloacid dehalogenase (EC:3.8.1.2)	1.65	0.75	1.33	0.42	1.49	0.16	1.38	0.22	1.61	0.09	1.50	0.12	1.05	0.75	1.15	0.35	1.10	0.05
SPOA0438		peptidyl-prolyl cis-trans isomerase, FKBP-type	-2.08	0.00	-1.17	0.15	-1.63	0.46	2.08	0.04	1.73	0.02	1.91	0.18	1.10	0.10	-1.05	0.36	0.03	1.08
SPOA0439	*fabI-3*	enoyl-ACP reductase (EC:1.3.1.9)	1.55	0.13	1.43	0.31	1.49	0.06	1.21	0.39	0.99	0.53	1.10	0.11	1.50	0.02	0.99	0.36	1.25	0.26
SPOA0440	*fabB*	3-oxoacyl-ACP synthase (EC:2.3.1.41)	1.80	0.03	1.26	0.61	1.53	0.27	1.08	0.52	1.16	0.57	1.12	0.04	1.23	0.40	1.14	0.98	1.19	0.05
SPOA0441		hypothetical protein	-1.84	0.34	-1.18	0.67	-1.51	0.33	1.51	0.74	1.62	0.41	1.57	0.06	-1.13	0.82	-1.10	0.97	-1.12	0.01
SPOA0442		hypothetical protein	-1.47	0.37	-1.08	0.81	-1.28	0.20	-3.48	0.02	1.02	X	-1.23	2.25	-1.62	0.17	1.05	X	-0.29	1.34
SPOA0443		hypothetical protein	-1.39	0.03	1.12	0.38	-0.14	1.26	-1.46	0.06	1.49	0.04	0.02	1.48	1.23	0.03	1.43	0.02	1.33	0.10
SPOA0444	*fabA*	3-hydroxydecanoyl-ACP dehydratase (EC:4.2.1.60)	-1.77	0.08	1.09	0.80	-0.34	1.43	0.81	0.46	1.01	0.69	0.91	0.10	1.13	0.48	1.21	0.36	1.17	0.04
SPOA0445		FUR family transcriptional regulator	-1.73	0.03	1.19	0.08	-0.27	1.46	-1.55	0.01	1.07	0.69	-0.24	1.31	1.70	0.00	1.41	0.08	1.56	0.15
SPOA0446		LysR family transcriptional regulator	-1.03	0.99	-1.19	0.86	-1.11	0.08	1.13	0.42	-1.46	0.53	-0.17	1.30	1.04	0.75	-0.96	0.81	0.04	1.00
SPOA0447		branched-chain amino acid ABC transporter ATP-binding protein	-1.37	0.72	-1.33	0.61	-1.35	0.02	-1.81	0.67	-1.04	0.96	-1.43	0.39	-1.24	0.76	1.09	0.86	-0.08	1.17
SPOA0448	*hutG*	N-formylglutamate amidohydrolase (EC:3.5.1.68)	1.05	0.50	-1.03	0.84	0.01	1.04	-2.54	0.02	-1.31	0.30	-1.93	0.62	-1.54	0.10	-1.44	0.43	-1.49	0.05
SPOA0449		phytanoyl-CoA dioxygenase family protein	2.34	0.08	1.41	0.07	1.88	0.47	-1.18	0.87	1.10	0.53	-0.04	1.14	1.76	0.04	2.31	0.04	2.04	0.27
SPOA0450		hypothetical protein	-0.97	0.98	1.10	0.75	0.07	1.04	-1.25	0.90	1.11	0.10	-0.07	1.18	-1.15	0.31	-1.40	0.10	-1.28	0.13
SPOA0451		MarR family transcriptional regulator	-1.31	0.03	1.00	0.92	-0.16	1.16	-1.21	0.02	1.27	0.36	0.03	1.24	1.17	0.32	1.61	0.09	1.39	0.22
SPOA0452		MarR family transcriptional regulator	-1.26	0.04	-1.04	0.81	-1.15	0.11	-1.35	0.03	1.04	0.95	-0.16	1.20	1.13	0.51	1.33	0.59	1.23	0.10

Columns show the gene number (*SPO*), name (if applicable), function of the gene product (as predicted by KEGG) and fold change in expression of the gene (compared to uninduced cells) in the different co-inducers; 5 mM DMSP (Dp), 2.5 mM acrylate (A), 5 mM DMS (Ds). The fold change for each of the two duplicate arrays, for each inducer, is given, followed by the P value (P). The calculated mean is provided, along with the standard error. Up- or down-regulated gene expression values are highlighted in green or red, respectively. P values <0.05 (and thus, statistically significant) are highlighted in yellow. Due to the normalisation procedure, some genes have an "X" label in the fold-change columns, and N/A indicates where a P-value was absent following normalisation.