

HETEROGENEOUS RIBOSOMES AND BS21: AN
INVESTIGATION OF IMPACTS AND MECHANISMS
OF ALTERED TRANSLATION IN FRANCISELLA
TULARENSIS

BY
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ABSTRACT

Francisella tularensis is a pathogenic bacterium that requires coordinated regulation of gene expression to cause disease. In this dissertation, we explore a novel area of translation-level gene regulation in *F. tularensis*: heterogeneous ribosomes that preferentially translate specific mRNAs. Through mass spectrometry and immunoblotting, we find that wild-type *F. tularensis* ribosomes are heterogeneous with respect to the small ribosomal protein bS21, ^{and} ~~with~~ all three bS21 homologs ^{are} ~~able~~ to ^{be} incorporate ^d into ribosomes. Comparing proteomics and transcriptomics data, we determine that cells lacking one homolog, bS21-2, have genome-wide changes in protein abundance that are not explained by changes in transcript abundance. Among the impacted genes are key virulence factors encoding the Type VI Secretion System. We also show that cells lacking bS21-2 are defective in intramacrophage replication.

We then explore the mechanism that causes these changes in gene expression ~~by~~ ^{that} using reporter fusion assays. We determine the 5' untranslated regions (UTRs) of some genes are sufficient to drive differences in reporter protein abundance, independently of the RNA chaperone protein Hfq. While we do not find conserved structural motifs in bS21-2-responsive 5' UTRs, we identify a 6-nucleotide sequence in the 5' UTR of *mraY* that is necessary to cause differences in translation when bS21-2 is absent. We also determine that genes with perfect Shine-Dalgarno sequences do not require bS21-2 for efficient translation. Together, these findings strongly suggest that *F. tularensis*

contains heterogeneous ribosomes that differentially translate mRNA molecules with specific leader sequences, causing downstream impacts on the Type VI Secretion System and virulence.

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PREFACE

This dissertation has been prepared in manuscript format according to the guidelines of the Graduate School of the University of Rhode Island. The dissertation includes an introductory chapter, two manuscripts, and a summary chapter:

Chapter 1: Literature Review and Introduction

Chapter 2: “A ribosomal protein homolog governs gene expression and virulence in a bacterial pathogen” was published in the Journal of Bacteriology in October 2022.

Chapter 3: “Ribosome heterogeneity results in leader sequence-mediated regulation of protein synthesis in *Francisella tularensis*” was prepared for submission to the Journal of Bacteriology, 2023.

Chapter 4: Conclusions and Open Questions

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CHAPTER 1

LITERATURE REVIEW AND INTRODUCTION

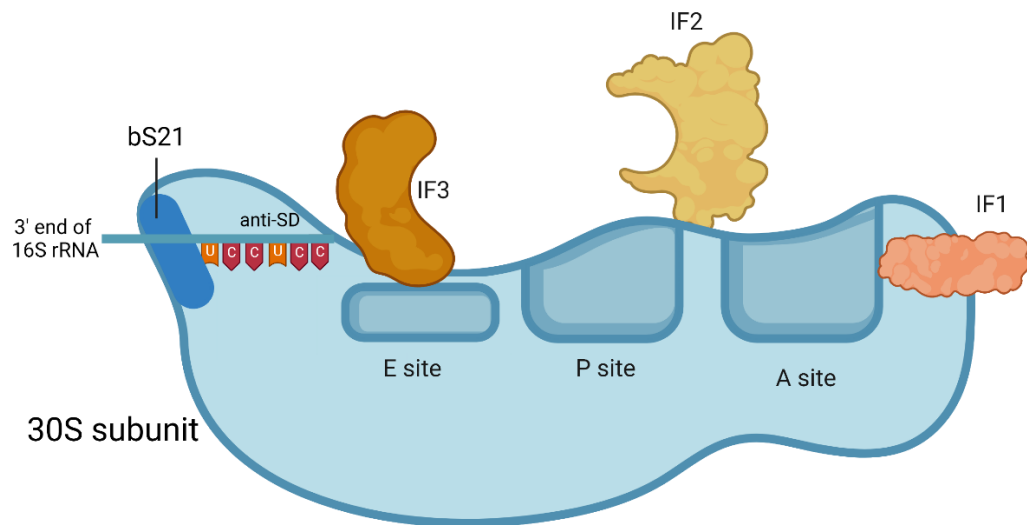
REVIEW OF THE LITERATURE

Translation initiation is a target for regulation

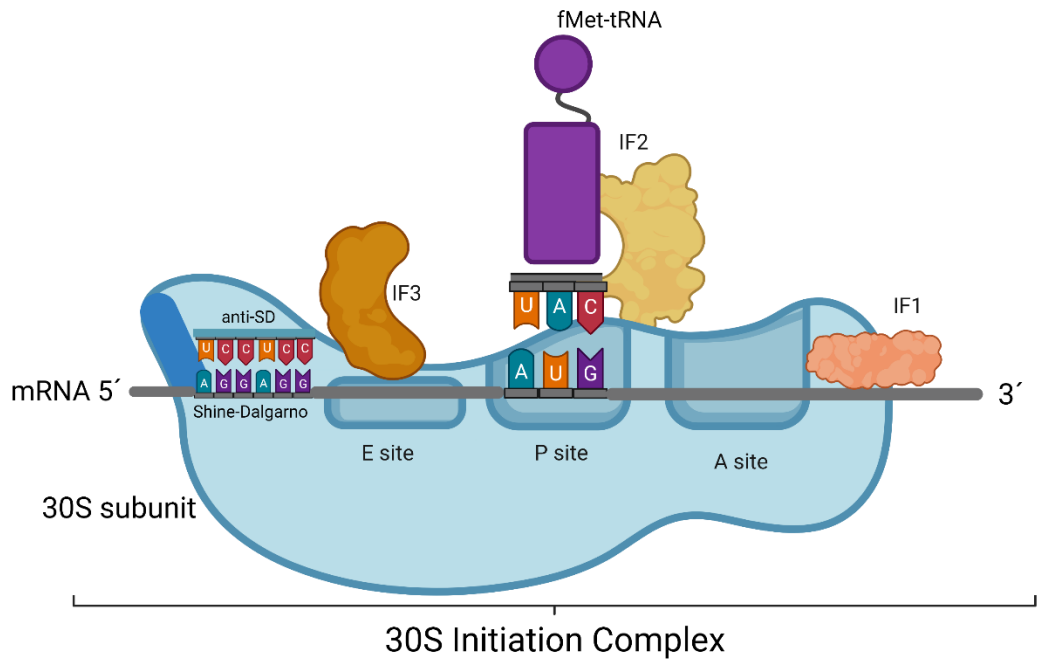
Regulation of gene expression through by modifying translation is a rapid way for bacteria to adapt to changing environmental or nutrient requirements. The ribosome is the highly conserved molecular machine that translates mRNA into protein and consists of two subunits composed of ribosomal RNAs (rRNAs) and ribosomal proteins (r-proteins). The complex process of protein synthesis is carried out through the coordinated actions of the ribosomes, tRNAs, and a number of additional factors. This process can be broken down into three major phases: translation initiation, elongation, and termination. While some regulation can occur during elongation, particularly in stress conditions (Taylor et al., 2013), initiation is the rate-limiting step of protein synthesis and the target of most regulatory mechanisms (Duval et al., 2015). As a brief overview, translation initiation begins with the formation of the 30S initiation complex, during which the Shine-Dalgarno (SD) sequence of mRNA can bind to the anti-Shine-Dalgarno (ASD) sequence of the 16S rRNA in the small ribosomal subunit (30S). The SD-ASD interaction increases the efficiency of translation initiation and assists in correctly positioning the initiation codon in the ribosome. Initiation factors help the anticodon on the initiating fMet-tRNA interact with the start codon of the mRNA in the P site. Subsequently, initiation factors are released and the large ribosomal subunit (50S) joins to form the 70S initiation

complex (Figure 1). The elongation phase can then begin (Laursen et al., 2005; Gualerzi & Pon, 2015; Milón & Rodnina, 2012). There are a number of mechanisms by which gene expression may be regulated at the level of translation initiation, including variations in recruitment of mRNA to the ribosome and factors that affect assembly of the translation initiation complex (Milón & Rodnina, 2012).

A



B



C

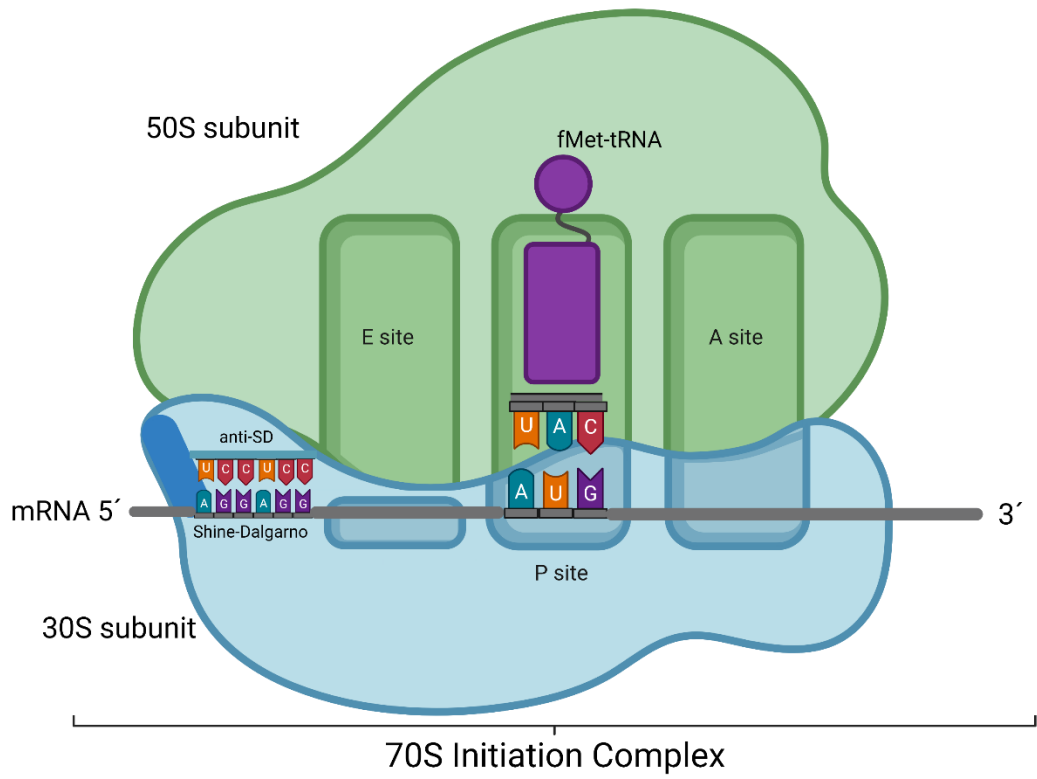


Figure 1: Translation initiation in bacteria. **A.** Start of translation initiation. Small ribosomal subunit (30S) of the ribosome with initiation factors (IF1, IF2, IF3). Key components of the 30S subunit including the anti-Shine-Dalgarno (anti-SD) and bS21 protein are indicated. **B.** 30S initiation complex. The Shine-Dalgarno sequence of the mRNA interacts with the anti-SD, facilitating binding between the start codon and the initiator tRNA in the P site. **C.** 70S initiation complex. Initiation factors are released and the large (50S) ribosomal subunit loads onto the 30S to create the 70S initiation complex, commencing the transition to elongation. Image generated on Biorender.com.

The Shine-Dalgarno sequence plays an important role in the initiation of translation in many bacterial species. In particular, the SD-ASD interaction anchors the mRNA onto the 30S subunit of the ribosome (Korostelev et al., 2007; Yusupova et al., 2006). Better complementarity between the SD and ASD improves ribosome occupancy on an mRNA and translation efficiency (Vellanworth & Rabinowitz, 1992; Saito et al., 2020). Some mRNAs, however, have weak Shine-Dalgarno sequences, lack SDs, or are completely without 5' UTRs (known as leaderless mRNAs). Indeed, in some species the majority of mRNAs have no SD sequence (e.g. *Bacteroidia*; Jha et al., 2020; McNutt et al., 2023; Wen et al., 2020), requiring other mechanisms for translation initiation. The ribosomal protein bS1 can assist with docking of mRNAs on the 30S ribosome in the absence of SD-ASD interactions, as in the case of the *thrS* mRNA in *E. coli* (Kolb et al., 1977; Duval et al., 2013). Leaderless mRNAs can be directly bound by 70S ribosomes, removing the need for formation of a 30S initiation complex (Leiva & Katz, 2022). Additionally, nucleoid protein H-NS can bind to AU-rich regions on mRNAs with weak SDs, repositioning 30S subunits and stimulating translation in *E. coli* (Park et al., 2010). Other mechanisms that

promote translation initiation in mRNAs with weak SDs likely exist (i.e. bS1 is nonessential in some species; H-NS is not present in some species), so further research in a greater variety of species is needed.

mRNAs can form a multitude of secondary structure motifs that impact formation of the initiation complex. In many bacterial mRNAs, the Shine-Dalgarno and initiating codon are in unstructured regions (Chiaruttini & Guillier, 2020); in other mRNAs, unfolding of 5' UTR secondary structures is necessary to allow access of the ribosome to the Shine-Dalgarno and/or initiating codon (Gualerzi & Pon, 2015). For instance, in *Bacillus subtilis*, the Shine-Dalgarno for *sigG* is entrapped in a hairpin loop which ensures translation is low during early spore formation; this is critical as the tightly-controlled switch from *sigF* to *sigG* expression leads to global changes in gene expression that progress spore development from early- to late-stages (Mearls et al., 2018). In mRNAs that have secondary structures blocking translation initiation, secondary sites known as standby sites may allow ribosomes to dock on the mRNA until the SD or start codon is accessible (de Smit & van Duin, 2003). The unfolding of secondary structures may be accomplished by small RNAs, RNA binding proteins, the ribosomal protein bS1, or small molecules, all of which can be limiting or abundant based on environmental signals (Meyer, 2017; Duval et al., 2013). Thus, mRNA structures can impact the efficiency of translation initiation and provide a mechanism to regulate gene expression.

Small RNAs (sRNAs) can contribute to gene regulation post-transcriptionally, frequently by binding complementary mRNAs to prevent or

promote translation (Harris et al., 2013). Often sRNAs require the RNA chaperone, Hfq, to facilitate interactions with target sequences. Hfq can play a significant role in mRNA and sRNA degradation by recruiting RNases and Hfq can directly impact translation initiation (Vogel & Luisi, 2011). Hfq-sRNA complexes can bind to the RBS on certain mRNAs to prevent 30S docking, as when Hfq mediates the interaction between the sRNA RhyB and the *sodB* mRNA in *E. coli* (Geissmann & Touati, 2004). Alternatively, Hfq-sRNA interactions with the mRNA can resolve secondary structures that block access to the SD, thereby promoting translation initiation, as in the case of the sRNA DsrA and the *rpoS* mRNA in *E. coli* (Soper & Woodson, 2008). The complex role of Hfq and small RNAs in translation regulation is worthy of continued investigation. In addition to these well described mechanisms, the ribosome itself may play a role in regulating gene expression.

Ribosomes may be heterogenous in structure and function

The ribosome, which translates mRNA into protein and is highly conserved in all domains of life, consists of three ribosomal RNAs (rRNAs) and around 50 ribosomal proteins (r-proteins). Typically, the ribosome is viewed as acting constitutively and without variability, translating every mRNA with equal efficiency. However, heterogeneity in ribosomes exists and arises via a number of mechanisms. These include diversity in rRNA sequences, r-proteins encoded by distinct homologs within the same cell, post-transcriptional modification of rRNA, and post-translational modification of r-proteins (Byrgazov et al., 2013; Sauert et al., 2015). The presence of these physical differences raises the possibility that heterogeneous ribosomes within the same organism have

functional differences. The term “specialized ribosomes” describes structurally diverse ribosomes that have altered activity (Xue & Barna, 2012). It should be noted that the concept of ribosomes with specialized functions has faced controversy due to conflicting results and claims that are insufficiently supported by the data. However, ribosome diversity is well documented and the scientific community agrees that thoughtful research into this field is warranted (Barna et al., 2022; Ferretti & Carbststein, 2019; Genuth & Barna, 2018). A recent publication, described further below, provides straightforward and compelling evidence for specialized ribosomes in some bacteria.

In the context of eukaryotic organisms, a significant number of studies focused on specialized ribosomes (reviewed in Xue & Barna, 2012). For example, in multiple species of the parasitic pathogen that causes malaria, *Plasmodium*, rRNA usage correlates to stages of the parasitic life-cycle and the distinct rRNAs have functional differences (Gunderson et al., 1987; Velichutina et al., 1998). When the parasite is growing in mosquitoes, one 18S rRNA is expressed (termed “S-type”), and when in mammals, a different 18S rRNA is expressed (termed “A-type”). When either A- or S-type *Plasmodium berghei* rRNAs were introduced to the yeast genome in the absence of native 18S rRNA, only cells with pure populations of A-type rRNA could be recovered. The inability for S-type rRNA cells to grow suggests that the two rRNAs have different functions (Velichutina et al., 1998). Similarly, in *P. falciparum*, A-type and S-type rRNAs show differential expression with changes in temperature (Fang & McCuthen, 2002). This raises the possibility not only that ribosomes are

heterogeneous in *Plasmodium* species, but that the expression of distinct rRNAs may be an adaption to the life-cycle requirements of the parasite.

In bacteria, recent studies have identified heterogeneous ribosomes may have functional differences, though there has been some controversy in the experimental approaches, as in the case of toxin-induced mutants of *Escherichia coli* (Vesper et al., 2011; Culviner & Laub, 2018). These studies took advantage of *E. coli* cells with induced expression of an endoribonuclease toxin called MazF. Initial studies suggested that the MazF toxin cleaves rRNA at sequence-specific sites and creates subsets of ribosomes lacking the anti-Shine-Dalgarno sequences in the 16S rRNA (Vesper et al., 2011). These studies led to a model proposing that the modified ribosomes consequently recognize leaderless mRNAs, also generated by MazF cleavage, which is supported by pulse labeling results *in vivo* and *in vitro* showing preferential translation of leaderless mRNA when MazF is active. These studies suggested that a class of ribosomes lacking the anti-Shine-Dalgarno sequences differentially translates subsets of mRNA to adapt to stress. However, a follow-up study published conflicting results, specifically finding that the 16S rRNAs lacking the anti-Shine-Dalgarno sequence were cleaved at additional sites and usually were not incorporated into mature ribosomes (Culviner & Laub, 2018). Additionally, MazF activity led to such substantial RNA cleavage throughout the cell such that very few full-length leaderless mRNA transcripts were present. This suggests that the “specialized” ribosomes are not controlling translation or gene regulation but instead that MazF activation results in major disruptions to

ribosome biogenesis and overall cell growth (Culviner & Laub, 2018). Given these conflicting results, additional studies would be necessary prior to citing toxin-induced ribosomes as bona fide specialized ribosomes.

A system in which ribosome heterogeneity is genetically-encoded, rather than the result of post-~~translational~~^{transcriptional} modifications, may provide more clarity in describing specialized ribosomes. In *Mycobacterium tuberculosis*, at least five ribosomal proteins have two paralogs. For each of these paralogs, one has a zinc-binding domain (the canonical paralog) and one does not (the alternative paralog). To elucidate differences in r-protein paralog functions, Prisic et al. (2015) focused on the two genes encoding the small subunit r-protein bS18. In high zinc conditions, expression of the alternative bS18 is repressed by a zinc uptake regulator (Zur), leading to a population of ribosomes with mostly the canonical bS18 present. In low-zinc conditions, repression of the alternative bS18 protein does not occur, leading to ribosomes with both canonical and alternative bS18 proteins, creating a more heterogeneous ribosome population (Prisic et al., 2015). The functional consequences of the distinct ribosome classes were analyzed in *M. smegmatis* using ribosome profiling of tagged-bS18 paralogs (Chen et al., 2020). While ribosomes with alternative r-proteins and canonical r-proteins were both able to partake in protein synthesis, the two subsets of ribosomes had distinct translational profiles with different efficiencies in translation of particular genes (Chen et al., 2020).

These experiments suggest a specific condition under which homologous r-proteins might regulate translation, specifically to adapt to zinc-

limiting conditions. Heterogeneous ribosomes in other species may be utilized to adapt to changes in other environmental conditions or metabolic requirements. However, the existence of five r-proteins with alternative paralogs complicated the interpretation of results in *Mycobacterium* – many combinations of the five canonical or alternative r-proteins could coexist within the same cell so it was not clear which “alternative” ribosomes were driving changes in translation. Hence, a simplified system with only one r-protein with multiple homologs may prove advantageous.

bS21 may play a regulatory role in translation

bS21 is a small ribosomal protein (~8 kDa) incorporated into the small subunit of many bacterial ribosomes. Early research investigating r-protein function identified that bS21 plays a role in *E. coli* translation initiation, ^{although} despite the fact that it is not encoded by all bacterial species. Using RNA from the bacteriophage MS2, a commonly used RNA substrate for studying translation, it was discovered that ribosomes lacking bS21 are fully functional in fMet-tRNA binding, can bind and translate synthesized poly(U) mRNA, but are unable to bind MS2 RNA. These results suggest that bS21 is necessary to mediate the interaction between the ribosome and some mRNA molecules during translation initiation (van Duin & Wijnands, 1981). In further support of this role, chemically damaged ribosomes that had lost their ability to bind bacteriophage RNA regained binding capabilities when four untreated purified r-proteins (bS1, uS12, uS13, and bS21) were added, with addition of bS21 alone providing significant recovery of activity (Chang & Craven, 1977).

Much of the work elucidating bacterial ribosome structures has been performed in *Thermus thermophilus*, a species that does not encode bS21, so less is known about the structural interactions of bS21 in the context of the bacterial ribosome compared with other r-proteins. However, crystallographic and cryogenic electron microscopy data of *E. coli* ribosomes shows that bS21 is found in the platform region of the 30S subunit, interacting with the central domain of the 16S rRNA, close to the exit channel of mRNA (Figure 2A) (Berk et al., 2006; Watson et al., 2020). In fact, there are direct interactions predicted between the anti-Shine-Dalgarno of the 16S rRNA and bS21 in both the *E. coli* (Figure 2B) and *Flavobacterium johnsoniae* ribosomes, bolstering support for a role of bS21 in translation initiation (Kaledhonkar et al., 2019; Jha et al., 2020). However, the observed bS21-ASD interactions in *E. coli* and *F. johnsoniae* are not alike, so the mechanism by which bS21 functions in different species is not likely to be conserved.

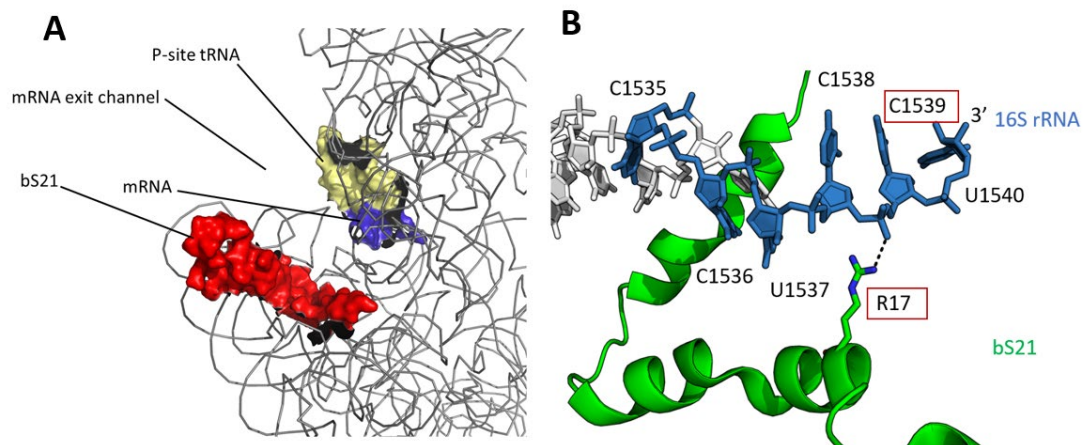


Figure 2: bS21 is proximal to anti-Shine-Dalgarno and mRNA channel in the *E. coli* ribosome. (A) Partial 30S subunit of *E. coli* ribosome as determined by cryogenic electron microscopy (cryoEM) showing bS21 location relative to mRNA. Red = bS21; blue = mRNA; grey = 16S rRNA and other 30S ribosomal

proteins. PDB entry 4V50 (Berk et al., 2006). **(B)** Predicted hydrogen bond interaction between R17 of bS21 and C1539 of 16S rRNA in *E. coli* ribosome. Blue = anti-Shine-Dalgarno; white = other 16S rRNA residues; green = bS21. PDB entry 6O7K (Kaledhonkar et al., 2019). Image courtesy of Dr. Steven Gregory.

In several species where the gene that encodes bS21, *rpsU*, has been mutagenized, distinct phenotypes have been observed. In *Bacillus subtilis*, bS21 mutants have defects in motility and biofilm formation (Takada et al., 2014) and in *Listeria monocytogenes*, null mutants have increased acid stress resistance and changes in transcription of stress resistance genes (Metselaar et al., 2015). In *Staphylococcus aureus*, some clinical isolates with mutations in *rpsU* have increased resistance to daptomycin and vancomycin (Basco et al., 2019; Blake & O'Neill, 2013; Friedman et al., 2006). In *Burkholderia pseudomallei*, bS21 was identified as a potential virulence factor during a transposon-sequencing (Tn-seq) mutagenesis screen in a mouse lung infections model (Gutierrez et al., 2015); similarly, in *Francisella tularensis*, one of the bS21-encoding genes, *rpsU1*, was flagged as a virulence gene in a transposon mutagenesis screen using a mouse infection model (Su et al., 2007). These data support the idea that in organisms which encode bS21, it may play a role in regulation of specific processes.

Recent research in the Bacteroidia species *Flavobacterium johnsoniae* shows clearly that incorporation of bS21 into the ribosome changes translation initiation for specific transcripts, unambiguously demonstrating that bS21 functions as a regulator of gene expression. The recently solved ribosome structure revealed interactions between the anti-Shine-Dalgarno (ASD) of the

16S rRNA, bS21, bS6 and bS18 (Jha et al., 2020) that result in sequestration of the ASD. This provides a rationale for why most genes in *F. johnsoniae* do not have Shine-Dalgarno sequences – transcripts cannot interact with the ASD because of the sequestration by r-proteins. Loss of bS21 results in increased translation from the *rpsU* mRNA, which has an extended Shine-Dalgarno, ~~along with other mRNA species containing strong SDs~~ (McNutt et al., 2023). Thus bS21 autoregulates its own protein production ~~and impacts the expression of other genes~~ through direct binding interactions with the ribosome (Jha et al., 2020; McNutt et al., 2023). This mechanism may differ in other classes of bacteria, in part because the interactions between bS21 and the ASD in *F. johnsoniae* that lead to sequestration of the ASD is in the C-terminal region of bS21, which is variable and lineage-specific. In particular, bS21 homologs in ~~G~~ammaproteobacteria have not been found to, and are not expected to, sequester the ASD. Indeed, many species including our model organism, *Francisella tularensis*, have many mRNAs with strong SDs.

Notably, a large number of *rpsU* homologs have been found in bacteriophage genomes. Over 1,300 bS21 homologs were found in viral genomes, infecting a wide range of bacterial clades (Al-Shayeb et al., 2020; Mizuno et al., 2019). Metatranscriptomic analyses identified bS21 transcripts associated with late stages of viral replication (Chen et al., 2022). At least one bS21 homolog was found to be encoded by a cultivated pelagiphage, *Pelagibacter* phage HTVC008M, and the purified viral bS21 protein was able to be incorporated into *E. coli* ribosomes (Mizuno et al., 2019). This is likely

Unless I'm mis-remembering, the only other strong SDs tested were introduced. This makes it sound like there are other native mRNAs w/ strong SDs - but an interesting point is it's really only *rpsU*! I think easier not to get into it.

possible because bS21 is one of the last-assembled r-proteins and is easily exchanged in *E. coli* (Mizushima & Nomura, 1970). Together, these findings raise the possibility that viruses may be utilizing bS21 to influence gene expression in host cells to increase viral replication.

While many bacteria genomes contain only one bS21 protein, some bacterial species, such as *Crocospaera watsonii*, *Nostoc punctiforme*, *Francisella tularensis* and *Burkholderia pseudomallei*, encode multiple homologs of bS21. The *Francisella tularensis* genome contains three homologs (*rpsU1*, *rpsU2*, and *rpsU3*, encoding bS21-1, bS21-2, and bS21-3, respectively), which is especially noteworthy given the significantly reduced genome of *F. tularensis* (~1.8 Mbp). *F. tularensis* is an ideal organism to study the role of bS21 homologs in ribosome heterogeneity as the genome does not encode multiple homologs of other r-proteins and all the rRNA operons are identical.

***Francisella tularensis* is an intracellular human pathogen**

F. tularensis is a highly infectious, Gram-negative, facultative intracellular bacterium that causes the human disease tularemia (Sjostedt, 2007). Infection of humans can occur through respiration, insect bites, and ingestion of contaminated food or water (McLendon et al., 2006). With a low infectious dose (as few as 10 organisms are able to cause the disease) and the potential to be fatal, *F. tularensis* is considered a bioweapon (Dennis et al., 2001). There is variability in pathogenicity within *Francisella* species: *F. tularensis* subspecies *holarctica* and *tularensis* are strains well described to cause human infection, while *Francisella novicida* is rarely associated with human disease (Kingry & Peterson, 2014).

There are multiple *F. tularensis* strains used in laboratory settings, with different advantages. Most commonly used are *F. tularensis* subsp. *holarctica* LVS (live vaccine strain), *F. tularensis* subsp. *tularensis* Schu S4, and *F. novicida* U112. Genome data has been available since 2005 for *Francisella tularensis* (Larsson et al., 2005), and all three of these strains retain more than 97% identity at the nucleotide level (Larsson et al., 2009). Schu S4 is an excellent model because it is highly virulent in humans and only 1 organism is sufficient to cause lethality in mice (Bell et al., 1955). Consequently, however, Schu S4 requires study within BSL-3 laboratories.

F. novicida U112 includes only a single copy of the Francisella Pathogenicity Island, the set of genes encoding the key virulence factor, the type VI secretion system (described in more detail below), while *F. tularensis* subspecies encode two identical copies (Nano et al., 2004). This makes *F. novicida* the preferred model for mutagenic studies of the FPI. Despite the fact that U112 retains pathogenicity in mouse models at a higher infectious dose, it is not a human pathogen and thus has limitations in its application to understanding human disease (Kingry & Peterson, 2014).

Our lab utilizes *F. tularensis* subsp. *holarctica* live vaccine strain, which was attenuated in Russian laboratories and is nonpathogenic to humans. This allows research to be conducted in BSL-2 laboratories with minimal risk to researchers. Yet, LVS can infect macrophage cells and cause pathogenicity in mouse models, allowing research on virulence to be conducted in this strain (Bell et al., 1955; Kingry & Peterson, 2014). LVS differs genetically from closely

related virulent strains by only 0.08% of nucleotide sequences (Rohmer et al., 2006). While 35 protein-coding regions are altered in LVS compared to its closest relative, many of which are SNPs (Rohmer et al., 2006), experimentally validated mutations that cause attenuation are an alteration in the type IV pili (Forslund et al., 2006) and fusion of two genes called *fupA/B* which facilitate iron transport across the outer membrane (Ramakrishnan & Sen, 2014). LVS is thus an ideal candidate to work with in a laboratory setting, as there is no risk of human infection, it can be used in animal infection models, and it is genetically very similar to the highly pathogenic strains.

Gene regulation is incompletely understood in *F. tularensis*

F. tularensis is able to survive in a wide variety of hosts and vectors, including ticks, flies, rabbits, rodents, and humans, as well as in soil and aquatic environments (Sjostedt, 2007). Thus, there must be regulation of gene expression to adapt to changing environments. In many bacteria, key regulators of gene expression in response to extracellular cues are two-component systems. In these systems, a membrane-bound sensor kinase relays environmental cues via phosphorylation to a DNA-binding response regulator, which then acts as a transcription factor to change expression of certain genes (Stock et al., 2000). Typically, the response regulator and sensor kinase are transcribed together in an operon; when the two genes are separated, they are referred to as “orphans” (Stock et al., 2000). In LVS, there is only one known response regulator, PmrA, and one orphan sensor kinase, QseC (described in more detail below) (Spidlova et al., 2020; Dai et al., 2011). In comparison, *E. coli* contains at least 30 two-component systems (Stock et al., 2000).

Essential for transcription, RNA polymerase sigma factors permit binding of RNA polymerase to specific promoters and coordinately regulate gene expression. In *F. tularensis*, there are only two sigma factors: σ^{70} (RpoD), which is the housekeeping sigma-factor, and σ^{32} (RpoH), which is a heat-stress alternative sigma factor that positively regulates heat-shock response genes (Grall et al., 2009). There are no homologs of RpoN, RpoS, RpoE, or other well-described sigma factors identified in *F. tularensis*. ^{no higher}

Several well-conserved transcription factors, some of which respond to environmental conditions, have been described in *F. tularensis* (Spidlova et al., 2020; Dai et al., 2011). Fur (ferric uptake regulator) is a DNA-binding protein that primarily represses transcription ^{when} ~~by~~ coordinating ferrous ions (Escolar et al., 1999). In *F. tularensis*, Fur binds promoters called Fur boxes to regulate iron homeostasis, in part through siderophore synthesis ^{regulating} (Pérard et al., 2018; Deng et al., 2006). IclR is a transcriptional regulator that impacts expression of at least 17 genes in LVS, but does not lead to attenuated virulence (Mortensen et al., 2010). OxyR is an oxidative response regulator that has widespread impacts on gene expression in *F. tularensis* (128 proteins impacted by *oxyR* deletion) and protects cells from exposure to peroxide and superoxide radicals (Ma et al., 2016). Both Fur and OxyR are implicated in virulence, with cells displaying deficient survival in macrophage and mouse models if these transcription factors are lost; in *oxyR* mutants, the loss of virulence was attributed to LVS being unable to escape the host phagosome (Pérard et al., 2018, Ma et al., 2016). Beyond these transcription factors, a significant amount of *F. tularensis*

gene regulation research has focused on transcription factors that control expression of a key virulence factor, the Francisella Pathogenicity Island (FPI), which encodes the Type VI secretion system (T6SS; discussed further below).

Regulated production of the *F. tularensis* type VI secretion system is necessary for virulence

While capable of replicating in a wide variety of cell types, *F. tularensis* must be able to replicate in macrophage to cause disease (Nano et al., 2004). *F. tularensis* cells use a subclass II Type VI secretion system (T6SS), distinct from other bacterial T6SSs, to escape the host phagosome and replicate in host macrophage cells (Barker et al., 2009; Clemens et al., 2018). Present in nearly a quarter of Gram-negative species, the T6SS is a contractile nanomachine, similar in structure to a phage, which anchors to the membrane and functions by injecting effector molecules into target cells (Cherrak et al., 2019). In *F. tularensis* LVS, the T6SS is encoded on the Francisella Pathogenicity Island (FPI), a set of 16 genes encoded in two operons, the *pdpA* operon and the *igla* operon. The entire FPI (both operons) is duplicated in the *F. tularensis* genome (Nano & Schmerk, 2007). Most of the FPI genes are essential for virulence in animals and growth in macrophages, with the exception of PdpC and PdpD which are essential in animals but not in macrophages, and PdpE, which is essential in neither animals nor macrophages (Clemens et al., 2018). Significant research has been performed to understand how transcription of the FPI operons are regulated.

MglA, SspA, PigR, and ppGpp

The FPI is known to be controlled at the level of transcription by the coordinate action of several factors, including MglA, SspA, PigR, and the small molecules guanosine pentaphosphate (pppGpp) and guanosine tetraphosphate (ppGpp) (referred to here as [p]ppGpp) (Brotcke et al., 2006; Brotcke & Monack, 2008; Charity et al., 2007; Ramsey et al., 2015; Rohlfing et al., 2018; Cuthbert et al., 2017). Specifically, MglA and SspA are transcription factors that are always associated with *F. tularensis* RNA polymerase (RNAP) at promoters and influence transcription of hundreds of genes, including the FPI (Brotcke et al., 2006; Brotcke & Monack, 2008; Charity et al., 2007; Ramsey et al., 2015; Travis et al., 2021). The small molecule (p)ppGpp, which is often produced during nutrient starvation or under stress conditions, is required for another transcription factor, PigR, to interact with the MglA-SspA complex (Charity et al., 2009; Cuthbert et al., 2017; Travis et al., 2021). When PigR interacts with the MglA-SspA-RNAP complex, it is thought to recognize a specific sequence called the PigR responsive element (PRE) in promoters of regulated genes (Ramsey et al., 2015; Travis et al., 2021). This stabilizes the interaction between the DNA and RNA polymerase to promote transcription of PigR-regulated genes (Ramsey et al., 2015; Rohlfing & Dove, 2014; Travis et al., 2021). All four of these factors – MglA, SspA, PigR, and (p)ppGpp – have been shown to positively control transcription of the FPI, are necessary for intramacrophage growth, and are important for survival in mice (Charity et al., 2007; Charity et al., 2009; Ramsey et al., 2015; Lauriano et al., 2004; Travis et al., 2021).

PmrA and QseC

PmrA is a response regulator in all *Francisella* species (Mohapatra et al., 2007; Sammons-Jackson et al., 2008). In both *F. tularensis* LVS and *F. novicida*, *PmrA* is important for intramacrophage replication. The mechanism by which *PmrA* promotes intramacrophage growth is somewhat controversial. An initial model proposed that *PmrA* positively regulates FPI genes, which is why its loss would result in lack of intramacrophage replication (Mohapatra et al., 2007; Sammons-Jackson et al., 2008). In support of this model, it was found that *PmrA* can bind directly to the *pdpD* promoter and the *pmrA* promoter *in vitro*, suggesting direct regulation of the FPI (Bell et al., 2010). In contrast, a ChIP-Seq analysis in LVS found no association of *PmrA* at *pdpA* and *igIA* FPI promoters *in vivo* (there is no *pdpD* promoter in LVS), and transcriptomics did not identify FPI genes impacted by *PmrA* (Ramsey & Dove, 2016). Instead, they identified *PmrA* directly represses expression of *prim*. Intramacrophage assays indicated that the intramacrophage growth defect in *pmrA* mutant cells is due to production of PriM, so an alternate model was proposed: *PmrA* functions to regulate virulence by repressing the anti-virulence factor PriM (Ramsey & Dove, 2016). Several lines of evidence indicated that PriM functions as an anti-virulence factor, among them the finding that a *pmrA/prim* double mutant had restored growth in macrophage. While a subsequent study did not replicate the *pmrA/prim* double mutant phenotype, it did confirm that cells lacking *PmrA* do not have altered FPI transcript abundance (Hoang et al., 2020). Since multiple studies rule out *PmrA* regulation of the FPI, the mechanism by which *PmrA* promotes intramacrophage growth has not been entirely resolved.

Further difficulty occurs in trying to identify the sensor kinase associated with PmrA. PmrA is phosphorylated at residue D51, which improves association of the regulator to DNA in *F. novicida* and impacts downstream gene expression in *F. tularensis* LVS (Bell et al., 2010; Hoang et al., 2020). It was reported that KdpD phosphorylates PmrA in *F. novicida*, but *F. tularensis* LVS does not have an intact *kdpD* gene and phosphorylation of PmrA in *F. tularensis* LVS by any sensor kinase has not been documented (Bell et al., 2010; Hoang et al., 2020). There is evidence of increased *prim* expression after inactivation of QseC, the only known sensor kinase in *F. tularensis* LVS, which suggests that loss of QseC ~~leads to less~~ *reduces the* PmrA-mediated repression of *prim* (Hoang et al., 2020). QseC has also been shown to play a role in virulence in *F. novicida* (Weiss et al., 2007). More work is required to definitively link PmrA to QseC (or any sensor kinase) and clarify the mechanism of PmrA regulation of intramacrophage growth.

Hfq and sRNAs

Hfq is an RNA chaperone that impacts mRNA stability and translation initiation, often in conjunction with sRNAs. In *F. tularensis*, multiple studies have looked at the impact of Hfq on expression of the T6SS with conflicting results. In one study, when *hfq* was deleted, *F. tularensis* LVS had increased transcript abundance of genes encoded on the *pdpA* operon but not those encoded on the *iglA* operon (Meibom et al., 2009). A study of the *F. tularensis* LVS proteome found that IglA, IglB, IglC, and IglH are less abundant when Hfq is absent (Lenco et al., 2014). This inconsistency may be due to differences in methodology or

may suggest post-transcriptional regulation – the study observing the protein-level differences may not detect transcript-level differences if there is another layer of regulation. Additionally, in *F. novicida*, loss of *hfq* led to decreased transcript abundance of *pdpA* and *pdpB* (Chambers & Bender, 2011), which conflicts with the previous study in LVS (Meibom et al., 2009). The differing results between *F. tularensis* and *F. novicida* may suggest species-specific differences in the Hfq regulon. Regardless of the specific impact on FPI genes, Hfq plays an important role in stress response in *F. novicida* and in virulence in mouse infection assays for *F. tularensis* clinical isolates (Chambers & Bender, 2011; Meibom et al., 2009).

As Hfq often works coordinately with sRNAs, it is worth pointing out that very few sRNAs have been identified in *F. tularensis*. In addition to identification of well-known sRNAs (4.5S rRNA, tmRNA), researchers found two novel sRNAs, referred to as FtrA and FtrB, which impact the transcript abundance of several genes (Postic et al., 2010). However, none of the impacted genes are on the FPI, and FtrA and FtrB do not play an important role in virulence (Postic et al., 2010). A distinct sRNA, FtrC, impacts transcript abundance of the hypothetical protein FTL_1293 independently of Hfq. Overexpression of FtrC does impact intramacrophage growth and infection in mice, though the mechanism is not understood (Postic et al., 2012). Hfq and sRNAs undoubtedly merit further research to uncover the specific role they play in regulating gene expression and virulence, particularly given the conflicting Hfq results and scarcity of sRNAs identified.

HU

HU (histone-like protein U) is a highly conserved bacterial protein that functions similarly to a eukaryotic histone by binding DNA in a sequence-independent manner and altering its structure to affect gene expression and DNA replication (Pettijohn, 1988; Verma et al., 2023). In *F. tularensis*, the genes that encodes HU, *hupB*, is essential for replication in macrophage and pathogenicity in mouse models (Stojkova et al., 2018). The FPI genes and *pigR* were found to both less abundant in the *hupB* mutant at the transcript and protein level, although the mechanism by which HU positively regulates their expression is not clear (Stojkova et al., 2018).

OsrR

A recently described transcriptional regulator called OsrR appears to play a role in regulating gene expression in response to oxidative stress. OsrR not only regulates the oxidative response, but leads to global changes in transcription and virulence. In cells lacking OsrR, transcripts of *pdpE* and *iglJ* are decreased significantly upon exposure to the superoxide-generating compound menadione, which causes oxidative stress. Further, the *osrR* deletion mutant leads to decreases in intramacrophage growth and pathogenicity in mice (Marghani et al., 2021).

While *F. tularensis* survives in diverse environments and requires coordinated regulation of the T6SS to replicate in macrophages and infect hosts, there is limited knowledge of regulatory networks in this bacterium. The regulation of FPI transcription is well-studied and there are a few recent advances in identifying novel virulence factors that regulate transcription (OsrR

and HU). However, there has been limited research into post-transcriptional regulation of virulence genes in this pathogen, an area of pursuit that may help to increase our understanding of *Francisella* gene regulation as a whole.

***F. tularensis* encodes three distinct bS21 homologs, suggesting ribosome heterogeneity**

The presence of three homologs of the gene encoding bS21, *rpsU*, in *F. tularensis*, led us to hypothesize that each of these genes encode distinct bS21 proteins that can incorporate into ribosomes, generating heterogeneous ribosomes. Prior to investigating this empirically, we compared the predicted protein sequences. An amino acid alignment of the three bS21 homologs, along with the single *E. coli* bS21 homolog, was generated using ClustalOmega multiple sequencing alignment tool (Figure 3A). While some amino acids are highly conserved, the *F. tularensis* homologs are distinct from each other and *E. coli*, with percent identities from 48-72% to each other and 51-60% to *E. coli* (Chapter 2, Figure S2).

→ **Fig 3 here?**

Structures of the F. tularensis bS21 homologs have not been determined

While structures of the *F. tularensis* ribosomes and bS21 homologs have not yet been determined through crystallography or cryogenic electron microscopy, three dimensional structural predictions can be made using the software AlphaFold. All three of the predicted structures for bS21 homologs appear identical (Figure 3B); however, these predictions do not consider the complexities and steric interactions that exist in the ribosome quaternary structure. To better understand where the regions of variability exist in the

A.

F. johnsoniae

E. coli MFVIRKRENEFFDVALRRFR
(F. johnsoniae) MLIIPIKDGENIDRALKRYKI
* : : : * : * : *

abbrviate
& indicate
in
legend
to prevent
new line issue

B.

B.



C.

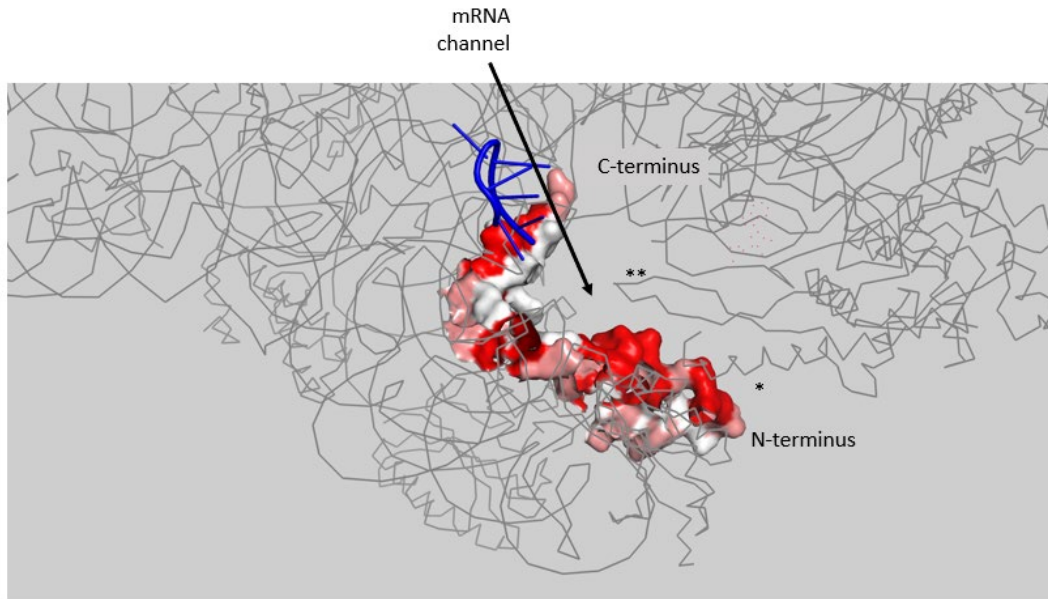


Figure 3: *F. tularensis* bS21 homologs have distinct sequences, similar predicted structures, and regions of variability near the mRNA channel. (A) Amino acid alignment of the three bS21 homologs in *F. tularensis* and the single bS21 proteins in *F. johnsoniae* and *E. coli*, from ClustalOmega sequence alignment tool. (B) Alignment of predicted structures of *F. tularensis* bS21 homologs using AlphaFold. Pink = bS21-2; Turquoise = bS21-1; Yellow = bS21-3. (C) Conserved and variable residues of *F. tularensis* bS21 homologs shown on *E. coli* bS21 structure in 30S particle. Red = identical amino acids; pink = similar amino acids; white = non-similar amino acids on bS21; blue = mRNA; grey = 16S rRNA and other 30S ribosomal proteins. To clarify perspective, * = portion of uS7 in foreground, and ** = portion of uS7 in background (behind bS21). PDB entry 4V50 (Berk et al., 2006).

The *E. coli* bS21 has numerous potential interactions with nearby r-proteins and rRNA. As mentioned previously, among several likely bonds between the 16S rRNA and bS21, there is a predicted hydrogen bond interaction between R17 of bS21 and C1539 of 16S rRNA in the 30S initiation complex (2.7Å distance) (Kaledhonkar et al., 2019). R17 is conserved in all three of the *F. tularensis* bS21 homologs, and the ASD is identical in *F. tularensis* and *E. coli*, leading us to hypothesize that this structure may be consistent in *Francisella*. Interestingly, this interaction is seen in the 30S

initiation complex (PDB 6O7K; Kaledhonkar et al., 2019) but not in the 70S structures that occur during elongation (PDB 4V6P; Agirrezabala et al., 2012) (Figure 4). Rather, in the translocating 70S structure, there is no proximity less than 3Å between the ASD and bS21, though there is a potential interaction between C1538 of the ASD and K57 and/or R54 of bS21 (3.5Å or 3.4Å distance, respectively). K57 and R54 residues are partially conserved amongst the three bS21 proteins in *F. tularensis* (specifically, R54 is present in bS21-1 and 2; K57 is present in bS21-2 and 3). These findings suggest that interactions between the *E. coli* bS21 and the anti-Shine Dalgarno are dynamic and may be partially conserved in *F. tularensis*.

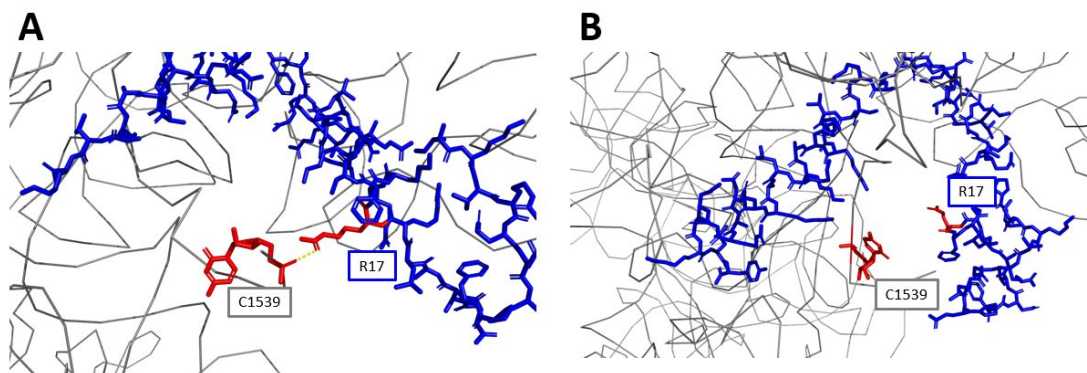


Figure 4: bS21 interactions with 16S rRNA anti-Shine-Dalgarno are dynamic. **A.** bS21 residue R17 forms a hydrogen bond with 16S rRNA residue C1539, a component of the anti-Shine Dalgarno, in the 30S initiation complex of *E. coli*. PDB 6O7K (Kaledhonkar et al., 2019). **B.** R17 and C1539 are too far apart from each other to interact directly during translation elongation. PDB 4V6P (Agirrezabala et al., 2012). Grey = 16S rRNA; Blue = bS21.

In *F. johnsoniae*, the bS21 protein has also been shown to interact with the ASD. In this species, the bS21-ASD interaction is a mechanism of bS21-based gene regulation, as bS21 acts with other r-proteins to sequester the anti-Shine Dalgarno of the 16S rRNA (Jha et al., 2020; McNutt et al., 2023). The

structure of the *F. johnsoniae* ribosome reveals three bS21 residues interact with the ASD: K51, Y54, and I55. Neither K51 or Y54 are conserved in the *F. tularensis* bS21 homologs (Figure 3A). I55 is partially conserved, as bS21-3 also has an isoleucine in that position, and bS21-1 and bS21-2 have a valine, which has similar properties to isoleucine (Figure 3A). Because of these differences, we do not expect the *F. tularensis* bS21 homologs to sequester the ASD; there may be another mechanism that allows bS21 homologs in *F. tularensis* to impact gene expression.

In addition to the 16S rRNA, bS21 also interacts with the r-proteins bS18 and uS11 in the *E. coli* ribosome (Berk et al., 2006). At least four bS21 residues are likely to interact with bS18: two are conserved in all of the *F. tularensis* bS21 homologs (C22, K19), one is a partially conserved (I3), and one is not conserved (K4). Ten bS21 residues may interact with uS11, spanning most of the bS21 protein. Again, some of these residues are completely conserved in the *F. tularensis* bS21 homologs, some are partially conserved, and some are not conserved (Berk et al., 2006). These comparisons draw attention to the importance of solving a structure of the *F. tularensis* ribosome, to determine where bS21 homologs interact with rRNA and other proteins, how these interactions might differ between the three homologs, and whether these may suggest functional mechanisms of bS21.

not sure what this means.
maybe function differences amongst
bS21 homologs?

The evolutionary history of bS21 homologs is not known

While Chen et al. (2020) looked at the divergent evolution of bS21 homologs in Bacteroidia and phages, no publications to our knowledge have

explored the evolutionary history of bS21 in species with multiple bS21 homologs. Many species have one bS21 protein, some have none, and still others have multiple homologs, including most of the close relatives of *F. tularensis* within the *Francisella* genus. A preliminary phylogenetic tree was created using RAxML (Randomized Axelerated Maximum Likelihood; Stamatakis, 2014), including a variety of bS21 seed sequences and eukaryotic proteins with similar domains obtained from Pfam, for a total of 330 amino acid sequences analyzed (Figure 5A). While there is close association of the three *F. tularensis* LVS bS21 proteins, bS21-2 appears to be in a distinct clade from bS21-1 and bS21-3. bS21-1 and bS21-3 are grouped with their corresponding proteins in *F. tularensis* ~~subs.~~ ^{subsp.} *tularensis* Schu S4 (FRATT in Figure 5B), which is unsurprising as they are identical at the nucleotide level. A nearby neighbor of bS21-1 and bS21-3 is *Coxiella burnetti* (COXBU), also a member of Gammaproteobacteria, though this species encodes only one bS21 protein. bS21-2 is also linked to its Schu S4 counterpart, and is in a clade with other non-*Francisella* species as well, including *Hydrogenovibrio crunogenus* (HYDCU) and *Ruthia magnifica* (RUTMC). Both of these genes are Gammaproteobacteria with one bS21 homolog. Given this preliminary phylogenetic tree and the high sequence identity between bS21-1 and bS21-3, it may be that bS21-2 evolved from an ancestral gene, and the duplication of bS21-1 and bS21-3 occurred more recently. However, given the relatively low bootstrap values, a more in-depth phylogenetic analysis is needed to elucidate the details of the evolutionary history of bS21 and draw any formal conclusions.

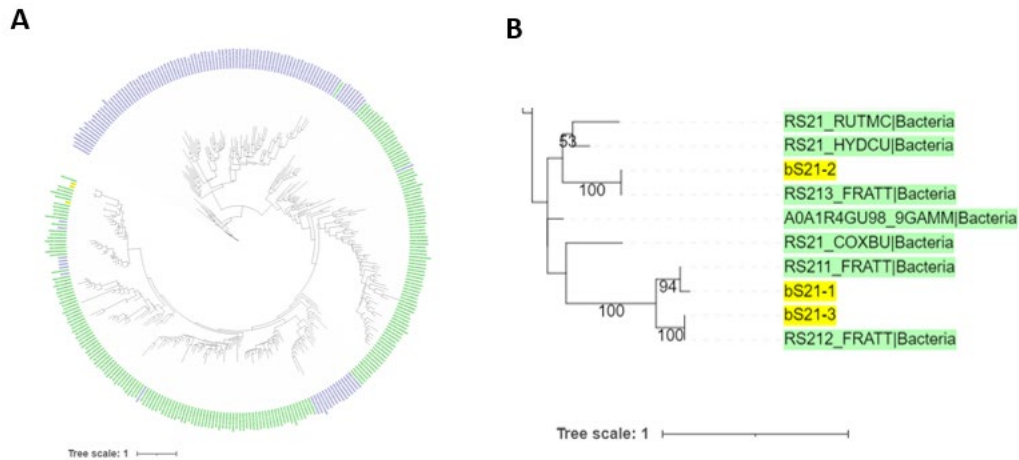


Figure 5. Phylogenetic analysis of bS21 proteins. **A.** Phylogenetic tree of 330 amino acid sequences with bS21-like domains. Purple = eukaryotic species; Green = bacterial species. **B.** Region of tree including *F. tularensis* bS21 homologs, highlighted in yellow, and nearby neighbors (*F. tularensis* subs. *tularensis* Schu S4 [FRATT]; *Coxiella burnetti* [COXBU]; *Methylophaga muralis* [9GAMM]; *Hydrogenovibrio crunogenus* [HYDCU]; and *Ruthia magnifica* [RUTMC]). Bootstrap values greater than fifty are indicated on tree branches. Tree kindly generated by Dr. Ying Zhang.

The genomic locations of the *rpsU* genes are partially conserved and support the phylogenetic analysis of bS21 proteins. *rpsU1* is located downstream of the gene *cspC*, which encodes a cold shock protein (Chapter 2, Figure S1). Homologs of *rpsU* are found in similar genomic contexts in many species across diverse bacterial classes, primarily within the phylum of Pseudomonadota. Species with *rpsU* genes syntenic with *F. tularensis* *rpsU1* are a part of betaproteobacteria (e.g. *Burkholderia* species), alpha-proteobacterial (e.g. *Agrobacterium fabacearum*), deltaproteobacteria (e.g. *Geobacter sulfurreducens*), and Flavobacteriia phylum (e.g. *Tenacibaculum jejuense*), amongst others (KEGG synteny tool; Kanehisa et al., 2023). There is

variety in the identity of the cold-shock protein gene (i.e. *cspA* instead of *cspC*) and the order of the operon (i.e. *rpsU* may be first or second), and there are at times other genes between *rpsU* and the cold shock protein gene.

rpsU2 is a part of a macromolecular synthesis operon that also encodes DNA primase and sigma-70 of RNA polymerase (Chapter 2, Figure S1), which is syntenic to *rpsU* genes in an even wider range of bacteria phyla: Pseudomonadota (e.g. *E. coli*), Bacillota (e.g. *Streptococcus* species), Spirochaetes (e.g. *Leptospira interrogans*), and Thermodesulfobacteria, to name a few examples (KEGG synteny tool; Kanehisa et al., 2023). As with *rpsU1*, the exact makeup of these operons varies across species, with some including additional genes like one encoding DNA mismatch repair protein in *Thermodesulfatator indicus*. Indeed, the *F. tularensis* operon also includes the gene *yqeY* which may encode a protein necessary for tRNA aminoacylation (Deniziak et al., 2007).

rpsU3 does not contain annotated genes in close proximity on the *F. tularensis* genome (Chapter 2, Figure S1). This is also true for several *rpsU* genes in a limited portion of the bacterial phyla, including in Cyanobacteria (e.g. one of the *Nostoc* sp. PCC 7120 *rpsU* genes) and Bacteroidia (e.g. *Salinobacter ruber*) (RAST FIGfam viewer; Meyer et al., 2009). Together these data are consistent with the idea that *rpsU1* and *rpsU3* duplication occurred more recently in the evolutionary history of these homologs, as the *rpsU2* genomic context is more broadly conserved across bacterial phyla.

One hallmark of horizontal gene transfer is a significant difference in GC content of the genes of interest compared to the remaining genome. A clear example of this in *F. tularensis* is the Francisella Pathogenicity Island, which has a GC content of only 27% while the entire genome has a GC content of 32%. *rpsU1* and *rpsU2* both have GC contents near 36%, which is marginally higher than the *F. tularensis* genome; however, assessing the operons to which they belong indicates GC contents of 34% and 32%, respectively, which are similar to the *F. tularensis* genome. This may suggest that the individual *rpsU* genes were acquired separately from the operons, but may also be an artifact reflecting that the *rpsU* genes are too small to show representative GC contents (~180 nt each). *rpsU3* has a GC content of 32%, which is the same as the genome's GC content. Together, the GC content analysis neither supports nor disallows the possibility of horizontal gene transfer.

SUMMARY AND OBJECTIVES

Bacterial ribosomes can be heterogeneous in structure and function, allowing bacteria to rapidly modulate their proteome in response to changing conditions. In the intracellular pathogen *Francisella tularensis*, there are three distinct homologs of the small ribosomal protein bS21, which may lead to ribosome heterogeneity. *F. tularensis* requires highly controlled regulation of virulence genes, but our knowledge of the mechanisms of gene regulation in this organism remain limited.

In the chapters that follow, I show that *F. tularensis* ribosomes are heterogeneous with respect to bS21 content and find genome-wide differences

in protein abundance when one bS21 homolog, bS21-2, is lost. In cells lacking bS21-2, I see specific changes in expression of known virulence genes on the FPI at the protein level but not the transcript level, with a corresponding decrease in virulence. I report that bS21-2 modulates the expression of some proteins in a 5' UTR-specific manner, and I identify a 6-nt sequence required for efficient translation in at least one bS21-2-responsive 5' UTR.

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CHAPTER 2

Manuscript 1

A ribosomal protein homolog governs gene expression and virulence in a bacterial pathogen

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**A ribosomal protein homolog governs gene expression and
virulence in a bacterial pathogen**

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Abstract

The molecular machine necessary for protein synthesis, the ribosome, is generally considered constitutively functioning and lacking any inherent regulatory capacity. Yet ribosomes are commonly heterogenous in composition and the impact of ribosome heterogeneity on translation is not well understood. Here we determine that changes in ribosome protein composition governs gene expression in the intracellular bacterial pathogen *Francisella tularensis*. *F. tularensis* encodes three distinct homologs for bS21, a ribosomal protein involved in translation initiation, and analysis of purified *F. tularensis* ribosomes reveals they are heterogenous with respect to bS21. Loss of one homolog, bS21-2, results in significant changes to the cellular proteome unlinked to changes in the transcriptome. Among the reduced proteins are components of the type VI secretion system (T6SS), an essential virulence factor encoded by the Francisella Pathogenicity Island. Furthermore, loss of bS21-2 leads to an intramacrophage growth defect. Although multiple bS21 homologs complement loss of bS21-2 with respect to T6SS protein abundance, bS21-2 is uniquely necessary for robust intramacrophage growth, suggesting bS21-2 modulates additional virulence gene(s) distinct from the T6SS. Our results indicate that ribosome composition in *F. tularensis*, either directly or indirectly, post-transcriptionally modulates gene expression and virulence. Our findings are consistent with a model in which bS21 homologs function as post-transcriptional regulators, allowing preferential translation of specific subsets of mRNAs, likely at the stage of translation initiation. This work also raises the possibility that bS21 in other organisms may function

similarly and that ribosome heterogeneity may permit many bacteria to post-transcriptionally regulate gene expression.

Importance

While bacterial ribosomes are commonly heterogenous in composition (e.g., incorporating different homologs for a ribosomal protein), how heterogeneity impacts translation is unclear. We found that the intracellular human pathogen *Francisella tularensis* has heterogenous ribosomes, incorporating one of three homologs for ribosomal protein bS21. Furthermore, one bS21 homolog post-transcriptionally governs expression of the *F. tularensis* type VI secretion system, an essential virulence factor. This bS21 homolog is also uniquely important for robust intracellular growth. Our data support a model in which bS21 heterogeneity leads to modulation of translation, providing another source of post-transcriptional gene regulation. Regulation of translation by bS21, or other sources of ribosomal heterogeneity, may be a conserved mechanism to control gene expression across the bacterial phylogeny.

Introduction

Regulation of translation provides bacteria with a rapid way to modify gene expression. While many distinct mechanisms permit this fine-tuning (1, 2) the impact of ribosome composition on gene expression remains poorly-understood. In bacteria, ribosomes are diverse and commonly heterogenous with respect to ribosomal protein (r-protein) content, post-translational modifications, rRNA

content, or post-transcriptional modifications (reviewed in (3)). The functional consequences of ribosome heterogeneity are unclear but may include the formation of “specialized ribosomes,” or ribosomes with altered activity due to their distinct composition (4). Although specialized ribosomes are not well described in bacteria, exciting recent studies have connected altered rRNA content of ribosomes and gene regulation (5, 6) and, in *Mycobacterium smegmatis*, ribosomes containing alternate r-protein homologs translate some genes with differential efficiency (7).

Francisella tularensis is a Gram-negative, facultative intracellular bacterium that causes the potentially fatal human disease tularemia (8). After internalization into host cells, *F. tularensis* must escape from the Francisella-containing phagosome to replicate inside the cytosol. This escape process requires a type VI secretion system (T6SS), which modifies the host cell by delivery of effector proteins (9–12). Production of this T6SS is coordinately regulated by the transcription factors MglA, SspA, and PigR, as well as the signaling molecule ppGpp (13–20). Regulation of the T6SS is arguably the most well-understood virulence regulatory network in *F. tularensis*. However, much remains to be learned about the regulation of other virulence factors.

Despite its relatively small genome (< 2 Mbp), *F. tularensis* encodes three distinct *rpsU* genes (*rpsU1*, *rpsU2*, and *rpsU3*), which encode homologs of the small ribosomal subunit protein bS21 (bS21-1, bS21-2, and bS21-3, respectively). This is the only apparent source of ribosome heterogeneity in *F. tularensis*, as the three rRNA operon sequences are identical and no other r-proteins are encoded

by multiple homologs. In *Escherichia coli*, bS21 is involved in translation initiation (21, 22) and, consistent with this activity, is found on the ribosome close to the anti-Shine-Dalgarno sequence near the mRNA exit channel (23, 24). Furthermore, bS21 is one of the last r-proteins to assemble into the ribosome, is considered “loosely associated,” and is easily exchanged among assembled ribosomes (25, 26).

Using mass spectrometry and immunoblot analyses, we show that ribosomes in *F. tularensis* are heterogenous with respect to bS21 content and can incorporate any of the three bS21 homologs into actively-translating ribosomes. Using quantitative whole-cell proteomics, quantitative immunoblots, and transcriptomic analyses, we demonstrate that loss of a particular bS21 homolog, bS21-2, leads to changes in abundance for a subset of proteins that cannot be explained by changes in transcript abundance. Among the impacted proteins are multiple virulence factors, including those that comprise the T6SS. Finally, using intramacrophage growth assays, we provide evidence that bS21-2, and not the other bS21 homologs, promotes intramacrophage growth. Our findings reveal that a specific r-protein homolog in *F. tularensis*, bS21-2, governs gene expression at the level of protein abundance and positively impacts virulence.

Results

***Francisella* species encode three bS21 homologs**

The genomes of multiple *Francisella* species contain three distinct genes encoding bS21 (*rpsU1*, *rpsU2*, and *rpsU3*), raising the possibility that cells contain ribosomes that are heterogenous with respect to bS21 content. The gene encoding one homolog in *F. tularensis*, *rpsU2* (encoding bS21-2), is syntenic with the single bS21-encoding gene in *Escherichia coli* (**Figure S1**). In *E. coli*, *rpsU* is the first in an operon referred to as the macromolecular synthesis operon, encoding key proteins for initiation of translation (bS21), DNA replication (DNA primase), and transcription (RNA polymerase σ^{70}) (27). The corresponding operon in *Francisella* species, including *F. tularensis*, also contains *yqeY*, which may encode a protein necessary for correct tRNA aminoacylation (28). Another bS21 homolog, bS21-1, is encoded by *rpsU1* in an apparent operon downstream of the gene for cold shock protein CspC. There are no annotated genes in the same transcriptional context as *rpsU3*, the gene encoding the third homolog, bS21-3. The bS21 homologs in *F. tularensis* are distinct but similar, with amino acid identities ranging from 48 – 72%, and are similar to *E. coli* bS21 (51 – 60% identical, with bS21-2 having the highest identity; **Figure S2**).

***F. tularensis* ribosomes are heterogenous**

The presence of three distinct genes encoding bS21 raises the potential for *F. tularensis* ribosomes to be heterogenous with respect to bS21. To investigate

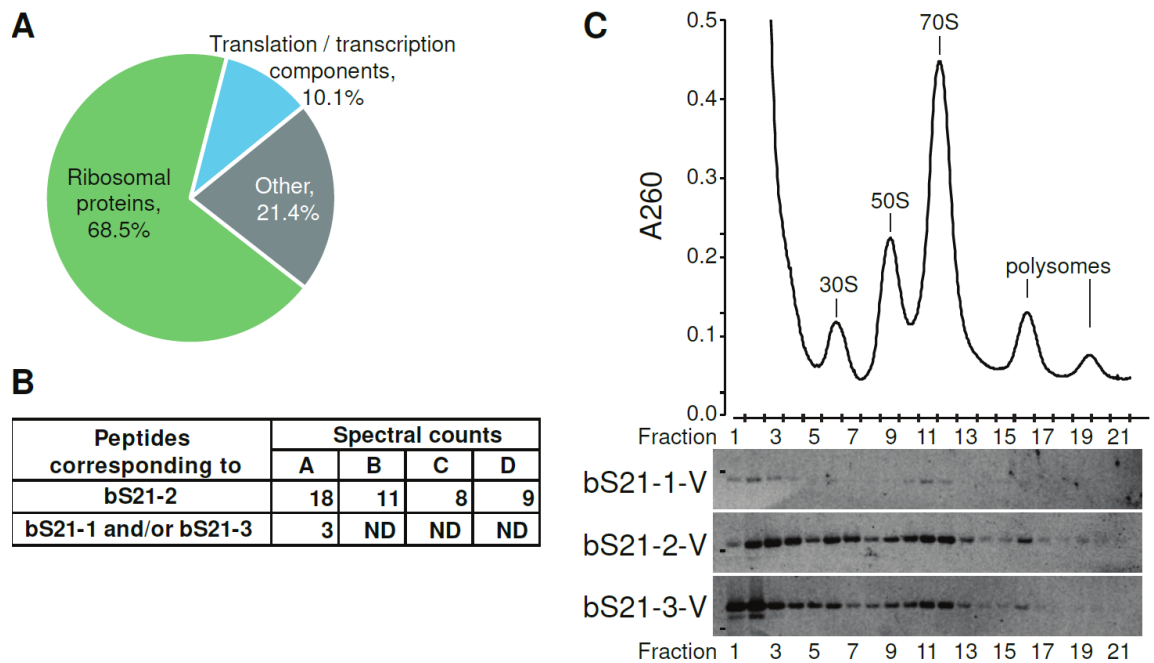


Figure 1. *F. tularensis* ribosomes are heterogenous with respect to bS21. A. Chart demonstrating purity of wild-type ribosomes. Categories represent classification of proteins identified by mass spectrometry of ribosomes purified from wild-type *F. tularensis* LVS cells. Numbers represent the percentage of spectral counts corresponding to proteins in each category, combined from quadruplicate samples. **B.** Wild-type *F. tularensis* LVS ribosomes contain more than one bS21 homolog. Table detailing the number of spectral counts corresponding to bS21 homologs identified from individual ribosome purifications (A – D) from wild-type cells. Spectral counts corresponding to bS21-1 and/or bS21-3 cannot be unambiguously assigned due to complete sequence identity of detected peptides. ND: not detected. **C.** Each bS21 homolog can be incorporated into ribosomes. Top: Sucrose gradient sedimentation profile from actively-translating wild-type cells containing an empty vector. Nucleic acid content was monitored by A260 (y-axis). Peaks corresponding to the 30S, 50S, 70S, and polysomes are indicated. Fractions collected are indicated on the x-axis. Bottom: Immunoblot analysis of fractions from sucrose gradient sedimentation performed on actively-translating cells ectopically expressing indicated bS21 homolog with VSV-G epitope tag. Wells correspond to fractions 1 – 21 from profile above.

this possibility, we used sucrose cushion centrifugation to isolate ribosomes from *F. tularensis* LVS grown *in vitro* in quadruplicate and analyzed their protein composition using liquid chromatography tandem mass spectrometry (LC-MS/MS). Approximately 80% of the spectral counts corresponded to ribosomal proteins or proteins associated with transcription and translation complexes (e.g., RNA polymerase, translation release factors, SRP), indicating *F. tularensis* ribosomes purified in this manner are highly pure (**Figure 1A, Table S1**). Despite the small size of bS21 (approx. 8 kDa), we identified multiple peptides corresponding to bS21-2 in all samples. In one sample, peptides shared between bS21-1 and bS21-3 were detected (**Figure 1B**). This suggests that bS21-2 is the most abundant homolog in wild-type cells, consistent with its production from an operon encoding proteins essential for transcription and DNA replication. It also suggests that either bS21-1, bS21-3, or both, are incorporated into ribosomes in LVS. However, it did not allow us to determine the next-most abundant homolog (bS21-1 or bS21-3) or confirm incorporation of both of these other homologs. Regardless, these results demonstrate that multiple bS21 homologs are incorporated into wild-type *F. tularensis* ribosomes and that ribosomes in *F. tularensis* are heterogenous, containing different bS21 homologs.

We next wanted to determine if each bS21 homolog can be found in actively-translating ribosomes. To track each bS21, we modified each homolog to encode a C-terminal vesicular stomatitis virus glycoprotein (VSV-G) tag and individually ectopically expressed them, using the same promoter, from a plasmid in wild-type cells. Lysate fractions of these cells were analyzed by immunoblotting

after sucrose gradient sedimentation (**Figure 1C**; **Figure S3**). When ectopically expressed (rather than produced from its native locus), bS21-1 was the least abundant homolog while bS21-3 was produced at the highest level. Each homolog was found in fractions corresponding to the 30S, 70S, and polysomes. Although bS21 is thought to function primarily in translation initiation, our findings indicate that each bS21 homolog associates with the ribosome throughout the translation cycle.

Loss of bS21-2 leads to changes in protein, not transcript, abundance

Because the ribosomal protein bS21 is involved in translation initiation, we hypothesized that loss of a bS21 homolog may impact translation and result in changes in abundance in a subset of proteins. To test this hypothesis, we individually deleted each of the three genes encoding bS21 homologs. This led us to determine that no single bS21 homolog is essential for cell growth. We subsequently grew wild-type cells and cells lacking single bS21 homologs to mid-log *in vitro* and used data-independent acquisition (DIA) mass spectrometry analysis (29) to compare relative protein abundance in cell lysates. Using this method, 68% of the total proteins predicted to be encoded by *F. tularensis* LVS were identified and analyzed (1194 of 1754). When compared to wild-type, we did not detect any significant changes in protein abundance in cells lacking either of the two lower-abundance bS21 homologs, bS21-1 and bS21-3 (>1.5-fold altered with an adjusted p-value <0.05, excluding bS21). In contrast, cells lacking the most abundant homolog, bS21-2 ($\Delta rpsU2$), had significant proteomic differences

compared to wild-type cells. Specifically, we found 185 unique proteins (~16% of detected proteins) had altered abundance in cells without bS21-2 compared to wild-type cells (**Figure 2**, data on y-axis, **Table S2**).

To determine if these changes in protein abundance can be explained by corresponding changes in transcription, we performed transcriptomic analyses on wild-type cells, cells lacking bS21-2 ($\Delta rpsU2$), and cells lacking the native bS21-2 but ectopically expressing bS21-2-V from a plasmid. Comparing cells with and without native bS21-2, we identified 105 differentially expressed genes (>2-fold altered with an adjusted p-value <0.05, excluding *rpsU*; **Figure 2**, data on x-axis, **Table S3**). All of these changes were complemented by ectopic expression of bS21-2-V on a plasmid.

Our analysis revealed that in cells lacking bS21-2, the largest change in transcript abundance was a six-fold increase in *yqeY*, the gene directly downstream from *rpsU2* (which encodes bS21-2). This increase in transcript abundance was complemented by ectopic expression of bS21-2-V, suggesting that bS21-2 functions as a negative regulator of its own operon. Translational feedback regulation is well-established for multiple ribosomal proteins but, to the best of our knowledge, this is the first report of translational regulation of ribosomal proteins in *F. tularensis* and the first report that bS21 governs its own production (30, 31).

Comparison of our proteomic and transcriptomic analyses reveals that the changes in protein abundance were not generally due to changes in transcript

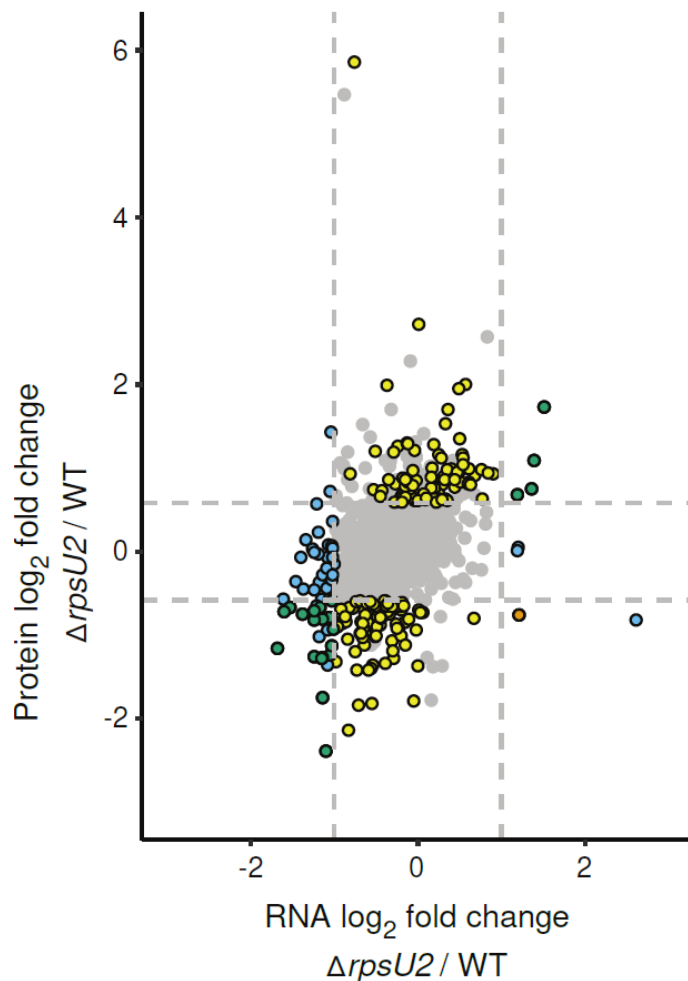


Figure 2. Loss of bS21-2 leads to changes in protein abundance that cannot be explained by changes in transcript abundance. Cells with (WT, wild-type) and without bS21-2 ($\Delta rpsU2$) were analyzed using RNA-Seq (x-axis) and DIA whole cell mass spectrometry (y-axis). Genes are represented by dots. Most genes with changes in protein (161 yellow dots) do not have corresponding changes in transcript abundance. One gene (orange dot) has discordant changes in transcript and protein abundance. Green dots (23) represent genes with concordant changes in transcript and protein abundance. Blue dots (60) indicate genes with altered transcript abundance only. Horizontal dashed lines indicate ± 1.5 -fold cutoff for differential protein abundance; vertical dashes indicate ± 2 -fold cutoff for differential transcript abundance. Colored dots with black outlines represent genes with significant changes in protein (± 1.5 -fold change, adjusted p-value < 0.05) and/or transcript (± 2 -fold change, adjusted p-value < 0.05) abundance as indicated above, while grey dots without outline represent genes with changes that did not meet the statistical thresholds. Three grey dots are located outside the bounds of the axis as represented.

abundance. Of the 185 differentially abundant proteins in cells lacking bS21-2, only ~12% (23) could be explained by altered transcription (**Figure 2**, yellow dots), while about 88% (162; **Figure 2**, blue dots and orange dot) had changes in protein abundance without a corresponding change in transcript abundance. These discrepancies between transcript abundance and protein abundance support a model in which bS21-2 controls expression, either directly or indirectly, of some genes at the level of translation.

bS21-2 governs the abundance of type VI secretion system proteins, which are essential for virulence

Among the proteins with altered abundance in cells lacking bS21-2, we identified twelve out of sixteen proteins encoded on the Francisella pathogenicity island (FPI). The FPI encodes a unique type VI secretion system (T6SS) that is absolutely essential for intramacrophage growth and virulence of *F. tularensis* (32–34). Using quantitative immunoblotting and antibodies specific to a subset of *F. tularensis* T6SS proteins, we validated that cells lacking bS21-2 have differences in those T6SS proteins (**Figure 3**). Consistent with the mass spectrometry results, we found reductions in virtually all probed T6SS proteins, including an ~4-fold reduction in PdpB, the TssM/IcmF homolog. Using this approach, we also found an ~2.4-fold reduction in IgIA and ~1.7-fold reduction in IgIB, T6SS proteins that are just below the cutoff for statistical significance in our mass spectrometry analysis. Since we identified this differential abundance using a more sensitive method of comparison, it raises the possibility that all FPI-

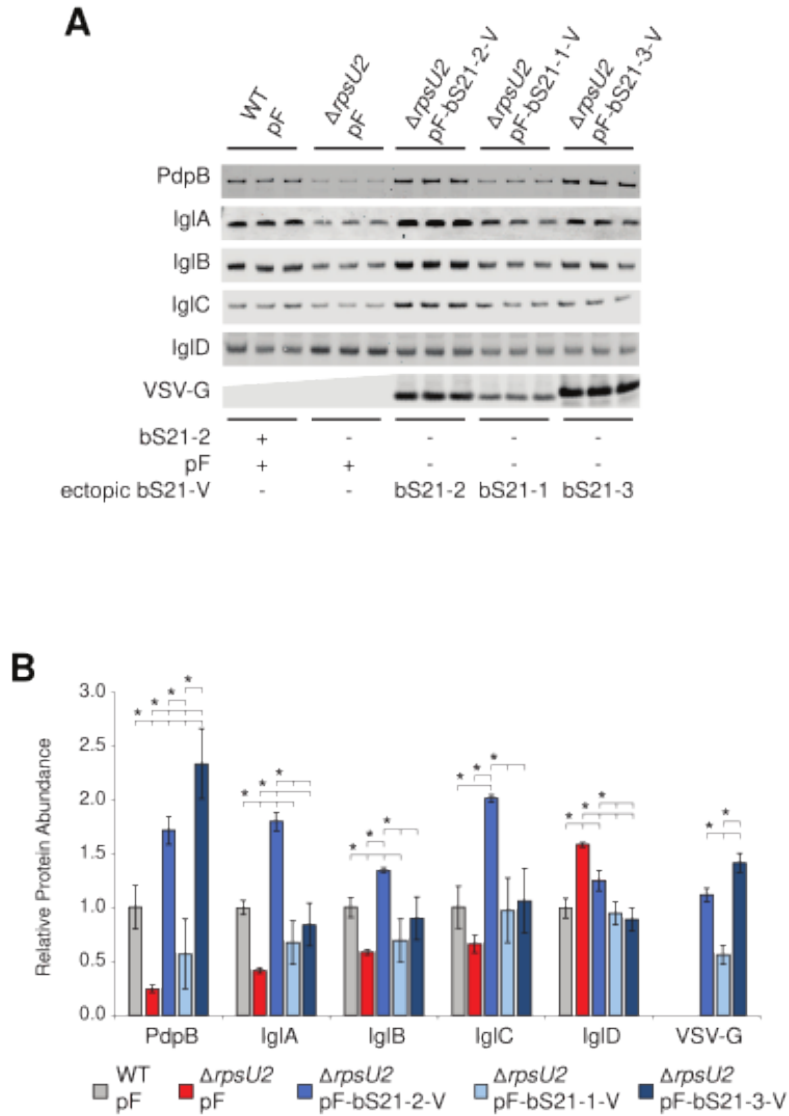


Figure 3. bS21-2 impacts T6SS protein abundance. A. Immunoblot analysis of indicated T6SS protein abundance. Cells either contained (wild-type) or lacked ($\Delta rpsU2$) bS21-2 and either an empty vector control (pF) or a vector ectopically expressing VSV-G-tagged bS21 homologs (pF-bS21-1-V, pF-bS21-2-V, or pF-bS21-3-V). Immunoblot against VSV-G was included to demonstrate production of VSV-G-tagged bS21 homologs. **B.** Quantification of immunoblots from (A). Band intensities for each protein were normalized to total protein per well on the membrane. Error bars represent 1 SD. Experiments were repeated at least twice and data from a representative experiment are shown. Lines above bars indicate statistical comparison among groups by t-test. Asterisk indicates group to which all other groups are compared, if horizontal line connects to line above group, $*p < 0.05$ using Benjamini-Hochberg correction.

encoded proteins may be differentially abundant in cells lacking bS21-2 compared to wild-type cells, but we do not have antibodies specific to the remaining proteins (i.e., PdpE and VgrG) to test this hypothesis. Also consistent with our mass spectrometry findings, IglD (the homolog of TssK) was the only T6SS protein with increased, rather than decreased, protein abundance (**Figure 3**). Each of these changes in protein abundance could be complemented by ectopic expression of bS21-2-V, driven by the *groES* promoter on a plasmid (**Figure 3**).

These changes in protein abundance likely reflect positive regulation of most, but not all, T6SS proteins by bS21-2 at the level of translation, either directly or indirectly. Our findings are inconsistent with bS21 positively regulating transcription; it is well-established that transcription of FPI operons are coordinately controlled and our RNA-Seq analysis reveals that cells lacking bS21-2 do not have FPI-wide transcript reductions (13–16, 20, 35); **Table S3**). In a complementary approach, we compared the transcript abundance for specific FPI genes using quantitative RT-PCR and included cells lacking PigR, a transcription factor critical for positive transcriptional regulation of FPI genes (14–16, 20, 35); **Figure S4**). We confirmed that cells lacking PigR have major decreases in FPI transcript abundance but cells lacking bS21-2 did not have compelling (2-fold or greater) changes in FPI transcript abundance or in transcript abundance of the positive regulator PigR, consistent with the RNA-Seq results. We considered the possibility that loss of bS21-2 could indirectly impact T6SS protein abundance by altering protein stability, but the half-life of one of the most differentially abundant proteins, PdpB, was unchanged in cells with and without bS21-2 (longer than 120

minutes, **Figure S5**). Our results are consistent with bS21-2 controlling expression of T6SS proteins at the level of translation.

Other bS21 homologs impact the abundance of type VI secretion system proteins

Our findings indicate that bS21-2 is the most abundant bS21 homolog in wild-type cells. However, it is not clear if the majority of ribosomes in cells lacking bS21-2 incorporate another bS21 homolog or no bS21 at all. This leads to the question: do all bS21 homologs affect T6SS protein translation or does bS21-2 specifically modulate translation of T6SS proteins? To answer this question, we ectopically expressed either bS21-1-V or bS21-3-V in cells lacking bS21-2, similarly to the ectopic expression of bS21-2-V. We subsequently used quantitative immunoblot analyses to assess the abundance of each ectopically expressed bS21 homolog and a subset of T6SS proteins (**Figure 3**). While this strategy resulted in comparable amounts of bS21-2 and bS21-3, ectopic expression resulted in approximately 2-fold less bS21-1 than the other homologs, consistent with its lower expression in wild-type cells (**Figure 3, Figure 1**). With respect to T6SS protein abundance, ectopic expression of bS21-3 restored all probed proteins to wild-type levels, complementing the loss of bS21-2 (**Figure 3**). However, bS21-1 did not appear to complement T6SS protein production completely (**Figure 3**). This may be due to reduced levels of bS21-1, lack of specific ability to regulate T6SS proteins, or a combination of the two factors. Notably, loss of bS21-2 resulted in a growth defect (**Table S4**) that could be

complemented by ectopic expression of bS21-2 or bS21-1, but not bS21-3. That cells lacking bS21-2 with ectopic expression of bS21-3 have wild-type levels of T6SS proteins and yet still have a growth defect reveals that changes in T6SS proteins are not due simply to changes in growth rate. Our findings allow us to conclude that incorporation of either bS21-2 or bS21-3 – and to a lesser extent, bS21-1 – into ribosomes modulates production of T6SS proteins.

bS21-2 is important for intramacrophage growth

A functional T6SS is essential for *F. tularensis* intramacrophage replication and is a strict requirement for virulence (32–34). The observed differences in FPI protein abundance led us to hypothesize that T6SS function may be compromised in cells lacking bS21-2 and these cells may be attenuated for intramacrophage growth. We tested the ability of cells lacking bS21-2 ($\Delta rpsU2$) to survive in murine macrophage-like J774A.1 cells. This revealed a significant defect in the ability of bS21-2 mutant cells to replicate in macrophage; we recovered ten-fold fewer bS21-2 mutant bacteria after 24 hours compared to wild-type (**Figure 4**). The intramacrophage growth defect of cells lacking bS21-2 could be restored by ectopic expression of bS21-2 from a plasmid (**Figure 4**). This is in contrast to ectopic expression of bS21-1 and bS21-3, neither of which restored the intramacrophage growth of cells lacking bS21-2 (**Figure 4**). These results indicate that bS21-2 is specifically required for intramacrophage survival, despite the fact that ectopic expression of bS21-1 restored *in vitro* growth rates and ectopic

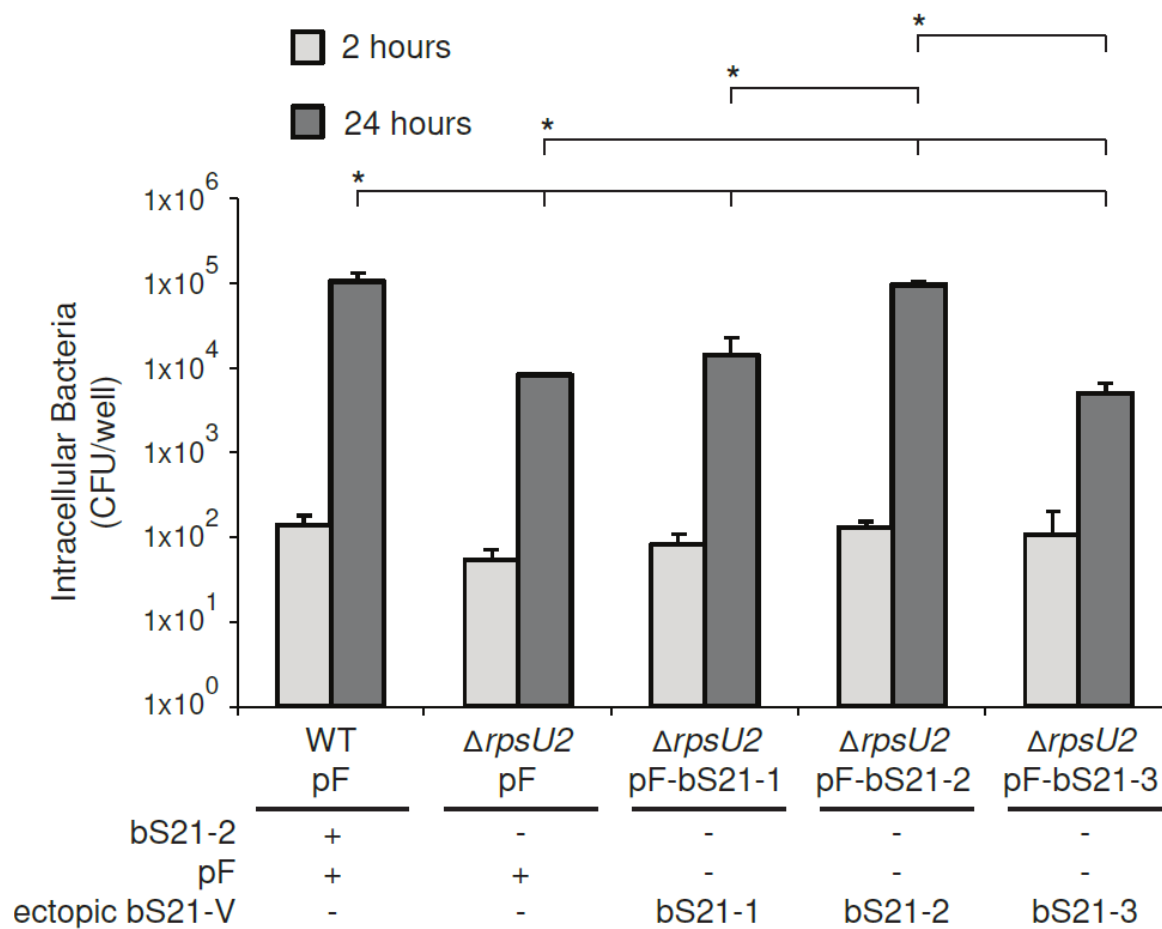


Figure 4. Cells without bS21-2 have an intramacrophage growth defect, which can be complemented by ectopic expression of bS21-2. Growth and survival of *F. tularensis* LVS cells within J774A.1 cells. Murine macrophage-like J774A.1 cells were infected with indicated bacterial cells at a multiplicity of infection of 5 – 10. J774A.1 cells were lysed and bacteria were plated for enumeration (colony forming units [CFU]) at 2- and 24-hours post-infection. Error bars represent 1 SD. Experiments were repeated at least twice and data from a representative experiment are shown. Lines above bars indicate statistical comparison among groups by t-test. Asterisk indicates group to which all other groups are compared, if horizontal line connects to line above group, * $p < 0.05$ using Benjamini-Hochberg correction.

expression of bS21-3 restored T6SS protein production *in vitro* (**Figure 3, Table S4**).

In summary, only the presence of bS21-2, not bS21-1 or bS21-3, could restore the intramacrophage growth defect of cells without bS21-2. This reveals that bS21-2 is critical for *F. tularensis* virulence and fits a model in which bS21-2 specifically regulates one or more genes necessary for intramacrophage growth in addition to T6SS genes, a topic still under investigation.

Discussion

The findings described here reveal that ribosome composition in *F. tularensis* is heterogeneous with respect to the small ribosomal protein bS21 and that this heterogeneity impacts gene expression at the level of translation. In particular, by studying cells that contain ribosomes either with or without one of the three bS21 homologs, we have identified that bS21-2 governs the abundance of most T6SS proteins. Additionally, cells lacking bS21-2 are defective for intramacrophage growth; since this defect can only be complemented by bS21-2, even though bS21-3 and (to a lesser extent) bS21-1 can restore T6SS protein abundance, this intramacrophage growth defect is likely independent of the impact bS21-2 has on the T6SS. This allows us to conclude that bS21-2 is important for intramacrophage growth of *F. tularensis*, potentially by regulating the translation of one or more proteins (in addition to the T6SS) necessary for virulence.

To examine the impact of bS21 homologs on gene expression, we used tools that assess the steady-state abundance of protein and transcripts: mass spectrometry and RNA-Seq, respectively. Our analyses revealed that when compared to wild-type cells, cells lacking bS21-2 have changes in protein abundance that cannot be explained by steady-state changes in corresponding mRNAs. Yet for some proteins with altered abundance in cells lacking bS21-2, there are corresponding modest differences in transcript abundance that do not reach statistical significance (**Figure 2**, yellow dots). It is possible that loss of bS21-2 leads to modest transcript abundance changes that result in more significant changes in protein abundance. But given the role of bS21 in translation, and specifically translation initiation, we propose a model in which bS21-2 impacts gene expression by modulating translation initiation for particular mRNAs. Since an mRNA can be stabilized by translation, increased translation can increase stability and, conversely, less translation can lead to faster degradation (reviewed in 36); this effect may impact the abundance of many transcripts in cells lacking bS21-2 and may explain the observed weak correlation between some protein and transcript abundances. Consequently, additional work will be required to validate our model.

Our approach in studying bS21 homologs in *F. tularensis* has thus far focused on the homolog bS21-2, whose loss led to phenotypic changes. Our data suggest that bS21-2 is the most abundant homolog in the conditions studied. We hypothesize that cells without bS21-1 and bS21-3 did not exhibit distinct phenotypes under the conditions of our experiments due to their relatively low

abundance. Both of these homologs may also influence gene expression under conditions when they are more abundant, but these conditions are not yet identified. Additionally, in our study of cells without bS21-2, it is not clear if the majority of ribosomes lack bS21 entirely or instead incorporate bS21-1 or bS21-3; our findings only extend to heterogeneity with respect to the presence or absence of bS21-2.

Comparison of *rpsU* genes across the bacterial phylogeny reveals that many clades and species do not encode bS21, suggesting that it is not essential for translation (37, 38). However, targeted deletion of the single *rpsU* gene in *E. coli* has not been successful, suggesting bS21 is essential in *E. coli* (39–41). We reported in previous work that the *F. tularensis* homolog syntenic with *E. coli* *rpsU*, *rpsU2*, is essential *in vitro* using transposon-insertion sequencing (Tn-Seq) (42). Yet using a targeted allelic exchange approach, we have been able to successfully delete each *rpsU* homolog individually, indicating that none of the *F. tularensis* bS21 homologs is individually essential. Our identification of *rpsU2* as an essential gene was likely due to the polar effects of transposon insertion into the first gene of an operon containing other known essential genes (*dnaG*, encoding primase, and *rpoD*, encoding the σ^{70} subunit of RNA polymerase). It is unclear if *F. tularensis* cells lacking all three *rpsU* genes are viable.

The literature reflects that bS21 may regulate gene expression in other bacteria. A recent study of the *Flavobacterium johnsoniae* ribosome revealed that bS21 plays a role in sequestering the anti-Shine-Dalgarno sequence (43). This

occlusion occurs through contacts with the C-terminal region of bS21 that are conserved across Bacteroidetes species and provides a rationale to explain why most Bacteroidetes mRNAs lack Shine-Dalgarno sequences. Notably, the mRNA encoding bS21 in *F. johnsoniae* encodes a perfect Shine-Dalgarno sequence, strongly suggesting that bS21 regulates its own expression through translational autoregulation (43). *F. tularensis*, however, is a member of the Gammaproteobacteria, has bS21 homologs that exhibit significant differences from *F. johnsoniae* at the C-terminal region, and encodes mRNAs that commonly contain sequences similar to the consensus Shine-Dalgarno sequence. This suggests that in *F. tularensis*, bS21 exerts its effects on gene expression in a different manner.

In other bacteria that encode it, loss of bS21 leads to a variety of phenotypic changes. In *B. subtilis*, loss of bS21 results in biofilm and motility defects (44) and in *Listeria monocytogenes*, inactivation of bS21 is linked to stress resistance and altered transcript abundance(45, 46). *Staphylococcus aureus* lacking functional bS21 exhibit increased resistance to the antibiotics daptomycin and vancomycin (47–49). Both *Burkholderia pseudomallei* and *F. tularensis* encode multiple bS21 homologs and in both organisms, virulence screens using transposon mutagenesis have identified one homolog as important for virulence (50, 51). Together, these findings suggest that bS21 may regulate gene expression in diverse bacterial species.

The idea that bS21 might modulate translation for a subset of mRNAs is further supported by the recent discovery that bS21 is encoded by thousands of sequenced bacteriophage genomes and is one of the most commonly encoded phage ribosomal proteins (52, 53). Transcripts encoding bS21 have been detected in metatranscriptomic samples along with transcripts for late-stage replication proteins (54) and at least one phage-encoded bS21 can be incorporated into *E. coli* ribosomes (52). All of this raises the possibility that incorporation of a viral bS21 into the host ribosome may co-opt the translation machinery in favor of viral proteins and replication.

Our work, together with these earlier findings, strongly suggests that incorporation of bS21 into the ribosome can impact translation of a subset of mRNAs. Considering that bS21 can easily be exchanged among ribosomes, this provides an excellent mechanism to quickly fine-tune the cellular proteome. While the molecular mechanism leading to the modulation of translation has yet to be identified, it is reasonable to speculate that bS21 impacts translation during initiation through specific interactions with the 5' untranslated regions of a specific set of mRNAs. These findings also support the idea that changes in ribosome composition may impact translation and provide another source for bacterial control of gene expression.

Materials and Methods

Bacterial strains and growth conditions

Unless otherwise noted, bacterial strains were grown as indicated here. *Francisella tularensis* subsp. *holarctica* Live Vaccine Strain (LVS) cells were grown in Mueller-Hinton broth (BD Difco) supplemented with 0.025% iron pyrophosphate, 0.1% glucose, and 2% Isovitalex (sMHB), shaking aerobically or on cystine heart agar plates with 1% hemoglobin (CHA-H) at 37°C. *Escherichia coli* XL1-Blue cells were grown in lysogeny broth (LB) shaking aerobically or on LB agar plates at 37°C. Kanamycin was used at concentrations of 5 µg/mL (*F. tularensis*) or 50 µg/mL (*E. coli*).

Vector construction

Complementation plasmids for each bS21 homolog were created from a plasmid derived from pFNLTP6 (55), pKL42 (pF-PmrA-V). Specifically, the complementation plasmids produce bS21 homologs with a C-terminal VSV-G epitope under the control of the *F. tularensis* *groES* promoter. Each *rpsU* gene was amplified using a 5' primer specifying an EcoRI site and an ideal Shine-Dalgarno sequence (5'-AGGAGG-3') located six nucleotides upstream from the translation start site. The 3' primer did not include the native stop codon and included DNA specifying a NotI site. The fragment was cloned into EcoRI/NotI digested pKL42, such that the 3' end of each *rpsU* is in frame with codons specifying three alanines followed by the VSV-G epitope. The resulting plasmids were pKR6 pF-bS21-1-V, pKR7 pF-bS21-2-V, and pKR8 pF-bS21-3-V. The control plasmid pF is the original

pFNLT6 plasmid (containing the *groES* promoter but not any *rpsU* genes nor the VSV-G epitope).

The plasmid pEX18kan was modified to generate in-frame deletions of each *rpsU* gene as previously described (14). Flanking regions of ~600 base pairs from both sides of each *rpsU* gene were amplified by PCR. Primers amplifying the DNA adjacent to each *rpsU* gene included the first three or last three codons of the open reading frame and DNA specifying a NotI site, which also encodes an alanine linker (5'-GCGGCCGCT-3'). The two fragments were cloned into BamHI/KpnI-digested pEX18kan for each *rpsU* gene respectively, yielding pKL122 pEXΔ*rpsU1*, pKR11 pEXΔ*rpsU2*, and pKR12 pEXΔ*rpsU3*; these plasmids were used to construct deletions via allelic exchange as described below.

Strain construction

Deletion strains were constructed by allelic exchange as previously (56). Briefly, competent cells were made by washing *F. tularensis* LVS cells in 10% sucrose and resuspending in an equal volume of 10% sucrose to cells. At least 1 μg of allelic exchange plasmid was electroporated into 50 μL competent cells in 0.2 cm cuvettes with a 2.5 kV pulse. Cells were allowed to recover in 4 – 5 mL sMHB for 4-8 hours at 37°C, shaking. Cells in which a single integration event occurred were selected for on CHA-H plates with kanamycin. These cells were subsequently plated on CHA-H containing 10% sucrose and lacking NaCl, allowing for survival only of cells that had crossed out the non-homologous portion of the vector,

including *sacB* and kanamycin resistance gene. Colonies that were sucrose-resistant and kanamycin-sensitive were screened for deletions using PCR. Candidate strains were confirmed by amplification of genomic DNA outside of the flanking regions on each side of the deletion and Sanger sequencing (Rhode Island Genomics and Sequencing Center). Plasmid pKL122 pEXΔ*rpsU1* was used to make LVS Δ*rpsU1*, plasmid pRK11 pEXΔ*rpsU2* was used to make LVS Δ*rpsU2*, and plasmid pKR12 pEXΔ*rpsU3* was used to make LVS Δ*rpsU3*.

Complementation plasmids were electroporated into LVS or LVS Δ*rpsU2* cells as described above and selected for on CHA-H plates with kanamycin.

Immunoblotting

Cells were collected from mid-log cultures (OD₆₀₀ 0.3-0.4) and resuspended in sample loading buffer (SLB: 1X NuPAGE LDS with 50 mM DTT) normalized to OD₆₀₀ and heated at 95°C for 10 minutes. Cell lysates and fractions were separated by SDS-PAGE on 4-12% Bis-Tris NuPAGE gels in MES or MOPS running buffer (Invitrogen) and transferred to PVDF with the Mini Blot Module transfer system (Invitrogen; 20V for 1 hour on ice) or the Criterion cell for midi gels (BioRad; 60V for 40 minutes on ice) with 1X NuPAGE transfer buffer and 10% methanol. Whole cell lysates were analyzed for total protein with the Invitrogen No-Stain Protein labeling reagent and all membranes were blocked with Odyssey blocking buffer diluted 1:5 in PBS overnight. For each antibody, the linear range of protein detection was determined by plotting sequential dilutions of one lysate from

each strain as a standard curve to establish appropriate volume of lysate to load. Membranes were probed with indicated monoclonal antibodies (BEI Resources, diluted 1:1000 in blocking buffer for all antibodies except anti-PdpB, which was diluted 1:250) or the VSV-G epitope (Sigma, diluted 1:2222). Proteins were detected using IRDye 800 CW donkey anti-mouse IgG or donkey anti-rabbit IgG (Li-Cor, diluted 1:10,000). Fluorescence was measured and quantified on the LiCor Odyssey CLx imager and software, and protein abundance was calculated relative to total protein in each lane. Experiments were performed at least twice in biological triplicate and two to three technical replicates.

RNA isolation and qRT-PCR

Cells were collected from mid-log cultures (OD₆₀₀ 0.3-0.4). Nucleic acids were isolated using the Direct-Zol RNA purification kit (Zymo Research) according to the manufacturer's protocol. Purified nucleic acids were treated with RQ1 Dnase (Promega) for 1 hour at 37°C and RNA was purified with the Direct-Zol RNA purification kit. cDNA was synthesized using Superscript III reverse transcriptase (Life Technologies) as previously described (14). qRT-PCR was performed using PowerUp SYBR Green Master Mix (Applied Biosystems) and a Roche LightCycler 480 (University of Rhode Island Genomics and Sequencing Center) essentially as described (14). Transcript abundances of *pdpA*, *pdpB*, *iglA*, and *pigR* were compared to three different control genes (*tul4*, *rpoA1*, and *bfr*) and since all results were similar, relative abundance is reported to *tul4*. Experiments comparing wild-

type and *rpsU2* mutant cells were performed three times in biological triplicate; experiment with cells lacking PigR was performed once.

RNA-Seq

Approximately 1.5 µg of RNA isolated as above was sent to the Microbial Genome Sequencing Center (MiGS) for RNA-Seq analysis, in biological triplicate (LVS pF) or duplicate (LVS $\Delta rpsU2$ pF, LVS $\Delta rpsU2$ pF-bS21-2-V). After using RiboZero Plus rRNA depletion, libraries were made using Illumina Stranded RNA library preparation and sequenced for a minimum of 12 million paired end reads. Paired-end sequencing reads were mapped to the *F. tularensis* LVS genome (NCBI RefSeq accession number NC_007880) using bowtie2 version 2.2.4. Reads that mapped to annotated genes were counted using HTSeq version 0.11.2, and analysis of differential gene expression was conducted using DESeq2 version 1.32.0. Reported genes had a 2-fold-higher or -lower abundance than the wild type, all with an adjusted p-value of 0.05 or lower.

70S ribosome purification

70S ribosomes were isolated using sucrose cushion centrifugation essentially as described (57). Briefly, wild-type *F. tularensis* cells were grown in 500 mL sMHB to mid-log (OD_{600} 0.3-0.4). Cells were chilled on ice for 20 minutes, centrifuged at 11,000 x g for 5 minutes at 4°C, then washed once with buffer H¹⁰M¹⁰A¹⁰⁰⁰ (10 mM HEPES KOH pH 7.6, 10 mM MgCl₂, and 100 mM NH₄Cl) to remove ribonucleases. The pellet was then washed twice with buffer H¹⁰M¹⁰A⁵⁰ (10 mM HEPES KOH pH

7.6, 10 mM MgCl₂, and 50 mM NH₄Cl, with or without 5 mM β-mercaptoethanol [BME]), and resuspended in ~15 mL of H¹⁰M¹⁰A⁵⁰ with 20 U Dnase I. Cells were lysed by passing through a French press three times at 800 psi and cell debris were removed by centrifugation at 146,000 x g for 15 minutes at 4°C. Supernatant was incubated with 0.5% Brij58 for 30 minutes and layered on top of H¹⁰M¹⁰A⁵⁰⁰ + 20% sucrose (10 mM HEPES KOH pH 7.6, 10 mM MgCl₂, 500 mM NH₄Cl, 20% sucrose, with or without 5 mM BME). Ribosomes were pelleted by ultracentrifugation in 70 Ti rotor for 4 hours at 146,000 x g at 4°C. The pellet was washed twice with H¹⁰M¹⁰A⁵⁰ and gently resuspended in H¹⁰M¹⁰A⁵⁰. This suspension was then layered onto another sucrose cushion (H¹⁰M¹⁰A⁵⁰ with 40% sucrose) and centrifuged for 14 hours at 146,000 x g at 4°C to further purify the ribosomes. Purified 70S ribosomes were gently resuspended in ~250 µL of H¹⁰M¹⁰A⁵⁰ and stored at -80°C.

LC-MS/MS of purified LVS ribosomes

70S ribosomes from wild-type LVS cells were prepared as described above. Samples were either purified via gel stacking prior to mass spectrometry analysis or maintained in H¹⁰M¹⁰A⁵⁰ and delivered to the Northwestern Proteomics Core. The proteins were in-gel digested or in-solution digested and liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis was completed based on internal protocols, matching peptides to the *F. tularensis* LVS proteome (NC_007880).

DIA mass spectrometry

Cells were collected from mid-log cultures (OD_{600} 0.3-0.4) and resuspended in Buffer 1 (20 mM KHEPES pH 7.9, 50 mM KCl, 0.5 mM DTT) with protease inhibitor tablets (Complete Mini, EDTA-free, Roche). Cells were lysed by sonication and protein concentration was determined using a BCA protein assay (Pierce). Lysates with concentrations between 620 and 862 $\mu\text{g/mL}$ were used by the University of Arkansas for Medical Sciences (UAMS) Proteomics Core for analysis. Protein extraction and protease digestion was completed according to UAMS internal protocols. Data-independent acquisition (DIA) was completed with the Orbitrap Exploris 480 mass spectrometer.

Polysome purification and sucrose gradient sedimentation

Polysomes were isolated essentially as described (58). *F. tularensis* cells were grown until early log (OD_{600} 0.2-0.25). Liquid cultures were rapidly filtered through 0.2 μm nitrocellulose membranes and transferred to a conical tube filled with liquid nitrogen. Cells were lysed by bead-beating with 650 μL flash frozen lysis buffer (25 mM HEPES pH 7.6, 100 mM NH_4Cl , 10 mM MgCl_2 , 0.4% Triton X-100, 0.1% NP-40, 100 U/mL Rnase-free Dnase) using the TissueLyser II (Qiagen) five times (15 Hz, 3 mins). Cell debris was pelleted and the polysome-containing lysates were stored at -80°C .

Sucrose gradients were prepared using 10 and 55% sucrose solutions in 25 mM HEPES pH 7.6, 100 mM NH_4Cl , 10 mM MgCl_2 with the BioComp Instruments 153

Gradient Station (BioComp). Cell lysates were layered onto gradients and centrifuged with the Beckman-Coulter SW40 Ti rotor at 40,000 rpm for 2.5 hr at 4°C. Gradients were fractionated using the Triax full spectrum flow cell and fractionator (BioComp; 0.2 mm/s, 28 fractions) and A260 was measured every second. Collected fractions were stored at -80°C. 20 µL of each fraction was combined with 10 µL of sample loading buffer (3X NuPAGE LDS with 50 mM DTT) and immunoblotted as described above.

Intramacrophage replication assays

Intramacrophage growth assays were performed as previously described (56). Briefly, approximately 2.5×10^4 cells of murine macrophage-like J774A.1 cells were incubated at 37°C in 5% CO₂ overnight in 96-well plates in DMEM (Invitrogen) supplemented with 10% fetal bovine serum (Gemini Bio-Products; DMEM-F). Macrophage cells were infected with LVS and indicated derivative strains at an MOI of approximately 5 – 10. After two hours, cells were washed twice with PBS and media was replaced with DMEM-F containing 10 µg/mL gentamycin. After 2 or 24 hours of infection, macrophage were lysed for 30 minutes in 1% saponin in PBS and plated for enumeration.

Antibiotic chase experiment

Indicated *F. tularensis* LVS cells were grown to mid-log in liquid culture (OD₆₀₀ 0.3-0.4). Spectinomycin was added to a final concentration of 200 µg/mL. Cells were collected at the indicated time points after antibiotic addition and resuspended in

sample loading buffer normalized to OD₆₀₀ at t=0. Immunoblotting was conducted as described above and analysis was conducted using one-phase decay equation on Prism 9 (GraphPad). Data represents two experiments in biological triplicate.

Data availability

RNA-Seq reads are available in the National Center for Biotechnology Information Gene Expression Omnibus (NCBI GEO) under accession number GSE210766.

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SUPPLEMENTAL FIGURES

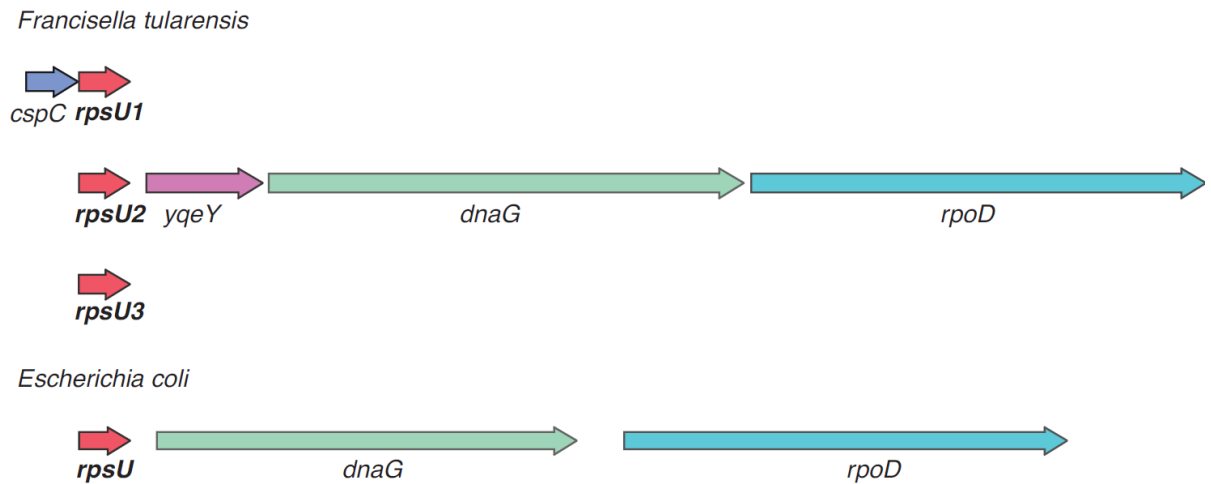


Figure S1. *F. tularensis* encodes three *rpsU* genes. *F. tularensis* *rpsU2*, which encodes bS21-2, is syntenic with the only *rpsU* in *E. coli*, which is located in the macromolecular synthesis operon (1). This operon in *E. coli* includes *rpsU* (encoding bS21), *dnaG* (encoding DNA primase), and *rpoD* (encoding RNA polymerase σ^{70}). In *F. tularensis*, this operon also includes *yqeY*, the product of which may be involved in tRNA aminoacylation. *rpsU1*, encoding bS21-1, is located immediately downstream of *cspC* (encoding cold-shock protein CspC), while *rpsU3*, encoding bS21-3, is not apparently in an operon with other genes. Genomic locations of *rpsU* genes were determined using RefSeq NC_007880 for *F. tularensis* and NC_000913 for *E. coli*.

	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-1	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-3	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-2	<i>E. coli</i> bS21
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-1	100.0	72.3	54.0	50.8
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-3		100.0	47.6	48.5
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-2			100.0	60.0
<i>E. coli</i> bS21				100.0

Figure S2. The three bS21 homologs in *F. tularensis* are distinct. Percent identities of amino acid sequences for *F. tularensis* LVS bS21-1, bS21-2, bS21-3 and *E. coli* bS21 were calculated using the multiple sequence alignment tool ClustalOmega (2). The bS21 homologs in *F. tularensis* are similar to each other, particularly bS21-1 and bS21-3 which are 72% identical at the amino acid level. bS21-2, encoded by the *rpsU* homolog gene syntenic to the single *E. coli rpsU* gene, is also the most similar to *E. coli* bS21, with 60% amino acid identity.

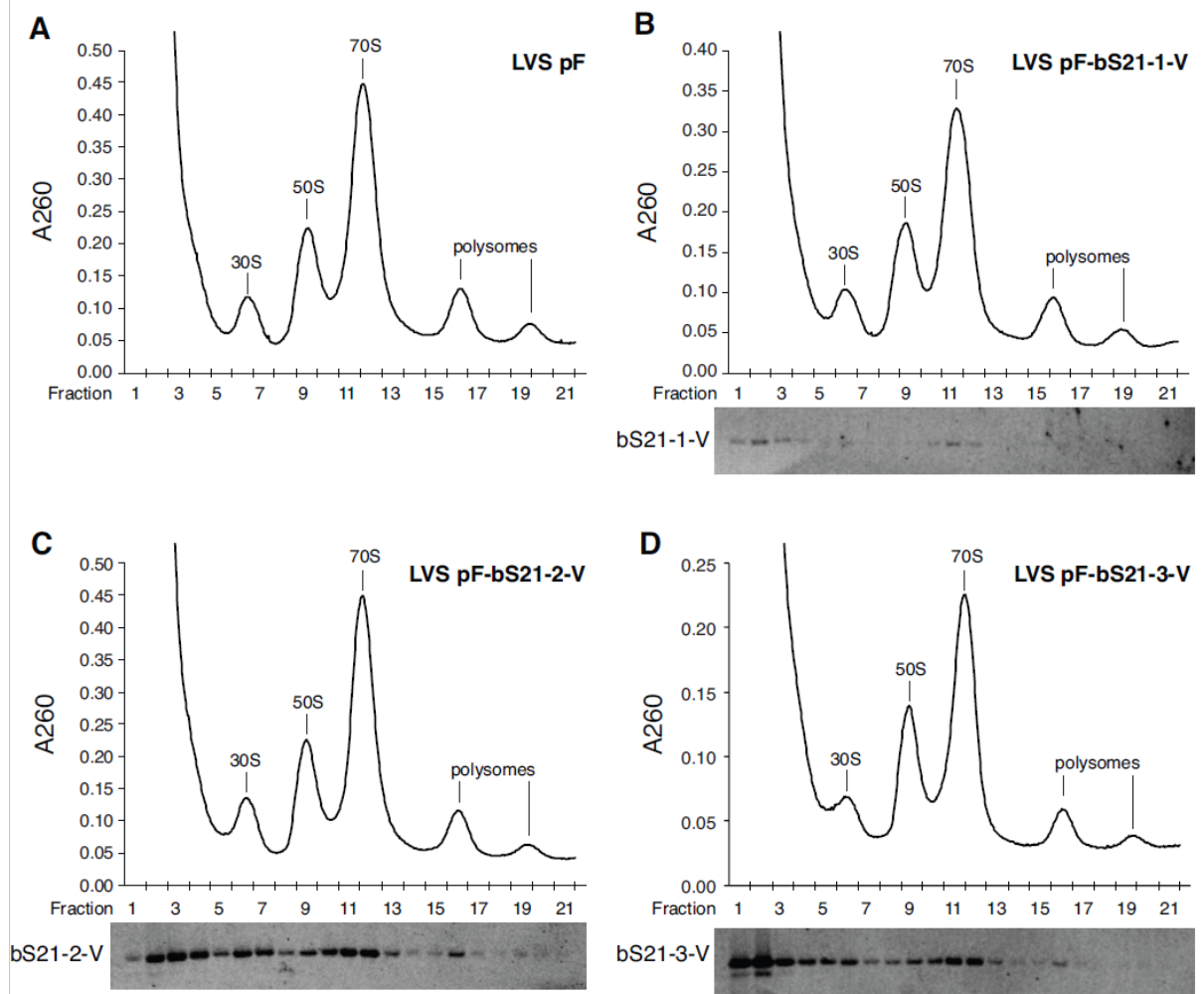


Figure S3. Each bS21 homolog can be detected in translationally-active ribosomes. For **A – D**, top: Sucrose gradient sedimentation profile from actively-translating wild-type *F. tularensis* cells with either empty vector or ectopic expression of indicated bS21 homolog. Nucleic acid content was monitored by A260 (y-axis). Peaks corresponding to the 30S, 50S, 70S, and polysomes are indicated. Fractions collected are indicated on the x-axis. For **A – D**, bottom: Immunoblot analysis of fractions from sucrose gradient sedimentation (above), probing for VSV-G. Wells correspond to fractions 1 – 21 from profile above. **A.** Cells from wild-type *F. tularensis* LVS with empty vector (LVS pF). **B.** Cells from wild-type *F. tularensis* LVS with ectopic expression of bS21-1 (LVS pF-bS21-1-V). **C.** Cells from wild-type *F. tularensis* LVS with ectopic expression of bS21-2 (LVS pF-bS21-2-V). **D.** Cells from wild-type *F. tularensis* LVS with ectopic expression of bS21-3 (LVS pF-bS21-3-V).

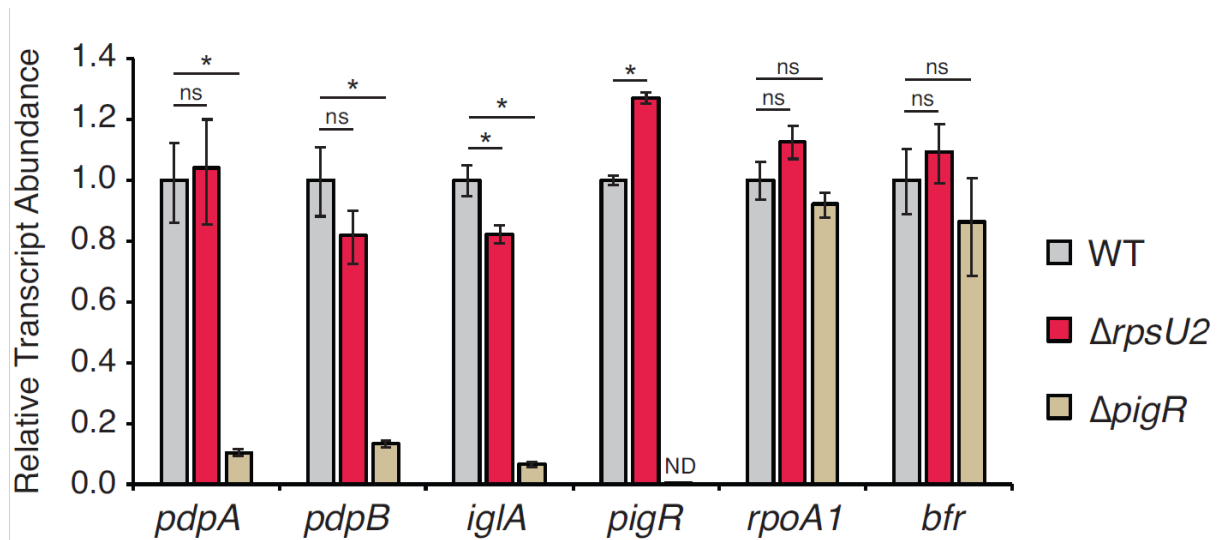


Figure S4. Loss of bS21-2 does not affect transcript abundance of FPI-encoded genes. Quantitative real-time PCR was used to determine the relative transcript abundance for indicated FPI genes in wild-type cells, cells lacking bS21-2 ($\Delta rpsU2$), or cells lacking the transcription factor PigR ($\Delta pigR$). Cells lacking PigR serve as a positive control, as PigR positively regulates its own transcription and the transcription of *pdpA*, *pdpB*, and *iglA*. The *rpoA1* and *bfr* genes are included as negative controls, as their expression is not influenced by bS21-2 or PigR. Transcript abundances are normalized to *tul4*, whose expression is not influenced by bS21-2 or PigR. Error bars represent 1 SD from the value (calculated using the mean threshold cycle). ns: not significant. ND: not detected *adjusted $p < 0.05$ by t-test with Bonferroni correction.

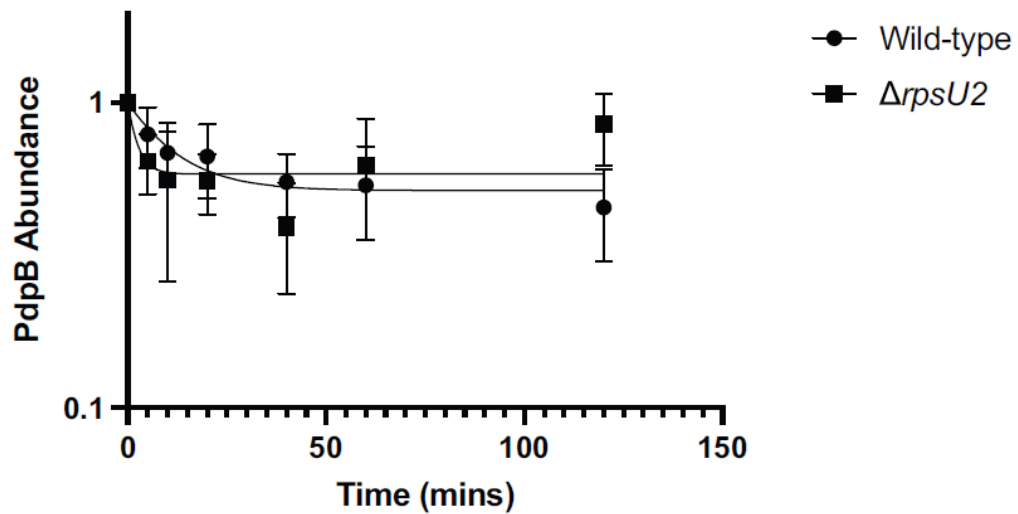


Figure S5. Loss of bS21-2 does not affect protein degradation of PdpB. One-phase decay of PdpB from antibiotic-chase experiment from wild-type cells and cells lacking bS21-2 ($\Delta rpsU2$). Neither strain showed significant degradation of PdpB through the time points assessed; the calculated half-life for both was greater than 120 minutes. Y-axis is logarithmic and error bars represent 1 SD from the mean.

Supplemental References

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Table S1. Proteins associated with purified *F. tularensis* ribosomes. LC-MS/MS analysis of four samples of ribosomes purified from wild-type cells by sucrose cushions. Total spectral counts (columns F-I) were filtered with the following parameters: 99% protein threshold, 95% peptide threshold, minimum of 2 peptides. Hypothetical proteins with no known function were not categorized as transcription or translation-related. Proteins were primarily ribosomal (69%) or associated with transcription and translation processes (10%).

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_514345.1	57	FTL_1714	<i>groEL</i>	chaperonin GroEL
YP_514522.1	62	FTL_1912	<i>rpsA</i>	30S ribosomal protein S1
YP_513037.1	25	FTL_0242	<i>rpsC</i>	30S ribosomal protein S3
YP_513727.1	16	FTL_1026	<i>rplI</i>	50S ribosomal protein L9
YP_513045.1	14	FTL_0250	<i>rpsH</i>	30S ribosomal protein S8
YP_514378.1	25	FTL_1747	<i>rplA</i>	50S ribosomal protein L1
YP_513101.1	100	FTL_0309	<i>aceE</i>	pyruvate dehydrogenase subunit E1
YP_514376.1	13	FTL_1745	<i>rplL</i>	50S ribosomal protein L7/L12
YP_513044.1	12	FTL_0249	<i>rpsN</i>	30S ribosomal protein S14
YP_514377.1	19	FTL_1746	<i>rplJ</i>	50S ribosomal protein L10
YP_513055.1	23	FTL_0260	<i>rpsD</i>	30S ribosomal protein S4
YP_513032.1	23	FTL_0237	<i>rplD</i>	50S ribosomal protein L4

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513043.1	20	FTL_0248	<i>rplE</i>	50S ribosomal protein L5
YP_513030.1	12	FTL_0235	<i>rpsJ</i>	30S ribosomal protein S10
YP_513019.1	26	FTL_0224	<i>rpsB</i>	30S ribosomal protein S2
YP_513031.1	22	FTL_0236	<i>rplC</i>	50S ribosomal protein L3
YP_513041.1	13	FTL_0246	<i>rplN</i>	50S ribosomal protein L14
YP_513102.1	57	FTL_0310	-	dihydrolipoamide acetyltransferase
YP_513036.1	12	FTL_0241	<i>rplV</i>	50S ribosomal protein L22
YP_513046.1	19	FTL_0251	<i>rplF</i>	50S ribosomal protein L6
YP_513048.1	18	FTL_0253	<i>rpsE</i>	30S ribosomal protein S5
YP_513034.1	30	FTL_0239	<i>rplB</i>	50S ribosomal protein L2
YP_514399.1	103	FTL_1772	-	aconitate hydratase
YP_513039.1	8	FTL_0244	-	50S ribosomal protein L29
YP_514411.1	66	FTL_1786	-	succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit
YP_513870.1	16	FTL_1187	<i>rplM</i>	50S ribosomal protein L13
YP_513042.1	11	FTL_0247	<i>rplX</i>	50S ribosomal protein L24
YP_513869.1	15	FTL_1186	<i>rpsI</i>	30S ribosomal protein S9
YP_513057.1	17	FTL_0262	<i>rplQ</i>	50S ribosomal protein L17
YP_513468.1	96	FTL_0717	<i>rne</i>	ribonuclease E
YP_513038.1	16	FTL_0243	<i>rplP</i>	50S ribosomal protein L16
YP_514420.1	50	FTL_1795	-	F0F1 ATP synthase subunit beta
YP_513028.1	18	FTL_0233	<i>rpsG</i>	30S ribosomal protein S7
YP_513345.1	83	FTL_0585	<i>fadE</i>	acyl-CoA dehydrogenase

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_514379.1	15	FTL_1748	<i>rplK</i>	50S ribosomal protein L11
YP_513047.1	13	FTL_0252	<i>rplR</i>	50S ribosomal protein L18
YP_513103.1	51	FTL_0311	-	dihydrolipoamide dehydrogenase
YP_513874.1	69	FTL_1191	<i>dnaK</i>	molecular chaperone DnaK
YP_514408.1	53	FTL_1783	<i>sucB</i>	dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex
YP_514115.1	71	FTL_1464	-	ATP-dependent metalloprotease
YP_514366.1	13	FTL_1735	<i>rplS</i>	50S ribosomal protein L19
YP_513053.1	13	FTL_0258	<i>rpsM</i>	30S ribosomal protein S13
YP_513054.1	14	FTL_0259	-	30S ribosomal protein S11
YP_514198.1	70	FTL_1552	-	hypothetical protein FTL_1552
YP_514374.1	157	FTL_1743	-	DNA-directed RNA polymerase subunit beta
YP_513622.1	40	FTL_0903	<i>hflK</i>	FtsH protease activity modulator
YP_514409.1	106	FTL_1784	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component
YP_514108.1	12	FTL_1453	<i>rplU</i>	50S ribosomal protein L21
YP_513726.1	8	FTL_1025	<i>rpsR</i>	30S ribosomal protein S18
YP_513661.1	11	FTL_0950	-	50S ribosomal protein L25
YP_514446.1	87	FTL_1824	-	NADH dehydrogenase subunit G
YP_514059.1	13	FTL_1404	<i>rplT</i>	50S ribosomal protein L20
YP_513725.1	13	FTL_1024	<i>rpsF</i>	30S ribosomal protein S6
YP_514184.1	10	FTL_1538	<i>rpsO</i>	30S ribosomal protein S15

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513559.1	53	FTL_0837	<i>metIQ</i>	D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein
YP_513050.1	15	FTL_0255	<i>rpIO</i>	50S ribosomal protein L15
YP_514183.1	76	FTL_1537	<i>pnp</i>	polynucleotide phosphorylase/polyadenylase
YP_513639.1	19	FTL_0926	-	Ferritin-like protein
YP_513033.1	11	FTL_0238	<i>rpIW</i>	50S ribosomal protein L23
YP_513788.1	40	FTL_1096	<i>dsbA</i>	Disulfide bond formation protein A / FipB
YP_514154.1	81	FTL_1504	<i>katG</i>	peroxidase/catalase
YP_514517.1	40	FTL_1907	-	cell division protein FtsZ
YP_514539.1	34	FTL_1936	-	periplasmic solute binding family protein
YP_512944.1	49	FTL_0146	-	ABC transporter ATP-binding protein
YP_513027.1	14	FTL_0232	<i>rpsL</i>	30S ribosomal protein S12
YP_514375.1	151	FTL_1744	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
YP_514422.1	56	FTL_1797	-	F0F1 ATP synthase subunit alpha
YP_513291.1	9	FTL_0522	<i>rpmB</i>	50S ribosomal protein L28
YP_513974.2	8	FTL_1303	<i>rpmE</i>	50S ribosomal protein L31
YP_513035.1	10	FTL_0240	<i>rpsS</i>	30S ribosomal protein S19
YP_514307.1	113	FTL_1672	-	AcrB/AcrD/AcrF family transporter
YP_513615.1	55	FTL_0896	-	peptidyl-prolyl cis-trans isomerase D
YP_514047.1	64	FTL_1392	<i>deaD</i>	cold-shock DEAD-box protein A
YP_514382.1	43	FTL_1751	-	elongation factor Tu
YP_514071.1	45	FTL_1416	<i>capB</i>	capsule biosynthesis protein capB

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513570.1	70	FTL_0848	<i>secD</i>	preprotein translocase subunit SecD
YP_513438.1	38	FTL_0687	-	HlyD family secretion protein
YP_514229.1	25	FTL_1590	-	hypothetical protein FTL_1590
YP_513040.1	10	FTL_0245	<i>rpsQ</i>	30S ribosomal protein S17
YP_514410.1	27	FTL_1785	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit
YP_514303.1	67	FTL_1668	<i>msbA</i>	lipid A transport protein ABC transporter ATP-binding protein/permease
YP_514421.1	33	FTL_1796	-	F0F1 ATP synthase subunit gamma
YP_513829.1	7	FTL_1143	<i>rpmF</i>	50S ribosomal protein L32
YP_513965.1	31	FTL_1294	-	short-chain dehydrogenase
YP_514434.1	92	FTL_1809	<i>infB</i>	translation initiation factor IF-2
YP_513610.1	50	FTL_0891	<i>tig</i>	trigger factor
YP_513260.1	57	FTL_0488	-	4-alpha-glucanotransferase
YP_513919.1	50	FTL_1239	<i>ffh</i>	signal recognition particle protein, Ffh
YP_513652.1	26	FTL_0939	-	aldolase/adducin class II family protein
YP_514069.1	44	FTL_1414	<i>capA</i>	hypothetical membrane protein, capA
YP_513862.1	11	FTL_1179	<i>hfp</i>	ribosome hibernation-promoting factor
YP_512874.1	10	FTL_0070	<i>rpsT</i>	30S ribosomal protein S20
YP_513049.1	7	FTL_0254	<i>rpmD</i>	50S ribosomal protein L30
YP_513747.1	8	FTL_1047	<i>rpsU2</i>	30S ribosomal protein S21-2
YP_514109.1	104	FTL_1458	<i>secA</i>	preprotein translocase subunit SecA
YP_513144.1	22	FTL_0361	-	LemA-like protein
YP_514369.1	9	FTL_1738	<i>rpsP</i>	30S ribosomal protein S16

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513551.1	30	FTL_0829	-	glycerophosphoryl diester phosphodiesterase
YP_513790.1	15	FTL_1100	<i>rsfS</i>	ribosomal silencing factor RsfS
YP_514488.1	37	FTL_1874	<i>obgE</i>	GTPase ObgE
YP_514310.1	38	FTL_1678	-	hypothetical protein FTL_1678
YP_514129.1	52	FTL_1478	<i>guaB</i>	inosine-5-monophosphate dehydrogenase
YP_513623.1	35	FTL_0904	<i>hflC</i>	protease modulator HflC
YP_514140.1	115	FTL_1489	-	FAD-binding family protein
YP_512961.1	30	FTL_0166	-	universal stress protein
YP_514306.1	50	FTL_1671	-	RND efflux transporter
YP_513537.1	150	FTL_0805	-	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase
YP_512931.1	81	FTL_0133	<i>feoB</i>	ferrous iron transport protein
YP_512973.1	62	FTL_0178	<i>yidC</i>	inner-membrane protein
YP_513113.1	47	FTL_0325	-	OmpA family protein
YP_513349.1	33	FTL_0589	-	hypothetical membrane protein FTL_0589
YP_513560.1	39	FTL_0838	<i>metN</i>	D-methionine transport protein, ABC transporter,ATP-binding subunit
YP_514354.1	24	FTL_1723	-	hypothetical protein FTL_1723
YP_513202.1	33	FTL_0430	-	hypothetical protein FTL_0430
YP_514185.1	63	FTL_1539	<i>ftsI</i>	penicillin binding protein (peptidoglycan synthetase)

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_514040.1	13	FTL_1384	-	hypothetical protein FTL_1384
YP_514107.1	9	FTL_1452	<i>rpmA</i>	50S ribosomal protein L27
YP_514451.1	17	FTL_1829	-	NADH dehydrogenase subunit B
YP_514447.1	46	FTL_1825	-	NADH dehydrogenase I subunit F
YP_512984.1	64	FTL_0189	-	cytochrome d terminal oxidase, polypeptide subunit I
YP_514250.1	36	FTL_1611	-	glycosyl transferase family protein
YP_514336.1	92	FTL_1705	<i>ftsK</i>	cell division protein
YP_513572.1	20	FTL_0850	-	hypothetical protein FTL_0850
YP_513208.1	107	FTL_0436	<i>ileS</i>	isoleucyl-tRNA synthetase
YP_513322.1	86	FTL_0556	<i>rnr</i>	ribonuclease R
YP_513187.1	52	FTL_0414	<i>engA</i>	GTP-binding protein EngA
YP_514341.1	28	FTL_1710	-	ProP osmoprotectant transporter, fragment, partial
YP_513409.1	45	FTL_0656	-	hypothetical membrane protein FTL_0656
YP_514524.1	21	FTL_1914	<i>ripA</i>	hypothetical membrane protein, ripA
YP_513957.1	15	FTL_1286	-	hypothetical membrane protein FTL_1286
YP_513310.1	22	FTL_0541	-	hypothetical membrane protein FTL_0541
YP_513309.1	43	FTL_0540	<i>lpxB</i>	lipid-A-disaccharide synthase
YP_513875.1	41	FTL_1192	-	chaperone protein DnaJ
YP_514424.1	17	FTL_1799	-	F0F1 ATP synthase subunit B
YP_513352.1	66	FTL_0592	<i>wbtA</i>	dTDP-glucose 4,6-dehydratase
YP_513408.1	40	FTL_0655	-	hypothetical membrane protein FTL_0655

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_514276.1	38	FTL_1637	-	lipoprotein
YP_512895.1	96	FTL_0094	<i>clpB</i>	ClpB protein
YP_513246.1	48	FTL_0474	-	lipoprotein releasing system, subunit C, putative membrane protein
YP_513660.1	35	FTL_0949	-	ribose-phosphate pyrophosphokinase
YP_513029.1	78	FTL_0234	-	elongation factor G
YP_513426.1	31	FTL_0674	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase
YP_514060.1	7	FTL_1405	<i>rpml</i>	50S ribosomal protein L35
YP_514346.1	10	FTL_1715	<i>groES</i>	co-chaperonin GroES
YP_513375.1	35	FTL_0616	<i>rpoA2</i>	DNA-directed RNA polymerase subunit alpha
YP_514221.1	45	FTL_1582	<i>potF</i>	putrescine-binding periplasmic protein
YP_513354.1	30	FTL_0594	<i>wbtC</i>	UDP-glucose 4-epimerase
YP_513364.1	33	FTL_0604	<i>wbtK</i>	glycosyltransferase
YP_512987.1	76	FTL_0192	-	cytochrome O ubiquinol oxidase subunit I
YP_513211.1	58	FTL_0439	-	hypothetical protein FTL_0439
YP_513381.1	36	FTL_0625	<i>gtrB</i>	glycosyl transferase family protein
YP_513890.1	31	FTL_1207	-	MRP like protein
YP_513662.1	47	FTL_0951	-	hypothetical membrane protein FTL_0951
YP_513519.1	67	FTL_0784	-	lipoprotein
YP_513617.1	12	FTL_0898	<i>hfq</i>	host factor I for bacteriophage Q beta replication
YP_512875.1	66	FTL_0071	-	GTP-binding protein LepA

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513308.1	28	FTL_0539	-	UDP-N-acetylglucosamine acyltransferase
YP_513332.1	52	FTL_0572	-	hypothetical protein FTL_0572
YP_513433.1	42	FTL_0681	<i>potG</i>	polyamine transporter, ABC transporter, ATP-binding protein
YP_513288.1	30	FTL_0519	<i>minD</i>	septum site-determining protein MinD
YP_512888.1	28	FTL_0087	-	acetyltransferase protein
YP_512910.1	58	FTL_0112	<i>iglB</i>	intracellular growth locus, subunit B
YP_513180.1	64	FTL_0407	<i>ubiB</i>	2-polyprenylphenol 6-hydroxylase
YP_512982.1	28	FTL_0187	-	cyclohexadienyl dehydratase
YP_513955.1	37	FTL_1284	-	glutathione synthetase
YP_514168.1	84	FTL_1521	-	chitinase family 18 protein
YP_513056.1	35	FTL_0261	-	DNA-directed RNA polymerase subunit alpha
YP_514174.1	50	FTL_1527	<i>eno</i>	phosphopyruvate hydratase
YP_513398.1	15	FTL_0645	-	lipoprotein
YP_514518.1	45	FTL_1908	-	cell division protein FtsA
YP_514423.1	19	FTL_1798	-	F0F1 ATP synthase subunit delta
YP_513109.1	12	FTL_0317	-	hypothetical protein FTL_0317
YP_513716.1	20	FTL_1015	-	AhpC/TSA family protein
YP_512923.1	128	FTL_0125	<i>pdpB</i>	Type VI Secretion protein PdpB
YP_513117.1	30	FTL_0329	<i>pssA</i>	CDP-alcohol phosphatidyltransferase
YP_514293.1	49	FTL_1658	<i>fimV</i>	hypothetical protein, fimV
YP_513437.1	55	FTL_0686	-	outer membrane efflux protein

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_514231.1	16	FTL_1592	<i>accB</i>	Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit
YP_513413.1	60	FTL_0661	-	hypothetical protein FTL_0661
YP_512889.1	29	FTL_0088	-	acetyltransferase protein
YP_512998.1	37	FTL_0203	-	hypothetical protein FTL_0203
YP_513823.1	44	FTL_1137	-	3-oxoacyl-ACP synthase
YP_513977.1	40	FTL_1306	-	hypothetical protein FTL_1306
YP_514130.1	52	FTL_1479	<i>pepA</i>	cytosol aminopeptidase
YP_513886.1	55	FTL_1203	-	cardiolipin synthetase
YP_513427.1	27	FTL_0675	<i>panG</i>	hypothetical protein, putative ketopantoate reductase
YP_512975.1	36	FTL_0180	<i>htrB</i>	acyltransferase
YP_513912.1	15	FTL_1231	-	hypothetical protein, FeS assembly SUF system regulator
YP_513348.1	82	FTL_0588	-	isocitrate dehydrogenase
YP_513908.1	26	FTL_1225	-	hypothetical protein FTL_1225
YP_514514.1	37	FTL_1904	-	peptide chain release factor 2
YP_513506.1	18	FTL_0761	<i>smpB</i>	SsrA-binding protein
YP_513194.1	16	FTL_0421	<i>tul4</i>	lipoprotein
YP_513994.1	41	FTL_1328	<i>fopA</i>	outer membrane associated protein
YP_513290.1	6	FTL_0521	<i>rpmG</i>	50S ribosomal protein L33
YP_514444.1	19	FTL_1822	-	NADH dehydrogenase subunit I
YP_514449.1	48	FTL_1827	-	NADH dehydrogenase subunit D

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513550.1	67	FTL_0828	-	Type IV pili nucleotide binding protein, ABC transporter ATP-binding protein
YP_513237.1	43	FTL_0465	-	BNR/Asp-box repeat-containing protein
YP_513828.1	38	FTL_1142	-	putative glycerol-3-phosphate acyltransferase PlsX
YP_512904.1	14	FTL_0105	-	hypothetical membrane protein FTL_0105
YP_513742.1	29	FTL_1042	-	FKBP-type peptidyl-prolyl cis-trans isomerase family protein
YP_513894.1	21	FTL_1211	-	lipoprotein
YP_513329.1	20	FTL_0569	-	hypothetical protein FTL_0569
YP_514450.1	25	FTL_1828	-	NADH dehydrogenase I
YP_513757.1	48	FTL_1060	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase
YP_513355.1	42	FTL_0595	-	galacturonosyl transferase
YP_514188.1	79	FTL_1542	-	hypothetical protein FTL_1542
YP_514419.1	16	FTL_1794	<i>atpC</i>	FOF1 ATP synthase subunit epsilon
YP_513746.1	51	FTL_1046	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase
YP_514074.1	29	FTL_1419	-	cyanophycinase
YP_513119.1	26	FTL_0331	-	TolQ protein
YP_513587.1	50	FTL_0865	-	major facilitator transporter
YP_512882.1	40	FTL_0078	-	riboflavin biosynthesis protein ribD
YP_513646.1	54	FTL_0933	-	DNA recombination protein RmuC family protein

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513540.1	43	FTL_0808	-	bifunctional 4'-phosphopantothienoylcysteine decarboxylase,phosphopantothienoylcysteine synthetase
YP_513532.1	64	FTL_0800	-	Type IV pilin multimeric outer membrane protein
YP_513376.1	17	FTL_0617	-	hypothetical protein FTL_0617
YP_514146.1	66	FTL_1495	-	cysteine/glutathione ABC transporter membrane/ATP-binding protein
YP_514236.1	99	FTL_1597	-	organic solvent tolerance protein
YP_512914.1	156	FTL_0116	<i>pdpC</i>	Type VI Secretion Protein PdpC
YP_514242.1	10	FTL_1603	-	RNA-binding protein
YP_514435.1	55	FTL_1810	<i>nusA</i>	transcription elongation factor NusA
YP_514021.1	8	FTL_0456 / FTL_1360	<i>rpsU1</i> / <i>rpsU3</i>	30S ribosomal protein S21
YP_513087.1	35	FTL_0295	-	acetyl-CoA carboxylase carboxyltransferase subunit alpha
YP_512970.1	5	FTL_0175	<i>rpmH</i>	50S ribosomal protein L34
YP_513548.1	15	FTL_0823	-	hypothetical lipoprotein FTL_0823
YP_513051.1	48	FTL_0256	<i>secY</i>	preprotein translocase subunit SecY
YP_512829.1	67	FTL_0020	<i>aspS</i>	aspartyl-tRNA synthetase
YP_514352.1	40	FTL_1721	<i>prfA</i>	peptide chain release factor 1
YP_514097.1	28	FTL_1442	<i>fabI</i>	enoyl-[acyl-carrier-protein] reductase (NADH)

Accession Number	Molecular Weight (kDa)	Gene Locus	Gene Name	Identified Proteins (245)
YP_513160.1	44	FTL_0387	<i>aspC1</i>	aspartate aminotransferase
YP_513200.1	35	FTL_0428	-	chromosome partition protein B
YP_513344.1	101	FTL_0584	-	bifunctional 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein
YP_513372.1	34	FTL_0612	<i>ppx</i>	exopolyphosphatase
YP_512917.1	25	FTL_0119	<i>dotU</i>	Type VI Secretion Protein DotU
YP_514482.1	57	FTL_1865	-	outer membrane protein tolC
YP_513195.1	19	FTL_0423	-	hypothetical protein FTL_0423
YP_514196.1	28	FTL_1550	-	lipoprotein
YP_512994.1	16	FTL_0199	-	hypothetical lipoprotein FTL_0199
YP_513001.1	61	FTL_0206	-	hypothetical protein FTL_0206
YP_513711.1	53	FTL_1005	-	hypothetical protein FTL_1005
YP_513307.1	18	FTL_0538	<i>fabZ</i>	(3R)-hydroxymyristoyl-ACP dehydratase
YP_514160.1	39	FTL_1511	-	glycerophosphoryl diester phosphodiesterase family protein
YP_513896.1	73	FTL_1213	-	hypothetical protein FTL_1213

Total spectra

99% protein
threshold, 95%
peptide
threshold,
minimum of 2
peptides

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_514345.1	141	248	273	257	NO	YES
YP_514522.1	756	245	192	277	YES	YES
YP_513037.1	255	232	225	247	YES	YES
YP_513727.1	295	220	228	228	YES	YES
YP_513045.1	299	183	163	175	YES	YES
YP_514378.1	252	164	159	199	YES	YES
YP_513101.1	67	154	139	161	NO	NO
YP_514376.1	414	151	165	212	YES	YES
YP_513044.1	166	139	131	123	YES	YES
YP_514377.1	296	128	141	156	YES	YES

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513055.1	304	125	76	157	YES	YES
YP_513032.1	385	123	142	128	YES	YES
YP_513043.1	157	109	102	105	YES	YES
YP_513030.1	177	105	93	141	YES	YES
YP_513019.1	135	104	115	112	YES	YES
YP_513031.1	173	101	108	109	YES	YES
YP_513041.1	168	96	104	105	YES	YES
YP_513102.1	39	96	71	95	NO	NO
YP_513036.1	240	95	86	55	YES	YES
YP_513046.1	283	82	128	93	YES	YES
YP_513048.1	189	71	67	81	YES	YES
YP_513034.1	184	67	62	75	YES	YES
YP_514399.1	10	67	70	68	NO	NO
YP_513039.1	24	65	67	63	YES	YES
YP_514411.1	16	64	60	46	NO	NO
YP_513870.1	85	52	50	48	YES	YES
YP_513042.1	72	52	50	65	YES	YES
YP_513869.1	64	50	53	42	YES	YES
YP_513057.1	82	49	40	49	YES	YES
YP_513468.1	75	47	39	35	NO	YES
YP_513038.1	61	47	38	44	YES	YES
YP_514420.1	25	47	60	62	NO	NO
YP_513028.1	80	46	39	54	YES	YES

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513345.1	22	46	58	55	NO	NO
YP_514379.1	51	42	38	39	YES	YES
YP_513047.1	192	41	35	35	YES	YES
YP_513103.1	31	41	28	44	NO	NO
YP_513874.1	18	40	35	37	NO	YES
YP_514408.1	4	39	34	34	NO	NO
YP_514115.1	7	36	39	34	NO	NO
YP_514366.1	75	35	37	43	YES	YES
YP_513053.1	68	35	32	34	YES	YES
YP_513054.1	94	33	41	39	YES	YES
YP_514198.1	4	33	34	34	NO	NO
YP_514374.1	65	32	27	29	NO	YES
YP_513622.1	10	30	35	31	NO	NO
YP_514409.1	3	29	25	25	NO	NO
YP_514108.1	321	27	25	30	YES	YES
YP_513726.1	34	27	31	29	YES	YES
YP_513661.1	33	27	26	27	YES	YES
YP_514446.1	10	26	29	23	NO	NO
YP_514059.1	84	25	30	33	YES	YES
YP_513725.1	49	25	27	25	YES	YES
YP_514184.1	38	25	18	19	YES	YES
YP_513559.1	5	25	32	26	NO	NO
YP_513050.1	110	24	25	27	YES	YES

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_514183.1	48	24	27	37	NO	YES
YP_513639.1	16	24	26	30	NO	NO
YP_513033.1	115	23	28	30	YES	YES
YP_513788.1	4	23	27	24	NO	NO
YP_514154.1	3	23	26	28	NO	NO
YP_514517.1	24	22	16	17	NO	NO
YP_514539.1	11	22	27	30	NO	NO
YP_512944.1	1	21	26	21	NO	NO
YP_513027.1	138	20	19	22	YES	YES
YP_514375.1	70	20	18	20	NO	YES
YP_514422.1	7	20	30	22	NO	NO
YP_513291.1	33	19	22	23	YES	YES
YP_513974.2	108	18	37	30	YES	YES
YP_513035.1	49	18	12	17	YES	YES
YP_514307.1	5	18	17	16	NO	NO
YP_513615.1	0	18	18	14	NO	YES
YP_514047.1	8	17	16	14	NO	YES
YP_514382.1	5	17	18	20	NO	YES
YP_514071.1	1	17	16	17	NO	NO
YP_513570.1	4	16	17	20	NO	YES
YP_513438.1	4	16	19	15	NO	NO
YP_514229.1	0	16	14	13	NO	NO
YP_513040.1	38	15	14	15	YES	YES

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_514410.1	2	15	20	18	NO	NO
YP_514303.1	0	15	17	16	NO	NO
YP_514421.1	0	15	22	18	NO	NO
YP_513829.1	16	14	16	14	YES	YES
YP_513965.1	2	14	13	12	NO	NO
YP_514434.1	0	13	11	14	NO	YES
YP_513610.1	41	12	18	20	NO	YES
YP_513260.1	35	12	10	16	NO	NO
YP_513919.1	17	12	11	12	NO	YES
YP_513652.1	9	12	8	12	NO	NO
YP_514069.1	0	12	19	14	NO	NO
YP_513862.1	30	11	11	13	NO	YES
YP_512874.1	19	11	11	10	YES	YES
YP_513049.1	18	11	13	15	YES	YES
YP_513747.1	18	11	8	9	YES	YES
YP_514109.1	3	11	6	1	NO	YES
YP_513144.1	0	11	19	19	NO	NO
YP_514369.1	0	11	15	14	YES	YES
YP_513551.1	17	10	11	10	NO	NO
YP_513790.1	16	9	8	9	NO	YES
YP_514488.1	7	9	5	10	NO	YES
YP_514310.1	6	9	11	8	NO	NO
YP_514129.1	6	9	6	7	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513623.1	3	9	16	12	NO	NO
YP_514140.1	3	9	7	5	NO	NO
YP_512961.1	3	9	8	8	NO	NO
YP_514306.1	1	9	10	10	NO	NO
YP_513537.1	1	9	7	7	NO	NO
YP_512931.1	0	9	18	14	NO	NO
YP_512973.1	0	9	10	10	NO	NO
YP_513113.1	0	9	18	19	NO	NO
YP_513349.1	0	9	9	11	NO	NO
YP_513560.1	0	9	10	7	NO	NO
YP_514354.1	0	9	10	8	NO	NO
YP_513202.1	0	9	12	12	NO	NO
YP_514185.1	0	9	18	15	NO	NO
YP_514040.1	0	9	8	9	NO	NO
YP_514107.1	18	8	7	8	YES	YES
YP_514451.1	6	8	11	10	NO	NO
YP_514447.1	5	8	14	7	NO	NO
YP_512984.1	3	8	14	14	NO	NO
YP_514250.1	0	8	14	9	NO	NO
YP_514336.1	0	8	6	7	NO	NO
YP_513572.1	0	8	8	5	NO	NO
YP_513208.1	0	8	9	6	NO	YES
YP_513322.1	32	7	11	11	NO	YES

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513187.1	8	7	6	12	NO	YES
YP_514341.1	2	7	7	7	NO	NO
YP_513409.1	1	7	7	6	NO	NO
YP_514524.1	1	7	6	4	NO	NO
YP_513957.1	0	7	9	8	NO	NO
YP_513310.1	4	6	7	9	NO	NO
YP_513309.1	2	6	5	6	NO	NO
YP_513875.1	1	6	6	4	NO	YES
YP_514424.1	0	6	11	10	NO	NO
YP_513352.1	0	6	15	13	NO	NO
YP_513408.1	0	6	12	13	NO	NO
YP_514276.1	0	6	6	6	NO	NO
YP_512895.1	0	6	5	7	NO	YES
YP_513246.1	0	6	8	8	NO	NO
YP_513660.1	0	6	8	12	NO	NO
YP_513029.1	0	6	3	7	NO	YES
YP_513426.1	0	6	2	6	NO	NO
YP_514060.1	0	6	6	6	YES	YES
YP_514346.1	0	6	5	8	NO	YES
YP_513375.1	18	5	10	8	NO	YES
YP_514221.1	0	5	5	5	NO	NO
YP_513354.1	0	5	10	8	NO	NO
YP_513364.1	0	5	9	4	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_512987.1	0	5	4	6	NO	NO
YP_513211.1	0	5	7	5	NO	NO
YP_513381.1	0	5	4	6	NO	NO
YP_513890.1	0	5	4	5	NO	NO
YP_513662.1	0	5	8	0	NO	NO
YP_513519.1	0	5	6	3	NO	NO
YP_513617.1	12	4	8	5	NO	YES
YP_512875.1	6	4	3	0	NO	YES
YP_513308.1	2	4	10	9	NO	NO
YP_513332.1	0	4	3	4	NO	NO
YP_513433.1	0	4	8	8	NO	NO
YP_513288.1	0	4	6	5	NO	NO
YP_512888.1	0	4	4	2	NO	NO
YP_512910.1	0	4	4	4	NO	NO
YP_513180.1	0	4	4	4	NO	NO
YP_512982.1	0	4	6	5	NO	NO
YP_513955.1	0	4	4	3	NO	NO
YP_514168.1	0	4	6	4	NO	NO
YP_513056.1	16	3	4	4	NO	YES
YP_514174.1	1	3	6	4	NO	NO
YP_513398.1	0	3	4	8	NO	NO
YP_514518.1	0	3	4	10	NO	NO
YP_514423.1	0	3	5	6	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513109.1	0	3	4	4	NO	NO
YP_513716.1	0	3	2	5	NO	NO
YP_512923.1	0	3	16	5	NO	NO
YP_513117.1	0	3	2	3	NO	NO
YP_514293.1	0	3	8	2	NO	NO
YP_513437.1	0	3	11	6	NO	NO
YP_514231.1	0	3	3	4	NO	NO
YP_513413.1	0	3	2	1	NO	NO
YP_512889.1	0	3	2	4	NO	NO
YP_512998.1	0	3	10	7	NO	NO
YP_513823.1	18	3	3	2	NO	NO
YP_513977.1	0	3	14	9	NO	NO
YP_514130.1	0	3	4	6	NO	YES
YP_513886.1	0	3	3	5	NO	NO
YP_513427.1	0	3	4	4	NO	NO
YP_512975.1	0	3	2	4	NO	NO
YP_513912.1	0	3	4	5	NO	NO
YP_513348.1	0	3	0	4	NO	NO
YP_513908.1	0	3	2	2	NO	NO
YP_514514.1	28	2	2	3	NO	YES
YP_513506.1	11	2	8	6	NO	YES
YP_513194.1	6	2	14	16	NO	NO
YP_513994.1	4	2	15	12	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513290.1	3	2	4	3	YES	YES
YP_514444.1	2	2	3	2	NO	NO
YP_514449.1	1	2	4	4	NO	NO
YP_513550.1	1	2	1	2	NO	NO
YP_513237.1	1	2	5	4	NO	NO
YP_513828.1	0	2	2	4	NO	NO
YP_512904.1	0	2	6	6	NO	NO
YP_513742.1	0	2	6	5	NO	YES
YP_513894.1	0	2	3	3	NO	NO
YP_513329.1	0	2	4	5	NO	NO
YP_514450.1	0	2	2	4	NO	NO
YP_513757.1	0	2	3	4	NO	NO
YP_513355.1	0	2	7	4	NO	NO
YP_514188.1	0	2	7	8	NO	NO
YP_514419.1	0	2	4	4	NO	NO
YP_513746.1	0	2	6	2	NO	NO
YP_514074.1	0	2	3	4	NO	NO
YP_513119.1	0	2	4	4	NO	NO
YP_513587.1	0	2	2	4	NO	NO
YP_512882.1	0	2	3	2	NO	NO
YP_513646.1	0	2	2	3	NO	NO
YP_513540.1	0	2	5	2	NO	NO
YP_513532.1	0	1	5	6	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513376.1	0	1	1	3	NO	NO
YP_514146.1	0	1	4	0	NO	NO
YP_514236.1	0	1	3	1	NO	NO
YP_512914.1	0	1	4	2	NO	NO
YP_514242.1	20	0	3	8	NO	YES
YP_514435.1	7	0	0	0	NO	YES
YP_514021.1	3	0	0	0	YES	YES
YP_513087.1	2	0	4	4	NO	NO
YP_512970.1	2	0	0	0	YES	YES
YP_513548.1	2	0	0	0	NO	NO
YP_513051.1	2	0	0	0	NO	YES
YP_512829.1	2	0	0	0	NO	YES
YP_514352.1	2	0	0	0	NO	YES
YP_514097.1	2	0	0	0	NO	NO
YP_513160.1	1	0	0	0	NO	NO
YP_513200.1	1	0	0	0	NO	NO
YP_513344.1	1	0	0	0	NO	NO
YP_513372.1	1	0	0	0	NO	NO
YP_512917.1	1	0	0	0	NO	NO
YP_514482.1	0	0	3	1	NO	NO
YP_513195.1	0	0	2	3	NO	NO
YP_514196.1	0	0	4	2	NO	NO
YP_512994.1	0	0	4	4	NO	NO

Accession Number	Sample A	Sample B	Sample C	Sample D	Ribosomal Protein	Reported transcription/translation complex component
YP_513001.1	0	0	6	0	NO	NO
YP_513711.1	0	0	3	2	NO	NO
YP_513307.1	0	0	4	1	NO	NO
YP_514160.1	0	0	2	3	NO	NO
YP_513896.1	0	0	5	0	NO	NO

	Sample A	Sample B	Sample C	Sample D	Total
Total spectra	8524.0	5626.0	5879.0	6158.0	26187.0
Total spectra from ribosomal proteins	7323.0	3454.0	3401.0	3739.0	17917.0
Percent spectra from ribosomal proteins	85.91%	61.39%	57.85%	60.72%	68.42%
Total spectra from translation/transcription components	8036.0	4081.0	4052.0	4401.0	20570.0
Percent spectra from translation/transcription components	94.27%	72.54%	68.92%	71.47%	78.55%

Table S2. Cells lacking bS21-2 exhibit genome-wide changes in protein abundance. Data-independent acquisition (DIA) mass spectrometry analysis of cellular lysates was used to quantify genome-wide protein abundance in wild-type cells (WT), cells lacking bS21-1 (delt_rpsU1), cells lacking bS21-2 (delt_rpsU2), and cells lacking bS21-3 (delt_rpsU3). Each deletion strain was compared to wild-type, but significant changes (>1.5-fold change, adjusted p-value <0.05, excluding bS21) were only observed in the cells lacking bS21-2. Cells are highlighted if the fold-change (columns R, U, and X) is greater than 1.5 (log2FC>0.58 or <-0.58). Green indicates less abundant in deletion strains compared to wild-type, and red indicates more abundant. Adjusted p-values are highlighted red if <0.05 (columns T, W, and Z).

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513747.1	YP_513747.1	FTL_1047	<i>rpsU2</i>	30S ribosomal protein S21-2
YP_513580.1	YP_513580.1	FTL_0858	-	hypothetical protein
YP_513220.1	YP_513220.1	FTL_0448	-	hypothetical protein
YP_513851.1	YP_513851.1	FTL_1167	<i>iglG</i>	hypothetical protein
YP_512919.1	YP_512919.1	FTL_0121	<i>iglG</i>	hypothetical protein
YP_514254.1	YP_514254.1	FTL_1615	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase
YP_513010.1	YP_513010.1	FTL_0215	-	dihydropteridine reductase
YP_513017.1	YP_513017.1	FTL_0222	-	hypothetical protein
YP_513601.1	YP_513601.1	FTL_0881	-	hypothetical protein
YP_513628.1	YP_513628.1	FTL_0915	-	acetolactate synthase small subunit
YP_514496.1	YP_514496.1	FTL_1883	-	potassium-transporting ATPase subunit A
YP_513787.1	YP_513787.1	FTL_1093	-	bifunctional methionine sulfoxide reductase B/A protein
YP_514317.1	YP_514317.1	FTL_1685	-	major facilitator transporter
YP_513786.1	YP_513786.1	FTL_1090	-	rRNA methyltransferase
YP_514023.1	YP_514023.1	FTL_1362	-	hypothetical protein
YP_513363.1	YP_513363.1	FTL_0603	<i>wzx</i>	O-antigen flippase
YP_514324.1	YP_514324.1	FTL_1693	-	hypothetical protein
YP_513465.1	YP_513465.1	FTL_0714	-	D-3-phosphoglycerate dehydrogenase
YP_513000.1	YP_513000.1	FTL_0205	-	hypothetical protein
YP_513080.1	YP_513080.1	FTL_0287	-	hypothetical protein
YP_514527.1	YP_514527.1	FTL_1917	-	30S ribosomal protein S6
YP_514530.1	YP_514530.1	FTL_1922	-	YggT family protein
YP_512896.1	YP_512896.1	FTL_0097	-	hypothetical protein
YP_513245.1	YP_513245.1	FTL_0473	-	peptide deformylase
YP_514476.1	YP_514476.1	FTL_1854	-	hypothetical protein
YP_512853.1	YP_512853.1	FTL_0045	-	orotidine 5'-phosphate decarboxylase
YP_513848.1	YP_513848.1	FTL_1164	<i>iglI</i>	hypothetical protein
YP_512916.1	YP_512916.1	FTL_0118	<i>iglI</i>	hypothetical protein
YP_513849.1	YP_513849.1	FTL_1165	<i>dotU</i>	hypothetical protein
YP_512917.1	YP_512917.1	FTL_0119	<i>dotU</i>	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513347.1	YP_513347.1	FTL_0587	-	arsenate reductase
YP_513542.1	YP_513542.1	FTL_0814	-	hypothetical protein
YP_514284.1	YP_514284.1	FTL_1645	<i>ansP</i>	major facilitator transporter, asparagine transporter
YP_512985.1	YP_512985.1	FTL_0190	-	major facilitator transporter
YP_514131.1	YP_514131.1	FTL_1480	-	YjgP/YjgQ family permease
YP_513847.1	YP_513847.1	FTL_1163	<i>iglI</i>	hypothetical protein
YP_512915.1	YP_512915.1	FTL_0117	<i>iglI</i>	hypothetical protein
YP_513137.1	YP_513137.1	FTL_0354	-	hypothetical protein
YP_513268.1	YP_513268.1	FTL_0499	-	S-adenosylmethionine decarboxylase
YP_513402.1	YP_513402.1	FTL_0649	-	aspartate/tyrosine/aromatic aminotransferase family protein
YP_513471.1	YP_513471.1	FTL_0720	-	DNA repair protein recO
YP_512943.1	YP_512943.1	FTL_0145	-	ABC transporter membrane protein
YP_513448.1	YP_513448.1	FTL_0697	-	ABC transporter membrane protein
YP_514358.1	YP_514358.1	FTL_1727	<i>ampD</i>	N-acetyl-anhydromuranmyl-L-alanine amidase
YP_513899.1	YP_513899.1	FTL_1216	-	hypothetical protein
YP_514486.1	YP_514486.1	FTL_1869	-	Na ⁺ /H ⁺ antiporter
YP_513856.1	YP_513856.1	FTL_1172	<i>pdpA</i>	PdpA protein
YP_512924.1	YP_512924.1	FTL_0126	<i>pdpA</i>	PdpA protein
YP_513850.1	YP_513850.1	FTL_1166	<i>iglH</i>	hypothetical protein
YP_512918.1	YP_512918.1	FTL_0120	<i>iglH</i>	hypothetical protein
YP_513852.1	YP_513852.1	FTL_1168	<i>iglF</i>	hypothetical protein
YP_512920.1	YP_512920.1	FTL_0122	<i>iglF</i>	hypothetical protein
YP_514064.1	YP_514064.1	FTL_1409	-	glycine cleavage system protein H
YP_514154.1	YP_514154.1	FTL_1504	<i>katG</i>	peroxidase/catalase
YP_513902.1	YP_513902.1	FTL_1219	-	hypothetical protein
YP_513486.1	YP_513486.1	FTL_0737	-	hypothetical protein
YP_514110.1	YP_514110.1	FTL_1459	-	hypothetical protein
YP_514037.1	YP_514037.1	FTL_1376	-	carbohydrate kinase family protein (YjeF-related protein)
YP_514415.1	YP_514415.1	FTL_1790	<i>ampG</i>	major facilitator superfamily transporter

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513802.1	YP_513802.1	FTL_1115	-	hypothetical protein
YP_513452.1	YP_513452.1	FTL_0701	<i>mreA</i>	FAD binding family protein
YP_513525.1	YP_513525.1	FTL_0790	<i>era</i>	GTP-binding protein Era
YP_514402.1	YP_514402.1	FTL_1775	-	oxygen-independent coproporphyrinogen III oxidase
YP_513855.1	YP_513855.1	FTL_1171	<i>pdpB</i>	PdpB protein
YP_512923.1	YP_512923.1	FTL_0125	<i>pdpB</i>	PdpB protein
YP_513854.1	YP_513854.1	FTL_1170	<i>iglE</i>	hypothetical protein
YP_512922.1	YP_512922.1	FTL_0124	<i>iglE</i>	hypothetical protein
YP_513926.1	YP_513926.1	FTL_1246	-	hypothetical protein
YP_513160.1	YP_513160.1	FTL_0387	<i>aspC1</i>	aspartate aminotransferase
YP_513018.1	YP_513018.1	FTL_0223	-	dihydrofolate reductase type I
YP_513546.1	YP_513546.1	FTL_0821	<i>hemH</i>	ferrochelatase
YP_513748.1	YP_513748.1	FTL_1048	-	hypothetical protein
YP_513887.1	YP_513887.1	FTL_1204	-	cardiolipin synthetase
YP_514137.1	YP_514137.1	FTL_1486	-	tRNA-(ms(2)io(6)a)-hydroxylase
YP_512944.1	YP_512944.1	FTL_0146	-	ABC transporter ATP-binding protein
YP_512846.1	YP_512846.1	FTL_0038	<i>emrA2</i>	HlyD family secretion protein
YP_513002.1	YP_513002.1	FTL_0207	-	pyrrolidone-carboxylate peptidase
YP_514111.1	YP_514111.1	FTL_1460	-	hypothetical protein
YP_514133.1	YP_514133.1	FTL_1482	-	peptidase M16 family protein
YP_512897.1	YP_512897.1	FTL_0098	<i>trpA</i>	tryptophan synthase subunit alpha
YP_514471.1	YP_514471.1	FTL_1849	-	hypothetical protein
YP_513392.1	YP_513392.1	FTL_0639	-	oxidoreductase
YP_513896.1	YP_513896.1	FTL_1213	-	hypothetical protein
YP_513929.1	YP_513929.1	FTL_1249	-	hypothetical protein
YP_513595.1	YP_513595.1	FTL_0875	<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
YP_513843.1	YP_513843.1	FTL_1159	<i>iglC</i>	intracellular growth locus, subunit C
YP_512911.1	YP_512911.1	FTL_0113	<i>iglC</i>	intracellular growth locus, subunit C
YP_512837.1	YP_512837.1	FTL_0029	<i>carB</i>	carbamoyl phosphate synthase large subunit
YP_513183.1	YP_513183.1	FTL_0410	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514504.1	YP_514504.1	FTL_1892	-	hypothetical protein
YP_513988.1	YP_513988.1	FTL_1317	-	hypothetical protein
YP_513059.1	YP_513059.1	FTL_0265	-	hypothetical protein
YP_513447.1	YP_513447.1	FTL_0696	-	ABC transporter ATP-binding protein
YP_512838.1	YP_512838.1	FTL_0030	<i>carA</i>	carbamoyl phosphate synthase small subunit
YP_513244.1	YP_513244.1	FTL_0472	-	DNA polymerase III subunit alpha
YP_512872.1	YP_512872.1	FTL_0068	-	phosphoheptose isomerase
YP_514019.1	YP_514019.1	FTL_1358	-	cation-efflux family protein
YP_513792.1	YP_513792.1	FTL_1105	-	hypothetical protein
YP_512887.1	YP_512887.1	FTL_0086	-	hypothetical protein
YP_513428.1	YP_513428.1	FTL_0676	-	DNA ligase
YP_513785.1	YP_513785.1	FTL_1089	-	chologlyglycine hydrolase family protein
YP_513846.1	YP_513846.1	FTL_1162	<i>pdpC</i>	hypothetical protein
YP_512914.1	YP_512914.1	FTL_0116	<i>pdpC</i>	PdpC protein
YP_513083.1	YP_513083.1	FTL_0290	<i>xerC</i>	integrase/recombinase XerC
YP_513669.1	YP_513669.1	FTL_0958	-	hypothetical protein
YP_512836.1	YP_512836.1	FTL_0028	<i>pyrB</i>	aspartate carbamoyltransferase
YP_513111.1	YP_513111.1	FTL_0319	-	hypothetical protein
YP_513109.1	YP_513109.1	FTL_0317	-	hypothetical protein
YP_512854.1	YP_512854.1	FTL_0046	-	diyrorotate dehydrogenase
YP_513968.1	YP_513968.1	FTL_1297	-	hypothetical protein
YP_513964.1	YP_513964.1	FTL_1293	-	hypothetical protein
YP_512865.1	YP_512865.1	FTL_0057	-	hypothetical protein
YP_513911.1	YP_513911.1	FTL_1230	-	cysteine desulfurase activator complex subunit SufB
YP_513773.1	YP_513773.1	FTL_1076	-	short chain dehydrogenase family protein
YP_513806.1	YP_513806.1	FTL_1119	<i>rdgC</i>	recombination associated protein
YP_513221.1	YP_513221.1	FTL_0449	<i>pigR</i>	pathogenicity island gene regulator
YP_514492.1	YP_514492.1	FTL_1879	-	osmosensitive K ⁺ channel His kinase sensor
YP_513639.1	YP_513639.1	FTL_0926	-	Ferritin-like protein
YP_513928.1	YP_513928.1	FTL_1248	-	glutathione reductase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514189.1	YP_514189.1	FTL_1543	-	formamidopyrimidine-DNA glycosylase
YP_513886.1	YP_513886.1	FTL_1203	-	cardiolipin synthetase
YP_513510.1	YP_513510.1	FTL_0765	-	VacJ lipoprotein
YP_514205.1	YP_514205.1	FTL_1566	-	CutC family protein
YP_513938.1	YP_513938.1	FTL_1264	-	dihydroneopterin aldolase
YP_513433.1	YP_513433.1	FTL_0681	<i>potG</i>	ATP-binding cassette putrescine uptake system, ATP-binding protein
YP_514192.1	YP_514192.1	FTL_1546	-	pyridoxal biosynthesis lyase PdxS
YP_513599.1	YP_513599.1	FTL_0879	-	beta-lactamase
YP_513011.1	YP_513011.1	FTL_0216	-	MutT/nudix family protein
YP_513070.1	YP_513070.1	FTL_0277	-	mercuric reductase protein
YP_513469.1	YP_513469.1	FTL_0718	-	cysteine desulfurase
YP_514134.1	YP_514134.1	FTL_1483	-	peptidase M16 family protein
YP_512964.1	YP_512964.1	FTL_0169	-	hypothetical protein
YP_514014.1	YP_514014.1	FTL_1351	-	TatD related DNase family protein
YP_513539.1	YP_513539.1	FTL_0807	-	major facilitator transporter
YP_513140.1	YP_513140.1	FTL_0357	<i>rph</i>	ribonuclease PH
YP_513168.1	YP_513168.1	FTL_0395	<i>purM</i>	phosphoribosylaminoimidazole synthetase
YP_513159.1	YP_513159.1	FTL_0383	<i>manA</i>	mannose-6-phosphate isomerase, fragment
YP_513676.1	YP_513676.1	FTL_0965	<i>hsIV</i>	ATP-dependent protease peptidase subunit
YP_513368.1	YP_513368.1	FTL_0608	<i>manC</i>	mannose-1-phosphate guanylttransferase
YP_513269.1	YP_513269.1	FTL_0500	-	spermidine synthase
YP_512857.1	YP_512857.1	FTL_0049	-	D-tyrosyl-tRNA(Tyr) deacylase
YP_512826.1	YP_512826.1	FTL_0016	<i>pta</i>	phosphate acetyltransferase
YP_514514.1	YP_514514.1	FTL_1904	-	peptide chain release factor 2
YP_513423.1	YP_513423.1	FTL_0671	-	pantothenate kinase
YP_513359.1	YP_513359.1	FTL_0599	<i>wbtG</i>	glycosyl transferase family protein
YP_513472.1	YP_513472.1	FTL_0721	-	DedA family protein
YP_512936.1	YP_512936.1	FTL_0138	-	ribonuclease II family protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513235.1	YP_513235.1	FTL_0463	-	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
YP_513737.1	YP_513737.1	FTL_1037	-	hypothetical protein
YP_513939.1	YP_513939.1	FTL_1265	-	2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine pyrophosphokinase
YP_513155.1	YP_513155.1	FTL_0379	-	methionine sulfoxide reductase B
YP_513912.1	YP_513912.1	FTL_1231	-	hypothetical protein
YP_514559.1	YP_514559.1	FTL_1961	-	hypothetical protein
YP_514508.1	YP_514508.1	FTL_1898	-	DNA polymerase III subunit delta
YP_513841.1	YP_513841.1	FTL_1157	<i>iglA</i>	intracellular growth locus, subunit A
YP_512909.1	YP_512909.1	FTL_0111	<i>iglA</i>	intracellular growth locus, subunit A
YP_514046.1	YP_514046.1	FTL_1391	<i>gmk</i>	guanylate kinase
YP_514128.1	YP_514128.1	FTL_1477	-	thiamine pyrophosphokinase
YP_513982.1	YP_513982.1	FTL_1311	<i>pyrG</i>	CTP synthetase
YP_513249.1	YP_513249.1	FTL_0477	<i>gcvT</i>	glycine cleavage system aminomethyltransferase T
YP_514196.1	YP_514196.1	FTL_1550	-	lipoprotein
YP_513842.1	YP_513842.1	FTL_1158	<i>iglB</i>	intracellular growth locus, subunit B
YP_512910.1	YP_512910.1	FTL_0112	<i>iglB</i>	intracellular growth locus, subunit B
YP_513277.1	YP_513277.1	FTL_0508	<i>mpl</i>	UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
YP_514441.1	YP_514441.1	FTL_1819	-	NADH dehydrogenase I subunit L
YP_513683.1	YP_513683.1	FTL_0974	-	50S ribosomal protein L11 methyltransferase
YP_513805.1	YP_513805.1	FTL_1118	-	hypothetical protein
YP_513709.1	YP_513709.1	FTL_1003	-	DNA polymerase III subunit epsilon
YP_513958.1	YP_513958.1	FTL_1287	<i>rlmL</i>	23S rRNA m(2)G2445 methyltransferase
YP_514515.1	YP_514515.1	FTL_1905	-	DNA polymerase III subunit gamma and tau
YP_513339.1	YP_513339.1	FTL_0579	-	putative nicotinate phosphoribosyltransferase
YP_513393.1	YP_513393.1	FTL_0640	-	hypothetical protein
YP_514209.1	YP_514209.1	FTL_1570	-	phospholipase D
YP_513587.1	YP_513587.1	FTL_0865	-	major facilitator transporter

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513438.1	YP_513438.1	FTL_0687	-	HlyD family secretion protein
YP_513331.1	YP_513331.1	FTL_0571	-	hypothetical protein
YP_512899.1	YP_512899.1	FTL_0100	-	carboxypeptidase,fragment
YP_514453.1	YP_514453.1	FTL_1831	<i>fur</i>	ferric uptake regulation protein
YP_513446.1	YP_513446.1	FTL_0695	-	cell entry (mce) related family protein
YP_512893.1	YP_512893.1	FTL_0092	<i>purT</i>	phosphoribosylglycinamide formyltransferase 2
YP_514291.1	YP_514291.1	FTL_1656	<i>uvrD</i>	DNA helicase II
YP_513445.1	YP_513445.1	FTL_0694	-	hypothetical protein
YP_513684.1	YP_513684.1	FTL_0975	-	Nif3 family protein
YP_513870.1	YP_513870.1	FTL_1187	<i>rplM</i>	50S ribosomal protein L13
YP_514153.1	YP_514153.1	FTL_1503	<i>dgt</i>	deoxyguanosinetriphosphate triphosphohydrolase
YP_513456.1	YP_513456.1	FTL_0705	-	hypothetical protein
YP_513470.1	YP_513470.1	FTL_0719	-	hypothetical protein
YP_513745.1	YP_513745.1	FTL_1045	-	lipoprotein
YP_513845.1	YP_513845.1	FTL_1161	<i>pdpE</i>	hypothetical protein
YP_512913.1	YP_512913.1	FTL_0115	<i>pdpE</i>	hypothetical protein
YP_514071.1	YP_514071.1	FTL_1416	<i>capB</i>	capsule biosynthesis protein capB
YP_514006.1	YP_514006.1	FTL_1341	-	hypothetical protein
YP_513693.1	YP_513693.1	FTL_0985	<i>grxA</i>	glutaredoxin
YP_513925.1	YP_513925.1	FTL_1245	-	short chain dehydrogenase
YP_513088.1	YP_513088.1	FTL_0296	-	hypothetical protein
YP_513803.1	YP_513803.1	FTL_1116	-	ATP-dependent DNA helicase
YP_513005.1	YP_513005.1	FTL_0210	<i>valS</i>	valyl-tRNA synthetase
YP_513459.1	YP_513459.1	FTL_0708	-	hypothetical protein
YP_513091.1	YP_513091.1	FTL_0299	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase
YP_513096.1	YP_513096.1	FTL_0304	<i>nhaP</i>	Na ⁺ /H ⁺ antiporter
YP_513332.1	YP_513332.1	FTL_0572	-	hypothetical protein
YP_513029.1	YP_513029.1	FTL_0234	-	elongation factor G
YP_514357.1	YP_514357.1	FTL_1726	<i>parE</i>	DNA topoisomerase IV subunit B
YP_513910.1	YP_513910.1	FTL_1229	-	ABC transporter ATP-binding protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513288.1	YP_513288.1	FTL_0519	<i>minD</i>	septum site-determining protein MinD
YP_513372.1	YP_513372.1	FTL_0612	<i>ppx</i>	exopolyphosphatase
YP_513857.1	YP_513857.1	FTL_1173	-	hypothetical protein
YP_513535.1	YP_513535.1	FTL_0803	-	hypothetical protein
YP_514536.1	YP_514536.1	FTL_1931	-	hypoxanthine-guanine phosphoribosyltransferase
YP_512825.1	YP_512825.1	FTL_0015	<i>ackA</i>	propionate kinase
YP_513352.1	YP_513352.1	FTL_0592	<i>wbtA</i>	dTDP-glucose 4,6-dehydratase
YP_513701.1	YP_513701.1	FTL_0995	-	haloacid dehalogenase
YP_513238.1	YP_513238.1	FTL_0466	<i>slt</i>	soluble lytic murein transglycosylase
YP_512898.1	YP_512898.1	FTL_0099	-	tryptophan synthase subunit beta
YP_513858.1	YP_513858.1	FTL_1174	-	cystathionine beta-synthase (cystein synthase)
YP_513974.2	YP_513974.2	FTL_1303	<i>rpmE</i>	50S ribosomal protein L31
YP_513909.1	YP_513909.1	FTL_1228	-	hypothetical protein
YP_514129.1	YP_514129.1	FTL_1478	<i>guaB</i>	inosine-5-monophosphate dehydrogenase
YP_513231.1	YP_513231.1	FTL_0459	-	methionine aminopeptidase
YP_513533.1	YP_513533.1	FTL_0801	<i>aroK</i>	shikimate kinase I
YP_513744.1	YP_513744.1	FTL_1044	-	hypothetical protein
YP_513317.1	YP_513317.1	FTL_0549	<i>proC</i>	pyrroline-5-carboxylate reductase
YP_512966.1	YP_512966.1	FTL_0171	-	tetrapyrrole methyltransferase family protein
YP_513532.1	YP_513532.1	FTL_0800	-	Type IV pilin multimeric outer membrane protein
YP_513057.1	YP_513057.1	FTL_0262	<i>rplQ</i>	50S ribosomal protein L17
YP_513692.1	YP_513692.1	FTL_0984	-	bifunctional gluaredoxin/ribonucleoside-diphosphate reductase subunit beta
YP_514310.1	YP_514310.1	FTL_1678	-	hypothetical protein
YP_513033.1	YP_513033.1	FTL_0238	<i>rplW</i>	50S ribosomal protein L23
YP_513167.1	YP_513167.1	FTL_0394	<i>folD</i>	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase
YP_514393.1	YP_514393.1	FTL_1762	<i>qseC</i>	sensor histidine kinase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514248.1	YP_514248.1	FTL_1609	-	dolichyl-phosphate-mannose-protein mannosyltransferase family protein
YP_514188.1	YP_514188.1	FTL_1542	-	hypothetical protein
YP_512994.1	YP_512994.1	FTL_0199	-	hypothetical protein
YP_513997.1	YP_513997.1	FTL_1331	-	hypothetical protein
YP_513932.1	YP_513932.1	FTL_1252	<i>rhIE</i>	ATP-dependent RNA helicase RhIE
YP_513346.1	YP_513346.1	FTL_0586	-	long chain fatty acid CoA ligase
YP_514316.1	YP_514316.1	FTL_1684	-	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase
YP_513819.1	YP_513819.1	FTL_1132	-	inositol-1-monophosphatase
YP_512848.1	YP_512848.1	FTL_0040	-	LysR family transcriptional regulator
YP_514278.1	YP_514278.1	FTL_1639	-	hypothetical protein
YP_514015.1	YP_514015.1	FTL_1352	-	DNA replication and repair protein RecF
YP_513086.1	YP_513086.1	FTL_0294	<i>mutS</i>	DNA mismatch repair protein MutS
YP_513113.1	YP_513113.1	FTL_0325	-	OmpA family protein
YP_513356.1	YP_513356.1	FTL_0596	-	UDP-glucose/GDP-mannose dehydrogenase
YP_514535.1	YP_514535.1	FTL_1930	<i>purA</i>	adenylosuccinate synthetase
YP_514138.1	YP_514138.1	FTL_1487	-	uridine phosphorylase
YP_514451.1	YP_514451.1	FTL_1829	-	NADH dehydrogenase subunit B
YP_514221.1	YP_514221.1	FTL_1582	<i>potF</i>	putrescine-binding periplasmic protein
YP_513281.1	YP_513281.1	FTL_0512	-	BolA-like protein
YP_513032.1	YP_513032.1	FTL_0237	<i>rplD</i>	50S ribosomal protein L4
YP_512947.1	YP_512947.1	FTL_0149	-	carbonic anhydrase
YP_514078.1	YP_514078.1	FTL_1423	-	glycosyl transferase family protein
YP_513354.1	YP_513354.1	FTL_0594	<i>wbtC</i>	UDP-glucose 4-epimerase
YP_513943.1	YP_513943.1	FTL_1272	<i>bioB</i>	biotin synthase
YP_513035.1	YP_513035.1	FTL_0240	<i>rpsS</i>	30S ribosomal protein S19
YP_514160.1	YP_514160.1	FTL_1511	-	glycerophosphoryl diester phosphodiesterase family protein
YP_513234.1	YP_513234.1	FTL_0462	-	DNA topoisomerase IV subunit A
YP_514315.1	YP_514315.1	FTL_1683	<i>cysS</i>	cysteinyI-tRNA synthetase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513908.1	YP_513908.1	FTL_1225	-	hypothetical protein
YP_513246.1	YP_513246.1	FTL_0474	-	lipoprotein releasing system, subunit C, putative membrane protein
YP_513087.1	YP_513087.1	FTL_0295	-	acetyl-CoA carboxylase carboxyltransferase subunit alpha
YP_513953.1	YP_513953.1	FTL_1282	-	beta-glucosidase
YP_514158.1	YP_514158.1	FTL_1509	-	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase
YP_513536.1	YP_513536.1	FTL_0804	-	hypothetical protein
YP_513209.1	YP_513209.1	FTL_0437	-	riboflavin biosynthesis protein RibF
YP_513905.1	YP_513905.1	FTL_1222	-	hypothetical protein
YP_513304.1	YP_513304.1	FTL_0535	-	outer membrane protein
YP_514048.1	YP_514048.1	FTL_1393	<i>ppiC</i>	peptidyl-prolyl cis-trans isomerase
YP_514418.1	YP_514418.1	FTL_1793	-	hypothetical protein
YP_513485.1	YP_513485.1	FTL_0736	-	ribose-5-phosphate isomerase A
YP_513192.1	YP_513192.1	FTL_0419	-	oligopeptidase A
YP_514377.1	YP_514377.1	FTL_1746	<i>rplJ</i>	50S ribosomal protein L10
YP_514293.1	YP_514293.1	FTL_1658	<i>fimV</i>	hypothetical protein
YP_513527.1	YP_513527.1	FTL_0795	<i>adk</i>	adenylate kinase
YP_513740.1	YP_513740.1	FTL_1040	-	hypothetical protein
YP_514147.1	YP_514147.1	FTL_1496	-	cysteine/glutathione ABC transporter membrane/ATP-binding protein
YP_513108.1	YP_513108.1	FTL_0316	-	arsenate reductase
YP_513293.1	YP_513293.1	FTL_0524	-	ATP-dependent DNA helicase RecG
YP_513914.1	YP_513914.1	FTL_1233	<i>argP</i>	amino acid antiporter, high affinity arginine transporter
YP_513907.1	YP_513907.1	FTL_1224	-	thioredoxin
YP_513223.1	YP_513223.1	FTL_0451	-	hypothetical protein
YP_514444.1	YP_514444.1	FTL_1822	-	NADH dehydrogenase subunit I
YP_514447.1	YP_514447.1	FTL_1825	-	NADH dehydrogenase I subunit F
YP_513427.1	YP_513427.1	FTL_0675	<i>panG</i>	hypothetical protein, putative ketopantoate reductase
YP_513662.1	YP_513662.1	FTL_0951	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513310.1	YP_513310.1	FTL_0541	-	hypothetical protein
YP_513667.1	YP_513667.1	FTL_0956	<i>pth</i>	peptidyl-tRNA hydrolase
YP_514379.1	YP_514379.1	FTL_1748	<i>rplK</i>	50S ribosomal protein L11
YP_513162.1	YP_513162.1	FTL_0389	-	DNA repair protein recN
YP_513264.1	YP_513264.1	FTL_0492	<i>murF</i>	UDP-N--acetylmuramoylalanyl-D-glutamyl-2,6- diaminopimelate-D-alanyl-D-alanyl ligase
YP_514069.1	YP_514069.1	FTL_1414	<i>capA</i>	hypothetical protein
YP_514488.1	YP_514488.1	FTL_1874	<i>obgE</i>	GTPase ObgE
YP_513038.1	YP_513038.1	FTL_0243	<i>rplP</i>	50S ribosomal protein L16
YP_513831.1	YP_513831.1	FTL_1145	-	transketolase
YP_514417.1	YP_514417.1	FTL_1792	-	glutaredoxin-like protein
YP_514051.1	YP_514051.1	FTL_1396	-	galactose-1-phosphate uridylyltransferase
YP_514210.1	YP_514210.1	FTL_1571	-	thioredoxin reductase
YP_513248.1	YP_513248.1	FTL_0476	-	lysine decarboxylase, inducible
YP_513561.1	YP_513561.1	FTL_0839	-	hypothetical protein
YP_513206.1	YP_513206.1	FTL_0434	-	hypothetical protein
YP_513312.1	YP_513312.1	FTL_0544	<i>ppk</i>	polyphosphate kinase 2
YP_514253.1	YP_514253.1	FTL_1614	<i>murD</i>	UDP-N-acetylmuramoylalanine--D-glutamate ligase
YP_513458.1	YP_513458.1	FTL_0707	-	glycosyl transferase family protein
YP_513502.1	YP_513502.1	FTL_0754	<i>xseA</i>	exodeoxyribonuclease VII large subunit
YP_514059.1	YP_514059.1	FTL_1404	<i>rplT</i>	50S ribosomal protein L20
YP_512977.1	YP_512977.1	FTL_0182	-	elongation factor P
YP_514130.1	YP_514130.1	FTL_1479	<i>pepA</i>	cytosol aminopeptidase
YP_513807.1	YP_513807.1	FTL_1120	-	hypothetical protein
YP_513044.1	YP_513044.1	FTL_0249	<i>rpsN</i>	30S ribosomal protein S14
YP_513937.1	YP_513937.1	FTL_1263	<i>fadD2</i>	AMP-binding family protein
YP_512840.1	YP_512840.1	FTL_0032	<i>tmpT</i>	thiopurine S-methyltransferase
YP_513040.1	YP_513040.1	FTL_0245	<i>rpsQ</i>	30S ribosomal protein S17
YP_513483.1	YP_513483.1	FTL_0732	-	lactoylglutathione lyase
YP_513217.1	YP_513217.1	FTL_0445	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513679.1	YP_513679.1	FTL_0968	<i>tyrS</i>	tyrosyl-tRNA synthetase
YP_512930.1	YP_512930.1	FTL_0132	-	pyruvate phosphate dikinase
YP_514193.1	YP_514193.1	FTL_1547	-	DNA gyrase subunit B
YP_514159.1	YP_514159.1	FTL_1510	-	glycerol-3-phosphate transporter
YP_513894.1	YP_513894.1	FTL_1211	-	lipoprotein
YP_513148.1	YP_513148.1	FTL_0372	<i>gpsA</i>	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
YP_513743.1	YP_513743.1	FTL_1043	-	C32 tRNA thiolase
YP_513357.1	YP_513357.1	FTL_0597	<i>wbtF</i>	NAD dependent epimerase
YP_513283.1	YP_513283.1	FTL_0514	-	hypothetical protein
YP_512839.1	YP_512839.1	FTL_0031	-	acid phosphatase
YP_514474.1	YP_514474.1	FTL_1852	-	hypothetical protein
YP_513360.1	YP_513360.1	FTL_0600	<i>wbtH</i>	asparagine synthase
YP_513418.1	YP_513418.1	FTL_0666	<i>recC</i>	exodeoxyribonuclease V subunit gamma
YP_513467.1	YP_513467.1	FTL_0716	-	prolipoprotein diacylglyceryl transferase
YP_513861.1	YP_513861.1	FTL_1178	-	hypothetical protein
YP_513237.1	YP_513237.1	FTL_0465	-	BNR/Asp-box repeat-containing protein
YP_514185.1	YP_514185.1	FTL_1539	<i>ftsI</i>	penicillin binding protein (peptidoglycan synthetase)
YP_513830.1	YP_513830.1	FTL_1144	-	hypothetical protein
YP_513756.1	YP_513756.1	FTL_1059	-	hypothetical protein
YP_513853.1	YP_513853.1	FTL_1169	<i>vgrG</i>	hypothetical protein
YP_512921.1	YP_512921.1	FTL_0123	<i>vgrG</i>	hypothetical protein
YP_514178.1	YP_514178.1	FTL_1532	-	hypothetical protein
YP_513711.1	YP_513711.1	FTL_1005	-	hypothetical protein
YP_513511.1	YP_513511.1	FTL_0766	<i>ggt</i>	gamma-glutamyltranspeptidase
YP_513772.1	YP_513772.1	FTL_1075	-	hypothetical protein
YP_512968.1	YP_512968.1	FTL_0173	<i>aroE</i>	shikimate 5-dehydrogenase
YP_514208.1	YP_514208.1	FTL_1569	-	phosphoglycolate phosphatase
YP_513440.1	YP_513440.1	FTL_0689	-	transcriptional regulator araC family protein
YP_514387.1	YP_514387.1	FTL_1756	<i>glpD</i>	anaerobic glycerol-3-phosphate dehydrogenase
YP_514448.1	YP_514448.1	FTL_1826	-	NADH dehydrogenase I subunit E

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513746.1	YP_513746.1	FTL_1046	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase
YP_513187.1	YP_513187.1	FTL_0414	<i>engA</i>	GTP-binding protein EngA
YP_514380.1	YP_514380.1	FTL_1749	-	transcription antitermination protein nusG
YP_513642.1	YP_513642.1	FTL_0929	-	hypothetical protein
YP_514170.1	YP_514170.1	FTL_1523	<i>tdh</i>	L-threonine 3-dehydrogenase
YP_512879.1	YP_512879.1	FTL_0075	-	riboflavin synthase beta subunit (6,7-dimethyl-8-ribityllumazine synthase)
YP_513030.1	YP_513030.1	FTL_0235	<i>rpsI</i>	30S ribosomal protein S10
YP_514223.1	YP_514223.1	FTL_1584	<i>perM</i>	PerM family protein
YP_513586.1	YP_513586.1	FTL_0864	-	SIS domain-containing protein
YP_513460.1	YP_513460.1	FTL_0709	-	glycosyl transferases group 1 family protein
YP_513420.1	YP_513420.1	FTL_0668	-	ATP-dependent DNA helicase
YP_513409.1	YP_513409.1	FTL_0656	-	hypothetical protein
YP_514195.1	YP_514195.1	FTL_1549	-	tRNA-dihydrouridine synthase A
YP_514560.1	YP_514560.1	FTL_1962	-	hypothetical protein
YP_513355.1	YP_513355.1	FTL_0595	-	galacturonosyl transferase
YP_514446.1	YP_514446.1	FTL_1824	-	NADH dehydrogenase subunit G
YP_512973.1	YP_512973.1	FTL_0178	<i>yidC</i>	inner-membrane protein
YP_514450.1	YP_514450.1	FTL_1828	-	NADH dehydrogenase I
YP_513107.1	YP_513107.1	FTL_0315	-	MutT protein
YP_514522.1	YP_514522.1	FTL_1912	<i>rpsA</i>	30S ribosomal protein S1
YP_514348.1	YP_514348.1	FTL_1717	-	hypothetical protein
YP_514332.1	YP_514332.1	FTL_1701	<i>glpX</i>	fructose 1,6-bisphosphatase II
YP_514371.1	YP_514371.1	FTL_1740	-	fatty acid desaturase
YP_513375.1	YP_513375.1	FTL_0616	<i>rpoA2</i>	DNA-directed RNA polymerase subunit alpha
YP_513871.1	YP_513871.1	FTL_1188	-	hypothetical protein
YP_513660.1	YP_513660.1	FTL_0949	-	ribose-phosphate pyrophosphokinase
YP_513141.1	YP_513141.1	FTL_0358	-	hypothetical protein
YP_514083.1	YP_514083.1	FTL_1428	-	ABC transporter ATP-binding and membrane protein
YP_514318.1	YP_514318.1	FTL_1686	-	acetyltransferase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514462.1	YP_514462.1	FTL_1840	-	hypothetical protein
YP_514040.1	YP_514040.1	FTL_1384	-	hypothetical protein
YP_514279.1	YP_514279.1	FTL_1640	-	amino acid transporter protein, fragment
YP_513479.1	YP_513479.1	FTL_0728	-	hypothetical protein
YP_514378.1	YP_514378.1	FTL_1747	<i>rplA</i>	50S ribosomal protein L1
YP_513610.1	YP_513610.1	FTL_0891	<i>tig</i>	trigger factor
YP_513031.1	YP_513031.1	FTL_0236	<i>rplC</i>	50S ribosomal protein L3
YP_513694.1	YP_513694.1	FTL_0986	<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha
YP_513552.1	YP_513552.1	FTL_0830	-	molybdopterin binding family protein, fragment
YP_514207.1	YP_514207.1	FTL_1568	-	LysR family transcriptional regulator
YP_513653.1	YP_513653.1	FTL_0940	-	methylpurine-DNA glycosylase family protein
YP_512904.1	YP_512904.1	FTL_0105	-	hypothetical protein
YP_512991.1	YP_512991.1	FTL_0196	-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
YP_513774.1	YP_513774.1	FTL_1077	<i>ruvB</i>	Holliday junction DNA helicase RuvB
YP_514022.1	YP_514022.1	FTL_1361	-	cold shock protein
YP_514018.1	YP_514018.1	FTL_1357	-	UTP--glucose-1-phosphate uridylyltransferase
YP_513230.1	YP_513230.1	FTL_0458	-	hypothetical protein
YP_513048.1	YP_513048.1	FTL_0253	<i>rpsE</i>	30S ribosomal protein S5
YP_513895.1	YP_513895.1	FTL_1212	<i>leuS</i>	leucyl-tRNA synthetase
YP_514140.1	YP_514140.1	FTL_1489	-	FAD-binding family protein
YP_513396.1	YP_513396.1	FTL_0643	-	N utilisation substance protein B
YP_513537.1	YP_513537.1	FTL_0805	-	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase
YP_513520.1	YP_513520.1	FTL_0785	-	GTP-binding protein
YP_514243.1	YP_514243.1	FTL_1604	-	DNA polymerase III, delta prime subunit
YP_514449.1	YP_514449.1	FTL_1827	-	NADH dehydrogenase subunit D
YP_513099.1	YP_513099.1	FTL_0307	<i>coaE</i>	dephospho-CoA kinase
YP_513413.1	YP_513413.1	FTL_0661	-	hypothetical protein
YP_514229.1	YP_514229.1	FTL_1590	-	hypothetical protein
YP_514143.1	YP_514143.1	FTL_1492	-	fructokinase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513421.1	YP_513421.1	FTL_0669	<i>recB</i>	exodeoxyribonuclease V subunit beta
YP_514506.1	YP_514506.1	FTL_1896	-	hypothetical protein
YP_514002.1	YP_514002.1	FTL_1336	-	prephenate dehydratase
YP_514276.1	YP_514276.1	FTL_1637	-	lipoprotein
YP_514452.1	YP_514452.1	FTL_1830	-	NADH dehydrogenase I subunit A
YP_513251.1	YP_513251.1	FTL_0479	-	glycine dehydrogenase subunit 1
YP_513500.1	YP_513500.1	FTL_0752	-	hypothetical protein
YP_514292.1	YP_514292.1	FTL_1657	<i>ftsY</i>	signal recognition particle receptor FtsY
YP_513661.1	YP_513661.1	FTL_0950	-	50S ribosomal protein L25
YP_513285.1	YP_513285.1	FTL_0516	-	ABC transporter membrane protein
YP_514382.1	YP_514382.1	FTL_1751	-	elongation factor Tu
YP_514538.1	YP_514538.1	FTL_1935	-	ABC transporter ATP-binding protein
YP_513252.1	YP_513252.1	FTL_0480	-	glycine dehydrogenase subunit 2
YP_513124.1	YP_513124.1	FTL_0336	-	peptidoglycan-associated lipoprotein
YP_514523.1	YP_514523.1	FTL_1913	-	Sua5/YciO/YrdC family protein
YP_513276.1	YP_513276.1	FTL_0507	<i>pyrE</i>	orotate phosphoribosyltransferase
YP_514025.1	YP_514025.1	FTL_1364	-	hypothetical protein
YP_514031.1	YP_514031.1	FTL_1370	-	hypothetical protein
YP_513980.1	YP_513980.1	FTL_1309	-	Acetyl-CoA carboxylase beta subunit
YP_513550.1	YP_513550.1	FTL_0828	-	Type IV pili nucleotide binding protein, ABC transporter ATP-binding protein
YP_514135.1	YP_514135.1	FTL_1484	-	methylese
YP_514252.1	YP_514252.1	FTL_1613	<i>ftsW</i>	cell division protein FtsW
YP_513449.1	YP_513449.1	FTL_0698	-	hypothetical protein
YP_513194.1	YP_513194.1	FTL_0421	<i>tul4</i>	lipoprotein
YP_513316.1	YP_513316.1	FTL_0548	<i>rdgB</i>	putative deoxyribonucleotide triphosphate pyrophosphatase
YP_513734.1	YP_513734.1	FTL_1034	<i>cysN</i>	sulfate adenyllyltransferase
YP_512821.1	YP_512821.1	FTL_0011	<i>secB1</i>	preprotein translocase subunit SecB
YP_513114.1	YP_513114.1	FTL_0326	-	FKBP-type 16 kDa peptidyl-prolyl cis-transisomerase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513577.1	YP_513577.1	FTL_0855	-	L-asparaginase
YP_514233.1	YP_514233.1	FTL_1594	<i>apaH</i>	diadenosine tetraphosphatase
YP_513153.1	YP_513153.1	FTL_0377	-	chorismate synthase
YP_513377.1	YP_513377.1	FTL_0620	<i>tatD</i>	deoxyribonuclease
YP_513548.1	YP_513548.1	FTL_0823	-	hypothetical protein
YP_514295.1	YP_514295.1	FTL_1660	<i>tmk</i>	thymidylate kinase
YP_514045.1	YP_514045.1	FTL_1390	-	quinolinate synthetase
YP_513741.1	YP_513741.1	FTL_1041	-	octaprenyl-diphosphate synthase
YP_513556.1	YP_513556.1	FTL_0834	-	rhodanese-like family protein
YP_513719.1	YP_513719.1	FTL_1018	-	phosphoserine aminotransferase
YP_513371.1	YP_513371.1	FTL_0611	<i>trx1</i>	thioredoxin
YP_512812.1	YP_512812.1	FTL_0002	-	DNA polymerase III subunit beta
YP_513742.1	YP_513742.1	FTL_1042	-	FKBP-type peptidyl-prolyl cis-trans isomerase family protein
YP_512967.1	YP_512967.1	FTL_0172	<i>murC</i>	UDP-N-acetylmuramate--L-alanine ligase
YP_513512.1	YP_513512.1	FTL_0767	-	hypothetical protein
YP_513302.1	YP_513302.1	FTL_0533	-	DNA gyrase subunit A
YP_514366.1	YP_514366.1	FTL_1735	<i>rplS</i>	50S ribosomal protein L19
YP_513171.1	YP_513171.1	FTL_0398	<i>purE</i>	phosphoribosylaminoimidazole carboxylase, catalytic subunit
YP_513954.1	YP_513954.1	FTL_1283	-	glutamate-1-semialdehyde aminotransferase
YP_513344.1	YP_513344.1	FTL_0584	-	bifunctional 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein
YP_513216.1	YP_513216.1	FTL_0444	<i>metG</i>	methionyl-tRNA synthetase
YP_513119.1	YP_513119.1	FTL_0331	-	TolQ protein
YP_513077.1	YP_513077.1	FTL_0284	-	hypothetical protein
YP_513085.1	YP_513085.1	FTL_0293	<i>secB2</i>	preprotein translocase subunit SecB
YP_512969.1	YP_512969.1	FTL_0174	-	hypothetical protein
YP_513012.1	YP_513012.1	FTL_0217	<i>fumC</i>	fumarate hydratase
YP_513225.1	YP_513225.1	FTL_0453	-	UDP-N-acetylglucosamine pyrophosphorylase/glucosamine-1-phosphate N-acetyltransferase
YP_514554.1	YP_514554.1	FTL_1956	<i>pepN</i>	aminopeptidase N

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_512864.1	YP_512864.1	FTL_0056	-	NADH dehydrogenase
YP_513172.1	YP_513172.1	FTL_0399	<i>purK</i>	phosphoribosylaminoimidazole carboxylase ATPase subunit
YP_514062.1	YP_514062.1	FTL_1407	<i>thrS</i>	threonyl-tRNA synthetase
YP_513574.1	YP_513574.1	FTL_0852	-	3-phosphoshikimate 1-carboxyvinyltransferase
YP_512993.1	YP_512993.1	FTL_0198	-	pyridoxal kinase
YP_514277.1	YP_514277.1	FTL_1638	-	3-demethylubiquinone-9 3-methyltransferase
YP_513650.1	YP_513650.1	FTL_0937	-	hypothetical protein
YP_513715.1	YP_513715.1	FTL_1014	-	oxidative stress transcriptional regulator
YP_513476.1	YP_513476.1	FTL_0725	-	hypothetical protein
YP_513832.1	YP_513832.1	FTL_1146	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase
YP_513804.1	YP_513804.1	FTL_1117	-	hypothetical protein
YP_513540.1	YP_513540.1	FTL_0808	-	bifunctional 4'-phosphopantothenoylcysteine decarboxylase,phosphopantothenoylcysteine synthetase
YP_513053.1	YP_513053.1	FTL_0258	<i>rpsM</i>	30S ribosomal protein S13
YP_513731.1	YP_513731.1	FTL_1030	-	ribosomal large subunit pseudouridine synthase B
YP_513435.1	YP_513435.1	FTL_0684	-	hypothetical protein
YP_513166.1	YP_513166.1	FTL_0393	<i>lpxE</i>	lipid A 1-phosphatase
YP_513654.1	YP_513654.1	FTL_0941	-	hypothetical protein
YP_513955.1	YP_513955.1	FTL_1284	-	glutathione synthetase
YP_512875.1	YP_512875.1	FTL_0071	-	GTP-binding protein LepA
YP_514244.1	YP_514244.1	FTL_1605	-	putative periplasmic protease
YP_513521.1	YP_513521.1	FTL_0786	-	N-acetylglucosamine-6-phosphate deacetylase
YP_512877.1	YP_512877.1	FTL_0073	-	hypothetical protein
YP_513298.1	YP_513298.1	FTL_0529	-	uracil-DNA glycosylase
YP_513700.1	YP_513700.1	FTL_0994	-	hypothetical protein
YP_513381.1	YP_513381.1	FTL_0625	<i>gtrB</i>	glycosyl transferase family protein
YP_513611.1	YP_513611.1	FTL_0892	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit
YP_514376.1	YP_514376.1	FTL_1745	<i>rplL</i>	50S ribosomal protein L7/L12
YP_513047.1	YP_513047.1	FTL_0252	<i>rplR</i>	50S ribosomal protein L18
YP_513652.1	YP_513652.1	FTL_0939	-	aldolase/adducin class II family protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513061.1	YP_513061.1	FTL_0267	<i>htpG</i>	heat shock protein 90
YP_514354.1	YP_514354.1	FTL_1723	-	hypothetical protein
YP_514542.1	YP_514542.1	FTL_1941	-	tRNA processing ribonuclease BN
YP_512818.1	YP_512818.1	FTL_0008	-	peptidase
YP_513675.1	YP_513675.1	FTL_0964	<i>hslU</i>	ATP-dependent protease ATP-binding subunit HslU
YP_513180.1	YP_513180.1	FTL_0407	<i>ubiB</i>	2-polyprenylphenol 6-hydroxylase
YP_513382.1	YP_513382.1	FTL_0626	<i>ppnK</i>	inorganic phosphate/ATP-NAD kinase
YP_514435.1	YP_514435.1	FTL_1810	<i>nusA</i>	transcription elongation factor NusA
YP_513455.1	YP_513455.1	FTL_0704	-	hypothetical protein
YP_513041.1	YP_513041.1	FTL_0246	<i>rplN</i>	50S ribosomal protein L14
YP_513630.1	YP_513630.1	FTL_0917	-	transcription-repair coupling factor
YP_513045.1	YP_513045.1	FTL_0250	<i>rpsH</i>	30S ribosomal protein S8
YP_514250.1	YP_514250.1	FTL_1611	-	glycosyl transferase family protein
YP_512971.1	YP_512971.1	FTL_0176	-	ribonuclease P protein component
YP_514085.1	YP_514085.1	FTL_1430	-	UDP-glucose 4-epimerase
YP_513796.2	YP_513796.2	FTL_1109	-	transaldolase B
YP_513139.1	YP_513139.1	FTL_0356	<i>ubiC</i>	chorismate pyruvate lyase
YP_513695.1	YP_513695.1	FTL_0987	<i>mdh</i>	malate dehydrogenase
YP_513493.1	YP_513493.1	FTL_0744	-	exodeoxyribonuclease I
YP_512984.1	YP_512984.1	FTL_0189	-	cytochrome d terminal oxidase, polypeptide subunit I
YP_513403.1	YP_513403.1	FTL_0650	-	prolyl-tRNA synthetase
YP_513265.1	YP_513265.1	FTL_0493	-	hypothetical protein
YP_513314.1	YP_513314.1	FTL_0546	<i>ispA</i>	geranyltranstransferase
YP_513795.1	YP_513795.1	FTL_1108	-	cytosol aminopeptidase
YP_512995.1	YP_512995.1	FTL_0200	-	methanol dehydrogenase regulatory protein
YP_513944.1	YP_513944.1	FTL_1273	<i>bioF</i>	8-amino-7-oxononanoate synthase
YP_512953.1	YP_512953.1	FTL_0157	-	hypothetical protein
YP_513006.1	YP_513006.1	FTL_0211	-	hypothetical protein
YP_513882.1	YP_513882.1	FTL_1199	-	regulatory protein
YP_513668.1	YP_513668.1	FTL_0957	<i>blaA</i>	Beta-lactamase class A

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513210.1	YP_513210.1	FTL_0438	-	malate dehydrogenase
YP_513178.1	YP_513178.1	FTL_0405	<i>ubiE</i>	menaquinone biosynthesis methyltransferase
YP_513369.1	YP_513369.1	FTL_0609	<i>manB</i>	phosphomannomutase
YP_513477.1	YP_513477.1	FTL_0726	-	2-octaprenyl-6-methoxyphenyl hydroxylase
YP_513046.1	YP_513046.1	FTL_0251	<i>rplF</i>	50S ribosomal protein L6
YP_513028.1	YP_513028.1	FTL_0233	<i>rpsG</i>	30S ribosomal protein S7
YP_513713.1	YP_513713.1	FTL_1012	-	hypothetical protein
YP_514534.1	YP_514534.1	FTL_1929	<i>purH</i>	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
YP_514465.1	YP_514465.1	FTL_1843	-	Glu-tRNA ^{Gln} amidotransferase C subunit
YP_513678.1	YP_513678.1	FTL_0967	<i>lplA</i>	lipocate-protein ligase A
YP_513690.1	YP_513690.1	FTL_0981	-	DNA polymerase IV
YP_514367.1	YP_514367.1	FTL_1736	<i>trmD</i>	tRNA (guanine-N(1)-)-methyltransferase
YP_513523.1	YP_513523.1	FTL_0788	-	glutamine amidotransferases class-II family protein
YP_513226.1	YP_513226.1	FTL_0454	-	glucosamine--fructose-6-phosphate aminotransferase
YP_513513.1	YP_513513.1	FTL_0768	-	GTP binding translational elongation factor Tu and G family protein
YP_513406.1	YP_513406.1	FTL_0653	-	hypothetical protein
YP_513727.1	YP_513727.1	FTL_1026	<i>rplI</i>	50S ribosomal protein L9
YP_513554.1	YP_513554.1	FTL_0832	-	Mur ligase family protein
YP_513054.1	YP_513054.1	FTL_0259	-	30S ribosomal protein S11
YP_513306.1	YP_513306.1	FTL_0537	<i>lpxD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
YP_514360.1	YP_514360.1	FTL_1729	<i>nudH</i>	dinucleoside polyphosphate hydrolase
YP_513398.1	YP_513398.1	FTL_0645	-	lipoprotein
YP_512876.1	YP_512876.1	FTL_0072	<i>mnmA</i>	tRNA-specific 2-thiouridylase MnmA
YP_513063.1	YP_513063.1	FTL_0269	<i>gdh</i>	glutamate dehydrogenase
YP_513193.1	YP_513193.1	FTL_0420	-	hypothetical protein
YP_513098.1	YP_513098.1	FTL_0306	-	tryptophanyl-tRNA synthetase
YP_514548.1	YP_514548.1	FTL_1947	-	putative ABC transporter ATP-binding protein
YP_512992.1	YP_512992.1	FTL_0197	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514513.1	YP_514513.1	FTL_1903	-	lysyl-tRNA synthetase
YP_513901.1	YP_513901.1	FTL_1218	-	hypothetical protein
YP_513106.1	YP_513106.1	FTL_0314	<i>isftu1</i>	transposase
YP_514545.1	YP_514545.1	FTL_1944	<i>isftu1</i>	transposase
YP_514532.1	YP_514532.1	FTL_1925	<i>isftu1</i>	transposase
YP_514503.1	YP_514503.1	FTL_1891	<i>isftu1</i>	transposase
YP_514499.1	YP_514499.1	FTL_1886	<i>isftu1</i>	transposase
YP_514438.1	YP_514438.1	FTL_1815	<i>isftu1</i>	transposase
YP_514388.1	YP_514388.1	FTL_1757	<i>isftu1</i>	transposase
YP_514349.1	YP_514349.1	FTL_1718	<i>isftu1</i>	transposase
YP_514344.1	YP_514344.1	FTL_1713	<i>isftu1</i>	transposase
YP_514319.1	YP_514319.1	FTL_1687	<i>isftu1</i>	transposase
YP_514313.1	YP_514313.1	FTL_1681	<i>isftu1</i>	transposase
YP_514282.1	YP_514282.1	FTL_1643	<i>isftu1</i>	transposase
YP_514269.1	YP_514269.1	FTL_1630	<i>isftu1</i>	transposase
YP_514266.1	YP_514266.1	FTL_1627	<i>isftu1</i>	transposase
YP_514249.1	YP_514249.1	FTL_1610	<i>isftu1</i>	transposase
YP_514190.1	YP_514190.1	FTL_1544	<i>isftu1</i>	transposase
YP_514155.1	YP_514155.1	FTL_1505	<i>isftu1</i>	transposase
YP_514113.1	YP_514113.1	FTL_1462	<i>isftu1</i>	transposase
YP_514101.1	YP_514101.1	FTL_1446	<i>isftu1</i>	transposase
YP_514057.1	YP_514057.1	FTL_1402	<i>isftu1</i>	transposase
YP_514030.1	YP_514030.1	FTL_1369	<i>isftu1</i>	transposase
YP_514012.1	YP_514012.1	FTL_1349	<i>isftu1</i>	transposase
YP_513987.1	YP_513987.1	FTL_1316	<i>isftu1</i>	transposase
YP_513969.1	YP_513969.1	FTL_1298	<i>isftu1</i>	transposase
YP_513961.1	YP_513961.1	FTL_1290	<i>isftu1</i>	transposase
YP_513921.1	YP_513921.1	FTL_1241	<i>isftu1</i>	transposase
YP_513878.1	YP_513878.1	FTL_1195	<i>isftu1</i>	transposase
YP_513838.1	YP_513838.1	FTL_1153	<i>isftu1</i>	transposase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513814.1	YP_513814.1	FTL_1127	<i>isftu1</i>	transposase
YP_513721.1	YP_513721.1	FTL_1020	<i>isftu1</i>	transposase
YP_513680.1	YP_513680.1	FTL_0969	<i>isftu1</i>	transposase
YP_513518.1	YP_513518.1	FTL_0783	<i>isftu1</i>	transposase
YP_513484.1	YP_513484.1	FTL_0733	<i>isftu1</i>	transposase
YP_513434.1	YP_513434.1	FTL_0682	<i>isftu1</i>	transposase
YP_513430.1	YP_513430.1	FTL_0678	<i>isftu1</i>	transposase
YP_513384.1	YP_513384.1	FTL_0631	<i>isftu1</i>	transposase
YP_513367.1	YP_513367.1	FTL_0607	<i>isftu1</i>	transposase
YP_513279.1	YP_513279.1	FTL_0510	<i>isftu1</i>	transposase
YP_513272.1	YP_513272.1	FTL_0503	<i>isftu1</i>	transposase
YP_513212.1	YP_513212.1	FTL_0440	<i>isftu1</i>	transposase
YP_513190.1	YP_513190.1	FTL_0417	<i>isftu1</i>	transposase
YP_513136.1	YP_513136.1	FTL_0353	<i>isftu1</i>	transposase
YP_513126.1	YP_513126.1	FTL_0339	<i>isftu1</i>	transposase
YP_513062.1	YP_513062.1	FTL_0268	<i>isftu1</i>	transposase
YP_513060.1	YP_513060.1	FTL_0266	<i>isftu1</i>	transposase
YP_513058.1	YP_513058.1	FTL_0263	<i>isftu1</i>	transposase
YP_512980.1	YP_512980.1	FTL_0185	<i>isftu1</i>	transposase
YP_512959.1	YP_512959.1	FTL_0164	<i>isftu1</i>	transposase
YP_512951.1	YP_512951.1	FTL_0153	<i>isftu1</i>	transposase
YP_512933.1	YP_512933.1	FTL_0135	<i>isftu1</i>	transposase
YP_512926.1	YP_512926.1	FTL_0128	<i>isftu1</i>	transposase
YP_512905.1	YP_512905.1	FTL_0107	<i>isftu1</i>	transposase
YP_512884.1	YP_512884.1	FTL_0080	<i>isftu1</i>	transposase
YP_512862.1	YP_512862.1	FTL_0054	<i>isftu1</i>	transposase
YP_512831.1	YP_512831.1	FTL_0023	<i>isftu1</i>	transposase
YP_512827.1	YP_512827.1	FTL_0018	<i>isftu1</i>	transposase
YP_512814.1	YP_512814.1	FTL_0004	<i>isftu1</i>	transposase
YP_513294.1	YP_513294.1	FTL_0525	-	fumerate hydratase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514539.1	YP_514539.1	FTL_1936	-	periplasmic solute binding family protein
YP_514052.1	YP_514052.1	FTL_1397	-	galactokinase
YP_514529.1	YP_514529.1	FTL_1921	-	ABC transporter ATP-binding protein
YP_513788.1	YP_513788.1	FTL_1096	<i>dsbA</i>	Disulfide bond formation protein A / FipB
YP_513917.1	YP_513917.1	FTL_1237	-	hypothetical protein
YP_514556.1	YP_514556.1	FTL_1958	-	bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase
YP_514021	YP_514021	FTL_1360	<i>rpsU3</i>	30S ribosomal protein S21-3
YP_513228.1	YP_513228.1	FTL_0456	<i>rpsU1</i>	30S ribosomal protein S21-1
YP_513534.1	YP_513534.1	FTL_0802	<i>aroB</i>	3-dehydroquinate synthase
YP_513019.1	YP_513019.1	FTL_0224	<i>rpsB</i>	30S ribosomal protein S2
YP_514304.1	YP_514304.1	FTL_1669	-	tRNA CCA-pyrophosphorylase
YP_513749.1	YP_513749.1	FTL_1049	<i>dnaG</i>	DNA primase
YP_513020.1	YP_513020.1	FTL_0225	<i>tsf</i>	elongation factor Ts
YP_513920.1	YP_513920.1	FTL_1240	-	phospho-2-dehydro-3-deoxyheptonate aldolase
YP_514420.1	YP_514420.1	FTL_1795	-	F0F1 ATP synthase subunit beta
YP_513481.1	YP_513481.1	FTL_0730	-	haloacid dehalogenase-like hydrolase family protein
YP_513307.1	YP_513307.1	FTL_0538	<i>fabZ</i>	(3R)-hydroxymyristoyl-ACP dehydratase
YP_513222.1	YP_513222.1	FTL_0450	<i>psd</i>	phosphatidylserine decarboxylase
YP_514374.1	YP_514374.1	FTL_1743	-	DNA-directed RNA polymerase subunit beta
YP_514001.1	YP_514001.1	FTL_1335	-	hypothetical protein
YP_514087.1	YP_514087.1	FTL_1432	-	D-ribulose-phosphate 3-epimerase
YP_512946.1	YP_512946.1	FTL_0148	-	Sodium/hydrogen exchanger (antiporter) family protein
YP_513100.1	YP_513100.1	FTL_0308	-	hypothetical protein
YP_513385.1	YP_513385.1	FTL_0632	-	ArsR family transcriptional regulator
YP_513362.1	YP_513362.1	FTL_0602	<i>wbtI</i>	hypothetical protein
YP_513530.1	YP_513530.1	FTL_0798	-	Type IV pili glycosylation protein
YP_513186.1	YP_513186.1	FTL_0413	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
YP_513097.1	YP_513097.1	FTL_0305	-	hypothetical protein
YP_514340.1	YP_514340.1	FTL_1709	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513365.1	YP_513365.1	FTL_0605	<i>wbtL</i>	glucose-1-phosphate thymidyltransferase
YP_513170.1	YP_513170.1	FTL_0397	<i>purN</i>	phosphoribosylglycinamide formyltransferase
YP_512890.1	YP_512890.1	FTL_0089	-	ferredoxin
YP_512880.1	YP_512880.1	FTL_0076	-	riboflavin biosynthesis protein ribA/GTP-cyclohydrolase II
YP_513549.1	YP_513549.1	FTL_0827	-	Type IV pili polytopic inner membrane protein
YP_514036.1	YP_514036.1	FTL_1375	-	heat shock protein 15 (HSP15)
YP_514274.1	YP_514274.1	FTL_1635	-	chitinase, fragment
YP_513379.1	YP_513379.1	FTL_0623	-	ABC transporter ATP-binding protein
YP_514141.1	YP_514141.1	FTL_1490	-	phosphoglyceromutase
YP_514365.1	YP_514365.1	FTL_1734	-	integrase/recombinase
YP_513151.1	YP_513151.1	FTL_0375	-	hypothetical protein
YP_514472.1	YP_514472.1	FTL_1850	<i>purB</i>	adenylosuccinate lyase
YP_513437.1	YP_513437.1	FTL_0686	-	outer membrane efflux protein
YP_512847.1	YP_512847.1	FTL_0039	-	hypothetical protein
YP_513291.1	YP_513291.1	FTL_0522	<i>rpmB</i>	50S ribosomal protein L28
YP_513208.1	YP_513208.1	FTL_0436	<i>ileS</i>	isoleucyl-tRNA synthetase
YP_514039.1	YP_514039.1	FTL_1383	-	glutathione peroxidase
YP_514237.1	YP_514237.1	FTL_1598	<i>argS</i>	arginyl-tRNA synthetase
YP_513646.1	YP_513646.1	FTL_0933	-	DNA recombination protein RmuC family protein
YP_513994.1	YP_513994.1	FTL_1328	<i>fopA</i>	OmpA family protein, outer membrane associated protein
YP_514330.1	YP_514330.1	FTL_1699	-	hypothetical protein
YP_512982.1	YP_512982.1	FTL_0187	-	cyclohexadienyl dehydratase
YP_513422.1	YP_513422.1	FTL_0670	<i>recD</i>	exodeoxyribonuclease V subunit alpha
YP_513946.1	YP_513946.1	FTL_1275	<i>bioD</i>	dethiobiotin synthetase
YP_513043.1	YP_513043.1	FTL_0248	<i>rplE</i>	50S ribosomal protein L5
YP_513578.1	YP_513578.1	FTL_0856	-	carbonic anhydrase
YP_514256.1	YP_514256.1	FTL_1617	<i>glnS</i>	glutaminyl-tRNA synthetase
YP_513519.1	YP_513519.1	FTL_0784	-	lipoprotein
YP_513474.1	YP_513474.1	FTL_0723	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513247.1	YP_513247.1	FTL_0475	-	lipoprotein releasing system, subunit D, ABC transporter ATP-binding protein
YP_514294.1	YP_514294.1	FTL_1659	<i>prfC</i>	peptide chain release factor 3
YP_513037.1	YP_513037.1	FTL_0242	<i>rpsC</i>	30S ribosomal protein S3
YP_513723.1	YP_513723.1	FTL_1022	-	coproporphyrinogen III oxidase
YP_512822.1	YP_512822.1	FTL_0012	<i>recA</i>	recombinase A
YP_513034.1	YP_513034.1	FTL_0239	<i>rplB</i>	50S ribosomal protein L2
YP_513408.1	YP_513408.1	FTL_0655	-	hypothetical protein
YP_513555.1	YP_513555.1	FTL_0833	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
YP_513635.1	YP_513635.1	FTL_0922	-	Iron-sulfur cluster-binding protein
YP_513560.1	YP_513560.1	FTL_0838	<i>metN</i>	D-methionine transport protein, ABC transporter,ATP-binding subunit
YP_512935.1	YP_512935.1	FTL_0137	-	lipopolysaccharide protein
YP_513898.1	YP_513898.1	FTL_1215	-	hypothetical protein
YP_513885.1	YP_513885.1	FTL_1202	-	hypothetical protein
YP_514555.1	YP_514555.1	FTL_1957	-	heat shock protein
YP_513927.1	YP_513927.1	FTL_1247	-	hypothetical protein
YP_513348.1	YP_513348.1	FTL_0588	-	isocitrate dehydrogenase
YP_513411.1	YP_513411.1	FTL_0659	-	cell division protein
YP_514194.1	YP_514194.1	FTL_1548	<i>chaC</i>	hypothetical protein
YP_514097.1	YP_514097.1	FTL_1442	<i>fabI</i>	enoyl-[acyl-carrier-protein] reductase (NADH)
YP_513965.1	YP_513965.1	FTL_1294	-	short-chain dehydrogenase
YP_513424.1	YP_513424.1	FTL_0672	<i>panD</i>	aspartate alpha-decarboxylase
YP_513257.1	YP_513257.1	FTL_0485	<i>glgC</i>	glucose-1-phosphate adenyllyltransferase
YP_513768.1	YP_513768.1	FTL_1071	<i>guaA</i>	GMP synthase
YP_513522.1	YP_513522.1	FTL_0787	-	glycoprotease family protein
YP_513013.1	YP_513013.1	FTL_0218	<i>gltX</i>	glutamyl-tRNA synthetase
YP_514127.1	YP_514127.1	FTL_1476	<i>pgi</i>	glucose-6-phosphate isomerase
YP_513195.1	YP_513195.1	FTL_0423	-	hypothetical protein
YP_513666.1	YP_513666.1	FTL_0955	-	GTP-dependent nucleic acid-binding protein EngD

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513869.1	YP_513869.1	FTL_1186	<i>rpsL</i>	30S ribosomal protein S9
YP_513764.1	YP_513764.1	FTL_1067	-	hypothetical protein
YP_513956.1	YP_513956.1	FTL_1285	-	methionyl-tRNA formyltransferase
YP_513812.1	YP_513812.1	FTL_1125	-	transcriptional regulator
YP_514198.1	YP_514198.1	FTL_1552	-	hypothetical protein
YP_513345.1	YP_513345.1	FTL_0585	<i>fadE</i>	acyl-CoA dehydrogenase
YP_513790.1	YP_513790.1	FTL_1100	<i>rsfS</i>	ribosomal silencing factor RsfS
YP_513227.1	YP_513227.1	FTL_0455	-	acetyltransferase
YP_513933.1	YP_513933.1	FTL_1253	<i>folE</i>	GTP cyclohydrolase I
YP_514217.1	YP_514217.1	FTL_1578	-	hypothetical protein
YP_512820.1	YP_512820.1	FTL_0010	<i>glpe</i>	thiosulfate sulfurtransferase
YP_514423.1	YP_514423.1	FTL_1798	-	FOF1 ATP synthase subunit delta
YP_514510.1	YP_514510.1	FTL_1900	-	L-glutaminase
YP_513883.1	YP_513883.1	FTL_1200	-	cobalamin (vitamin B12) synthesis protein/P47K family protein
YP_513940.1	YP_513940.1	FTL_1266	-	lipase/esterase
YP_513900.1	YP_513900.1	FTL_1217	-	hypothetical protein
YP_513303.1	YP_513303.1	FTL_0534	-	1-deoxy-D-xylulose 5-phosphate reductoisomerase
YP_514262.1	YP_514262.1	FTL_1623	-	hypothetical protein
YP_513177.1	YP_513177.1	FTL_0404	<i>glk</i>	glucose kinase
YP_514112.1	YP_514112.1	FTL_1461	<i>deoD</i>	purine nucleoside phosphorylase
YP_514050.1	YP_514050.1	FTL_1395	<i>galP1</i>	major facilitator superfamily galactose-proton symporter
YP_513507.1	YP_513507.1	FTL_0762	-	hypothetical protein
YP_514564.1	YP_514564.1	FTL_1968	-	ribonuclease G
YP_514139.1	YP_514139.1	FTL_1488	-	cytidine deaminase
YP_513597.1	YP_513597.1	FTL_0877	-	peptidase, M24 family protein
YP_513103.1	YP_513103.1	FTL_0311	-	dihydrolipoamide dehydrogenase
YP_513860.1	YP_513860.1	FTL_1177	<i>trmE</i>	tRNA modification GTPase TrmE
YP_514104.1	YP_514104.1	FTL_1449	-	ribonuclease D
YP_513957.1	YP_513957.1	FTL_1286	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_512998.1	YP_512998.1	FTL_0203	-	hypothetical protein
YP_514035.1	YP_514035.1	FTL_1374	-	organic solvent tolerance protein
YP_513881.1	YP_513881.1	FTL_1198	<i>pheT</i>	phenylalanyl-tRNA synthetase subunit beta
YP_513102.1	YP_513102.1	FTL_0310	-	dihydrolipoamide acetyltransferase
YP_514199.1	YP_514199.1	FTL_1553	<i>sucC</i>	succinyl-CoA synthetase subunit beta
YP_513570.1	YP_513570.1	FTL_0848	<i>secD</i>	preprotein translocase subunit SecD
YP_513835.1	YP_513835.1	FTL_1149	<i>fbaA</i>	fructose-1,6-bisphosphate aldolase
YP_513342.1	YP_513342.1	FTL_0582	-	hypothetical protein
YP_513750.1	YP_513750.1	FTL_1050	<i>rpoD</i>	RNA polymerase sigma-70 factor
YP_514187.1	YP_514187.1	FTL_1541	<i>mraW</i>	S-adenosyl-methyltransferase Mrw
YP_513572.1	YP_513572.1	FTL_0850	-	hypothetical protein
YP_513410.1	YP_513410.1	FTL_0657	-	hydroxyacylglutathione hydrolase
YP_514478.1	YP_514478.1	FTL_1861	<i>purF</i>	amidophosphoribosyltransferase
YP_514245.1	YP_514245.1	FTL_1606	<i>sspA</i>	stringent starvation protein A
YP_513973.1	YP_513973.1	FTL_1302	-	phenol hydroxylase
YP_513636.1	YP_513636.1	FTL_0923	-	glutaredoxin
YP_514337.1	YP_514337.1	FTL_1706	<i>lolA</i>	lipoprotein releasing system subunit A, outer membrane lipoproteins carrier
YP_513656.1	YP_513656.1	FTL_0943	-	Sodium/hydrogen exchanger family protein
YP_514520.1	YP_514520.1	FTL_1910	-	D-alanyl-alanine synthetase A
YP_514184.1	YP_514184.1	FTL_1538	<i>rpsO</i>	30S ribosomal protein S15
YP_514299.1	YP_514299.1	FTL_1664	<i>deoB</i>	phosphopentomutase
YP_513833.1	YP_513833.1	FTL_1147	<i>pgk</i>	phosphoglycerate kinase
YP_513290.1	YP_513290.1	FTL_0521	<i>rpmG</i>	50S ribosomal protein L33
YP_513397.1	YP_513397.1	FTL_0644	-	carbon-nitrogen hydrolase
YP_513524.1	YP_513524.1	FTL_0789	-	aspartate aminotransferase
YP_513936.1	YP_513936.1	FTL_1262	-	chorismate binding family protein
YP_512940.1	YP_512940.1	FTL_0142	-	hypothetical protein
YP_513329.1	YP_513329.1	FTL_0569	-	hypothetical protein
YP_512873.1	YP_512873.1	FTL_0069	-	outer membrane lipoprotein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514075.1	YP_514075.1	FTL_1420	-	carbohydrate/purine kinase pfkB family protein
YP_513023.1	YP_513023.1	FTL_0228	<i>uppS</i>	undecaprenyl pyrophosphate synthase
YP_514109.1	YP_514109.1	FTL_1458	<i>secA</i>	preprotein translocase subunit SecA
YP_513913.1	YP_513913.1	FTL_1232	<i>trkA</i>	potassium transporter peripheral membrane protein
YP_514146.1	YP_514146.1	FTL_1495	-	cysteine/glutathione ABC transporter membrane/ATP-binding protein
YP_513224.1	YP_513224.1	FTL_0452	-	bifunctional nicotinamide mononucleotide adenylyltransferase/ADP-ribose pyrophosphatase
YP_513181.1	YP_513181.1	FTL_0408	<i>hitA</i>	histidine triad (HIT) family protein
YP_514000.1	YP_514000.1	FTL_1334	-	L-serine dehydratase 1
YP_514179.1	YP_514179.1	FTL_1533	-	DNA-directed RNA polymerase subunit omega
YP_513834.1	YP_513834.1	FTL_1148	<i>pyk</i>	pyruvate kinase
YP_514107.1	YP_514107.1	FTL_1452	<i>rpmA</i>	50S ribosomal protein L27
YP_514370.1	YP_514370.1	FTL_1739	-	S-adenosylmethionine synthetase
YP_513618.1	YP_513618.1	FTL_0899	-	protease, GTP-binding subunit
YP_513144.1	YP_513144.1	FTL_0361	-	LemA-like protein
YP_514080.1	YP_514080.1	FTL_1425	-	hypothetical protein
YP_513565.1	YP_513565.1	FTL_0843	<i>tgt</i>	queueine tRNA-ribosyltransferase
YP_513478.1	YP_513478.1	FTL_0727	-	monooxygenase family protein
YP_514483.1	YP_514483.1	FTL_1866	-	protein-L-isoaspartate O-methyltransferase
YP_514355.1	YP_514355.1	FTL_1724	-	lipoprotein
YP_512895.1	YP_512895.1	FTL_0094	<i>clpB</i>	ClpB protein
YP_513439.1	YP_513439.1	FTL_0688	-	major facilitator transporter
YP_513318.1	YP_513318.1	FTL_0552	<i>pmrA</i>	two-component response regulator
YP_512878.1	YP_512878.1	FTL_0074	-	peptide deformylase
YP_513376.1	YP_513376.1	FTL_0617	-	hypothetical protein
YP_513049.1	YP_513049.1	FTL_0254	<i>rpmD</i>	50S ribosomal protein L30
YP_514341.1	YP_514341.1	FTL_1710	-	ProP osmoprotectant transporter, fragment
YP_513407.1	YP_513407.1	FTL_0654	-	uroporphyrinogen III synthase
YP_513450.1	YP_513450.1	FTL_0699	-	ribosomal large subunit pseudouridine synthase D

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514218.1	YP_514218.1	FTL_1579	-	hypothetical protein
YP_514487.1	YP_514487.1	FTL_1873	-	amino acid transporter
YP_514226.1	YP_514226.1	FTL_1587	-	lysyl-tRNA synthetase
YP_513287.1	YP_513287.1	FTL_0518	<i>minE</i>	cell division topological specificity factor MinE
YP_513606.1	YP_513606.1	FTL_0886	-	(dimethylallyl)adenosine tRNA methylthiotransferase
YP_513055.1	YP_513055.1	FTL_0260	<i>rpsD</i>	30S ribosomal protein S4
YP_514400.1	YP_514400.1	FTL_1773	-	hypothetical protein
YP_514255.1	YP_514255.1	FTL_1616	<i>pckA</i>	phosphoenolpyruvate carboxykinase
YP_513480.1	YP_513480.1	FTL_0729	<i>queA</i>	S-adenosylmethionine--tRNA ribosyltransferase-isomerase
YP_513671.1	YP_513671.1	FTL_0960	<i>udhA</i>	soluble pyridine nucleotide transhydrogenase
YP_513082.1	YP_513082.1	FTL_0289	-	hypothetical protein
YP_513022.1	YP_513022.1	FTL_0227	<i>frr</i>	ribosome recycling factor
YP_513584.1	YP_513584.1	FTL_0862	-	hypothetical protein
YP_513315.1	YP_513315.1	FTL_0547	<i>kdtA</i>	3-deoxy-D-manno-octulosonic-acid transferase
YP_513793.1	YP_513793.1	FTL_1106	<i>alaS</i>	alanyl-tRNA synthetase
YP_512997.1	YP_512997.1	FTL_0202	-	hypothetical protein
YP_513568.1	YP_513568.1	FTL_0846	-	isochorismatase hydrolase family protein
YP_513697.1	YP_513697.1	FTL_0989	-	ubiquinone biosynthesis protein
YP_513718.1	YP_513718.1	FTL_1017	-	cytidylate kinase
YP_513417.1	YP_513417.1	FTL_0665	<i>gltB</i>	hypothetical protein (glutamate synthase domain-containing 2)
YP_513333.1	YP_513333.1	FTL_0573	-	hypothetical protein
YP_513614.1	YP_513614.1	FTL_0895	<i>hupB</i>	histone-like protein HU form B
YP_513615.1	YP_513615.1	FTL_0896	-	hypothetical protein
YP_514181.1	YP_514181.1	FTL_1535	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase
YP_513475.1	YP_513475.1	FTL_0724	-	5-formyltetrahydrofolate cyclo-ligase
YP_513717.1	YP_513717.1	FTL_1016	-	short chain dehydrogenase
YP_513184.1	YP_513184.1	FTL_0411	-	hypothetical protein
YP_514149.1	YP_514149.1	FTL_1498	-	translation initiation inhibitor
YP_513645.1	YP_513645.1	FTL_0932	<i>ruvA</i>	Holliday junction DNA helicase RuvA

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513305.1	YP_513305.1	FTL_0536	-	outer membrane protein OmpH
YP_514413.1	YP_514413.1	FTL_1788	-	succinate dehydrogenase, cytochrome b556
YP_514345.1	YP_514345.1	FTL_1714	<i>groEL</i>	chaperonin GroEL
YP_513763.1	YP_513763.1	FTL_1066	-	fumarylacetoacetate hydrolase family protein
YP_513492.1	YP_513492.1	FTL_0743	-	oxidoreductase, short-chain dehydrogenase family protein
YP_513489.1	YP_513489.1	FTL_0740	-	hypothetical protein
YP_513056.1	YP_513056.1	FTL_0261	-	DNA-directed RNA polymerase subunit alpha
YP_513116.1	YP_513116.1	FTL_0328	-	chorismate mutase
YP_513612.1	YP_513612.1	FTL_0893	<i>clpX</i>	ATP-dependent protease ATP-binding subunit ClpX
YP_514215.1	YP_514215.1	FTL_1576	-	DNA mismatch repair protein
YP_513366.1	YP_513366.1	FTL_0606	<i>wbtM</i>	dTDP-D-glucose 4,6-dehydratase
YP_513202.1	YP_513202.1	FTL_0430	-	hypothetical protein
YP_513872.1	YP_513872.1	FTL_1189	<i>mltA</i>	membrane-bound lytic murein transglycosylase A (MLT) family protein
YP_512978.1	YP_512978.1	FTL_0183	-	oligoribonuclease
YP_513258.1	YP_513258.1	FTL_0486	<i>glgA</i>	glycogen synthase
YP_512867.1	YP_512867.1	FTL_0059	<i>gidB</i>	16S rRNA methyltransferase GidB
YP_514301.1	YP_514301.1	FTL_1666	-	DNA polymerase I
YP_514421.1	YP_514421.1	FTL_1796	-	F0F1 ATP synthase subunit gamma
YP_512937.1	YP_512937.1	FTL_0139	-	carboxylesterase/phospholipase family protein
YP_513602.1	YP_513602.1	FTL_0882	-	apolipoprotein N-acyltransferase
YP_514336.1	YP_514336.1	FTL_1705	<i>ftsK</i>	cell division protein
YP_513101.1	YP_513101.1	FTL_0309	<i>aceE</i>	pyruvate dehydrogenase subunit E1
YP_514364.1	YP_514364.1	FTL_1733	-	oxidoreductase iron/ascorbate family protein
YP_513629.1	YP_513629.1	FTL_0916	-	ketol-acid reductoisomerase
YP_513729.1	YP_513729.1	FTL_1028	-	radical SAM superfamily protein
YP_512987.1	YP_512987.1	FTL_0192	-	cytochrome O ubiquinol oxidase subunit I
YP_513613.1	YP_513613.1	FTL_0894	<i>lon</i>	DNA-binding, ATP-dependent protease La
YP_514516.1	YP_514516.1	FTL_1906	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514303.1	YP_514303.1	FTL_1668	<i>msbA</i>	lipid A transport protein ABC transporter ATP-binding protein/permease
YP_514424.1	YP_514424.1	FTL_1799	-	F0F1 ATP synthase subunit B
YP_513261.1	YP_513261.1	FTL_0489	<i>glyQ</i>	glycyl-tRNA synthetase subunit alpha
YP_513457.1	YP_513457.1	FTL_0706	<i>wyz</i>	predicted O-antigen ligase
YP_512829.1	YP_512829.1	FTL_0020	<i>aspS</i>	aspartyl-tRNA synthetase
YP_513426.1	YP_513426.1	FTL_0674	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase
YP_513198.1	YP_513198.1	FTL_0426	-	DNA topoisomerase I
YP_513122.1	YP_513122.1	FTL_0334	-	TolB protein precursor
YP_514168.1	YP_514168.1	FTL_1521	-	chitinase family 18 protein
YP_513050.1	YP_513050.1	FTL_0255	<i>rplO</i>	50S ribosomal protein L15
YP_514068.1	YP_514068.1	FTL_1413	<i>spoT</i>	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase/(p)ppGpp synthase
YP_513981.1	YP_513981.1	FTL_1310	<i>ndk</i>	nucleoside diphosphate kinase
YP_514125.1	YP_514125.1	FTL_1474	<i>greA</i>	transcription elongation factor GreA
YP_514043.1	YP_514043.1	FTL_1388	-	L-aspartate oxidase
YP_514524.1	YP_514524.1	FTL_1914	<i>ripA</i>	hypothetical protein
YP_514563.1	YP_514563.1	FTL_1967	-	trp operon repressor
YP_513275.1	YP_513275.1	FTL_0506	<i>lpxH</i>	UDP-2,3-diacylglucosamine hydrolase
YP_513880.1	YP_513880.1	FTL_1197	<i>pheS</i>	phenylalanyl-tRNA synthetase subunit alpha
YP_514419.1	YP_514419.1	FTL_1794	<i>atpC</i>	F0F1 ATP synthase subunit epsilon
YP_512811.1	YP_512811.1	FTL_0001	<i>dnaA</i>	chromosomal replication initiation protein
YP_513259.1	YP_513259.1	FTL_0487	-	maltodextrin phosphorylase
YP_513975.1	YP_513975.1	FTL_1304	-	glutamate--cysteine ligase
YP_514260.1	YP_514260.1	FTL_1621	-	ABC transporter ATP-binding
YP_513797.1	YP_513797.1	FTL_1110	-	hypothetical protein
YP_513121.1	YP_513121.1	FTL_0333	-	hypothetical protein
YP_513494.1	YP_513494.1	FTL_0745	-	excinuclease ABC subunit B
YP_513229.1	YP_513229.1	FTL_0457	-	cold shock protein
YP_514003.1	YP_514003.1	FTL_1338	-	alanine racemase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514169.1	YP_514169.1	FTL_1522	-	2-amino-3-ketobutyrate coenzyme A ligase
YP_514307.1	YP_514307.1	FTL_1672	-	AcrB/AcrD/AcrF family transporter
YP_512888.1	YP_512888.1	FTL_0087	-	acetyltransferase protein
YP_513256.1	YP_513256.1	FTL_0484	<i>pgm</i>	phosphoglucomutase
YP_513569.1	YP_513569.1	FTL_0847	<i>yajC</i>	preprotein translocase family protein
YP_514464.1	YP_514464.1	FTL_1842	<i>gatA</i>	aspartyl/glutamyl-tRNA amidotransferase subunit A
YP_514088.1	YP_514088.1	FTL_1433	-	arabinose phosphate isomerase
YP_514241.1	YP_514241.1	FTL_1602	-	delta-aminolevulinic acid dehydratase
YP_513505.1	YP_513505.1	FTL_0760	-	C32 tRNA thiolase
YP_513205.1	YP_513205.1	FTL_0433	-	ribosomal large subunit methyltransferase J
YP_514375.1	YP_514375.1	FTL_1744	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
YP_514103.1	YP_514103.1	FTL_1448	<i>uvrC</i>	excinuclease ABC subunit C
YP_513759.1	YP_513759.1	FTL_1062	-	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
YP_514222.1	YP_514222.1	FTL_1583	<i>gadC</i>	glutamate:gamma-aminobutyric acid antiporter family protein, putative glutamate transporter
YP_513185.1	YP_513185.1	FTL_0412	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase
YP_513147.1	YP_513147.1	FTL_0371	-	hypothetical protein
YP_513758.1	YP_513758.1	FTL_1061	-	inorganic pyrophosphatase
YP_514230.1	YP_514230.1	FTL_1591	<i>accC</i>	Acetyl-CoA carboxylase, biotin carboxylase subunit
YP_513596.1	YP_513596.1	FTL_0876	-	hypothetical protein
YP_513468.1	YP_513468.1	FTL_0717	<i>rne</i>	ribonuclease E
YP_514434.1	YP_514434.1	FTL_1809	<i>infB</i>	translation initiation factor IF-2
YP_512996.1	YP_512996.1	FTL_0201	-	hypothetical protein
YP_513079.1	YP_513079.1	FTL_0286	-	hypothetical protein
YP_513623.1	YP_513623.1	FTL_0904	<i>hflC</i>	protease modulator HflC
YP_514306.1	YP_514306.1	FTL_1671	-	RND efflux transporter
YP_512841.1	YP_512841.1	FTL_0033	<i>pyrC</i>	dihydroorotase
YP_514283.1	YP_514283.1	FTL_1644	-	glycerol kinase
YP_513286.1	YP_513286.1	FTL_0517	-	ABC transporter ATP-binding protein
YP_513998.1	YP_513998.1	FTL_1332	-	hesB family protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514013.1	YP_514013.1	FTL_1350	-	glycyl-tRNA synthetase subunit beta
YP_514240.1	YP_514240.1	FTL_1601	-	tRNA/rRNA methyltransferase
YP_513634.1	YP_513634.1	FTL_0921	-	endonuclease III
YP_514410.1	YP_514410.1	FTL_1785	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit
YP_513282.1	YP_513282.1	FTL_0513	-	hypothetical protein
YP_514183.1	YP_514183.1	FTL_1537	<i>pnp</i>	polynucleotide phosphorylase/polyadenylase
YP_514074.1	YP_514074.1	FTL_1419	-	cyanophycinase
YP_512851.1	YP_512851.1	FTL_0043	-	chorismate mutase
YP_513559.1	YP_513559.1	FTL_0837	<i>metIQ</i>	D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein
YP_513115.1	YP_513115.1	FTL_0327	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
YP_514073.1	YP_514073.1	FTL_1418	-	asparaginase
YP_513829.1	YP_513829.1	FTL_1143	<i>rpmF</i>	50S ribosomal protein L32
YP_513714.1	YP_513714.1	FTL_1013	-	hypothetical protein
YP_512819.1	YP_512819.1	FTL_0009	-	outer membrane protein
YP_513999.1	YP_513999.1	FTL_1333	-	selenocysteine lyase
YP_513551.1	YP_513551.1	FTL_0829	-	glycerophosphoryl diester phosphodiesterase
YP_513441.1	YP_513441.1	FTL_0690	-	Acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)
YP_514372.1	YP_514372.1	FTL_1741	-	putative DNA-binding/iron metalloprotein/AP endonuclease
YP_513828.1	YP_513828.1	FTL_1142	-	putative glycerol-3-phosphate acyltransferase PlsX
YP_514409.1	YP_514409.1	FTL_1784	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component
YP_513425.1	YP_513425.1	FTL_0673	<i>panC</i>	pantoate-beta-alanine ligase
YP_513769.1	YP_513769.1	FTL_1072	-	1-deoxy-D-xylulose-5-phosphate synthase
YP_513009.1	YP_513009.1	FTL_0214	-	L-lactate dehydrogenase
YP_513370.1	YP_513370.1	FTL_0610	<i>rho</i>	transcription termination factor Rho
YP_514484.1	YP_514484.1	FTL_1867	-	protease yegQ
YP_514352.1	YP_514352.1	FTL_1721	<i>prfA</i>	peptide chain release factor 1
YP_512874.1	YP_512874.1	FTL_0070	<i>rpsT</i>	30S ribosomal protein S20
YP_514331.1	YP_514331.1	FTL_1700	-	Sodium/proline permease
YP_513891.1	YP_513891.1	FTL_1208	<i>dcd</i>	deoxycytidine triphosphate deaminase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514408.1	YP_514408.1	FTL_1783	<i>sucB</i>	dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex
YP_513890.1	YP_513890.1	FTL_1207	-	MRP like protein
YP_514518.1	YP_514518.1	FTL_1908	-	cell division protein FtsA
YP_514220.1	YP_514220.1	FTL_1581	-	lipoprotein
YP_513823.1	YP_513823.1	FTL_1137	-	3-oxoacyl-ACP synthase
YP_514024.1	YP_514024.1	FTL_1363	-	hypothetical protein
YP_514047.1	YP_514047.1	FTL_1392	<i>deaD</i>	cold-shock DEAD-box protein A
YP_514540.1	YP_514540.1	FTL_1939	-	outer membrane lipoprotein
YP_512889.1	YP_512889.1	FTL_0088	-	acetyltransferase protein
YP_513142.1	YP_513142.1	FTL_0359	-	Type IV pili fiber building block protein
YP_513199.1	YP_513199.1	FTL_0427	-	chromosome partition protein A
YP_514562.1	YP_514562.1	FTL_1966	-	anthranilate synthase component I
YP_513321.1	YP_513321.1	FTL_0555	<i>truB</i>	tRNA pseudouridine synthase B
YP_513875.1	YP_513875.1	FTL_1192	-	chaperone protein DnaJ
YP_513488.1	YP_513488.1	FTL_0739	-	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA
YP_513308.1	YP_513308.1	FTL_0539	-	UDP-N-acetylglucosamine acyltransferase
YP_514561.1	YP_514561.1	FTL_1963	-	hypothetical protein
YP_514517.1	YP_514517.1	FTL_1907	-	cell division protein FtsZ
YP_513143.1	YP_513143.1	FTL_0360	-	heat shock protein HtpX
YP_514428.1	YP_514428.1	FTL_1803	<i>ileP</i>	major facilitator transporter, isoleucine transporter
YP_513553.1	YP_513553.1	FTL_0831	-	cyanophycin synthetase
YP_513506.1	YP_513506.1	FTL_0761	<i>smpB</i>	SsrA-binding protein
YP_514407.1	YP_514407.1	FTL_1782	<i>apt</i>	adenine phosphoribosyltransferase
YP_513919.1	YP_513919.1	FTL_1239	<i>ffh</i>	signal recognition particle protein, Ffh
YP_513529.1	YP_513529.1	FTL_0797	-	Type IV pili associated protein
YP_513816.1	YP_513816.1	FTL_1129	-	acetyltransferase
YP_513643.1	YP_513643.1	FTL_0930	<i>ruvC</i>	Holliday junction resolvase
YP_513640.1	YP_513640.1	FTL_0927	-	lipoyl synthase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513945.1	YP_513945.1	FTL_1274	<i>bioC</i>	biotin synthesis protein BioC
YP_513862.1	YP_513862.1	FTL_1179	<i>hfp</i>	ribosome hibernation-promoting factor
YP_512999.1	YP_512999.1	FTL_0204	-	hypothetical protein
YP_513873.1	YP_513873.1	FTL_1190	-	heat shock protein GrpE
YP_513538.1	YP_513538.1	FTL_0806	-	amino acid transporter family protein
YP_513977.1	YP_513977.1	FTL_1306	-	hypothetical protein
YP_513622.1	YP_513622.1	FTL_0903	<i>hflK</i>	FtsH protease activity modulator
YP_514437.1	YP_514437.1	FTL_1812	<i>hemE</i>	uroporphyrinogen decarboxylase
YP_513051.1	YP_513051.1	FTL_0256	<i>secY</i>	preprotein translocase subunit SecY
YP_514142.1	YP_514142.1	FTL_1491	-	seryl-tRNA synthetase
YP_513169.1	YP_513169.1	FTL_0396	<i>purCD</i>	fusion protein PurC/PurD
YP_513025.1	YP_513025.1	FTL_0230	<i>dut</i>	deoxyuridine 5'-triphosphate nucleotidohydrolase
YP_512986.1	YP_512986.1	FTL_0191	-	cytochrome O ubiquinol oxidase subunit II
YP_514053.1	YP_514053.1	FTL_1398	-	hypothetical protein
YP_513255.1	YP_513255.1	FTL_0483	<i>glgB</i>	glycogen branching protein
YP_513710.1	YP_513710.1	FTL_1004	-	D-alanyl-D-alanine carboxypeptidase
YP_512882.1	YP_512882.1	FTL_0078	-	riboflavin biosynthesis protein ribD
YP_514404.1	YP_514404.1	FTL_1779	<i>secG</i>	preprotein translocase subunit SecG
YP_514242.1	YP_514242.1	FTL_1603	-	RNA-binding protein
YP_514443.1	YP_514443.1	FTL_1821	-	NADH dehydrogenase I subunit J
YP_514482.1	YP_514482.1	FTL_1865	-	outer membrane protein tolC
YP_514406.1	YP_514406.1	FTL_1781	<i>glmM</i>	phosphoglucosamine mutase
YP_513090.1	YP_513090.1	FTL_0298	-	hypothetical protein
YP_512975.1	YP_512975.1	FTL_0180	<i>htrB</i>	acyltransferase
YP_514231.1	YP_514231.1	FTL_1592	<i>accB</i>	Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit
YP_512903.1	YP_512903.1	FTL_0104	-	hypothetical protein
YP_513924.1	YP_513924.1	FTL_1244	-	exodeoxyribonuclease III
YP_513757.1	YP_513757.1	FTL_1060	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase
YP_512983.1	YP_512983.1	FTL_0188	-	cytochrome d terminal oxidase, polypeptide subunit II

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_512868.1	YP_512868.1	FTL_0060	-	hypothetical protein
YP_514236.1	YP_514236.1	FTL_1597	-	organic solvent tolerance protein
YP_514200.1	YP_514200.1	FTL_1554	<i>sucD</i>	succinyl-CoA synthetase, alpha subunit
YP_514232.1	YP_514232.1	FTL_1593	<i>aroD</i>	3-dehydroquinate dehydratase
YP_512832.1	YP_512832.1	FTL_0024	-	serine transporter
YP_513761.1	YP_513761.1	FTL_1064	-	hypothetical protein
YP_513716.1	YP_513716.1	FTL_1015	-	AhpC/TSA family protein
YP_513200.1	YP_513200.1	FTL_0428	-	chromosome partition protein B
YP_513641.1	YP_513641.1	FTL_0928	-	isoprenoid biosynthesis protein with amidotransferase-like domain
YP_513603.1	YP_513603.1	FTL_0883	-	metal ion transporter protein
YP_513196.1	YP_513196.1	FTL_0424	-	lipoprotein
YP_514026.1	YP_514026.1	FTL_1365	-	hypothetical protein
YP_513466.1	YP_513466.1	FTL_0715	<i>thyA</i>	thymidylate synthase
YP_513451.1	YP_513451.1	FTL_0700	-	lipoprotein
YP_513730.1	YP_513730.1	FTL_1029	-	Type IV pili lipoprotein
YP_514430.1	YP_514430.1	FTL_1805	-	ATPase
YP_513232.1	YP_513232.1	FTL_0460	-	hypothetical protein
YP_514333.1	YP_514333.1	FTL_1702	-	hypothetical protein
YP_513161.1	YP_513161.1	FTL_0388	-	cation transporter
YP_513495.1	YP_513495.1	FTL_0746	-	hypothetical protein
YP_513996.1	YP_513996.1	FTL_1330	<i>coaD</i>	phosphopantetheine adenyltransferase
YP_512948.1	YP_512948.1	FTL_0150	-	lipoprotein releasing system, subunit B, outer membrane lipoprotein
YP_513547.1	YP_513547.1	FTL_0822	-	hypothetical protein
YP_513211.1	YP_513211.1	FTL_0439	-	hypothetical protein
YP_513726.1	YP_513726.1	FTL_1025	<i>rpsR</i>	30S ribosomal protein S18
YP_514175.1	YP_514175.1	FTL_1528	-	major facilitator transporter
YP_513253.1	YP_513253.1	FTL_0481	-	shikimate 5-dehydrogenase
YP_513179.1	YP_513179.1	FTL_0406	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513827.1	YP_513827.1	FTL_1141	-	3-oxoacyl-ACP synthase
YP_514280.1	YP_514280.1	FTL_1641	-	hypothetical protein
YP_513074.1	YP_513074.1	FTL_0281	-	heat shock protein, hsp40
YP_513250.1	YP_513250.1	FTL_0478	-	glycine cleavage system H protein
YP_514076.1	YP_514076.1	FTL_1421	-	haloacid dehalogenase-like hydrolase family protein
YP_514219.1	YP_514219.1	FTL_1580	-	hypothetical protein
YP_513760.1	YP_513760.1	FTL_1063	-	hypothetical protein
YP_514119.1	YP_514119.1	FTL_1468	-	ATP-dependent metalloprotease
YP_514115.1	YP_514115.1	FTL_1464	-	ATP-dependent metalloprotease
YP_513260.1	YP_513260.1	FTL_0488	-	4-alpha-glucanotransferase
YP_514191.1	YP_514191.1	FTL_1545	-	glutamine amidotransferase subunit PdxT
YP_514224.1	YP_514224.1	FTL_1585	-	single-stranded-DNA-specific exonuclease
YP_513262.1	YP_513262.1	FTL_0490	-	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
YP_513868.1	YP_513868.1	FTL_1185	<i>mgIA</i>	macrophage growth locus subunit A
YP_513770.1	YP_513770.1	FTL_1073	-	hypothetical protein
YP_513598.1	YP_513598.1	FTL_0878	-	DNA/RNA endonuclease family protein, DNA/RNA endonuclease G
YP_514558.1	YP_514558.1	FTL_1960	-	peptide methionine sulfoxide reductase MsrA
YP_514338.1	YP_514338.1	FTL_1707	-	hypothetical protein
YP_513036.1	YP_513036.1	FTL_0241	<i>rplV</i>	50S ribosomal protein L22
YP_513353.1	YP_513353.1	FTL_0593	<i>wbtB</i>	galactosyl transferase
YP_513390.1	YP_513390.1	FTL_0637	-	hypothetical protein
YP_514098.1	YP_514098.1	FTL_1443	-	hypothetical protein
YP_513531.1	YP_513531.1	FTL_0799	-	Type IV pili lipoprotein
YP_514126.1	YP_514126.1	FTL_1475	<i>fimT</i>	Type IV pili fiber building block protein
YP_513117.1	YP_513117.1	FTL_0329	<i>pssA</i>	CDP-alcohol phosphatidyltransferase
YP_514353.1	YP_514353.1	FTL_1722	-	glutamyl-tRNA reductase
YP_513482.1	YP_513482.1	FTL_0731	-	YhhQ family protein
YP_514177.1	YP_514177.1	FTL_1531	<i>rumA</i>	23S rRNA 5-methyluridine methyltransferase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514065.1	YP_514065.1	FTL_1410	<i>murG</i>	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
YP_514541.1	YP_514541.1	FTL_1940	-	trp repressor binding protein
YP_513732.1	YP_513732.1	FTL_1031	-	hypothetical protein
YP_513442.1	YP_513442.1	FTL_0691	-	proton-dependent oligopeptide transport (POT) family protein
YP_514167.1	YP_514167.1	FTL_1520	<i>upp</i>	uracil phosphoribosyltransferase
YP_514273.1	YP_514273.1	FTL_1634	-	LysR family transcriptional regulator
YP_514086.1	YP_514086.1	FTL_1431	-	sugar transferase
YP_514509.1	YP_514509.1	FTL_1899	-	glutamine synthetase
YP_513444.1	YP_513444.1	FTL_0693	-	hypothetical protein
YP_513089.1	YP_513089.1	FTL_0297	-	hypothetical protein
YP_513874.1	YP_513874.1	FTL_1191	<i>dnaK</i>	molecular chaperone DnaK
YP_513039.1	YP_513039.1	FTL_0244	-	50S ribosomal protein L29
YP_514405.1	YP_514405.1	FTL_1780	-	triosephosphate isomerase
YP_513361.1	YP_513361.1	FTL_0601	<i>wbtI</i>	sugar transamine/perosamine synthetase
YP_513625.1	YP_513625.1	FTL_0906	<i>engB</i>	ribosome biogenesis GTP-binding protein YsxC
YP_514182.1	YP_514182.1	FTL_1536	-	iron-sulfur cluster insertion protein ErpA
YP_513916.1	YP_513916.1	FTL_1236	<i>infA</i>	translation initiation factor IF-1
YP_514433.1	YP_514433.1	FTL_1808	-	ribosome-binding factor A
YP_513309.1	YP_513309.1	FTL_0540	<i>lpxB</i>	lipid-A-disaccharide synthase
YP_513765.1	YP_513765.1	FTL_1068	<i>truA</i>	tRNA pseudouridine synthase A
YP_514425.1	YP_514425.1	FTL_1800	-	F0F1 ATP synthase subunit C
YP_513150.1	YP_513150.1	FTL_0374	-	DNA repair protein RadA
YP_513496.1	YP_513496.1	FTL_0747	-	glutamate racemase
YP_514302.1	YP_514302.1	FTL_1667	<i>lpxK</i>	tetraacyldisaccharide 4'-kinase
YP_513978.1	YP_513978.1	FTL_1307	-	nucleotide-binding protein, yjeE
YP_513364.1	YP_513364.1	FTL_0604	<i>wbtK</i>	glycosyltransferase
YP_514477.1	YP_514477.1	FTL_1860	<i>purL</i>	phosphoribosylformylglycinamide synthase
YP_514285.1	YP_514285.1	FTL_1646	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514079.1	YP_514079.1	FTL_1424	-	glycosyl transferase family protein
YP_514422.1	YP_514422.1	FTL_1797	-	F0F1 ATP synthase subunit alpha
YP_513762.1	YP_513762.1	FTL_1065	-	ABC transporter ATP-binding protein
YP_513616.1	YP_513616.1	FTL_0897	<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate transferase
YP_513322.1	YP_513322.1	FTL_0556	<i>rnr</i>	ribonuclease R
YP_514067.1	YP_514067.1	FTL_1412	-	recombination protein RecR
YP_514463.1	YP_514463.1	FTL_1841	<i>gatB</i>	aspartyl/glutamyl-tRNA amidotransferase subunit B
YP_513254.1	YP_513254.1	FTL_0482	-	pullulanase
YP_512894.1	YP_512894.1	FTL_0093	<i>chiB</i>	chitinase
YP_513508.1	YP_513508.1	FTL_0763	-	hypothetical protein
YP_514481.1	YP_514481.1	FTL_1864	-	hypothetical protein
YP_513383.1	YP_513383.1	FTL_0627	<i>rhtB</i>	threonine efflux protein
YP_513042.1	YP_513042.1	FTL_0247	<i>rplX</i>	50S ribosomal protein L24
YP_513794.1	YP_513794.1	FTL_1107	-	hypothetical protein
YP_513733.1	YP_513733.1	FTL_1032	-	ribosomal-protein-alanine acetyltransferase
YP_513343.1	YP_513343.1	FTL_0583	-	acetyl-CoA acetyltransferase
YP_514519.1	YP_514519.1	FTL_1909	-	cell division protein FtsQ
YP_514399.1	YP_514399.1	FTL_1772	-	aconitate hydratase
YP_513078.1	YP_513078.1	FTL_0285	-	GTP pyrophosphokinase
YP_513575.1	YP_513575.1	FTL_0853	-	hypothetical protein
YP_513979.1	YP_513979.1	FTL_1308	-	bifunctional folylpolyglutamate synthase/ dihydrofolate synthase
YP_514055.1	YP_514055.1	FTL_1400	-	hypothetical protein
YP_514429.1	YP_514429.1	FTL_1804	-	ribosomal large subunit pseudouridine synthase C
YP_513789.1	YP_513789.1	FTL_1097	<i>fipA</i>	Macrophage infectivity potentiator, fragment, FipA
YP_512949.1	YP_512949.1	FTL_0151	<i>ipk</i>	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
YP_513725.1	YP_513725.1	FTL_1024	<i>rpsF</i>	30S ribosomal protein S6
YP_513349.1	YP_513349.1	FTL_0589	-	hypothetical protein
YP_512929.1	YP_512929.1	FTL_0131	-	branched-chain amino acid aminotransferase
YP_513149.1	YP_513149.1	FTL_0373	-	hypothetical protein

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514454.1	YP_514454.1	FTL_1832	<i>fsIA</i>	hypothetical protein
YP_512938.1	YP_512938.1	FTL_0140	<i>hemC</i>	porphobilinogen deaminase
YP_513454.1	YP_513454.1	FTL_0703	<i>glyA</i>	serine hydroxymethyltransferase
YP_513289.1	YP_513289.1	FTL_0520	<i>minC</i>	septum site-determining protein MinC
YP_514084.1	YP_514084.1	FTL_1429	-	glycosyl transferases group 1 family protein
YP_514173.1	YP_514173.1	FTL_1526	-	cell division protein
YP_513707.1	YP_513707.1	FTL_1001	-	hypothetical protein
YP_513934.1	YP_513934.1	FTL_1258	-	aldo/keto reductase
YP_513755.1	YP_513755.1	FTL_1058	<i>lipB</i>	lipoate-protein ligase B
YP_513670.1	YP_513670.1	FTL_0959	<i>pilD</i>	Type IV pili leader peptidase and methylase.
YP_514247.1	YP_514247.1	FTL_1608	-	hypothetical protein
YP_513722.1	YP_513722.1	FTL_1021	-	hypothetical protein
YP_513942.1	YP_513942.1	FTL_1271	<i>bioA</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
YP_514082.1	YP_514082.1	FTL_1427	-	hypothetical protein
YP_513576.1	YP_513576.1	FTL_0854	-	ribonuclease H
YP_513844.1	YP_513844.1	FTL_1160	<i>iglD</i>	intracellular growth locus, subunit D
YP_512912.1	YP_512912.1	FTL_0114	<i>iglD</i>	intracellular growth locus, subunit D
YP_514235.1	YP_514235.1	FTL_1596	<i>surA</i>	peptidyl-prolyl cis-trans isomerase
YP_513571.1	YP_513571.1	FTL_0849	<i>secF</i>	preprotein translocase subunit SecF
YP_514180.1	YP_514180.1	FTL_1534	-	uridine kinase
YP_514108.1	YP_514108.1	FTL_1453	<i>rplU</i>	50S ribosomal protein L21
YP_514525.1	YP_514525.1	FTL_1915	-	putative acyltransferase
YP_513021.1	YP_513021.1	FTL_0226	<i>pyrH</i>	uridylyate kinase
YP_514061.1	YP_514061.1	FTL_1406	-	translation initiation factor IF-3
YP_513826.1	YP_513826.1	FTL_1140	-	malonyl CoA-acyl carrier protein transacylase
YP_514368.1	YP_514368.1	FTL_1737	<i>rimM</i>	16S rRNA-processing protein RimM
YP_513319.1	YP_513319.1	FTL_0553	<i>lepB</i>	signal peptidase I
YP_514174.1	YP_514174.1	FTL_1527	<i>eno</i>	phosphopyruvate hydratase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514411.1	YP_514411.1	FTL_1786	-	succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit
YP_514432.1	YP_514432.1	FTL_1807	<i>hisS</i>	histidyl-tRNA synthetase
YP_514334.1	YP_514334.1	FTL_1703	<i>lysP</i>	lysine:H ⁺ symporter
YP_514512.1	YP_514512.1	FTL_1902	-	hypothetical protein
YP_514124.1	YP_514124.1	FTL_1473	<i>uvrA</i>	DNA excision repair protein subunit A
YP_513528.1	YP_513528.1	FTL_0796	-	hypothetical protein
YP_513651.1	YP_513651.1	FTL_0938	-	histidine decarboxylase
YP_514445.1	YP_514445.1	FTL_1823	-	NADH dehydrogenase I subunit H
YP_514298.1	YP_514298.1	FTL_1663	<i>deoC</i>	deoxyribose-phosphate aldolase
YP_513509.1	YP_513509.1	FTL_0764	-	lipoprotein
YP_514325.1	YP_514325.1	FTL_1694	-	hypothetical protein
YP_512842.1	YP_512842.1	FTL_0034	-	hypothetical protein
YP_513605.1	YP_513605.1	FTL_0885	-	phoH-like protein
YP_514300.1	YP_514300.1	FTL_1665	-	pantothenate kinase
YP_513573.1	YP_513573.1	FTL_0851	-	RNA polymerase factor sigma-32
YP_512931.1	YP_512931.1	FTL_0133	<i>feoB</i>	ferrous iron transport protein
YP_513350.1	YP_513350.1	FTL_0590	-	ATp-dependent helicase
YP_513453.1	YP_513453.1	FTL_0702	<i>prfM</i>	hypothetical protein
YP_514414.1	YP_514414.1	FTL_1789	-	citrate synthase
YP_514225.1	YP_514225.1	FTL_1586	-	biotin--acetyl-CoA-carboxylase ligase
YP_514081.1	YP_514081.1	FTL_1426	-	hypothetical protein
YP_513865.1	YP_513865.1	FTL_1182	<i>rnhB</i>	ribonuclease HII
YP_513334.1	YP_513334.1	FTL_0574	-	hypothetical protein
YP_512961.1	YP_512961.1	FTL_0166	-	universal stress protein
YP_513443.1	YP_513443.1	FTL_0692	-	16S ribosomal RNA methyltransferase RsmE
YP_513464.1	YP_513464.1	FTL_0713	-	PP-loop family protein
YP_513607.1	YP_513607.1	FTL_0887	-	o-methyltransferase family protein
YP_513412.1	YP_513412.1	FTL_0660	<i>feoA</i>	ferrous iron transport protein A
YP_513728.1	YP_513728.1	FTL_1027	-	replicative DNA helicase

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_513791.1	YP_513791.1	FTL_1101	-	hypothetical protein
YP_512823.1	YP_512823.1	FTL_0013	<i>recX</i>	regulatory protein recX
YP_513027.1	YP_513027.1	FTL_0232	<i>rpsL</i>	30S ribosomal protein S12
YP_514544.1	YP_514544.1	FTL_1943	-	primosomal protein N'
YP_512824.1	YP_512824.1	FTL_0014	<i>ssb</i>	single-strand binding protein
YP_513228.1 YP_514021.1_s hared	YP_513228.1_YP_5	FTL_0456 and FTL_1360	<i>rpsU1</i> and <i>rpsU3</i>	30S ribosomal protein S21-1 and 30S ribosomal protein S21-3
YP_514436.1	YP_514436.1	FTL_1811	-	hypothetical protein
YP_514145.1	YP_514145.1	FTL_1494	-	hypothetical protein
YP_514132.1	YP_514132.1	FTL_1481	-	YjgP/YjgQ family permease
YP_513970.1	YP_513970.1	FTL_1299	-	hypothetical protein
YP_514457.1	YP_514457.1	FTL_1835	<i>fsiD</i>	hypothetical protein
YP_513503.1	YP_513503.1	FTL_0755	-	hypothetical protein
YP_513120.1	YP_513120.1	FTL_0332	-	TolR protein
YP_514054.1	YP_514054.1	FTL_1399	-	3-deoxy-manno-octulosonate cytidyltransferase
YP_514234.1	YP_514234.1	FTL_1595	<i>ksgA</i>	dimethyladenosine transferase
YP_513156.1	YP_513156.1	FTL_0380	-	superoxide dismutase (Cu-Zn) precursor
YP_513436.1	YP_513436.1	FTL_0685	-	NH(3)-dependent NAD(+) synthetase
YP_514381.2	YP_514381.2	FTL_1750	<i>secE</i>	preprotein translocase subunit SecE
YP_513864.1	YP_513864.1	FTL_1181	-	SpoU rRNA methylase family protein
YP_513825.1	YP_513825.1	FTL_1139	-	3-oxoacyl-(acyl-carrier-protein) reductase
YP_512881.1	YP_512881.1	FTL_0077	-	riboflavin synthase subunit alpha
YP_513931.1	YP_513931.1	FTL_1251	<i>dptA</i>	proton-dependent oligopeptide transport (POT) family protein
YP_514416.1	YP_514416.1	FTL_1791	-	superoxide dismutase
YP_512974.1	YP_512974.1	FTL_0179	<i>ddg</i>	acyltransferase
YP_513490.1	YP_513490.1	FTL_0741	-	hypothetical protein
YP_514044.1	YP_514044.1	FTL_1389	-	nicotinate-nucleotide pyrophosphorylase
YP_512955.1	YP_512955.1	FTL_0159	-	hydrolase subunit

Protein Metadata				
id	Protein IDs	Locus	Gene Name	Protein Name
YP_514346.1	YP_514346.1	FTL_1715	<i>groES</i>	co-chaperonin GroES
YP_514049.1	YP_514049.1	FTL_1394	<i>galP2</i>	major facilitator superfamily galactose-proton symporter
YP_513867.1	YP_513867.1	FTL_1184	-	ClpXP protease specificity-enhancing factor
YP_513320.1	YP_513320.1	FTL_0554	<i>rnc</i>	ribonuclease III
YP_513340.1	YP_513340.1	FTL_0580	-	hypothetical protein
YP_513609.1	YP_513609.1	FTL_0890	-	thymidine kinase
YP_512970.1	YP_512970.1	FTL_0175	<i>rpmH</i>	50S ribosomal protein L34
YP_514066.1	YP_514066.1	FTL_1411	-	hypothetical protein
YP_514172.1	YP_514172.1	FTL_1525	-	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
YP_514033.1	YP_514033.1	FTL_1372	-	lipoprotein
YP_514507.1	YP_514507.1	FTL_1897	-	outer membrane lipoprotein
YP_514456.1	YP_514456.1	FTL_1834	<i>fsiC</i>	diaminopimelate decarboxylase
YP_514403.1	YP_514403.1	FTL_1776	-	hypothetical protein
YP_514363.1	YP_514363.1	FTL_1732	-	acid phosphatase
YP_513415.1	YP_513415.1	FTL_0663	-	hypothetical protein
YP_513633.1	YP_513633.1	FTL_0920	-	hypothetical protein
YP_513617.1	YP_513617.1	FTL_0898	<i>hfq</i>	host factor I for bacteriophage Q beta replication
YP_513822.1	YP_513822.1	FTL_1136	-	hypothetical protein
YP_514493.1	YP_514493.1	FTL_1880	-	potassium-transporting ATPase C chain
YP_512942.1	YP_512942.1	FTL_0144	-	hypothetical protein
YP_514339.1	YP_514339.1	FTL_1708	<i>tkrH</i>	potassium uptake protein

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513747.1	32.3	32.3	32.7	32.2	33.1	33.0	0.0	0.0	0.0	33.7	32.4
YP_513580.1	18.6	16.2	16.9	17.7	18.0	17.1	0.0	19.1	0.0	18.4	17.0
YP_513220.1	18.4	14.7	18.2	14.8	16.3	18.2	0.0	16.6	16.7	18.2	18.0
YP_513851.1	23.5	23.8	23.5	23.1	22.9	23.2	22.4	21.0	20.3	24.3	23.6
YP_512919.1	23.5	23.8	23.5	23.1	22.9	23.2	22.4	21.0	20.3	24.3	23.6
YP_514254.1	25.7	26.0	25.4	25.8	25.1	25.0	22.9	24.1	23.8	24.5	26.1
YP_513010.1	23.2	23.1	22.8	23.2	23.2	22.6	21.0	20.9	21.6	22.0	22.7
YP_513017.1	25.2	25.3	25.3	25.3	25.2	25.0	23.2	23.6	23.5	25.1	25.0
YP_513601.1	21.7	20.7	21.5	21.3	20.6	20.8	19.7	20.4	18.4	21.6	21.2
YP_513628.1	22.0	18.2	16.4	20.3	16.9	18.9	17.4	14.5	19.3	14.5	20.0
YP_514496.1	26.9	27.0	26.8	27.1	26.6	26.7	25.2	25.5	24.7	26.1	27.1
YP_513787.1	30.0	30.0	30.1	30.0	30.2	30.0	28.7	28.5	28.8	30.3	30.1
YP_514317.1	25.0	25.4	25.0	25.5	24.6	24.8	24.0	23.9	23.4	24.4	25.3
YP_513786.1	24.3	24.3	23.9	24.2	24.0	23.7	22.2	23.0	23.0	24.0	23.9
YP_514023.1	24.6	23.2	21.2	21.3	21.0	24.6	21.1	20.1	23.6	20.8	24.0
YP_513363.1	24.4	24.4	24.4	24.4	24.3	24.0	23.5	23.6	22.0	23.0	24.6
YP_514324.1	19.4	20.4	20.9	19.5	20.0	20.9	19.4	19.4	17.8	19.0	19.4
YP_513465.1	26.7	26.5	26.6	26.6	26.4	26.4	25.3	25.3	25.1	26.4	26.5
YP_513000.1	18.2	16.8	19.0	17.2	18.1	16.2	18.4	16.9	14.6	18.0	16.1
YP_513080.1	23.9	24.3	24.3	24.2	24.5	24.3	23.0	23.1	22.4	24.0	23.8
YP_514527.1	20.6	20.6	20.4	20.6	19.4	20.5	18.9	19.0	19.7	19.2	19.7
YP_514530.1	24.5	24.6	24.4	24.5	24.3	24.1	23.2	24.0	22.5	24.0	24.5
YP_512896.1	29.2	28.7	29.2	29.1	29.4	29.6	27.8	27.8	27.7	29.7	29.0
YP_513245.1	27.4	27.5	27.3	27.4	27.3	27.3	26.1	26.2	26.0	27.2	27.5
YP_514476.1	20.4	20.0	20.2	20.1	20.2	19.9	18.5	19.3	19.1	17.6	19.8
YP_512853.1	30.8	30.8	30.9	30.7	30.9	30.8	29.6	29.5	29.5	31.1	30.7
YP_513848.1	30.2	30.2	30.0	30.2	30.0	30.1	29.0	28.9	28.8	30.0	30.3
YP_512916.1	30.2	30.2	30.0	30.2	30.0	30.1	29.0	28.9	28.8	30.0	30.3
YP_513849.1	26.4	26.5	26.1	26.4	25.8	26.3	25.1	25.3	25.0	25.5	26.8
YP_512917.1	26.4	26.5	26.1	26.4	25.8	26.3	25.1	25.3	25.0	25.5	26.8

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513347.1	26.4	26.7	26.9	26.6	26.8	26.9	25.4	25.5	25.7	27.2	26.7
YP_513542.1	26.3	26.2	26.4	26.0	26.1	26.4	25.1	25.1	25.2	26.6	26.3
YP_514284.1	22.3	22.9	22.6	23.2	21.8	22.1	21.5	21.9	21.1	21.9	22.9
YP_512985.1	20.4	19.7	19.8	19.2	18.3	18.5	18.7	19.6	18.1	17.0	16.7
YP_514131.1	25.6	25.5	25.6	25.7	25.4	25.6	24.5	24.7	24.1	25.2	25.7
YP_513847.1	27.5	27.5	27.4	27.4	27.4	27.4	26.4	26.3	26.3	27.4	27.7
YP_512915.1	27.5	27.5	27.4	27.4	27.4	27.4	26.4	26.3	26.3	27.4	27.7
YP_513137.1	24.3	24.0	23.9	24.3	23.8	20.3	22.7	22.7	23.5	23.3	24.5
YP_513268.1	22.1	22.3	22.4	22.9	22.1	23.0	21.1	21.9	20.5	21.8	22.3
YP_513402.1	23.6	23.7	23.3	23.6	23.1	23.3	22.1	22.8	22.5	22.2	23.7
YP_513471.1	21.5	21.4	21.7	21.0	21.7	21.5	20.0	20.5	21.0	21.5	21.1
YP_512943.1	25.5	25.0	25.7	25.3	25.3	25.4	24.6	24.5	24.1	25.4	25.5
YP_513448.1	23.8	24.3	24.3	24.3	23.6	23.7	23.1	23.4	22.8	23.7	23.9
YP_514358.1	26.1	26.3	26.3	26.3	26.0	26.1	25.4	25.3	24.9	26.1	26.1
YP_513899.1	27.1	27.0	27.0	27.1	26.9	26.9	25.9	26.1	26.0	26.6	27.0
YP_514486.1	24.3	24.3	23.9	24.6	23.6	23.5	23.4	23.2	22.9	23.2	24.5
YP_513856.1	30.0	29.8	29.8	29.8	29.8	29.9	29.0	28.9	28.8	29.7	30.0
YP_512924.1	30.0	29.8	29.8	29.8	29.8	29.9	29.0	28.9	28.8	29.7	30.0
YP_513850.1	30.3	30.2	30.1	30.2	30.0	30.2	29.3	29.2	29.2	30.0	30.3
YP_512918.1	30.3	30.2	30.1	30.2	30.0	30.2	29.3	29.2	29.2	30.0	30.3
YP_513852.1	26.2	26.2	26.0	26.1	26.0	26.2	25.3	25.1	25.3	26.2	26.4
YP_512920.1	26.2	26.2	26.0	26.1	26.0	26.2	25.3	25.1	25.3	26.2	26.4
YP_514064.1	27.8	28.0	28.2	27.9	27.9	27.8	26.9	27.0	27.2	28.8	27.9
YP_514154.1	33.8	33.9	34.0	33.8	34.1	33.9	33.0	32.7	33.1	34.6	33.8
YP_513902.1	31.5	31.4	31.3	31.4	31.1	31.2	30.6	30.6	30.3	30.9	31.3
YP_513486.1	21.3	21.4	21.6	21.6	20.8	20.7	20.7	20.7	20.1	21.3	20.9
YP_514110.1	25.5	25.6	25.6	25.6	25.3	25.4	24.7	24.6	24.7	25.4	25.5
YP_514037.1	25.7	25.5	25.2	25.2	25.4	25.2	24.9	24.9	23.9	25.1	24.9
YP_514415.1	27.8	28.0	27.9	27.9	27.5	27.7	27.1	27.2	26.8	27.3	28.2

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513802.1	30.1	30.2	30.1	30.2	30.1	30.0	29.2	29.3	29.3	29.9	30.1
YP_513452.1	24.8	23.7	24.5	24.3	23.9	24.0	23.4	23.8	23.2	24.6	23.8
YP_513525.1	27.7	27.7	27.7	27.7	27.7	27.7	26.9	27.0	26.7	27.6	27.7
YP_514402.1	25.4	25.7	25.4	25.5	25.4	25.5	24.6	24.8	24.6	25.2	25.5
YP_513855.1	31.0	30.9	30.8	31.0	30.8	31.0	30.2	30.2	29.9	30.6	31.0
YP_512923.1	31.0	30.9	30.8	31.0	30.8	31.0	30.2	30.2	29.9	30.6	31.0
YP_513854.1	27.9	28.0	27.8	27.9	27.8	27.9	27.0	27.2	26.9	28.3	28.1
YP_512922.1	27.9	28.0	27.8	27.9	27.8	27.9	27.0	27.2	26.9	28.3	28.1
YP_513926.1	21.9	22.0	21.4	22.0	21.4	21.6	20.6	21.3	20.8	21.1	21.4
YP_513160.1	33.6	33.5	33.5	33.6	33.6	33.5	32.8	32.6	32.7	33.3	33.6
YP_513018.1	27.6	27.6	27.7	27.7	27.8	27.7	26.9	26.9	26.6	27.6	27.6
YP_513546.1	25.6	25.4	25.5	25.6	25.1	25.3	24.8	25.0	24.2	24.4	25.6
YP_513748.1	28.3	27.9	28.8	28.0	29.3	29.2	27.4	27.1	27.9	30.0	28.2
YP_513887.1	24.4	24.4	24.4	24.4	24.3	24.3	23.5	23.9	23.3	24.1	24.5
YP_514137.1	28.8	28.9	28.7	28.8	28.7	28.5	28.0	27.9	28.0	28.6	28.8
YP_512944.1	30.0	30.2	30.0	30.1	30.1	30.0	29.2	29.4	29.2	29.9	30.2
YP_512846.1	29.4	29.3	29.2	29.1	28.8	29.2	28.5	28.6	28.3	28.8	29.2
YP_513002.1	31.9	31.9	31.8	31.9	31.7	31.8	31.1	31.1	31.0	31.8	31.9
YP_514111.1	24.8	24.9	24.8	25.0	24.7	24.6	24.0	24.1	24.0	24.5	24.8
YP_514133.1	25.1	25.2	25.3	25.1	25.4	25.3	24.5	24.1	24.7	25.5	25.2
YP_512897.1	29.0	29.0	28.8	28.9	28.9	28.9	28.2	28.2	28.2	28.9	28.9
YP_514471.1	21.2	20.2	20.3	20.5	19.5	19.3	19.5	20.2	19.6	19.4	20.2
YP_513392.1	25.0	25.1	25.0	25.0	25.0	25.0	24.3	24.5	23.9	24.6	25.1
YP_513896.1	29.3	29.3	29.1	29.2	29.0	29.1	28.5	28.5	28.3	29.0	29.2
YP_513929.1	28.9	29.0	28.9	29.0	28.7	28.8	28.1	28.3	28.1	28.9	29.1
YP_513595.1	30.7	30.8	30.7	30.8	30.5	30.6	29.9	30.2	29.8	30.2	30.7
YP_513843.1	34.9	34.9	34.7	34.8	34.6	34.5	34.4	34.1	33.8	34.5	34.7
YP_512911.1	34.9	34.9	34.7	34.8	34.6	34.5	34.4	34.1	33.8	34.5	34.7
YP_512837.1	32.4	32.5	32.2	32.4	32.2	32.3	31.7	31.6	31.5	32.0	32.3
YP_513183.1	26.7	26.7	26.5	26.8	26.4	26.5	26.0	26.1	25.6	25.9	26.6

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514504.1	31.7	31.8	31.5	31.7	31.4	31.5	30.9	31.0	30.8	31.4	31.7	
YP_513988.1	31.7	31.8	31.5	31.7	31.4	31.5	30.9	31.0	30.8	31.4	31.7	
YP_513059.1	31.7	31.8	31.5	31.7	31.4	31.5	30.9	31.0	30.8	31.4	31.7	
YP_513447.1	27.2	27.2	27.1	27.2	27.1	27.1	26.3	26.8	26.3	26.7	27.1	
YP_512838.1	30.7	30.5	30.7	30.7	30.6	30.6	29.9	30.0	29.8	30.3	30.7	
YP_513244.1	28.9	28.9	28.8	28.9	28.8	28.8	28.3	28.1	28.1	28.6	28.7	
YP_512872.1	26.2	26.4	25.8	26.1	26.3	26.4	25.8	24.7	25.9	27.1	26.1	
YP_514019.1	28.3	28.4	28.2	28.4	28.1	28.2	27.6	27.8	27.5	28.1	28.4	
YP_513792.1	25.8	26.1	25.9	26.2	25.6	25.6	25.3	25.6	24.8	25.2	25.7	
YP_512887.1	26.0	26.1	26.0	26.1	25.9	26.1	25.4	25.4	25.3	25.9	26.0	
YP_513428.1	28.5	28.7	28.6	28.6	28.6	28.5	27.9	27.8	28.0	28.5	28.5	
YP_513785.1	29.8	29.7	29.6	29.7	29.4	29.6	29.0	29.2	28.8	29.1	29.8	
YP_513846.1	31.9	31.6	31.8	31.6	31.5	31.8	31.2	31.1	30.9	31.8	32.0	
YP_512914.1	31.9	31.6	31.8	31.6	31.5	31.8	31.2	31.1	30.9	31.8	32.0	
YP_513083.1	24.8	24.8	24.8	24.9	24.6	24.8	24.3	24.0	24.1	24.7	24.9	
YP_513669.1	26.8	26.9	26.7	26.8	26.4	26.6	26.1	26.2	26.0	26.3	26.7	
YP_512836.1	29.7	29.7	29.6	29.7	29.6	29.7	28.9	29.0	29.0	29.5	29.7	
YP_513111.1	23.7	23.7	23.8	23.7	23.5	23.4	23.3	23.1	22.7	22.6	23.8	
YP_513109.1	32.1	32.0	32.3	32.0	32.2	32.1	30.8	31.4	32.1	33.5	31.8	
YP_512854.1	28.2	28.0	28.2	28.2	28.2	28.1	27.5	27.3	27.5	28.2	27.9	
YP_513968.1	23.8	24.0	24.3	24.2	24.3	23.6	23.3	23.3	23.5	24.5	23.9	
YP_513964.1	26.3	26.4	26.6	26.3	26.5	26.4	25.6	25.6	26.0	27.3	26.5	
YP_512865.1	23.2	21.9	23.2	22.2	23.0	23.1	22.1	22.5	21.7	22.4	23.0	
YP_513911.1	30.1	30.1	30.1	30.0	30.1	30.0	29.4	29.5	29.4	29.9	30.0	
YP_513773.1	25.9	26.2	25.9	26.1	25.9	25.8	25.3	25.4	25.3	25.6	26.2	
YP_513806.1	27.9	28.0	28.0	28.1	28.0	28.0	27.4	27.3	27.3	27.7	27.9	
YP_513221.1	26.6	26.6	26.4	26.6	26.5	26.6	25.7	25.8	26.1	26.9	26.9	
YP_514492.1	24.7	24.7	24.7	24.8	24.9	24.9	23.7	24.4	24.1	24.7	24.9	
YP_513639.1	26.1	26.2	26.3	26.5	26.7	26.2	25.4	25.9	25.4	26.6	26.3	
YP_513928.1	29.3	29.4	29.4	29.3	29.4	29.4	28.8	28.7	28.8	29.6	29.4	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514189.1	28.2	28.2	28.1	28.2	28.1	28.1	27.6	27.6	27.4	27.9	28.1	
YP_513886.1	26.3	26.3	26.1	26.2	25.8	25.9	25.7	25.8	25.3	25.6	26.0	
YP_513510.1	25.8	25.9	25.6	25.9	25.6	25.5	25.3	25.5	24.7	24.9	26.0	
YP_514205.1	17.3	18.0	17.3	18.7	17.2	17.9	17.1	17.5	16.2	0.0	17.5	
YP_513938.1	25.6	25.5	25.5	25.8	25.6	25.4	25.0	25.0	24.8	25.4	25.6	
YP_513433.1	30.7	30.5	30.8	30.6	30.8	30.8	30.1	30.3	29.9	30.4	30.7	
YP_514192.1	32.0	32.1	32.0	32.2	31.9	32.0	31.4	31.6	31.3	31.9	32.2	
YP_513599.1	30.6	30.6	30.5	30.6	30.4	30.5	29.9	30.1	29.9	30.4	30.8	
YP_513011.1	27.7	27.8	27.8	27.7	27.8	27.7	27.0	27.2	27.2	27.6	27.7	
YP_513070.1	25.2	25.2	25.0	25.2	25.0	24.9	24.5	24.5	24.6	24.9	25.1	
YP_513469.1	26.0	26.0	25.9	25.9	25.7	25.8	25.5	25.5	25.2	25.8	26.0	
YP_514134.1	24.9	25.3	25.1	25.3	25.2	25.1	24.4	24.8	24.5	24.9	24.9	
YP_512964.1	26.7	26.8	26.6	26.7	26.4	26.3	26.2	26.2	25.9	26.0	26.5	
YP_514014.1	22.1	22.2	22.2	22.4	22.2	21.9	21.6	21.8	21.3	20.9	22.0	
YP_513539.1	24.6	24.8	24.6	24.9	23.7	24.3	24.3	24.1	23.8	24.0	24.8	
YP_513140.1	29.8	29.9	29.9	29.8	29.7	29.8	29.2	29.3	29.3	29.7	29.8	
YP_513168.1	29.1	29.3	29.1	29.2	29.1	29.2	28.6	28.7	28.5	29.1	29.2	
YP_513159.1	28.9	29.0	29.3	29.0	29.2	28.8	28.4	28.1	28.9	30.4	28.9	
YP_513676.1	29.8	29.9	29.9	29.9	29.9	29.9	29.3	29.3	29.3	29.9	29.9	
YP_513368.1	28.6	28.6	28.5	28.6	28.5	28.6	28.0	28.1	28.0	28.3	28.6	
YP_513269.1	26.5	26.5	26.4	26.3	26.0	26.1	25.9	25.9	25.9	25.6	26.3	
YP_512857.1	27.7	27.7	27.7	27.6	27.6	27.7	27.1	27.3	27.1	27.7	27.6	
YP_512826.1	30.7	30.8	30.6	30.8	30.5	30.6	30.1	30.4	29.9	30.2	30.8	
YP_514514.1	27.9	28.0	28.2	27.9	28.1	28.0	27.4	27.5	27.5	28.5	28.0	
YP_513423.1	32.4	32.6	32.2	32.5	32.2	32.3	31.8	31.9	31.7	31.9	32.5	
YP_513359.1	27.8	27.7	27.9	27.8	27.9	27.9	27.3	27.3	27.2	28.0	27.8	
YP_513472.1	27.7	27.7	27.7	27.8	27.5	27.6	27.2	27.4	26.8	27.5	27.8	
YP_512936.1	24.8	25.0	24.9	24.8	24.8	24.8	24.4	24.4	24.2	25.1	24.7	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513235.1	28.1	28.3	28.2	28.3	28.1	28.1	27.8	27.7	27.5	27.9	28.2
YP_513737.1	26.9	26.8	26.9	26.7	26.7	26.8	26.3	26.4	26.2	26.7	27.0
YP_513939.1	30.2	30.3	30.3	30.3	30.2	30.4	29.7	29.8	29.7	30.2	30.4
YP_513155.1	28.1	27.9	28.3	28.0	28.7	28.6	27.7	27.3	27.8	29.2	28.2
YP_513912.1	30.6	30.7	30.5	30.5	30.4	30.5	30.0	30.1	30.0	30.3	30.5
YP_514559.1	26.4	26.4	26.9	26.4	26.8	26.5	25.7	25.8	26.5	28.1	25.8
YP_514508.1	24.8	24.9	24.9	25.0	25.0	24.9	24.4	24.4	24.1	24.8	25.0
YP_513841.1	32.9	32.8	32.6	32.8	32.8	32.7	32.3	32.3	32.2	32.6	32.8
YP_512909.1	32.9	32.8	32.6	32.8	32.8	32.7	32.3	32.3	32.2	32.6	32.8
YP_514046.1	29.1	29.4	29.1	29.2	29.0	29.0	28.6	28.7	28.7	29.4	29.2
YP_514128.1	26.7	26.7	26.4	26.5	26.2	26.3	25.9	26.2	26.2	26.3	26.5
YP_513982.1	30.6	30.7	30.7	30.6	30.7	30.6	30.2	30.2	30.1	30.7	30.6
YP_513249.1	31.4	31.5	31.4	31.5	31.3	31.4	31.0	31.0	30.8	31.2	31.5
YP_514196.1	27.4	27.6	27.6	27.6	27.5	27.6	27.1	27.0	27.0	27.8	27.6
YP_513842.1	34.4	34.3	34.1	34.3	34.0	34.2	33.8	33.8	33.6	33.8	34.4
YP_512910.1	34.4	34.3	34.1	34.3	34.0	34.2	33.8	33.8	33.6	33.8	34.4
YP_513277.1	26.7	26.8	26.7	26.8	26.6	26.7	26.2	26.3	26.3	26.5	26.8
YP_514441.1	25.6	26.0	25.5	26.1	25.0	25.4	25.1	25.4	25.0	25.0	25.7
YP_513683.1	27.1	27.2	27.1	27.0	27.0	27.0	26.5	26.9	26.5	26.8	27.1
YP_513805.1	30.1	30.2	30.2	30.1	30.2	30.1	29.7	29.7	29.6	30.2	30.0
YP_513709.1	27.2	27.0	27.3	27.1	27.5	27.3	26.6	26.7	26.7	27.6	27.1
YP_513958.1	29.6	29.7	29.5	29.6	29.4	29.5	29.1	29.2	29.1	29.3	29.6
YP_514515.1	28.1	28.0	27.9	28.0	28.0	27.9	27.5	27.6	27.5	27.9	27.9
YP_513339.1	24.9	25.0	24.7	24.8	24.7	24.5	24.3	24.7	24.1	24.4	24.6
YP_513393.1	25.4	25.6	25.6	25.4	25.5	25.5	24.9	25.4	24.9	25.1	25.4
YP_514209.1	27.4	27.3	27.4	27.5	27.2	27.4	26.8	27.1	26.8	27.1	27.4
YP_513587.1	28.9	29.1	29.0	29.0	28.8	28.8	28.6	28.8	28.2	28.7	29.1

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513438.1	28.2	28.1	28.0	28.2	27.8	28.0	27.6	27.9	27.5	27.7	28.1	
YP_513331.1	30.9	30.9	30.8	30.8	30.8	30.8	30.4	30.5	30.3	30.6	30.9	
YP_512899.1	27.3	27.4	27.3	27.4	27.2	27.5	26.9	27.0	26.7	27.0	27.4	
YP_514453.1	29.8	30.0	29.9	29.9	29.8	29.8	29.4	29.6	29.4	30.0	29.9	
YP_513446.1	29.7	29.7	29.6	29.7	29.5	29.6	29.2	29.4	29.1	29.5	29.7	
YP_512893.1	28.4	28.4	28.3	28.4	28.3	28.2	27.9	28.0	27.9	28.2	28.5	
YP_514291.1	28.0	28.1	28.1	28.1	28.2	28.2	27.7	27.6	27.6	28.2	28.2	
YP_513445.1	27.1	27.1	27.2	27.2	27.2	27.2	26.9	26.6	26.6	27.4	27.2	
YP_513684.1	25.3	25.3	25.2	25.2	25.1	25.2	24.8	24.8	24.9	24.8	25.1	
YP_513870.1	31.8	32.0	31.8	32.0	31.8	31.9	31.3	31.8	31.2	31.7	32.0	
YP_514153.1	29.0	29.0	28.8	29.0	28.9	28.8	28.6	28.6	28.3	28.7	28.9	
YP_513456.1	26.1	26.3	26.2	26.3	26.0	26.1	25.8	25.8	25.7	26.0	26.1	
YP_513470.1	25.5	25.7	25.5	25.7	25.6	25.6	25.2	25.0	25.2	26.0	25.6	
YP_513745.1	26.6	26.6	26.7	26.8	26.5	26.6	26.2	26.2	26.2	26.4	26.8	
YP_513845.1	28.4	28.3	28.2	28.3	28.2	28.3	27.9	27.9	27.8	28.4	28.4	
YP_512913.1	28.4	28.3	28.2	28.3	28.2	28.3	27.9	27.9	27.8	28.4	28.4	
YP_514071.1	30.4	30.4	30.3	30.3	30.1	30.1	29.9	30.0	29.8	30.1	30.3	
YP_514006.1	25.5	25.4	25.4	25.4	25.6	25.5	25.0	25.1	24.8	25.2	25.3	
YP_513693.1	29.2	29.2	29.5	29.2	29.5	29.4	28.7	28.9	29.0	29.6	29.3	
YP_513925.1	25.4	25.2	25.4	25.3	25.2	25.1	24.6	25.2	24.9	25.1	25.2	
YP_513088.1	22.6	22.7	22.4	22.7	22.4	22.2	22.3	22.7	21.4	20.3	22.2	
YP_513803.1	21.6	21.9	21.9	21.2	21.2	21.4	20.9	21.2	22.1	20.3	21.9	
YP_513005.1	31.8	31.8	31.9	31.8	31.8	31.9	31.4	31.5	31.3	31.7	31.8	
YP_513459.1	27.1	27.4	27.1	26.9	27.1	27.3	26.8	27.0	26.5	26.7	27.0	
YP_513091.1	26.8	26.7	26.8	26.7	26.9	26.7	26.3	26.2	26.4	27.1	26.7	
YP_513096.1	24.3	24.3	24.0	24.3	24.3	24.1	23.9	23.8	23.5	23.9	24.4	
YP_513332.1	32.3	32.3	32.2	32.2	32.3	32.2	31.8	31.8	31.9	32.5	32.3	
YP_513029.1	34.7	34.7	34.9	34.7	34.9	34.9	34.3	34.5	34.2	34.3	34.8	
YP_514357.1	28.7	28.6	28.7	28.6	28.9	28.9	28.3	28.2	28.2	28.8	28.6	
YP_513910.1	30.5	30.6	30.6	30.5	30.6	30.6	30.1	30.1	30.2	30.6	30.5	

log2 Cyclic Loess Normalized Exclusive Intensities for DIA												
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513288.1	33.2	33.1	33.0	33.1	33.0	33.0	32.7	32.8	32.6	32.7	33.1	
YP_513372.1	29.6	29.6	29.4	29.5	29.3	29.3	29.1	29.2	29.0	29.3	29.5	
YP_513857.1	27.3	27.3	27.4	27.3	27.1	27.0	27.0	27.1	26.6	26.8	27.3	
YP_513535.1	27.6	27.6	27.8	27.4	27.7	27.6	27.0	27.2	27.6	28.0	27.5	
YP_514536.1	28.2	28.4	28.2	28.3	28.1	28.3	27.8	28.0	27.8	27.9	28.3	
YP_512825.1	28.7	28.9	28.7	28.8	28.7	28.7	28.3	28.4	28.4	28.7	28.7	
YP_513352.1	31.1	31.1	31.0	31.1	30.9	31.1	30.7	30.7	30.6	30.8	31.0	
YP_513701.1	28.0	28.1	27.9	28.0	27.8	27.8	27.6	27.8	27.5	27.6	28.0	
YP_513238.1	29.1	29.2	29.1	29.2	29.1	29.0	28.8	28.8	28.6	28.7	29.1	
YP_512898.1	28.7	28.7	28.7	28.7	28.8	28.9	28.5	27.9	28.4	29.3	28.8	
YP_513858.1	28.5	28.6	28.5	28.5	28.5	28.4	28.0	28.2	28.2	28.5	28.6	
YP_513974.2	29.7	30.1	30.2	29.8	30.1	30.1	29.4	29.5	29.9	30.5	29.5	
YP_513909.1	28.6	28.6	28.5	28.6	28.7	28.7	28.3	28.2	28.2	28.8	28.6	
YP_514129.1	33.3	33.3	33.2	33.3	33.4	33.4	32.9	32.9	32.9	33.2	33.2	
YP_513231.1	29.5	29.5	29.5	29.4	29.5	29.6	29.1	29.2	29.1	29.4	29.6	
YP_513533.1	31.2	31.3	31.3	31.3	31.4	31.3	30.9	31.0	30.9	31.3	31.3	
YP_513744.1	28.5	28.5	28.4	28.5	28.4	28.3	28.0	28.2	28.1	28.5	28.6	
YP_513317.1	27.3	27.3	27.4	27.3	27.3	27.3	27.0	27.0	26.9	27.2	27.3	
YP_512966.1	23.8	24.5	23.6	23.8	23.8	23.9	23.4	23.8	23.6	23.5	24.3	
YP_513532.1	29.0	29.1	29.0	29.0	28.8	28.8	28.6	28.7	28.6	28.8	28.9	
YP_513057.1	33.6	33.7	33.6	33.6	33.5	33.5	33.3	33.3	33.2	33.6	33.6	
YP_513692.1	31.0	31.1	31.0	30.9	30.9	30.9	30.6	30.7	30.6	30.7	30.9	
YP_514310.1	30.1	29.8	29.9	29.9	29.8	29.9	29.5	29.5	29.6	30.0	29.9	
YP_513033.1	32.8	33.0	33.1	32.9	33.0	33.0	32.5	32.5	32.8	33.4	32.9	
YP_513167.1	28.8	28.9	28.8	28.8	28.9	28.9	28.5	28.3	28.6	29.1	28.7	
YP_514393.1	28.1	28.2	28.1	28.3	28.0	28.1	27.9	27.9	27.6	27.7	28.1	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514248.1	27.9	27.9	27.9	28.0	27.7	27.7	27.6	27.6	27.4	27.5	27.9
YP_514188.1	31.1	31.2	31.1	31.1	31.0	31.0	30.8	30.8	30.7	30.8	31.1
YP_512994.1	29.7	29.5	29.7	29.7	29.7	29.7	29.2	29.3	29.4	30.1	29.8
YP_513997.1	28.1	28.2	28.3	28.0	28.2	28.1	27.7	28.1	27.7	28.2	28.0
YP_513932.1	26.9	26.8	27.1	27.0	26.8	27.1	26.7	26.6	26.5	26.4	26.4
YP_513346.1	29.7	29.8	29.7	29.7	29.6	29.8	29.4	29.5	29.3	29.6	29.8
YP_514316.1	29.3	29.6	29.4	29.5	29.3	29.3	29.1	29.1	29.1	29.3	29.5
YP_513819.1	29.2	28.7	29.4	28.9	29.5	29.6	28.7	28.8	28.6	29.2	29.0
YP_512848.1	26.3	26.3	26.3	26.2	26.2	26.4	26.0	26.1	25.8	25.8	26.3
YP_514278.1	27.1	27.1	27.0	27.1	26.9	27.0	26.9	26.9	26.4	26.6	27.2
YP_514015.1	24.6	24.4	24.9	24.6	24.6	24.9	23.9	25.2	23.8	25.7	24.7
YP_513086.1	29.1	29.1	29.0	29.1	29.1	29.1	28.8	28.8	28.7	28.9	29.2
YP_513113.1	31.0	31.0	30.9	31.0	30.9	31.1	30.6	30.7	30.5	30.9	31.1
YP_513356.1	32.0	32.0	31.8	31.9	31.8	31.8	31.5	31.7	31.5	31.5	31.8
YP_514535.1	30.5	30.4	30.3	30.5	30.3	30.4	30.1	30.0	30.1	30.3	30.4
YP_514138.1	28.6	28.6	28.6	28.7	28.6	28.6	28.3	28.3	28.2	28.4	28.6
YP_514451.1	27.8	27.8	27.7	27.8	27.8	27.9	27.6	27.7	27.0	27.6	27.9
YP_514221.1	28.7	28.8	28.7	28.8	28.8	28.8	28.4	28.4	28.3	28.8	28.7
YP_513281.1	26.8	26.9	27.0	26.9	27.0	27.0	26.5	26.5	26.8	27.9	26.9
YP_513032.1	32.7	32.8	32.7	32.8	32.6	32.6	32.3	32.4	32.5	33.0	32.7
YP_512947.1	27.2	27.0	27.0	27.0	26.9	26.7	26.7	26.5	26.9	28.0	27.0
YP_514078.1	27.2	27.0	26.9	27.2	27.0	27.1	26.8	26.6	26.8	27.2	27.2
YP_513354.1	29.9	29.9	29.8	29.9	29.7	29.8	29.6	29.6	29.4	29.7	29.9
YP_513943.1	32.1	31.9	31.9	32.1	31.9	31.9	31.6	31.7	31.6	31.7	32.0
YP_513035.1	32.4	32.5	32.5	32.4	32.7	32.5	32.1	32.2	32.1	33.0	32.5
YP_514160.1	31.3	31.3	31.3	31.3	31.3	31.2	30.9	31.0	31.0	31.3	31.3
YP_513234.1	29.4	29.4	29.2	29.4	29.2	29.2	29.0	29.0	29.0	29.3	29.2
YP_514315.1	30.6	30.6	30.7	30.5	30.7	30.7	30.3	30.3	30.3	30.6	30.6

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513908.1	31.4	31.4	31.7	31.4	31.7	31.7	31.1	30.9	31.5	32.7	31.5
YP_513246.1	28.8	28.7	28.6	28.7	28.4	28.6	28.4	28.6	28.1	28.0	28.7
YP_513087.1	33.5	33.4	33.3	33.5	33.2	33.4	33.1	33.2	33.0	33.0	33.4
YP_513953.1	26.4	26.2	26.3	26.2	26.4	26.4	25.9	26.0	26.0	26.2	26.1
YP_514158.1	25.0	24.5	25.1	24.9	24.4	25.2	24.6	24.5	24.5	25.2	25.0
YP_513536.1	26.9	26.9	27.3	26.8	27.4	27.3	26.6	26.4	27.0	28.7	26.9
YP_513209.1	27.8	27.8	27.6	27.7	27.7	27.6	27.3	27.6	27.3	27.4	27.7
YP_513905.1	21.9	21.8	22.3	22.5	22.0	22.0	21.3	22.2	21.5	21.2	21.7
YP_513304.1	27.0	26.9	27.0	27.0	26.8	26.9	26.7	26.8	26.5	26.6	27.1
YP_514048.1	33.2	33.3	33.4	33.3	33.5	33.5	33.0	32.8	33.2	34.3	33.2
YP_514418.1	30.1	30.2	30.2	30.1	30.2	30.2	29.8	29.7	30.0	30.6	30.1
YP_513485.1	26.8	26.8	26.7	26.7	26.7	26.8	26.3	26.3	26.7	27.0	26.7
YP_513192.1	29.9	30.0	30.0	30.0	29.9	29.9	29.6	29.8	29.5	29.9	30.0
YP_514377.1	33.6	33.6	33.4	33.5	33.2	33.3	33.2	33.3	33.1	33.4	33.6
YP_514293.1	31.2	31.2	31.3	31.2	31.2	31.2	30.9	31.1	30.8	31.4	31.2
YP_513527.1	32.3	32.2	32.4	32.2	32.3	32.3	32.0	32.0	31.9	32.2	32.2
YP_513740.1	27.7	27.6	27.8	27.6	27.9	27.9	27.3	27.2	27.7	28.9	27.7
YP_514147.1	27.4	27.5	27.4	27.5	27.3	27.3	27.1	27.4	26.9	26.9	27.4
YP_513108.1	27.8	27.4	28.1	27.6	28.2	28.2	27.5	27.4	27.5	28.4	27.8
YP_513293.1	25.6	25.7	25.6	25.6	25.4	25.7	25.5	25.4	25.2	25.3	25.4
YP_513914.1	26.5	26.6	26.5	26.6	26.0	26.2	26.2	26.4	26.1	26.0	26.4
YP_513907.1	30.8	30.9	30.9	30.8	30.7	30.7	30.5	30.5	30.6	31.1	30.9
YP_513223.1	29.5	29.4	29.6	29.4	29.5	29.5	29.2	29.3	29.2	29.9	29.3
YP_514444.1	29.1	29.2	29.1	29.2	29.0	29.0	28.8	28.9	28.8	29.1	29.0
YP_514447.1	31.3	31.3	31.3	31.3	31.3	31.3	31.0	31.2	30.9	31.1	31.2
YP_513427.1	31.7	31.6	31.4	31.7	31.5	31.5	31.3	31.4	31.2	31.3	31.6
YP_513662.1	27.9	27.8	27.9	27.9	27.5	27.7	27.7	27.7	27.4	27.3	27.6

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513310.1	28.8	28.6	28.5	28.8	28.5	28.6	28.3	28.4	28.4	28.7	28.6	
YP_513667.1	24.8	24.8	24.6	24.6	24.6	24.7	24.6	24.6	24.0	24.1	24.6	
YP_514379.1	33.3	33.2	33.3	33.3	33.4	33.2	33.0	33.0	33.0	33.4	33.3	
YP_513162.1	28.7	28.8	28.8	28.8	29.0	28.8	28.5	28.5	28.5	28.8	28.7	
YP_513264.1	29.9	29.9	29.8	29.9	29.9	29.9	29.5	29.7	29.5	29.5	29.9	
YP_514069.1	30.3	30.2	30.3	30.3	30.2	30.2	30.0	30.1	29.9	30.1	30.2	
YP_514488.1	28.1	28.2	28.0	28.2	28.0	27.9	27.8	27.8	27.8	27.8	28.3	
YP_513038.1	32.8	32.9	33.0	32.8	32.9	32.9	32.6	32.6	32.6	33.2	32.8	
YP_513831.1	31.1	30.9	31.0	31.0	31.1	31.1	30.7	30.8	30.6	30.6	31.1	
YP_514417.1	30.6	30.6	31.0	30.6	31.1	30.9	30.5	30.2	30.7	32.0	30.6	
YP_514051.1	30.0	29.8	30.0	29.9	30.0	30.0	29.6	29.8	29.6	29.7	29.9	
YP_514210.1	30.2	29.8	30.3	30.2	30.2	30.1	29.8	29.9	29.7	30.3	30.1	
YP_513248.1	29.6	29.6	29.5	29.6	29.4	29.4	29.3	29.4	29.2	29.1	29.5	
YP_513561.1	29.1	29.2	29.0	29.2	28.7	28.8	28.8	29.0	28.6	28.7	29.1	
YP_513206.1	28.6	28.4	28.4	28.4	28.5	28.4	28.2	28.2	28.2	28.6	28.4	
YP_513312.1	28.4	28.5	28.3	28.4	28.3	28.4	28.2	28.2	28.1	28.2	28.5	
YP_514253.1	28.7	28.8	28.7	28.7	28.6	28.7	28.4	28.5	28.5	28.6	28.8	
YP_513458.1	27.7	27.8	27.7	27.8	27.9	27.9	27.5	27.4	27.5	27.8	27.7	
YP_513502.1	27.1	27.2	27.0	27.2	27.1	27.3	26.8	27.0	26.7	26.8	27.0	
YP_514059.1	32.4	32.5	32.4	32.4	32.4	32.4	32.1	32.2	32.2	32.9	32.5	
YP_512977.1	29.2	29.3	29.3	29.2	29.2	29.1	28.9	29.1	29.0	29.8	29.1	
YP_514130.1	31.7	31.7	31.6	31.8	31.6	31.6	31.5	31.5	31.4	31.5	31.7	
YP_513807.1	27.3	27.3	27.5	27.2	27.5	27.3	27.0	27.0	27.4	28.6	27.2	
YP_513044.1	32.2	32.3	32.3	32.2	32.2	32.2	32.0	32.1	32.0	32.5	32.2	
YP_513937.1	25.8	25.7	25.6	25.8	25.8	25.8	25.6	25.3	25.5	25.3	25.6	
YP_512840.1	25.7	25.6	25.5	25.9	25.4	25.5	25.3	25.6	25.2	25.3	25.7	
YP_513040.1	30.5	30.5	30.4	30.4	30.4	30.3	29.9	30.2	30.5	30.7	30.1	
YP_513483.1	25.9	25.9	26.2	26.0	26.0	26.1	26.0	25.6	25.6	26.7	26.1	
YP_513217.1	24.3	23.8	24.0	24.3	23.9	23.8	23.6	24.1	23.7	22.9	24.1	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513679.1	29.8	29.9	29.9	29.9	30.0	29.9	29.7	29.7	29.6	29.9	29.9	
YP_512930.1	29.5	29.6	29.4	29.5	29.3	29.4	29.2	29.3	29.1	29.0	29.5	
YP_514193.1	32.4	32.4	32.4	32.4	32.4	32.4	32.2	32.2	32.1	32.2	32.4	
YP_514159.1	28.0	27.8	27.9	28.0	27.6	27.9	27.7	28.0	27.3	27.3	28.0	
YP_513894.1	28.4	28.4	28.4	28.4	28.2	28.3	28.2	28.1	28.2	28.9	28.4	
YP_513148.1	29.3	29.3	29.2	29.2	29.2	29.2	29.0	29.1	28.9	28.9	29.2	
YP_513743.1	27.4	27.5	27.4	27.5	27.2	27.2	27.3	27.2	27.1	27.2	27.3	
YP_513357.1	30.9	30.9	30.9	30.9	30.8	30.9	30.7	30.8	30.6	30.5	30.9	
YP_513283.1	28.2	28.4	28.4	28.2	28.4	28.4	28.0	28.0	28.3	28.8	28.3	
YP_512839.1	26.2	26.2	26.1	26.0	26.1	26.3	25.7	26.2	25.9	26.0	26.2	
YP_514474.1	27.0	27.1	26.9	27.0	26.8	26.9	26.6	26.8	26.9	27.1	27.0	
YP_513360.1	30.1	30.1	30.0	30.2	30.1	30.1	29.9	29.9	29.7	29.7	30.0	
YP_513418.1	26.0	25.6	25.9	25.8	26.1	26.0	25.7	25.5	25.6	26.2	26.1	
YP_513467.1	24.7	24.6	24.7	24.7	24.4	24.6	24.4	24.5	24.4	24.6	24.7	
YP_513861.1	25.8	25.8	25.7	25.8	25.6	25.6	25.4	25.7	25.5	25.6	25.7	
YP_513237.1	26.9	26.9	26.8	26.9	26.7	27.0	26.7	26.6	26.6	27.0	26.9	
YP_514185.1	29.1	29.1	29.0	29.0	28.8	28.9	28.8	29.0	28.7	28.6	29.1	
YP_513830.1	26.5	26.5	26.4	26.7	26.5	26.8	26.0	26.5	26.3	26.8	26.6	
YP_513756.1	29.5	29.6	29.9	29.6	29.8	29.6	29.4	29.3	29.7	30.9	29.7	
YP_513853.1	26.2	25.0	26.1	25.7	25.9	26.3	25.6	25.6	25.4	27.0	26.0	
YP_512921.1	26.2	25.0	26.1	25.7	25.9	26.3	25.6	25.6	25.4	27.0	26.0	
YP_514178.1	30.5	30.6	30.6	30.6	30.5	30.5	30.3	30.4	30.3	30.5	30.6	
YP_513711.1	27.2	27.3	27.4	27.3	27.3	27.4	27.0	27.2	27.0	27.2	27.6	
YP_513511.1	29.3	29.4	29.4	29.4	29.4	29.3	29.2	29.1	29.1	29.5	29.3	
YP_513772.1	30.9	31.0	31.1	30.9	31.0	31.0	30.8	30.7	30.8	31.2	30.9	
YP_512968.1	29.0	29.1	28.9	28.9	29.1	29.1	28.8	28.7	28.8	29.1	28.9	
YP_514208.1	23.0	22.7	22.7	23.0	22.5	22.9	23.0	22.4	22.3	22.5	22.5	
YP_513440.1	27.5	27.6	27.6	27.5	27.6	27.6	27.3	27.4	27.3	27.6	27.5	
YP_514387.1	31.3	31.2	31.2	31.2	31.2	31.2	31.0	31.0	30.9	30.9	31.2	
YP_514448.1	28.4	28.5	28.7	28.4	28.5	28.5	28.3	28.3	28.4	29.4	28.4	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513746.1	29.5	29.4	29.3	29.3	29.3	29.4	29.2	29.3	29.0	29.2	29.4	
YP_513187.1	29.7	29.7	29.7	29.7	29.8	29.7	29.5	29.4	29.5	29.8	29.7	
YP_514380.1	32.1	32.2	32.3	32.1	32.3	32.2	31.9	32.0	32.0	32.4	32.1	
YP_513642.1	29.4	29.5	29.7	29.5	29.6	29.3	29.3	29.2	29.5	30.6	29.4	
YP_514170.1	30.2	30.2	30.2	30.2	30.2	30.1	30.0	29.9	30.0	30.1	30.2	
YP_512879.1	28.5	28.5	28.5	28.5	28.5	28.4	28.3	28.4	28.3	28.4	28.6	
YP_513030.1	33.9	34.0	33.8	33.9	33.7	33.8	33.6	33.8	33.6	33.6	33.8	
YP_514223.1	23.8	23.4	23.9	24.2	23.0	23.5	23.7	23.9	22.9	23.0	23.8	
YP_513586.1	29.2	28.9	29.2	29.1	29.1	29.1	28.9	29.0	28.8	28.8	29.2	
YP_513460.1	26.6	26.6	26.5	26.6	26.2	26.5	26.3	26.5	26.2	26.3	26.5	
YP_513420.1	27.0	26.9	26.9	26.9	26.9	26.9	26.7	26.8	26.8	27.0	26.8	
YP_513409.1	29.0	28.9	28.8	29.0	28.6	28.8	28.7	28.8	28.5	28.6	29.0	
YP_514195.1	27.6	27.6	27.6	27.5	27.5	27.6	27.4	27.6	27.2	28.1	27.5	
YP_514560.1	26.7	26.6	26.7	26.6	26.8	26.9	26.4	26.4	26.6	27.5	26.7	
YP_513355.1	29.2	29.2	29.1	29.1	29.0	29.0	28.9	29.0	28.9	28.9	29.1	
YP_514446.1	31.6	31.7	31.6	31.6	31.5	31.5	31.3	31.5	31.4	31.6	31.5	
YP_512973.1	30.4	30.5	30.4	30.5	30.2	30.2	30.3	30.3	30.0	30.0	30.5	
YP_514450.1	30.8	30.7	30.8	30.7	30.7	30.8	30.6	30.6	30.5	30.8	30.7	
YP_513107.1	29.1	29.3	29.1	29.2	29.1	28.9	28.9	29.1	28.9	28.9	29.1	
YP_514522.1	34.3	34.3	34.3	34.3	34.3	34.3	34.0	34.1	34.1	34.1	34.3	
YP_514348.1	29.7	29.5	29.6	29.6	29.8	29.8	29.4	29.4	29.3	29.5	29.7	
YP_514332.1	32.1	32.1	32.1	32.2	32.1	32.1	32.0	31.9	31.9	32.0	32.1	
YP_514371.1	28.3	28.3	28.2	28.3	28.1	28.1	28.1	28.1	28.0	28.2	28.3	
YP_513375.1	32.7	32.7	32.7	32.7	32.6	32.6	32.5	32.6	32.4	32.5	32.7	
YP_513871.1	26.9	27.1	26.8	26.9	26.5	26.7	26.6	27.1	26.6	26.3	26.8	
YP_513660.1	32.2	32.4	32.2	32.3	32.1	32.1	32.1	32.2	31.9	31.8	32.2	
YP_513141.1	27.4	27.5	27.3	27.3	27.3	27.3	27.3	27.2	27.1	27.3	27.3	
YP_514083.1	26.6	26.6	26.5	25.6	26.5	26.2	26.2	26.5	26.4	25.5	26.5	
YP_514318.1	25.8	26.0	25.6	26.1	25.8	25.7	25.7	25.7	25.4	25.3	25.8	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514462.1	29.8	29.8	29.7	29.8	29.7	29.7	29.5	29.7	29.6	29.8	29.7	
YP_514040.1	26.9	27.1	27.3	27.0	27.3	27.3	26.9	26.7	27.1	28.3	27.1	
YP_514279.1	22.4	22.1	22.1	22.5	22.2	22.3	22.1	22.2	21.8	22.5	22.2	
YP_513479.1	27.0	27.1	27.2	27.0	27.1	27.1	27.0	26.9	26.8	27.8	27.1	
YP_514378.1	33.1	33.2	33.1	33.2	33.1	33.1	33.0	33.0	32.9	33.1	33.2	
YP_513610.1	32.5	32.6	32.7	32.5	32.7	32.6	32.4	32.4	32.5	33.2	32.5	
YP_513031.1	31.8	31.6	32.1	31.6	32.3	32.1	31.6	31.6	31.8	32.7	31.9	
YP_513694.1	30.3	30.3	30.2	30.3	30.3	30.4	30.0	30.0	30.2	30.7	30.3	
YP_513552.1	28.5	28.5	28.4	28.4	28.3	28.2	28.2	28.4	28.2	28.1	28.5	
YP_514207.1	25.7	25.9	25.8	25.9	25.7	25.6	25.5	25.8	25.5	25.5	25.8	
YP_513653.1	25.9	25.9	25.8	25.8	26.0	25.8	25.5	25.8	25.8	26.1	25.7	
YP_512904.1	33.0	33.0	32.9	33.0	32.8	32.8	32.8	32.9	32.7	32.7	33.0	
YP_512991.1	26.0	26.1	26.1	26.3	26.1	26.0	25.7	26.1	25.8	26.0	26.2	
YP_513774.1	28.5	28.5	28.6	28.5	28.4	28.5	28.3	28.4	28.3	28.5	28.4	
YP_514022.1	23.4	23.9	24.5	24.2	24.7	24.4	23.8	23.3	24.1	25.9	23.5	
YP_514018.1	29.9	29.9	30.0	29.9	30.0	30.0	29.8	29.7	29.8	30.2	30.0	
YP_513230.1	24.4	24.3	24.1	24.3	24.8	24.7	24.4	23.4	24.4	25.0	24.4	
YP_513048.1	33.3	33.3	33.3	33.2	33.3	33.2	33.2	33.1	33.1	33.5	33.3	
YP_513895.1	31.1	31.2	31.1	31.1	31.1	31.1	31.0	30.9	31.0	31.2	31.1	
YP_514140.1	29.9	29.8	29.8	29.8	29.6	29.8	29.6	29.7	29.6	29.5	29.7	
YP_513396.1	29.8	29.6	29.8	29.7	29.6	29.6	29.5	29.7	29.5	29.5	29.8	
YP_513537.1	32.6	32.6	32.5	32.7	32.5	32.5	32.5	32.5	32.3	32.1	32.6	
YP_513520.1	27.5	27.4	27.6	27.6	27.9	27.8	27.5	27.3	27.3	27.8	27.6	
YP_514243.1	23.7	23.8	23.6	23.7	23.3	23.4	23.7	23.8	23.1	22.7	23.7	
YP_514449.1	31.8	31.8	31.7	31.8	31.6	31.7	31.6	31.8	31.5	31.4	31.8	
YP_513099.1	29.0	29.1	29.1	29.1	29.1	29.1	28.9	28.9	28.9	29.0	29.1	
YP_513413.1	30.5	30.6	30.6	30.6	30.4	30.5	30.4	30.5	30.3	30.2	30.6	
YP_514229.1	29.4	29.5	29.3	29.5	29.1	29.3	29.3	29.3	29.1	29.1	29.3	
YP_514143.1	28.5	28.5	28.5	28.5	28.6	28.6	28.4	28.3	28.3	28.6	28.5	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513421.1	26.4	26.4	26.4	26.5	26.3	26.5	26.2	26.4	26.2	26.1	26.5	
YP_514506.1	27.3	27.1	27.2	27.3	27.3	27.2	27.1	27.1	27.0	27.1	27.2	
YP_514002.1	29.4	29.5	29.4	29.5	29.4	29.3	29.3	29.3	29.2	29.2	29.4	
YP_514276.1	28.8	28.9	28.9	29.0	28.7	28.8	28.6	28.9	28.6	30.1	28.8	
YP_514452.1	22.7	23.1	23.1	24.2	23.4	22.8	22.8	22.2	23.4	24.7	25.0	
YP_513251.1	30.7	30.8	30.6	30.7	30.6	30.6	30.5	30.6	30.5	30.4	30.8	
YP_513500.1	21.0	21.3	21.1	21.8	20.4	21.2	20.4	21.2	21.3	19.9	20.5	
YP_514292.1	29.8	29.9	29.7	29.8	29.6	29.7	29.6	29.8	29.5	29.8	29.8	
YP_513661.1	33.6	33.6	33.7	33.6	33.6	33.6	33.4	33.5	33.6	34.2	33.5	
YP_513285.1	24.3	23.9	23.8	24.2	23.9	23.9	23.8	24.0	23.8	23.5	23.3	
YP_514382.1	36.3	36.0	36.3	36.3	36.3	36.3	36.0	36.0	36.0	36.5	36.3	
YP_514538.1	26.3	26.3	26.2	26.1	25.7	25.8	26.0	26.3	26.1	25.8	26.1	
YP_513252.1	32.2	32.2	32.1	32.3	32.2	32.2	32.0	32.1	32.0	32.2	32.3	
YP_513124.1	33.0	32.9	32.8	32.9	32.7	32.8	32.7	32.9	32.7	32.7	32.9	
YP_514523.1	26.9	26.9	26.8	26.9	27.0	26.9	26.7	26.7	26.7	26.8	27.0	
YP_513276.1	28.6	28.7	28.6	28.7	28.5	28.6	28.5	28.6	28.3	28.3	28.6	
YP_514025.1	32.4	32.3	32.3	32.4	32.2	32.3	32.3	32.3	32.1	32.0	32.4	
YP_514031.1	26.1	26.1	26.1	26.2	26.1	26.2	26.0	25.7	26.2	26.8	26.0	
YP_513980.1	33.0	33.0	33.0	32.9	33.0	33.1	32.9	32.8	32.9	32.8	32.9	
YP_513550.1	29.9	30.0	29.9	29.9	29.9	29.9	29.8	29.9	29.7	29.5	29.9	
YP_514135.1	23.9	24.8	24.1	24.5	24.3	24.4	24.3	24.1	24.0	23.6	24.4	
YP_514252.1	25.7	25.7	25.6	25.7	25.3	25.3	25.6	25.7	25.3	24.6	25.7	
YP_513449.1	27.6	26.6	27.5	27.1	27.6	27.6	27.1	27.1	27.2	27.7	27.6	
YP_513194.1	34.3	34.4	34.3	34.4	34.0	34.3	34.1	34.4	34.1	33.7	34.3	
YP_513316.1	27.0	27.0	26.9	27.0	26.9	26.9	26.8	26.7	27.0	27.4	27.0	
YP_513734.1	26.1	26.3	26.0	26.4	26.1	26.0	26.0	25.9	26.0	25.9	26.2	
YP_512821.1	30.4	30.5	30.6	30.5	30.4	30.4	30.4	30.4	30.3	30.8	30.5	
YP_513114.1	29.5	29.5	29.8	29.5	29.8	29.6	29.5	29.0	29.9	31.3	29.4	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513577.1	26.8	26.8	26.8	26.8	26.7	26.6	26.6	26.9	26.6	26.5	26.9
YP_514233.1	28.2	28.2	28.1	28.1	28.0	28.1	28.0	28.1	28.0	27.9	28.1
YP_513153.1	28.8	28.8	28.8	28.8	28.8	28.8	28.7	28.7	28.7	28.4	28.7
YP_513377.1	24.3	23.9	23.7	23.7	23.5	23.8	24.0	23.7	23.8	23.4	23.7
YP_513548.1	26.5	26.5	26.6	26.5	26.6	26.6	26.4	26.2	26.6	27.4	26.6
YP_514295.1	28.5	28.6	28.5	28.6	28.7	28.7	28.4	28.3	28.5	28.5	28.5
YP_514045.1	30.9	30.8	30.9	30.9	30.9	30.9	30.8	30.7	30.7	30.8	30.9
YP_513741.1	29.6	29.7	29.5	29.6	29.5	29.4	29.4	29.6	29.4	29.4	29.5
YP_513556.1	31.6	31.7	31.7	31.5	31.8	31.7	31.6	31.3	31.7	32.0	31.6
YP_513719.1	28.6	28.7	28.6	28.7	28.6	28.6	28.5	28.6	28.6	28.7	28.6
YP_513371.1	31.6	31.7	31.9	31.6	31.9	31.8	31.5	31.6	31.8	32.2	31.5
YP_512812.1	32.7	32.7	32.6	32.7	32.5	32.5	32.6	32.7	32.4	32.1	32.7
YP_513742.1	31.2	31.2	31.4	31.2	31.3	31.3	31.1	31.2	31.2	31.6	31.2
YP_512967.1	24.0	23.9	23.9	23.7	23.8	23.7	23.6	24.0	23.8	23.8	23.9
YP_513512.1	29.4	29.2	29.2	29.3	29.2	29.3	29.2	29.2	29.1	29.3	29.5
YP_513302.1	31.6	31.5	31.6	31.5	31.6	31.7	31.5	31.6	31.3	31.6	31.7
YP_514366.1	32.0	32.0	31.9	32.0	31.9	31.9	31.8	31.8	31.9	32.3	31.9
YP_513171.1	30.8	30.7	30.7	30.7	30.7	30.7	30.6	30.8	30.6	30.4	30.6
YP_513954.1	30.1	30.1	30.0	30.1	30.1	30.0	30.0	30.0	30.0	29.9	30.1
YP_513344.1	32.6	32.6	32.4	32.6	32.6	32.6	32.5	32.5	32.3	32.2	32.7
YP_513216.1	31.2	31.1	31.2	31.3	31.2	31.2	31.1	31.1	31.0	31.1	31.2
YP_513119.1	30.0	29.9	29.9	29.9	29.8	29.8	29.7	29.9	29.8	29.9	29.9
YP_513077.1	27.3	27.4	27.5	27.4	27.5	27.4	27.2	27.3	27.3	27.8	27.4
YP_513085.1	29.9	30.0	30.1	30.0	30.1	30.0	29.8	29.8	30.1	31.0	29.9
YP_512969.1	29.4	29.4	29.6	29.2	29.8	29.6	28.9	29.0	30.1	31.3	29.2
YP_513012.1	26.1	26.2	26.2	26.0	26.1	26.0	26.2	25.7	26.2	26.3	26.5
YP_513225.1	32.0	32.1	32.0	32.1	32.0	32.0	31.9	32.0	31.9	32.0	32.0
YP_514554.1	30.1	30.0	30.1	30.1	30.1	30.2	30.0	30.0	29.9	29.9	30.2

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_512864.1	27.4	27.2	27.3	27.1	27.4	27.3	27.2	27.2	27.2	27.3	27.2
YP_513172.1	30.9	30.9	30.9	30.9	30.9	30.9	30.8	30.9	30.8	30.6	30.9
YP_514062.1	32.0	32.0	31.9	32.0	32.0	32.0	31.9	31.9	31.8	31.8	31.9
YP_513574.1	30.5	30.3	30.4	30.4	30.3	30.4	30.3	30.5	30.2	29.9	30.4
YP_512993.1	25.2	25.3	25.2	25.1	25.3	24.9	24.8	25.2	25.5	24.8	25.2
YP_514277.1	27.5	27.5	27.6	27.5	27.5	27.4	27.4	27.5	27.4	27.5	27.4
YP_513650.1	28.4	27.6	28.4	27.9	28.3	28.4	28.1	28.1	27.9	28.1	28.4
YP_513715.1	28.1	28.1	28.1	28.0	28.3	28.5	28.1	27.8	28.1	28.5	28.2
YP_513476.1	27.9	28.0	28.0	28.0	28.0	27.9	27.8	27.9	27.9	28.1	28.1
YP_513832.1	33.0	33.1	33.0	33.1	33.0	33.0	33.0	33.0	32.9	33.1	33.0
YP_513804.1	25.9	26.1	25.8	26.0	25.5	25.7	25.8	26.1	25.7	25.6	26.0
YP_513540.1	28.9	28.7	28.7	28.8	28.5	28.7	28.6	28.8	28.7	28.7	28.7
YP_513053.1	33.9	34.0	33.9	33.9	33.8	33.8	33.8	33.9	33.9	33.9	33.9
YP_513731.1	29.6	29.7	29.6	29.6	29.7	29.7	29.6	29.5	29.6	29.8	29.6
YP_513435.1	18.0	18.4	17.8	18.0	18.5	18.6	18.2	18.2	17.6	16.1	17.9
YP_513166.1	24.5	24.4	24.5	24.6	24.5	24.4	24.5	24.7	24.1	24.6	24.6
YP_513654.1	30.2	30.1	30.2	30.1	30.3	30.3	30.1	30.1	30.1	30.3	30.3
YP_513955.1	29.0	29.1	29.0	28.9	29.0	29.0	29.0	29.0	28.9	28.7	29.0
YP_512875.1	30.4	30.5	30.4	30.5	30.3	30.3	30.5	30.3	30.4	30.3	30.5
YP_514244.1	30.9	30.9	30.8	30.9	30.6	30.8	30.8	30.9	30.6	30.4	30.8
YP_513521.1	28.5	28.5	28.5	28.5	28.5	28.5	28.4	28.4	28.5	28.6	28.5
YP_512877.1	30.5	30.7	30.5	30.6	30.4	30.5	30.5	30.6	30.4	30.4	30.6
YP_513298.1	23.3	23.4	23.3	23.6	23.3	23.1	23.5	23.1	23.2	23.1	23.5
YP_513700.1	28.0	28.1	28.2	28.1	28.1	28.2	28.1	27.9	28.1	28.4	27.9
YP_513381.1	27.5	27.3	27.4	27.4	27.9	27.9	27.7	27.1	27.2	27.5	27.3
YP_513611.1	30.7	30.8	30.7	30.8	30.7	30.7	30.6	30.8	30.6	30.4	30.8
YP_514376.1	34.5	34.4	34.6	34.4	34.5	34.7	34.3	34.2	34.8	35.2	34.3
YP_513047.1	32.5	32.7	32.6	32.6	32.5	32.5	32.5	32.5	32.6	32.8	32.6
YP_513652.1	27.7	27.7	27.7	27.7	27.8	27.8	27.7	27.6	27.7	27.8	27.8

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	delt_rpsU3 .3
YP_513061.1	34.4	34.5	34.4	34.5	34.4	34.6	34.4	34.6	34.2	34.0	34.5	
YP_514354.1	29.7	29.8	29.7	29.8	29.6	29.8	29.8	29.7	29.5	29.6	29.7	
YP_514542.1	27.9	28.2	28.5	27.8	28.6	28.4	28.1	27.5	28.8	29.6	27.8	
YP_512818.1	28.7	28.8	28.7	28.8	28.7	28.9	28.6	28.9	28.6	29.0	28.8	
YP_513675.1	31.6	31.5	31.6	31.7	31.7	31.7	31.4	31.5	31.5	31.7	31.6	
YP_513180.1	27.7	27.5	27.6	27.5	27.7	27.7	27.5	27.6	27.4	27.7	27.5	
YP_513382.1	25.8	25.8	25.8	25.7	25.7	25.7	25.6	25.9	25.6	25.9	25.7	
YP_514435.1	33.0	33.1	32.9	33.1	33.0	32.9	32.9	33.1	32.9	32.8	33.0	
YP_513455.1	28.0	28.1	28.2	28.0	28.1	28.0	28.0	28.0	28.0	28.3	28.0	
YP_513041.1	31.9	32.0	31.9	32.0	31.9	31.9	32.0	31.7	31.9	32.1	31.9	
YP_513630.1	28.0	27.8	27.8	27.7	27.6	27.8	27.7	27.9	27.8	27.4	27.8	
YP_513045.1	32.9	32.9	32.9	32.9	32.8	32.8	32.8	32.8	32.8	32.9	32.9	
YP_514250.1	30.5	30.3	30.5	30.4	30.2	30.4	30.4	30.6	30.1	30.1	30.4	
YP_512971.1	21.8	21.2	20.6	20.8	21.9	21.0	21.4	20.6	21.4	19.5	20.7	
YP_514085.1	29.6	29.6	29.6	29.7	29.7	29.7	29.5	29.5	29.7	29.9	29.6	
YP_513796.2	30.4	30.4	30.4	30.4	30.3	30.3	30.3	30.3	30.4	30.2	30.3	
YP_513139.1	27.5	27.0	27.4	27.4	27.6	27.6	27.3	27.2	27.2	27.8	27.5	
YP_513695.1	32.7	32.7	32.7	32.7	32.9	32.9	32.7	32.7	32.6	32.4	32.7	
YP_513493.1	28.5	28.6	28.5	28.6	28.5	28.6	28.5	28.6	28.4	28.4	28.6	
YP_512984.1	31.1	31.0	31.1	31.1	31.2	31.2	31.1	31.1	31.0	31.2	31.1	
YP_513403.1	30.4	30.4	30.4	30.4	30.3	30.3	30.3	30.5	30.3	30.1	30.4	
YP_513265.1	26.8	27.1	26.9	26.9	26.7	26.5	26.7	26.7	27.2	28.0	26.9	
YP_513314.1	26.6	26.6	26.6	26.5	26.4	26.4	26.5	26.7	26.4	26.0	26.6	
YP_513795.1	29.9	29.9	29.8	29.8	29.9	29.9	29.8	29.9	29.8	29.6	29.7	
YP_512995.1	29.2	29.4	29.2	29.2	29.1	29.1	29.1	29.4	29.2	29.1	29.2	
YP_513944.1	28.7	28.8	28.6	28.6	28.6	28.5	28.7	28.6	28.7	28.4	28.6	
YP_512953.1	29.9	30.1	29.9	30.1	29.8	29.9	30.0	30.1	29.8	29.5	30.1	
YP_513006.1	22.4	22.4	22.5	22.1	22.1	22.5	22.5	22.5	22.2	22.3	22.3	
YP_513882.1	23.9	23.9	24.0	24.2	23.9	24.0	23.9	23.6	24.1	24.8	23.2	
YP_513668.1	25.1	25.2	25.1	25.3	25.1	25.1	25.0	25.2	25.1	24.8	24.7	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513210.1	32.5	32.4	32.4	32.5	32.3	32.3	32.4	32.4	32.3	32.1	32.4	
YP_513178.1	29.4	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	
YP_513369.1	28.1	28.1	28.0	28.2	28.1	28.1	28.1	28.1	28.0	27.7	28.1	
YP_513477.1	26.7	26.8	26.7	26.7	26.6	26.6	26.7	26.7	26.6	26.5	26.8	
YP_513046.1	32.6	32.7	32.8	32.8	32.7	32.8	32.8	32.5	32.8	33.0	32.8	
YP_513028.1	34.0	34.1	34.1	34.0	34.1	34.0	34.0	34.0	34.1	34.4	34.0	
YP_513713.1	25.6	25.7	25.6	25.5	25.7	25.8	25.4	25.5	25.8	26.3	25.7	
YP_514534.1	30.3	30.4	30.5	30.3	30.6	30.5	30.3	30.3	30.4	31.0	30.3	
YP_514465.1	29.2	29.5	29.6	29.4	29.4	29.3	29.2	29.6	29.4	29.8	29.4	
YP_513678.1	27.5	27.4	27.5	27.4	27.5	27.5	27.3	27.3	27.7	28.0	27.4	
YP_513690.1	23.9	25.3	24.7	24.4	24.5	24.5	24.7	24.1	25.0	24.6	23.1	
YP_514367.1	27.9	27.9	27.8	27.8	27.9	27.9	27.9	27.8	27.8	27.6	27.8	
YP_513523.1	23.1	23.6	22.9	23.4	23.2	23.3	23.1	23.2	23.1	23.3	23.6	
YP_513226.1	31.2	31.2	31.1	31.1	31.2	31.2	31.2	31.1	31.2	31.2	31.2	
YP_513513.1	31.1	31.1	31.2	31.2	31.2	31.2	31.1	31.2	31.1	31.2	31.2	
YP_513406.1	28.1	28.2	28.4	28.2	28.4	28.3	28.2	28.0	28.3	29.0	28.1	
YP_513727.1	33.2	33.2	33.5	33.2	33.4	33.3	33.2	33.1	33.5	34.2	33.2	
YP_513554.1	31.3	31.1	31.3	31.2	31.3	31.3	31.2	31.3	31.1	31.2	31.4	
YP_513054.1	32.8	32.8	33.0	32.8	33.0	32.9	32.8	32.9	32.8	33.1	32.8	
YP_513306.1	30.2	30.3	30.3	30.2	30.4	30.4	30.4	30.1	30.3	30.4	30.2	
YP_514360.1	28.3	28.4	28.3	28.3	28.2	28.3	28.3	28.4	28.1	27.9	28.3	
YP_513398.1	31.7	31.9	31.7	31.8	31.4	31.6	31.7	31.9	31.6	31.5	31.7	
YP_512876.1	27.6	27.4	27.3	27.5	27.4	27.5	27.4	27.4	27.4	27.3	27.3	
YP_513063.1	35.2	35.2	35.2	35.2	35.2	35.2	35.3	35.3	35.0	34.7	35.2	
YP_513193.1	29.1	29.0	29.1	28.9	29.2	29.1	29.0	29.0	29.2	29.7	29.0	
YP_513098.1	29.8	30.0	29.7	29.9	29.7	29.7	29.8	30.0	29.7	29.6	29.9	
YP_514548.1	30.9	30.7	30.9	30.8	31.0	31.0	30.8	30.9	30.8	30.8	30.8	
YP_512992.1	26.6	26.7	26.3	26.6	26.3	26.1	26.5	26.6	26.4	26.5	26.5	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514513.1	31.3	31.3	31.4	31.3	31.3	31.3	31.3	31.4	31.3	31.4	31.4	
YP_513901.1	26.4	26.5	26.5	26.4	26.5	26.5	26.4	26.5	26.5	26.2	26.4	
YP_513106.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514545.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514532.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514503.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514499.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514438.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514388.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514349.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514344.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514319.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514313.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514282.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514269.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514266.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514249.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514190.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514155.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514113.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514101.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514057.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514030.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_514012.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513987.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513969.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513961.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513921.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513878.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513838.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513814.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513721.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513680.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513518.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513484.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513434.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513430.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513384.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513367.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513279.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513272.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513212.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513190.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513136.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513126.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513062.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513060.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513058.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512980.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512959.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512951.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512933.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512926.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512905.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512884.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512862.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512831.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512827.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_512814.1	24.2	24.2	24.2	24.2	24.2	24.3	24.2	24.2	24.2	24.3	24.2	
YP_513294.1	31.0	31.0	31.1	31.0	31.1	31.1	31.1	31.0	31.0	31.2	31.0	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514539.1	29.7	29.6	29.7	29.7	29.8	29.8	29.9	29.4	29.7	29.9	29.7
YP_514052.1	27.8	27.8	27.8	27.7	27.8	27.7	27.9	27.8	27.7	27.5	27.8
YP_514529.1	27.8	28.0	27.7	27.8	27.8	27.8	27.8	28.0	27.7	27.6	27.9
YP_513788.1	31.5	31.5	31.5	31.5	31.6	31.6	31.5	31.4	31.6	31.6	31.6
YP_513917.1	23.9	24.0	23.8	24.3	24.3	23.7	24.0	24.0	23.7	23.1	24.0
YP_514556.1	29.9	30.1	30.0	30.0	30.0	30.0	29.9	30.1	30.0	29.7	29.9
YP_514021	0.0	0.0	0.0	28.6	28.8	28.7	0.0	0.0	0.0	0.0	0.0
YP_513228.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	26.1	26.2
YP_513534.1	29.0	29.1	28.9	29.0	28.9	28.9	28.9	29.1	28.9	28.7	29.0
YP_513019.1	33.7	33.6	33.5	33.7	33.6	33.6	33.7	33.6	33.6	33.4	33.7
YP_514304.1	24.4	24.4	24.5	24.5	24.4	24.4	24.8	24.1	24.4	24.9	24.4
YP_513749.1	26.3	26.4	26.4	26.3	26.4	26.4	26.3	26.4	26.3	26.1	26.1
YP_513020.1	34.2	34.0	34.4	34.1	34.4	34.4	34.1	34.2	34.3	34.9	34.1
YP_513920.1	30.2	30.3	30.2	30.1	30.4	30.2	30.4	29.9	30.4	30.5	30.1
YP_514420.1	33.4	33.4	33.4	33.5	33.4	33.4	33.4	33.6	33.2	33.2	33.5
YP_513481.1	19.7	19.8	18.0	19.4	20.1	20.3	19.9	18.1	19.5	20.9	20.4
YP_513307.1	32.8	33.0	32.9	33.0	32.9	33.1	32.7	33.2	32.9	33.0	33.0
YP_513222.1	29.0	29.1	29.0	29.1	29.3	29.2	29.3	29.0	29.0	29.0	29.0
YP_514374.1	34.7	34.7	34.8	34.7	34.8	34.8	34.8	34.8	34.6	34.5	34.9
YP_514001.1	21.4	20.8	21.7	21.1	21.2	21.1	21.6	22.0	20.4	20.1	21.2
YP_514087.1	28.8	29.0	28.9	28.9	28.8	28.9	28.9	28.8	29.0	29.0	28.9
YP_512946.1	27.8	27.8	27.7	27.8	27.7	27.6	27.8	27.9	27.6	27.3	27.7
YP_513100.1	22.8	22.9	22.6	23.0	22.4	22.6	22.6	22.9	22.8	21.3	22.8
YP_513385.1	25.0	25.2	25.2	25.1	25.3	25.1	25.1	25.2	25.2	25.5	25.2
YP_513362.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.2	31.1	31.0	31.1
YP_513530.1	24.4	24.7	24.9	24.4	24.4	24.7	24.5	24.9	24.6	24.4	25.0
YP_513186.1	29.0	28.8	29.0	28.9	28.9	29.0	29.0	29.0	28.9	28.6	28.9
YP_513097.1	25.3	25.3	25.4	25.5	25.5	25.4	25.2	25.4	25.5	25.8	25.3
YP_514340.1	28.4	28.3	28.4	28.4	28.4	28.5	28.5	28.3	28.4	28.8	28.2

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513365.1	30.7	30.5	30.6	30.6	30.6	30.6	30.6	30.6	30.7	30.5	30.6	
YP_513170.1	26.5	26.5	26.5	26.5	26.4	26.3	26.5	26.6	26.5	26.6	26.4	
YP_512890.1	28.3	27.9	28.6	28.0	28.7	28.5	28.0	28.2	28.7	30.0	28.2	
YP_512880.1	29.4	29.6	29.4	29.6	29.5	29.5	29.5	29.6	29.5	29.4	29.6	
YP_513549.1	29.3	29.3	29.2	29.3	29.1	29.2	29.3	29.4	29.2	29.1	29.3	
YP_514036.1	25.5	25.6	25.7	25.5	25.8	25.7	25.7	25.2	26.0	26.8	25.6	
YP_514274.1	20.7	20.9	21.3	21.1	20.8	21.4	20.8	21.5	20.7	20.6	21.0	
YP_513379.1	28.0	28.2	28.1	28.1	28.1	28.2	28.2	28.2	28.1	27.9	28.2	
YP_514141.1	30.6	30.5	30.6	30.5	30.7	30.7	30.6	30.6	30.6	30.5	30.5	
YP_514365.1	24.7	24.8	24.7	25.0	24.6	24.6	24.7	25.0	24.6	24.0	24.9	
YP_513151.1	27.3	27.1	27.5	27.1	27.7	27.7	27.2	27.4	27.3	28.1	27.4	
YP_514472.1	31.0	30.8	31.0	30.9	31.0	31.0	30.9	31.0	30.9	30.7	31.0	
YP_513437.1	28.6	28.3	28.7	28.4	28.4	28.6	28.7	28.6	28.4	28.2	28.4	
YP_512847.1	29.7	29.7	29.6	29.5	29.5	29.8	29.9	29.4	29.8	30.1	29.6	
YP_513291.1	33.2	33.3	33.2	33.2	33.3	33.3	33.3	33.3	33.3	33.5	33.4	
YP_513208.1	32.1	32.2	32.1	32.2	32.0	32.1	32.2	32.3	32.0	31.8	32.2	
YP_514039.1	28.7	28.6	29.0	28.6	29.2	29.1	28.9	28.6	28.9	29.6	28.7	
YP_514237.1	31.5	31.6	31.5	31.5	31.6	31.5	31.6	31.7	31.6	31.5	31.5	
YP_513646.1	28.4	28.3	28.5	28.4	28.6	28.5	28.5	28.5	28.5	28.4	28.5	
YP_513994.1	34.8	34.8	35.0	35.0	35.0	35.0	34.9	34.9	34.9	34.9	35.0	
YP_514330.1	24.9	24.9	24.7	25.1	24.8	24.6	24.9	25.1	24.7	23.9	24.8	
YP_512982.1	30.0	29.9	30.1	30.1	30.2	30.2	30.2	29.9	30.0	30.2	30.1	
YP_513422.1	27.2	26.6	27.2	26.6	27.3	27.2	27.1	26.8	27.2	27.4	26.9	
YP_513946.1	30.3	30.4	30.1	30.3	30.1	30.1	30.2	30.4	30.3	30.0	30.3	
YP_513043.1	33.9	34.0	33.8	34.0	33.7	33.7	34.0	34.0	33.9	33.4	34.0	
YP_513578.1	30.8	30.8	30.6	30.7	30.5	30.6	30.7	30.9	30.7	30.6	30.9	
YP_514256.1	30.3	30.4	30.3	30.3	30.4	30.3	30.4	30.3	30.4	30.2	30.3	
YP_513519.1	28.1	28.0	28.1	27.9	28.2	28.3	28.2	28.2	28.0	28.0	28.1	
YP_513474.1	28.6	28.8	28.9	28.6	28.9	28.8	28.8	28.8	28.9	29.5	28.8	

log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513247.1	28.6	28.5	28.6	28.5	28.5	28.6	28.6	28.5	28.6	28.5	28.5
YP_514294.1	29.7	29.8	29.7	29.7	29.7	29.7	29.8	29.8	29.8	29.6	29.7
YP_513037.1	34.0	34.1	33.8	34.0	34.1	34.0	34.1	34.0	34.0	33.7	34.0
YP_513723.1	28.5	28.5	28.4	28.6	28.4	28.4	28.6	28.6	28.5	28.3	28.5
YP_512822.1	31.8	31.7	31.8	31.7	31.8	31.8	31.9	31.9	31.8	31.8	31.8
YP_513034.1	33.5	33.5	33.6	33.6	33.9	33.7	33.7	33.2	33.9	34.2	33.5
YP_513408.1	30.1	30.0	30.1	30.1	29.9	30.0	30.1	30.2	30.1	30.1	30.1
YP_513555.1	26.6	26.7	26.4	26.6	26.5	26.5	26.6	26.7	26.7	26.7	26.6
YP_513635.1	27.2	27.1	27.5	27.2	27.7	27.4	27.2	27.1	27.6	28.4	27.1
YP_513560.1	30.2	29.7	30.2	30.1	30.1	30.1	30.2	30.2	29.9	29.8	30.2
YP_512935.1	29.5	29.6	29.4	29.6	29.2	29.3	29.6	29.8	29.4	29.0	29.5
YP_513898.1	26.4	26.6	26.6	26.5	26.6	26.6	26.6	26.6	26.7	26.7	26.3
YP_513885.1	26.1	26.4	26.2	26.3	26.3	26.0	26.1	26.4	26.4	26.5	26.6
YP_514555.1	31.6	31.5	32.0	31.6	32.4	32.4	31.8	31.7	31.9	32.3	31.5
YP_513927.1	28.4	28.0	28.4	28.2	28.4	28.2	28.3	28.4	28.2	28.7	28.3
YP_513348.1	33.5	33.4	33.6	33.4	33.5	33.5	33.6	33.7	33.4	33.6	33.5
YP_513411.1	28.5	28.5	28.5	28.5	28.3	28.3	28.5	28.7	28.4	28.3	28.4
YP_514194.1	27.6	27.6	27.7	27.6	27.4	27.5	27.7	27.7	27.6	27.4	27.5
YP_514097.1	33.5	33.6	33.3	33.4	33.2	33.4	33.5	33.6	33.4	33.1	33.6
YP_513965.1	27.7	27.7	27.7	27.7	27.6	27.5	27.8	27.9	27.6	26.9	27.7
YP_513424.1	26.3	26.4	26.1	26.5	25.9	26.0	26.8	25.5	26.6	26.4	26.6
YP_513257.1	31.3	31.3	31.2	31.3	31.3	31.2	31.4	31.3	31.3	31.2	31.3
YP_513768.1	29.9	30.0	29.8	30.0	29.8	29.9	30.0	30.1	29.8	29.5	30.0
YP_513522.1	25.3	25.6	25.1	25.2	25.3	25.5	25.4	25.4	25.4	25.5	25.4
YP_513013.1	30.9	30.9	30.9	30.8	31.0	31.0	31.0	30.9	30.9	30.9	31.0
YP_514127.1	30.6	30.5	30.5	30.6	30.5	30.5	30.6	30.7	30.5	30.3	30.6
YP_513195.1	29.3	29.2	29.3	29.4	29.2	29.2	29.5	29.2	29.2	29.4	29.3
YP_513666.1	28.4	28.5	28.4	28.5	28.6	28.5	28.5	28.4	28.6	28.6	28.5

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513869.1	32.1	32.1	32.3	32.1	32.3	32.2	32.2	32.2	32.4	32.8	32.1
YP_513764.1	29.2	29.4	29.3	29.4	29.2	29.3	29.4	29.5	29.3	29.0	29.4
YP_513956.1	27.9	28.2	28.0	28.1	28.0	28.0	28.1	28.2	28.0	27.8	28.0
YP_513812.1	24.6	24.5	24.5	24.8	24.6	24.5	24.7	24.6	24.6	24.5	24.4
YP_514198.1	31.3	31.4	31.3	31.4	31.3	31.3	31.5	31.5	31.3	31.3	31.4
YP_513345.1	31.9	31.8	31.6	31.8	31.6	31.7	31.9	32.0	31.7	31.5	31.8
YP_513790.1	28.7	28.9	29.3	28.7	29.3	29.1	29.0	28.5	29.6	31.0	28.8
YP_513227.1	27.1	26.7	27.1	27.0	27.1	27.1	27.1	27.1	27.0	27.0	27.1
YP_513933.1	27.2	27.2	27.2	27.1	27.3	27.2	27.5	26.8	27.6	27.7	27.2
YP_514217.1	23.5	23.5	24.0	23.5	23.9	24.0	23.8	23.5	23.9	24.4	23.6
YP_512820.1	29.6	29.5	29.5	29.5	29.5	29.5	29.8	29.4	29.7	29.8	29.5
YP_514423.1	29.9	29.9	30.1	29.9	30.0	30.0	30.0	30.1	30.1	30.0	29.8
YP_514510.1	28.0	28.1	28.0	28.1	28.2	28.2	28.2	27.9	28.2	28.3	28.2
YP_513883.1	26.0	26.2	26.2	26.2	26.2	26.1	26.3	26.0	26.4	26.9	26.3
YP_513940.1	30.4	30.3	30.3	30.4	30.4	30.4	30.5	30.3	30.5	30.7	30.4
YP_513900.1	24.7	24.5	25.1	24.5	24.3	25.3	25.0	24.5	25.1	24.7	25.9
YP_513303.1	29.0	29.0	29.0	29.0	28.9	29.0	29.1	29.2	29.0	28.6	29.0
YP_514262.1	27.6	27.1	27.6	27.4	27.2	27.5	27.5	28.0	27.1	26.5	27.4
YP_513177.1	29.8	29.8	29.8	29.4	29.2	29.2	29.7	29.7	30.2	29.9	29.8
YP_514112.1	32.9	33.0	32.9	33.0	33.0	33.0	33.1	33.1	33.0	32.9	33.0
YP_514050.1	27.2	27.3	27.1	27.4	27.0	27.1	27.4	27.4	27.2	26.9	27.3
YP_513507.1	28.3	28.4	28.0	28.2	28.3	28.2	28.1	28.3	28.6	28.6	28.3
YP_514564.1	24.6	24.5	24.4	24.7	24.7	24.7	24.9	24.8	24.1	25.0	24.8
YP_514139.1	26.4	26.0	26.6	26.2	26.7	26.7	26.5	26.4	26.4	26.8	26.4
YP_513597.1	30.4	30.4	30.3	30.3	30.3	30.4	30.5	30.5	30.4	30.2	30.5
YP_513103.1	32.3	32.4	32.2	32.3	32.1	32.2	32.4	32.4	32.4	32.3	32.3
YP_513860.1	28.6	28.5	28.6	28.6	28.5	28.6	28.7	28.6	28.7	29.2	28.5
YP_514104.1	25.8	26.0	25.8	26.0	25.9	25.8	26.1	25.9	25.9	25.5	25.6
YP_513957.1	23.6	23.3	23.6	23.3	23.4	23.8	23.8	23.6	23.4	23.7	23.3

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	delt_rpsU3 .3
YP_512998.1	26.4	26.5	26.4	26.8	26.4	26.5	26.4	27.0	26.3	25.7	26.7	
YP_514035.1	20.8	21.5	21.3	21.9	21.3	22.2	21.2	21.4	21.2	22.0	21.5	
YP_513881.1	31.2	31.2	31.2	31.1	31.2	31.0	31.2	31.3	31.3	31.2	31.1	
YP_513102.1	33.3	33.2	33.2	33.2	33.2	33.3	33.3	33.5	33.3	33.3	33.3	
YP_514199.1	34.2	34.2	34.3	34.2	34.3	34.1	34.2	34.4	34.4	34.4	34.2	
YP_513570.1	30.3	30.4	30.2	30.4	30.1	30.2	30.5	30.6	30.2	30.0	30.5	
YP_513835.1	31.2	31.0	31.1	31.1	31.2	31.2	31.2	31.3	31.1	31.0	31.1	
YP_513342.1	27.3	27.0	27.2	27.1	27.2	27.2	27.2	27.3	27.3	27.3	27.3	
YP_513750.1	31.2	31.1	31.4	31.2	31.5	31.4	31.4	31.4	31.3	31.5	31.4	
YP_514187.1	27.2	26.9	27.3	27.3	27.2	27.1	27.3	27.4	27.1	27.1	27.3	
YP_513572.1	29.3	29.3	29.4	29.3	29.5	29.4	29.5	29.5	29.3	29.2	29.4	
YP_513410.1	27.9	27.9	28.0	28.0	27.9	28.0	28.1	28.1	27.9	27.7	28.0	
YP_514478.1	30.7	30.7	30.6	30.6	30.6	30.6	30.7	30.8	30.7	30.3	30.7	
YP_514245.1	29.4	29.3	29.4	29.5	29.3	29.3	29.5	29.6	29.4	29.5	29.6	
YP_513973.1	30.5	29.7	30.6	30.0	30.6	30.6	30.4	30.6	30.2	30.2	30.4	
YP_513636.1	30.6	30.3	30.6	30.3	30.9	30.9	30.7	30.4	30.7	31.0	30.5	
YP_514337.1	28.6	28.7	29.0	28.7	29.0	28.9	28.8	28.7	29.1	30.1	28.8	
YP_513656.1	23.6	24.0	23.5	23.6	23.2	23.2	23.9	24.0	23.6	23.3	23.9	
YP_514520.1	30.8	30.8	30.9	30.9	31.0	30.9	30.9	30.9	31.1	31.1	30.8	
YP_514184.1	30.2	30.4	30.5	30.4	30.4	30.3	30.4	30.5	30.6	31.1	30.3	
YP_514299.1	30.3	30.2	30.3	30.2	30.3	30.3	30.4	30.4	30.4	30.3	30.2	
YP_513833.1	31.1	31.2	31.1	31.1	31.0	31.1	31.2	31.4	31.2	31.0	31.2	
YP_513290.1	27.2	27.3	27.8	27.3	27.7	27.8	27.2	27.5	27.8	29.3	27.8	
YP_513397.1	29.2	29.3	29.2	29.3	29.3	29.3	29.3	29.4	29.4	29.4	29.3	
YP_513524.1	30.3	30.3	30.4	30.4	30.3	30.5	30.5	30.3	30.5	30.6	30.5	
YP_513936.1	27.0	27.2	27.0	27.0	26.9	27.0	27.2	27.2	27.2	26.7	27.0	
YP_512940.1	26.2	25.9	26.2	26.2	26.2	26.2	26.1	26.3	26.3	26.9	26.3	
YP_513329.1	32.5	32.5	32.5	32.5	32.5	32.5	32.6	32.6	32.6	32.5	32.5	
YP_512873.1	27.0	26.9	27.1	26.8	27.2	27.4	27.2	27.1	27.1	27.5	27.0	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514075.1	29.8	29.7	29.7	29.8	29.7	29.7	29.8	30.0	29.9	29.8	29.8	
YP_513023.1	27.3	27.2	27.2	27.2	27.7	27.7	27.4	27.3	27.4	27.5	27.2	
YP_514109.1	31.1	31.1	31.0	31.1	31.1	31.1	31.2	31.2	31.1	30.8	31.1	
YP_513913.1	28.9	29.1	28.9	29.0	29.0	28.9	29.1	29.1	29.1	28.9	29.1	
YP_514146.1	26.6	26.0	26.5	26.3	26.3	26.4	26.4	26.5	26.5	26.3	26.3	
YP_513224.1	28.0	27.8	27.9	27.9	28.0	28.0	28.1	28.0	27.9	27.7	27.9	
YP_513181.1	28.7	28.9	28.7	28.7	28.6	28.6	28.9	28.8	29.0	29.4	28.7	
YP_514000.1	31.3	31.2	31.2	31.2	31.3	31.3	31.4	31.3	31.4	31.3	31.3	
YP_514179.1	29.5	29.5	29.8	29.4	29.8	29.5	29.5	29.6	30.0	30.5	29.6	
YP_513834.1	32.9	32.9	32.9	32.9	32.9	32.9	33.0	33.0	33.0	33.2	32.9	
YP_514107.1	31.4	30.5	31.8	31.1	31.9	31.7	31.3	31.3	31.5	32.0	31.3	
YP_514370.1	29.2	29.2	29.2	29.3	29.1	29.2	29.3	29.5	29.3	29.2	29.3	
YP_513618.1	27.6	27.8	27.5	27.7	27.5	27.5	27.8	28.0	27.6	27.1	27.7	
YP_513144.1	30.9	30.9	30.8	30.9	30.8	30.8	31.1	30.9	31.0	31.1	31.0	
YP_514080.1	25.9	26.0	26.0	26.0	26.1	26.1	26.1	26.3	26.0	26.5	26.0	
YP_513565.1	29.3	29.3	29.4	29.3	29.5	29.5	29.4	29.6	29.5	29.4	29.2	
YP_513478.1	26.3	26.1	26.3	26.3	26.3	26.4	26.5	26.5	26.2	26.5	26.3	
YP_514483.1	29.9	29.9	30.1	29.9	30.3	30.3	30.3	29.9	30.2	30.4	29.8	
YP_514355.1	27.8	27.7	27.9	27.8	27.7	27.8	27.9	28.1	27.7	27.5	27.7	
YP_512895.1	34.1	34.2	34.2	34.2	34.2	34.2	34.2	34.4	34.4	34.3	34.1	
YP_513439.1	17.0	19.3	18.3	16.3	17.7	16.8	19.2	17.9	18.0	0.0	17.7	
YP_513318.1	31.9	32.0	32.1	31.9	32.0	31.9	32.1	32.2	32.1	32.1	32.0	
YP_512878.1	27.4	27.7	27.6	27.6	27.6	27.5	27.6	27.7	27.9	28.0	27.6	
YP_513376.1	36.0	36.7	36.0	36.0	36.0	36.0	36.3	36.4	36.4	36.2	36.0	
YP_513049.1	31.1	31.3	31.2	31.5	31.2	31.4	31.3	31.5	31.2	31.7	31.1	
YP_514341.1	26.3	25.8	26.7	26.2	26.7	26.7	26.5	26.0	26.8	27.9	25.8	
YP_513407.1	25.4	25.5	25.2	25.4	25.3	25.2	25.4	25.8	25.5	24.5	25.4	
YP_513450.1	26.1	26.4	26.4	26.4	26.3	26.3	26.4	26.4	26.6	26.4	26.2	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514218.1	30.1	30.1	30.4	30.2	30.3	30.3	30.3	30.4	30.4	30.9	30.2	
YP_514487.1	27.5	27.6	27.5	27.6	27.3	27.5	27.8	27.8	27.5	27.3	27.5	
YP_514226.1	27.3	27.3	27.2	27.3	27.2	27.1	27.3	27.7	27.3	26.6	27.2	
YP_513287.1	30.7	30.7	30.7	30.6	30.6	30.6	30.9	30.8	30.9	30.5	30.6	
YP_513606.1	30.9	31.1	31.0	31.0	31.0	31.0	31.1	31.2	31.1	31.1	30.9	
YP_513055.1	33.7	33.7	33.7	33.7	33.7	33.7	33.9	33.7	34.0	34.1	33.8	
YP_514400.1	29.2	29.3	29.4	29.3	29.6	29.4	29.6	29.3	29.5	29.5	29.3	
YP_514255.1	28.6	28.5	28.6	28.5	28.6	28.7	28.6	28.8	28.8	28.7	28.6	
YP_513480.1	27.3	27.4	27.3	27.3	27.4	27.4	27.4	27.6	27.4	27.4	27.4	
YP_513671.1	31.1	31.1	31.1	31.2	31.1	31.0	31.2	31.5	31.2	30.9	31.1	
YP_513082.1	24.6	24.7	24.6	24.8	24.9	24.4	24.4	25.0	25.1	23.6	24.1	
YP_513022.1	31.7	31.7	32.0	31.7	32.0	31.8	31.9	31.9	32.2	33.0	31.7	
YP_513584.1	26.2	26.1	26.2	26.2	26.3	26.2	26.3	26.6	26.2	25.9	26.2	
YP_513315.1	28.9	28.7	28.9	28.8	29.0	29.1	29.1	29.1	28.8	28.8	28.9	
YP_513793.1	30.3	30.2	30.4	30.3	30.3	30.3	30.4	30.5	30.5	30.3	30.3	
YP_512997.1	24.3	24.3	24.4	24.4	24.3	24.7	24.4	25.3	23.9	23.9	24.8	
YP_513568.1	25.9	26.3	26.5	25.8	26.3	26.5	26.4	25.9	26.9	27.0	26.1	
YP_513697.1	27.8	27.7	27.8	27.8	27.8	27.8	28.0	27.9	27.9	27.7	27.8	
YP_513718.1	29.5	29.4	29.5	29.4	29.5	29.5	29.6	29.6	29.7	29.6	29.5	
YP_513417.1	26.6	26.2	26.6	26.3	26.4	26.4	26.7	26.7	26.5	26.8	26.4	
YP_513333.1	29.7	29.7	29.8	29.7	30.0	29.8	29.9	29.7	30.2	30.7	29.7	
YP_513614.1	30.0	29.7	30.4	29.8	30.6	30.3	30.2	29.6	30.8	31.3	29.6	
YP_513615.1	30.0	29.9	29.9	30.0	29.9	30.0	30.2	30.1	29.9	29.8	30.0	
YP_514181.1	29.6	29.6	29.5	29.6	29.5	29.6	29.7	29.8	29.7	29.4	29.5	
YP_513475.1	25.0	24.9	24.8	25.0	25.3	25.1	25.3	24.9	25.1	24.9	24.7	
YP_513717.1	31.0	31.0	30.9	31.1	30.8	30.9	31.2	31.2	31.1	30.6	31.0	
YP_513184.1	27.6	27.7	27.9	27.7	28.1	27.9	27.8	27.5	28.5	29.7	27.7	
YP_514149.1	30.3	30.4	30.2	30.4	30.0	30.1	30.4	30.6	30.5	30.7	30.4	
YP_513645.1	28.2	28.4	28.2	28.1	28.2	28.1	28.4	28.5	28.4	28.2	28.3	

log2 Cyclic Loess Normalized Exclusive Intensities for DIA												
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513305.1	29.3	29.2	29.6	29.4	29.8	29.6	29.4	29.1	30.1	31.6	29.4	
YP_514413.1	29.6	29.7	29.5	29.7	29.3	29.5	29.8	30.0	29.6	29.4	29.7	
YP_514345.1	36.6	36.3	36.6	36.6	36.7	36.6	36.7	36.7	36.7	36.9	36.6	
YP_513763.1	27.1	26.3	26.8	26.7	27.0	26.9	26.8	26.7	27.2	28.3	26.6	
YP_513492.1	31.1	31.1	31.1	31.0	30.9	31.1	31.2	31.4	31.1	31.1	31.2	
YP_513489.1	24.7	24.6	24.6	24.7	24.5	24.5	24.9	24.9	24.7	24.4	24.6	
YP_513056.1	32.6	32.7	32.5	32.7	32.7	32.7	32.8	32.7	32.8	32.4	32.7	
YP_513116.1	29.6	29.7	29.5	29.6	29.5	29.6	29.7	29.8	29.8	29.8	29.6	
YP_513612.1	31.0	31.1	31.0	31.0	31.1	31.1	31.3	31.2	31.3	31.1	31.0	
YP_514215.1	25.8	25.8	25.8	26.0	25.7	25.7	25.9	26.3	25.8	25.4	26.0	
YP_513366.1	29.9	30.0	29.9	30.0	29.9	30.0	30.1	30.3	30.0	29.6	30.0	
YP_513202.1	28.1	28.3	28.0	28.3	27.9	28.0	28.4	28.5	28.2	27.6	28.1	
YP_513872.1	28.2	28.2	28.1	28.1	28.1	28.1	28.4	28.5	28.3	27.9	28.0	
YP_512978.1	26.8	26.8	26.7	26.9	26.9	26.8	26.9	27.1	26.9	26.5	26.8	
YP_513258.1	29.2	29.2	29.1	29.2	29.2	29.2	29.4	29.4	29.3	28.9	29.2	
YP_512867.1	27.1	27.1	27.0	27.2	27.1	27.1	27.3	27.5	27.1	26.8	27.2	
YP_514301.1	29.1	29.4	29.2	29.3	29.3	29.1	29.4	29.4	29.5	29.1	29.2	
YP_514421.1	30.5	30.5	30.5	30.5	30.5	30.5	30.7	30.8	30.7	30.1	30.5	
YP_512937.1	27.6	27.5	27.8	27.6	27.9	27.8	28.0	27.5	28.0	28.1	27.6	
YP_513602.1	26.4	26.1	26.3	26.4	25.9	26.0	26.4	26.8	26.2	25.7	26.3	
YP_514336.1	30.5	30.5	30.5	30.5	30.3	30.5	30.7	30.8	30.6	30.1	30.4	
YP_513101.1	34.6	34.6	34.5	34.6	34.7	34.7	34.9	34.7	34.7	34.2	34.6	
YP_514364.1	30.6	30.6	30.8	30.7	30.9	30.8	31.0	30.9	30.8	30.8	30.7	
YP_513629.1	31.9	32.1	31.8	31.9	31.7	31.8	32.2	32.2	32.1	31.7	32.0	
YP_513729.1	27.0	27.2	27.1	27.0	27.0	26.9	27.2	27.5	27.3	26.9	27.2	
YP_512987.1	31.3	31.3	31.2	31.3	31.1	31.2	31.5	31.7	31.2	31.0	31.3	
YP_513613.1	31.8	31.8	31.8	31.9	31.8	31.9	32.1	32.0	32.0	31.8	31.9	
YP_514516.1	29.9	30.0	29.9	29.9	29.9	29.8	30.1	30.0	30.3	30.1	29.8	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514303.1	31.4	31.4	31.3	31.3	31.2	31.2	31.6	31.6	31.5	31.1	31.3
YP_514424.1	32.5	32.2	32.5	32.3	32.5	32.6	32.6	32.8	32.6	32.7	32.5
YP_513261.1	29.3	29.6	29.3	29.5	29.4	29.3	29.7	29.7	29.6	29.3	29.5
YP_513457.1	25.4	25.3	25.3	25.5	25.1	25.4	25.5	25.8	25.3	24.7	25.3
YP_512829.1	32.7	32.6	32.8	32.6	32.8	32.8	32.9	33.0	32.7	32.2	32.6
YP_513426.1	31.8	31.8	31.7	31.9	31.7	31.6	32.0	32.1	31.8	31.5	31.9
YP_513198.1	30.6	30.7	30.8	30.7	30.8	30.7	31.0	30.8	31.0	30.9	30.7
YP_513122.1	30.2	30.3	30.2	30.2	30.0	30.0	30.4	30.7	30.2	29.7	30.2
YP_514168.1	31.5	31.5	31.5	31.4	31.4	31.4	31.7	31.7	31.7	31.6	31.4
YP_513050.1	33.4	33.2	33.7	33.3	33.6	33.6	33.6	33.4	34.0	34.6	33.4
YP_514068.1	29.3	29.2	29.3	29.3	29.4	29.4	29.5	29.5	29.5	29.3	29.3
YP_513981.1	31.7	31.8	31.9	31.8	32.1	32.0	32.1	31.9	32.2	32.6	31.7
YP_514125.1	32.6	32.7	33.0	32.7	32.9	32.8	32.9	32.7	33.3	33.9	32.5
YP_514043.1	26.4	26.3	26.3	26.4	26.3	26.2	26.6	26.7	26.5	26.3	26.5
YP_514524.1	31.2	31.2	31.2	31.2	31.0	31.0	31.4	31.6	31.2	30.9	31.2
YP_514563.1	23.3	23.5	23.2	23.4	23.7	23.6	23.4	23.4	24.0	24.4	23.2
YP_513275.1	25.7	25.6	25.5	25.7	25.5	25.6	25.8	26.1	25.6	25.1	25.5
YP_513880.1	30.7	30.6	30.7	30.8	30.8	30.7	30.9	31.0	30.9	30.8	30.7
YP_514419.1	30.7	30.8	31.1	30.7	31.0	30.8	31.0	30.9	31.4	32.1	30.7
YP_512811.1	30.3	30.1	30.2	30.3	30.2	30.2	30.5	30.5	30.3	30.2	30.2
YP_513259.1	30.0	30.0	29.9	30.0	30.0	29.9	30.3	30.1	30.2	30.0	30.0
YP_513975.1	30.1	30.0	30.0	30.0	30.0	30.0	30.3	30.4	30.2	29.6	30.1
YP_514260.1	28.4	28.3	28.3	28.9	28.8	29.0	28.7	28.2	29.0	28.6	28.8
YP_513797.1	28.3	28.6	28.8	28.5	28.6	28.5	28.7	28.5	29.2	30.1	28.4
YP_513121.1	26.8	26.8	26.9	26.9	26.8	26.8	27.1	27.3	26.9	26.5	26.8
YP_513494.1	28.3	28.3	28.2	28.3	28.1	28.1	28.5	28.6	28.4	28.3	28.3
YP_513229.1	29.3	29.3	29.8	29.3	29.6	29.5	29.6	29.5	30.2	31.2	29.6
YP_514003.1	26.5	26.6	26.4	26.6	26.6	26.6	26.8	26.6	27.0	27.0	26.7

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514169.1	31.3	31.3	31.2	31.3	31.4	31.3	31.6	31.1	31.8	31.9	31.3
YP_514307.1	28.6	28.4	28.5	28.7	28.3	28.4	28.8	28.9	28.7	28.1	28.8
YP_512888.1	28.8	28.9	28.8	28.7	28.8	28.9	29.0	29.1	29.1	29.2	28.9
YP_513256.1	30.8	30.6	30.8	30.7	30.7	30.7	31.0	30.9	31.1	30.9	30.7
YP_513569.1	30.1	30.1	30.3	30.3	30.2	30.2	30.5	30.3	30.5	31.0	30.2
YP_514464.1	30.0	30.1	30.1	30.0	30.1	30.1	30.3	30.4	30.3	30.1	30.0
YP_514088.1	29.5	29.5	29.5	29.6	29.6	29.5	29.7	29.7	29.9	29.7	29.4
YP_514241.1	29.4	29.3	29.2	29.3	29.4	29.5	29.7	29.5	29.6	29.6	29.5
YP_513505.1	27.4	27.4	27.5	27.5	27.6	27.5	27.7	27.7	27.8	27.5	27.4
YP_513205.1	25.8	26.0	25.9	25.9	25.8	25.9	26.2	26.1	26.2	26.3	25.9
YP_514375.1	34.1	34.1	34.1	34.1	34.2	34.1	34.5	34.3	34.4	34.1	34.2
YP_514103.1	26.4	26.5	26.5	26.4	26.2	26.3	26.6	26.9	26.7	25.9	26.4
YP_513759.1	26.7	26.7	26.8	27.1	26.5	26.7	26.9	27.2	27.0	27.2	26.5
YP_514222.1	22.3	21.6	22.1	21.9	21.9	21.7	22.5	21.6	22.6	23.4	22.0
YP_513185.1	27.4	27.4	27.4	27.3	27.4	27.3	27.6	27.6	27.7	27.3	27.4
YP_513147.1	27.2	27.2	27.1	27.2	27.3	27.2	27.4	27.4	27.6	27.9	27.2
YP_513758.1	31.8	31.7	32.1	31.9	32.1	32.0	32.2	32.1	32.2	32.4	32.0
YP_514230.1	33.3	33.4	33.2	33.4	33.3	33.3	33.5	33.5	33.7	33.1	33.3
YP_513596.1	27.4	27.5	27.5	27.5	27.5	27.4	27.8	27.8	27.8	27.4	27.5
YP_513468.1	32.8	32.8	32.7	32.8	32.7	32.7	33.1	33.2	33.0	32.3	32.8
YP_514434.1	33.2	33.1	33.1	33.2	33.2	33.1	33.4	33.4	33.3	33.3	33.1
YP_512996.1	25.6	25.7	25.7	25.7	25.4	25.4	25.8	26.1	26.0	25.7	25.5
YP_513079.1	24.5	24.4	24.8	24.3	25.2	24.9	24.8	23.9	25.9	27.9	24.6
YP_513623.1	31.5	31.5	31.4	31.5	31.3	31.4	31.8	31.8	31.7	31.4	31.4
YP_514306.1	29.4	29.5	29.5	29.5	29.3	29.3	29.8	29.6	29.8	29.6	29.4
YP_512841.1	29.8	29.9	29.9	29.8	29.9	29.8	30.1	30.1	30.2	29.9	29.9
YP_514283.1	27.8	27.7	27.8	27.7	27.8	27.7	28.0	28.0	28.1	28.0	27.8
YP_513286.1	27.8	27.8	27.7	27.8	27.4	27.6	28.0	28.3	27.8	27.0	27.6
YP_513998.1	29.1	29.1	29.5	29.2	29.3	29.2	29.4	29.5	29.8	30.4	29.2

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514013.1	30.8	30.9	30.8	30.8	30.9	30.8	31.1	31.1	31.1	30.5	30.8	
YP_514240.1	24.9	25.0	24.8	24.9	24.9	24.8	25.2	25.3	25.1	24.7	25.1	
YP_513634.1	24.5	24.6	24.5	24.6	24.4	24.4	24.8	25.0	24.8	24.1	24.4	
YP_514410.1	33.4	33.5	33.2	33.4	33.1	33.2	33.7	33.9	33.5	32.9	33.4	
YP_513282.1	25.2	25.4	25.1	25.2	25.1	25.2	25.5	25.7	25.4	25.0	25.1	
YP_514183.1	32.1	32.1	32.0	32.1	32.0	32.0	32.4	32.4	32.3	31.9	32.1	
YP_514074.1	32.0	32.1	32.1	32.1	32.1	32.1	32.4	32.3	32.4	32.0	32.1	
YP_512851.1	26.7	26.4	26.5	26.6	26.7	26.7	26.8	26.9	26.8	26.4	26.6	
YP_513559.1	29.4	29.3	29.4	29.4	29.6	29.7	29.8	29.6	29.6	29.6	29.3	
YP_513115.1	29.4	29.0	29.3	29.4	29.6	29.3	29.7	29.2	29.8	30.2	29.3	
YP_514073.1	29.5	29.5	29.6	29.5	29.7	29.6	29.8	29.7	29.9	30.0	29.4	
YP_513829.1	31.6	31.7	32.0	31.8	32.1	31.9	32.0	31.8	32.5	33.2	31.8	
YP_513714.1	28.4	28.3	28.3	28.4	28.3	28.3	28.7	28.7	28.5	28.2	28.4	
YP_512819.1	32.9	32.8	33.4	33.0	33.3	33.0	33.1	32.9	34.1	35.1	33.1	
YP_513999.1	29.1	29.2	29.0	29.1	29.1	29.0	29.4	29.4	29.4	29.0	28.9	
YP_513551.1	26.8	26.7	26.8	26.8	26.6	26.6	27.0	27.2	27.0	26.6	26.7	
YP_513441.1	28.5	28.4	28.4	28.4	28.4	28.5	28.7	28.9	28.7	28.0	28.3	
YP_514372.1	27.1	27.1	27.0	27.0	27.2	27.1	27.3	27.4	27.6	27.3	27.1	
YP_513828.1	31.4	31.6	31.5	31.7	31.4	31.5	31.8	32.0	31.6	30.8	31.6	
YP_514409.1	32.9	33.0	32.8	32.9	32.9	32.9	33.3	33.3	33.1	32.5	32.9	
YP_513425.1	32.7	32.6	32.6	32.7	32.6	32.5	33.1	32.7	33.1	32.8	32.7	
YP_513769.1	29.2	28.9	29.3	29.1	29.4	29.4	29.5	29.4	29.5	29.3	29.1	
YP_513009.1	25.1	25.2	25.0	25.0	25.1	25.4	25.6	25.0	25.6	25.8	25.0	
YP_513370.1	31.0	31.0	31.2	31.0	31.4	31.3	31.4	31.3	31.6	31.6	31.0	
YP_514484.1	29.0	29.0	28.9	28.9	28.9	28.9	29.2	29.3	29.3	28.8	28.9	
YP_514352.1	29.5	29.5	29.8	29.5	29.9	29.7	29.9	29.8	30.1	30.3	29.3	
YP_512874.1	27.6	27.6	27.9	27.7	28.7	28.2	27.9	27.7	28.5	29.8	27.9	
YP_514331.1	26.0	25.9	25.8	25.9	25.9	26.0	26.3	26.0	26.4	26.4	25.9	
YP_513891.1	28.0	28.1	28.1	28.1	28.2	28.2	28.3	28.4	28.6	28.5	28.1	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514408.1	33.1	32.9	33.1	33.0	33.1	33.2	33.4	33.4	33.3	33.3	33.2
YP_513890.1	27.5	27.6	27.6	27.6	27.6	27.5	27.9	27.8	28.0	27.5	27.6
YP_514518.1	31.5	31.5	31.4	31.5	31.5	31.4	31.8	31.9	31.7	31.3	31.5
YP_514220.1	28.9	29.1	29.0	29.0	28.7	28.8	29.3	29.5	29.3	29.0	29.0
YP_513823.1	31.6	31.6	31.6	31.7	31.6	31.6	31.9	32.1	31.9	31.4	31.5
YP_514024.1	26.0	25.9	25.9	25.9	25.7	25.9	26.2	26.5	26.1	25.6	25.8
YP_514047.1	32.5	32.4	32.4	32.5	32.3	32.3	32.7	32.8	32.7	32.0	32.3
YP_514540.1	28.5	28.4	28.5	28.5	28.3	28.4	28.8	28.9	28.8	28.5	28.5
YP_512889.1	29.8	29.8	29.7	29.8	29.7	29.8	30.1	30.3	29.9	29.4	29.8
YP_513142.1	25.7	25.5	25.7	25.7	25.4	25.5	25.9	26.3	25.7	24.7	25.7
YP_513199.1	28.8	28.8	28.6	28.7	28.7	28.6	29.1	28.8	29.3	29.1	28.6
YP_514562.1	29.7	29.8	29.7	29.8	29.8	29.8	30.2	29.9	30.1	29.8	29.9
YP_513321.1	25.2	25.4	25.5	25.4	25.7	25.4	25.7	26.0	25.6	26.1	25.2
YP_513875.1	29.7	29.8	29.8	29.8	29.9	29.9	30.0	30.2	30.2	29.9	29.8
YP_513488.1	30.4	30.3	30.4	30.4	30.6	30.5	30.8	30.7	30.7	30.5	30.4
YP_513308.1	30.0	30.0	29.9	30.0	29.9	29.9	30.3	30.4	30.3	30.1	30.0
YP_514561.1	25.3	24.6	25.4	24.9	25.7	25.9	25.4	25.6	25.4	25.2	25.3
YP_514517.1	34.0	33.8	33.9	33.8	33.8	33.9	34.2	34.3	34.3	34.0	33.9
YP_513143.1	27.0	27.0	27.0	27.2	27.0	27.0	27.4	27.4	27.4	27.4	27.2
YP_514428.1	24.4	24.6	24.0	24.5	23.7	24.0	24.9	24.7	24.6	23.8	24.5
YP_513553.1	31.8	31.9	31.7	31.8	31.7	31.7	32.2	32.1	32.1	31.7	31.8
YP_513506.1	24.4	24.7	24.3	24.4	24.8	24.8	25.0	24.8	24.8	24.4	24.4
YP_514407.1	30.9	31.0	30.9	30.9	30.8	30.8	31.2	31.4	31.2	30.7	31.0
YP_513919.1	31.5	31.6	31.6	31.5	31.5	31.5	31.9	32.0	31.8	31.4	31.6
YP_513529.1	26.8	26.8	26.7	26.8	26.6	26.8	27.2	27.3	27.0	26.7	26.9
YP_513816.1	29.6	29.4	29.6	29.5	29.6	29.5	29.9	30.0	29.8	29.7	29.7
YP_513643.1	27.1	27.3	27.0	27.2	27.0	27.0	27.5	27.7	27.3	26.7	27.2
YP_513640.1	28.7	28.7	28.8	28.7	29.0	29.0	29.1	28.8	29.4	29.7	28.7

log2 Cyclic Loess Normalized Exclusive Intensities for DIA												
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513945.1	28.8	28.8	28.6	28.8	28.6	28.7	29.1	29.2	29.0	28.6	28.8	
YP_513862.1	32.2	32.3	32.6	32.3	32.5	32.4	32.7	32.5	33.1	33.6	32.3	
YP_512999.1	26.3	26.1	26.2	26.3	26.2	26.5	26.6	26.8	26.3	25.9	26.2	
YP_513873.1	31.5	31.4	31.7	31.4	31.7	31.6	31.7	31.8	32.1	32.6	31.5	
YP_513538.1	27.6	27.7	27.5	27.8	27.6	27.6	28.2	28.4	27.3	26.9	27.9	
YP_513977.1	30.3	30.2	30.2	30.2	30.5	30.5	30.7	30.2	30.9	31.2	30.2	
YP_513622.1	31.9	31.9	31.8	31.9	31.8	32.0	32.3	32.3	32.2	31.7	31.8	
YP_514437.1	29.8	29.8	29.7	29.8	29.7	29.9	30.1	30.2	30.1	29.7	29.9	
YP_513051.1	30.1	29.4	30.0	29.9	29.7	29.8	30.2	30.5	30.0	29.6	30.0	
YP_514142.1	30.8	30.9	30.9	30.9	31.0	30.9	31.3	31.1	31.4	31.5	30.8	
YP_513169.1	30.2	30.2	30.2	30.1	30.5	30.3	30.6	30.4	30.6	30.3	30.2	
YP_513025.1	23.7	23.4	23.9	23.8	24.3	24.1	23.9	23.5	24.8	26.4	23.7	
YP_512986.1	29.1	29.2	29.1	29.1	28.9	29.1	29.6	29.6	29.4	29.2	29.2	
YP_514053.1	28.1	28.0	27.9	27.9	27.8	27.8	28.4	28.4	28.4	28.1	28.1	
YP_513255.1	29.8	29.8	29.7	29.8	29.6	29.6	30.1	30.4	30.0	29.2	29.8	
YP_513710.1	25.0	24.8	25.1	25.1	24.9	25.0	25.0	25.3	25.6	26.2	25.3	
YP_512882.1	27.0	27.0	26.9	27.1	27.1	27.0	27.3	27.5	27.2	26.5	27.1	
YP_514404.1	25.1	25.1	25.3	25.3	25.0	25.3	25.7	25.7	25.3	25.3	25.3	
YP_514242.1	26.9	26.2	27.3	27.0	27.2	27.4	27.2	27.1	27.3	28.0	27.0	
YP_514443.1	25.3	25.2	25.4	25.2	25.6	25.2	25.8	25.2	26.1	26.9	25.4	
YP_514482.1	29.6	29.3	29.5	29.5	29.4	29.4	29.9	29.9	29.8	29.6	29.5	
YP_514406.1	31.4	31.4	31.3	31.4	31.4	31.3	31.8	31.8	31.7	31.6	31.4	
YP_513090.1	24.4	23.9	24.3	23.8	23.8	24.0	24.6	24.7	24.5	23.7	24.1	
YP_512975.1	29.5	29.3	29.3	29.4	29.3	29.4	29.8	30.0	29.6	28.9	29.4	
YP_514231.1	33.1	32.9	33.1	33.0	33.1	33.1	33.4	33.5	33.4	33.1	33.0	
YP_512903.1	28.8	28.9	28.7	28.8	28.6	28.7	29.2	29.3	29.2	28.9	28.8	
YP_513924.1	26.5	26.7	26.6	26.7	27.0	26.7	26.7	26.6	27.8	27.5	26.7	
YP_513757.1	32.8	32.8	32.8	32.8	32.8	32.8	33.2	33.2	33.2	32.9	32.9	
YP_512983.1	24.0	23.6	23.8	24.2	23.7	24.4	24.4	24.4	23.9	24.5	24.1	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_512868.1	28.4	28.2	28.4	28.3	28.4	28.4	28.7	28.8	28.7	28.2	28.3
YP_514236.1	28.5	28.4	28.4	28.4	28.3	28.4	28.9	28.9	28.8	28.3	28.4
YP_514200.1	32.8	32.2	32.8	32.6	32.8	32.7	33.1	33.0	33.0	32.9	32.6
YP_514232.1	25.5	25.6	25.7	25.6	25.5	25.6	26.1	26.0	26.0	26.2	25.8
YP_512832.1	27.5	27.2	27.5	27.3	27.4	27.2	27.9	27.8	27.9	27.2	27.3
YP_513761.1	28.2	28.1	28.3	28.2	28.2	28.2	28.6	28.7	28.6	28.3	28.2
YP_513716.1	33.1	33.1	33.2	33.1	33.3	33.2	33.6	33.4	33.7	33.8	33.1
YP_513200.1	28.9	29.0	28.9	29.1	29.1	29.0	29.4	29.3	29.5	29.4	29.1
YP_513641.1	30.9	30.9	31.0	30.8	31.2	31.0	31.3	31.2	31.6	31.4	30.9
YP_513603.1	28.3	28.3	28.3	28.3	28.4	28.4	28.8	28.7	28.9	28.4	28.4
YP_513196.1	24.6	23.8	24.6	24.6	24.3	24.4	25.1	23.9	25.2	25.6	24.0
YP_514026.1	25.1	25.1	25.2	25.1	25.2	25.3	25.5	25.5	25.7	25.8	25.0
YP_513466.1	29.0	28.8	28.9	28.9	29.1	29.0	29.5	29.2	29.4	29.2	29.0
YP_513451.1	27.0	27.0	27.1	27.2	26.8	27.2	27.6	27.6	27.2	27.0	27.3
YP_513730.1	28.0	27.9	28.0	27.9	28.0	28.2	28.4	28.5	28.4	28.1	28.0
YP_514430.1	27.4	27.4	27.2	27.3	27.2	27.2	27.9	27.8	27.7	26.7	27.4
YP_513232.1	25.4	25.4	25.5	25.3	25.5	25.7	25.9	26.0	25.8	25.7	25.3
YP_514333.1	28.2	28.3	28.1	28.1	28.1	28.1	28.7	28.6	28.7	28.2	28.1
YP_513161.1	25.7	25.7	25.9	25.8	25.7	26.0	26.2	26.2	26.4	25.8	25.5
YP_513495.1	28.0	28.0	28.0	27.9	27.9	28.1	28.5	28.5	28.5	28.1	27.9
YP_513996.1	28.6	28.7	28.6	28.5	28.5	28.6	29.0	29.2	29.2	28.4	28.5
YP_512948.1	27.1	27.1	27.3	27.1	27.3	27.3	27.6	27.5	27.9	26.0	26.9
YP_513547.1	29.6	29.2	29.7	29.3	29.6	29.7	29.7	29.8	30.5	31.6	29.4
YP_513211.1	29.7	29.5	29.8	29.7	29.9	29.8	30.2	29.9	30.4	30.5	29.8
YP_513726.1	27.4	27.4	27.6	27.5	27.9	27.8	28.2	27.7	28.0	28.8	27.6
YP_514175.1	27.3	27.4	27.2	27.4	26.9	27.0	27.7	28.0	27.8	26.7	27.4
YP_513253.1	26.8	26.8	26.6	26.7	26.8	26.8	27.1	27.2	27.3	26.8	26.8
YP_513179.1	25.5	25.7	25.7	25.5	26.3	26.0	26.3	26.0	26.1	25.7	25.9

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_513827.1	30.9	30.8	30.9	30.9	31.1	31.1	31.4	31.4	31.5	31.1	30.9
YP_514280.1	19.9	21.2	19.4	20.9	20.9	20.6	20.2	19.8	21.9	20.9	20.0
YP_513074.1	30.4	30.3	30.7	30.4	30.8	30.7	30.9	31.0	31.1	31.3	30.4
YP_513250.1	26.7	26.8	27.2	26.7	27.2	26.9	27.2	26.8	28.1	28.9	26.9
YP_514076.1	24.5	24.6	24.7	24.7	24.5	24.5	25.2	25.1	25.0	23.7	24.5
YP_514219.1	28.1	27.9	28.0	28.0	28.0	28.1	28.6	28.5	28.5	27.6	27.9
YP_513760.1	27.2	27.2	27.2	27.2	27.2	27.2	27.8	27.6	27.7	27.4	27.1
YP_514119.1	31.0	31.0	31.0	31.0	30.9	30.9	31.5	31.5	31.4	30.7	30.9
YP_514115.1	31.0	31.0	31.0	31.0	30.9	30.9	31.5	31.5	31.4	30.7	30.9
YP_513260.1	25.1	25.2	25.2	25.4	25.2	25.2	25.6	25.6	25.8	25.6	25.4
YP_514191.1	29.2	29.4	29.2	29.3	29.2	29.2	29.8	29.9	29.7	29.2	29.4
YP_514224.1	27.1	27.3	27.1	26.8	27.0	27.2	27.6	27.7	27.8	26.6	26.7
YP_513262.1	27.9	27.9	27.9	28.0	27.9	28.0	28.4	28.3	28.5	28.3	28.2
YP_513868.1	30.5	30.4	30.5	30.6	30.4	30.4	31.0	31.0	31.0	30.5	30.6
YP_513770.1	27.2	27.2	27.2	27.2	27.3	27.2	27.6	27.5	28.1	28.0	27.2
YP_513598.1	25.9	25.9	26.0	25.9	26.2	26.3	26.5	26.3	26.6	26.5	26.0
YP_514558.1	28.1	28.0	28.2	28.1	28.8	28.7	28.8	28.1	28.9	29.1	28.0
YP_514338.1	28.2	27.9	28.3	28.0	28.4	28.3	28.8	28.2	29.1	29.5	28.0
YP_513036.1	30.2	30.1	30.4	30.1	30.6	30.6	30.9	29.9	31.5	32.2	30.3
YP_513353.1	28.8	28.6	28.8	28.5	29.0	29.1	29.4	29.1	29.4	29.1	28.7
YP_513390.1	28.9	28.8	28.7	28.7	28.8	28.7	29.3	29.3	29.4	29.0	28.8
YP_514098.1	29.5	29.5	29.5	29.5	29.5	29.4	29.9	30.3	30.0	29.4	29.6
YP_513531.1	27.0	27.0	27.2	27.0	27.3	27.1	27.5	27.6	27.6	27.2	27.0
YP_514126.1	26.9	26.9	26.8	26.9	26.6	26.7	27.5	27.5	27.4	27.0	27.1
YP_513117.1	29.3	28.6	29.3	28.9	29.4	29.7	29.7	29.8	29.4	29.3	29.4
YP_514353.1	27.2	27.2	27.2	27.2	27.3	27.3	27.7	27.7	27.9	27.2	27.2
YP_513482.1	24.0	23.8	24.0	24.3	24.4	24.1	24.7	23.7	25.1	26.0	24.0
YP_514177.1	29.5	29.2	29.4	29.4	29.5	29.4	29.9	29.9	30.0	29.5	29.3

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514065.1	26.5	25.9	26.9	26.0	27.2	27.2	27.1	26.8	27.1	27.0	25.9
YP_514541.1	26.2	26.4	26.3	26.5	26.5	26.4	26.9	26.9	26.9	26.9	26.2
YP_513732.1	14.9	17.9	18.8	18.1	18.7	17.6	18.0	16.1	19.2	18.6	18.4
YP_513442.1	26.8	26.7	26.8	26.8	26.9	26.8	27.4	27.1	27.5	27.4	26.9
YP_514167.1	29.7	29.8	29.6	29.7	29.7	29.7	30.2	30.5	30.2	29.4	29.7
YP_514273.1	24.4	24.0	24.3	24.4	24.4	24.1	24.7	24.9	24.9	24.5	24.3
YP_514086.1	25.9	26.1	25.9	26.0	25.8	25.9	26.5	26.8	26.4	25.4	25.9
YP_514509.1	32.0	32.0	31.9	32.1	31.9	31.9	32.6	32.6	32.5	31.9	31.9
YP_513444.1	25.5	25.0	25.7	25.2	25.5	25.9	26.0	26.1	25.9	24.9	25.5
YP_513089.1	24.9	24.6	24.9	24.7	25.0	25.0	25.3	25.5	25.4	25.1	24.9
YP_513874.1	33.8	33.8	34.2	33.9	34.5	34.3	34.6	34.1	34.9	35.4	33.9
YP_513039.1	31.2	31.3	31.3	31.2	31.7	31.4	32.2	31.2	32.3	32.9	31.2
YP_514405.1	31.2	31.3	31.1	31.2	31.2	31.1	31.7	31.9	31.8	31.3	31.1
YP_513361.1	30.6	30.6	30.6	30.5	30.7	30.7	31.3	31.2	31.2	30.5	30.5
YP_513625.1	29.9	30.0	29.9	30.0	29.9	29.9	30.6	30.6	30.5	29.9	29.9
YP_514182.1	26.0	26.1	26.7	26.4	26.7	26.2	26.6	26.6	27.5	28.4	26.6
YP_513916.1	29.9	30.3	30.3	30.2	30.2	30.2	30.6	30.8	30.9	30.9	30.1
YP_514433.1	29.4	29.6	29.4	29.6	29.4	29.5	30.1	30.2	30.1	29.5	29.6
YP_513309.1	29.4	29.4	29.3	29.4	29.3	29.5	30.1	30.1	29.9	29.3	29.3
YP_513765.1	25.5	25.4	25.3	25.4	25.5	25.3	26.0	26.0	26.1	25.4	25.2
YP_514425.1	26.6	25.5	25.7	25.4	26.3	26.3	26.9	25.9	26.9	27.8	25.5
YP_513150.1	22.5	22.5	22.3	22.3	22.3	22.9	23.0	23.0	23.2	23.0	22.6
YP_513496.1	27.6	27.7	27.4	27.6	27.4	27.4	28.1	28.3	28.2	27.2	27.6
YP_514302.1	26.2	26.3	26.2	26.2	26.0	26.2	26.8	26.9	26.9	26.4	26.2
YP_513978.1	24.8	24.4	24.4	24.4	24.5	24.5	25.2	25.0	25.3	24.9	24.3
YP_513364.1	29.2	28.9	29.1	29.1	29.3	29.3	29.7	29.8	29.6	29.2	29.1
YP_514477.1	31.4	31.4	31.4	31.4	31.5	31.4	32.1	32.1	32.0	31.5	31.4
YP_514285.1	24.3	24.3	24.5	24.4	24.8	24.8	25.0	24.7	25.4	25.9	24.5

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514079.1	23.3	23.3	23.8	24.2	23.8	23.5	24.3	24.0	24.0	23.5	23.4	
YP_514422.1	34.0	33.9	33.9	34.0	34.0	34.0	34.6	34.6	34.6	33.8	34.0	
YP_513762.1	28.0	27.9	28.1	27.9	28.0	28.0	28.5	28.7	28.7	28.0	27.8	
YP_513616.1	27.6	27.5	27.5	27.4	27.2	27.5	28.1	28.2	28.1	27.0	27.3	
YP_513322.1	29.5	29.5	29.4	29.6	29.4	29.4	30.2	30.2	30.0	29.2	29.5	
YP_514067.1	27.4	27.6	27.3	27.6	27.4	27.5	28.0	28.1	28.2	27.2	27.5	
YP_514463.1	30.0	29.7	30.1	29.8	30.5	30.4	30.8	30.2	30.8	31.0	29.9	
YP_513254.1	28.6	28.7	28.5	28.6	28.4	28.4	29.3	29.4	29.1	27.9	28.6	
YP_512894.1	25.8	25.8	25.9	25.6	26.5	26.5	26.5	26.3	26.8	27.0	25.6	
YP_513508.1	25.1	24.9	25.4	24.8	26.6	25.7	26.2	24.7	26.5	28.0	24.8	
YP_514481.1	26.2	26.0	26.0	26.4	26.6	26.8	26.8	26.3	27.1	27.5	26.4	
YP_513383.1	21.7	20.9	21.8	21.6	22.7	21.6	23.3	20.2	23.0	24.3	21.8	
YP_513042.1	31.0	31.0	31.4	31.0	31.8	31.4	31.9	31.1	32.4	33.3	31.0	
YP_513794.1	26.6	26.6	26.6	26.6	26.6	26.6	27.3	27.4	27.1	26.5	26.7	
YP_513733.1	24.7	22.8	25.0	23.5	25.3	25.3	23.7	25.4	25.5	25.4	23.5	
YP_513343.1	30.1	29.9	30.0	30.1	30.1	30.2	30.7	30.7	30.7	30.3	30.0	
YP_514519.1	24.9	24.9	25.0	24.8	25.4	25.3	25.8	25.3	25.8	25.5	25.0	
YP_514399.1	34.1	33.9	34.0	34.1	33.8	34.0	34.7	34.9	34.5	33.5	34.1	
YP_513078.1	28.9	29.0	28.9	28.9	29.0	29.1	29.6	29.7	29.6	29.0	28.9	
YP_513575.1	23.4	23.4	23.5	23.4	23.1	23.6	24.3	24.4	23.7	22.4	23.8	
YP_513979.1	26.5	26.4	26.3	26.5	26.2	26.3	27.2	27.3	26.8	25.7	26.4	
YP_514055.1	28.2	28.6	28.9	28.4	28.9	28.7	29.1	29.0	29.8	30.4	28.5	
YP_514429.1	25.3	25.3	25.3	25.4	26.0	25.8	26.2	25.7	26.2	26.4	25.4	
YP_513789.1	23.9	24.0	21.4	22.0	24.3	20.4	23.6	24.1	23.9	23.9	22.4	
YP_512949.1	25.2	24.7	24.9	25.0	25.2	25.0	25.6	25.6	25.8	25.2	24.7	
YP_513725.1	31.0	30.7	31.5	30.9	31.9	31.8	32.2	31.3	32.0	32.3	31.1	
YP_513349.1	30.8	30.5	30.7	30.8	30.7	30.8	31.7	31.3	31.3	30.7	30.8	
YP_512929.1	29.0	29.0	29.0	29.0	29.0	28.9	29.8	29.8	29.5	28.7	29.0	
YP_513149.1	23.4	21.7	23.7	22.6	24.3	23.9	23.8	23.6	23.6	23.8	23.0	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514454.1	28.7	28.7	28.6	28.6	28.5	28.5	29.3	29.6	29.4	28.5	28.9	
YP_512938.1	26.3	26.3	26.4	26.4	26.8	26.6	27.1	26.5	27.7	28.1	26.2	
YP_513454.1	31.4	31.2	31.5	31.4	31.8	31.6	32.3	31.8	32.3	32.3	31.4	
YP_513289.1	28.9	28.4	29.1	28.4	29.2	29.4	29.5	29.6	29.5	29.3	28.7	
YP_514084.1	26.6	26.5	26.7	26.7	26.7	26.8	27.4	27.0	27.6	27.3	26.8	
YP_514173.1	23.5	23.2	23.4	24.2	23.6	23.9	24.3	24.1	24.0	24.1	23.9	
YP_513707.1	19.0	17.1	18.6	18.5	18.9	19.2	19.7	18.5	18.8	19.6	0.0	
YP_513934.1	19.5	19.6	20.0	19.9	20.5	18.1	20.5	21.0	19.8	20.4	19.6	
YP_513755.1	25.6	25.6	25.4	25.5	25.9	25.7	26.2	26.4	26.3	26.0	25.4	
YP_513670.1	20.2	19.4	19.7	19.7	19.6	19.6	20.0	20.7	20.8	16.7	18.8	
YP_514247.1	29.4	28.6	29.8	28.9	30.0	29.9	29.9	29.9	30.4	31.1	29.0	
YP_513722.1	24.2	23.5	23.7	23.6	23.5	23.8	24.5	24.7	24.6	23.2	23.4	
YP_513942.1	28.3	27.9	28.4	28.1	28.9	28.7	29.1	28.7	29.1	28.8	28.0	
YP_514082.1	26.1	26.3	26.2	26.3	26.2	26.0	27.0	27.0	27.0	26.1	26.4	
YP_513576.1	25.3	24.9	25.3	25.1	25.6	25.5	26.0	25.6	26.2	26.3	25.1	
YP_513844.1	32.2	31.9	32.0	32.0	32.0	32.1	32.8	32.9	32.8	31.9	32.1	
YP_512912.1	32.2	31.9	32.0	32.0	32.0	32.1	32.8	32.9	32.8	31.9	32.1	
YP_514235.1	26.9	26.9	26.9	26.8	26.9	27.0	27.7	27.7	27.6	26.7	26.8	
YP_513571.1	29.3	28.5	29.3	29.0	29.4	29.4	30.0	29.9	29.7	29.5	29.4	
YP_514180.1	28.2	28.1	28.2	28.2	28.5	28.4	29.1	28.8	29.1	28.5	28.2	
YP_514108.1	33.0	32.4	33.5	32.5	33.9	33.8	33.9	33.3	34.2	34.8	32.8	
YP_514525.1	25.4	25.8	25.3	25.3	26.3	25.6	26.5	26.7	25.6	25.6	25.9	
YP_513021.1	27.7	27.3	27.8	27.5	27.7	27.8	28.4	28.6	28.4	27.6	27.8	
YP_514061.1	31.5	31.7	31.7	31.6	31.7	31.6	32.5	32.4	32.5	32.2	31.6	
YP_513826.1	32.7	32.5	32.8	32.6	32.7	32.7	33.5	33.7	33.4	32.4	32.6	
YP_514368.1	25.4	25.4	25.8	25.6	26.0	25.8	26.4	26.1	26.6	27.1	25.6	
YP_513319.1	28.8	28.8	28.7	28.8	28.7	28.7	29.6	29.8	29.4	28.6	28.8	
YP_514174.1	32.3	31.4	32.5	31.8	32.6	32.7	32.9	33.1	32.8	32.4	32.2	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA										
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2
YP_514411.1	32.3	32.3	32.3	32.3	32.4	32.4	33.3	33.0	33.2	32.6	32.4
YP_514432.1	30.0	30.1	30.0	30.0	30.2	30.1	31.0	30.7	31.0	30.4	30.1
YP_514334.1	28.1	27.6	28.1	27.8	28.3	28.3	28.8	28.8	28.7	28.2	28.1
YP_514512.1	27.7	27.5	27.6	27.6	28.0	27.8	28.8	27.6	29.0	29.5	27.5
YP_514124.1	30.2	30.1	30.2	30.2	30.2	30.2	31.0	31.1	31.0	30.0	30.2
YP_513528.1	27.3	27.2	27.2	27.1	27.5	27.6	28.2	28.0	28.1	27.3	27.3
YP_513651.1	26.5	26.5	26.7	26.5	26.8	26.8	27.6	27.3	27.4	26.6	26.6
YP_514445.1	26.0	25.8	26.0	25.9	27.0	26.9	27.2	26.2	27.1	27.3	25.9
YP_514298.1	27.5	27.5	27.3	27.5	27.4	27.4	28.3	28.4	28.4	27.6	27.5
YP_513509.1	23.7	23.6	23.0	23.5	23.4	23.4	24.6	24.5	24.0	23.4	23.4
YP_514325.1	21.1	20.3	22.0	19.6	21.7	21.9	21.9	22.3	21.9	21.4	20.6
YP_512842.1	27.7	27.8	27.7	27.7	27.6	27.6	28.6	28.7	28.6	27.9	27.7
YP_513605.1	28.1	28.1	28.1	28.3	28.2	28.1	29.0	29.1	29.0	27.7	28.0
YP_514300.1	22.2	23.0	22.7	22.2	22.6	22.1	23.8	23.7	23.1	22.8	21.5
YP_513573.1	27.2	27.2	27.4	27.2	27.8	27.6	28.1	28.1	28.3	28.2	27.4
YP_512931.1	29.1	29.1	29.1	29.2	29.0	29.0	30.0	30.1	29.9	28.9	29.1
YP_513350.1	25.2	25.1	25.0	24.9	24.7	24.5	26.1	26.2	25.9	25.5	25.2
YP_513453.1	25.0	24.3	24.6	24.7	24.7	25.7	25.4	25.8	25.6	26.3	24.3
YP_514414.1	33.1	32.9	32.9	33.0	32.9	32.9	34.0	34.0	33.7	32.5	33.1
YP_514225.1	22.9	23.1	23.4	23.4	23.4	23.0	24.3	23.9	24.1	23.7	22.8
YP_514081.1	27.9	27.9	28.0	28.1	28.1	28.1	28.9	29.0	28.8	27.8	28.0
YP_513865.1	27.1	27.2	27.2	27.2	27.1	27.1	28.1	28.3	28.1	26.5	27.0
YP_513334.1	27.0	27.0	27.1	27.1	27.1	27.2	28.0	28.0	28.0	26.9	27.1
YP_512961.1	28.8	28.4	28.8	28.6	29.9	29.6	30.2	28.6	30.2	30.3	28.7
YP_513443.1	22.9	22.3	23.3	22.8	24.7	24.3	24.0	22.9	24.4	24.5	22.5
YP_513464.1	23.1	23.3	22.9	23.3	22.8	22.7	24.3	24.1	23.9	22.2	23.1
YP_513607.1	25.3	25.5	25.4	25.4	25.6	25.6	26.4	26.4	26.5	25.9	25.3
YP_513412.1	22.5	22.4	23.2	22.6	25.0	23.5	24.4	22.0	24.6	24.9	21.8
YP_513728.1	28.7	28.8	28.7	28.7	28.8	28.7	29.7	29.8	29.7	29.1	28.7

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_513791.1	24.3	24.0	24.4	24.3	24.8	24.6	25.5	24.6	25.7	26.1	24.4	
YP_512823.1	24.3	23.7	26.0	24.2	24.8	24.6	25.3	25.7	26.0	25.3	24.0	
YP_513027.1	29.8	29.4	30.0	29.6	30.5	30.4	31.1	29.8	31.4	32.0	29.8	
YP_514544.1	26.0	26.0	26.2	26.0	26.1	25.9	26.1	29.1	26.1	25.9	25.9	
YP_512824.1	30.0	29.2	30.3	29.3	31.1	31.0	30.7	30.4	31.4	32.1	29.7	
YP_513228.1												
YP_514021.1_s hared	28.3	28.1	28.3	0.0	0.0	0.0	29.1	29.3	29.3	0.0	0.0	
YP_514436.1	29.6	29.6	29.9	29.7	30.4	30.3	30.8	30.6	30.9	31.0	29.6	
YP_514145.1	28.9	28.7	29.3	28.8	29.8	29.5	30.0	29.1	31.0	32.3	29.0	
YP_514132.1	19.8	19.1	19.5	19.8	20.3	19.5	21.5	19.6	20.6	19.6	18.3	
YP_513970.1	23.0	23.0	23.0	23.0	24.3	23.8	24.3	23.5	24.4	24.5	23.3	
YP_514457.1	20.3	21.1	20.8	20.7	19.2	19.8	21.8	22.5	21.1	20.3	20.9	
YP_513503.1	28.3	28.1	28.8	28.2	28.9	28.5	29.4	29.1	30.1	30.6	28.3	
YP_513120.1	26.3	25.8	26.3	26.1	27.1	27.2	27.3	27.0	27.4	27.7	26.3	
YP_514054.1	30.5	30.6	30.4	30.5	30.5	30.4	31.6	31.7	31.6	30.3	30.6	
YP_514234.1	24.7	24.5	24.7	24.6	24.9	24.7	25.8	25.8	25.7	24.4	24.7	
YP_513156.1	25.4	25.1	24.8	25.8	24.5	25.1	26.2	26.4	26.0	25.8	24.8	
YP_513436.1	26.1	25.3	26.6	25.7	27.1	27.1	27.2	26.9	27.3	27.4	25.8	
YP_514381.2	26.7	26.5	26.5	26.5	26.8	26.7	27.8	26.9	28.3	28.9	26.6	
YP_513864.1	28.0	28.2	28.1	28.1	28.0	28.0	29.2	29.4	29.2	27.4	27.8	
YP_513825.1	32.0	31.0	32.2	31.3	32.4	32.4	32.9	32.8	32.9	32.9	31.8	
YP_512881.1	21.4	21.7	21.9	22.8	22.5	22.7	22.8	23.2	22.5	22.0	22.1	
YP_513931.1	23.8	23.6	24.3	24.3	25.8	25.1	26.0	23.9	25.4	25.7	24.1	
YP_514416.1	30.4	30.1	30.5	30.3	31.0	30.9	31.7	31.2	31.7	31.3	30.4	
YP_512974.1	28.8	29.0	29.2	29.2	29.9	29.5	30.2	30.0	30.4	30.2	29.5	
YP_513490.1	20.0	22.0	21.0	21.4	21.6	22.3	22.6	21.7	22.4	21.3	21.6	
YP_514044.1	25.3	25.1	25.7	25.2	26.1	25.9	26.7	26.5	26.7	26.1	25.5	
YP_512955.1	21.0	20.3	19.9	20.4	21.4	21.3	22.0	21.3	21.8	21.6	20.8	

	log2 Cyclic Loess Normalized Exclusive Intensities for DIA											
id	WT.1	WT.2	WT.3	delt_rpsU1 .1	delt_rpsU1 .2	delt_rpsU1 .3	delt_rpsU2 .1	delt_rpsU2 .2	delt_rpsU2 .3	delt_rpsU3 .1	delt_rpsU3 .2	
YP_514346.1	33.8	33.7	34.0	33.7	34.2	33.9	35.0	35.0	35.3	35.0	33.7	
YP_514049.1	29.3	29.0	29.2	29.3	29.1	29.2	30.5	30.5	30.4	29.4	29.3	
YP_513867.1	25.6	25.5	26.0	25.6	26.4	26.1	26.9	26.2	28.0	28.9	25.8	
YP_513320.1	24.5	24.5	24.4	24.5	24.4	24.1	25.8	26.0	25.7	23.9	24.4	
YP_513340.1	21.2	21.0	20.9	21.5	21.5	21.8	21.8	22.3	23.3	25.2	21.3	
YP_513609.1	23.1	22.5	23.4	23.2	24.9	24.7	24.8	23.7	24.8	24.8	22.9	
YP_512970.1	28.4	28.1	28.8	28.3	29.5	29.0	29.9	28.5	31.2	33.0	28.4	
YP_514066.1	26.5	25.8	27.1	26.1	28.3	28.0	28.2	26.8	28.9	30.0	26.3	
YP_514172.1	26.2	26.2	26.3	26.2	26.4	26.1	27.6	27.8	27.8	26.3	26.2	
YP_514033.1	24.3	24.1	24.4	24.5	24.3	23.9	25.9	26.0	25.9	24.7	24.0	
YP_514507.1	25.9	25.5	26.1	25.6	27.7	27.3	28.2	26.5	27.9	27.7	25.8	
YP_514456.1	27.8	27.7	27.6	27.7	27.6	27.8	29.4	29.5	29.3	27.8	28.0	
YP_514403.1	25.7	25.6	26.0	25.5	26.2	25.9	27.5	27.2	28.5	28.1	25.6	
YP_514363.1	22.7	22.6	23.1	22.3	22.7	22.4	24.7	24.8	24.9	22.7	23.1	
YP_513415.1	17.8	18.9	19.3	18.9	19.8	19.7	20.4	21.6	19.9	17.9	19.2	
YP_513633.1	19.3	17.7	20.3	18.3	21.1	21.0	22.0	19.9	22.1	20.7	19.0	
YP_513617.1	29.3	28.9	29.5	29.1	30.6	30.1	31.8	30.2	33.5	33.8	29.2	
YP_513822.1	27.7	27.2	27.8	27.4	28.0	28.0	30.2	30.0	30.7	29.8	27.5	
YP_514493.1	18.8	18.6	0.0	20.2	19.8	20.1	16.5	18.7	18.6	17.8	19.3	
YP_512942.1	20.8	19.9	20.7	21.7	24.4	25.0	27.1	24.6	27.3	26.1	20.3	
YP_514339.1	16.4	0.0	14.8	16.9	14.8	14.6	15.1	17.6	17.0	0.0	14.4	

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513747.1	33.1	0.34	18.71	1.0E+00	-32.44	18.71	3.8E-21	0.64	18.71	6.0E-01
YP_513580.1	0.0	0.35	13.64	1.0E+00	-10.89	13.64	1.4E-01	-5.46	13.64	6.3E-01
YP_513220.1	15.0	-0.65	16.46	1.0E+00	-5.98	16.46	1.4E-01	-0.01	16.46	1.0E+00
YP_513851.1	24.1	-0.55	23.30	1.0E+00	-2.39	23.30	9.6E-05	0.40	23.30	6.3E-01
YP_512919.1	24.1	-0.55	23.30	1.0E+00	-2.39	23.30	9.6E-05	0.40	23.30	6.3E-01
YP_514254.1	25.3	-0.41	25.13	1.0E+00	-2.14	25.13	1.3E-03	-0.43	25.13	6.3E-01
YP_513010.1	22.5	-0.02	22.80	1.0E+00	-1.84	22.80	5.8E-06	-0.63	22.80	6.0E-01
YP_513017.1	25.1	-0.10	25.01	1.0E+00	-1.82	25.01	7.7E-07	-0.19	25.01	6.3E-01
YP_513601.1	21.2	-0.37	20.77	1.0E+00	-1.79	20.77	3.6E-03	0.06	20.77	9.5E-01
YP_513628.1	16.6	-0.20	18.17	1.0E+00	-1.78	18.17	4.6E-01	-1.85	18.17	6.3E-01
YP_514496.1	26.8	-0.12	26.23	1.0E+00	-1.75	26.23	1.2E-03	-0.22	26.23	7.3E-01
YP_513787.1	30.2	-0.01	29.86	1.0E+00	-1.42	29.86	1.9E-06	0.16	29.86	6.3E-01
YP_514317.1	24.9	-0.20	24.73	1.0E+00	-1.42	24.73	3.6E-04	-0.30	24.73	6.3E-01
YP_513786.1	23.4	-0.20	23.77	1.0E+00	-1.40	23.77	6.8E-05	-0.37	23.77	6.0E-01
YP_514023.1	24.0	-0.63	22.65	1.0E+00	-1.38	22.65	3.7E-01	-0.06	22.65	9.8E-01
YP_513363.1	23.9	-0.19	23.94	1.0E+00	-1.37	23.94	1.1E-02	-0.59	23.94	6.1E-01
YP_514324.1	19.6	-0.13	19.54	1.0E+00	-1.37	19.54	7.6E-02	-0.89	19.54	6.0E-01
YP_513465.1	26.5	-0.11	26.30	1.0E+00	-1.36	26.30	1.3E-08	-0.09	26.30	6.3E-01
YP_513000.1	17.5	-0.81	16.47	1.0E+00	-1.36	16.47	8.0E-01	-0.84	16.47	8.9E-01
YP_513080.1	24.1	0.20	24.14	1.0E+00	-1.34	24.14	5.8E-04	-0.18	24.14	7.0E-01
YP_514527.1	20.1	-0.36	19.96	1.0E+00	-1.32	19.96	1.1E-02	-0.84	19.96	6.0E-01
YP_514530.1	24.0	-0.23	24.06	1.0E+00	-1.28	24.06	2.6E-03	-0.34	24.06	6.3E-01
YP_512896.1	29.3	0.33	28.69	1.0E+00	-1.28	28.69	1.6E-04	0.30	28.69	6.1E-01
YP_513245.1	27.3	-0.06	27.03	1.0E+00	-1.27	27.03	9.7E-06	-0.05	27.03	8.6E-01
YP_514476.1	20.0	-0.13	19.28	1.0E+00	-1.27	19.28	2.0E-01	-1.09	19.28	6.1E-01
YP_512853.1	30.8	0.02	30.62	1.0E+00	-1.26	30.62	5.3E-06	0.06	30.62	8.4E-01
YP_513848.1	30.1	0.00	29.78	1.0E+00	-1.24	29.78	5.9E-07	0.02	29.78	9.4E-01
YP_512916.1	30.1	0.00	29.78	1.0E+00	-1.24	29.78	5.9E-07	0.02	29.78	9.4E-01
YP_513849.1	26.3	-0.15	25.74	1.0E+00	-1.20	25.74	1.6E-02	-0.15	25.74	8.2E-01
YP_512917.1	26.3	-0.15	25.74	1.0E+00	-1.20	25.74	1.6E-02	-0.15	25.74	8.2E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513347.1	26.8	0.07	26.82	1.0E+00	-1.19	26.82	1.0E-04	0.22	26.82	6.2E-01
YP_513542.1	26.5	-0.12	25.97	1.0E+00	-1.16	25.97	6.1E-04	0.17	25.97	6.7E-01
YP_514284.1	22.4	-0.23	22.41	1.0E+00	-1.13	22.41	2.0E-02	-0.21	22.41	7.4E-01
YP_512985.1	18.4	-1.29	18.00	1.0E+00	-1.12	18.00	8.7E-01	-2.59	18.00	6.8E-01
YP_514131.1	25.5	0.00	25.29	1.0E+00	-1.12	25.29	4.6E-05	-0.13	25.29	6.7E-01
YP_513847.1	27.6	-0.06	27.17	1.0E+00	-1.12	27.17	3.7E-08	0.12	27.17	6.0E-01
YP_512915.1	27.6	-0.06	27.17	1.0E+00	-1.12	27.17	3.7E-08	0.12	27.17	6.0E-01
YP_513137.1	24.0	-1.25	23.30	1.0E+00	-1.08	23.30	3.0E-01	-0.08	23.30	9.6E-01
YP_513268.1	22.6	0.39	22.47	1.0E+00	-1.07	22.47	4.2E-02	-0.05	22.47	9.6E-01
YP_513402.1	23.1	-0.20	23.29	1.0E+00	-1.05	23.29	6.1E-03	-0.55	23.29	6.0E-01
YP_513471.1	21.7	-0.16	21.35	1.0E+00	-1.03	21.35	4.8E-03	-0.08	21.35	8.7E-01
YP_512943.1	25.4	-0.10	24.98	1.0E+00	-1.02	24.98	1.4E-01	0.02	24.98	9.8E-01
YP_513448.1	23.6	-0.26	23.81	1.0E+00	-1.02	23.81	1.5E-02	-0.38	23.81	6.2E-01
YP_514358.1	26.0	-0.10	26.11	1.0E+00	-1.01	26.11	2.8E-05	-0.17	26.11	6.2E-01
YP_513899.1	26.6	-0.05	26.81	1.0E+00	-1.01	26.81	1.1E-03	-0.30	26.81	6.1E-01
YP_514486.1	23.9	-0.27	24.03	1.0E+00	-0.98	24.03	3.4E-02	-0.30	24.03	6.3E-01
YP_513856.1	30.0	-0.02	29.72	1.0E+00	-0.98	29.72	6.8E-07	0.00	29.72	1.0E+00
YP_512924.1	30.0	-0.02	29.72	1.0E+00	-0.98	29.72	6.8E-07	0.00	29.72	1.0E+00
YP_513850.1	30.3	-0.10	29.95	1.0E+00	-0.97	29.95	1.9E-06	-0.03	29.95	8.7E-01
YP_512918.1	30.3	-0.10	29.95	1.0E+00	-0.97	29.95	1.9E-06	-0.03	29.95	8.7E-01
YP_513852.1	26.3	-0.06	25.92	1.0E+00	-0.94	25.92	2.2E-03	0.13	25.92	7.3E-01
YP_512920.1	26.3	-0.06	25.92	1.0E+00	-0.94	25.92	2.2E-03	0.13	25.92	7.3E-01
YP_514064.1	27.9	-0.14	27.85	1.0E+00	-0.94	27.85	6.5E-02	0.18	27.85	7.9E-01
YP_514154.1	33.9	0.05	33.67	1.0E+00	-0.93	33.67	2.3E-03	0.19	33.67	6.3E-01
YP_513902.1	31.3	-0.18	31.27	1.0E+00	-0.92	31.27	1.6E-04	-0.27	31.27	6.0E-01
YP_513486.1	20.6	-0.39	20.83	1.0E+00	-0.92	20.83	1.1E-02	-0.50	20.83	6.0E-01
YP_514110.1	25.4	-0.11	25.32	1.0E+00	-0.92	25.32	5.5E-04	-0.15	25.32	6.3E-01
YP_514037.1	24.9	-0.21	25.13	1.0E+00	-0.90	25.13	8.0E-03	-0.51	25.13	6.0E-01
YP_514415.1	27.8	-0.23	27.70	1.0E+00	-0.90	27.70	2.8E-03	-0.15	27.70	6.9E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513802.1	30.0	-0.04	29.91	1.0E+00	-0.88	29.91	2.4E-06	-0.16	29.91	6.0E-01
YP_513452.1	23.5	-0.32	24.02	1.0E+00	-0.87	24.02	2.8E-02	-0.41	24.02	6.1E-01
YP_513525.1	27.6	0.00	27.65	1.0E+00	-0.87	27.65	7.8E-07	-0.09	27.65	6.3E-01
YP_514402.1	25.1	-0.05	25.19	1.0E+00	-0.86	25.19	3.5E-02	-0.21	25.19	7.0E-01
YP_513855.1	31.1	-0.02	30.74	1.0E+00	-0.86	30.74	5.8E-05	-0.01	30.74	9.8E-01
YP_512923.1	31.1	-0.02	30.74	1.0E+00	-0.86	30.74	5.8E-05	-0.01	30.74	9.8E-01
YP_513854.1	28.0	-0.02	27.78	1.0E+00	-0.85	27.78	1.6E-04	0.23	27.78	6.0E-01
YP_512922.1	28.0	-0.02	27.78	1.0E+00	-0.85	27.78	1.6E-04	0.23	27.78	6.0E-01
YP_513926.1	21.1	-0.10	21.21	1.0E+00	-0.85	21.21	3.6E-02	-0.57	21.21	6.0E-01
YP_513160.1	33.6	0.02	33.34	1.0E+00	-0.84	33.34	6.1E-06	-0.05	33.34	7.9E-01
YP_513018.1	27.7	0.09	27.48	1.0E+00	-0.84	27.48	6.4E-06	0.00	27.48	1.0E+00
YP_513546.1	25.1	-0.14	25.26	1.0E+00	-0.83	25.26	1.0E-01	-0.45	25.26	6.2E-01
YP_513748.1	29.2	0.54	27.78	1.0E+00	-0.82	27.78	2.5E-01	0.82	27.78	6.0E-01
YP_513887.1	23.9	-0.05	24.18	1.0E+00	-0.82	24.18	3.8E-03	-0.27	24.18	6.1E-01
YP_514137.1	28.5	-0.13	28.63	1.0E+00	-0.81	28.63	8.4E-05	-0.17	28.63	6.1E-01
YP_512944.1	30.0	0.00	29.89	1.0E+00	-0.81	29.89	8.5E-06	-0.07	29.89	7.1E-01
YP_512846.1	29.0	-0.20	28.71	1.0E+00	-0.81	28.71	1.0E-03	-0.28	28.71	6.0E-01
YP_513002.1	31.9	-0.07	31.60	1.0E+00	-0.80	31.60	1.9E-04	0.01	31.60	9.7E-01
YP_514111.1	24.6	-0.07	24.66	1.0E+00	-0.80	24.66	2.6E-03	-0.22	24.66	6.3E-01
YP_514133.1	25.5	0.04	25.24	1.0E+00	-0.79	25.24	8.6E-04	0.16	25.24	6.3E-01
YP_512897.1	28.9	-0.02	28.80	1.0E+00	-0.79	28.80	4.3E-07	-0.02	28.80	8.6E-01
YP_514471.1	19.1	-0.78	19.83	1.0E+00	-0.78	19.83	3.2E-01	-0.99	19.83	6.0E-01
YP_513392.1	24.8	-0.01	24.75	1.0E+00	-0.78	24.75	3.0E-03	-0.18	24.75	6.3E-01
YP_513896.1	29.2	-0.09	29.00	1.0E+00	-0.78	29.00	1.2E-05	-0.07	29.00	6.9E-01
YP_513929.1	28.8	-0.12	28.65	1.0E+00	-0.76	28.65	6.3E-05	-0.02	28.65	9.4E-01
YP_513595.1	30.4	-0.11	30.53	1.0E+00	-0.76	30.53	8.9E-04	-0.31	30.53	6.0E-01
YP_513843.1	34.9	-0.20	34.55	1.0E+00	-0.75	34.55	2.2E-03	-0.16	34.55	6.3E-01
YP_512911.1	34.9	-0.20	34.55	1.0E+00	-0.75	34.55	2.2E-03	-0.16	34.55	6.3E-01
YP_512837.1	32.3	-0.06	32.28	1.0E+00	-0.75	32.28	6.3E-05	-0.18	32.28	6.0E-01
YP_513183.1	26.4	-0.07	26.54	1.0E+00	-0.75	26.54	8.5E-03	-0.34	26.54	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514504.1	31.5	-0.10	31.50	1.0E+00	-0.73	31.50	2.7E-03	-0.12	31.50	6.9E-01
YP_513988.1	31.5	-0.10	31.50	1.0E+00	-0.73	31.50	2.7E-03	-0.12	31.50	6.9E-01
YP_513059.1	31.5	-0.10	31.50	1.0E+00	-0.73	31.50	2.7E-03	-0.12	31.50	6.9E-01
YP_513447.1	26.8	-0.07	27.07	1.0E+00	-0.73	27.07	3.6E-04	-0.31	27.07	6.0E-01
YP_512838.1	30.4	-0.03	30.50	1.0E+00	-0.72	30.50	4.4E-05	-0.17	30.50	6.0E-01
YP_513244.1	28.8	-0.03	28.85	1.0E+00	-0.72	28.85	3.7E-06	-0.21	28.85	6.0E-01
YP_512872.1	26.9	0.11	26.15	1.0E+00	-0.71	26.15	8.6E-02	0.55	26.15	6.0E-01
YP_514019.1	28.1	-0.12	28.00	1.0E+00	-0.71	28.00	5.8E-04	-0.12	28.00	6.4E-01
YP_513792.1	25.4	-0.13	25.80	1.0E+00	-0.71	25.80	2.4E-02	-0.50	25.80	6.0E-01
YP_512887.1	25.9	-0.04	25.97	1.0E+00	-0.70	25.97	1.6E-04	-0.10	25.97	6.5E-01
YP_513428.1	28.5	0.00	28.61	1.0E+00	-0.70	28.61	1.6E-05	-0.09	28.61	6.3E-01
YP_513785.1	29.5	-0.15	29.53	1.0E+00	-0.69	29.53	7.5E-03	-0.24	29.53	6.2E-01
YP_513846.1	32.1	-0.10	31.57	1.0E+00	-0.69	31.57	5.8E-04	0.21	31.57	6.0E-01
YP_512914.1	32.1	-0.10	31.57	1.0E+00	-0.69	31.57	5.8E-04	0.21	31.57	6.0E-01
YP_513083.1	24.6	-0.06	24.74	1.0E+00	-0.68	24.74	1.4E-03	-0.07	24.74	7.8E-01
YP_513669.1	26.4	-0.20	26.70	1.0E+00	-0.68	26.70	1.2E-03	-0.36	26.70	6.0E-01
YP_512836.1	29.6	0.01	29.54	1.0E+00	-0.67	29.54	2.4E-06	-0.06	29.54	6.7E-01
YP_513111.1	23.7	-0.19	23.57	1.0E+00	-0.67	23.57	3.7E-02	-0.37	23.57	6.0E-01
YP_513109.1	31.9	-0.04	32.01	1.0E+00	-0.67	32.01	2.1E-01	0.28	32.01	6.9E-01
YP_512854.1	28.2	0.02	28.00	1.0E+00	-0.67	28.00	2.5E-05	-0.04	28.00	8.2E-01
YP_513968.1	24.1	0.00	23.86	1.0E+00	-0.66	23.86	2.5E-02	0.11	23.86	7.9E-01
YP_513964.1	26.2	0.01	26.48	1.0E+00	-0.66	26.48	3.0E-02	0.23	26.48	6.3E-01
YP_512865.1	22.8	0.00	22.36	1.0E+00	-0.66	22.36	3.0E-01	-0.05	22.36	9.6E-01
YP_513911.1	30.0	-0.06	29.97	1.0E+00	-0.66	29.97	6.5E-07	-0.10	29.97	6.0E-01
YP_513773.1	25.8	-0.09	25.89	1.0E+00	-0.66	25.89	4.9E-03	-0.13	25.89	6.6E-01
YP_513806.1	27.9	0.08	27.98	1.0E+00	-0.65	27.98	4.4E-05	-0.15	27.98	6.0E-01
YP_513221.1	26.8	0.01	26.31	1.0E+00	-0.65	26.31	1.1E-01	0.34	26.31	6.3E-01
YP_514492.1	24.8	0.16	24.68	1.0E+00	-0.65	24.68	2.7E-02	0.07	24.68	8.7E-01
YP_513639.1	26.7	0.29	26.28	1.0E+00	-0.65	26.28	1.6E-01	0.32	26.28	6.3E-01
YP_513928.1	29.5	-0.04	29.20	1.0E+00	-0.63	29.20	4.2E-06	0.12	29.20	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514189.1	28.0	-0.04	28.05	1.0E+00	-0.62	28.05	1.2E-03	-0.15	28.05	6.3E-01
YP_513886.1	25.8	-0.23	26.08	1.0E+00	-0.62	26.08	8.0E-03	-0.40	26.08	6.0E-01
YP_513510.1	25.7	-0.11	25.65	1.0E+00	-0.62	25.65	1.7E-01	-0.28	25.65	6.5E-01
YP_514205.1	17.1	0.39	16.58	1.0E+00	-0.61	16.58	9.2E-01	-6.00	16.58	6.0E-01
YP_513938.1	25.4	0.05	25.38	1.0E+00	-0.61	25.38	6.3E-04	-0.08	25.38	6.9E-01
YP_513433.1	30.7	0.04	30.60	1.0E+00	-0.60	30.60	9.4E-04	-0.06	30.60	7.7E-01
YP_514192.1	32.0	-0.03	31.86	1.0E+00	-0.60	31.86	7.4E-04	-0.02	31.86	9.2E-01
YP_513599.1	30.6	-0.04	30.52	1.0E+00	-0.59	30.52	9.4E-05	0.03	30.52	8.7E-01
YP_513011.1	27.8	0.01	27.60	1.0E+00	-0.59	27.60	3.8E-06	-0.02	27.60	8.7E-01
YP_513070.1	25.0	-0.07	24.92	1.0E+00	-0.59	24.92	2.9E-02	-0.11	24.92	7.5E-01
YP_513469.1	25.6	-0.15	25.91	1.0E+00	-0.59	25.91	1.4E-03	-0.16	25.91	6.2E-01
YP_514134.1	25.1	0.06	25.02	1.0E+00	-0.58	25.02	1.6E-02	-0.14	25.02	6.6E-01
YP_512964.1	26.1	-0.22	26.38	1.0E+00	-0.58	26.38	8.0E-03	-0.49	26.38	6.0E-01
YP_514014.1	21.6	0.02	21.98	1.0E+00	-0.58	21.98	2.2E-01	-0.64	21.98	6.0E-01
YP_513539.1	24.6	-0.34	24.41	1.0E+00	-0.58	24.41	9.4E-02	-0.22	24.41	6.4E-01
YP_513140.1	29.8	-0.08	29.67	1.0E+00	-0.57	29.67	2.7E-05	-0.07	29.67	6.3E-01
YP_513168.1	29.1	-0.01	29.05	1.0E+00	-0.57	29.05	2.9E-04	-0.02	29.05	9.0E-01
YP_513159.1	29.2	-0.02	29.05	1.0E+00	-0.57	29.05	2.7E-01	0.49	29.05	6.2E-01
YP_513676.1	29.8	0.04	29.83	1.0E+00	-0.57	29.83	4.7E-05	0.03	29.83	8.5E-01
YP_513368.1	28.6	-0.01	28.51	1.0E+00	-0.57	28.51	1.6E-05	-0.07	28.51	6.3E-01
YP_513269.1	26.3	-0.32	26.14	1.0E+00	-0.57	26.14	9.3E-03	-0.40	26.14	6.0E-01
YP_512857.1	27.6	-0.07	27.58	1.0E+00	-0.56	27.58	1.6E-05	-0.08	27.58	6.3E-01
YP_512826.1	30.6	-0.06	30.55	1.0E+00	-0.56	30.55	8.7E-03	-0.19	30.55	6.2E-01
YP_514514.1	28.2	-0.02	28.00	1.0E+00	-0.56	28.00	2.2E-02	0.18	28.00	6.3E-01
YP_513423.1	32.2	-0.08	32.16	1.0E+00	-0.56	32.16	1.9E-02	-0.17	32.16	6.3E-01
YP_513359.1	27.8	0.03	27.69	1.0E+00	-0.55	27.69	5.6E-06	0.08	27.69	6.2E-01
YP_513472.1	27.7	-0.04	27.71	1.0E+00	-0.55	27.71	9.8E-03	-0.04	27.71	8.9E-01
YP_512936.1	24.9	-0.11	24.85	1.0E+00	-0.55	24.85	1.3E-03	0.01	24.85	9.6E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513235.1	28.1	-0.07	28.03	1.0E+00	-0.54	28.03	3.1E-03	-0.16	28.03	6.2E-01
YP_513737.1	27.0	-0.12	26.44	1.0E+00	-0.54	26.44	1.7E-02	0.05	26.44	8.9E-01
YP_513939.1	30.2	0.05	30.23	1.0E+00	-0.54	30.23	1.2E-03	-0.01	30.23	9.8E-01
YP_513155.1	28.7	0.32	28.29	1.0E+00	-0.53	28.29	2.8E-01	0.58	28.29	6.0E-01
YP_513912.1	30.4	-0.09	30.42	1.0E+00	-0.53	30.42	3.7E-03	-0.23	30.42	6.0E-01
YP_514559.1	26.7	0.01	26.60	1.0E+00	-0.53	26.60	4.5E-01	0.30	26.60	7.3E-01
YP_514508.1	24.7	0.09	24.88	1.0E+00	-0.52	24.88	1.2E-03	0.00	24.88	9.8E-01
YP_513841.1	32.9	-0.02	32.64	1.0E+00	-0.52	32.64	1.8E-03	0.00	32.64	1.0E+00
YP_512909.1	32.9	-0.02	32.64	1.0E+00	-0.52	32.64	1.8E-03	0.00	32.64	1.0E+00
YP_514046.1	29.0	-0.15	29.14	1.0E+00	-0.52	29.14	2.6E-03	-0.03	29.14	8.9E-01
YP_514128.1	26.0	-0.26	26.36	1.0E+00	-0.51	26.36	3.7E-02	-0.32	26.36	6.0E-01
YP_513982.1	30.6	-0.04	30.69	1.0E+00	-0.51	30.69	2.6E-05	-0.07	30.69	6.3E-01
YP_513249.1	31.4	-0.03	31.34	1.0E+00	-0.51	31.34	1.0E-04	-0.08	31.34	6.3E-01
YP_514196.1	27.7	0.03	27.44	1.0E+00	-0.51	27.44	4.2E-03	0.18	27.44	6.1E-01
YP_513842.1	34.3	-0.09	34.05	1.0E+00	-0.51	34.05	2.6E-02	-0.07	34.05	8.2E-01
YP_512910.1	34.3	-0.09	34.05	1.0E+00	-0.51	34.05	2.6E-02	-0.07	34.05	8.2E-01
YP_513277.1	26.6	-0.03	26.69	1.0E+00	-0.50	26.69	5.6E-04	-0.12	26.69	6.2E-01
YP_514441.1	25.0	-0.16	25.38	1.0E+00	-0.50	25.38	3.0E-01	-0.42	25.38	6.3E-01
YP_513683.1	26.9	-0.12	27.01	1.0E+00	-0.50	27.01	1.9E-03	-0.19	27.01	6.0E-01
YP_513805.1	30.1	-0.06	30.03	1.0E+00	-0.50	30.03	6.8E-05	-0.07	30.03	6.3E-01
YP_513709.1	27.4	0.16	27.28	1.0E+00	-0.50	27.28	8.4E-03	0.22	27.28	6.0E-01
YP_513958.1	29.4	-0.12	29.51	1.0E+00	-0.49	29.51	1.7E-02	-0.18	29.51	6.3E-01
YP_514515.1	27.8	-0.05	27.98	1.0E+00	-0.49	27.98	9.4E-05	-0.16	27.98	6.0E-01
YP_513339.1	24.1	-0.17	24.69	1.0E+00	-0.49	24.69	3.2E-02	-0.46	24.69	6.0E-01
YP_513393.1	25.3	-0.08	25.44	1.0E+00	-0.48	25.44	1.5E-02	-0.29	25.44	6.0E-01
YP_514209.1	27.1	-0.07	27.18	1.0E+00	-0.48	27.18	5.7E-03	-0.19	27.18	6.0E-01
YP_513587.1	28.9	-0.13	28.80	1.0E+00	-0.47	28.80	3.7E-02	-0.12	28.80	7.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513438.1	27.9	-0.13	27.93	1.0E+00	-0.47	27.93	4.6E-02	-0.24	27.93	6.1E-01
YP_513331.1	30.7	-0.07	30.86	1.0E+00	-0.46	30.86	1.0E-03	-0.13	30.86	6.1E-01
YP_512899.1	27.6	0.00	27.25	1.0E+00	-0.46	27.25	1.6E-02	-0.02	27.25	9.6E-01
YP_514453.1	29.8	-0.06	29.87	1.0E+00	-0.46	29.87	7.6E-04	-0.02	29.87	9.1E-01
YP_513446.1	29.6	-0.05	29.65	1.0E+00	-0.46	29.65	1.2E-03	-0.10	29.65	6.3E-01
YP_512893.1	28.3	-0.10	28.37	1.0E+00	-0.46	28.37	1.2E-03	-0.05	28.37	7.4E-01
YP_514291.1	28.3	0.11	28.07	1.0E+00	-0.45	28.07	4.3E-03	0.16	28.07	6.1E-01
YP_513445.1	27.4	0.07	27.05	1.0E+00	-0.45	27.05	1.7E-02	0.18	27.05	6.2E-01
YP_513684.1	25.2	-0.14	25.21	1.0E+00	-0.45	25.21	7.0E-03	-0.25	25.21	6.0E-01
YP_513870.1	31.6	0.02	31.65	1.0E+00	-0.45	31.65	6.6E-02	-0.11	31.65	7.3E-01
YP_514153.1	28.8	-0.07	28.89	1.0E+00	-0.45	28.89	5.5E-03	-0.13	28.89	6.3E-01
YP_513456.1	25.9	-0.07	26.16	1.0E+00	-0.45	26.16	5.4E-03	-0.18	26.16	6.0E-01
YP_513470.1	25.4	0.08	25.60	1.0E+00	-0.44	25.60	5.8E-02	0.12	25.60	7.0E-01
YP_513745.1	26.6	0.00	26.48	1.0E+00	-0.44	26.48	4.0E-01	-0.01	26.48	9.9E-01
YP_513845.1	28.3	-0.02	28.17	1.0E+00	-0.44	28.17	2.3E-03	0.06	28.17	7.4E-01
YP_512913.1	28.3	-0.02	28.17	1.0E+00	-0.44	28.17	2.3E-03	0.06	28.17	7.4E-01
YP_514071.1	30.2	-0.15	30.12	1.0E+00	-0.44	30.12	3.1E-03	-0.15	30.12	6.1E-01
YP_514006.1	25.5	0.09	25.27	1.0E+00	-0.44	25.27	1.3E-01	-0.09	25.27	8.2E-01
YP_513693.1	29.4	0.08	29.21	1.0E+00	-0.44	29.21	2.2E-01	0.13	29.21	7.9E-01
YP_513925.1	25.2	-0.08	25.15	1.0E+00	-0.43	25.15	1.4E-02	-0.11	25.15	6.3E-01
YP_513088.1	21.8	-0.14	22.30	1.0E+00	-0.43	22.30	4.4E-01	-1.18	22.30	6.0E-01
YP_513803.1	21.3	-0.56	21.44	1.0E+00	-0.43	21.44	4.6E-01	-0.66	21.44	6.0E-01
YP_513005.1	31.7	0.00	31.77	1.0E+00	-0.43	31.77	5.3E-05	-0.11	31.77	6.0E-01
YP_513459.1	27.1	-0.12	27.09	1.0E+00	-0.43	27.09	3.5E-02	-0.28	27.09	6.0E-01
YP_513091.1	26.9	0.01	26.70	1.0E+00	-0.43	26.70	7.0E-03	0.13	26.70	6.3E-01
YP_513096.1	24.4	0.01	24.04	1.0E+00	-0.43	24.04	5.1E-02	0.05	24.04	8.9E-01
YP_513332.1	32.4	-0.01	32.19	1.0E+00	-0.42	32.19	1.1E-03	0.15	32.19	6.0E-01
YP_513029.1	34.6	0.06	34.65	1.0E+00	-0.42	34.65	1.8E-02	-0.19	34.65	6.1E-01
YP_514357.1	28.8	0.11	28.80	1.0E+00	-0.42	28.80	6.3E-04	0.10	28.80	6.2E-01
YP_513910.1	30.5	0.00	30.48	1.0E+00	-0.42	30.48	4.3E-04	-0.04	30.48	7.5E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513288.1	33.0	-0.08	32.90	1.0E+00	-0.41	32.90	1.2E-02	-0.19	32.90	6.0E-01
YP_513372.1	29.3	-0.12	29.47	1.0E+00	-0.41	29.47	1.1E-02	-0.18	29.47	6.0E-01
YP_513857.1	27.2	-0.19	27.02	1.0E+00	-0.41	27.02	2.1E-01	-0.23	27.02	6.3E-01
YP_513535.1	27.7	-0.11	27.66	1.0E+00	-0.41	27.66	1.4E-01	0.04	27.66	9.2E-01
YP_514536.1	28.0	-0.03	28.08	1.0E+00	-0.41	28.08	9.0E-02	-0.20	28.08	6.3E-01
YP_512825.1	28.6	-0.05	28.70	1.0E+00	-0.40	28.70	3.3E-03	-0.13	28.70	6.1E-01
YP_513352.1	30.9	-0.03	31.02	1.0E+00	-0.40	31.02	9.1E-03	-0.15	31.02	6.1E-01
YP_513701.1	27.8	-0.15	27.96	1.0E+00	-0.40	27.96	3.6E-02	-0.19	27.96	6.2E-01
YP_513238.1	29.1	-0.04	29.10	1.0E+00	-0.39	29.10	1.3E-02	-0.16	29.10	6.1E-01
YP_512898.1	28.9	0.11	28.75	1.0E+00	-0.39	28.75	7.2E-02	0.31	28.75	6.0E-01
YP_513858.1	28.6	-0.08	28.46	1.0E+00	-0.39	28.46	1.6E-02	0.03	28.46	9.1E-01
YP_513974.2	29.8	0.02	29.69	1.0E+00	-0.38	29.69	3.5E-01	-0.03	29.69	9.6E-01
YP_513909.1	28.6	0.05	28.55	1.0E+00	-0.38	28.55	3.4E-04	0.06	28.55	6.3E-01
YP_514129.1	33.3	0.06	33.14	1.0E+00	-0.38	33.14	2.8E-04	-0.06	33.14	6.3E-01
YP_513231.1	29.5	0.01	29.44	1.0E+00	-0.38	29.44	4.9E-04	-0.02	29.44	8.7E-01
YP_513533.1	31.3	0.04	31.39	1.0E+00	-0.38	31.39	4.0E-04	-0.02	31.39	9.0E-01
YP_513744.1	28.5	-0.04	28.35	1.0E+00	-0.38	28.35	1.3E-03	0.08	28.35	6.3E-01
YP_513317.1	27.2	-0.05	27.22	1.0E+00	-0.38	27.22	1.1E-03	-0.09	27.22	6.2E-01
YP_512966.1	23.2	-0.15	23.89	1.0E+00	-0.37	23.89	3.7E-01	-0.29	23.89	6.3E-01
YP_513532.1	28.8	-0.14	28.85	1.0E+00	-0.37	28.85	1.2E-03	-0.16	28.85	6.0E-01
YP_513057.1	33.5	-0.10	33.57	1.0E+00	-0.37	33.57	5.4E-04	-0.02	33.57	8.9E-01
YP_513692.1	30.8	-0.09	30.93	1.0E+00	-0.37	30.93	2.9E-03	-0.21	30.93	6.0E-01
YP_514310.1	29.9	-0.04	29.85	1.0E+00	-0.37	29.85	7.1E-03	0.02	29.85	9.3E-01
YP_513033.1	33.1	0.02	32.98	1.0E+00	-0.36	32.98	7.3E-02	0.14	32.98	6.3E-01
YP_513167.1	28.9	0.06	28.89	1.0E+00	-0.36	28.89	4.2E-02	0.08	28.89	7.3E-01
YP_514393.1	28.0	0.00	28.11	1.0E+00	-0.36	28.11	6.2E-02	-0.22	28.11	6.1E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514248.1	27.8	-0.07	27.79	1.0E+00	-0.36	27.79	4.1E-02	-0.14	27.79	6.3E-01
YP_514188.1	31.0	-0.08	30.97	1.0E+00	-0.36	30.97	2.5E-02	-0.14	30.97	6.3E-01
YP_512994.1	29.6	0.03	29.65	1.0E+00	-0.36	29.65	2.5E-02	0.18	29.65	6.1E-01
YP_513997.1	27.9	-0.09	28.15	1.0E+00	-0.36	28.15	1.6E-01	-0.15	28.15	6.7E-01
YP_513932.1	27.2	0.03	26.82	1.0E+00	-0.36	26.82	1.7E-01	-0.29	26.82	6.1E-01
YP_513346.1	29.6	-0.05	29.46	1.0E+00	-0.35	29.46	9.1E-03	-0.11	29.46	6.3E-01
YP_514316.1	29.3	-0.10	29.28	1.0E+00	-0.35	29.28	7.1E-03	-0.06	29.28	7.3E-01
YP_513819.1	29.4	0.27	29.15	1.0E+00	-0.35	29.15	3.8E-01	0.14	29.15	7.9E-01
YP_512848.1	26.3	0.00	26.14	1.0E+00	-0.35	26.14	4.2E-02	-0.13	26.14	6.3E-01
YP_514278.1	27.2	-0.06	26.90	1.0E+00	-0.35	26.90	1.5E-01	-0.08	26.90	8.1E-01
YP_514015.1	24.7	0.03	24.80	1.0E+00	-0.35	24.80	6.1E-01	0.34	24.80	6.8E-01
YP_513086.1	29.1	0.03	29.09	1.0E+00	-0.35	29.09	1.1E-03	0.01	29.09	9.3E-01
YP_513113.1	31.1	0.05	30.97	1.0E+00	-0.35	30.97	5.0E-03	0.08	30.97	6.3E-01
YP_513356.1	31.7	-0.08	31.86	1.0E+00	-0.35	31.86	2.6E-02	-0.28	31.86	6.0E-01
YP_514535.1	30.3	-0.03	30.44	1.0E+00	-0.34	30.44	1.8E-02	-0.11	30.44	6.3E-01
YP_514138.1	28.5	0.04	28.48	1.0E+00	-0.34	28.48	7.0E-03	-0.09	28.48	6.3E-01
YP_514451.1	27.8	0.07	27.80	1.0E+00	-0.34	27.80	8.8E-02	-0.03	27.80	9.3E-01
YP_514221.1	28.8	0.06	28.65	1.0E+00	-0.34	28.65	2.0E-03	0.03	28.65	8.4E-01
YP_513281.1	27.0	0.04	27.05	1.0E+00	-0.34	27.05	2.4E-01	0.33	27.05	6.0E-01
YP_513032.1	32.5	-0.08	32.67	1.0E+00	-0.34	32.67	2.7E-02	0.00	32.67	1.0E+00
YP_512947.1	26.8	-0.19	26.91	1.0E+00	-0.34	26.91	3.1E-01	0.22	26.91	6.3E-01
YP_514078.1	27.2	0.01	26.89	1.0E+00	-0.33	26.89	1.2E-02	0.13	26.89	6.1E-01
YP_513354.1	29.7	-0.06	29.77	1.0E+00	-0.33	29.77	2.6E-02	-0.11	29.77	6.3E-01
YP_513943.1	31.8	-0.04	31.94	1.0E+00	-0.33	31.94	5.8E-02	-0.15	31.94	6.3E-01
YP_513035.1	32.6	0.05	32.42	1.0E+00	-0.33	32.42	1.3E-01	0.20	32.42	6.2E-01
YP_514160.1	31.3	-0.03	31.36	1.0E+00	-0.33	31.36	3.7E-05	-0.02	31.36	8.1E-01
YP_513234.1	29.2	-0.04	29.38	1.0E+00	-0.33	29.38	1.4E-02	-0.12	29.38	6.2E-01
YP_514315.1	30.7	0.02	30.55	1.0E+00	-0.32	30.55	5.3E-04	0.02	30.55	8.6E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513908.1	31.8	0.09	31.56	1.0E+00	-0.32	31.56	4.6E-01	0.48	31.56	6.0E-01
YP_513246.1	28.5	-0.13	28.61	1.0E+00	-0.32	28.61	1.9E-01	-0.30	28.61	6.0E-01
YP_513087.1	33.3	-0.04	33.31	1.0E+00	-0.32	33.31	6.4E-02	-0.16	33.31	6.2E-01
YP_513953.1	26.1	0.05	26.25	1.0E+00	-0.32	26.25	9.3E-03	-0.13	26.25	6.1E-01
YP_514158.1	25.3	-0.02	24.77	1.0E+00	-0.32	24.77	4.9E-01	0.26	24.77	6.7E-01
YP_513536.1	27.3	0.13	27.30	1.0E+00	-0.32	27.30	6.4E-01	0.62	27.30	6.1E-01
YP_513209.1	27.2	-0.04	27.61	1.0E+00	-0.32	27.61	1.5E-01	-0.27	27.61	6.0E-01
YP_513905.1	22.0	0.16	22.01	1.0E+00	-0.32	22.01	3.8E-01	-0.34	22.01	6.2E-01
YP_513304.1	27.0	-0.04	26.78	1.0E+00	-0.31	26.78	5.9E-02	-0.09	26.78	6.8E-01
YP_514048.1	33.5	0.11	33.38	1.0E+00	-0.31	33.38	3.7E-01	0.35	33.38	6.1E-01
YP_514418.1	30.2	0.02	30.22	1.0E+00	-0.31	30.22	4.8E-02	0.12	30.22	6.3E-01
YP_513485.1	26.9	-0.05	26.57	1.0E+00	-0.31	26.57	2.1E-02	0.11	26.57	6.3E-01
YP_513192.1	29.9	-0.03	29.87	1.0E+00	-0.30	29.87	9.6E-04	0.00	29.87	9.9E-01
YP_514377.1	33.4	-0.17	33.35	1.0E+00	-0.30	33.35	6.1E-02	-0.08	33.35	7.1E-01
YP_514293.1	31.2	-0.04	31.19	1.0E+00	-0.30	31.19	1.3E-02	0.04	31.19	7.8E-01
YP_513527.1	32.4	0.03	32.23	1.0E+00	-0.30	32.23	8.4E-03	0.00	32.23	9.8E-01
YP_513740.1	27.9	0.08	27.81	1.0E+00	-0.30	27.81	5.1E-01	0.47	27.81	6.1E-01
YP_514147.1	27.3	-0.10	27.42	1.0E+00	-0.29	27.42	1.3E-01	-0.25	27.42	6.0E-01
YP_513108.1	28.2	0.21	27.75	1.0E+00	-0.29	27.75	5.1E-01	0.37	27.75	6.2E-01
YP_513293.1	25.5	-0.10	25.69	1.0E+00	-0.29	25.69	9.0E-02	-0.24	25.69	6.0E-01
YP_513914.1	26.2	-0.27	26.36	1.0E+00	-0.29	26.36	2.2E-01	-0.29	26.36	6.0E-01
YP_513907.1	30.8	-0.11	30.76	1.0E+00	-0.29	30.76	1.2E-01	0.05	30.76	8.6E-01
YP_513223.1	29.4	-0.02	29.50	1.0E+00	-0.28	29.50	2.1E-01	0.01	29.50	9.8E-01
YP_514444.1	29.0	-0.06	28.99	1.0E+00	-0.28	28.99	3.0E-02	-0.05	28.99	7.6E-01
YP_514447.1	31.3	-0.01	31.21	1.0E+00	-0.28	31.21	2.1E-02	-0.10	31.21	6.3E-01
YP_513427.1	31.5	-0.01	31.41	1.0E+00	-0.28	31.41	5.9E-02	-0.10	31.41	6.3E-01
YP_513662.1	27.6	-0.18	27.81	1.0E+00	-0.28	27.81	2.2E-01	-0.35	27.81	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513310.1	28.5	-0.02	28.59	1.0E+00	-0.28	28.59	4.8E-02	-0.01	28.59	9.7E-01
YP_513667.1	24.4	-0.06	24.81	1.0E+00	-0.28	24.81	2.1E-01	-0.35	24.81	6.0E-01
YP_514379.1	33.2	0.05	33.26	1.0E+00	-0.28	33.26	1.8E-02	0.04	33.26	8.1E-01
YP_513162.1	28.8	0.05	28.93	1.0E+00	-0.28	28.93	2.9E-03	-0.06	28.93	6.4E-01
YP_513264.1	29.8	0.02	29.79	1.0E+00	-0.28	29.79	2.2E-02	-0.11	29.79	6.2E-01
YP_514069.1	30.3	-0.06	30.14	1.0E+00	-0.28	30.14	1.9E-03	-0.07	30.14	6.3E-01
YP_514488.1	28.1	-0.07	28.07	1.0E+00	-0.27	28.07	7.3E-02	-0.04	28.07	8.7E-01
YP_513038.1	32.8	0.00	32.84	1.0E+00	-0.27	32.84	1.0E-01	0.07	32.84	7.5E-01
YP_513831.1	31.1	0.07	30.95	1.0E+00	-0.27	30.95	7.8E-02	-0.05	30.95	8.3E-01
YP_514417.1	31.0	0.10	30.83	1.0E+00	-0.27	30.83	5.3E-01	0.42	30.83	6.1E-01
YP_514051.1	29.8	0.05	29.88	1.0E+00	-0.27	29.88	5.8E-02	-0.10	29.88	6.3E-01
YP_514210.1	30.1	0.10	30.18	1.0E+00	-0.26	30.18	4.1E-01	0.10	30.18	8.3E-01
YP_513248.1	29.4	-0.10	29.49	1.0E+00	-0.26	29.49	8.5E-02	-0.21	29.49	6.0E-01
YP_513561.1	28.8	-0.17	28.88	1.0E+00	-0.26	28.88	5.2E-01	-0.24	28.88	6.5E-01
YP_513206.1	28.6	-0.01	28.43	1.0E+00	-0.26	28.43	1.9E-02	0.09	28.43	6.3E-01
YP_513312.1	28.2	-0.05	28.43	1.0E+00	-0.26	28.43	1.6E-01	-0.13	28.43	6.3E-01
YP_514253.1	28.5	-0.04	28.63	1.0E+00	-0.26	28.63	7.5E-02	-0.11	28.63	6.3E-01
YP_513458.1	27.8	0.13	27.72	1.0E+00	-0.26	27.72	7.3E-03	0.02	27.72	8.8E-01
YP_513502.1	27.0	0.10	27.08	1.0E+00	-0.26	27.08	4.9E-02	-0.15	27.08	6.0E-01
YP_514059.1	32.4	-0.01	32.47	1.0E+00	-0.26	32.47	2.0E-01	0.15	32.47	6.3E-01
YP_512977.1	29.1	-0.09	29.39	1.0E+00	-0.26	29.39	4.1E-01	0.07	29.39	8.7E-01
YP_514130.1	31.6	-0.05	31.52	1.0E+00	-0.26	31.52	5.1E-02	-0.06	31.52	7.2E-01
YP_513807.1	27.4	-0.02	27.45	1.0E+00	-0.25	27.45	6.0E-01	0.36	27.45	6.3E-01
YP_513044.1	32.3	-0.06	32.20	1.0E+00	-0.25	32.20	2.6E-02	0.08	32.20	6.3E-01
YP_513937.1	25.8	0.08	25.63	1.0E+00	-0.25	25.63	1.3E-01	-0.15	25.63	6.2E-01
YP_512840.1	25.6	-0.03	25.56	1.0E+00	-0.25	25.56	2.1E-01	-0.07	25.56	7.9E-01
YP_513040.1	30.2	-0.08	30.25	1.0E+00	-0.25	30.25	2.3E-01	-0.14	30.25	6.3E-01
YP_513483.1	26.0	0.05	26.00	1.0E+00	-0.25	26.00	4.4E-01	0.29	26.00	6.2E-01
YP_513217.1	24.1	-0.02	24.06	1.0E+00	-0.25	24.06	5.8E-01	-0.34	24.06	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513679.1	29.9	0.03	29.97	1.0E+00	-0.25	29.97	1.1E-01	0.01	29.97	9.7E-01
YP_512930.1	29.4	-0.08	29.27	1.0E+00	-0.25	29.27	1.2E-01	-0.16	29.27	6.2E-01
YP_514193.1	32.4	-0.04	32.39	1.0E+00	-0.24	32.39	1.8E-02	-0.09	32.39	6.2E-01
YP_514159.1	27.8	-0.10	27.77	1.0E+00	-0.24	27.77	3.5E-01	-0.24	27.77	6.2E-01
YP_513894.1	28.2	-0.08	28.33	1.0E+00	-0.24	28.33	1.3E-01	0.12	28.33	6.3E-01
YP_513148.1	29.1	-0.06	29.25	1.0E+00	-0.24	29.25	3.5E-02	-0.22	29.25	6.0E-01
YP_513743.1	27.1	-0.16	27.30	1.0E+00	-0.24	27.30	1.2E-01	-0.24	27.30	6.0E-01
YP_513357.1	30.8	-0.04	30.90	1.0E+00	-0.24	30.90	1.3E-01	-0.20	30.90	6.0E-01
YP_513283.1	28.2	-0.01	28.37	1.0E+00	-0.24	28.37	3.3E-01	0.08	28.37	8.1E-01
YP_512839.1	26.2	0.00	26.09	1.0E+00	-0.24	26.09	2.0E-01	0.01	26.09	9.8E-01
YP_514474.1	26.8	-0.11	26.94	1.0E+00	-0.24	26.94	3.0E-01	-0.07	26.94	8.2E-01
YP_513360.1	30.0	0.05	30.03	1.0E+00	-0.23	30.03	7.5E-02	-0.15	30.03	6.0E-01
YP_513418.1	26.0	0.15	25.94	1.0E+00	-0.23	25.94	2.9E-01	0.26	25.94	6.0E-01
YP_513467.1	24.6	-0.12	24.39	1.0E+00	-0.23	24.39	7.2E-01	-0.05	24.39	9.6E-01
YP_513861.1	25.6	-0.10	25.61	1.0E+00	-0.23	25.61	6.8E-01	-0.10	25.61	8.9E-01
YP_513237.1	26.9	0.00	26.87	1.0E+00	-0.23	26.87	6.9E-02	0.07	26.87	6.7E-01
YP_514185.1	29.0	-0.14	28.83	1.0E+00	-0.23	28.83	2.0E-01	-0.17	28.83	6.2E-01
YP_513830.1	26.0	0.15	26.55	1.0E+00	-0.23	26.55	3.4E-01	-0.03	26.55	9.4E-01
YP_513756.1	29.7	-0.03	29.71	1.0E+00	-0.22	29.71	6.6E-01	0.38	29.71	6.3E-01
YP_513853.1	25.9	0.19	25.75	1.0E+00	-0.22	25.75	8.3E-01	0.55	25.75	6.3E-01
YP_512921.1	25.9	0.19	25.75	1.0E+00	-0.22	25.75	8.3E-01	0.55	25.75	6.3E-01
YP_514178.1	30.5	-0.05	30.50	1.0E+00	-0.22	30.50	2.6E-02	-0.06	30.50	6.7E-01
YP_513711.1	27.6	0.07	27.16	1.0E+00	-0.22	27.16	3.0E-01	0.14	27.16	6.3E-01
YP_513511.1	29.4	0.00	29.37	1.0E+00	-0.22	29.37	2.4E-02	0.04	29.37	7.8E-01
YP_513772.1	30.9	0.01	30.90	1.0E+00	-0.22	30.90	1.5E-01	0.02	30.90	9.2E-01
YP_512968.1	29.0	0.02	29.09	1.0E+00	-0.22	29.09	2.1E-02	-0.01	29.09	9.2E-01
YP_514208.1	22.8	0.02	22.86	1.0E+00	-0.22	22.86	3.7E-01	-0.18	22.86	6.3E-01
YP_513440.1	27.5	0.04	27.48	1.0E+00	-0.22	27.48	3.7E-02	-0.01	27.48	9.4E-01
YP_514387.1	31.2	-0.04	31.14	1.0E+00	-0.22	31.14	2.7E-02	-0.11	31.14	6.0E-01
YP_514448.1	28.4	-0.05	28.52	1.0E+00	-0.22	28.52	5.5E-01	0.20	28.52	6.7E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513746.1	29.4	-0.04	29.36	1.0E+00	-0.22	29.36	8.4E-02	-0.04	29.36	8.2E-01
YP_513187.1	29.7	0.06	29.70	1.0E+00	-0.21	29.70	1.3E-02	0.04	29.70	7.1E-01
YP_514380.1	32.2	-0.02	32.22	1.0E+00	-0.21	32.22	2.5E-01	0.06	32.22	8.3E-01
YP_513642.1	29.5	-0.07	29.61	1.0E+00	-0.21	29.61	6.7E-01	0.28	29.61	6.4E-01
YP_514170.1	30.1	-0.02	30.07	1.0E+00	-0.21	30.07	1.6E-02	-0.03	30.07	7.7E-01
YP_512879.1	28.5	-0.01	28.40	1.0E+00	-0.21	28.40	1.0E-01	-0.05	28.40	7.9E-01
YP_513030.1	33.7	-0.09	33.80	1.0E+00	-0.21	33.80	1.5E-01	-0.19	33.80	6.0E-01
YP_514223.1	23.2	-0.15	23.47	1.0E+00	-0.21	23.47	7.1E-01	-0.40	23.47	6.3E-01
YP_513586.1	29.0	0.01	29.08	1.0E+00	-0.21	29.08	1.3E-01	-0.11	29.08	6.3E-01
YP_513460.1	26.2	-0.13	26.46	1.0E+00	-0.21	26.46	3.1E-01	-0.21	26.46	6.1E-01
YP_513420.1	26.9	-0.06	26.93	1.0E+00	-0.21	26.93	6.1E-03	-0.04	26.93	7.1E-01
YP_513409.1	28.8	-0.09	28.69	1.0E+00	-0.21	28.69	2.2E-01	-0.08	28.69	7.2E-01
YP_514195.1	27.5	-0.09	27.60	1.0E+00	-0.21	27.60	2.7E-01	0.12	27.60	6.5E-01
YP_514560.1	26.8	0.12	26.67	1.0E+00	-0.20	26.67	3.7E-01	0.34	26.67	6.0E-01
YP_513355.1	28.9	-0.09	29.04	1.0E+00	-0.20	29.04	2.2E-01	-0.15	29.04	6.2E-01
YP_514446.1	31.6	-0.07	31.57	1.0E+00	-0.20	31.57	1.6E-02	-0.06	31.57	6.3E-01
YP_512973.1	30.2	-0.11	30.23	1.0E+00	-0.20	30.23	3.0E-01	-0.17	30.23	6.3E-01
YP_514450.1	30.7	-0.04	30.74	1.0E+00	-0.20	30.74	1.7E-02	-0.04	30.74	7.3E-01
YP_513107.1	29.1	-0.09	29.05	1.0E+00	-0.20	29.05	2.2E-01	-0.14	29.05	6.3E-01
YP_514522.1	34.2	0.02	34.19	1.0E+00	-0.20	34.19	1.1E-02	-0.08	34.19	6.1E-01
YP_514348.1	29.7	0.18	29.59	1.0E+00	-0.20	29.59	3.0E-01	0.08	29.59	7.5E-01
YP_514332.1	32.1	0.02	32.11	1.0E+00	-0.20	32.11	1.1E-02	-0.04	32.11	6.7E-01
YP_514371.1	28.3	-0.06	28.12	1.0E+00	-0.20	28.12	1.3E-01	0.00	28.12	9.9E-01
YP_513375.1	32.5	-0.04	32.64	1.0E+00	-0.20	32.64	6.9E-02	-0.13	32.64	6.0E-01
YP_513871.1	26.5	-0.26	26.70	1.0E+00	-0.20	26.70	4.0E-01	-0.40	26.70	6.0E-01
YP_513660.1	32.1	-0.07	32.22	1.0E+00	-0.19	32.22	3.5E-01	-0.20	32.22	6.1E-01
YP_513141.1	27.2	-0.08	27.30	1.0E+00	-0.19	27.30	2.3E-02	-0.14	27.30	6.0E-01
YP_514083.1	26.3	-0.48	26.34	1.0E+00	-0.19	26.34	5.7E-01	-0.44	26.34	6.0E-01
YP_514318.1	25.7	0.06	25.76	1.0E+00	-0.19	25.76	4.5E-01	-0.23	25.76	6.2E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514462.1	29.6	-0.08	29.66	1.0E+00	-0.19	29.66	1.4E-01	-0.08	29.66	6.4E-01
YP_514040.1	27.3	0.10	27.20	1.0E+00	-0.19	27.20	6.4E-01	0.47	27.20	6.0E-01
YP_514279.1	22.5	0.15	22.05	1.0E+00	-0.18	22.05	4.3E-01	0.21	22.05	6.2E-01
YP_513479.1	27.0	-0.03	27.10	1.0E+00	-0.18	27.10	5.2E-01	0.19	27.10	6.3E-01
YP_514378.1	33.0	-0.03	33.09	1.0E+00	-0.18	33.09	8.4E-02	-0.03	33.09	8.6E-01
YP_513610.1	32.7	0.00	32.71	1.0E+00	-0.18	32.71	4.8E-01	0.18	32.71	6.3E-01
YP_513031.1	32.0	0.13	31.91	1.0E+00	-0.18	31.91	6.4E-01	0.37	31.91	6.1E-01
YP_513694.1	30.3	0.05	30.29	1.0E+00	-0.18	30.29	1.7E-01	0.17	30.29	6.0E-01
YP_513552.1	28.3	-0.12	28.28	1.0E+00	-0.17	28.28	2.0E-01	-0.13	28.28	6.2E-01
YP_514207.1	25.8	-0.05	25.73	1.0E+00	-0.17	25.73	3.9E-01	-0.10	25.73	7.1E-01
YP_513653.1	26.0	0.02	25.81	1.0E+00	-0.17	25.81	2.1E-01	0.09	25.81	6.3E-01
YP_512904.1	32.8	-0.07	32.83	1.0E+00	-0.17	32.83	2.3E-01	-0.13	32.83	6.2E-01
YP_512991.1	26.1	0.09	26.11	1.0E+00	-0.17	26.11	1.8E-01	0.00	26.11	9.8E-01
YP_513774.1	28.5	-0.04	28.66	1.0E+00	-0.17	28.66	1.5E-01	-0.05	28.66	7.8E-01
YP_514022.1	24.4	0.53	24.42	1.0E+00	-0.17	24.42	9.0E-01	0.66	24.42	6.3E-01
YP_514018.1	30.1	0.04	29.89	1.0E+00	-0.17	29.89	1.7E-01	0.17	29.89	6.0E-01
YP_513230.1	24.9	0.33	24.50	1.0E+00	-0.17	24.50	7.3E-01	0.53	24.50	6.0E-01
YP_513048.1	33.2	-0.04	33.26	1.0E+00	-0.17	33.26	1.9E-01	0.03	33.26	8.6E-01
YP_513895.1	31.2	-0.04	31.15	1.0E+00	-0.17	31.15	4.6E-02	0.04	31.15	7.3E-01
YP_514140.1	29.6	-0.07	29.73	1.0E+00	-0.17	29.73	1.8E-01	-0.18	29.73	6.0E-01
YP_513396.1	29.5	-0.05	29.66	1.0E+00	-0.16	29.66	3.5E-01	-0.14	29.66	6.3E-01
YP_513537.1	32.5	-0.03	32.56	1.0E+00	-0.16	32.56	4.6E-01	-0.17	32.56	6.3E-01
YP_513520.1	27.7	0.23	27.58	1.0E+00	-0.16	27.58	4.8E-01	0.20	27.58	6.2E-01
YP_514243.1	23.6	-0.18	23.59	1.0E+00	-0.16	23.59	7.4E-01	-0.34	23.59	6.3E-01
YP_514449.1	31.6	-0.05	31.75	1.0E+00	-0.16	31.75	3.5E-01	-0.19	31.75	6.0E-01
YP_513099.1	29.0	0.05	29.10	1.0E+00	-0.16	29.10	1.5E-01	-0.04	29.10	7.7E-01
YP_513413.1	30.5	-0.04	30.46	1.0E+00	-0.16	30.46	1.8E-01	-0.12	30.46	6.2E-01
YP_514229.1	29.3	-0.11	29.36	1.0E+00	-0.16	29.36	3.6E-01	-0.16	29.36	6.2E-01
YP_514143.1	28.6	0.06	28.53	1.0E+00	-0.16	28.53	1.6E-01	0.08	28.53	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513421.1	26.3	0.03	26.39	1.0E+00	-0.16	26.39	2.5E-01	-0.11	26.39	6.3E-01
YP_514506.1	27.3	0.04	27.05	1.0E+00	-0.16	27.05	4.5E-01	0.01	27.05	9.7E-01
YP_514002.1	29.3	-0.06	29.40	1.0E+00	-0.16	29.40	3.1E-01	-0.13	29.40	6.3E-01
YP_514276.1	28.7	-0.01	28.75	1.0E+00	-0.15	28.75	6.8E-01	0.35	28.75	6.1E-01
YP_514452.1	23.7	0.54	23.35	1.0E+00	-0.15	23.35	8.7E-01	1.55	23.35	6.0E-01
YP_513251.1	30.6	-0.06	30.46	1.0E+00	-0.15	30.46	4.1E-01	-0.12	30.46	6.3E-01
YP_513500.1	20.8	0.01	20.76	1.0E+00	-0.15	20.76	8.3E-01	-0.72	20.76	6.0E-01
YP_514292.1	29.7	-0.12	29.76	1.0E+00	-0.15	29.76	2.1E-01	-0.01	29.76	9.5E-01
YP_513661.1	33.6	-0.08	33.69	1.0E+00	-0.15	33.69	6.0E-01	0.14	33.69	6.9E-01
YP_513285.1	23.5	-0.02	23.69	1.0E+00	-0.15	23.69	5.4E-01	-0.57	23.69	5.8E-01
YP_514382.1	36.3	0.11	36.19	1.0E+00	-0.15	36.19	4.3E-01	0.17	36.19	6.2E-01
YP_514538.1	25.8	-0.41	26.20	1.0E+00	-0.15	26.20	5.3E-01	-0.38	26.20	6.0E-01
YP_513252.1	32.3	0.03	32.03	1.0E+00	-0.15	32.03	1.5E-01	0.06	32.03	6.9E-01
YP_513124.1	32.7	-0.13	32.87	1.0E+00	-0.15	32.87	2.8E-01	-0.15	32.87	6.1E-01
YP_514523.1	26.7	0.03	26.87	1.0E+00	-0.14	26.87	3.3E-01	-0.04	26.87	8.4E-01
YP_513276.1	28.3	-0.03	28.63	1.0E+00	-0.14	28.63	5.0E-01	-0.21	28.63	6.1E-01
YP_514025.1	32.2	-0.04	32.30	1.0E+00	-0.14	32.30	3.6E-01	-0.15	32.30	6.2E-01
YP_514031.1	26.2	0.05	26.15	1.0E+00	-0.14	26.15	5.1E-01	0.22	26.15	6.1E-01
YP_513980.1	33.0	0.00	32.95	1.0E+00	-0.14	32.95	1.3E-01	-0.05	32.95	6.8E-01
YP_513550.1	29.8	-0.03	29.89	1.0E+00	-0.14	29.89	3.6E-01	-0.20	29.89	6.0E-01
YP_514135.1	24.1	0.13	24.10	1.0E+00	-0.14	24.10	7.7E-01	-0.22	24.10	6.7E-01
YP_514252.1	25.3	-0.25	25.40	1.0E+00	-0.14	25.40	8.0E-01	-0.47	25.40	6.1E-01
YP_513449.1	27.6	0.21	27.13	1.0E+00	-0.14	27.13	9.0E-01	0.40	27.13	6.8E-01
YP_513194.1	34.1	-0.13	34.22	1.0E+00	-0.14	34.22	5.9E-01	-0.33	34.22	6.0E-01
YP_513316.1	27.0	-0.04	26.94	1.0E+00	-0.14	26.94	3.5E-01	0.17	26.94	6.0E-01
YP_513734.1	25.9	0.05	26.11	1.0E+00	-0.14	26.11	3.7E-01	-0.09	26.11	6.5E-01
YP_512821.1	30.4	-0.03	30.46	1.0E+00	-0.13	30.46	2.7E-01	0.10	30.46	6.3E-01
YP_513114.1	29.8	-0.02	29.83	1.0E+00	-0.13	29.83	8.9E-01	0.58	29.83	6.2E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513577.1	26.6	-0.09	26.63	1.0E+00	-0.13	26.63	5.5E-01	-0.13	26.63	6.4E-01
YP_514233.1	28.0	-0.08	27.95	1.0E+00	-0.13	27.95	4.7E-01	-0.18	27.95	6.1E-01
YP_513153.1	28.7	-0.06	28.87	1.0E+00	-0.13	28.87	2.4E-01	-0.22	28.87	6.0E-01
YP_513377.1	23.3	-0.25	23.73	1.0E+00	-0.12	23.73	7.9E-01	-0.50	23.73	6.0E-01
YP_513548.1	26.7	0.02	26.42	1.0E+00	-0.12	26.42	7.9E-01	0.33	26.42	6.2E-01
YP_514295.1	28.7	0.11	28.61	1.0E+00	-0.12	28.61	1.5E-01	0.05	28.61	6.9E-01
YP_514045.1	30.9	0.04	30.83	1.0E+00	-0.12	30.83	1.2E-01	0.01	30.83	9.6E-01
YP_513741.1	29.3	-0.09	29.57	1.0E+00	-0.12	29.57	2.9E-01	-0.19	29.57	6.0E-01
YP_513556.1	31.9	0.04	31.63	1.0E+00	-0.11	31.63	5.8E-01	0.20	31.63	6.1E-01
YP_513719.1	28.5	-0.01	28.59	1.0E+00	-0.11	28.59	3.4E-01	-0.04	28.59	7.9E-01
YP_513371.1	31.8	0.03	31.84	1.0E+00	-0.11	31.84	7.5E-01	0.08	31.84	8.4E-01
YP_512812.1	32.5	-0.08	32.56	1.0E+00	-0.11	32.56	6.7E-01	-0.24	32.56	6.1E-01
YP_513742.1	31.3	0.00	31.30	1.0E+00	-0.11	31.30	5.8E-01	0.13	31.30	6.3E-01
YP_512967.1	23.8	-0.17	23.81	1.0E+00	-0.11	23.81	5.8E-01	-0.07	23.81	7.9E-01
YP_513512.1	29.3	0.00	29.25	1.0E+00	-0.11	29.25	4.3E-01	0.08	29.25	6.8E-01
YP_513302.1	31.6	0.07	31.67	1.0E+00	-0.11	31.67	3.1E-01	0.05	31.67	7.1E-01
YP_514366.1	31.9	-0.01	31.86	1.0E+00	-0.11	31.86	7.3E-01	0.09	31.86	8.1E-01
YP_513171.1	30.6	-0.02	30.71	1.0E+00	-0.11	30.71	3.7E-01	-0.20	30.71	6.0E-01
YP_513954.1	30.0	-0.04	30.01	1.0E+00	-0.11	30.01	3.6E-01	-0.09	30.01	6.3E-01
YP_513344.1	32.7	0.04	32.43	1.0E+00	-0.11	32.43	4.9E-01	-0.04	32.43	8.6E-01
YP_513216.1	31.1	0.03	31.20	1.0E+00	-0.11	31.20	4.6E-01	-0.05	31.20	7.7E-01
YP_513119.1	29.9	-0.09	29.83	1.0E+00	-0.10	29.83	2.5E-01	-0.04	29.83	7.2E-01
YP_513077.1	27.5	0.02	27.51	1.0E+00	-0.10	27.51	7.3E-01	0.18	27.51	6.3E-01
YP_513085.1	30.0	0.02	30.08	1.0E+00	-0.10	30.08	8.6E-01	0.33	30.08	6.3E-01
YP_512969.1	29.6	0.06	29.70	1.0E+00	-0.10	29.70	9.2E-01	0.59	29.70	6.2E-01
YP_513012.1	26.4	-0.12	26.05	1.0E+00	-0.10	26.05	6.4E-01	0.24	26.05	6.0E-01
YP_513225.1	31.9	0.01	31.97	1.0E+00	-0.10	31.97	3.5E-01	-0.06	31.97	6.7E-01
YP_514554.1	30.1	0.05	30.11	1.0E+00	-0.10	30.11	2.3E-01	0.00	30.11	9.7E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_512864.1	27.4	-0.01	27.22	1.0E+00	-0.10	27.22	4.4E-01	0.01	27.22	9.6E-01
YP_513172.1	30.8	-0.02	30.88	1.0E+00	-0.10	30.88	3.3E-01	-0.15	30.88	6.0E-01
YP_514062.1	31.9	0.02	31.97	1.0E+00	-0.09	31.97	2.4E-01	-0.08	31.97	6.2E-01
YP_513574.1	30.2	-0.05	30.36	1.0E+00	-0.09	30.36	6.4E-01	-0.23	30.36	6.0E-01
YP_512993.1	25.0	-0.10	25.06	1.0E+00	-0.09	25.06	8.8E-01	-0.22	25.06	6.8E-01
YP_514277.1	27.4	-0.05	27.50	1.0E+00	-0.09	27.50	3.7E-01	-0.07	27.50	6.3E-01
YP_513650.1	28.3	0.09	28.17	1.0E+00	-0.09	28.17	8.7E-01	0.13	28.17	7.9E-01
YP_513715.1	28.3	0.19	28.16	1.0E+00	-0.09	28.16	6.2E-01	0.22	28.16	6.0E-01
YP_513476.1	28.0	0.02	27.94	1.0E+00	-0.09	27.94	4.3E-01	0.10	27.94	6.2E-01
YP_513832.1	33.1	-0.01	33.05	1.0E+00	-0.09	33.05	4.0E-01	0.04	33.05	7.4E-01
YP_513804.1	25.6	-0.20	25.76	1.0E+00	-0.08	25.76	7.9E-01	-0.21	25.76	6.3E-01
YP_513540.1	28.6	-0.08	28.66	1.0E+00	-0.08	28.66	4.9E-01	-0.10	28.66	6.3E-01
YP_513053.1	33.8	-0.12	33.89	1.0E+00	-0.08	33.89	3.9E-01	-0.09	33.89	6.2E-01
YP_513731.1	29.7	0.04	29.64	1.0E+00	-0.08	29.64	5.5E-01	0.09	29.64	6.3E-01
YP_513435.1	18.7	0.28	17.88	1.0E+00	-0.08	17.88	9.2E-01	-0.51	17.88	6.4E-01
YP_513166.1	24.5	0.04	24.42	1.0E+00	-0.08	24.42	7.7E-01	0.09	24.42	7.6E-01
YP_513654.1	30.3	0.07	30.13	1.0E+00	-0.08	30.13	6.0E-01	0.16	30.13	6.0E-01
YP_513955.1	28.9	-0.07	28.93	1.0E+00	-0.08	28.93	5.8E-01	-0.14	28.93	6.0E-01
YP_512875.1	30.5	-0.09	30.41	1.0E+00	-0.07	30.41	5.1E-01	-0.03	30.41	8.3E-01
YP_514244.1	30.6	-0.07	30.77	1.0E+00	-0.07	30.77	7.9E-01	-0.21	30.77	6.2E-01
YP_513521.1	28.6	-0.02	28.57	1.0E+00	-0.07	28.57	3.6E-01	0.06	28.57	6.3E-01
YP_512877.1	30.5	-0.08	30.51	1.0E+00	-0.07	30.51	6.4E-01	-0.06	30.51	7.3E-01
YP_513298.1	23.3	-0.03	23.22	1.0E+00	-0.07	23.22	7.8E-01	-0.02	23.22	9.6E-01
YP_513700.1	28.2	0.01	28.15	1.0E+00	-0.07	28.15	6.1E-01	0.07	28.15	6.8E-01
YP_513381.1	28.0	0.32	27.54	1.0E+00	-0.07	27.54	8.5E-01	0.18	27.54	6.3E-01
YP_513611.1	30.6	0.01	30.63	1.0E+00	-0.07	30.63	7.4E-01	-0.15	30.63	6.3E-01
YP_514376.1	34.5	0.06	34.56	1.0E+00	-0.07	34.56	8.9E-01	0.19	34.56	6.8E-01
YP_513047.1	32.5	-0.08	32.63	1.0E+00	-0.07	32.63	6.7E-01	0.01	32.63	9.8E-01
YP_513652.1	27.7	0.04	27.66	1.0E+00	-0.07	27.66	5.9E-01	0.05	27.66	7.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513061.1	34.3	0.04	34.38	1.0E+00	-0.07	34.38	8.3E-01	-0.17	34.38	6.3E-01
YP_514354.1	29.6	-0.01	29.76	1.0E+00	-0.07	29.76	6.2E-01	-0.10	29.76	6.3E-01
YP_514542.1	28.3	0.06	28.46	1.0E+00	-0.07	28.46	9.2E-01	0.35	28.46	6.9E-01
YP_512818.1	28.9	0.03	28.78	1.0E+00	-0.07	28.78	7.3E-01	0.13	28.78	6.3E-01
YP_513675.1	31.6	0.11	31.71	1.0E+00	-0.07	31.71	5.0E-01	0.09	31.71	6.2E-01
YP_513180.1	27.8	0.07	27.53	1.0E+00	-0.06	27.53	5.8E-01	0.10	27.53	6.2E-01
YP_513382.1	25.7	-0.08	25.75	1.0E+00	-0.06	25.75	7.0E-01	-0.04	25.75	8.3E-01
YP_514435.1	32.8	-0.04	32.94	1.0E+00	-0.06	32.94	6.8E-01	-0.18	32.94	6.0E-01
YP_513455.1	28.1	-0.05	28.21	1.0E+00	-0.06	28.21	7.6E-01	0.07	28.21	7.4E-01
YP_513041.1	31.9	0.01	31.89	1.0E+00	-0.06	31.89	6.5E-01	0.06	31.89	7.0E-01
YP_513630.1	27.7	-0.13	27.81	1.0E+00	-0.06	27.81	7.6E-01	-0.21	27.81	6.0E-01
YP_513045.1	32.8	-0.02	32.86	1.0E+00	-0.06	32.86	4.8E-01	-0.04	32.86	6.8E-01
YP_514250.1	30.2	-0.08	30.40	1.0E+00	-0.06	30.40	7.3E-01	-0.19	30.40	6.0E-01
YP_512971.1	20.5	0.02	20.56	1.0E+00	-0.06	20.56	9.4E-01	-0.97	20.56	6.0E-01
YP_514085.1	29.7	0.06	29.74	1.0E+00	-0.05	29.74	6.3E-01	0.11	29.74	6.1E-01
YP_513796.2	30.2	-0.07	30.40	1.0E+00	-0.05	30.40	6.5E-01	-0.15	30.40	6.0E-01
YP_513139.1	27.6	0.20	27.34	1.0E+00	-0.05	27.34	8.6E-01	0.31	27.34	6.0E-01
YP_513695.1	32.9	0.11	32.68	1.0E+00	-0.05	32.68	8.0E-01	-0.03	32.68	8.9E-01
YP_513493.1	28.6	0.03	28.52	1.0E+00	-0.05	28.52	7.1E-01	-0.01	28.52	9.7E-01
YP_512984.1	31.3	0.09	31.01	1.0E+00	-0.05	31.01	6.4E-01	0.09	31.01	6.2E-01
YP_513403.1	30.2	-0.08	30.39	1.0E+00	-0.05	30.39	8.2E-01	-0.18	30.39	6.1E-01
YP_513265.1	26.6	-0.23	26.94	1.0E+00	-0.05	26.94	9.2E-01	0.23	26.94	7.3E-01
YP_513314.1	26.5	-0.15	26.57	1.0E+00	-0.05	26.57	8.8E-01	-0.24	26.57	6.0E-01
YP_513795.1	29.8	0.02	29.82	1.0E+00	-0.05	29.82	7.0E-01	-0.15	29.82	6.0E-01
YP_512995.1	29.1	-0.10	29.27	1.0E+00	-0.04	29.27	8.0E-01	-0.15	29.27	6.1E-01
YP_513944.1	28.6	-0.14	28.68	1.0E+00	-0.04	28.68	7.9E-01	-0.20	28.68	6.0E-01
YP_512953.1	29.9	-0.07	29.85	1.0E+00	-0.04	29.85	9.0E-01	-0.16	29.85	6.3E-01
YP_513006.1	22.3	-0.21	22.20	1.0E+00	-0.04	22.20	9.0E-01	-0.13	22.20	6.3E-01
YP_513882.1	23.8	0.12	24.01	1.0E+00	-0.04	24.01	9.2E-01	0.06	24.01	9.1E-01
YP_513668.1	24.7	0.03	25.31	1.0E+00	-0.04	25.31	8.4E-01	-0.40	25.31	2.6E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513210.1	32.3	-0.06	32.37	1.0E+00	-0.04	32.37	8.6E-01	-0.18	32.37	6.0E-01
YP_513178.1	29.3	-0.04	29.34	1.0E+00	-0.04	29.34	6.4E-01	-0.03	29.34	7.8E-01
YP_513369.1	28.0	0.06	28.11	1.0E+00	-0.04	28.11	9.0E-01	-0.11	28.11	6.8E-01
YP_513477.1	26.6	-0.08	26.61	1.0E+00	-0.03	26.61	9.0E-01	-0.07	26.61	7.7E-01
YP_513046.1	32.9	0.06	32.71	1.0E+00	-0.03	32.71	7.9E-01	0.21	32.71	6.0E-01
YP_513028.1	33.9	-0.04	34.07	1.0E+00	-0.03	34.07	9.2E-01	0.04	34.07	8.9E-01
YP_513713.1	25.7	0.04	25.47	1.0E+00	-0.03	25.47	9.2E-01	0.27	25.47	6.2E-01
YP_514534.1	30.5	0.11	30.48	1.0E+00	-0.03	30.48	9.2E-01	0.23	30.48	6.2E-01
YP_514465.1	29.3	-0.06	29.47	1.0E+00	-0.03	29.47	9.2E-01	0.07	29.47	8.7E-01
YP_513678.1	27.5	0.05	27.56	1.0E+00	-0.03	27.56	9.2E-01	0.15	27.56	6.3E-01
YP_513690.1	24.4	-0.16	24.41	1.0E+00	-0.03	24.41	9.6E-01	-0.60	24.41	6.1E-01
YP_514367.1	27.8	0.02	27.90	1.0E+00	-0.03	27.90	8.1E-01	-0.14	27.90	6.0E-01
YP_513523.1	23.1	0.11	23.17	1.0E+00	-0.03	23.17	9.2E-01	0.12	23.17	6.9E-01
YP_513226.1	31.2	0.00	31.17	1.0E+00	-0.03	31.17	8.2E-01	0.04	31.17	7.4E-01
YP_513513.1	31.2	0.04	31.14	1.0E+00	-0.03	31.14	8.6E-01	0.03	31.14	8.4E-01
YP_513406.1	28.4	0.10	28.35	1.0E+00	-0.02	28.35	9.4E-01	0.31	28.35	6.2E-01
YP_513727.1	33.4	0.01	33.40	1.0E+00	-0.02	33.40	9.4E-01	0.27	33.40	6.3E-01
YP_513554.1	31.3	0.04	31.05	1.0E+00	-0.02	31.05	9.1E-01	0.08	31.05	6.5E-01
YP_513054.1	32.9	0.04	32.90	1.0E+00	-0.02	32.90	9.2E-01	0.07	32.90	6.8E-01
YP_513306.1	30.4	0.05	30.26	1.0E+00	-0.02	30.26	9.1E-01	0.08	30.26	6.3E-01
YP_514360.1	28.2	-0.05	28.40	1.0E+00	-0.02	28.40	9.2E-01	-0.18	28.40	6.1E-01
YP_513398.1	31.4	-0.16	31.73	1.0E+00	-0.02	31.73	9.2E-01	-0.24	31.73	6.0E-01
YP_512876.1	27.3	0.05	27.51	1.0E+00	-0.02	27.51	9.2E-01	-0.12	27.51	6.1E-01
YP_513063.1	35.2	0.00	35.16	1.0E+00	-0.02	35.16	9.3E-01	-0.17	35.16	6.3E-01
YP_513193.1	29.1	0.00	29.15	1.0E+00	-0.02	29.15	9.5E-01	0.18	29.15	6.4E-01
YP_513098.1	29.6	-0.03	29.77	1.0E+00	-0.02	29.77	9.2E-01	-0.11	29.77	6.3E-01
YP_514548.1	30.9	0.06	30.97	1.0E+00	-0.02	30.97	9.2E-01	-0.01	30.97	9.6E-01
YP_512992.1	26.0	-0.21	26.46	1.0E+00	-0.01	26.46	9.5E-01	-0.17	26.46	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514513.1	31.2	-0.04	31.35	1.0E+00	-0.01	31.35	9.2E-01	-0.01	31.35	9.7E-01
YP_513901.1	26.3	0.00	26.40	1.0E+00	-0.01	26.40	9.5E-01	-0.14	26.40	6.2E-01
YP_513106.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514545.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514532.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514503.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514499.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514438.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514388.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514349.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514344.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514319.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514313.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514282.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514269.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514266.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514249.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514190.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514155.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514113.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514101.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514057.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514030.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_514012.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513987.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513969.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513961.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513921.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513878.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513838.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513814.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513721.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513680.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513518.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513484.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513434.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513430.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513384.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513367.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513279.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513272.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513212.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513190.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513136.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513126.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513062.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513060.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513058.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512980.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512959.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512951.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512933.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512926.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512905.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512884.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512862.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512831.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512827.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_512814.1	24.3	0.01	24.22	1.0E+00	-0.01	24.22	9.2E-01	0.06	24.22	6.3E-01
YP_513294.1	31.1	0.06	31.02	1.0E+00	-0.01	31.02	9.4E-01	0.07	31.02	6.7E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514539.1	30.1	0.11	29.77	1.0E+00	-0.01	29.77	9.5E-01	0.20	29.77	6.0E-01
YP_514052.1	27.7	-0.02	27.70	1.0E+00	-0.01	27.70	9.4E-01	-0.12	27.70	6.0E-01
YP_514529.1	27.4	-0.07	27.68	1.0E+00	-0.01	27.68	9.7E-01	-0.20	27.68	6.1E-01
YP_513788.1	31.6	0.02	31.47	1.0E+00	-0.01	31.47	9.5E-01	0.13	31.47	6.0E-01
YP_513917.1	24.0	0.19	23.84	1.0E+00	0.00	23.84	9.9E-01	-0.21	23.84	7.2E-01
YP_514556.1	29.9	0.00	30.02	1.0E+00	0.00	30.02	1.0E+00	-0.14	30.02	6.1E-01
YP_514021	0.0	28.71	8.60	7.0E-30	0.00	8.60	1.0E+00	0.00	8.60	1.0E+00
YP_513228.1	25.8	0.00	8.07	1.0E+00	0.00	8.07	1.0E+00	26.04	8.07	1.0E-26
YP_513534.1	28.8	-0.06	28.88	1.0E+00	0.00	28.88	9.9E-01	-0.15	28.88	6.3E-01
YP_513019.1	33.6	0.00	33.60	1.0E+00	0.00	33.60	9.7E-01	-0.06	33.60	7.3E-01
YP_514304.1	24.5	0.00	24.51	1.0E+00	0.01	24.51	9.8E-01	0.19	24.51	6.3E-01
YP_513749.1	26.1	0.00	25.72	1.0E+00	0.01	25.72	9.5E-01	-0.22	25.72	6.0E-01
YP_513020.1	34.4	0.08	34.29	1.0E+00	0.01	34.29	9.8E-01	0.24	34.29	6.2E-01
YP_513920.1	30.2	0.03	30.17	1.0E+00	0.01	30.17	9.5E-01	0.07	30.17	7.9E-01
YP_514420.1	33.5	0.03	33.41	1.0E+00	0.01	33.41	9.2E-01	-0.02	33.41	9.4E-01
YP_513481.1	20.3	0.77	20.06	1.0E+00	0.01	20.06	9.8E-01	1.38	20.06	6.0E-01
YP_513307.1	32.9	0.10	32.99	1.0E+00	0.01	32.99	9.5E-01	0.04	32.99	9.1E-01
YP_513222.1	29.3	0.14	29.11	1.0E+00	0.02	29.11	9.2E-01	0.02	29.11	9.3E-01
YP_514374.1	34.7	0.05	34.67	1.0E+00	0.02	34.67	9.2E-01	-0.02	34.67	9.2E-01
YP_514001.1	19.9	-0.15	21.28	1.0E+00	0.02	21.28	9.8E-01	-0.91	21.28	6.0E-01
YP_514087.1	28.8	-0.04	28.93	1.0E+00	0.02	28.93	9.2E-01	0.01	28.93	9.6E-01
YP_512946.1	27.6	-0.09	27.71	1.0E+00	0.02	27.71	9.2E-01	-0.24	27.71	6.0E-01
YP_513100.1	22.2	-0.09	22.64	1.0E+00	0.02	22.64	9.7E-01	-0.64	22.64	6.0E-01
YP_513385.1	25.0	0.00	25.19	1.0E+00	0.02	25.19	9.2E-01	0.10	25.19	6.7E-01
YP_513362.1	31.1	0.03	31.05	1.0E+00	0.02	31.05	9.2E-01	-0.03	31.05	8.9E-01
YP_513530.1	24.5	-0.13	24.58	1.0E+00	0.02	24.58	9.6E-01	-0.02	24.58	9.8E-01
YP_513186.1	28.9	-0.01	28.81	1.0E+00	0.02	28.81	9.1E-01	-0.14	28.81	6.1E-01
YP_513097.1	25.4	0.08	25.49	1.0E+00	0.02	25.49	9.2E-01	0.16	25.49	6.3E-01
YP_514340.1	28.6	0.05	28.45	1.0E+00	0.03	28.45	9.2E-01	0.17	28.45	6.1E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513365.1	30.6	-0.01	30.53	1.0E+00	0.03	30.53	8.3E-01	-0.05	30.53	6.9E-01
YP_513170.1	26.2	-0.09	26.46	1.0E+00	0.03	26.46	8.8E-01	-0.11	26.46	6.3E-01
YP_512890.1	28.4	0.08	28.55	1.0E+00	0.03	28.55	9.5E-01	0.60	28.55	6.1E-01
YP_512880.1	29.4	0.05	29.45	1.0E+00	0.03	29.45	8.2E-01	0.00	29.45	9.8E-01
YP_513549.1	29.2	-0.11	29.21	1.0E+00	0.03	29.21	8.3E-01	-0.07	29.21	6.5E-01
YP_514036.1	25.7	0.04	25.75	1.0E+00	0.03	25.75	9.4E-01	0.40	25.75	6.2E-01
YP_514274.1	20.7	0.10	20.91	1.0E+00	0.04	20.91	9.3E-01	-0.22	20.91	6.8E-01
YP_513379.1	28.1	0.04	28.12	1.0E+00	0.04	28.12	8.8E-01	0.00	28.12	1.0E+00
YP_514141.1	30.7	0.06	30.58	1.0E+00	0.04	30.58	7.7E-01	0.01	30.58	9.8E-01
YP_514365.1	24.7	-0.02	24.50	1.0E+00	0.04	24.50	9.4E-01	-0.21	24.50	7.2E-01
YP_513151.1	27.7	0.27	27.36	1.0E+00	0.04	27.36	9.4E-01	0.49	27.36	6.1E-01
YP_514472.1	31.0	0.05	30.93	1.0E+00	0.04	30.93	8.3E-01	0.00	30.93	9.8E-01
YP_513437.1	28.5	-0.04	28.48	1.0E+00	0.04	28.48	8.8E-01	-0.15	28.48	6.3E-01
YP_512847.1	29.7	-0.09	29.53	1.0E+00	0.04	29.53	9.2E-01	0.15	29.53	6.5E-01
YP_513291.1	33.3	0.03	33.30	1.0E+00	0.04	33.30	8.5E-01	0.14	33.30	6.2E-01
YP_513208.1	32.0	-0.04	32.11	1.0E+00	0.04	32.11	8.8E-01	-0.15	32.11	6.3E-01
YP_514039.1	29.0	0.18	28.89	1.0E+00	0.04	28.89	9.2E-01	0.35	28.89	6.2E-01
YP_514237.1	31.5	-0.03	31.61	1.0E+00	0.04	31.61	7.2E-01	-0.07	31.61	6.3E-01
YP_513646.1	28.7	0.06	28.41	1.0E+00	0.04	28.41	8.5E-01	0.10	28.41	6.5E-01
YP_513994.1	35.0	0.11	34.91	1.0E+00	0.04	34.91	6.2E-01	0.09	34.91	6.0E-01
YP_514330.1	24.4	-0.02	24.78	1.0E+00	0.05	24.78	9.2E-01	-0.46	24.78	6.0E-01
YP_512982.1	30.2	0.20	30.07	1.0E+00	0.05	30.07	9.1E-01	0.15	30.07	6.7E-01
YP_513422.1	27.1	0.06	27.02	1.0E+00	0.05	27.02	9.2E-01	0.13	27.02	8.2E-01
YP_513946.1	30.1	-0.08	30.16	1.0E+00	0.05	30.16	8.7E-01	-0.17	30.16	6.3E-01
YP_513043.1	33.7	-0.09	33.85	1.0E+00	0.05	33.85	8.6E-01	-0.19	33.85	6.2E-01
YP_513578.1	30.7	-0.13	30.70	1.0E+00	0.05	30.70	8.2E-01	0.02	30.70	9.4E-01
YP_514256.1	30.3	0.05	30.36	1.0E+00	0.06	30.36	5.0E-01	-0.05	30.36	6.3E-01
YP_513519.1	28.2	0.03	28.22	1.0E+00	0.06	28.22	6.6E-01	-0.01	28.22	9.4E-01
YP_513474.1	28.7	-0.01	28.94	1.0E+00	0.06	28.94	9.0E-01	0.24	28.94	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513247.1	28.5	-0.03	28.56	1.0E+00	0.06	28.56	4.6E-01	-0.01	28.56	9.0E-01
YP_514294.1	29.6	-0.03	29.74	1.0E+00	0.06	29.74	5.6E-01	-0.08	29.74	6.3E-01
YP_513037.1	34.0	0.07	33.94	1.0E+00	0.06	33.94	7.2E-01	-0.06	33.94	7.6E-01
YP_513723.1	28.4	-0.03	28.46	1.0E+00	0.06	28.46	6.3E-01	-0.10	28.46	6.2E-01
YP_512822.1	31.8	0.01	31.80	1.0E+00	0.06	31.80	4.7E-01	0.03	31.80	7.8E-01
YP_513034.1	33.8	0.19	33.65	1.0E+00	0.06	33.65	8.9E-01	0.29	33.65	6.1E-01
YP_513408.1	30.1	-0.03	30.02	1.0E+00	0.06	30.02	6.0E-01	0.05	30.02	7.2E-01
YP_513555.1	26.5	-0.02	26.48	1.0E+00	0.06	26.48	7.0E-01	0.03	26.48	8.9E-01
YP_513635.1	27.5	0.14	27.41	1.0E+00	0.06	27.41	9.2E-01	0.38	27.41	6.3E-01
YP_513560.1	30.2	0.04	30.00	1.0E+00	0.06	30.00	8.1E-01	0.04	30.00	8.9E-01
YP_512935.1	29.2	-0.16	29.42	1.0E+00	0.06	29.42	8.5E-01	-0.28	29.42	6.0E-01
YP_513898.1	26.5	0.00	26.61	1.0E+00	0.06	26.61	8.3E-01	-0.06	26.61	8.6E-01
YP_513885.1	26.4	-0.03	26.20	1.0E+00	0.07	26.20	8.3E-01	0.27	26.20	6.0E-01
YP_514555.1	32.1	0.39	32.31	1.0E+00	0.07	32.31	9.1E-01	0.26	32.31	6.3E-01
YP_513927.1	28.3	0.01	28.24	1.0E+00	0.07	28.24	8.8E-01	0.20	28.24	6.4E-01
YP_513348.1	33.5	0.01	33.60	1.0E+00	0.07	33.60	4.5E-01	0.02	33.60	8.8E-01
YP_513411.1	28.2	-0.12	28.57	1.0E+00	0.07	28.57	5.8E-01	-0.18	28.57	6.0E-01
YP_514194.1	27.4	-0.09	27.54	1.0E+00	0.07	27.54	5.2E-01	-0.18	27.54	6.0E-01
YP_514097.1	33.3	-0.10	33.33	1.0E+00	0.07	33.33	7.9E-01	-0.12	33.33	6.7E-01
YP_513965.1	27.5	-0.12	27.61	1.0E+00	0.07	27.61	8.5E-01	-0.35	27.61	6.0E-01
YP_513424.1	26.4	-0.10	26.18	1.0E+00	0.07	26.18	9.2E-01	0.21	26.18	7.3E-01
YP_513257.1	31.3	-0.01	31.23	1.0E+00	0.07	31.23	5.5E-01	-0.02	31.23	8.9E-01
YP_513768.1	29.8	0.04	29.91	1.0E+00	0.07	29.91	8.3E-01	-0.14	29.91	6.8E-01
YP_513522.1	25.2	0.02	25.42	1.0E+00	0.07	25.42	7.0E-01	0.08	25.42	7.3E-01
YP_513013.1	31.0	0.07	30.94	1.0E+00	0.08	30.94	4.4E-01	0.09	30.94	6.2E-01
YP_514127.1	30.5	-0.02	30.45	1.0E+00	0.08	30.45	6.0E-01	-0.06	30.45	7.4E-01
YP_513195.1	29.4	-0.01	29.19	1.0E+00	0.08	29.19	9.1E-01	0.12	29.19	8.3E-01
YP_513666.1	28.6	0.05	28.48	1.0E+00	0.08	28.48	7.8E-01	0.11	28.48	6.9E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513869.1	32.3	0.06	32.19	1.0E+00	0.08	32.19	7.9E-01	0.24	32.19	6.1E-01
YP_513764.1	29.3	-0.01	29.29	1.0E+00	0.08	29.29	7.4E-01	-0.10	29.29	7.2E-01
YP_513956.1	27.9	-0.01	27.96	1.0E+00	0.08	27.96	6.4E-01	-0.15	27.96	6.2E-01
YP_513812.1	24.5	0.07	24.39	1.0E+00	0.08	24.39	5.7E-01	-0.06	24.39	7.3E-01
YP_514198.1	31.4	-0.04	31.30	1.0E+00	0.08	31.30	3.4E-01	0.04	31.30	7.3E-01
YP_513345.1	31.6	-0.08	31.65	1.0E+00	0.08	31.65	7.6E-01	-0.14	31.65	6.3E-01
YP_513790.1	29.1	0.05	29.27	1.0E+00	0.08	29.27	9.2E-01	0.66	29.27	6.2E-01
YP_513227.1	27.1	0.06	25.03	1.0E+00	0.08	25.03	9.2E-01	0.11	25.03	8.8E-01
YP_513933.1	27.4	0.01	27.29	1.0E+00	0.09	27.29	7.8E-01	0.24	27.29	6.2E-01
YP_514217.1	23.7	0.14	23.73	1.0E+00	0.09	23.73	8.6E-01	0.25	23.73	6.3E-01
YP_512820.1	29.7	-0.04	29.51	1.0E+00	0.09	29.51	5.1E-01	0.13	29.51	6.1E-01
YP_514423.1	30.0	-0.02	29.95	1.0E+00	0.09	29.95	4.5E-01	-0.05	29.95	7.4E-01
YP_514510.1	28.2	0.15	28.12	1.0E+00	0.09	28.12	5.5E-01	0.21	28.12	6.0E-01
YP_513883.1	26.4	0.01	26.02	1.0E+00	0.09	26.02	6.4E-01	0.37	26.02	6.0E-01
YP_513940.1	30.4	0.06	30.40	1.0E+00	0.09	30.40	4.8E-01	0.16	30.40	6.0E-01
YP_513900.1	25.5	-0.02	24.88	1.0E+00	0.09	24.88	9.0E-01	0.62	24.88	6.0E-01
YP_513303.1	29.0	-0.03	28.98	1.0E+00	0.09	28.98	5.5E-01	-0.17	28.98	6.0E-01
YP_514262.1	27.3	-0.04	27.23	1.0E+00	0.09	27.23	8.5E-01	-0.37	27.23	6.1E-01
YP_513177.1	29.2	-0.51	29.58	1.0E+00	0.10	29.58	7.8E-01	-0.16	29.58	6.8E-01
YP_514112.1	33.0	0.02	33.00	1.0E+00	0.10	33.00	3.6E-01	-0.01	33.00	9.7E-01
YP_514050.1	27.2	-0.08	27.12	1.0E+00	0.10	27.12	6.3E-01	-0.09	27.12	7.1E-01
YP_513507.1	27.9	0.01	28.20	1.0E+00	0.10	28.20	7.7E-01	0.05	28.20	9.0E-01
YP_514564.1	24.6	0.21	24.42	1.0E+00	0.10	24.42	7.5E-01	0.33	24.42	6.0E-01
YP_514139.1	26.7	0.20	26.47	1.0E+00	0.10	26.47	7.8E-01	0.30	26.47	6.1E-01
YP_513597.1	30.4	-0.05	30.33	1.0E+00	0.10	30.33	3.0E-01	-0.02	30.33	9.1E-01
YP_513103.1	32.2	-0.08	32.26	1.0E+00	0.10	32.26	3.3E-01	-0.06	32.26	6.4E-01
YP_513860.1	28.5	0.00	28.66	1.0E+00	0.10	28.66	5.7E-01	0.15	28.66	6.2E-01
YP_514104.1	25.6	0.05	26.00	1.0E+00	0.10	26.00	5.0E-01	-0.27	26.00	6.0E-01
YP_513957.1	22.4	-0.04	23.09	1.0E+00	0.10	23.09	8.9E-01	-0.40	23.09	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_512998.1	26.4	0.07	26.42	1.0E+00	0.10	26.42	7.8E-01	-0.18	26.42	6.5E-01
YP_514035.1	21.0	0.61	21.32	1.0E+00	0.10	21.32	9.2E-01	0.32	21.32	7.2E-01
YP_513881.1	31.1	-0.05	31.20	1.0E+00	0.10	31.20	1.8E-01	-0.02	31.20	8.8E-01
YP_513102.1	33.3	-0.01	33.29	1.0E+00	0.11	33.29	2.6E-01	0.04	33.29	7.8E-01
YP_514199.1	34.2	-0.01	34.26	1.0E+00	0.11	34.26	2.3E-01	0.04	34.26	7.3E-01
YP_513570.1	30.3	-0.07	30.18	1.0E+00	0.11	30.18	6.4E-01	-0.08	30.18	7.9E-01
YP_513835.1	31.2	0.04	31.10	1.0E+00	0.11	31.10	3.8E-01	0.00	31.10	1.0E+00
YP_513342.1	27.2	-0.01	27.11	1.0E+00	0.11	27.11	5.8E-01	0.12	27.11	6.3E-01
YP_513750.1	31.4	0.12	31.28	1.0E+00	0.11	31.28	4.6E-01	0.20	31.28	6.0E-01
YP_514187.1	27.1	0.05	27.04	1.0E+00	0.11	27.04	7.3E-01	0.02	27.04	9.6E-01
YP_513572.1	29.8	0.09	29.40	1.0E+00	0.11	29.40	5.1E-01	0.13	29.40	6.3E-01
YP_513410.1	28.1	0.04	27.85	1.0E+00	0.12	27.85	5.0E-01	-0.02	27.85	9.6E-01
YP_514478.1	30.7	-0.03	30.65	1.0E+00	0.12	30.65	4.6E-01	-0.10	30.65	6.4E-01
YP_514245.1	29.3	0.01	29.29	1.0E+00	0.12	29.29	5.0E-01	0.09	29.29	6.8E-01
YP_513973.1	30.5	0.11	30.34	1.0E+00	0.12	30.34	8.3E-01	0.10	30.34	8.7E-01
YP_513636.1	31.0	0.22	30.61	1.0E+00	0.12	30.61	7.4E-01	0.35	30.61	6.0E-01
YP_514337.1	28.9	0.10	28.92	1.0E+00	0.12	28.92	8.5E-01	0.49	28.92	6.1E-01
YP_513656.1	23.6	-0.34	23.69	1.0E+00	0.12	23.69	7.1E-01	-0.11	23.69	7.6E-01
YP_514520.1	30.9	0.09	30.98	1.0E+00	0.12	30.98	4.3E-01	0.09	30.98	6.4E-01
YP_514184.1	30.2	-0.04	30.42	1.0E+00	0.12	30.42	7.3E-01	0.15	30.42	7.1E-01
YP_514299.1	30.3	-0.03	30.35	1.0E+00	0.12	30.35	3.5E-01	-0.01	30.35	9.6E-01
YP_513833.1	31.1	-0.06	31.07	1.0E+00	0.12	31.07	3.4E-01	-0.05	31.07	7.7E-01
YP_513290.1	27.9	0.21	27.54	1.0E+00	0.12	27.54	9.0E-01	0.90	27.54	6.0E-01
YP_513397.1	29.2	0.02	29.26	1.0E+00	0.12	29.26	1.6E-01	0.05	29.26	7.0E-01
YP_513524.1	30.5	0.04	30.36	1.0E+00	0.12	30.36	2.1E-01	0.19	30.36	6.0E-01
YP_513936.1	26.7	-0.11	27.09	1.0E+00	0.12	27.09	3.8E-01	-0.26	27.09	6.0E-01
YP_512940.1	26.1	0.08	26.11	1.0E+00	0.12	26.11	7.3E-01	0.33	26.11	6.0E-01
YP_513329.1	32.6	0.02	32.56	1.0E+00	0.12	32.56	2.9E-01	0.06	32.56	6.9E-01
YP_512873.1	27.3	0.18	27.17	1.0E+00	0.13	27.17	5.8E-01	0.26	27.17	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514075.1	29.7	0.00	29.75	1.0E+00	0.13	29.75	2.2E-01	-0.02	29.75	9.2E-01
YP_513023.1	27.4	0.30	27.48	1.0E+00	0.13	27.48	5.0E-01	0.14	27.48	6.3E-01
YP_514109.1	31.0	0.02	31.09	1.0E+00	0.13	31.09	2.4E-01	-0.10	31.09	6.2E-01
YP_513913.1	28.9	-0.01	29.01	1.0E+00	0.13	29.01	4.0E-01	-0.02	29.01	9.4E-01
YP_514146.1	26.4	-0.02	26.39	1.0E+00	0.13	26.39	6.3E-01	-0.03	26.39	9.5E-01
YP_513224.1	27.9	0.13	27.87	1.0E+00	0.13	27.87	2.4E-01	0.00	27.87	9.8E-01
YP_513181.1	28.5	-0.11	28.73	1.0E+00	0.13	28.73	6.7E-01	0.07	28.73	8.6E-01
YP_514000.1	31.3	0.04	31.24	1.0E+00	0.13	31.24	6.3E-02	0.06	31.24	6.3E-01
YP_514179.1	29.6	0.00	29.67	1.0E+00	0.14	29.67	7.8E-01	0.34	29.67	6.2E-01
YP_513834.1	33.0	0.01	32.97	1.0E+00	0.14	32.97	2.0E-01	0.17	32.97	6.0E-01
YP_514107.1	31.7	0.36	31.23	1.0E+00	0.14	31.23	9.0E-01	0.49	31.23	6.3E-01
YP_514370.1	29.2	-0.02	29.28	1.0E+00	0.14	29.28	9.6E-02	0.01	29.28	9.5E-01
YP_513618.1	27.6	-0.11	27.57	1.0E+00	0.14	27.57	5.8E-01	-0.20	27.57	6.3E-01
YP_513144.1	31.0	0.00	30.88	1.0E+00	0.14	30.88	1.5E-01	0.18	30.88	6.0E-01
YP_514080.1	26.2	0.08	26.02	1.0E+00	0.15	26.02	4.8E-01	0.28	26.02	6.0E-01
YP_513565.1	29.4	0.07	29.35	1.0E+00	0.15	29.35	2.6E-01	0.00	29.35	1.0E+00
YP_513478.1	26.4	0.10	26.28	1.0E+00	0.15	26.28	2.4E-01	0.16	26.28	6.0E-01
YP_514483.1	30.4	0.22	30.18	1.0E+00	0.15	30.18	6.2E-01	0.26	30.18	6.2E-01
YP_514355.1	27.7	-0.03	27.83	1.0E+00	0.15	27.83	2.6E-01	-0.15	27.83	6.0E-01
YP_512895.1	34.1	0.03	34.36	1.0E+00	0.15	34.36	2.5E-01	-0.01	34.36	9.8E-01
YP_513439.1	18.2	-1.24	16.84	1.0E+00	0.15	16.84	9.7E-01	-6.22	16.84	6.0E-01
YP_513318.1	31.9	-0.06	31.99	1.0E+00	0.15	31.99	3.7E-01	0.04	31.99	8.7E-01
YP_512878.1	27.5	0.04	27.55	1.0E+00	0.16	27.55	4.3E-01	0.18	27.55	6.2E-01
YP_513376.1	36.0	-0.23	36.19	1.0E+00	0.16	36.19	5.3E-01	-0.16	36.19	6.3E-01
YP_513049.1	31.0	0.16	31.32	1.0E+00	0.16	31.32	6.4E-01	0.05	31.32	9.1E-01
YP_514341.1	26.7	0.28	26.45	1.0E+00	0.16	26.45	8.8E-01	0.55	26.45	6.3E-01
YP_513407.1	25.0	-0.07	25.26	1.0E+00	0.16	25.26	7.5E-01	-0.45	25.26	6.1E-01
YP_513450.1	26.1	0.00	26.40	1.0E+00	0.16	26.40	1.8E-01	-0.08	26.40	6.4E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514218.1	30.4	0.03	30.40	1.0E+00	0.16	30.40	6.6E-01	0.28	30.40	6.3E-01
YP_514487.1	27.5	-0.07	27.49	1.0E+00	0.16	27.49	2.2E-01	-0.11	27.49	6.3E-01
YP_514226.1	27.0	-0.09	27.34	1.0E+00	0.16	27.34	4.3E-01	-0.37	27.34	6.0E-01
YP_513287.1	30.6	-0.07	30.67	1.0E+00	0.16	30.67	1.2E-01	-0.15	30.67	6.0E-01
YP_513606.1	30.8	-0.01	31.04	1.0E+00	0.17	31.04	1.3E-01	-0.04	31.04	8.1E-01
YP_513055.1	33.7	-0.02	33.76	1.0E+00	0.17	33.76	1.6E-01	0.17	33.76	6.0E-01
YP_514400.1	29.6	0.10	29.40	1.0E+00	0.17	29.40	3.1E-01	0.15	29.40	6.2E-01
YP_514255.1	28.7	0.04	28.60	1.0E+00	0.17	28.60	4.0E-01	0.09	28.60	7.3E-01
YP_513480.1	27.4	0.06	27.39	1.0E+00	0.17	27.39	1.0E-01	0.05	27.39	7.0E-01
YP_513671.1	30.8	0.00	31.12	1.0E+00	0.17	31.12	3.5E-01	-0.16	31.12	6.2E-01
YP_513082.1	24.4	0.08	24.69	1.0E+00	0.17	24.69	8.3E-01	-0.59	24.69	6.2E-01
YP_513022.1	31.8	0.02	32.08	1.0E+00	0.17	32.08	7.2E-01	0.35	32.08	6.3E-01
YP_513584.1	26.2	0.05	26.30	1.0E+00	0.18	26.30	1.7E-01	-0.07	26.30	7.0E-01
YP_513315.1	29.1	0.12	28.87	1.0E+00	0.18	28.87	3.2E-01	0.08	28.87	7.3E-01
YP_513793.1	30.4	0.02	30.34	1.0E+00	0.18	30.34	3.1E-02	0.05	30.34	6.7E-01
YP_512997.1	24.4	0.12	24.26	1.0E+00	0.18	24.26	6.8E-01	0.02	24.26	9.7E-01
YP_513568.1	26.5	-0.04	26.07	1.0E+00	0.18	26.07	8.3E-01	0.29	26.07	7.2E-01
YP_513697.1	27.8	0.05	27.81	1.0E+00	0.18	27.81	1.7E-01	0.00	27.81	9.8E-01
YP_513718.1	29.5	0.02	29.47	1.0E+00	0.18	29.47	1.3E-01	0.07	29.47	6.8E-01
YP_513417.1	26.4	-0.09	26.49	1.0E+00	0.18	26.49	4.0E-01	0.09	26.49	7.3E-01
YP_513333.1	29.9	0.08	29.90	1.0E+00	0.18	29.90	6.4E-01	0.37	29.90	6.1E-01
YP_513614.1	30.4	0.20	30.13	1.0E+00	0.18	30.13	8.3E-01	0.42	30.13	6.3E-01
YP_513615.1	30.0	0.05	29.90	1.0E+00	0.18	29.90	7.1E-02	0.01	29.90	9.3E-01
YP_514181.1	29.5	-0.01	29.67	1.0E+00	0.18	29.67	7.1E-02	-0.09	29.67	6.3E-01
YP_513475.1	25.3	0.24	25.10	1.0E+00	0.18	25.10	4.4E-01	0.07	25.10	8.3E-01
YP_513717.1	30.9	-0.08	30.96	1.0E+00	0.18	30.96	3.8E-01	-0.18	30.96	6.3E-01
YP_513184.1	28.1	0.14	28.07	1.0E+00	0.19	28.07	8.3E-01	0.72	28.07	6.1E-01
YP_514149.1	30.0	-0.13	30.37	1.0E+00	0.19	30.37	4.9E-01	0.05	30.37	9.0E-01
YP_513645.1	28.1	-0.10	28.27	1.0E+00	0.19	28.27	2.7E-02	-0.06	28.27	6.3E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513305.1	29.7	0.24	29.68	1.0E+00	0.19	29.68	8.3E-01	0.87	29.68	6.0E-01
YP_514413.1	29.5	-0.12	29.47	1.0E+00	0.19	29.47	3.9E-01	-0.10	29.47	7.3E-01
YP_514345.1	36.7	0.12	36.64	1.0E+00	0.19	36.64	3.2E-01	0.19	36.64	6.1E-01
YP_513763.1	26.8	0.15	26.89	1.0E+00	0.19	26.89	7.7E-01	0.53	26.89	6.1E-01
YP_513492.1	31.0	-0.03	31.11	1.0E+00	0.19	31.11	9.7E-02	0.01	31.11	9.5E-01
YP_513489.1	24.6	-0.06	24.72	1.0E+00	0.19	24.72	4.3E-01	-0.12	24.72	6.9E-01
YP_513056.1	32.7	0.11	32.58	1.0E+00	0.20	32.58	1.0E-01	0.06	32.58	7.2E-01
YP_513116.1	29.5	-0.02	29.53	1.0E+00	0.20	29.53	8.8E-02	0.06	29.53	6.9E-01
YP_513612.1	31.2	0.05	31.07	1.0E+00	0.20	31.07	1.6E-02	0.07	31.07	6.3E-01
YP_514215.1	25.8	-0.02	25.85	1.0E+00	0.20	25.85	3.9E-01	-0.11	25.85	7.1E-01
YP_513366.1	29.8	0.01	29.86	1.0E+00	0.20	29.86	2.2E-01	-0.13	29.86	6.3E-01
YP_513202.1	27.8	-0.08	28.01	1.0E+00	0.20	28.01	6.3E-01	-0.28	28.01	6.3E-01
YP_513872.1	28.1	-0.05	28.20	1.0E+00	0.20	28.20	7.2E-02	-0.18	28.20	6.0E-01
YP_512978.1	26.6	0.09	26.87	1.0E+00	0.20	26.87	7.2E-02	-0.16	26.87	6.0E-01
YP_513258.1	29.1	0.04	29.16	1.0E+00	0.20	29.16	1.5E-01	-0.11	29.16	6.3E-01
YP_512867.1	27.0	0.08	27.10	1.0E+00	0.21	27.10	3.4E-01	-0.07	27.10	8.2E-01
YP_514301.1	29.2	0.00	29.35	1.0E+00	0.21	29.35	1.1E-01	-0.07	29.35	7.0E-01
YP_514421.1	30.5	0.00	30.42	1.0E+00	0.21	30.42	1.3E-01	-0.12	30.42	6.3E-01
YP_512937.1	28.1	0.15	27.72	1.0E+00	0.21	27.72	4.0E-01	0.30	27.72	6.0E-01
YP_513602.1	25.9	-0.15	26.15	1.0E+00	0.21	26.15	4.1E-01	-0.26	26.15	6.1E-01
YP_514336.1	30.4	-0.06	30.54	1.0E+00	0.21	30.54	7.5E-02	-0.17	30.54	6.0E-01
YP_513101.1	34.7	0.12	34.58	1.0E+00	0.22	34.58	2.3E-01	-0.06	34.58	7.9E-01
YP_514364.1	30.8	0.13	30.83	1.0E+00	0.22	30.83	6.4E-02	0.11	30.83	6.2E-01
YP_513629.1	31.7	-0.11	31.91	1.0E+00	0.22	31.91	1.5E-01	-0.16	31.91	6.1E-01
YP_513729.1	26.9	-0.12	27.05	1.0E+00	0.22	27.05	1.4E-01	-0.08	27.05	7.1E-01
YP_512987.1	31.2	-0.09	31.24	1.0E+00	0.22	31.24	1.9E-01	-0.13	31.24	6.3E-01
YP_513613.1	31.8	0.05	31.83	1.0E+00	0.22	31.83	2.0E-03	0.01	31.83	8.9E-01
YP_514516.1	29.9	-0.04	30.01	1.0E+00	0.22	30.01	1.5E-01	0.06	30.01	7.9E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514303.1	31.2	-0.08	31.46	1.0E+00	0.22	31.46	2.1E-01	-0.13	31.46	6.3E-01
YP_514424.1	32.6	0.05	32.48	1.0E+00	0.22	32.48	2.3E-01	0.17	32.48	6.2E-01
YP_513261.1	29.2	0.00	29.43	1.0E+00	0.22	29.43	2.7E-01	-0.07	29.43	7.9E-01
YP_513457.1	25.2	0.00	25.30	1.0E+00	0.23	25.30	6.3E-01	-0.25	25.30	6.7E-01
YP_512829.1	32.7	0.06	32.70	1.0E+00	0.23	32.70	3.2E-01	-0.16	32.70	6.3E-01
YP_513426.1	31.7	-0.04	31.67	1.0E+00	0.23	31.67	1.3E-01	-0.05	31.67	8.2E-01
YP_513198.1	30.8	0.02	30.78	1.0E+00	0.23	30.78	7.1E-02	0.10	30.78	6.3E-01
YP_513122.1	30.0	-0.11	30.22	1.0E+00	0.23	30.22	2.6E-01	-0.25	30.22	6.0E-01
YP_514168.1	31.4	-0.09	31.48	1.0E+00	0.23	31.48	9.3E-03	-0.05	31.48	6.8E-01
YP_513050.1	33.6	0.13	33.59	1.0E+00	0.23	33.59	6.0E-01	0.48	33.59	6.0E-01
YP_514068.1	29.4	0.08	29.38	1.0E+00	0.23	29.38	1.9E-02	0.07	29.38	6.3E-01
YP_513981.1	32.0	0.14	31.98	1.0E+00	0.24	31.98	4.6E-01	0.31	31.98	6.2E-01
YP_514125.1	32.8	0.06	32.91	1.0E+00	0.24	32.91	5.8E-01	0.33	32.91	6.3E-01
YP_514043.1	26.3	-0.05	26.31	1.0E+00	0.24	26.31	1.8E-01	0.01	26.31	9.6E-01
YP_514524.1	31.1	-0.10	31.19	1.0E+00	0.24	31.19	1.6E-01	-0.10	31.19	6.5E-01
YP_514563.1	23.2	0.21	23.56	1.0E+00	0.24	23.56	5.3E-01	0.25	23.56	6.3E-01
YP_513275.1	25.2	0.02	25.72	1.0E+00	0.24	25.72	2.5E-01	-0.37	25.72	6.0E-01
YP_513880.1	30.7	0.07	30.79	1.0E+00	0.25	30.79	1.2E-03	0.04	30.79	6.4E-01
YP_514419.1	31.0	-0.03	31.01	1.0E+00	0.25	31.01	6.1E-01	0.38	31.01	6.3E-01
YP_512811.1	30.2	0.04	30.23	1.0E+00	0.25	30.23	5.4E-02	-0.02	30.23	9.4E-01
YP_513259.1	30.0	-0.01	29.96	1.0E+00	0.26	29.96	4.5E-02	0.02	29.96	9.2E-01
YP_513975.1	30.0	-0.04	30.14	1.0E+00	0.26	30.14	4.0E-02	-0.12	30.14	6.2E-01
YP_514260.1	29.1	0.54	28.68	1.0E+00	0.26	28.68	3.8E-01	0.49	28.68	6.0E-01
YP_513797.1	28.5	0.00	28.74	1.0E+00	0.26	28.74	6.7E-01	0.45	28.74	6.3E-01
YP_513121.1	26.7	-0.02	26.85	1.0E+00	0.26	26.85	7.5E-02	-0.20	26.85	6.0E-01
YP_513494.1	28.1	-0.05	28.22	1.0E+00	0.26	28.22	3.7E-02	0.01	28.22	9.7E-01
YP_513229.1	29.7	0.00	29.71	1.0E+00	0.26	29.71	7.2E-01	0.68	29.71	6.1E-01
YP_514003.1	26.6	0.07	26.58	1.0E+00	0.26	26.58	8.7E-02	0.24	26.58	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514169.1	31.8	0.09	31.39	1.0E+00	0.26	31.39	2.4E-01	0.39	31.39	6.0E-01
YP_514307.1	28.4	-0.06	28.42	1.0E+00	0.26	28.42	2.7E-01	-0.09	28.42	7.7E-01
YP_512888.1	28.8	-0.04	28.76	1.0E+00	0.27	28.76	2.5E-02	0.13	28.76	6.1E-01
YP_513256.1	30.7	-0.03	30.71	1.0E+00	0.27	30.71	7.7E-02	0.03	30.71	8.9E-01
YP_513569.1	30.3	0.05	30.29	1.0E+00	0.27	30.29	3.5E-01	0.35	30.29	6.0E-01
YP_514464.1	30.1	-0.01	30.07	1.0E+00	0.27	30.07	2.7E-04	0.01	30.07	9.6E-01
YP_514088.1	29.5	0.07	29.55	1.0E+00	0.27	29.55	6.0E-03	0.05	29.55	6.9E-01
YP_514241.1	29.6	0.08	29.41	1.0E+00	0.27	29.41	1.2E-02	0.28	29.41	4.8E-01
YP_513505.1	27.5	0.06	27.52	1.0E+00	0.27	27.52	6.2E-03	0.02	27.52	8.7E-01
YP_513205.1	25.9	-0.02	26.05	1.0E+00	0.28	26.05	4.9E-02	0.11	26.05	6.3E-01
YP_514375.1	34.2	0.01	34.13	1.0E+00	0.28	34.13	8.0E-03	0.02	34.13	9.0E-01
YP_514103.1	26.2	-0.12	26.49	1.0E+00	0.28	26.49	8.2E-02	-0.30	26.49	6.0E-01
YP_513759.1	26.5	0.07	26.97	1.0E+00	0.28	26.97	3.4E-01	0.00	26.97	1.0E+00
YP_514222.1	22.2	-0.13	22.01	1.0E+00	0.28	22.01	5.8E-01	0.55	22.01	6.0E-01
YP_513185.1	27.5	0.00	27.39	1.0E+00	0.28	27.39	2.7E-03	0.05	27.39	6.8E-01
YP_513147.1	27.3	0.06	27.23	1.0E+00	0.28	27.23	2.2E-01	0.29	27.23	6.0E-01
YP_513758.1	32.1	0.10	32.04	1.0E+00	0.28	32.04	2.2E-01	0.28	32.04	6.0E-01
YP_514230.1	33.2	0.03	33.35	1.0E+00	0.28	33.35	1.1E-01	-0.04	33.35	8.6E-01
YP_513596.1	27.3	-0.02	27.45	1.0E+00	0.28	27.45	2.7E-03	-0.11	27.45	6.0E-01
YP_513468.1	32.7	-0.04	32.84	1.0E+00	0.28	32.84	8.0E-02	-0.19	32.84	6.0E-01
YP_514434.1	33.2	0.05	33.14	1.0E+00	0.28	33.14	1.3E-02	0.12	33.14	6.1E-01
YP_512996.1	25.4	-0.15	25.66	1.0E+00	0.28	25.66	8.9E-02	-0.14	25.66	6.3E-01
YP_513079.1	25.2	0.23	25.03	1.0E+00	0.29	25.03	8.3E-01	1.29	25.03	6.0E-01
YP_513623.1	31.4	-0.07	31.53	1.0E+00	0.29	31.53	6.1E-03	-0.08	31.53	6.3E-01
YP_514306.1	29.5	-0.05	29.50	1.0E+00	0.29	29.50	6.5E-03	0.04	29.50	7.9E-01
YP_512841.1	29.8	0.01	29.94	1.0E+00	0.29	29.94	2.1E-03	0.04	29.94	7.5E-01
YP_514283.1	28.0	0.00	27.81	1.0E+00	0.29	27.81	4.6E-03	0.18	27.81	6.0E-01
YP_513286.1	27.5	-0.15	27.67	1.0E+00	0.30	27.67	2.0E-01	-0.39	27.67	6.0E-01
YP_513998.1	29.2	-0.01	29.31	1.0E+00	0.30	29.31	6.5E-01	0.37	29.31	6.4E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514013.1	30.8	0.02	30.83	1.0E+00	0.30	30.83	1.9E-02	-0.09	30.83	6.3E-01
YP_514240.1	24.8	-0.04	24.77	1.0E+00	0.30	24.77	2.3E-01	-0.04	24.77	9.0E-01
YP_513634.1	24.0	-0.10	24.53	1.0E+00	0.30	24.53	1.2E-01	-0.42	24.53	6.0E-01
YP_514410.1	33.2	-0.12	33.28	1.0E+00	0.30	33.28	1.0E-01	-0.23	33.28	6.0E-01
YP_513282.1	25.0	-0.07	25.26	1.0E+00	0.30	25.26	1.3E-01	-0.21	25.26	6.1E-01
YP_514183.1	32.0	-0.02	32.08	1.0E+00	0.30	32.08	1.5E-02	-0.08	32.08	6.3E-01
YP_514074.1	32.0	0.01	32.10	1.0E+00	0.30	32.10	2.2E-03	-0.05	32.10	6.8E-01
YP_512851.1	26.7	0.13	26.50	1.0E+00	0.30	26.50	2.0E-02	0.03	26.50	8.7E-01
YP_513559.1	29.8	0.21	29.42	1.0E+00	0.30	29.42	1.7E-01	0.22	29.42	6.2E-01
YP_513115.1	29.9	0.19	29.46	1.0E+00	0.30	29.46	5.0E-01	0.59	29.46	6.0E-01
YP_514073.1	29.7	0.10	29.62	1.0E+00	0.30	29.62	2.7E-01	0.17	29.62	6.4E-01
YP_513829.1	31.8	0.13	31.89	1.0E+00	0.30	31.89	6.8E-01	0.44	31.89	6.3E-01
YP_513714.1	28.4	-0.01	28.29	1.0E+00	0.30	28.29	2.8E-03	0.00	28.29	9.9E-01
YP_512819.1	33.4	0.06	33.34	1.0E+00	0.31	33.34	6.7E-01	0.82	33.34	6.0E-01
YP_513999.1	29.0	-0.02	29.18	1.0E+00	0.31	29.18	2.1E-02	-0.11	29.18	6.3E-01
YP_513551.1	26.5	-0.07	26.85	1.0E+00	0.31	26.85	1.9E-02	-0.11	26.85	6.3E-01
YP_513441.1	28.3	-0.01	28.50	1.0E+00	0.31	28.50	9.0E-02	-0.24	28.50	6.0E-01
YP_514372.1	27.0	-0.03	27.20	1.0E+00	0.32	27.20	7.5E-03	0.02	27.20	9.0E-01
YP_513828.1	31.5	-0.01	31.51	1.0E+00	0.32	31.51	4.8E-01	-0.20	31.51	7.2E-01
YP_514409.1	32.9	-0.04	32.86	1.0E+00	0.32	32.86	1.0E-01	-0.17	32.86	6.3E-01
YP_513425.1	32.8	-0.03	32.60	1.0E+00	0.32	32.60	1.1E-02	0.14	32.60	6.0E-01
YP_513769.1	29.4	0.15	29.27	1.0E+00	0.32	29.27	2.0E-01	0.13	29.27	7.0E-01
YP_513009.1	25.7	0.09	25.19	1.0E+00	0.32	25.19	3.5E-01	0.40	25.19	6.0E-01
YP_513370.1	31.4	0.18	31.29	1.0E+00	0.32	31.29	1.6E-01	0.22	31.29	6.2E-01
YP_514484.1	28.9	-0.05	28.93	1.0E+00	0.33	28.93	3.4E-04	-0.09	28.93	6.0E-01
YP_514352.1	29.8	0.13	29.85	1.0E+00	0.33	29.85	4.0E-01	0.23	29.85	6.6E-01
YP_512874.1	28.7	0.47	28.07	1.0E+00	0.33	28.07	6.8E-01	1.07	28.07	6.0E-01
YP_514331.1	26.1	0.01	26.03	1.0E+00	0.33	26.03	4.6E-01	0.25	26.03	6.7E-01
YP_513891.1	28.2	0.09	28.14	1.0E+00	0.33	28.14	1.6E-02	0.19	28.14	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514408.1	33.1	0.05	33.04	1.0E+00	0.33	33.04	2.0E-02	0.17	33.04	6.0E-01
YP_513890.1	27.5	0.00	27.66	1.0E+00	0.33	27.66	5.2E-03	-0.02	27.66	8.9E-01
YP_514518.1	31.4	-0.01	31.48	1.0E+00	0.34	31.48	2.4E-03	-0.05	31.48	6.9E-01
YP_514220.1	28.7	-0.17	28.91	1.0E+00	0.34	28.91	4.1E-02	-0.12	28.91	6.3E-01
YP_513823.1	31.4	0.05	31.64	1.0E+00	0.34	31.64	1.1E-02	-0.12	31.64	6.2E-01
YP_514024.1	25.7	-0.10	25.87	1.0E+00	0.34	25.87	7.2E-03	-0.21	25.87	6.0E-01
YP_514047.1	32.3	-0.06	32.46	1.0E+00	0.34	32.46	1.5E-02	-0.17	32.46	6.0E-01
YP_514540.1	28.4	-0.06	28.44	1.0E+00	0.34	28.44	1.9E-02	0.04	28.44	8.6E-01
YP_512889.1	29.6	0.02	29.75	1.0E+00	0.35	29.75	4.7E-02	-0.15	29.75	6.3E-01
YP_513142.1	25.6	-0.12	25.61	1.0E+00	0.35	25.61	2.9E-01	-0.32	25.61	6.2E-01
YP_513199.1	28.7	-0.03	28.72	1.0E+00	0.35	28.72	7.2E-02	0.10	28.72	7.0E-01
YP_514562.1	29.9	0.04	29.80	1.0E+00	0.35	29.80	5.6E-04	0.12	29.80	6.0E-01
YP_513321.1	25.5	0.11	25.55	1.0E+00	0.35	25.55	3.5E-01	0.20	25.55	6.9E-01
YP_513875.1	29.7	0.07	29.92	1.0E+00	0.35	29.92	1.1E-02	0.03	29.92	8.8E-01
YP_513488.1	30.5	0.13	30.51	1.0E+00	0.36	30.51	1.4E-02	0.08	30.51	6.7E-01
YP_513308.1	29.9	-0.04	29.99	1.0E+00	0.36	29.99	1.1E-03	0.01	29.99	9.4E-01
YP_514561.1	25.6	0.41	25.24	1.0E+00	0.36	25.24	3.8E-01	0.25	25.24	6.4E-01
YP_514517.1	33.9	-0.04	33.99	1.0E+00	0.36	33.99	3.2E-04	0.04	33.99	7.1E-01
YP_513143.1	27.2	0.06	27.13	1.0E+00	0.36	27.13	7.9E-03	0.25	27.13	6.0E-01
YP_514428.1	24.1	-0.29	24.39	1.0E+00	0.36	24.39	2.1E-01	-0.22	24.39	6.3E-01
YP_513553.1	31.8	-0.07	31.73	1.0E+00	0.36	31.73	4.9E-05	-0.03	31.73	7.7E-01
YP_513506.1	24.6	0.19	24.60	1.0E+00	0.37	24.60	2.6E-01	0.00	24.60	1.0E+00
YP_514407.1	30.9	-0.07	30.85	1.0E+00	0.37	30.85	3.3E-03	-0.06	30.85	6.9E-01
YP_513919.1	31.5	-0.02	31.59	1.0E+00	0.37	31.59	1.2E-02	-0.05	31.59	7.9E-01
YP_513529.1	26.7	-0.06	26.83	1.0E+00	0.37	26.83	2.1E-02	-0.04	26.83	8.7E-01
YP_513816.1	29.5	0.00	29.62	1.0E+00	0.37	29.62	2.8E-03	0.09	29.62	6.3E-01
YP_513643.1	26.8	-0.07	27.18	1.0E+00	0.37	27.18	1.2E-01	-0.21	27.18	6.3E-01
YP_513640.1	29.1	0.20	28.97	1.0E+00	0.37	28.97	2.2E-01	0.44	28.97	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513945.1	28.7	0.00	28.75	1.0E+00	0.37	28.75	6.0E-03	-0.06	28.75	7.3E-01
YP_513862.1	32.4	0.01	32.58	1.0E+00	0.38	32.58	4.3E-01	0.38	32.58	6.3E-01
YP_512999.1	26.3	0.10	26.25	1.0E+00	0.38	26.25	3.4E-02	-0.08	26.25	7.3E-01
YP_513873.1	31.5	0.08	31.83	1.0E+00	0.38	31.83	3.5E-01	0.35	31.83	6.3E-01
YP_513538.1	27.7	0.10	27.57	1.0E+00	0.38	27.57	3.2E-01	-0.07	27.57	9.0E-01
YP_513977.1	30.7	0.19	30.40	1.0E+00	0.38	30.40	2.1E-01	0.51	30.40	6.0E-01
YP_513622.1	31.9	0.03	31.95	1.0E+00	0.38	31.95	6.2E-03	-0.07	31.95	6.9E-01
YP_514437.1	29.9	0.05	29.77	1.0E+00	0.39	29.77	8.4E-03	0.03	29.77	8.7E-01
YP_513051.1	29.8	-0.05	29.79	1.0E+00	0.39	29.79	2.9E-01	-0.05	29.79	9.2E-01
YP_514142.1	31.0	0.06	31.02	1.0E+00	0.39	31.02	7.0E-02	0.25	31.02	6.0E-01
YP_513169.1	30.6	0.16	30.36	1.0E+00	0.39	30.36	2.0E-02	0.18	30.36	6.1E-01
YP_513025.1	24.4	0.38	24.16	1.0E+00	0.39	24.16	6.7E-01	1.16	24.16	6.0E-01
YP_512986.1	29.0	-0.10	29.07	1.0E+00	0.40	29.07	1.1E-02	-0.01	29.07	9.7E-01
YP_514053.1	27.9	-0.14	27.87	1.0E+00	0.40	27.87	1.6E-03	0.08	27.87	6.3E-01
YP_513255.1	29.5	-0.03	29.75	1.0E+00	0.40	29.75	6.5E-02	-0.23	29.75	6.1E-01
YP_513710.1	25.4	0.06	25.08	1.0E+00	0.40	25.08	2.8E-01	0.68	25.08	6.0E-01
YP_512882.1	26.9	0.12	27.06	1.0E+00	0.41	27.06	5.5E-02	-0.13	27.06	6.6E-01
YP_514404.1	25.3	0.03	25.03	1.0E+00	0.41	25.03	2.1E-01	0.14	25.03	7.4E-01
YP_514242.1	26.9	0.41	26.94	1.0E+00	0.41	26.94	6.3E-01	0.52	26.94	6.3E-01
YP_514443.1	25.9	0.03	25.37	1.0E+00	0.41	25.37	4.5E-01	0.76	25.37	6.0E-01
YP_514482.1	29.5	-0.01	29.52	1.0E+00	0.41	29.52	1.6E-03	0.13	29.52	6.1E-01
YP_514406.1	31.3	-0.03	31.43	1.0E+00	0.41	31.43	2.6E-03	0.08	31.43	6.3E-01
YP_513090.1	24.0	-0.31	24.06	1.0E+00	0.41	24.06	6.4E-02	-0.28	24.06	6.0E-01
YP_512975.1	29.2	-0.03	29.56	1.0E+00	0.41	29.56	1.7E-02	-0.21	29.56	6.0E-01
YP_514231.1	33.1	-0.03	33.20	1.0E+00	0.41	33.20	1.2E-02	-0.01	33.20	9.6E-01
YP_512903.1	28.6	-0.10	28.77	1.0E+00	0.42	28.77	2.0E-02	-0.05	28.77	8.5E-01
YP_513924.1	27.2	0.23	26.76	1.0E+00	0.42	26.76	2.3E-01	0.53	26.76	6.0E-01
YP_513757.1	33.0	0.02	32.90	1.0E+00	0.43	32.90	2.5E-05	0.12	32.90	6.0E-01
YP_512983.1	24.4	0.29	23.84	1.0E+00	0.43	23.84	9.6E-02	0.52	23.84	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_512868.1	28.4	0.05	28.33	1.0E+00	0.43	28.33	3.4E-03	0.01	28.33	9.6E-01
YP_514236.1	28.4	-0.05	28.44	1.0E+00	0.43	28.44	4.6E-05	-0.04	28.44	7.3E-01
YP_514200.1	32.8	0.10	32.70	1.0E+00	0.44	32.70	1.0E-01	0.16	32.70	6.7E-01
YP_514232.1	25.6	-0.02	25.73	1.0E+00	0.44	25.73	2.2E-02	0.30	25.73	6.0E-01
YP_512832.1	27.5	-0.08	27.53	1.0E+00	0.44	27.53	3.6E-03	-0.09	27.53	6.5E-01
YP_513761.1	28.2	-0.02	28.30	1.0E+00	0.45	28.30	1.2E-03	0.04	28.30	8.0E-01
YP_513716.1	33.4	0.09	33.37	1.0E+00	0.45	33.37	2.9E-02	0.33	33.37	6.0E-01
YP_513200.1	29.2	0.10	29.09	1.0E+00	0.45	29.09	1.1E-03	0.26	29.09	6.0E-01
YP_513641.1	31.2	0.11	31.06	1.0E+00	0.46	31.06	6.2E-02	0.26	31.06	6.1E-01
YP_513603.1	28.4	0.06	28.36	1.0E+00	0.46	28.36	1.6E-05	0.09	28.36	6.1E-01
YP_513196.1	24.7	0.12	24.22	1.0E+00	0.46	24.22	4.4E-01	0.47	24.22	6.3E-01
YP_514026.1	25.4	0.11	25.04	1.0E+00	0.46	25.04	6.1E-02	0.30	25.04	6.0E-01
YP_513466.1	29.1	0.08	28.98	1.0E+00	0.46	28.98	4.9E-03	0.16	28.98	6.1E-01
YP_513451.1	27.3	0.04	27.09	1.0E+00	0.47	27.09	8.6E-02	0.18	27.09	6.4E-01
YP_513730.1	28.2	0.07	28.08	1.0E+00	0.47	28.08	6.3E-05	0.11	28.08	6.0E-01
YP_514430.1	27.2	-0.09	27.21	1.0E+00	0.47	27.21	3.7E-02	-0.25	27.21	6.1E-01
YP_513232.1	25.3	0.07	25.54	1.0E+00	0.48	25.54	1.1E-02	0.02	25.54	9.6E-01
YP_514333.1	28.1	-0.09	28.16	1.0E+00	0.48	28.16	9.7E-03	-0.09	28.16	7.0E-01
YP_513161.1	25.8	0.08	25.78	1.0E+00	0.48	25.78	3.8E-01	-0.09	25.78	9.0E-01
YP_513495.1	28.0	-0.05	28.05	1.0E+00	0.48	28.05	1.3E-04	0.02	28.05	8.9E-01
YP_513996.1	28.4	-0.09	28.74	1.0E+00	0.48	28.74	9.5E-04	-0.19	28.74	6.0E-01
YP_512948.1	27.3	0.04	27.14	1.0E+00	0.49	27.14	3.4E-01	-0.44	27.14	6.2E-01
YP_513547.1	29.9	0.05	29.84	1.0E+00	0.49	29.84	4.8E-01	0.79	29.84	6.0E-01
YP_513211.1	30.0	0.10	29.79	1.0E+00	0.49	29.79	7.5E-02	0.40	29.79	6.0E-01
YP_513726.1	28.0	0.25	27.62	1.0E+00	0.49	27.62	2.9E-01	0.66	27.62	6.0E-01
YP_514175.1	27.0	-0.22	27.27	1.0E+00	0.49	27.27	6.2E-02	-0.28	27.27	6.1E-01
YP_513253.1	26.6	0.07	26.72	1.0E+00	0.49	26.72	2.6E-03	0.02	26.72	9.2E-01
YP_513179.1	26.0	0.29	25.90	1.0E+00	0.49	25.90	2.6E-02	0.22	25.90	6.2E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513827.1	30.9	0.12	31.03	1.0E+00	0.49	31.03	3.8E-03	0.05	31.03	8.1E-01
YP_514280.1	20.9	0.67	19.77	1.0E+00	0.50	19.77	9.2E-01	0.45	19.77	9.6E-01
YP_513074.1	30.6	0.15	30.79	1.0E+00	0.50	30.79	1.2E-01	0.30	30.79	6.2E-01
YP_513250.1	27.1	0.05	26.93	1.0E+00	0.51	26.93	6.4E-01	0.73	26.93	6.3E-01
YP_514076.1	24.8	-0.03	24.52	1.0E+00	0.51	24.52	1.9E-01	-0.27	24.52	6.3E-01
YP_514219.1	27.9	0.02	28.16	1.0E+00	0.51	28.16	1.2E-03	-0.23	28.16	6.0E-01
YP_513760.1	27.3	-0.01	27.42	1.0E+00	0.51	27.42	4.4E-03	0.03	27.42	8.9E-01
YP_514119.1	30.9	-0.03	31.06	1.0E+00	0.51	31.06	1.3E-05	-0.12	31.06	6.0E-01
YP_514115.1	30.9	-0.03	31.06	1.0E+00	0.51	31.06	1.3E-05	-0.12	31.06	6.0E-01
YP_513260.1	25.3	0.10	25.31	1.0E+00	0.51	25.31	1.1E-02	0.26	25.31	6.0E-01
YP_514191.1	29.3	-0.02	29.23	1.0E+00	0.52	29.23	5.8E-04	0.04	29.23	8.4E-01
YP_514224.1	26.6	-0.16	27.15	1.0E+00	0.52	27.15	2.3E-03	-0.49	27.15	2.0E-01
YP_513262.1	28.1	0.05	28.00	1.0E+00	0.53	28.00	2.9E-04	0.29	28.00	6.0E-01
YP_513868.1	30.4	-0.01	30.49	1.0E+00	0.53	30.49	5.3E-04	0.00	30.49	1.0E+00
YP_513770.1	27.4	0.05	27.42	1.0E+00	0.53	27.42	3.1E-02	0.33	27.42	6.0E-01
YP_513598.1	26.5	0.21	26.25	1.0E+00	0.53	26.25	6.2E-03	0.41	26.25	6.0E-01
YP_514558.1	28.8	0.45	28.26	1.0E+00	0.54	28.26	2.7E-01	0.54	28.26	6.1E-01
YP_514338.1	28.7	0.08	28.34	1.0E+00	0.54	28.34	2.3E-01	0.60	28.34	6.0E-01
YP_513036.1	31.1	0.19	30.49	1.0E+00	0.55	30.49	4.1E-01	0.99	30.49	6.0E-01
YP_513353.1	29.1	0.16	28.91	1.0E+00	0.55	28.91	1.6E-02	0.26	28.91	6.0E-01
YP_513390.1	28.8	-0.04	28.84	1.0E+00	0.55	28.84	7.6E-05	0.08	28.84	6.3E-01
YP_514098.1	29.4	-0.07	29.50	1.0E+00	0.55	29.50	1.5E-04	-0.07	29.50	6.8E-01
YP_513531.1	27.2	0.09	27.22	1.0E+00	0.56	27.22	1.1E-03	0.11	27.22	6.3E-01
YP_514126.1	26.9	-0.13	26.92	1.0E+00	0.56	26.92	6.9E-04	0.11	26.92	6.3E-01
YP_513117.1	29.5	0.27	29.12	1.0E+00	0.56	29.12	1.2E-01	0.33	29.12	6.2E-01
YP_514353.1	27.2	0.05	27.41	1.0E+00	0.57	27.41	2.7E-05	-0.01	27.41	9.3E-01
YP_513482.1	24.8	0.29	24.16	1.0E+00	0.57	24.16	3.5E-01	1.04	24.16	6.0E-01
YP_514177.1	29.4	0.05	29.67	1.0E+00	0.57	29.67	4.4E-04	0.03	29.67	8.8E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514065.1	27.0	0.38	26.67	1.0E+00	0.57	26.67	3.4E-01	0.26	26.67	7.3E-01
YP_514541.1	26.4	0.11	26.55	1.0E+00	0.57	26.55	1.2E-02	0.21	26.55	6.2E-01
YP_513732.1	18.0	1.00	17.59	1.0E+00	0.58	17.59	7.3E-01	1.19	17.59	6.3E-01
YP_513442.1	27.1	0.11	26.90	1.0E+00	0.58	26.90	1.5E-03	0.36	26.90	6.0E-01
YP_514167.1	29.5	0.00	29.98	1.0E+00	0.58	29.98	2.2E-03	-0.15	29.98	6.2E-01
YP_514273.1	24.0	0.06	24.35	1.0E+00	0.59	24.35	1.2E-02	0.03	24.35	9.4E-01
YP_514086.1	25.7	-0.09	26.08	1.0E+00	0.59	26.08	1.0E-02	-0.32	26.08	6.0E-01
YP_514509.1	31.7	0.00	32.00	1.0E+00	0.59	32.00	4.4E-04	-0.14	32.00	6.2E-01
YP_513444.1	25.5	0.13	25.54	1.0E+00	0.60	25.54	8.4E-02	-0.09	25.54	8.6E-01
YP_513089.1	25.1	0.10	24.94	1.0E+00	0.60	24.94	1.2E-03	0.22	24.94	6.0E-01
YP_513874.1	34.5	0.27	34.40	1.0E+00	0.60	34.40	1.8E-01	0.65	34.40	6.0E-01
YP_513039.1	32.1	0.17	31.50	1.0E+00	0.61	31.50	3.9E-01	0.83	31.50	6.0E-01
YP_514405.1	31.1	-0.04	31.23	1.0E+00	0.61	31.23	4.9E-06	-0.03	31.23	8.3E-01
YP_513361.1	30.6	0.04	30.74	1.0E+00	0.61	30.74	3.3E-05	-0.05	30.74	7.4E-01
YP_513625.1	29.9	-0.04	30.04	1.0E+00	0.61	30.04	5.9E-07	-0.05	30.04	6.3E-01
YP_514182.1	27.0	0.17	26.58	1.0E+00	0.61	26.58	3.2E-01	1.08	26.58	6.0E-01
YP_513916.1	30.1	0.02	30.37	1.0E+00	0.62	30.37	5.2E-02	0.19	30.37	6.7E-01
YP_514433.1	29.4	0.03	29.53	1.0E+00	0.62	29.53	2.9E-05	0.02	29.53	8.8E-01
YP_513309.1	29.3	0.00	29.45	1.0E+00	0.62	29.45	1.6E-05	-0.05	29.45	7.3E-01
YP_513765.1	25.4	-0.03	25.52	1.0E+00	0.63	25.52	2.8E-05	-0.07	25.52	6.4E-01
YP_514425.1	26.3	0.04	26.05	1.0E+00	0.63	26.05	3.5E-01	0.60	26.05	6.2E-01
YP_513150.1	22.7	0.08	22.51	1.0E+00	0.63	22.51	4.2E-02	0.30	22.51	6.2E-01
YP_513496.1	27.4	-0.12	27.59	1.0E+00	0.63	27.59	9.7E-04	-0.16	27.59	6.2E-01
YP_514302.1	26.2	-0.05	26.38	1.0E+00	0.63	26.38	3.4E-04	0.05	26.38	7.9E-01
YP_513978.1	24.5	-0.05	24.66	1.0E+00	0.63	24.66	4.1E-02	0.05	24.66	9.1E-01
YP_513364.1	29.4	0.14	29.20	1.0E+00	0.64	29.20	6.2E-04	0.16	29.20	6.2E-01
YP_514477.1	31.5	0.04	31.54	1.0E+00	0.64	31.54	2.7E-07	0.07	31.54	6.2E-01
YP_514285.1	24.9	0.33	24.60	1.0E+00	0.64	24.60	1.6E-01	0.70	24.60	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514079.1	23.0	0.39	23.52	1.0E+00	0.64	23.52	1.8E-01	-0.14	23.52	8.4E-01
YP_514422.1	34.1	0.03	34.09	1.0E+00	0.65	34.09	3.3E-06	0.01	34.09	9.5E-01
YP_513762.1	28.1	0.01	28.24	1.0E+00	0.65	28.24	9.3E-05	0.00	28.24	1.0E+00
YP_513616.1	27.3	-0.14	27.55	1.0E+00	0.65	27.55	9.1E-04	-0.33	27.55	6.0E-01
YP_513322.1	29.4	0.00	29.57	1.0E+00	0.66	29.57	1.3E-05	-0.13	29.57	6.0E-01
YP_514067.1	27.3	0.04	27.67	1.0E+00	0.66	27.67	2.9E-04	-0.11	27.67	6.3E-01
YP_514463.1	30.7	0.29	30.15	1.0E+00	0.66	30.15	1.3E-01	0.61	30.15	6.0E-01
YP_513254.1	28.4	-0.15	28.53	1.0E+00	0.66	28.53	9.1E-03	-0.31	28.53	6.0E-01
YP_512894.1	26.5	0.36	26.20	1.0E+00	0.67	26.20	1.7E-01	0.52	26.20	6.1E-01
YP_513508.1	25.8	0.57	25.44	1.0E+00	0.67	25.44	5.6E-01	1.09	25.44	6.1E-01
YP_514481.1	27.1	0.48	26.45	1.0E+00	0.67	26.45	5.1E-02	0.91	26.45	4.8E-01
YP_513383.1	23.8	0.51	22.01	1.0E+00	0.67	22.01	6.0E-01	1.85	22.01	6.0E-01
YP_513042.1	31.8	0.28	31.51	1.0E+00	0.67	31.51	3.8E-01	0.91	31.51	6.0E-01
YP_513794.1	26.6	0.03	26.73	1.0E+00	0.68	26.73	3.0E-06	-0.01	26.73	9.5E-01
YP_513733.1	25.1	0.54	24.50	1.0E+00	0.68	24.50	5.1E-01	0.48	24.50	7.2E-01
YP_513343.1	30.1	0.13	30.11	1.0E+00	0.68	30.11	4.0E-05	0.12	30.11	6.2E-01
YP_514519.1	25.5	0.25	25.23	1.0E+00	0.68	25.23	4.6E-03	0.44	25.23	6.0E-01
YP_514399.1	34.0	-0.04	34.09	1.0E+00	0.69	34.09	2.6E-03	-0.17	34.09	6.3E-01
YP_513078.1	29.0	0.06	29.12	1.0E+00	0.69	29.12	5.9E-07	0.02	29.12	9.0E-01
YP_513575.1	23.3	-0.04	23.54	1.0E+00	0.69	23.54	1.1E-01	-0.25	23.54	6.8E-01
YP_513979.1	26.2	-0.09	26.52	1.0E+00	0.69	26.52	9.4E-03	-0.30	26.52	6.0E-01
YP_514055.1	28.9	0.11	28.85	1.0E+00	0.71	28.85	2.3E-01	0.71	28.85	6.0E-01
YP_514429.1	26.1	0.43	25.60	1.0E+00	0.72	25.60	5.4E-02	0.67	25.60	6.0E-01
YP_513789.1	21.4	-0.88	21.86	1.0E+00	0.72	21.86	9.2E-01	-0.55	21.86	9.5E-01
YP_512949.1	24.8	0.13	25.21	1.0E+00	0.73	25.21	7.6E-03	-0.05	25.21	9.0E-01
YP_513725.1	32.2	0.41	31.45	1.0E+00	0.73	31.45	3.0E-01	0.75	31.45	6.1E-01
YP_513349.1	30.9	0.07	30.82	1.0E+00	0.73	30.82	1.4E-04	0.12	30.82	6.3E-01
YP_512929.1	29.0	0.02	29.03	1.0E+00	0.74	29.03	5.6E-06	-0.04	29.03	7.9E-01
YP_513149.1	23.9	0.69	23.20	1.0E+00	0.74	23.20	4.7E-01	0.64	23.20	6.4E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514454.1	28.8	-0.10	28.62	1.0E+00	0.75	28.62	9.6E-05	0.07	28.62	7.3E-01
YP_512938.1	26.8	0.26	26.64	1.0E+00	0.75	26.64	2.1E-01	0.70	26.64	6.0E-01
YP_513454.1	32.0	0.21	31.62	1.0E+00	0.75	31.62	1.4E-01	0.52	31.62	6.1E-01
YP_513289.1	29.3	0.23	29.02	1.0E+00	0.76	29.02	9.1E-02	0.33	29.02	6.3E-01
YP_514084.1	26.5	0.14	26.81	1.0E+00	0.76	26.81	2.5E-03	0.29	26.81	6.0E-01
YP_514173.1	23.5	0.52	23.78	1.0E+00	0.76	23.78	2.7E-02	0.41	23.78	6.0E-01
YP_513707.1	19.4	0.64	17.85	1.0E+00	0.76	17.85	9.2E-01	-5.21	17.85	6.0E-01
YP_513934.1	19.8	-0.17	19.90	1.0E+00	0.77	19.90	3.1E-01	0.23	19.90	8.3E-01
YP_513755.1	25.6	0.16	25.74	1.0E+00	0.77	25.74	9.8E-04	0.14	25.74	6.3E-01
YP_513670.1	19.7	-0.10	19.60	1.0E+00	0.77	19.60	5.8E-01	-1.35	19.60	6.1E-01
YP_514247.1	29.9	0.31	29.71	1.0E+00	0.78	29.71	3.3E-01	0.74	29.71	6.2E-01
YP_513722.1	23.5	-0.17	23.86	1.0E+00	0.78	23.86	5.5E-03	-0.43	23.86	6.0E-01
YP_513942.1	28.9	0.39	28.48	1.0E+00	0.78	28.48	6.1E-02	0.40	28.48	6.2E-01
YP_514082.1	26.1	-0.05	26.40	1.0E+00	0.79	26.40	5.7E-06	-0.02	26.40	8.9E-01
YP_513576.1	25.6	0.23	25.43	1.0E+00	0.79	25.43	1.2E-01	0.51	25.43	6.2E-01
YP_513844.1	32.2	0.05	32.09	1.0E+00	0.80	32.09	5.6E-06	0.07	32.09	6.6E-01
YP_512912.1	32.2	0.05	32.09	1.0E+00	0.80	32.09	5.6E-06	0.07	32.09	6.6E-01
YP_514235.1	26.8	0.04	27.01	1.0E+00	0.80	27.01	1.1E-07	-0.08	27.01	6.2E-01
YP_513571.1	29.7	0.18	29.19	1.0E+00	0.81	29.19	2.4E-02	0.46	29.19	6.0E-01
YP_514180.1	28.6	0.21	28.40	1.0E+00	0.81	28.40	9.0E-04	0.24	28.40	6.1E-01
YP_514108.1	34.0	0.46	33.39	1.0E+00	0.82	33.39	3.7E-01	0.88	33.39	6.2E-01
YP_514525.1	24.5	0.26	25.34	1.0E+00	0.82	25.34	1.9E-01	-0.12	25.34	8.9E-01
YP_513021.1	27.7	0.04	27.79	1.0E+00	0.83	27.79	1.8E-03	0.07	27.79	8.5E-01
YP_514061.1	31.7	-0.03	31.91	1.0E+00	0.83	31.91	1.6E-04	0.17	31.91	6.2E-01
YP_513826.1	32.6	-0.02	32.86	1.0E+00	0.83	32.86	4.4E-05	-0.13	32.86	6.3E-01
YP_514368.1	26.1	0.29	25.92	1.0E+00	0.83	25.92	1.0E-01	0.74	25.92	6.0E-01
YP_513319.1	28.7	-0.04	28.92	1.0E+00	0.85	28.92	5.3E-06	-0.09	28.92	6.3E-01
YP_514174.1	32.6	0.31	32.30	1.0E+00	0.86	32.30	1.1E-01	0.31	32.30	6.8E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514411.1	32.5	0.01	32.40	1.0E+00	0.86	32.40	2.5E-07	0.17	32.40	6.0E-01
YP_514432.1	30.3	0.05	30.07	1.0E+00	0.86	30.07	1.4E-05	0.23	30.07	6.0E-01
YP_514334.1	28.4	0.25	28.00	1.0E+00	0.86	28.00	2.2E-02	0.29	28.00	6.3E-01
YP_514512.1	28.4	0.17	27.91	1.0E+00	0.86	27.91	1.8E-01	0.83	27.91	6.0E-01
YP_514124.1	30.1	0.01	30.36	1.0E+00	0.86	30.36	3.7E-08	-0.07	30.36	6.2E-01
YP_513528.1	27.6	0.15	27.49	1.0E+00	0.88	27.49	1.2E-05	0.22	27.49	6.0E-01
YP_513651.1	26.7	0.17	26.80	1.0E+00	0.88	26.80	3.3E-04	0.10	26.80	7.3E-01
YP_514445.1	27.1	0.65	26.37	1.0E+00	0.88	26.37	1.5E-01	0.82	26.37	6.0E-01
YP_514298.1	27.4	-0.06	27.57	1.0E+00	0.89	27.57	6.9E-07	0.03	27.57	8.6E-01
YP_513509.1	23.4	-0.04	23.41	1.0E+00	0.90	23.41	2.4E-02	-0.07	23.41	9.0E-01
YP_514325.1	21.9	-0.06	21.36	1.0E+00	0.90	21.36	3.7E-01	0.19	21.36	8.9E-01
YP_512842.1	27.6	-0.08	27.90	1.0E+00	0.91	27.90	3.5E-06	0.04	27.90	8.4E-01
YP_513605.1	27.9	0.06	28.25	1.0E+00	0.92	28.25	2.4E-06	-0.24	28.25	6.0E-01
YP_514300.1	22.0	-0.33	22.53	1.0E+00	0.93	22.53	5.1E-02	-0.52	22.53	6.1E-01
YP_513573.1	27.9	0.26	27.66	1.0E+00	0.93	27.66	4.7E-03	0.56	27.66	6.0E-01
YP_512931.1	29.0	-0.03	29.23	1.0E+00	0.93	29.23	1.3E-05	-0.10	29.23	6.4E-01
YP_513350.1	25.1	-0.42	25.19	1.0E+00	0.94	25.19	1.0E-04	0.15	25.19	6.3E-01
YP_513453.1	24.5	0.41	24.88	1.0E+00	0.95	24.88	1.5E-01	0.39	24.88	6.7E-01
YP_514414.1	32.9	0.00	33.03	1.0E+00	0.95	33.03	1.2E-03	-0.14	33.03	6.9E-01
YP_514225.1	22.9	0.13	23.56	1.0E+00	0.95	23.56	1.0E-03	-0.04	23.56	9.1E-01
YP_514081.1	28.1	0.15	28.08	1.0E+00	0.97	28.08	8.5E-05	0.05	28.08	8.7E-01
YP_513865.1	26.8	-0.05	27.41	1.0E+00	0.98	27.41	2.4E-05	-0.39	27.41	6.0E-01
YP_513334.1	27.2	0.09	27.28	1.0E+00	0.98	27.28	7.7E-07	0.05	27.28	7.7E-01
YP_512961.1	30.3	0.70	29.15	1.0E+00	0.99	29.15	1.9E-01	1.09	29.15	6.0E-01
YP_513443.1	25.0	1.17	23.59	1.0E+00	0.99	23.59	3.4E-01	1.21	23.59	6.0E-01
YP_513464.1	23.0	-0.14	23.14	1.0E+00	0.99	23.14	3.5E-02	-0.32	23.14	6.3E-01
YP_513607.1	25.7	0.12	25.76	1.0E+00	0.99	25.76	4.3E-05	0.24	25.76	6.0E-01
YP_513412.1	24.9	0.98	23.27	1.0E+00	1.00	23.27	5.2E-01	1.19	23.27	6.3E-01
YP_513728.1	28.7	-0.02	28.98	1.0E+00	1.00	28.98	1.4E-06	0.08	28.98	6.6E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_513791.1	25.3	0.32	24.62	1.0E+00	1.01	24.62	1.0E-01	1.02	24.62	6.0E-01
YP_512823.1	25.9	-0.10	24.80	1.0E+00	1.02	24.80	1.7E-01	0.39	24.80	7.0E-01
YP_513027.1	30.9	0.43	30.16	1.0E+00	1.02	30.16	2.0E-01	1.17	30.16	6.0E-01
YP_514544.1	26.0	-0.08	26.10	1.0E+00	1.03	26.10	1.3E-01	-0.17	26.10	8.7E-01
YP_512824.1	31.2	0.65	30.34	1.0E+00	1.03	30.34	3.0E-01	1.16	30.34	6.0E-01
YP_513228.1										
YP_514021.1_s hared	0.0	-28.23	8.21	8.9E-32	1.04	8.21	9.2E-10	-28.23	8.21	8.9E-32
YP_514436.1	30.3	0.39	30.09	1.0E+00	1.04	30.09	4.7E-02	0.60	30.09	6.0E-01
YP_514145.1	29.9	0.38	29.53	1.0E+00	1.06	29.53	3.0E-01	1.40	29.53	6.0E-01
YP_514132.1	21.5	0.38	19.86	1.0E+00	1.06	19.86	4.0E-01	0.34	19.86	8.5E-01
YP_513970.1	24.1	0.71	23.43	1.0E+00	1.08	23.43	1.2E-01	0.96	23.43	6.0E-01
YP_514457.1	20.4	-0.78	20.38	1.0E+00	1.09	20.38	4.3E-02	-0.17	20.38	8.3E-01
YP_513503.1	28.8	0.13	28.84	1.0E+00	1.09	28.84	1.3E-01	0.80	28.84	6.1E-01
YP_513120.1	27.2	0.66	26.62	1.0E+00	1.09	26.62	6.9E-02	0.90	26.62	6.0E-01
YP_514054.1	30.5	-0.04	30.58	1.0E+00	1.12	30.58	5.9E-07	-0.03	30.58	8.7E-01
YP_514234.1	24.7	0.10	25.01	1.0E+00	1.12	25.01	2.5E-07	-0.02	25.01	8.9E-01
YP_513156.1	23.7	0.03	25.09	1.0E+00	1.13	25.09	1.4E-01	-0.35	25.09	7.3E-01
YP_513436.1	27.0	0.62	26.47	1.0E+00	1.13	26.47	1.7E-01	0.74	26.47	6.2E-01
YP_514381.2	27.1	0.10	26.87	1.0E+00	1.14	26.87	7.7E-02	0.99	26.87	6.0E-01
YP_513864.1	27.6	-0.07	28.49	1.0E+00	1.16	28.49	8.1E-07	-0.48	28.49	2.0E-01
YP_513825.1	32.4	0.35	32.05	1.0E+00	1.16	32.05	9.0E-02	0.67	32.05	6.2E-01
YP_512881.1	22.1	0.95	22.23	1.0E+00	1.16	22.23	2.0E-02	0.39	22.23	6.3E-01
YP_513931.1	26.3	1.14	24.54	1.0E+00	1.19	24.54	2.2E-01	1.44	24.54	6.0E-01
YP_514416.1	31.0	0.38	30.72	1.0E+00	1.19	30.72	6.7E-03	0.54	30.72	6.0E-01
YP_512974.1	29.6	0.49	29.43	1.0E+00	1.20	29.43	1.7E-02	0.71	29.43	6.0E-01
YP_513490.1	21.4	0.75	21.42	1.0E+00	1.21	21.42	3.9E-02	0.41	21.42	6.3E-01
YP_514044.1	26.1	0.33	25.91	1.0E+00	1.26	25.91	2.6E-03	0.51	25.91	6.0E-01
YP_512955.1	21.9	0.60	21.02	1.0E+00	1.28	21.02	2.6E-02	1.02	21.02	6.0E-01

		01_delt_rpsU1_vs_WT			02_delt_rpsU2_vs_WT			03_delt_rpsU3_vs_WT		
id	delt_rpsU3 .3	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val	logFC	AveExpr	adj.P.Val
YP_514346.1	34.0	0.12	34.29	1.0E+00	1.29	34.29	9.7E-04	0.41	34.29	6.0E-01
YP_514049.1	29.3	0.05	29.36	1.0E+00	1.30	29.36	5.3E-06	0.14	29.36	6.3E-01
YP_513867.1	26.7	0.33	26.12	1.0E+00	1.31	26.12	1.8E-01	1.44	26.12	6.0E-01
YP_513320.1	24.4	-0.13	24.64	1.0E+00	1.35	24.64	5.3E-05	-0.24	24.64	6.2E-01
YP_513340.1	21.5	0.51	22.10	1.0E+00	1.37	22.10	1.7E-01	1.61	22.10	6.0E-01
YP_513609.1	24.7	1.23	23.63	1.0E+00	1.41	23.63	1.0E-01	1.11	23.63	6.0E-01
YP_512970.1	29.8	0.49	29.16	1.0E+00	1.43	29.16	3.2E-01	1.96	29.16	6.0E-01
YP_514066.1	28.4	1.01	27.37	1.0E+00	1.52	27.37	3.0E-01	1.75	27.37	6.0E-01
YP_514172.1	26.0	0.04	26.54	1.0E+00	1.53	26.54	1.0E-08	-0.06	26.54	7.1E-01
YP_514033.1	23.8	0.00	24.86	1.0E+00	1.70	24.86	1.2E-05	-0.06	24.86	8.8E-01
YP_514507.1	27.8	1.05	26.55	1.0E+00	1.70	26.55	1.0E-01	1.28	26.55	6.0E-01
YP_514456.1	28.0	0.02	27.73	1.0E+00	1.73	27.73	1.2E-07	0.21	27.73	6.0E-01
YP_514403.1	26.0	0.11	26.40	1.0E+00	1.95	26.40	1.5E-02	0.81	26.40	6.1E-01
YP_514363.1	22.7	-0.33	23.21	1.0E+00	1.99	23.21	7.7E-07	0.02	23.21	9.6E-01
YP_513415.1	18.5	0.83	19.00	1.0E+00	2.00	19.00	3.5E-03	-0.10	19.00	9.2E-01
YP_513633.1	21.1	1.07	19.76	1.0E+00	2.28	19.76	1.2E-01	1.21	19.76	6.3E-01
YP_513617.1	30.8	0.65	30.27	1.0E+00	2.57	30.27	6.6E-02	2.01	30.27	6.0E-01
YP_513822.1	28.0	0.23	28.24	1.0E+00	2.72	28.24	2.9E-04	0.85	28.24	6.0E-01
YP_514493.1	18.9	7.57	18.12	1.0E+00	5.47	18.12	2.2E-01	6.20	18.12	6.0E-01
YP_512942.1	24.8	3.24	23.38	1.0E+00	5.86	23.38	2.0E-03	3.27	23.38	6.0E-01
YP_514339.1	0.0	4.99	11.88	1.0E+00	6.15	11.88	3.1E-01	-5.63	11.88	6.2E-01

Table S3. Cells lacking bS21-2 have significant changes in transcript abundance. RNA-Seq was used to compare genome-wide transcript abundance from wild-type cells with an empty vector (LVS pF), cells lacking bS21-2 and containing an empty vector (LVS Δ rpsU2 pF), and bS21-2 mutant cells with bS21-2-V ectopically expressed (LVS Δ rpsU2 pF-rpsU2-V). Transcripts with significant differences in cells lacking bS21-2 compared to wild-type (>2 -fold change, adjusted p-value <0.05) are highlighted in yellow (columns E, G, I). All changes were complemented by ectopic expression of bS21-2-V (column G). Base mean (column D) reflects a measure of transcript abundance across all strains. NA = not available, generally due to low read abundance.

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0001	<i>dnaA</i>	chromosomal replication initiation protein	6426.0	0.09	4.80E-01
FTL_0002	-	DNA polymerase III subunit beta	9636.3	-0.04	8.69E-01
FTL_0003	-	hypothetical protein	6.9	0.27	2.79E-01
FTL_0004	<i>isftu1</i>	transposase	549.6	0.06	7.56E-01
FTL_0005	-	Na ⁺ /H ⁺ antiporter NHAP, fragment	13.5	0.69	5.88E-02
FTL_0006	-	indolepyruvate decarboxylase	96.2	1.10	8.88E-06
FTL_0007	-	hypothetical protein	177.5	-0.17	4.39E-01
FTL_0008	-	peptidase	2173.6	-1.08	6.41E-30
FTL_0009	-	outer membrane protein	48301.5	-0.61	3.02E-06
FTL_0010	<i>glpe</i>	thiosulfate sulfurtransferase	2237.8	-0.04	7.38E-01
FTL_0011	<i>secB1</i>	preprotein translocase subunit SecB	2263.0	-0.44	3.14E-04
FTL_0012	<i>recA</i>	recombinase A	11355.0	-0.34	3.14E-04
FTL_0013	<i>recX</i>	regulatory protein recX	354.5	0.15	3.58E-01
FTL_0014	<i>ssb</i>	single-strand binding protein	7330.6	-0.89	3.68E-17
FTL_0015	<i>ackA</i>	propionate kinase	2657.5	-0.44	4.73E-05
FTL_0016	<i>pta</i>	phosphate acetyltransferase	4249.9	-0.38	8.03E-06
FTL_0017	-	-	1119.0	-0.29	2.05E-03
FTL_0018	<i>isftu1</i>	transposase	542.2	0.04	8.31E-01
FTL_0019	-	sugar transferase	154.1	0.00	9.91E-01
FTL_0020	<i>aspS</i>	aspartyl-tRNA synthetase	18464.0	-0.12	2.11E-01
FTL_0021	-	MFS superfamily proline/ betaine transporte	45.8	1.89	1.20E-11
FTL_0022	-	-	11.6	0.00	9.84E-01
FTL_0023	<i>isftu1</i>	transposase	525.0	0.11	5.80E-01

				LVS Δ rrpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0024	-	serine transporter	5882.0	0.19	1.36E-01
FTL_0025	-	hypothetical protein	1.6	0.01	NA
FTL_0026	-	3-hydroxyisobutyrate dehydrogenase	1374.4	-0.44	5.88E-03
FTL_0027	-	3-hydroxyisobutyrate dehydrogenase	282.2	-0.49	1.23E-02
FTL_0028	-	aspartate carbamoyltransferase	1235.2	-1.53	3.38E-31
FTL_0029	<i>carB</i>	carbamoyl phosphate synthase large subunit	9724.0	-1.38	2.39E-58
FTL_0030	-	carbamoyl phosphate synthase small subunit	2527.4	-1.60	4.67E-62
FTL_0031	-	acid phosphatase	630.3	-0.81	2.37E-11
FTL_0032	<i>tmpT</i>	thiopurine S-methyltransferase	281.4	-0.15	4.26E-01
FTL_0033	<i>pyrC</i>	dihydroorotase	4027.8	-0.38	1.24E-04
FTL_0034	-	hypothetical protein	4926.1	0.68	1.34E-07
FTL_0035	-	hypothetical protein	2.9	0.07	NA
FTL_0036	-	hypothetical protein	167.6	-0.23	2.64E-01
FTL_0037	-	hypothetical protein	1025.6	-0.40	1.60E-05
FTL_0038	<i>emrA2</i>	HlyD family secretion protein	983.8	-1.03	1.26E-12
FTL_0039	-	hypothetical protein	4246.3	-0.11	6.47E-01
FTL_0040	-	LysR family transcriptional regulator	224.7	-0.16	3.30E-01
FTL_0041	-	hypothetical protein	11.3	0.38	1.98E-01
FTL_0042	<i>isftu2</i>	transposase	53.5	0.06	8.26E-01
FTL_0043	-	chorismate mutase	132.3	-0.29	1.20E-01
FTL_0044	-	transglutaminase	393.7	0.02	9.00E-01
FTL_0045	-	orotidine 5'-phosphate decarboxylase	1886.4	-1.24	2.67E-43
FTL_0046	-	diydroorotate dehydrogenase	1521.7	-1.17	4.58E-19

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0047	-	hypothetical protein	7.2	-0.11	6.38E-01
FTL_0048	-	prephenate dehydrogenase.	339.6	-0.55	2.00E-04
FTL_0049	-	D-tyrosyl-tRNA(Tyr) deacylase	144.4	-0.19	3.38E-01
FTL_0050	-	hypothetical protein	11.2	0.20	4.33E-01
FTL_0051	-	hypothetical protein	31.3	-0.13	6.43E-01
FTL_0052	-	hypothetical protein	8.4	0.15	5.52E-01
FTL_0053	-	Beta-fructofuranosidase	19.8	-0.05	8.58E-01
FTL_0054	<i>isftu1</i>	transposase	537.7	0.06	7.56E-01
FTL_0055	-	hypothetical protein	16.7	0.24	3.71E-01
FTL_0056	-	NADH dehydrogenase	433.0	-0.42	9.68E-04
FTL_0057	-	hypothetical protein	537.5	-0.69	1.77E-05
FTL_0058	-	aromatic amino acid HAAP transporter	1340.2	-0.40	2.74E-05
FTL_0059	<i>gidB</i>	16S rRNA methyltransferase GidB	300.5	-0.09	5.85E-01
FTL_0060	-	hypothetical protein	630.3	-0.18	1.54E-01
FTL_0061	-	hypothetical protein	48.9	-0.04	9.01E-01
FTL_0062	-	transcriptional regulator	14.5	0.14	6.05E-01
FTL_0063	-	major facilitator transporter	117.8	-0.47	1.34E-02
FTL_0064	-	-	3.0	0.17	NA
FTL_0065	-	-	40.2	-0.02	9.31E-01
FTL_0066	-	-	14.5	-0.36	2.01E-01
FTL_0067	-	-	149.7	-0.72	7.70E-05
FTL_0068	-	phosphoheptose isomerase	1640.8	-0.40	1.27E-06
FTL_0069	-	outer membrane lipoprotein	108.5	-0.33	8.55E-02

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0070	<i>rpsT</i>	30S ribosomal protein S20	5634.7	-0.37	5.58E-03
FTL_0071	-	GTP-binding protein LepA	5752.6	-0.40	9.48E-10
FTL_0072	<i>mnmA</i>	tRNA-specific 2-thiouridylase MnmA	2012.1	0.26	1.31E-02
FTL_0073	-	hypothetical protein	4079.4	-0.86	1.04E-25
FTL_0074	-	peptide deformylase	996.5	-0.59	1.59E-06
FTL_0075	-	riboflavin synthase beta subunit (6,7-dimeth	620.8	-0.62	7.66E-07
FTL_0076	-	riboflavin biosynthesis protein ribA/GTP-cycl	1851.8	-0.44	3.87E-07
FTL_0077	-	riboflavin synthase subunit alpha	130.0	0.25	1.79E-01
FTL_0078	-	riboflavin biosynthesis protein ribD	397.4	0.57	6.82E-06
FTL_0079	<i>isftu2</i>	transposase	55.7	0.20	4.37E-01
FTL_0080	<i>isftu1</i>	transposase	503.3	0.16	3.62E-01
FTL_0081	-	-	29.7	-0.02	9.52E-01
FTL_0082	-	B-type cytochrome	494.0	-0.95	3.60E-13
FTL_0083	-	-	19.2	0.21	4.55E-01
FTL_0084	-	-	614.9	-0.52	3.41E-06
FTL_0085	<i>nhaA</i>	pH-dependent sodium/proton antiporter	659.3	-0.26	2.63E-02
FTL_0086	-	hypothetical protein	489.4	-0.20	2.05E-01
FTL_0087	-	acetyltransferase protein	1035.9	0.06	6.77E-01
FTL_0088	-	acetyltransferase protein	1445.9	-0.12	2.95E-01
FTL_0089	-	ferredoxin	1302.4	-0.66	7.59E-05
FTL_0090	-	hypothetical protein	965.6	-0.70	9.97E-08
FTL_0091	-	O-methyltransferase	118.8	-0.57	3.33E-03
FTL_0092	<i>purT</i>	phosphoribosylglycinamide formyltransferas	2612.0	-0.82	1.01E-15

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0093	<i>chiB</i>	chitinase	2206.8	-0.29	7.52E-04
FTL_0094	<i>clpB</i>	ClpB protein	15884.8	-0.71	2.81E-10
FTL_0095	-	-	527.6	-0.12	4.49E-01
FTL_0096	-	-	147.7	-0.14	5.35E-01
FTL_0097	-	hypothetical protein	343.8	-0.29	2.85E-01
FTL_0098	<i>trpA</i>	tryptophan synthase subunit alpha	2373.5	-1.06	9.11E-16
FTL_0099	-	tryptophan synthase subunit beta	4828.4	-0.94	1.10E-19
FTL_0100	-	carboxypeptidase, fragment	972.9	-0.59	4.92E-08
FTL_0101	-	voltage-gated ClC-type chloride channel clcA	411.6	0.25	5.88E-02
FTL_0102	-	hypothetical protein	363.8	-0.18	2.71E-01
FTL_0103	-	hypothetical protein	415.6	-0.60	1.30E-05
FTL_0104	-	hypothetical protein	4986.5	-0.45	5.42E-07
FTL_0105	-	hypothetical protein	6904.3	-0.62	1.54E-13
FTL_0106	-	-	14.0	0.27	3.24E-01
FTL_0107	<i>isftu1</i>	transposase	539.8	0.08	7.19E-01
FTL_0108	-	hypothetical protein	3.3	-0.03	NA
FTL_0109	-	hypothetical protein	3.9	0.04	NA
FTL_0110	-	hypothetical protein	1.9	-0.06	NA
FTL_0111 / FTL_	<i>iglA</i>	intracellular growth locus, subunit A	5682.9	-0.93	6.56E-12
FTL_0112 / FTL_	<i>iglB</i>	intracellular growth locus, subunit B	30794.2	-0.37	3.91E-03
FTL_0113 / FTL_	<i>iglC</i>	intracellular growth locus, subunit C	19436.1	-0.34	1.64E-02
FTL_0114 / FTL_	<i>iglD</i>	intracellular growth locus, subunit D	15432.1	0.29	4.92E-02
FTL_0115 / FTL_	<i>pdpE</i>	PdpE protein	399.0	-0.21	2.22E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0116 / FTL	<i>pdpC</i>	PdpC protein	8687.8	-0.57	2.40E-04
FTL_0117 / FTL	<i>iglJ</i>	IglJ protein	497.6	-0.64	5.78E-03
FTL_0118 / FTL	<i>iglI</i>	IglI protein	1438.0	-1.05	6.98E-14
FTL_0119 / FTL	<i>dotU</i>	DotU	858.7	-0.75	6.73E-08
FTL_0120 / FTL	<i>iglH</i>	IglH protein	2250.6	-0.63	4.29E-04
FTL_0121 / FTL	<i>iglG</i>	IglG protein	1612.3	-1.10	8.68E-34
FTL_0122 / FTL	<i>iglF</i>	IglF protien	612.9	-0.02	9.25E-01
FTL_0123 / FTL	<i>vgrG</i>	VgrG	307.7	-0.33	3.82E-02
FTL_0124 / FTL	<i>iglE</i>	IglE protein	93.5	-0.16	5.49E-01
FTL_0125 / FTL	<i>pdpB</i>	PdpB protein	3030.3	-0.90	1.68E-13
FTL_0126 / FTL	<i>pdpA</i>	PdpA protein	4109.1	-0.69	1.03E-05
FTL_0127	-	formate dehydrogenase	2515.5	-0.51	8.61E-12
FTL_0128	<i>isftu1</i>	transposase	533.5	0.03	8.93E-01
FTL_0129	-	2-isopropylmalate synthase	1886.0	-0.51	4.04E-06
FTL_0130	-	isopropylmalate/homocitrate/citramalate sy	317.7	-0.64	1.47E-05
FTL_0131	-	branched-chain amino acid aminotransferase	4735.1	-0.53	1.67E-07
FTL_0132	-	pyruvate phosphate dikinase	6069.9	-0.78	2.04E-17
FTL_0133	<i>feoB</i>	ferrous iron transport protein	5486.6	0.90	1.15E-36
FTL_0134	-	hypothetical protein	12.7	0.37	2.08E-01
FTL_0135	<i>isftu1</i>	transposase	533.0	0.09	6.22E-01
FTL_0136	-	hypothetical protein	59.7	0.39	1.34E-01
FTL_0137	-	lipopolysaccharide protein	942.3	-0.44	7.10E-05
FTL_0138	-	ribonuclease II family protein	2440.5	-0.23	7.26E-03

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0139	-	carboxylesterase/phospholipase family prote	576.1	0.10	4.72E-01
FTL_0140	<i>hemC</i>	porphobilinogen deaminase	480.6	-0.21	1.96E-01
FTL_0141	-	camphor resistance protein CrcB	91.4	-0.14	5.65E-01
FTL_0142	-	hypothetical protein	123.2	-0.57	7.26E-03
FTL_0143	-	hypothetical protein	19.6	0.58	8.60E-02
FTL_0144	-	hypothetical protein	307.5	-0.76	6.91E-05
FTL_0145	-	ABC transporter membrane protein	1602.8	-1.18	3.59E-25
FTL_0146	-	ABC transporter ATP-binding protein	3757.6	-1.14	2.52E-42
FTL_0147	-	hypothetical protein	672.6	-0.18	2.36E-01
FTL_0148	-	Sodium/hydrogen exchanger (antiporter) fan	1412.8	-0.07	5.41E-01
FTL_0149	-	carbonic anhydrase	1601.5	-0.13	1.70E-01
FTL_0150	-	lipoprotein releasing system, subunit B, oute	335.9	-0.01	9.57E-01
FTL_0151	<i>ipk</i>	4-diphosphocytidyl-2-C-methyl-D-erythritol k	329.1	-0.10	5.67E-01
FTL_0152	-	hypothetical protein	563.7	-0.15	2.40E-01
FTL_0153	<i>isftu1</i>	transposase	533.7	0.02	9.07E-01
FTL_0154	-	-	8.4	0.25	3.23E-01
FTL_0155	-	-	247.8	-0.76	6.01E-06
FTL_0156	-	phosphate transport protein	1668.7	-0.31	1.04E-03
FTL_0157	-	hypothetical protein	1243.3	-0.85	4.12E-11
FTL_0158	<i>acpA</i>	acid phosphatase, phospholipase C (EC:3.1.4	1616.2	-0.73	9.78E-18
FTL_0159	-	hydrolase subunit	339.7	0.19	2.07E-01
FTL_0160	-	LamB/YcsF family protein	670.2	0.22	3.95E-02
FTL_0161	-	-	599.8	0.39	7.75E-03

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0162	-	hypothetical protein	62.6	0.79	6.64E-04
FTL_0163	-	MFS transporter	3.3	0.00	NA
FTL_0164	<i>isftu1</i>	transposase	534.1	0.03	8.93E-01
FTL_0165	-	dicarboxylate MFS transporter	25.9	-0.48	1.05E-01
FTL_0166	-	universal stress protein	26437.3	-0.88	7.46E-17
FTL_0167	-	DNA/RNA helicase	73.1	0.37	9.78E-02
FTL_0168	-	hypothetical protein	264.6	0.60	1.08E-03
FTL_0169	-	hypothetical protein	293.2	-0.32	3.51E-02
FTL_0170	-	hypothetical protein	60.5	-0.46	6.56E-02
FTL_0171	-	tetrapyrrole methyltransferase family protein	471.6	-0.26	5.14E-02
FTL_0172	<i>murC</i>	UDP-N-acetylmuramate--L-alanine ligase	1357.8	-0.01	9.25E-01
FTL_0173	<i>aroE</i>	shikimate 5-dehydrogenase	1188.1	-0.10	4.56E-01
FTL_0174	-	hypothetical protein	699.9	-0.80	3.03E-10
FTL_0175	<i>rpmH</i>	50S ribosomal protein L34	55.9	-1.04	1.58E-03
FTL_0176	-	ribonuclease P protein component	2617.0	-0.69	4.12E-07
FTL_0177	-	hypothetical protein	281.2	-0.71	9.60E-04
FTL_0178	<i>yidC</i>	inner-membrane protein	7406.7	-0.82	6.76E-11
FTL_0179	<i>ddg</i>	acyltransferase	1008.2	-0.51	2.15E-06
FTL_0180	<i>htrB</i>	acyltransferase	2199.0	-0.10	4.51E-01
FTL_0181	-	Type IV pili fiber building block protein	168.1	0.05	8.22E-01
FTL_0182	-	elongation factor P	2594.0	-0.59	1.32E-05
FTL_0183	-	oligoribonuclease	1131.7	-0.87	6.35E-24
FTL_0184	-	hypothetical protein	21.3	-0.23	4.03E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0185	<i>isftu1</i>	transposase	539.9	-0.02	9.34E-01
FTL_0186	-	hypothetical protein	95.4	0.69	2.24E-03
FTL_0187	-	cyclohexadienyl dehydratase	2263.8	1.20	4.13E-16
FTL_0188	-	cytochrome d terminal oxidase, polypeptide	16179.2	-0.02	8.32E-01
FTL_0189	-	cytochrome d terminal oxidase, polypeptide	20484.4	-0.19	1.06E-01
FTL_0190	-	major facilitator transporter	692.9	-0.56	1.20E-04
FTL_0191	-	cytochrome O ubiquinol oxidase subunit II	9279.9	-0.35	1.78E-04
FTL_0192	-	cytochrome O ubiquinol oxidase subunit I	30098.3	-0.64	1.14E-12
FTL_0193	-	cytochrome O ubiquinol oxidase, subunit III	4267.8	-0.45	3.18E-04
FTL_0194	-	cytochrome O ubiquinol oxidase subunit IV	1386.5	-0.49	3.60E-05
FTL_0195	-	protoheme IX farnesyltransferase	794.4	0.15	3.06E-01
FTL_0196	-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N	8823.3	-0.79	1.23E-16
FTL_0197	-	hypothetical protein	986.0	-0.02	9.00E-01
FTL_0198	-	pyridoxal kinase	1142.7	-0.38	6.16E-05
FTL_0199	-	hypothetical protein	734.8	-0.45	4.97E-03
FTL_0200	-	methanol dehydrogenase regulatory protein	1620.0	-0.27	1.99E-03
FTL_0201	-	hypothetical protein	563.8	-0.13	4.04E-01
FTL_0202	-	hypothetical protein	80.5	-0.02	9.25E-01
FTL_0203	-	hypothetical protein	324.5	-0.27	1.32E-01
FTL_0204	-	hypothetical protein	141.4	-0.33	1.36E-01
FTL_0205	-	hypothetical protein	111.4	-1.08	7.49E-04
FTL_0206	-	hypothetical protein	725.7	-0.76	1.22E-10
FTL_0207	-	pyrrolidone-carboxylate peptidase	4572.4	0.67	6.38E-15

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0208	-	putative cytochrome c-type biogenesis prote	1022.8	0.65	6.03E-06
FTL_0209	-	DNA polymerase III subunit chi	508.4	0.41	3.73E-03
FTL_0210	<i>valS</i>	valyl-tRNA synthetase	8389.0	-0.59	1.76E-18
FTL_0211	-	hypothetical protein	1336.5	-0.42	5.57E-03
FTL_0212	-	hypothetical protein	455.2	0.16	3.27E-01
FTL_0213	-	hypothetical protein	102.8	-0.21	3.44E-01
FTL_0214	-	L-lactate dehydrogenase	858.6	-0.45	2.41E-05
FTL_0215	-	dihydropteridine reductase	793.2	-0.71	1.49E-10
FTL_0216	-	MutT/nudix family protein	76.3	-0.39	1.14E-01
FTL_0217	<i>fumC</i>	fumarate hydratase	1098.5	-0.27	1.11E-02
FTL_0218	<i>gltX</i>	glutamyl-tRNA synthetase	6294.6	-0.54	9.41E-10
FTL_0219	-	hypothetical protein	125.5	0.34	6.48E-02
FTL_0220	<i>isftu2</i>	transposase	52.5	0.21	3.91E-01
FTL_0221	-	amino acid permease	623.1	0.06	6.96E-01
FTL_0222	-	hypothetical protein	2987.2	-0.55	3.04E-10
FTL_0223	-	dihydrofolate reductase type I	1549.9	-0.68	2.24E-15
FTL_0224	<i>rpsB</i>	30S ribosomal protein S2	9138.9	-0.27	1.52E-03
FTL_0225	<i>tsf</i>	elongation factor Ts	14334.6	0.00	9.69E-01
FTL_0226	<i>pyrH</i>	uridylate kinase	3256.1	0.61	3.21E-06
FTL_0227	<i>frr</i>	ribosome recycling factor	2274.3	0.13	5.71E-01
FTL_0228	<i>uppS</i>	undecaprenyl pyrophosphate synthase	1022.3	0.04	8.62E-01
FTL_0229	<i>cdsA</i>	phosphatidate cytidyltransferase	704.0	-0.78	4.01E-08
FTL_0230	<i>dut</i>	deoxyuridine 5'-triphosphate nucleotidohydr	1723.3	-0.46	9.72E-06

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0231	<i>pgsA</i>	phosphatidylglycerophosphate synthetase	855.1	-0.20	6.63E-02
FTL_0232	<i>rpsL</i>	30S ribosomal protein S12	6687.6	-0.34	3.27E-02
FTL_0233	<i>rpsG</i>	30S ribosomal protein S7	9194.0	-0.73	6.55E-03
FTL_0234	-	elongation factor G	83936.8	-0.56	3.07E-05
FTL_0235	<i>rpsJ</i>	30S ribosomal protein S10	4064.7	-0.48	1.07E-04
FTL_0236	<i>rplC</i>	50S ribosomal protein L3	45522.2	-0.43	3.75E-03
FTL_0237	<i>rplD</i>	50S ribosomal protein L4	21957.0	-0.93	3.20E-17
FTL_0238	<i>rplW</i>	50S ribosomal protein L23	1821.6	-1.46	2.39E-04
FTL_0239	<i>rplB</i>	50S ribosomal protein L2	15295.2	-1.03	3.79E-09
FTL_0240	<i>rpsS</i>	30S ribosomal protein S19	3239.8	-0.93	4.11E-14
FTL_0241	<i>rplV</i>	50S ribosomal protein L22	10796.4	-0.90	3.19E-08
FTL_0242	<i>rpsC</i>	30S ribosomal protein S3	19852.1	-0.86	6.51E-08
FTL_0243	<i>rplP</i>	50S ribosomal protein L16	15769.1	-0.47	5.08E-05
FTL_0244	-	50S ribosomal protein L29	3124.3	-0.55	4.22E-04
FTL_0245	<i>rpsQ</i>	30S ribosomal protein S17	1962.3	-0.33	3.12E-03
FTL_0246	<i>rplN</i>	50S ribosomal protein L14	5714.0	-0.41	1.26E-01
FTL_0247	<i>rplX</i>	50S ribosomal protein L24	3907.0	-0.43	1.00E-02
FTL_0248	<i>rplE</i>	50S ribosomal protein L5	20788.7	0.00	9.62E-01
FTL_0249	<i>rpsN</i>	30S ribosomal protein S14	13331.8	-0.08	6.22E-01
FTL_0250	<i>rpsH</i>	30S ribosomal protein S8	6960.7	-0.05	7.62E-01
FTL_0251	<i>rplF</i>	50S ribosomal protein L6	9051.5	-0.30	1.56E-02
FTL_0252	<i>rplR</i>	50S ribosomal protein L18	6671.0	-0.40	5.38E-03
FTL_0253	<i>rpsE</i>	30S ribosomal protein S5	11078.6	-0.64	4.15E-08

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0254	<i>rpmD</i>	50S ribosomal protein L30	2179.1	-0.59	5.11E-06
FTL_0255	<i>rplO</i>	50S ribosomal protein L15	8140.6	-0.36	3.18E-05
FTL_0256	<i>secY</i>	preprotein translocase subunit SecY	24096.5	0.01	9.41E-01
FTL_0257	<i>rpmJ</i>	50S ribosomal protein L36	611.1	-0.44	1.36E-03
FTL_0258	<i>rpsM</i>	30S ribosomal protein S13	5278.5	-0.06	5.47E-01
FTL_0259	-	30S ribosomal protein S11	7099.6	0.02	8.82E-01
FTL_0260	<i>rpsD</i>	30S ribosomal protein S4	18241.4	-0.39	6.20E-05
FTL_0261	-	DNA-directed RNA polymerase subunit alpha	17763.4	-0.13	3.72E-01
FTL_0262	<i>rplQ</i>	50S ribosomal protein L17	10763.9	-1.18	8.87E-41
FTL_0263	<i>isftu1</i>	transposase	522.6	0.06	7.70E-01
FTL_0264	-	-	56.5	0.21	3.81E-01
FTL_0265	-	hypothetical protein	6512.3	0.06	6.80E-01
FTL_0266	<i>isftu1</i>	transposase	537.0	0.10	6.29E-01
FTL_0267	<i>htpG</i>	heat shock protein 90	18207.7	-1.00	1.20E-10
FTL_0268	<i>isftu1</i>	transposase	529.3	0.10	5.58E-01
FTL_0269	<i>gdh</i>	glutamate dehydrogenase	21959.6	-0.70	1.17E-11
FTL_0270	<i>isftu2</i>	transposase	55.8	-0.07	7.88E-01
FTL_0271	-	hypothetical protein	55.1	0.35	1.52E-01
FTL_0272	-	diaminopimelate decarboxylase	91.7	0.16	4.72E-01
FTL_0273	-	glutamate/gamma-aminobutyrate anti-porter	133.7	-0.23	2.20E-01
FTL_0274	-	-	77.6	-0.10	7.09E-01
FTL_0275	-	methylated-DNA--protein-cysteine methyltra	98.6	-0.31	1.44E-01
FTL_0276	-	hypothetical protein	415.8	-0.77	1.47E-05

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0277	-	mercuric reductase protein	1768.8	-0.40	7.97E-05
FTL_0278	-	hypothetical protein	113.5	-0.34	1.39E-01
FTL_0279	-	hypothetical protein	576.3	-0.47	5.58E-04
FTL_0280	-	amino acid permease	428.0	-0.93	5.10E-15
FTL_0281	-	heat shock protein, hsp40	4535.6	-0.61	2.31E-03
FTL_0282	-	hypothetical protein	641.0	-0.75	2.61E-10
FTL_0283	-	aromatic amino acid HAAP transporter	148.2	0.05	8.07E-01
FTL_0284	-	hypothetical protein	316.2	-0.23	1.61E-01
FTL_0285	-	GTP pyrophosphokinase	2736.4	0.25	5.00E-03
FTL_0286	-	hypothetical protein	389.7	-0.87	7.79E-08
FTL_0287	-	hypothetical protein	100.6	-0.39	1.15E-01
FTL_0288	-	hypothetical protein	215.9	-0.46	2.27E-02
FTL_0289	-	hypothetical protein	210.7	-0.16	3.97E-01
FTL_0290	<i>xerC</i>	integrase/recombinase XerC	944.3	-0.78	3.35E-13
FTL_0291	-	aromatic amino acid HAAP transporter	886.1	-0.64	1.65E-07
FTL_0292	-	-	57.3	0.10	6.82E-01
FTL_0293	<i>secB2</i>	preprotein translocase subunit SecB	1690.5	-0.68	1.27E-06
FTL_0294	<i>mutS</i>	DNA mismatch repair protein MutS	2217.8	-0.64	6.11E-11
FTL_0295	-	acetyl-CoA carboxylase carboxyltransferase s	16205.4	-0.65	3.01E-20
FTL_0296	-	hypothetical protein	1300.3	-0.59	1.05E-04
FTL_0297	-	hypothetical protein	844.7	-0.24	3.96E-02
FTL_0298	-	hypothetical protein	452.9	0.28	1.76E-02
FTL_0299	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	438.3	-0.47	2.17E-04

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0300	-	hypothetical protein	203.6	-0.94	1.30E-08
FTL_0301	-	hypothetical protein	22.8	1.05	3.84E-03
FTL_0302	<i>isftu2</i>	transposase	47.9	0.11	6.96E-01
FTL_0303	-	hypothetical protein	4.2	0.16	NA
FTL_0304	<i>nhaP</i>	Na ⁺ /H ⁺ antiporter	1135.9	-0.28	9.37E-03
FTL_0305	-	hypothetical protein	1043.1	0.02	8.53E-01
FTL_0306	-	tryptophanyl-tRNA synthetase	4064.6	-0.09	3.71E-01
FTL_0307	<i>coaE</i>	dephospho-CoA kinase	3786.8	-0.56	5.86E-11
FTL_0308	-	hypothetical protein	478.3	0.44	5.06E-04
FTL_0309	<i>aceE</i>	pyruvate dehydrogenase subunit E1	35692.9	-0.34	8.25E-04
FTL_0310	-	dihydrolipoamide acetyltransferase	16476.6	-0.49	1.35E-05
FTL_0311	-	dihydrolipoamide dehydrogenase	24474.2	-0.41	1.89E-03
FTL_0312	-	transposase	0.0	NA	NA
FTL_0313	-	hypothetical protein	0.0	NA	NA
FTL_0314	<i>isftu1</i>	transposase	540.2	0.14	4.49E-01
FTL_0315	-	MutT protein	1085.4	-0.56	8.02E-07
FTL_0316	-	arsenate reductase	679.7	-0.55	1.23E-03
FTL_0317	-	hypothetical protein	5291.2	-0.93	1.06E-16
FTL_0318	-	lipoprotein	112.5	-0.72	4.72E-04
FTL_0319	-	hypothetical protein	1733.1	-0.82	6.70E-20
FTL_0320	-	aspartate aminotransferase	112.7	0.06	7.83E-01
FTL_0321	-	-	3.8	0.02	NA
FTL_0322	-	-	124.2	0.18	3.83E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0323	-	-	41.7	0.73	9.11E-03
FTL_0324	-	-	63.3	0.11	6.08E-01
FTL_0325	-	OmpA family protein	11044.2	-0.52	7.81E-05
FTL_0326	-	FKBP-type 16 kDa peptidyl-prolyl cis-transiso	1356.3	-0.44	1.19E-02
FTL_0327	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate r	4270.5	-0.41	5.68E-04
FTL_0328	-	chorismate mutase	1057.4	-0.10	5.13E-01
FTL_0329	<i>pssA</i>	CDP-alcohol phosphatidyltransferase	2281.3	-0.37	1.65E-04
FTL_0330	-	hypothetical protein	62.7	-0.40	1.08E-01
FTL_0331	-	TolQ protein	1437.8	-0.36	1.79E-03
FTL_0332	-	TolR protein	367.8	-0.39	1.38E-03
FTL_0333	-	hypothetical protein	264.7	0.16	4.15E-01
FTL_0334	-	TolB protein precursor	1426.9	-0.70	7.65E-11
FTL_0335	-	lipoprotein	195.5	-0.73	9.39E-04
FTL_0336	-	peptidoglycan-associated lipoprotein	9300.8	-0.48	2.47E-05
FTL_0337	-	-	8615.5	-0.21	7.67E-03
FTL_0338	-	N-acetyltransferase GCN5	220.3	0.04	8.75E-01
FTL_0339	<i>isftu1</i>	transposase	535.4	0.16	3.88E-01
FTL_0340	-	hypothetical protein	1.9	0.12	NA
FTL_0341	-	deoxyribodipyrimidine photolyase	46.5	0.07	7.92E-01
FTL_0342	-	deoxyribodipyrimidine photolyase	16.4	1.00	1.56E-02
FTL_0343	-	hypothetical protein	68.5	0.12	6.65E-01
FTL_0344	-	hypothetical protein	0.6	-0.03	NA
FTL_0345	-	bile acid symporter family protein	773.2	-0.75	2.40E-08

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0346	-	hypothetical protein	130.7	-0.19	4.55E-01
FTL_0347	-	hypothetical protein	102.2	-0.20	3.56E-01
FTL_0348	-	-	607.4	-0.93	1.55E-12
FTL_0349	-	-	34.5	-1.84	2.16E-05
FTL_0350	-	-	34.8	-0.19	4.90E-01
FTL_0351	-	-	3.8	0.08	NA
FTL_0352	-	hypothetical protein	10.9	0.12	6.46E-01
FTL_0353	<i>isftu1</i>	transposase	533.1	0.18	3.58E-01
FTL_0354	-	hypothetical protein	242.6	-0.52	2.38E-04
FTL_0355	<i>ubiA</i>	4-hydroxybenzoate polyprenyltransferase	382.0	-0.38	6.77E-03
FTL_0356	<i>ubiC</i>	chorismate pyruvate lyase	554.2	-0.28	2.68E-02
FTL_0357	<i>rph</i>	ribonuclease PH	2027.6	-1.15	5.75E-18
FTL_0358	-	hypothetical protein	752.2	-0.18	1.95E-01
FTL_0359	-	Type IV pili fiber building block protein	846.7	0.29	1.72E-02
FTL_0360	-	heat shock protein HtpX	3585.4	-1.02	2.92E-18
FTL_0361	-	LemA-like protein	3857.0	-1.34	7.37E-38
FTL_0362	-	-	19.5	0.74	3.88E-02
FTL_0363	-	-	299.0	-0.11	4.94E-01
FTL_0364	-	-	11.2	0.12	5.86E-01
FTL_0365	-	-	70.5	0.41	1.07E-01
FTL_0366	-	-	37.6	0.20	4.53E-01
FTL_0367	<i>isftu2</i>	transposase	57.5	0.20	4.22E-01
FTL_0368	-	-	118.7	-0.06	7.91E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0369	-	-	281.1	-0.16	4.72E-01
FTL_0370	-	arsenical resistance operon repressor	138.2	-0.25	2.39E-01
FTL_0371	-	hypothetical protein	254.0	-0.97	1.99E-09
FTL_0372	<i>gpsA</i>	NAD(P)H-dependent glycerol-3-phosphate de	1544.2	-0.58	8.22E-11
FTL_0373	-	hypothetical protein	96.2	0.21	3.32E-01
FTL_0374	-	DNA repair protein RadA	841.5	0.01	9.26E-01
FTL_0375	-	hypothetical protein	1402.9	-0.25	7.88E-02
FTL_0376	-	hypothetical protein	585.2	-0.18	1.82E-01
FTL_0377	-	chorismate synthase	2325.0	-0.35	2.00E-04
FTL_0378	-	hypothetical protein	199.0	-0.07	7.17E-01
FTL_0379	-	methionine sulfoxide reductase B	487.4	-0.78	7.08E-10
FTL_0380	-	superoxide dismutase (Cu-Zn) precursor	2365.7	-0.02	9.09E-01
FTL_0381	-	hypothetical protein	822.7	0.18	1.54E-01
FTL_0382	-	amino acid permease	36413.4	-1.48	1.32E-52
FTL_0383	<i>manA</i>	mannose-6-phosphate isomerase, fragment	307.8	-1.61	2.10E-09
FTL_0384	-	-	1626.0	-0.90	6.87E-17
FTL_0385	-	-	455.8	-0.79	9.98E-06
FTL_0386	-	-	77.9	-0.49	6.88E-02
FTL_0387	<i>aspC1</i>	aspartate aminotransferase	18763.8	-0.86	2.34E-30
FTL_0388	-	cation transporter	324.9	-0.12	5.04E-01
FTL_0389	-	DNA repair protein recN	2624.8	-0.71	5.92E-12
FTL_0390	-	Type IV pili fiber building block protein	442.8	0.26	1.04E-01
FTL_0391	-	hypothetical protein	298.1	-0.09	6.58E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0392	-	Type IV pili fiber building block protein	137.1	-1.40	9.91E-07
FTL_0393	<i>lpxE</i>	lipid A 1-phosphatase	582.2	-0.49	2.94E-06
FTL_0394	<i>folD</i>	bifunctional 5,10-methylene-tetrahydrofolat	4695.8	-0.65	1.38E-16
FTL_0395	<i>purM</i>	phosphoribosylaminoimidazole synthetase	4704.3	-1.06	9.52E-30
FTL_0396	<i>purCD</i>	fusion protein PurC/PurD	9409.5	-0.55	1.17E-11
FTL_0397	<i>purN</i>	phosphoribosylglycinamide formyltransferas	606.9	-0.26	5.64E-02
FTL_0398	<i>purE</i>	phosphoribosylaminoimidazole carboxylase,	1179.2	-0.66	2.53E-08
FTL_0399	<i>purK</i>	phosphoribosylaminoimidazole carboxylase,	3054.5	-0.53	6.94E-08
FTL_0400	<i>isftu2</i>	transposase	51.6	-0.16	5.49E-01
FTL_0401	-	Sua5_yciO_yrdC family protein	602.0	0.09	7.15E-01
FTL_0402	<i>ispZ</i>	intracellular septation protein A family prote	1786.5	-0.55	8.45E-04
FTL_0403	-	hypothetical protein	250.1	0.01	9.67E-01
FTL_0404	<i>glk</i>	glucose kinase	2498.6	-0.36	8.82E-04
FTL_0405	<i>ubiE</i>	menaquinone biosynthesis methyltransferas	2691.7	-0.23	5.25E-02
FTL_0406	-	hypothetical protein	668.1	-0.22	1.04E-01
FTL_0407	<i>ubiB</i>	2-polyprenylphenol 6-hydroxylase	1633.2	-0.41	1.32E-06
FTL_0408	<i>hitA</i>	histidine triad (HIT) family protein	403.6	-0.36	4.12E-02
FTL_0409	-	purine/pyrimidine phosphoribosyl transferas	118.9	-0.19	4.09E-01
FTL_0410	-	hypothetical protein	943.7	-0.44	1.96E-03
FTL_0411	-	hypothetical protein	1978.5	-0.20	7.26E-02
FTL_0412	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine redu	629.4	0.08	6.11E-01
FTL_0413	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltran	3694.9	-0.10	2.66E-01
FTL_0414	<i>engA</i>	GTP-binding protein EngA	4860.1	-0.62	2.19E-18

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0415	-	hypothetical protein	18.2	0.38	1.95E-01
FTL_0416	<i>isftu2</i>	transposase	66.0	0.12	6.37E-01
FTL_0417	<i>isftu1</i>	transposase	519.4	0.03	8.81E-01
FTL_0418	-	hypothetical protein	124.2	-0.29	1.31E-01
FTL_0419	-	oligopeptidase A	4089.1	-0.50	2.33E-07
FTL_0420	-	hypothetical protein	604.6	-0.49	9.44E-05
FTL_0421	-	lipoprotein	24342.1	-0.50	2.13E-07
FTL_0422	-	-	251.0	0.44	1.97E-03
FTL_0423	-	hypothetical protein	2089.9	-1.07	6.43E-15
FTL_0424	-	lipoprotein	3931.5	-0.08	5.59E-01
FTL_0425	-	Type IV pili glycosylation protein	3129.0	-0.92	7.05E-24
FTL_0426	-	DNA topoisomerase I	10052.0	0.10	3.56E-01
FTL_0427	-	chromosome partition protein A	2579.1	-0.34	1.46E-02
FTL_0428	-	chromosome partition protein B	1988.3	-0.24	2.77E-03
FTL_0429	-	glutamine amidotransferase	649.0	-0.11	5.27E-01
FTL_0430	-	hypothetical protein	1464.4	-0.22	5.18E-02
FTL_0431	-	hypothetical protein	152.7	-0.14	5.59E-01
FTL_0432	-	hypothetical protein	35.8	0.26	3.45E-01
FTL_0433	-	ribosomal large subunit methyltransferase J	344.1	-0.47	5.79E-04
FTL_0434	-	hypothetical protein	1149.9	-0.58	1.29E-07
FTL_0435	<i>lspA</i>	lipoprotein signal peptidase	1044.7	0.17	2.90E-01
FTL_0436	<i>ileS</i>	isoleucyl-tRNA synthetase	18488.5	-0.18	5.52E-02
FTL_0437	-	riboflavin biosynthesis protein RibF	1308.2	-0.64	4.11E-13

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0438	-	malate dehydrogenase	25896.9	0.01	9.34E-01
FTL_0439	-	hypothetical protein	11809.2	0.02	8.69E-01
FTL_0440	<i>isftu1</i>	transposase	511.9	0.06	7.85E-01
FTL_0441	<i>isftu2</i>	transposase	89.4	0.55	1.11E-02
FTL_0442	-	hypothetical protein	124.2	0.85	8.65E-06
FTL_0443	-	major facilitator transporter	1564.7	0.01	9.40E-01
FTL_0444	<i>metG</i>	methionyl-tRNA synthetase	7971.8	-0.47	7.43E-09
FTL_0445	-	hypothetical protein	144.6	-0.78	4.05E-05
FTL_0446	-	hypothetical protein	18.5	-0.02	9.43E-01
FTL_0447	-	hypothetical protein	259.0	0.29	8.30E-02
FTL_0448	-	hypothetical protein	659.9	-0.76	2.74E-11
FTL_0449	<i>pigR</i>	pathogenicity island gene regulator	3998.2	-0.19	1.39E-01
FTL_0450	<i>psd</i>	phosphatidylserine decarboxylase	2897.3	-0.71	3.68E-17
FTL_0451	-	hypothetical protein	1657.8	-0.32	1.75E-03
FTL_0452	-	bifunctional nicotinamide mononucleotide a	1747.8	-0.23	1.33E-02
FTL_0453	-	UDP-N-acetylglucosamine pyrophosphorylas	5061.6	-0.53	1.09E-07
FTL_0454	-	glucosamine--fructose-6-phosphate aminotr	10883.8	-0.47	1.32E-08
FTL_0455	-	acetyltransferase	616.6	-0.57	2.03E-05
FTL_0456	<i>rpsU</i>	30S ribosomal protein S21	7227.8	-0.48	2.68E-03
FTL_0457	-	cold shock protein	1468.8	-0.22	5.21E-02
FTL_0458	-	hypothetical protein	82.9	-0.70	9.67E-03
FTL_0459	-	methionine aminopeptidase	1725.2	-0.60	1.09E-05
FTL_0460	-	hypothetical protein	1636.1	-0.07	6.65E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0461	-	hypothetical protein	825.1	0.78	2.98E-06
FTL_0462	-	DNA topoisomerase IV subunit A	4251.3	-0.46	5.42E-09
FTL_0463	-	5'-methylthioadenosine/S-adenosylhomocys	939.2	-0.99	1.32E-17
FTL_0464	-	hypothetical protein	242.8	-0.36	3.31E-02
FTL_0465	-	BNR/Asp-box repeat-containing protein	1278.1	-0.30	7.41E-03
FTL_0466	-	soluble lytic murein transglycosylase	3894.2	-0.47	2.13E-07
FTL_0467	-	hypothetical protein	5.6	0.14	NA
FTL_0468	<i>isftu2</i>	transposase	55.7	0.04	9.03E-01
FTL_0469	-	hypothetical protein	2.1	0.15	NA
FTL_0470	-	hypothetical protein	795.0	-0.23	2.67E-01
FTL_0471	-	hypothetical protein	9.2	0.13	5.96E-01
FTL_0472	-	DNA polymerase III subunit alpha	4880.6	-0.36	1.84E-05
FTL_0473	-	peptide deformylase	1228.7	-1.14	6.15E-35
FTL_0474	-	lipoprotein releasing system, subunit C, putat	1738.9	-0.28	6.93E-03
FTL_0475	-	lipoprotein releasing system, subunit D, ABC	784.0	-0.09	4.41E-01
FTL_0476	-	lysine decarboxylase, inducible	5251.9	-0.72	7.02E-18
FTL_0477	<i>gcvT</i>	glycine cleavage system aminomethyltransfe	6334.5	-0.77	3.37E-17
FTL_0478	-	glycine cleavage system H protein	4407.6	-0.69	2.12E-08
FTL_0479	-	glycine dehydrogenase subunit 1	9013.1	-1.00	1.28E-19
FTL_0480	-	glycine dehydrogenase subunit 2	12677.2	-0.45	3.67E-05
FTL_0481	-	shikimate 5-dehydrogenase	891.6	0.18	1.90E-01
FTL_0482	-	pullulanase	5169.0	0.05	6.67E-01
FTL_0483	<i>glgB</i>	glycogen branching protein	6977.1	-0.14	1.76E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0484	<i>pgm</i>	phosphoglucomutase	2794.3	-0.58	2.72E-10
FTL_0485	<i>glgC</i>	glucose-1-phosphate adenylyltransferase	3625.8	-0.98	2.50E-17
FTL_0486	<i>glgA</i>	glycogen synthase	2612.0	-0.55	8.84E-09
FTL_0487	-	maltodextrin phosphorylase	6156.9	-0.37	6.10E-04
FTL_0488	-	4-alpha-glucanotransferase	1274.1	-0.50	9.31E-05
FTL_0489	<i>glyQ</i>	glycyl-tRNA synthetase subunit alpha	3050.6	-0.25	3.44E-03
FTL_0490	-	UDP-N-acetylmuramoylalanyl-D-glutamate--2	1650.5	0.05	7.62E-01
FTL_0491	-	outer membrane lipoprotein	677.4	-0.44	1.79E-02
FTL_0492	-	UDP-N--acetylmuramoylalanyl-D-glutamyl-2,	3421.6	-0.42	3.16E-06
FTL_0493	-	hypothetical protein	2080.5	-0.78	7.82E-22
FTL_0494	-	aspartate-semialdehyde dehydrogenase	4.9	0.16	NA
FTL_0495	-	-	6.0	0.18	4.01E-01
FTL_0496	-	-	0.3	0.00	NA
FTL_0497	-	-	0.7	0.02	NA
FTL_0498	-	threonine synthase	38.5	0.00	9.98E-01
FTL_0499	-	S-adenosylmethionine decarboxylase	1554.3	-0.31	6.56E-03
FTL_0500	-	spermidine synthase	869.3	0.42	9.78E-04
FTL_0501	-	putative arginine decarboxylase	21.0	0.18	5.12E-01
FTL_0502	-	hypothetical protein	45.5	-0.24	3.67E-01
FTL_0503	<i>isftu1</i>	transposase	545.1	0.08	7.03E-01
FTL_0504	-	beta-alanine synthase or beta-ureidopropion	1.5	-0.01	NA
FTL_0505	-	carbon-nitrogen hydrolase family protein	9.7	-0.05	8.38E-01
FTL_0506	<i>lpxH</i>	UDP-2,3-diacetylglucosamine hydrolase	383.6	-0.03	9.00E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0507	<i>pyrE</i>	orotate phosphoribosyltransferase	939.8	-0.18	1.36E-01
FTL_0508	<i>mpl</i>	UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamate ligase	2929.2	-0.78	2.28E-20
FTL_0509	<i>yjfh</i>	tRNA/rRNA methyltransferase	577.7	-0.80	1.21E-12
FTL_0510	<i>isftu1</i>	transposase	549.0	0.04	8.12E-01
FTL_0511	-	hypothetical protein	686.0	-0.64	9.86E-04
FTL_0512	-	BolA-like protein	233.7	-0.55	1.35E-03
FTL_0513	-	hypothetical protein	301.6	-0.09	6.28E-01
FTL_0514	-	hypothetical protein	1164.5	-0.68	5.59E-09
FTL_0515	-	ABC transporter substrate-binding protein	590.1	-0.40	1.70E-03
FTL_0516	-	ABC transporter membrane protein	324.9	-0.11	5.47E-01
FTL_0517	-	ABC transporter ATP-binding protein	687.7	-0.20	1.99E-01
FTL_0518	<i>minE</i>	cell division topological specificity factor MinE	617.6	-0.29	1.21E-02
FTL_0519	<i>minD</i>	septum site-determining protein MinD	9437.7	-0.45	4.95E-07
FTL_0520	<i>minC</i>	septum site-determining protein MinC	8721.5	-0.31	1.14E-04
FTL_0521	<i>rpmG</i>	50S ribosomal protein L33	297.3	-0.42	1.73E-02
FTL_0522	<i>rpmB</i>	50S ribosomal protein L28	1743.9	-0.30	1.63E-03
FTL_0523	-	hypothetical protein	1439.2	-0.72	3.10E-10
FTL_0524	-	ATP-dependent DNA helicase RecG	1459.2	-0.11	3.58E-01
FTL_0525	-	fumarate hydratase	7963.4	-0.28	7.99E-03
FTL_0526	<i>isftu1</i>	transposase	448.2	0.09	6.55E-01
FTL_0527	-	endonuclease	22.0	0.28	3.22E-01
FTL_0528	-	Type III restriction enzyme	835.3	0.44	4.89E-03
FTL_0529	-	uracil-DNA glycosylase	186.6	0.08	7.18E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0530	-	hypothetical protein	3.3	-0.10	NA
FTL_0531	-	hypothetical protein	1.2	0.04	NA
FTL_0532	-	hypothetical protein	32.0	-1.07	2.30E-03
FTL_0533	-	DNA gyrase subunit A	24474.7	-0.43	2.80E-08
FTL_0534	-	1-deoxy-D-xylulose 5-phosphate reductoisom	3357.2	-0.06	6.30E-01
FTL_0535	-	outer membrane protein	3457.0	0.22	3.77E-02
FTL_0536	-	outer membrane protein OmpH	7214.7	-0.31	5.08E-04
FTL_0537	<i>lpxD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine M	6065.6	-0.53	9.42E-04
FTL_0538	<i>fabZ</i>	(3R)-hydroxymyristoyl-ACP dehydratase	4618.8	-0.21	1.21E-01
FTL_0539	-	UDP-N-acetylglucosamine acyltransferase	11325.6	-0.06	6.06E-01
FTL_0540	<i>lpxB</i>	lipid-A-disaccharide synthase	4022.2	0.09	3.71E-01
FTL_0541	-	hypothetical protein	1568.6	-0.40	3.21E-05
FTL_0542	-	hypothetical protein	264.4	0.05	7.83E-01
FTL_0543	-	-	1187.4	-0.28	4.70E-03
FTL_0544	<i>ppk</i>	polyphosphate kinase 2	1438.9	-0.42	1.67E-03
FTL_0545	<i>pcs</i>	phosphatidylcholine synthase	1110.7	-0.51	2.22E-04
FTL_0546	<i>ispA</i>	geranyltranstransferase	891.5	0.32	5.68E-03
FTL_0547	<i>kdtA</i>	3-deoxy-D-manno-octulosonic-acid transfera	2093.0	-0.22	9.70E-03
FTL_0548	<i>rdgB</i>	putative deoxyribonucleotide triphosphate p	458.9	-0.65	1.87E-08
FTL_0549	<i>proC</i>	pyrroline-5-carboxylate reductase	760.2	-0.36	2.73E-03
FTL_0550	-	-	7.4	-0.08	7.07E-01
FTL_0551	-	-	83.6	1.27	6.89E-09
FTL_0552	<i>pmrA</i>	two-component response regulator	8257.8	-0.32	3.96E-02

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0553	<i>lepB</i>	signal peptidase I	2185.3	-0.02	9.10E-01
FTL_0554	<i>rnc</i>	ribonuclease III	456.0	0.50	3.35E-04
FTL_0555	<i>truB</i>	tRNA pseudouridine synthase B	835.9	0.24	7.37E-02
FTL_0556	<i>rnr</i>	ribonuclease R	8366.0	0.14	1.17E-01
FTL_0557	-	Delta 9 acyl-lipid fatty acid desaturase	7.1	0.03	8.85E-01
FTL_0558	-	oxidoreductase	44.8	-0.59	3.50E-02
FTL_0559	-	hypothetical protein	22.1	-0.91	1.20E-02
FTL_0560	-	hypothetical protein	3.7	0.29	NA
FTL_0561	-	cyclopropane-fatty-acyl-phospholipid synthase	40.2	0.60	3.24E-02
FTL_0562	-	-	56.1	-0.97	1.02E-03
FTL_0563	-	-	7.0	0.14	5.59E-01
FTL_0564	-	-	3.8	0.43	NA
FTL_0565	-	-	7.6	1.44	1.23E-02
FTL_0566	-	-	43.3	0.16	5.45E-01
FTL_0567	-	-	1.7	-0.08	NA
FTL_0568	<i>isftu2</i>	transposase	51.7	0.16	5.39E-01
FTL_0569	-	hypothetical protein	7278.5	-0.74	8.92E-18
FTL_0570	-	hypothetical protein	260.0	-0.12	6.16E-01
FTL_0571	-	hypothetical protein	3871.6	-0.72	4.29E-10
FTL_0572	-	hypothetical protein	16095.1	-0.98	3.53E-21
FTL_0573	-	hypothetical protein	6661.6	-0.55	5.17E-11
FTL_0574	-	hypothetical protein	2596.4	0.76	2.80E-12
FTL_0575	<i>isftu2</i>	transposase	51.6	-0.07	7.97E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0576	-	hypothetical protein	13.9	0.21	4.39E-01
FTL_0577	-	hypothetical protein	0.2	0.02	NA
FTL_0578	-	ornithine cyclodeaminase	3809.6	0.47	6.47E-10
FTL_0579	-	putative nicotinate phosphoribosyltransferase	1436.7	-0.33	1.15E-03
FTL_0580	-	hypothetical protein	1218.2	-0.57	1.54E-03
FTL_0581	-	sugar transport protein	1257.4	0.44	5.96E-04
FTL_0582	-	hypothetical protein	1244.7	-0.21	1.37E-01
FTL_0583	-	acetyl-CoA acetyltransferase	10920.0	-0.19	1.93E-01
FTL_0584	-	bifunctional 3-hydroxacyl-CoA dehydrogenase	29149.4	-0.26	2.01E-02
FTL_0585	<i>fadE</i>	acyl-CoA dehydrogenase	43720.2	-0.21	9.77E-02
FTL_0586	-	long chain fatty acid CoA ligase	2560.1	-0.51	4.29E-12
FTL_0587	-	arsenate reductase	707.1	-0.30	1.06E-01
FTL_0588	-	isocitrate dehydrogenase	31533.8	-0.58	8.14E-07
FTL_0589	-	hypothetical protein	6231.7	-0.43	6.66E-06
FTL_0590	-	ATP-dependent helicase	3362.5	0.84	1.03E-29
FTL_0591	<i>isftu2</i>	transposase	49.8	-0.03	9.18E-01
FTL_0592	<i>wbtA</i>	dTDP-glucose 4,6-dehydratase	4285.1	-0.29	9.83E-03
FTL_0593	<i>wbtB</i>	galactosyl transferase	1916.0	-0.66	3.83E-04
FTL_0594	<i>wbtC</i>	UDP-glucose 4-epimerase	4226.5	-0.54	7.34E-11
FTL_0595	-	galacturonosyl transferase	3114.1	-0.27	9.10E-02
FTL_0596	-	UDP-glucose/GDP-mannose dehydrogenase	12618.6	-0.51	6.52E-11
FTL_0597	<i>wbtF</i>	NAD dependent epimerase	2722.1	-0.67	1.37E-04
FTL_0598	<i>wzy</i>	membrane protein/O-antigen protein	556.5	0.68	6.34E-06

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0599	<i>wbtG</i>	glycosyl transferase family protein	1578.3	0.37	4.70E-02
FTL_0600	<i>wbtH</i>	asparagine synthase	5365.4	-0.59	1.25E-12
FTL_0601	<i>wbtI</i>	sugar transamine/perosamine synthetase	5355.7	-0.04	7.83E-01
FTL_0602	<i>wbtJ</i>	hypothetical protein	3790.2	-0.13	3.82E-01
FTL_0603	<i>wzx</i>	O-antigen flippase	1579.3	0.00	9.91E-01
FTL_0604	<i>wbtK</i>	glycosyltransferase	4235.6	-0.21	1.48E-01
FTL_0605	<i>wbtL</i>	glucose-1-phosphate thymidyltransferase	4127.1	-0.13	2.46E-01
FTL_0606	<i>wbtM</i>	dTDP-D-glucose 4,6-dehydratase	3294.6	-0.13	3.10E-01
FTL_0607	<i>isftu1</i>	transposase	534.9	0.19	3.24E-01
FTL_0608	<i>manC</i>	mannose-1-phosphate guanylyltransferase	2422.5	-0.60	9.32E-11
FTL_0609	<i>manB</i>	phosphomannomutase	1988.1	-0.49	3.71E-08
FTL_0610	<i>rho</i>	transcription termination factor Rho	9402.3	-0.27	2.40E-03
FTL_0611	<i>trx1</i>	thioredoxin	1698.3	-0.17	1.29E-01
FTL_0612	<i>ppx</i>	exopolyphosphatase	1121.8	-0.26	9.36E-02
FTL_0613	<i>isftu2</i>	transposase	54.6	0.03	9.15E-01
FTL_0614	-	-	1.4	0.04	NA
FTL_0615	-	recombination factor protein RarA	17.1	-0.04	8.81E-01
FTL_0616	<i>rpoA2</i>	DNA-directed RNA polymerase subunit alpha	11143.7	0.65	6.94E-06
FTL_0617	-	hypothetical protein	46886.4	-0.06	7.32E-01
FTL_0618	-	-	127.4	-0.08	7.19E-01
FTL_0619	-	-	17.8	0.09	7.50E-01
FTL_0620	<i>tatD</i>	deoxyribonuclease	441.3	0.16	2.65E-01
FTL_0621	-	-	468.1	-0.05	7.72E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0622	<i>isftu2</i>	transposase	51.4	-0.11	6.90E-01
FTL_0623	-	ABC transporter ATP-binding protein	1117.7	-0.47	1.16E-03
FTL_0624	-	ABC transporter membrane protein	886.8	-0.46	1.08E-05
FTL_0625	<i>gtrB</i>	glycosyl transferase family protein	1178.3	-0.64	7.95E-11
FTL_0626	<i>ppnK</i>	inorganic phosphate/ATP-NAD kinase	878.8	0.45	2.13E-05
FTL_0627	<i>rhtB</i>	threonine efflux protein	285.2	-0.98	4.27E-11
FTL_0628	-	-	808.1	-0.30	2.10E-02
FTL_0629	-	-	702.0	-0.40	1.04E-03
FTL_0630	-	-	8.4	0.08	7.56E-01
FTL_0631	<i>isftu1</i>	transposase	542.4	0.07	7.04E-01
FTL_0632	-	ArsR family transcriptional regulator	37.3	-0.35	1.99E-01
FTL_0633	-	hypothetical protein	189.7	0.30	1.49E-01
FTL_0634	-	NADH oxidase	0.5	0.04	NA
FTL_0635	-	FAD-dependent pyridine nucleotide-disulfide	72.9	0.58	8.87E-03
FTL_0636	-	NADH oxidase	35.0	-0.24	3.78E-01
FTL_0637	-	hypothetical protein	1880.8	-0.24	2.50E-02
FTL_0638	-	hypothetical protein	1222.7	0.31	1.21E-02
FTL_0639	-	oxidoreductase	311.3	-0.49	5.79E-04
FTL_0640	-	hypothetical protein	1265.6	-0.28	1.59E-02
FTL_0641	-	hypothetical protein	1.2	0.01	NA
FTL_0642	-	lipoprotein	31.7	-0.09	7.63E-01
FTL_0643	-	N utilisation substance protein B	1525.3	-0.34	1.15E-03
FTL_0644	-	carbon-nitrogen hydrolase	2292.8	-0.64	3.20E-07

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0645	-	lipoprotein	5692.2	-0.33	3.62E-02
FTL_0646	-	hypothetical protein	13.8	-0.04	8.90E-01
FTL_0647	-	hypothetical protein	9.3	0.14	5.84E-01
FTL_0648	-	aminotransferase	246.1	-0.69	2.01E-05
FTL_0649	-	aspartate/tyrosine/aromatic aminotransfera	1108.0	-0.84	3.19E-13
FTL_0650	-	prolyl-tRNA synthetase	6718.4	-0.05	6.49E-01
FTL_0651	-	transposase	23.2	0.39	1.86E-01
FTL_0652	-	hypothetical protein	748.3	-1.12	1.67E-23
FTL_0653	-	hypothetical protein	822.2	0.06	6.41E-01
FTL_0654	-	uroporphyrinogen III synthase	306.9	-0.02	9.28E-01
FTL_0655	-	hypothetical protein	2331.9	-0.39	3.98E-03
FTL_0656	-	hypothetical protein	1812.3	-0.69	1.35E-13
FTL_0657	-	hydroxyacylglutathione hydrolase	891.7	0.08	5.66E-01
FTL_0659	-	cell division protein	679.7	-0.67	6.25E-09
FTL_0660	<i>feoA</i>	ferrous iron transport protein A	60.5	-0.63	1.59E-02
FTL_0661	-	hypothetical protein	6347.2	-0.71	3.33E-15
FTL_0662	-	prophage repressor protein	418.0	0.39	1.52E-03
FTL_0663	-	hypothetical protein	370.7	0.57	7.86E-02
FTL_0664	-	hypothetical protein	563.2	-0.34	7.71E-02
FTL_0665	<i>gltB</i>	hypothetical protein (glutamate synthase do	1349.7	-0.51	2.87E-06
FTL_0666	<i>recC</i>	exodeoxyribonuclease V subunit gamma	2029.0	-0.51	3.05E-08
FTL_0667	-	hypothetical protein	154.4	-0.42	4.51E-02
FTL_0668	-	ATP-dependent DNA helicase	1097.6	-0.45	2.82E-05

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0669	<i>recB</i>	exodeoxyribonuclease V subunit beta	1563.6	-0.29	3.90E-03
FTL_0670	<i>recD</i>	exodeoxyribonuclease V subunit alpha	616.7	-0.01	9.69E-01
FTL_0671	-	pantothenate kinase	14539.4	-0.85	1.30E-28
FTL_0672	<i>panD</i>	aspartate alpha-decarboxylase	1718.4	-0.79	1.02E-07
FTL_0673	<i>panC</i>	pantoate-beta-alanine ligase	22195.0	-0.82	4.28E-15
FTL_0674	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltra	17739.6	-1.19	7.16E-11
FTL_0675	<i>panG</i>	hypothetical protein, putative ketopantoate	3595.0	-0.64	7.19E-06
FTL_0676	-	DNA ligase	2957.5	0.01	9.09E-01
FTL_0677	-	hypothetical protein	57.4	0.00	9.99E-01
FTL_0678	<i>isftu1</i>	transposase	535.9	0.05	8.26E-01
FTL_0679	<i>potI</i>	ATP-binding cassette putrescine uptake syste	1906.6	-1.00	7.04E-14
FTL_0680	<i>potH</i>	ATP-binding cassette putrescine uptake syste	2114.8	-0.68	3.53E-10
FTL_0681	<i>potG</i>	ATP-binding cassette putrescine uptake syste	6924.3	-0.74	1.45E-19
FTL_0682	<i>isftu1</i>	transposase	531.3	0.10	5.98E-01
FTL_0683	-	-	32.8	-0.31	2.62E-01
FTL_0684	-	hypothetical protein	696.6	-0.58	5.39E-06
FTL_0685	-	NH(3)-dependent NAD(+) synthetase	1894.5	-0.02	8.66E-01
FTL_0686	-	outer membrane efflux protein	7415.6	0.13	2.07E-01
FTL_0687	-	HlyD family secretion protein	6451.5	-0.18	7.11E-02
FTL_0688	-	major facilitator transporter	3526.6	0.18	4.12E-02
FTL_0689	-	transcriptional regulator araC family protein	285.9	-0.32	3.48E-02
FTL_0690	-	Acyl-CoA synthetase (long-chain-fatty-acid--C	1926.0	-0.32	1.24E-04
FTL_0691	-	proton-dependent oligopeptide transport (P	14034.0	-0.09	3.54E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0692	-	16S ribosomal RNA methyltransferase RsmE	215.3	-0.05	8.52E-01
FTL_0693	-	hypothetical protein	89.9	-0.12	6.49E-01
FTL_0694	-	hypothetical protein	1252.7	-1.37	4.28E-15
FTL_0695	-	cell entry (mce) related family protein	648.0	-1.24	1.10E-16
FTL_0696	-	ABC transporter ATP-binding protein	1184.2	-0.60	1.52E-09
FTL_0697	-	ABC transporter membrane protein	1233.9	-0.51	4.46E-07
FTL_0698	-	hypothetical protein	399.8	0.12	3.82E-01
FTL_0699	-	ribosomal large subunit pseudouridine synth	1072.6	-0.27	4.29E-02
FTL_0700	-	lipoprotein	636.7	-0.11	5.47E-01
FTL_0701	<i>mreA</i>	FAD binding family protein	717.0	-0.26	2.85E-02
FTL_0702	<i>priM</i>	hypothetical protein	357.3	0.49	4.31E-04
FTL_0703	<i>glyA</i>	serine hydroxymethyltransferase	15419.1	-0.58	1.03E-09
FTL_0704	-	hypothetical protein	1125.1	0.12	5.85E-01
FTL_0705	-	hypothetical protein	424.1	0.16	4.95E-01
FTL_0706	<i>wyz</i>	predicted O-antigen ligase	218.5	0.30	7.62E-02
FTL_0707	-	glycosyl transferase family protein	1162.2	-0.77	3.53E-10
FTL_0708	-	hypothetical protein	779.4	-0.20	1.41E-01
FTL_0709	-	glycosyl transferases group 1 family protein	833.4	-0.43	6.21E-03
FTL_0710	-	choloylglycine hydrolase family protein	10.1	0.10	7.05E-01
FTL_0711	-	proton-dependent oligopeptide transport (P	63.2	0.52	3.40E-02
FTL_0712	-	hypothetical protein	6.0	0.00	9.86E-01
FTL_0713	-	PP-loop family protein	421.9	0.40	3.55E-03
FTL_0714	-	D-3-phosphoglycerate dehydrogenase	3861.7	-0.54	1.73E-06

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0715	<i>thyA</i>	thymidylate synthase	2140.7	-0.13	3.04E-01
FTL_0716	-	prolipoprotein diacylglycerol transferase	3663.6	0.09	5.30E-01
FTL_0717	-	ribonuclease E	21253.7	0.46	6.15E-07
FTL_0718	-	cysteine desulfurase	868.4	-0.69	3.67E-09
FTL_0719	-	hypothetical protein	167.5	-0.49	8.70E-03
FTL_0720	-	DNA repair protein recO	164.4	-0.66	5.06E-04
FTL_0721	-	DedA family protein	607.9	-0.46	5.21E-05
FTL_0722	-	DedA family protein	679.3	0.33	9.88E-03
FTL_0723	-	hypothetical protein	471.8	0.20	3.16E-01
FTL_0724	-	5-formyltetrahydrofolate cyclo-ligase	984.6	0.27	3.59E-02
FTL_0725	-	hypothetical protein	598.0	-0.29	9.84E-02
FTL_0726	-	2-octaprenyl-6-methoxyphenyl hydroxylase	1846.1	0.34	1.29E-03
FTL_0727	-	monooxygenase family protein	1677.5	0.26	2.09E-03
FTL_0728	-	hypothetical protein	267.9	-0.05	8.18E-01
FTL_0729	<i>queA</i>	S-adenosylmethionine--tRNA ribosyltransferase	620.4	-0.59	2.24E-06
FTL_0730	-	haloacid dehalogenase-like hydrolase family	3152.1	-0.31	4.95E-02
FTL_0731	-	YhhQ family protein	1781.4	-1.21	2.05E-23
FTL_0732	-	lactoylglutathione lyase	346.6	-0.42	2.30E-02
FTL_0733	<i>isf1</i>	transposase	533.1	0.00	9.99E-01
FTL_0734	-	-	91.2	0.62	3.37E-03
FTL_0735	-	-	2.3	0.06	NA
FTL_0736	-	ribose-5-phosphate isomerase A	2553.0	-0.05	6.62E-01
FTL_0737	-	hypothetical protein	1309.6	-0.23	2.81E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0738	-	hypothetical protein	486.7	-0.01	9.76E-01
FTL_0739	-	tRNA uridine 5-carboxymethylaminomethyl r	8946.8	-0.20	5.48E-02
FTL_0740	-	hypothetical protein	294.8	0.28	1.24E-01
FTL_0741	-	hypothetical protein	328.3	-0.04	8.30E-01
FTL_0742	-	LysR family transcriptional regulator	10.8	-0.09	7.12E-01
FTL_0743	-	oxidoreductase, short-chain dehydrogenase	2570.3	-0.74	5.19E-11
FTL_0744	-	exodeoxyribonuclease I	1942.8	-0.22	7.76E-03
FTL_0745	-	excinuclease ABC subunit B	1622.3	-0.16	1.96E-01
FTL_0746	-	hypothetical protein	564.1	-0.15	4.21E-01
FTL_0747	-	glutamate racemase	409.2	0.33	3.29E-02
FTL_0748	-	major facilitator transporter	1027.2	-0.29	3.59E-02
FTL_0749	<i>isftu2</i>	transposase	51.0	-0.18	4.68E-01
FTL_0750	-	-	256.9	0.13	4.49E-01
FTL_0751	-	lipoprotein	422.0	1.18	3.54E-17
FTL_0752	-	hypothetical protein	410.4	-0.09	5.64E-01
FTL_0753	-	aminoacylase	99.5	-0.35	9.87E-02
FTL_0754	<i>xseA</i>	exodeoxyribonuclease VII large subunit	1005.0	-0.08	5.43E-01
FTL_0755	-	hypothetical protein	764.3	0.42	1.89E-05
FTL_0756	-	-	794.7	0.22	1.51E-01
FTL_0757	-	-	296.2	0.59	1.29E-05
FTL_0758	-	-	71.0	0.50	3.84E-02
FTL_0759	-	hypothetical protein	91.0	-1.37	1.11E-07
FTL_0760	-	C32 tRNA thiolase	1101.5	-0.25	4.89E-02

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0761	<i>smpB</i>	SsrA-binding protein	450.9	-0.43	1.01E-03
FTL_0762	-	hypothetical protein	741.2	-0.52	1.26E-05
FTL_0763	-	hypothetical protein	906.1	-0.19	2.57E-01
FTL_0764	-	lipoprotein	421.7	0.31	1.02E-02
FTL_0765	-	VacJ lipoprotein	583.5	-0.25	6.63E-02
FTL_0766	<i>ggt</i>	gamma-glutamyltranspeptidase	2730.0	0.04	8.17E-01
FTL_0767	-	hypothetical protein	1866.9	-0.59	7.41E-07
FTL_0768	-	GTP binding translational elongation factor T	13155.9	-0.52	1.83E-09
FTL_0769	-	hypothetical protein	23.6	0.74	2.44E-02
FTL_0770	-	-	5.6	0.05	NA
FTL_0771	-	-	60.8	0.17	5.17E-01
FTL_0772	-	-	1.8	0.01	NA
FTL_0773	-	-	0.8	-0.03	NA
FTL_0774	-	-	0.4	-0.02	NA
FTL_0775	-	-	0.3	0.03	NA
FTL_0776	-	hypothetical protein	41.5	-0.11	6.97E-01
FTL_0777	-	hypothetical protein	1.4	0.03	NA
FTL_0778	-	-	21.3	0.08	7.70E-01
FTL_0779	-	-	38.9	-0.02	9.58E-01
FTL_0780	-	cold shock protein (DNA-binding)	20.8	0.49	1.07E-01
FTL_0781	-	-	69.7	0.30	1.81E-01
FTL_0782	-	-	9.9	0.14	5.66E-01
FTL_0783	<i>isftu1</i>	transposase	548.6	0.10	6.09E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0784	-	lipoprotein	2575.0	-0.20	3.98E-02
FTL_0785	-	GTP-binding protein	985.3	-0.47	2.06E-04
FTL_0786	-	N-acetylglucosamine-6-phosphate deacetylase	2686.5	-0.23	7.35E-03
FTL_0787	-	glycoprotease family protein	930.7	-0.21	1.02E-01
FTL_0788	-	glutamine amidotransferases class-II family protein	789.0	-0.29	1.47E-02
FTL_0789	-	aspartate aminotransferase	3829.4	-0.63	1.34E-12
FTL_0790	<i>era</i>	GTP-binding protein Era	1688.8	-1.00	9.85E-23
FTL_0791	-	hypothetical protein	13.7	-0.01	9.63E-01
FTL_0792	-	-	997.3	-0.15	2.14E-01
FTL_0793	-	-	139.6	0.21	2.58E-01
FTL_0794	-	-	3.1	-0.04	NA
FTL_0795	<i>adk</i>	adenylate kinase	3381.9	-0.91	3.69E-15
FTL_0796	-	hypothetical protein	2030.5	0.42	4.55E-04
FTL_0797	-	Type IV pili associated protein	376.6	0.37	8.70E-03
FTL_0798	-	Type IV pili glycosylation protein	276.1	0.29	4.71E-02
FTL_0799	-	Type IV pili lipoprotein	427.8	0.43	1.11E-02
FTL_0800	-	Type IV pilin multimeric outer membrane protein	4694.6	0.57	3.44E-16
FTL_0801	<i>aroK</i>	shikimate kinase I	5263.4	0.28	1.28E-03
FTL_0802	<i>aroB</i>	3-dehydroquinate synthase	2452.6	0.10	3.43E-01
FTL_0803	-	hypothetical protein	3163.9	-0.46	2.09E-08
FTL_0804	-	hypothetical protein	401.3	-0.76	7.03E-07
FTL_0805	-	bifunctional proline dehydrogenase/pyrroline oxidase	30808.5	-0.35	1.14E-03
FTL_0806	-	amino acid transporter family protein	2680.6	-0.82	2.09E-15

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0807	-	major facilitator transporter	1150.9	0.09	5.09E-01
FTL_0808	-	bifunctional 4'-phosphopantothienoylcysteine	4277.0	0.02	8.74E-01
FTL_0809	-	-	2447.8	-0.19	6.57E-02
FTL_0810	-	cation transport regulator	17.2	-1.00	1.62E-02
FTL_0811	-	-	1.9	0.07	NA
FTL_0812	-	-	11.9	0.33	1.89E-01
FTL_0813	-	-	100.3	-0.34	1.61E-01
FTL_0814	-	hypothetical protein	131.5	-1.68	3.03E-10
FTL_0815	-	PRC-barrel protein	2.8	-0.19	NA
FTL_0816	-	hypothetical protein	23.8	-1.38	4.81E-03
FTL_0817	-	-	2.2	0.01	NA
FTL_0818	-	-	0.8	0.00	NA
FTL_0819	-	-	3.0	0.01	NA
FTL_0820	<i>isftu2</i>	transposase	53.0	-0.10	7.03E-01
FTL_0821	<i>hemH</i>	ferrochelatase	650.8	-0.16	2.71E-01
FTL_0822	-	hypothetical protein	673.5	-0.75	1.35E-04
FTL_0823	-	hypothetical protein	1438.9	0.22	4.18E-01
FTL_0824	-	-	619.2	-0.06	6.67E-01
FTL_0825	-	-	307.9	0.16	3.10E-01
FTL_0826	-	-	14.4	0.14	6.07E-01
FTL_0827	-	Type IV pili polytopic inner membrane protein	3336.0	-0.66	7.89E-18
FTL_0828	-	Type IV pili nucleotide binding protein, ABC transporter	5473.4	-0.49	4.12E-11
FTL_0829	-	glycerophosphoryl diester phosphodiesterase	518.1	0.37	1.22E-02

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0830	-	molybdopterin binding family protein, fragm	828.4	-0.33	1.48E-02
FTL_0831	-	cyanophycin synthetase	8936.9	-0.44	3.73E-06
FTL_0832	-	Mur ligase family protein	5552.7	-0.56	1.13E-13
FTL_0833	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate	1437.1	-0.43	1.09E-04
FTL_0834	-	rhodanese-like family protein	3887.9	-0.70	1.23E-13
FTL_0835	-	aromatic amino acid HAAP transporter	38.2	2.03	1.88E-08
FTL_0836	-	hypothetical protein	173.6	0.52	3.52E-03
FTL_0837	<i>metIQ</i>	D-methionine binding transport protein, ABC	3023.8	-0.61	3.42E-09
FTL_0838	<i>metN</i>	D-methionine transport protein, ABC transp	2928.2	-0.66	2.14E-12
FTL_0839	-	hypothetical protein	1215.5	-0.65	2.36E-09
FTL_0840	-	hypothetical protein	520.6	-0.34	2.12E-02
FTL_0841	-	lipoprotein	311.4	-0.25	1.54E-01
FTL_0842	-	transposase	6.3	0.30	2.03E-01
FTL_0843	<i>tgt</i>	queueine tRNA-ribosyltransferase	2378.1	-0.41	5.32E-06
FTL_0844	-	LysR transcriptional regulator family protein	80.5	1.54	5.92E-12
FTL_0845	-	hypothetical protein	28.2	-0.11	6.96E-01
FTL_0846	-	isochorismatase hydrolase family protein	475.7	-0.45	6.86E-04
FTL_0847	<i>yajC</i>	preprotein translocase family protein	4110.4	-0.80	5.32E-10
FTL_0848	<i>secD</i>	preprotein translocase subunit SecD	12509.7	-0.11	3.51E-01
FTL_0849	<i>secF</i>	preprotein translocase subunit SecF	2350.5	-0.27	2.20E-03
FTL_0850	-	hypothetical protein	8562.8	-0.61	2.85E-06
FTL_0851	-	RNA polymerase factor sigma-32	5318.6	-0.81	3.98E-35
FTL_0852	-	3-phosphoshikimate 1-carboxyvinyltransfera	3499.7	0.10	4.21E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0853	-	hypothetical protein	318.0	0.54	1.35E-04
FTL_0854	-	ribonuclease H	179.7	0.16	4.76E-01
FTL_0855	-	L-asparaginase	1954.4	-0.20	5.40E-02
FTL_0856	-	carbonic anhydrase	2614.8	-0.35	2.54E-04
FTL_0857	-	hypothetical protein	110.6	0.01	9.67E-01
FTL_0858	-	hypothetical protein	453.2	0.09	6.25E-01
FTL_0859	-	rubredoxin	474.2	-0.29	7.40E-02
FTL_0860	-	hypothetical protein	120.3	0.02	9.31E-01
FTL_0861	<i>isftu2</i>	transposase	52.0	-0.04	8.92E-01
FTL_0862	-	hypothetical protein	272.1	-0.09	6.30E-01
FTL_0863	-	Sodium-dicarboxylate symporter family prote	6294.2	-0.51	1.49E-05
FTL_0864	-	SIS domain-containing protein	3139.1	-0.53	2.74E-06
FTL_0865	-	major facilitator transporter	3083.8	-0.89	1.18E-19
FTL_0866	-	IS1 transposase	84.1	-0.42	5.83E-02
FTL_0867	-	hypothetical protein	381.4	0.96	1.16E-13
FTL_0868	<i>isftu2</i>	transposase	51.5	0.08	7.72E-01
FTL_0869	-	hypothetical protein	0.5	-0.03	NA
FTL_0870	-	hypothetical protein	0.1	0.00	NA
FTL_0871	-	Na ⁺ /H ⁺ antiporter	1.7	0.03	NA
FTL_0872	-	hypothetical protein	3.0	0.06	NA
FTL_0873	-	-	10.4	0.24	3.56E-01
FTL_0874	-	-	34.7	-0.08	7.88E-01
FTL_0875	<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphat	6148.9	1.21	7.03E-87

				LVS Δ rrpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0876	-	hypothetical protein	2089.9	0.25	6.09E-03
FTL_0877	-	peptidase, M24 family protein	10350.8	-0.36	1.35E-04
FTL_0878	-	DNA/RNA endonuclease family protein, DNA	774.8	-0.02	8.65E-01
FTL_0879	-	beta-lactamase	3133.3	-1.03	6.22E-22
FTL_0880	-	hypothetical protein	354.4	-0.45	9.67E-03
FTL_0881	-	hypothetical protein	171.3	-0.05	8.52E-01
FTL_0882	-	apolipoprotein N-acyltransferase	830.9	0.39	2.81E-04
FTL_0883	-	metal ion transporter protein	812.5	0.08	5.45E-01
FTL_0884	-	hypothetical protein	500.7	0.50	1.26E-04
FTL_0885	-	phoH-like protein	3500.4	0.37	3.98E-04
FTL_0886	-	(dimethylallyl)adenosine tRNA methylthiotra	9348.3	0.13	2.24E-01
FTL_0887	-	o-methyltransferase family protein	414.3	0.61	1.05E-07
FTL_0888	-	-	32.5	0.56	8.99E-02
FTL_0889	-	hypothetical protein	1.4	0.14	NA
FTL_0890	-	thymidine kinase	190.8	0.07	7.31E-01
FTL_0891	<i>tig</i>	trigger factor	7185.7	-0.32	2.95E-02
FTL_0892	<i>clpP</i>	ATP-dependent Clp protease proteolytic sub	4056.3	-0.39	5.61E-04
FTL_0893	<i>clpX</i>	ATP-dependent protease ATP-binding subun	6509.9	-0.21	1.92E-02
FTL_0894	<i>lon</i>	DNA-binding, ATP-dependent protease La	14002.8	-0.22	8.67E-03
FTL_0895	<i>hupB</i>	histone-like protein HU form B	8740.5	-0.95	1.27E-09
FTL_0896	-	hypothetical protein	3620.7	-0.42	3.23E-03
FTL_0897	<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate tra	869.7	0.13	2.70E-01
FTL_0898	<i>hfq</i>	host factor I for bacteriophage Q beta replica	8342.5	0.83	2.19E-18

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0899	-	protease, GTP-binding subunit	7561.3	0.14	1.72E-01
FTL_0900	-	monooxygenase	11.0	1.89	7.22E-04
FTL_0901	-	monooxygenase family protein	150.8	0.63	1.82E-04
FTL_0902	-	oxidoreductase	232.0	-0.49	6.70E-02
FTL_0903	-	hypothetical protein	13231.0	-0.23	1.98E-02
FTL_0904	-	hypothetical protein	13259.5	-0.01	9.18E-01
FTL_0905	-	low molecular weight (LMW) phosphotyrosin	1547.1	0.16	2.62E-01
FTL_0906	<i>engB</i>	ribosome biogenesis GTP-binding protein Ysa	4679.4	0.35	7.84E-04
FTL_0907	-	-	1128.4	-0.33	4.57E-03
FTL_0908	-	-	446.6	0.18	1.55E-01
FTL_0909	-	hypothetical protein	12.0	0.10	7.16E-01
FTL_0910	-	hypothetical protein	0.1	0.00	NA
FTL_0911	-	-	8.3	0.04	8.81E-01
FTL_0912	-	-	116.8	0.27	2.18E-01
FTL_0913	-	-	10409.5	0.29	5.58E-03
FTL_0914	-	-	1036.1	0.27	3.20E-02
FTL_0915	-	acetolactate synthase small subunit	564.6	0.16	4.44E-01
FTL_0916	-	ketol-acid reductoisomerase	8605.6	-0.40	2.96E-05
FTL_0917	-	transcription-repair coupling factor	5197.0	0.45	5.15E-05
FTL_0918	<i>yccA</i>	hypothetical protein	14557.4	-0.39	1.43E-04
FTL_0919	-	hypothetical protein	403.0	0.86	2.74E-04
FTL_0920	-	hypothetical protein	272.8	-0.09	6.25E-01
FTL_0921	-	endonuclease III	799.7	-0.08	6.37E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0922	-	Iron-sulfur cluster-binding protein	2496.9	-0.41	1.54E-05
FTL_0923	-	glutaredoxin	5467.7	-0.49	1.82E-04
FTL_0924	-	proton-dependent oligopeptide transporter	105.2	-0.07	7.86E-01
FTL_0925	-	proton-dependent oligopeptide transport (P	72.0	-0.05	8.55E-01
FTL_0926	-	Ferritin-like protein	4073.2	-1.21	8.28E-19
FTL_0927	-	lipoyl synthase	3478.7	-0.03	8.62E-01
FTL_0928	-	isoprenoid biosynthesis protein with amidot	4028.1	-0.02	8.20E-01
FTL_0929	-	hypothetical protein	3137.5	-0.26	1.57E-02
FTL_0930	<i>ruvC</i>	Holliday junction resolvase	1084.1	0.07	6.41E-01
FTL_0931	-	major facilitator transporter	1006.8	-0.60	2.49E-09
FTL_0932	<i>ruvA</i>	Holliday junction DNA helicase RuvA	583.9	-0.23	1.61E-01
FTL_0933	-	DNA recombination protein RmuC family pro	456.8	-0.46	9.29E-04
FTL_0934	-	hypothetical protein	7.7	-0.01	9.80E-01
FTL_0935	-	hypothetical protein	107.0	-0.69	6.65E-03
FTL_0936	-	hypothetical protein	3.5	0.06	NA
FTL_0937	-	hypothetical protein	836.9	-0.26	1.55E-01
FTL_0938	-	histidine decarboxylase	1811.3	-0.18	2.02E-01
FTL_0939	-	aldolase/adducin class II family protein	2441.0	-0.64	1.38E-06
FTL_0940	-	methylpurine-DNA glycosylase family protein	61.5	-0.80	4.51E-03
FTL_0941	-	hypothetical protein	1677.3	-0.53	1.02E-06
FTL_0942	-	nicotinamide mononucleotide transport (NM	2025.9	-0.20	1.28E-01
FTL_0943	-	Sodium/hydrogen exchanger family protein	240.6	-0.56	1.08E-03
FTL_0944	-	-	31.7	0.61	5.05E-02

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0945	-	hypothetical protein	143.1	0.01	9.73E-01
FTL_0946	-	major facilitator transporter	68.9	-0.11	6.75E-01
FTL_0947	-	-	15.1	1.58	9.03E-04
FTL_0948	-	hypothetical protein	146.4	-0.21	2.82E-01
FTL_0949	-	ribose-phosphate pyrophosphokinase	6405.3	-0.64	2.18E-09
FTL_0950	-	50S ribosomal protein L25	3790.0	-0.18	1.26E-01
FTL_0951	-	hypothetical protein	1510.2	-0.02	9.07E-01
FTL_0952	-	hypothetical protein	4.0	3.27	NA
FTL_0953	-	hypothetical protein	1913.9	0.65	4.78E-04
FTL_0954	-	hypothetical protein	147.9	-0.26	2.32E-01
FTL_0955	-	GTP-dependent nucleic acid-binding protein	3897.8	-0.56	3.69E-12
FTL_0956	<i>pth</i>	peptidyl-tRNA hydrolase	238.6	-0.05	8.12E-01
FTL_0957	<i>blaA</i>	Beta-lactamase class A	377.6	-0.04	8.23E-01
FTL_0958	-	hypothetical protein	644.8	-0.44	1.27E-03
FTL_0959	<i>pilD</i>	Type IV pili leader peptidase and methylase.	851.8	-0.03	8.45E-01
FTL_0960	<i>udhA</i>	soluble pyridine nucleotide transhydrogenas	4359.2	-0.35	1.19E-02
FTL_0961	-	potassium channel protein	56.1	-0.33	1.93E-01
FTL_0962	-	hypothetical protein	47.7	-0.15	6.01E-01
FTL_0963	-	proton-dependent oligopeptide transport (P	699.9	-1.14	1.47E-20
FTL_0964	<i>hslU</i>	ATP-dependent protease ATP-binding subun	2880.8	-1.40	3.65E-39
FTL_0965	<i>hslV</i>	ATP-dependent protease peptidase subunit	661.7	-0.96	5.50E-10
FTL_0966	-	hypothetical protein	543.1	-0.67	5.10E-04
FTL_0967	<i>lplA</i>	lipoate-protein ligase A	694.7	-0.59	7.83E-05

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0968	<i>tyrS</i>	tyrosyl-tRNA synthetase	3002.9	-0.51	8.88E-06
FTL_0969	<i>isftu1</i>	transposase	534.2	0.05	8.12E-01
FTL_0970	-	L-lactate dehydrogenase	35.0	-0.09	7.38E-01
FTL_0971	-	FAD linked oxidase	192.0	1.29	1.38E-15
FTL_0972	-	-	103.9	0.39	4.73E-02
FTL_0973	-	-	243.9	0.24	1.68E-01
FTL_0974	-	50S ribosomal protein L11 methyltransferase	784.4	-0.56	2.40E-06
FTL_0975	-	Nif3 family protein	1283.9	-0.21	1.26E-01
FTL_0976	-	hypothetical protein	174.5	0.27	1.92E-01
FTL_0977	-	hypothetical protein	6.9	0.36	1.58E-01
FTL_0978	-	hypothetical protein	15.4	-0.04	8.83E-01
FTL_0979	-	hypothetical protein	0.8	0.07	NA
FTL_0980	-	hypothetical protein	21.1	0.05	8.66E-01
FTL_0981	-	DNA polymerase IV	326.8	0.14	4.27E-01
FTL_0982	-	DJ-1/Pfpl family protein	491.5	0.00	9.98E-01
FTL_0983	-	-	927.5	-0.45	3.89E-05
FTL_0984	-	bifunctional glutaredoxin/ribonucleoside-diphosphate reductase	9336.5	-0.16	7.34E-02
FTL_0985	<i>grxA</i>	glutaredoxin	911.9	-0.29	1.61E-02
FTL_0986	<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha	6999.6	-0.47	5.60E-10
FTL_0987	<i>mdh</i>	malate dehydrogenase	9664.5	-0.60	5.91E-09
FTL_0988	-	hypothetical protein	388.2	-0.15	4.80E-01
FTL_0989	-	ubiquinone biosynthesis protein	1683.7	-0.40	4.31E-05
FTL_0990	-	lipoprotein	46.3	-0.09	7.62E-01

				LVS Δ rrpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_0991	-	-	0.8	-0.05	NA
FTL_0992	-	-	526.8	0.12	5.42E-01
FTL_0993	-	HesA/MoeB/ThiF family protein	86.3	-0.20	3.68E-01
FTL_0994	-	hypothetical protein	2558.7	-0.06	6.59E-01
FTL_0995	-	haloacid dehalogenase	2351.1	-0.28	2.22E-02
FTL_0996	-	AhpC/Tsa family protein	526.9	0.47	3.10E-04
FTL_0997	-	hypothetical protein	8.2	0.59	8.58E-02
FTL_0998	-	hypothetical protein	8.4	0.08	7.28E-01
FTL_0999	-	phosphonoacetate hydrolase	679.8	-0.55	1.57E-03
FTL_1000	-	hypothetical protein	138.8	0.30	1.26E-01
FTL_1001	-	hypothetical protein	101.2	-0.04	8.83E-01
FTL_1002	-	hypothetical protein	10.9	0.03	9.25E-01
FTL_1003	-	DNA polymerase III subunit epsilon	1086.3	-0.16	1.54E-01
FTL_1004	-	D-alanyl-D-alanine carboxypeptidase	613.0	-0.35	1.82E-02
FTL_1005	-	hypothetical protein	1430.2	-0.32	1.33E-03
FTL_1006	-	-	631.7	-0.25	9.27E-02
FTL_1007	-	-	207.8	-0.17	5.16E-01
FTL_1008	-	-	6.6	-0.07	7.83E-01
FTL_1009	-	aldehyde dehydrogenase	20.3	0.29	3.03E-01
FTL_1010	-	-	19.5	0.50	1.14E-01
FTL_1011	-	-	0.8	0.02	NA
FTL_1012	-	hypothetical protein	1067.0	-1.19	5.68E-15
FTL_1013	-	hypothetical protein	3811.5	-0.64	3.62E-07

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1014	-	oxidative stress transcriptional regulator	1414.2	-0.37	3.33E-03
FTL_1015	-	AhpC/TSA family protein	10511.9	-0.78	2.51E-18
FTL_1016	-	short chain dehydrogenase	12031.7	-0.37	1.63E-03
FTL_1017	-	cytidylate kinase	1246.7	-0.40	8.20E-04
FTL_1018	-	phosphoserine aminotransferase	2894.0	-0.11	5.73E-01
FTL_1019	-	hypothetical protein	0.0	NA	NA
FTL_1020	<i>isftu1</i>	transposase	531.5	0.11	5.47E-01
FTL_1021	-	hypothetical protein	742.5	-0.15	2.71E-01
FTL_1022	-	coproporphyrinogen III oxidase	1995.3	-0.59	2.81E-11
FTL_1023	<i>isftu2</i>	transposase	84.7	0.24	2.59E-01
FTL_1024	<i>rpsF</i>	30S ribosomal protein S6	6573.7	-0.52	4.80E-05
FTL_1025	<i>rpsR</i>	30S ribosomal protein S18	2055.5	-0.35	1.98E-02
FTL_1026	<i>rplI</i>	50S ribosomal protein L9	13436.2	-0.31	9.90E-03
FTL_1027	-	replicative DNA helicase	4066.3	0.17	1.20E-01
FTL_1028	-	radical SAM superfamily protein	4010.0	-0.08	3.82E-01
FTL_1029	-	Type IV pili lipoprotein	1824.9	-0.42	2.03E-07
FTL_1030	-	ribosomal large subunit pseudouridine synth	1660.4	0.00	9.80E-01
FTL_1031	-	hypothetical protein	58.6	0.14	6.04E-01
FTL_1032	-	ribosomal-protein-alanine acetyltransferase	83.1	0.68	6.88E-02
FTL_1033	-	-	39.3	0.90	3.34E-03
FTL_1034	<i>cysN</i>	sulfate adenyltransferase	852.5	-0.54	2.25E-07
FTL_1035	<i>cysC</i>	sulfate adenyltransferase	207.9	-0.25	1.35E-01
FTL_1036	-	adenylsulfate kinase, fragment	49.3	0.23	3.71E-01

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1037	-	hypothetical protein	959.2	-0.46	4.17E-05
FTL_1038	-	hypothetical protein	406.9	-0.06	8.00E-01
FTL_1039	-	hypothetical protein	39.9	0.24	3.82E-01
FTL_1040	-	hypothetical protein	612.3	0.12	4.29E-01
FTL_1041	-	octaprenyl-diphosphate synthase	2066.9	0.31	6.13E-03
FTL_1042	-	FKBP-type peptidyl-prolyl cis-trans isomerase	7042.0	-0.84	1.24E-16
FTL_1043	-	C32 tRNA thiolase	1949.2	-0.66	3.61E-12
FTL_1044	-	hypothetical protein	353.8	-0.69	3.21E-06
FTL_1045	-	lipoprotein	1198.3	-0.72	2.19E-10
FTL_1046	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase	5059.0	-0.46	8.88E-06
FTL_1047	<i>rpsU</i>	30S ribosomal protein S21	2094.7	-12.55	4.72E-14
FTL_1048	-	hypothetical protein	3960.9	2.61	#####
FTL_1049	<i>dnaG</i>	DNA primase	2811.8	1.19	2.28E-64
FTL_1050	<i>rpoD</i>	RNA polymerase sigma-70 factor	4901.2	-0.64	2.15E-12
FTL_1051	<i>ndh</i>	NADH dehydrogenase	3251.1	0.01	9.17E-01
FTL_1052	-	putative glycosidase	1.0	-0.01	NA
FTL_1053	-	putative alpha-xylosidase	25.1	0.71	2.85E-02
FTL_1054	-	putative alpha-xylosidase	56.8	-0.15	5.64E-01
FTL_1055	-	-	170.6	-0.44	1.19E-02
FTL_1056	-	-	20.0	-0.21	4.33E-01
FTL_1057	-	-	294.6	-0.77	3.37E-06
FTL_1058	<i>lipB</i>	lipoate-protein ligase B	1316.2	0.44	7.56E-04
FTL_1059	-	hypothetical protein	852.8	0.76	8.56E-08

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1060	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase	11993.8	-0.07	5.73E-01
FTL_1061	-	inorganic pyrophosphatase	1618.8	-0.60	1.78E-12
FTL_1062	-	3-deoxy-D-manno-octulosonate 8-phosphate	1140.0	0.03	8.56E-01
FTL_1063	-	hypothetical protein	498.6	0.43	2.35E-03
FTL_1064	-	hypothetical protein	844.4	0.00	9.99E-01
FTL_1065	-	ABC transporter ATP-binding protein	623.5	-0.18	3.63E-01
FTL_1066	-	fumarylacetoacetate hydrolase family protein	309.6	-0.43	4.31E-03
FTL_1067	-	hypothetical protein	2710.0	-0.24	1.86E-02
FTL_1068	<i>truA</i>	tRNA pseudouridine synthase A	285.0	-0.04	8.35E-01
FTL_1069	-	amino acid permease	248.3	-0.20	2.35E-01
FTL_1070	-	hypothetical protein	0.8	0.04	NA
FTL_1071	<i>guaA</i>	GMP synthase	6508.3	-0.18	5.97E-02
FTL_1072	-	1-deoxy-D-xylulose-5-phosphate synthase	7174.7	-0.34	3.22E-06
FTL_1073	-	hypothetical protein	862.6	-0.71	1.19E-06
FTL_1074	-	GDH-like lipase/acylhydrolase family protein	1021.3	-0.32	7.97E-03
FTL_1075	-	hypothetical protein	3852.7	-0.59	2.29E-07
FTL_1076	-	short chain dehydrogenase family protein	653.4	-0.39	9.03E-04
FTL_1077	<i>ruvB</i>	Holliday junction DNA helicase RuvB	2784.6	-0.41	1.92E-04
FTL_1078	-	-	194.8	0.51	6.54E-03
FTL_1079	-	helix-turn-helix family protein	21.8	0.11	6.84E-01
FTL_1080	-	hypothetical protein	83.3	0.02	9.31E-01
FTL_1081	-	hypothetical protein	8.0	0.25	2.85E-01
FTL_1082	-	hypothetical protein	1.9	0.06	NA

				LVS Δ rp _s U2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1083	-	hypothetical protein	0.8	0.03	NA
FTL_1084	-	hypothetical protein	0.9	0.01	NA
FTL_1085	-	hypothetical protein	1.2	0.09	NA
FTL_1086	-	proton-dependent oligopeptide transporter	270.7	0.27	2.39E-01
FTL_1087	<i>isftu2</i>	transposase	50.3	-0.04	8.91E-01
FTL_1088	-	hypothetical protein	682.9	-0.50	4.18E-03
FTL_1089	-	choloyleglycine hydrolase family protein	2535.9	-0.92	7.32E-21
FTL_1090	-	rRNA methyltransferase	358.5	-0.56	1.34E-04
FTL_1091	-	-	120.5	-0.48	2.34E-02
FTL_1092	-	-	32.2	-0.18	5.13E-01
FTL_1093	-	bifunctional methionine sulfoxide reductase	3947.1	-0.59	2.06E-10
FTL_1094	-	-	178.9	0.01	9.82E-01
FTL_1095	-	-	170.6	-0.46	2.85E-02
FTL_1096	<i>dsbA</i>	Disulfide bond formation protein A	19752.8	-0.80	2.39E-17
FTL_1097	-	hypothetical protein	2554.9	-1.05	1.91E-24
FTL_1098	-	-	25.5	0.47	1.18E-01
FTL_1099	-	-	591.2	-0.22	1.22E-01
FTL_1100	-	hypothetical protein	1312.4	-0.50	1.24E-04
FTL_1101	-	hypothetical protein	527.1	-0.03	9.25E-01
FTL_1102	-	-	86.5	-0.45	3.77E-02
FTL_1103	-	-	18.8	1.25	2.29E-03
FTL_1104	-	-	15.4	1.29	2.90E-03
FTL_1105	-	hypothetical protein	1147.4	-0.64	4.69E-08

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1106	<i>alaS</i>	alanyl-tRNA synthetase	8132.8	-0.17	1.04E-01
FTL_1107	-	hypothetical protein	1416.0	0.06	6.47E-01
FTL_1108	-	cytosol aminopeptidase	3038.4	-0.76	5.23E-14
FTL_1109	-	transaldolase B	4692.3	-0.57	7.16E-17
FTL_1110	-	hypothetical protein	1884.1	-0.98	1.96E-16
FTL_1111	-	isochorismatase hydrolase family protein	3.5	0.33	NA
FTL_1112	<i>isftu2</i>	transposase	63.4	0.10	6.96E-01
FTL_1113	-	hypothetical protein	92.7	1.36	5.74E-05
FTL_1114	-	isochorismatase hydrolase family protein	142.9	1.79	2.56E-13
FTL_1115	-	hypothetical protein	1559.6	-0.45	1.15E-04
FTL_1116	-	ATP-dependent DNA helicase	950.3	-0.39	2.38E-04
FTL_1117	-	hypothetical protein	1677.9	-0.42	2.51E-05
FTL_1118	-	hypothetical protein	2222.8	-0.68	2.38E-14
FTL_1119	<i>rdgC</i>	recombination associated protein	1945.6	-0.38	4.34E-04
FTL_1120	-	hypothetical protein	229.9	-0.28	1.28E-01
FTL_1121	-	hypothetical protein	350.6	-0.82	3.65E-09
FTL_1122	-	hypothetical protein	37.7	-0.28	3.11E-01
FTL_1123	-	hypothetical protein	53.8	-0.76	1.16E-02
FTL_1124	-	hypothetical protein	17.3	-0.24	3.82E-01
FTL_1125	-	transcriptional regulator	147.5	0.06	7.91E-01
FTL_1126	-	transcriptional regulator	17.3	-0.04	8.94E-01
FTL_1127	<i>isftu1</i>	transposase	548.8	0.08	6.67E-01
FTL_1128	-	hypothetical protein	0.0	NA	NA

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1129	-	acetyltransferase	1382.1	-0.20	1.98E-01
FTL_1130	-	ribosomal RNA small subunit methyltransferase	2.3	-0.06	NA
FTL_1131	-	Sun protein	278.8	0.01	9.75E-01
FTL_1132	-	inositol-1-monophosphatase	2390.7	-0.35	5.35E-04
FTL_1133	-	hypothetical protein	1123.0	-0.49	3.75E-05
FTL_1134	-	hypothetical protein	5358.3	-0.54	1.64E-07
FTL_1135	-	-	449.1	-0.51	2.88E-04
FTL_1136	-	hypothetical protein	1412.7	0.01	9.68E-01
FTL_1137	-	3-oxoacyl-ACP synthase	60812.5	0.14	3.16E-01
FTL_1138	<i>acpP</i>	acyl carrier protein	8080.1	-0.37	1.52E-03
FTL_1139	-	3-oxoacyl-(acyl-carrier-protein) reductase	10591.1	-0.31	4.10E-03
FTL_1140	-	malonyl CoA-acyl carrier protein transacylase	13809.2	-0.12	4.00E-01
FTL_1141	-	3-oxoacyl-ACP synthase	6210.5	-0.07	5.73E-01
FTL_1142	-	putative glycerol-3-phosphate acyltransferase	16502.4	-0.15	1.19E-01
FTL_1143	<i>rpmF</i>	50S ribosomal protein L32	762.0	-0.34	1.60E-02
FTL_1144	-	hypothetical protein	641.4	-0.40	1.22E-02
FTL_1145	-	transketolase	11352.6	-0.66	1.31E-10
FTL_1146	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase	13019.1	-0.48	1.86E-06
FTL_1147	<i>pgk</i>	phosphoglycerate kinase	10374.9	-0.38	2.51E-03
FTL_1148	<i>pyk</i>	pyruvate kinase	11485.7	-0.54	1.73E-03
FTL_1149	<i>fbaA</i>	fructose-1,6-bisphosphate aldolase	9713.8	-0.44	8.08E-05
FTL_1150	<i>treA</i>	Alpha, alpha-trehalase	4.1	-0.07	NA
FTL_1151	-	trehalase, pseudogene	14.0	0.11	6.77E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1152	-	-	0.1	0.00	NA
FTL_1153	<i>isftu1</i>	transposase	527.5	0.10	6.47E-01
FTL_1154	-	-	3.8	0.10	NA
FTL_1155	-	hypothetical protein	2.9	-0.01	NA
FTL_1156	-	hypothetical protein	2.8	0.01	NA
FTL_1173	-	hypothetical protein	1573.9	-0.82	2.60E-11
FTL_1174	-	cystathionine beta-synthase (cystein synthas	1897.8	-0.89	2.27E-14
FTL_1175	-	-	9.3	-0.10	6.67E-01
FTL_1176	-	LysR transcriptional regulator family protein	115.6	0.07	7.71E-01
FTL_1177	<i>trmE</i>	tRNA modification GTPase TrmE	3251.9	-0.13	3.02E-01
FTL_1178	-	hypothetical protein	0.5	-0.01	NA
FTL_1179	-	sigma-54 modulation protein	9348.8	-0.36	3.68E-05
FTL_1180	-	PEP-dependent sugar PTS system family prot	2097.7	0.15	1.54E-01
FTL_1181	-	SpoU rRNA methylase family protein	2214.8	0.53	9.68E-10
FTL_1182	<i>rnhB</i>	ribonuclease HII	713.3	0.35	1.27E-03
FTL_1183	-	Sodium-solute symporter family protein	340.2	0.55	9.74E-04
FTL_1184	-	ClpXP protease specificity-enhancing factor	1671.2	-0.03	8.53E-01
FTL_1185	-	macrophage growth locus subunit A	6602.9	-0.03	8.18E-01
FTL_1186	<i>rpsI</i>	30S ribosomal protein S9	8060.2	-0.56	1.44E-13
FTL_1187	<i>rplM</i>	50S ribosomal protein L13	8658.6	-0.75	1.28E-11
FTL_1188	-	hypothetical protein	1376.0	-0.14	2.23E-01
FTL_1189	<i>mltA</i>	membrane-bound lytic murein transglycosyla	873.9	0.14	2.57E-01
FTL_1190	-	heat shock protein GrpE	1410.5	-0.38	1.61E-01

				LVS Δ rrpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1191	<i>dnaK</i>	molecular chaperone DnaK	60679.2	-0.40	4.70E-03
FTL_1192	-	chaperone protein DnaJ	7950.7	-0.04	8.35E-01
FTL_1193	-	LysR transcriptional regulator family protein	3.4	0.00	NA
FTL_1194	-	pirin family protein	5.0	0.06	NA
FTL_1195	<i>isftu1</i>	transposase	527.9	0.05	7.97E-01
FTL_1196	-	hypothetical protein	64.9	0.34	1.42E-01
FTL_1197	<i>pheS</i>	phenylalanyl-tRNA synthetase subunit alpha	4341.6	-0.24	9.28E-02
FTL_1198	<i>pheT</i>	phenylalanyl-tRNA synthetase subunit beta	11205.5	0.14	1.57E-01
FTL_1199	-	regulatory protein	395.0	-0.06	7.24E-01
FTL_1200	-	cobalamin (vitamin B12) synthesis protein/P4	678.5	-0.05	7.96E-01
FTL_1201	-	ZIP metal transporter family protein	317.7	0.18	3.68E-01
FTL_1202	-	hypothetical protein	449.4	-0.97	1.47E-14
FTL_1203	-	cardiolipin synthetase	973.1	-0.61	1.25E-08
FTL_1204	-	cardiolipin synthetase	419.3	-1.24	2.05E-21
FTL_1205	-	hypothetical protein	3.6	0.10	NA
FTL_1206	-	major facilitator transporter	59.8	0.19	4.31E-01
FTL_1207	-	MRP like protein	2063.9	0.81	9.60E-16
FTL_1208	<i>dcd</i>	deoxycytidine triphosphate deaminase	1449.3	-0.15	1.00E-01
FTL_1209	-	hypothetical protein	38.6	0.14	6.18E-01
FTL_1210	-	hypothetical protein	105.1	0.07	7.09E-01
FTL_1211	-	lipoprotein	2531.8	-0.73	5.20E-11
FTL_1212	<i>leuS</i>	leucyl-tRNA synthetase	19799.6	-0.34	2.19E-04
FTL_1213	-	hypothetical protein	4221.2	-0.87	7.45E-10

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1214	-	hypothetical protein	6.4	-0.09	6.73E-01
FTL_1215	-	hypothetical protein	519.8	-0.14	3.43E-01
FTL_1216	-	hypothetical protein	1733.0	-0.20	6.38E-02
FTL_1217	-	hypothetical protein	923.5	-0.20	4.63E-01
FTL_1218	-	hypothetical protein	2926.7	-0.25	9.38E-02
FTL_1219	-	hypothetical protein	53616.2	-0.25	7.86E-03
FTL_1220	-	amino-acid permease	161.2	-0.06	7.96E-01
FTL_1221	-	hypothetical protein	31.2	0.73	4.69E-02
FTL_1222	-	hypothetical protein	28.8	0.00	9.97E-01
FTL_1223	-	hypothetical protein	1095.2	-0.61	2.81E-04
FTL_1224	-	thioredoxin	1858.0	-0.87	9.13E-20
FTL_1225	-	hypothetical protein	7724.2	-0.95	9.17E-16
FTL_1226	-	-	158.1	-0.04	8.55E-01
FTL_1227	-	-	846.5	-0.94	1.17E-08
FTL_1228	-	hypothetical protein	1384.4	-0.41	1.03E-02
FTL_1229	-	ABC transporter ATP-binding protein	1188.1	-0.45	6.72E-06
FTL_1230	-	cysteine desulfurase activator complex subu	4212.8	-0.51	3.10E-05
FTL_1231	-	hypothetical protein	385.1	-0.29	1.15E-01
FTL_1232	<i>trkA</i>	potassium transporter peripheral membrane	3203.5	-0.24	3.27E-02
FTL_1233	<i>argP</i>	amino acid antiporter, high affinity arginine t	2866.9	-0.48	7.61E-06
FTL_1234	-	hypothetical protein	67.9	0.28	2.53E-01
FTL_1235	-	-	81.5	-0.20	4.05E-01
FTL_1236	<i>infA</i>	translation initiation factor IF-1	1787.4	-0.11	5.27E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1237	-	hypothetical protein	1206.8	-0.53	3.64E-05
FTL_1238	-	hypothetical protein	2.0	-0.01	NA
FTL_1239	<i>ffh</i>	signal recognition particle protein, Ffh	15280.4	-0.15	1.07E-01
FTL_1240	-	phospho-2-dehydro-3-deoxyheptonate aldol	17023.2	-0.34	6.93E-05
FTL_1241	<i>isftu1</i>	transposase	549.1	0.08	7.34E-01
FTL_1242	-	ThiJ/Pfpl family protein	369.7	-0.57	4.26E-03
FTL_1243	-	hypothetical protein	1350.6	-0.40	1.24E-05
FTL_1244	-	exodeoxyribonuclease III	832.7	-0.49	1.07E-05
FTL_1245	-	short chain dehydrogenase	547.0	-0.50	2.51E-05
FTL_1246	-	hypothetical protein	304.4	-0.60	5.97E-06
FTL_1247	-	hypothetical protein	345.9	-1.03	1.53E-14
FTL_1248	-	glutathione reductase	3448.6	-0.53	8.38E-08
FTL_1249	-	hypothetical protein	303.3	-0.63	4.61E-05
FTL_1250	<i>isftu2</i>	transposase	52.1	-0.22	3.87E-01
FTL_1251	-	proton-dependent oligopeptide transport (P	6639.0	-0.84	5.64E-17
FTL_1252	-	ATP-dependent RNA helicase RhlE	2075.8	-0.52	2.65E-09
FTL_1253	<i>folE</i>	GTP cyclohydrolase I	759.0	0.15	2.15E-01
FTL_1254	-	-	76.6	0.19	4.39E-01
FTL_1255	-	-	53.4	0.43	1.09E-01
FTL_1256	-	-	875.4	-0.56	9.56E-05
FTL_1257	-	-	67.3	-0.19	4.50E-01
FTL_1258	-	aldo/keto reductase	1240.1	-0.15	1.89E-01
FTL_1259	-	-	88.9	0.42	4.12E-02

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1260	-	-	6.9	0.65	7.33E-02
FTL_1261	-	anthranilate synthase component II	217.7	0.00	9.82E-01
FTL_1262	-	chorismate binding family protein	1164.9	0.08	5.27E-01
FTL_1263	<i>fadD2</i>	AMP-binding family protein	703.9	-0.14	3.81E-01
FTL_1264	-	dihydroneopterin aldolase	216.4	-0.19	3.20E-01
FTL_1265	-	2-amino-4-hydroxy-6-hydroxymethyldihydro	6632.7	-0.18	2.22E-01
FTL_1266	-	lipase/esterase	11295.3	-0.81	1.49E-14
FTL_1267	-	hypothetical protein	1403.4	-0.34	3.28E-03
FTL_1268	-	-	20.2	-0.16	5.39E-01
FTL_1269	-	-	44.8	-0.16	5.54E-01
FTL_1270	-	-	97.8	0.15	5.45E-01
FTL_1271	<i>bioA</i>	adenosylmethionine-8-amino-7-oxononanoa	3445.1	-0.34	3.82E-04
FTL_1272	<i>bioB</i>	biotin synthase	9495.1	-0.13	3.80E-01
FTL_1273	<i>bioF</i>	8-amino-7-oxononanoate synthase	6407.4	0.44	3.38E-04
FTL_1274	<i>bioC</i>	biotin synthesis protein BioC	1171.8	0.63	6.18E-02
FTL_1275	<i>bioD</i>	dethiobiotin synthetase	3074.6	-0.22	1.28E-01
FTL_1276	<i>birA</i>	bifunctional biotin operon repressor/biotin s	389.1	-0.25	1.01E-01
FTL_1277	-	ROK family protein	419.9	-0.20	2.06E-01
FTL_1278	-	major facilitator transporter	348.5	-0.06	7.29E-01
FTL_1279	-	acetoacetate decarboxylase, fragment	236.4	-0.15	3.92E-01
FTL_1280	-	short-chain dehydrogenase	3.9	-0.08	NA
FTL_1281	-	hypothetical protein	55.8	0.19	4.44E-01
FTL_1282	-	beta-glucosidase	892.3	-0.16	3.19E-01

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1283	-	glutamate-1-semialdehyde aminotransferase	3408.6	-0.13	1.68E-01
FTL_1284	-	glutathione synthetase	2292.4	-0.04	7.06E-01
FTL_1285	-	methionyl-tRNA formyltransferase	1085.5	-0.14	2.98E-01
FTL_1286	-	hypothetical protein	839.9	-0.35	7.06E-04
FTL_1287	<i>rlmL</i>	23S rRNA m(2)G2445 methyltransferase	6958.4	-0.60	3.61E-12
FTL_1288	-	fatty acid hydroxylase	318.5	-0.12	6.72E-01
FTL_1289	-	hypothetical protein	7.1	0.11	6.06E-01
FTL_1290	<i>isftu1</i>	transposase	552.4	0.01	9.48E-01
FTL_1291	-	hypothetical protein	6.2	0.21	3.58E-01
FTL_1292	-	hypothetical protein	4.8	0.10	NA
FTL_1293	-	hypothetical protein	1048.8	-0.21	3.59E-02
FTL_1294	-	short-chain dehydrogenase	1356.5	-0.47	1.71E-06
FTL_1295	-	amino acid transporter	234.1	2.11	1.49E-42
FTL_1296	-	amino acid antiporter	167.1	0.31	1.87E-01
FTL_1297	-	hypothetical protein	121.0	-0.31	1.20E-01
FTL_1298	<i>isftu1</i>	transposase	512.2	0.04	8.31E-01
FTL_1299	-	hypothetical protein	188.6	-0.33	8.92E-02
FTL_1300	-	hypothetical protein	42.2	-0.17	5.40E-01
FTL_1301	<i>isftu2</i>	transposase	52.9	0.02	9.42E-01
FTL_1302	-	phenol hydroxylase	2778.8	-0.60	2.55E-12
FTL_1303	<i>rpmE</i>	50S ribosomal protein L31	1822.3	-0.86	5.15E-03
FTL_1304	-	glutamate--cysteine ligase	1930.8	-0.25	3.39E-03
FTL_1305	-	virulence factor MviN	645.9	0.21	1.29E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1306	-	hypothetical protein	6815.7	-0.64	4.95E-14
FTL_1307	-	nucleotide-binding protein, yjeE	221.0	0.26	8.55E-02
FTL_1308	-	bifunctional folylpolyglutamate synthase/ di	3162.4	0.17	7.73E-02
FTL_1309	-	Acetyl-CoA carboxylase beta subunit	24841.0	-0.27	1.26E-03
FTL_1310	<i>ndk</i>	nucleoside diphosphate kinase	3043.9	-0.63	5.79E-10
FTL_1311	<i>pyrG</i>	CTP synthetase	4275.8	-0.83	2.11E-14
FTL_1312	-	S-transferase	1137.9	-1.08	2.16E-23
FTL_1313	-	short-chain fatty acids transporter	533.8	-0.50	3.29E-04
FTL_1314	-	hypothetical protein	39.4	0.32	2.39E-01
FTL_1315	-	hypothetical protein	11.2	1.04	2.19E-02
FTL_1316	<i>isftu1</i>	transposase	505.1	0.12	5.75E-01
FTL_1317	-	hypothetical protein	7168.9	0.03	8.77E-01
FTL_1318	-	-	0.2	0.02	NA
FTL_1319	-	transposase	48.4	0.02	9.55E-01
FTL_1320	-	hypothetical protein	16.0	-0.05	8.44E-01
FTL_1321	-	hypothetical protein	6.3	-0.03	8.88E-01
FTL_1322	-	-	9.2	0.37	1.92E-01
FTL_1323	-	-	12.9	-0.10	7.03E-01
FTL_1324	-	-	0.0	NA	NA
FTL_1325	-	-	58.4	0.24	3.43E-01
FTL_1326	-	hypothetical protein	27.3	0.74	2.37E-02
FTL_1327	-	hypothetical protein	659.8	0.15	2.44E-01
FTL_1328	<i>fopA</i>	OmpA family protein, outer membrane assoc	82247.8	-0.20	6.64E-02

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1329	-	ferredoxin	248.4	0.19	2.85E-01
FTL_1330	<i>coaD</i>	phosphopantetheine adenylyltransferase	920.8	0.27	1.41E-01
FTL_1331	-	hypothetical protein	786.9	-0.07	7.29E-01
FTL_1332	-	hesB family protein	980.7	-0.07	6.77E-01
FTL_1333	-	selenocysteine lyase	1690.6	0.02	8.65E-01
FTL_1334	-	L-serine dehydratase 1	5240.1	-0.01	9.39E-01
FTL_1335	-	hypothetical protein	263.0	-0.02	9.38E-01
FTL_1336	-	prephenate dehydratase	1402.5	-0.45	1.02E-05
FTL_1337	-	-	512.2	-0.38	3.59E-03
FTL_1338	-	alanine racemase	392.8	-0.89	3.46E-09
FTL_1339	-	proton-dependent oligopeptide transport (P	548.8	-0.33	5.81E-02
FTL_1340	-	hypothetical protein	1597.3	-0.95	8.30E-21
FTL_1341	-	hypothetical protein	264.8	-0.22	2.11E-01
FTL_1342	-	hypothetical protein	701.6	-0.86	2.15E-16
FTL_1343	-	hypothetical protein	56.9	-0.14	6.20E-01
FTL_1344	-	hypothetical protein	229.3	-0.82	3.48E-06
FTL_1345	-	-	2729.8	-0.32	5.74E-03
FTL_1346	-	-	3.7	0.16	NA
FTL_1347	-	hypothetical protein	5.7	0.16	NA
FTL_1348	-	transposase	62.8	0.02	9.54E-01
FTL_1349	<i>isftu1</i>	transposase	554.0	0.07	7.30E-01
FTL_1350	-	glycyl-tRNA synthetase subunit beta	6672.4	-0.12	1.49E-01
FTL_1351	-	TatD related DNase family protein	186.2	-0.22	2.23E-01

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1352	-	DNA replication and repair protein RecF	214.4	0.03	9.18E-01
FTL_1353	-	hypothetical protein	6.0	0.14	5.17E-01
FTL_1354	-	hypothetical protein	1328.8	-0.40	6.13E-04
FTL_1355	-	-	457.4	-0.20	2.59E-01
FTL_1356	-	-	1105.8	-0.41	1.43E-04
FTL_1357	-	UTP--glucose-1-phosphate uridylyltransferas	1364.2	-0.74	3.69E-15
FTL_1358	-	cation-efflux family protein	2092.1	-1.24	7.54E-35
FTL_1359	-	hypothetical protein	203.2	-0.24	1.61E-01
FTL_1360	<i>rpsU</i>	30S ribosomal protein S21	410.6	0.31	6.44E-02
FTL_1361	-	cold shock protein	357.9	0.04	8.83E-01
FTL_1362	-	hypothetical protein	531.3	0.18	2.37E-01
FTL_1363	-	hypothetical protein	668.7	-0.21	1.14E-01
FTL_1364	-	hypothetical protein	6848.3	-0.74	3.20E-13
FTL_1365	-	hypothetical protein	922.8	0.00	9.98E-01
FTL_1366	-	membrane fusion protein	99.6	0.34	9.63E-02
FTL_1367	-	hypothetical protein	244.7	0.31	2.73E-02
FTL_1368	-	hypothetical protein	132.8	0.36	1.14E-01
FTL_1369	<i>isftu1</i>	transposase	551.5	0.08	7.13E-01
FTL_1370	-	hypothetical protein	968.7	-0.56	1.66E-07
FTL_1371	-	hypothetical protein	510.9	0.62	2.32E-04
FTL_1372	-	lipoprotein	2355.6	0.36	6.43E-02
FTL_1373	-	hypothetical protein	38.7	1.58	7.83E-08
FTL_1374	-	organic solvent tolerance protein	598.6	0.39	1.59E-03

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1375	-	heat shock protein 15 (HSP15)	25.1	-1.26	3.70E-03
FTL_1376	-	carbohydrate kinase family protein (YjeF-rela	375.7	-0.49	1.16E-04
FTL_1377	-	hypothetical protein	29.0	0.40	1.71E-01
FTL_1378	-	-	1.5	0.04	NA
FTL_1379	-	-	129.4	0.06	7.96E-01
FTL_1380	-	-	5.6	0.08	NA
FTL_1381	-	-	13.3	0.04	9.00E-01
FTL_1382	-	-	317.0	-0.43	1.06E-02
FTL_1383	-	glutathione peroxidase	491.4	-1.02	1.26E-12
FTL_1384	-	hypothetical protein	176.3	-0.56	2.47E-02
FTL_1385	-	hypothetical protein	34.1	0.11	6.97E-01
FTL_1386	<i>isftu2</i>	transposase	52.7	0.11	6.64E-01
FTL_1387	-	-	56.5	0.09	7.41E-01
FTL_1388	-	L-aspartate oxidase	1395.3	-0.35	4.36E-04
FTL_1389	-	nicotinate-nucleotide pyrophosphorylase	1898.2	-0.24	3.99E-02
FTL_1390	-	quinolinate synthetase	5431.5	-0.29	4.24E-03
FTL_1391	<i>gmk</i>	guanylate kinase	2082.6	-0.38	1.29E-04
FTL_1392	<i>deaD</i>	cold-shock DEAD-box protein A	18541.9	-0.57	2.18E-10
FTL_1393	<i>ppiC</i>	peptidyl-prolyl cis-trans isomerase	5117.8	-0.23	2.04E-01
FTL_1394	<i>galP2</i>	major facilitator superfamily galactose-proto	7549.0	-0.13	2.55E-01
FTL_1395	<i>galP1</i>	major facilitator superfamily galactose-proto	2787.5	-0.37	2.22E-03
FTL_1396	-	galactose-1-phosphate uridylyltransferase	4798.7	-0.27	2.86E-03
FTL_1397	-	galactokinase	2696.3	-0.33	4.32E-04

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1398	-	hypothetical protein	906.3	0.33	2.08E-03
FTL_1399	-	3-deoxy-manno-octulosonate cytidyltransferase	2513.9	0.54	4.83E-08
FTL_1400	-	hypothetical protein	369.4	0.20	2.58E-01
FTL_1401	-	hypothetical protein	25.4	-0.06	8.39E-01
FTL_1402	<i>isftu1</i>	transposase	549.5	0.04	8.33E-01
FTL_1403	-	hypothetical protein	386.1	0.46	3.51E-02
FTL_1404	<i>rplT</i>	50S ribosomal protein L20	7777.7	-0.75	1.57E-09
FTL_1405	<i>rpmI</i>	50S ribosomal protein L35	470.6	-0.43	1.32E-02
FTL_1406	-	translation initiation factor IF-3	23785.0	0.51	2.85E-03
FTL_1407	<i>thrS</i>	threonyl-tRNA synthetase	16292.5	-0.42	3.54E-06
FTL_1408	-	chitin binding protein	296.5	0.11	5.53E-01
FTL_1409	-	glycine cleavage system protein H	1701.1	-1.08	5.97E-27
FTL_1410	<i>murG</i>	undecaprenyldiphospho-muramoylpentapeptidase	1470.6	-0.17	1.28E-01
FTL_1411	-	hypothetical protein	890.0	-0.66	3.85E-06
FTL_1412	-	recombination protein RecR	1021.7	-0.45	2.77E-05
FTL_1413	<i>spoT</i>	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphatase	5079.8	-0.39	2.95E-07
FTL_1414	<i>capA</i>	hypothetical protein	6258.4	-1.14	4.89E-36
FTL_1415	<i>capC</i>	capsule biosynthesis protein CapC	1259.1	-1.21	4.98E-24
FTL_1416	<i>capB</i>	capsule biosynthesis protein capB	2201.6	-1.09	2.68E-28
FTL_1417	-	major facilitator transporter	1361.6	0.00	9.82E-01
FTL_1418	-	asparaginase	2274.7	-0.25	4.05E-02
FTL_1419	-	cyanophycinase	7971.3	-0.43	8.67E-06
FTL_1420	-	carbohydrate/purine kinase pfkB family protein	3039.0	-0.33	2.80E-04

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1421	-	haloacid dehalogenase-like hydrolase family	272.6	0.19	2.08E-01
FTL_1422	-	glycosyl transferases group 1 family protein	354.1	0.51	9.24E-04
FTL_1423	-	glycosyl transferase family protein	310.3	0.54	2.79E-04
FTL_1424	-	glycosyl transferase family protein	375.6	0.47	6.11E-03
FTL_1425	-	hypothetical protein	496.5	-0.15	3.54E-01
FTL_1426	-	hypothetical protein	747.5	-0.06	7.72E-01
FTL_1427	-	hypothetical protein	2140.5	-0.06	7.14E-01
FTL_1428	-	ABC transporter ATP-binding and membrane	605.6	0.08	5.65E-01
FTL_1429	-	glycosyl transferases group 1 family protein	1290.9	0.20	1.32E-01
FTL_1430	-	UDP-glucose 4-epimerase	2421.5	-0.11	2.45E-01
FTL_1431	-	sugar transferase	726.9	0.22	6.88E-02
FTL_1432	-	D-ribulose-phosphate 3-epimerase	931.2	-0.51	1.02E-05
FTL_1433	-	arabinose phosphate isomerase	1342.8	-0.43	3.81E-05
FTL_1434	-	DoxD-like family protein	19.0	0.13	6.54E-01
FTL_1435	-	hypothetical protein	1.4	0.05	NA
FTL_1436	-	hypothetical protein	3.4	0.02	NA
FTL_1437	-	hypothetical protein	12.0	-0.17	5.35E-01
FTL_1438	-	hypothetical protein	1.8	0.05	NA
FTL_1439	-	arylsulfatase	7.4	-0.01	9.80E-01
FTL_1440	-	beta-lactamase superfamily hydrolase	15.8	0.06	8.30E-01
FTL_1441	<i>isftu2</i>	transposase	52.4	-0.10	7.09E-01
FTL_1442	<i>fabI</i>	enoyl-[acyl-carrier-protein] reductase (NADH	11277.0	-0.48	1.03E-08
FTL_1443	-	hypothetical protein	2800.4	0.09	3.45E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1444	-	hypothetical protein	271.9	-0.20	3.78E-01
FTL_1445	<i>isftu2</i>	transposase	63.4	0.20	4.02E-01
FTL_1446	<i>isftu1</i>	transposase	544.5	0.06	7.72E-01
FTL_1447	-	hypothetical protein	20.6	-0.07	7.81E-01
FTL_1448	<i>uvrC</i>	excinuclease ABC subunit C	727.5	0.02	9.11E-01
FTL_1449	-	ribonuclease D	573.7	0.09	5.99E-01
FTL_1450	-	major facilitator transporter	3602.9	-0.30	8.07E-04
FTL_1451	-	hypothetical protein	502.4	-0.42	1.63E-03
FTL_1452	<i>rpmA</i>	50S ribosomal protein L27	2675.8	-0.17	1.57E-01
FTL_1453	<i>rplU</i>	50S ribosomal protein L21	1300.9	-0.26	2.01E-01
FTL_1454	-	-	42.0	-0.53	4.72E-02
FTL_1455	-	-	56.1	-0.25	3.17E-01
FTL_1456	-	-	15.7	0.25	3.64E-01
FTL_1457	-	-	17.3	0.11	6.92E-01
FTL_1458	<i>secA</i>	preprotein translocase subunit SecA	18357.6	-0.10	3.29E-01
FTL_1459	-	hypothetical protein	603.5	-0.65	5.39E-06
FTL_1460	-	hypothetical protein	284.9	-0.44	1.66E-03
FTL_1461	<i>deoD</i>	purine nucleoside phosphorylase	18976.0	-0.89	1.06E-21
FTL_1462	<i>isftu1</i>	transposase	544.5	0.00	9.86E-01
FTL_1463	<i>isftu2</i>	transposase	51.1	-0.08	7.50E-01
FTL_1464	-	ATP-dependent metalloprotease	4035.5	-0.32	4.38E-02
FTL_1465	-	hypothetical protein	20.1	-0.66	5.85E-02
FTL_1466	-	major facilitator transporter	19.0	0.08	7.72E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1467	<i>isftu2</i>	transposase	52.1	-0.11	6.76E-01
FTL_1468	-	ATP-dependent metalloprotease	4011.0	-0.28	1.14E-01
FTL_1469	-	hypothetical protein	21.4	-0.72	4.00E-02
FTL_1470	-	major facilitator transporter	18.2	0.20	4.68E-01
FTL_1471	<i>isftu2</i>	transposase	53.0	-0.09	7.29E-01
FTL_1472	-	hypothetical protein	52.3	-0.08	7.71E-01
FTL_1473	<i>uvrA</i>	DNA excision repair protein subunit A	5592.2	0.32	3.81E-05
FTL_1474	<i>greA</i>	transcription elongation factor GreA	1902.8	-0.41	1.67E-05
FTL_1475	<i>fimT</i>	Type IV pili fiber building block protein	1026.5	-0.09	3.79E-01
FTL_1476	<i>pgi</i>	glucose-6-phosphate isomerase	5226.6	-0.37	1.76E-04
FTL_1477	-	thiamine pyrophosphokinase	549.3	-0.01	9.58E-01
FTL_1478	<i>guaB</i>	inosine-5-monophosphate dehydrogenase	14927.4	-0.15	2.41E-01
FTL_1479	<i>pepA</i>	cytosol aminopeptidase	17097.1	-0.63	1.78E-07
FTL_1480	-	YjgP/YjgQ family permease	1258.8	-0.15	2.81E-01
FTL_1481	-	YjgP/YjgQ family permease	1185.5	-0.35	4.65E-04
FTL_1482	-	peptidase M16 family protein	1896.0	-0.45	1.58E-05
FTL_1483	-	peptidase M16 family protein	1040.7	-0.34	1.58E-03
FTL_1484	-	methylase	155.7	-0.14	5.30E-01
FTL_1485	-	hypothetical protein	682.8	0.60	3.85E-06
FTL_1486	-	tRNA-(ms(2)io(6)a)-hydroxylase	660.4	-0.11	3.42E-01
FTL_1487	-	uridine phosphorylase	1611.8	-0.57	2.60E-07
FTL_1488	-	cytidine deaminase	642.1	-0.73	4.20E-08
FTL_1489	-	FAD-binding family protein	7928.9	-0.25	8.59E-03

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1490	-	phosphoglyceromutase	10851.2	-0.64	1.37E-11
FTL_1491	-	seryl-tRNA synthetase	5595.3	-0.39	4.31E-05
FTL_1492	-	fructokinase	2328.5	-0.51	3.41E-09
FTL_1493	-	polysaccharide biosynthesis protein (export p	570.4	-0.26	3.35E-02
FTL_1494	-	hypothetical protein	3522.2	-0.93	2.01E-23
FTL_1495	-	cysteine/glutathione ABC transporter memb	1571.5	-0.36	2.12E-05
FTL_1496	-	cysteine/glutathione ABC transporter memb	1017.3	-0.29	7.81E-03
FTL_1497	-	C4-dicarboxylate transport protein	654.1	-0.58	4.94E-07
FTL_1498	-	translation initiation inhibitor	1334.0	-0.43	1.99E-04
FTL_1499	-	sulfate permease family protein	881.2	0.13	2.63E-01
FTL_1500	-	transposase	42.2	-0.27	3.04E-01
FTL_1501	-	-	0.1	0.00	NA
FTL_1502	-	major facilitator transporter	46.0	0.21	4.11E-01
FTL_1503	<i>dgt</i>	deoxyguanosinetriphosphate triphosphohyd	3612.3	-0.43	1.08E-06
FTL_1504	<i>katG</i>	peroxidase/catalase	61092.5	-1.01	6.61E-17
FTL_1505	<i>isftu1</i>	transposase	543.5	0.12	5.08E-01
FTL_1506	-	short-chain dehydrogenase	240.2	-0.69	8.20E-06
FTL_1507	-	3-oxoacyl-ACP reductase	294.1	-0.80	1.63E-07
FTL_1508	-	-	4.4	0.13	NA
FTL_1509	-	D-alanyl-D-alanine carboxypeptidase/D-alany	361.8	-0.71	1.78E-07
FTL_1510	-	glycerol-3-phosphate transporter	5937.5	-0.53	4.83E-10
FTL_1511	-	glycerophosphoryl diester phosphodiesteras	7373.0	-0.68	1.93E-14
FTL_1512	-	hypothetical protein	93.8	0.27	2.15E-01

				LVS Δ rpS2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1513	-	ABC transporter ATP-binding protein	36.3	0.03	9.20E-01
FTL_1514	-	ABC transporter permease	9.3	0.12	6.49E-01
FTL_1515	-	ABC transporter membrane protein	1.6	0.11	NA
FTL_1516	<i>isftu2</i>	transposase	48.6	-0.06	8.10E-01
FTL_1517	-	hypothetical protein	73.2	0.56	1.30E-02
FTL_1518	-	-	164.7	0.00	9.92E-01
FTL_1519	-	-	81.3	-0.35	1.34E-01
FTL_1520	<i>upp</i>	uracil phosphoribosyltransferase	2014.1	-0.85	8.51E-10
FTL_1521	-	chitinase family 18 protein	24560.1	-0.21	1.06E-01
FTL_1522	-	2-amino-3-ketobutyrate coenzyme A ligase	5919.0	-0.74	6.02E-13
FTL_1523	<i>tdh</i>	L-threonine 3-dehydrogenase	4703.7	-0.81	9.47E-13
FTL_1524	-	serine transporter	1629.3	-0.47	3.79E-03
FTL_1525	-	2-C-methyl-D-erythritol 4-phosphate cytidylyl	971.7	0.33	2.19E-02
FTL_1526	-	cell division protein	775.0	0.16	2.09E-01
FTL_1527	<i>eno</i>	phosphopyruvate hydratase	21353.6	-0.25	5.31E-03
FTL_1528	-	major facilitator transporter	2569.8	0.34	1.70E-02
FTL_1529	-	nicotinamide mononucleotide transport (NM	93.2	0.82	4.03E-04
FTL_1530	-	-	633.0	0.05	8.32E-01
FTL_1531	<i>rumA</i>	23S rRNA 5-methyluridine methyltransferase	3473.9	0.10	4.02E-01
FTL_1532	-	hypothetical protein	1860.0	-0.68	2.42E-08
FTL_1533	-	DNA-directed RNA polymerase subunit omega	1326.5	-0.09	6.22E-01
FTL_1534	-	uridine kinase	2052.0	0.60	5.57E-09
FTL_1535	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	4575.2	0.11	3.04E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1536	-	iron-sulfur cluster insertion protein ErpA	614.9	0.07	8.00E-01
FTL_1537	<i>pnp</i>	polynucleotide phosphorylase/polyadenylase	19297.8	-0.22	1.13E-01
FTL_1538	<i>rpsO</i>	30S ribosomal protein S15	3260.7	-0.27	6.44E-03
FTL_1539	<i>ftsI</i>	penicillin binding protein (peptidoglycan synt	2379.0	-0.02	9.18E-01
FTL_1540	-	hypothetical protein	107.9	0.03	9.00E-01
FTL_1541	<i>mraW</i>	S-adenosyl-methyltransferase MraW	1166.7	-0.31	5.59E-03
FTL_1542	-	hypothetical protein	6259.2	-0.51	9.41E-10
FTL_1543	-	formamidopyrimidine-DNA glycosylase	1458.0	-0.36	1.95E-03
FTL_1544	<i>isftu1</i>	transposase	515.0	-0.01	9.72E-01
FTL_1545	-	glutamine amidotransferase subunit PdxT	404.8	-0.80	1.76E-02
FTL_1546	-	pyridoxal biosynthesis lyase PdxS	3487.4	-0.57	3.20E-07
FTL_1547	-	DNA gyrase subunit B	28628.5	-0.06	5.53E-01
FTL_1548	-	hypothetical protein	912.0	-0.38	5.61E-04
FTL_1549	-	tRNA-dihydrouridine synthase A	1180.0	-0.24	2.02E-02
FTL_1550	-	lipoprotein	1442.5	-0.49	2.38E-07
FTL_1551	-	hypothetical protein	2.8	-0.17	NA
FTL_1552	-	hypothetical protein	8629.3	-0.78	7.22E-23
FTL_1553	<i>sucC</i>	succinyl-CoA synthetase subunit beta	20098.8	-0.72	2.75E-18
FTL_1554	<i>sucD</i>	succinyl-CoA synthetase, alpha subunit	20181.7	-0.58	2.64E-07
FTL_1555	-	hypothetical protein	152.5	-0.16	4.28E-01
FTL_1556	-	hypothetical protein	725.1	0.00	9.98E-01
FTL_1557	-	hypothetical protein	79.1	-0.82	5.58E-04
FTL_1558	-	hypothetical protein	112.5	-0.94	1.34E-04

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1559	-	-	176.6	0.83	9.97E-08
FTL_1560	-	-	1.3	0.01	NA
FTL_1561	-	-	2.4	0.06	NA
FTL_1562	-	-	121.9	-0.30	1.37E-01
FTL_1563	-	-	12.0	0.05	8.73E-01
FTL_1564	-	-	4.3	0.14	NA
FTL_1565	-	-	45.3	0.15	5.79E-01
FTL_1566	-	CutC family protein	610.6	-0.43	1.56E-04
FTL_1567	-	major facilitator transporter	190.2	0.45	1.95E-03
FTL_1568	-	LysR family transcriptional regulator	292.2	0.02	9.28E-01
FTL_1569	-	phosphoglycolate phosphatase	424.8	-0.27	3.97E-02
FTL_1570	-	phospholipase D	1120.2	-0.46	8.97E-06
FTL_1571	-	thioredoxin reductase	4908.4	-0.60	7.30E-15
FTL_1572	<i>isftu2</i>	transposase	44.2	-0.05	8.66E-01
FTL_1573	-	major facilitator transporter	11.3	0.81	4.71E-02
FTL_1574	-	hypothetical protein	2.6	0.14	NA
FTL_1575	-	hypothetical protein	230.4	0.25	1.54E-01
FTL_1576	-	DNA mismatch repair protein	1014.7	-0.03	8.52E-01
FTL_1577	-	hypothetical protein	396.0	-0.35	1.17E-01
FTL_1578	-	hypothetical protein	263.8	-0.37	9.70E-03
FTL_1579	-	hypothetical protein	8104.2	-0.07	5.66E-01
FTL_1580	-	hypothetical protein	1389.6	-0.17	1.92E-01
FTL_1581	-	lipoprotein	857.2	-0.09	6.19E-01

				LVS Δ rrpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1582	<i>potF</i>	putrescine-binding periplasmic protein	2451.5	-1.03	2.52E-30
FTL_1583	<i>gadC</i>	glutamate:gamma-aminobutyric acid antiporter	2548.1	-0.06	4.90E-01
FTL_1584	<i>perM</i>	PerM family protein	1647.6	-0.10	4.86E-01
FTL_1585	-	single-stranded-DNA-specific exonuclease	2203.2	0.38	3.02E-06
FTL_1586	-	biotin--acetyl-CoA-carboxylase ligase	589.9	0.49	3.63E-04
FTL_1587	-	lysyl-tRNA synthetase	816.8	-0.06	6.80E-01
FTL_1588	-	mechanosensitive ion channel protein	27.2	0.67	4.57E-02
FTL_1589	<i>isftu2</i>	transposase	56.3	0.00	9.88E-01
FTL_1590	-	hypothetical protein	2956.7	-0.18	1.66E-01
FTL_1591	<i>accC</i>	Acetyl-CoA carboxylase, biotin carboxylase subunit	21034.4	-0.12	2.40E-01
FTL_1592	<i>accB</i>	Acetyl-CoA carboxylase, biotin carboxyl carrier protein	3882.7	-0.25	8.45E-02
FTL_1593	<i>aroD</i>	3-dehydroquinate dehydratase	611.2	-0.38	3.71E-03
FTL_1594	<i>apaH</i>	diadenosine tetraphosphatase	1612.7	-0.14	3.91E-01
FTL_1595	<i>ksgA</i>	dimethyladenosine transferase	229.8	0.28	1.06E-01
FTL_1596	<i>surA</i>	peptidyl-prolyl cis-trans isomerase	931.8	0.63	1.07E-07
FTL_1597	-	organic solvent tolerance protein	4186.4	0.17	1.28E-01
FTL_1598	<i>argS</i>	arginyl-tRNA synthetase	8775.6	-0.56	2.32E-15
FTL_1599	-	hypothetical protein	261.6	0.25	1.95E-01
FTL_1600	-	periplasmic L-asparaginase II	145.5	0.56	1.26E-03
FTL_1601	-	tRNA/rRNA methyltransferase	1405.7	-0.12	2.93E-01
FTL_1602	-	delta-aminolevulinic acid dehydratase	6399.3	-0.34	2.41E-04
FTL_1603	-	RNA-binding protein	261.1	-0.35	7.52E-02
FTL_1604	-	DNA polymerase III, delta prime subunit	2771.5	-0.04	7.15E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1605	-	putative periplasmic protease	6424.8	-0.68	1.08E-16
FTL_1606	<i>sspA</i>	stringent starvation protein A	2895.8	-0.48	6.30E-07
FTL_1607	-	anaerobic sulfite reductase subunit	459.8	0.03	8.97E-01
FTL_1608	-	hypothetical protein	791.8	-0.79	5.03E-10
FTL_1609	-	dolichyl-phosphate-mannose-protein manno	2731.9	-0.38	7.26E-04
FTL_1610	<i>isftu1</i>	transposase	543.1	0.16	3.50E-01
FTL_1611	-	glycosyl transferase family protein	3546.6	-0.40	7.93E-06
FTL_1612	<i>nadX</i>	hypothetical protein, N-acetylhexosamine de	400.5	0.00	9.85E-01
FTL_1613	<i>ftsW</i>	cell division protein FtsW	812.4	0.04	7.97E-01
FTL_1614	<i>murD</i>	UDP-N-acetylmuramoylalanine--D-glutamate	1161.6	-0.22	2.72E-02
FTL_1615	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-tr	1778.5	-0.83	7.70E-19
FTL_1616	<i>pckA</i>	phosphoenolpyruvate carboxykinase	4030.8	-0.22	2.72E-03
FTL_1617	<i>glnS</i>	glutaminyl-tRNA synthetase	5415.7	-0.34	2.94E-06
FTL_1618	-	hypothetical protein	51.6	0.16	5.24E-01
FTL_1619	-	hypothetical protein	4.2	-0.03	NA
FTL_1620	-	proton-dependent oligopeptide transport (P	349.0	-0.53	1.43E-04
FTL_1621	-	ABC transporter ATP-binding	3443.3	-0.51	3.25E-11
FTL_1622	-	multidrug transporter (tetracycline resistanc	1113.4	-0.53	1.15E-06
FTL_1623	-	hypothetical protein	920.7	-0.24	1.16E-01
FTL_1624	-	major facilitator transporter	98.3	0.27	1.92E-01
FTL_1625	-	NADH dehydrogenase subunit	26.7	-0.01	9.80E-01
FTL_1626	-	rRNA methylase	0.1	0.00	NA
FTL_1627	<i>isftu1</i>	transposase	527.5	0.10	6.08E-01

				LVS Δ rpS2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1628	-	hypothetical protein	38.0	0.23	3.77E-01
FTL_1629	-	hypothetical protein	58.0	0.12	6.44E-01
FTL_1630	<i>isftu1</i>	transposase	534.8	0.05	7.92E-01
FTL_1631	-	hypothetical protein	22.5	0.58	7.06E-02
FTL_1632	-	hypothetical protein	6.4	-0.08	7.15E-01
FTL_1633	-	hypothetical protein	90.0	0.13	5.82E-01
FTL_1634	-	LysR family transcriptional regulator	371.6	-0.28	7.81E-02
FTL_1635	-	chitinase, fragment	370.2	0.15	2.65E-01
FTL_1636	-	hypothetical protein	2.7	-0.04	NA
FTL_1637	-	lipoprotein	2958.7	-0.45	1.73E-05
FTL_1638	-	3-demethylubiquinone-9 3-methyltransferase	949.4	-0.35	2.72E-03
FTL_1639	-	hypothetical protein	557.8	-0.05	7.91E-01
FTL_1640	-	amino acid transporter protein, fragment	2794.9	-0.95	1.57E-20
FTL_1641	-	hypothetical protein	58.7	0.25	3.69E-01
FTL_1642	-	hypothetical protein	0.1	0.02	NA
FTL_1643	<i>isftu1</i>	transposase	537.9	0.08	6.65E-01
FTL_1644	-	glycerol kinase	5752.7	-0.72	1.53E-11
FTL_1645	<i>ansP</i>	major facilitator transporter, asparagine tran	1404.8	-1.03	7.22E-14
FTL_1646	-	hypothetical protein	406.3	-0.98	1.14E-12
FTL_1647	-	major facilitator transporter	27.1	0.16	5.72E-01
FTL_1648	-	oligopeptide transporter, subunit D, ABC tran	31.1	0.07	8.12E-01
FTL_1649	-	-	17.2	-0.24	3.58E-01
FTL_1650	-	-	11.0	-0.10	6.64E-01

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1651	-	-	16.3	0.10	7.10E-01
FTL_1652	-	-	2.0	0.01	NA
FTL_1653	-	peptide transport system substrate-binding p	7.9	0.22	3.87E-01
FTL_1654	-	hypothetical protein	38.9	0.88	5.84E-03
FTL_1655	<i>isftu2</i>	transposase	49.3	0.08	7.72E-01
FTL_1656	<i>uvrD</i>	DNA helicase II	3340.0	-0.58	6.47E-10
FTL_1657	<i>ftsY</i>	signal recognition particle receptor FtsY	668.5	-0.50	6.56E-05
FTL_1658	<i>fimV</i>	hypothetical protein	3369.0	-0.32	7.27E-04
FTL_1659	<i>prfC</i>	peptide chain release factor 3	4206.5	-0.33	8.10E-04
FTL_1660	<i>tmk</i>	thymidylate kinase	628.7	-0.45	1.66E-05
FTL_1661	-	nucleoside permease NUP family protein	1357.8	0.12	3.32E-01
FTL_1662	<i>nupC1</i>	nucleoside permease NUP family protein	929.9	0.26	2.72E-02
FTL_1663	<i>deoC</i>	deoxyribose-phosphate aldolase	916.2	0.16	2.07E-01
FTL_1664	<i>deoB</i>	phosphopentomutase	4051.5	-0.05	6.22E-01
FTL_1665	-	pantothenate kinase	1653.5	0.10	4.41E-01
FTL_1666	-	DNA polymerase I	5696.6	0.11	2.12E-01
FTL_1667	<i>lpxK</i>	tetraacyldisaccharide 4'-kinase	797.4	0.77	1.78E-12
FTL_1668	<i>msbA</i>	lipid A transport protein ABC transporter ATP	7842.9	-0.17	5.01E-02
FTL_1669	-	tRNA CCA-pyrophosphorylase	365.6	-0.33	1.55E-02
FTL_1670	<i>dsbB</i>	disulfide bond formation protein	332.6	-0.45	1.47E-02
FTL_1671	-	RND efflux transporter	4513.6	-0.61	7.26E-13
FTL_1672	-	AcrB/AcrD/AcrF family transporter	6018.4	-0.45	5.37E-06
FTL_1673	-	major facilitator transporter	2211.6	-0.51	1.86E-09

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1674	-	hypothetical protein	41.5	0.03	9.31E-01
FTL_1675	-	-	0.2	0.02	NA
FTL_1676	-	-	0.8	0.09	NA
FTL_1677	-	-	10.8	0.26	2.93E-01
FTL_1678	-	hypothetical protein	12627.2	0.45	1.05E-04
FTL_1679	-	transposase	2.3	0.35	NA
FTL_1680	<i>isftu2</i>	transposase	56.9	0.05	8.61E-01
FTL_1681	<i>isftu1</i>	transposase	509.6	0.13	4.27E-01
FTL_1682	-	hypothetical protein	2.1	0.07	NA
FTL_1683	<i>cysS</i>	cysteinyl-tRNA synthetase	4020.0	-0.58	2.41E-13
FTL_1684	-	N5-glutamine S-adenosyl-L-methionine-depe	2906.6	-0.24	6.18E-03
FTL_1685	-	major facilitator transporter	1706.6	-0.73	9.85E-07
FTL_1686	-	acetyltransferase	396.8	0.06	7.18E-01
FTL_1687	<i>isftu1</i>	transposase	538.0	0.06	7.44E-01
FTL_1688	-	-	12.4	0.23	3.59E-01
FTL_1689	-	hypothetical protein	983.1	0.20	1.34E-01
FTL_1690	-	hypothetical protein	73.9	0.75	1.74E-03
FTL_1691	-	hypothetical protein	33.4	0.65	3.15E-02
FTL_1692	-	hypothetical protein	119.8	0.75	2.19E-04
FTL_1693	-	hypothetical protein	83.8	0.29	2.00E-01
FTL_1694	-	hypothetical protein	181.0	0.09	6.52E-01
FTL_1695	-	hypothetical protein	134.6	0.61	3.00E-04
FTL_1696	-	hypothetical protein	187.3	0.47	1.48E-02

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1697	-	metal ion transporter	3.3	0.06	NA
FTL_1698	-	hypothetical protein	3.3	0.10	NA
FTL_1699	-	hypothetical protein	680.6	-0.09	4.82E-01
FTL_1700	-	Sodium/proline permease	2289.2	-0.87	2.62E-20
FTL_1701	<i>glpX</i>	fructose 1,6-bisphosphatase II	5178.5	-0.54	4.13E-10
FTL_1702	-	hypothetical protein	1313.4	0.16	1.71E-01
FTL_1703	<i>lysP</i>	lysine:H ⁺ symporter	6924.0	-0.35	6.91E-05
FTL_1704	-	hypothetical protein	549.0	-0.61	2.15E-07
FTL_1705	<i>ftsK</i>	cell division protein	3439.1	-0.01	9.41E-01
FTL_1706	<i>lolA</i>	lipoprotein releasing system subunit A, outer	378.2	-0.34	6.60E-02
FTL_1707	-	hypothetical protein	744.3	-0.26	5.90E-02
FTL_1708	<i>tkrH</i>	potassium uptake protein	2093.7	0.75	4.90E-19
FTL_1709	-	hypothetical protein	1244.6	-0.41	3.01E-03
FTL_1710	-	ProP osmoprotectant transporter, fragment	2270.5	-0.18	2.02E-01
FTL_1711	-	HsdR protein, fragment	3.8	0.15	NA
FTL_1712	-	HsdR protein, fragment	8.0	0.15	5.50E-01
FTL_1713	<i>isftu1</i>	transposase	529.5	0.12	5.19E-01
FTL_1714	<i>groEL</i>	chaperonin GroEL	65234.3	-0.50	1.32E-03
FTL_1715	<i>groES</i>	co-chaperonin GroES	3444.0	-0.12	6.72E-01
FTL_1716	-	hypothetical protein	38.2	-0.39	1.52E-01
FTL_1717	-	hypothetical protein	1727.3	-0.53	4.51E-06
FTL_1718	<i>isftu1</i>	transposase	547.7	0.02	9.24E-01
FTL_1719	-	hypothetical protein	1.5	-0.08	NA

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1720	-	modification methylase	445.4	0.40	1.72E-03
FTL_1721	<i>prfA</i>	peptide chain release factor 1	2081.9	-0.48	4.87E-04
FTL_1722	-	glutamyl-tRNA reductase	2671.6	0.05	6.54E-01
FTL_1723	-	hypothetical protein	2608.1	-0.78	1.11E-08
FTL_1724	-	lipoprotein	3810.7	-0.43	3.02E-06
FTL_1725	-	efflux protein	1017.4	0.12	3.75E-01
FTL_1726	<i>parE</i>	DNA topoisomerase IV subunit B	3677.4	-0.34	2.62E-05
FTL_1727	<i>ampD</i>	N-acetyl-anhydromuranmyl-L-alanine amidase	420.6	-0.50	1.58E-03
FTL_1728	-	PAP2 family protein	539.5	-0.27	1.36E-01
FTL_1729	<i>nudH</i>	dinucleoside polyphosphate hydrolase	1259.6	-0.22	7.78E-02
FTL_1730	-	hypothetical protein	6.6	1.83	7.20E-03
FTL_1731	-	licB-like transmembrane protein	206.9	-0.35	8.64E-02
FTL_1732	-	acid phosphatase	448.1	-0.37	9.81E-03
FTL_1733	-	oxidoreductase iron/ascorbate family protein	2694.9	-0.48	7.51E-11
FTL_1734	-	integrase/recombinase	1414.1	0.79	1.51E-16
FTL_1735	<i>rplS</i>	50S ribosomal protein L19	10166.8	0.49	5.26E-05
FTL_1736	<i>trmD</i>	tRNA (guanine-N(1)-)-methyltransferase	12006.3	0.33	9.38E-03
FTL_1737	<i>rimM</i>	16S rRNA-processing protein RimM	4771.2	0.04	8.30E-01
FTL_1738	<i>rpsP</i>	30S ribosomal protein S16	7060.1	-0.55	4.78E-04
FTL_1739	-	S-adenosylmethionine synthetase	3593.4	-0.68	3.89E-11
FTL_1740	-	fatty acid desaturase	35710.3	-1.09	9.90E-36
FTL_1741	-	putative DNA-binding/iron metalloprotein/A	2075.4	-0.18	6.63E-02
FTL_1742	-	hypothetical protein	124.2	0.14	5.98E-01

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1743	-	DNA-directed RNA polymerase subunit beta	102363.2	-0.06	5.45E-01
FTL_1744	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	66676.5	0.24	1.01E-03
FTL_1745	<i>rplL</i>	50S ribosomal protein L7/L12	11510.0	-0.65	5.79E-04
FTL_1746	<i>rplI</i>	50S ribosomal protein L10	23216.4	-0.01	9.35E-01
FTL_1747	<i>rplA</i>	50S ribosomal protein L1	31199.0	-0.21	1.10E-01
FTL_1748	<i>rplK</i>	50S ribosomal protein L11	22659.5	-0.54	7.41E-06
FTL_1749	-	transcription antitermination protein nusG	1989.9	-0.71	9.87E-05
FTL_1750	<i>secE</i>	preprotein translocase subunit SecE	3678.2	-0.13	3.34E-01
FTL_1751	-	elongation factor Tu	265629.0	-0.49	4.89E-07
FTL_1752	-	helicase	79.3	0.27	2.03E-01
FTL_1753	-	ion channel protein, fragment	241.5	-0.19	3.31E-01
FTL_1754	-	hypothetical protein	351.3	0.59	7.02E-04
FTL_1755	<i>glpF</i>	glycerol uptake facilitator protein	1977.1	-0.16	2.19E-01
FTL_1756	<i>glpD</i>	anaerobic glycerol-3-phosphate dehydrogenase	5771.0	-0.26	1.19E-03
FTL_1757	<i>isftu1</i>	transposase	520.1	0.19	2.36E-01
FTL_1758	-	hypothetical protein	14.7	-0.03	9.02E-01
FTL_1759	-	hypothetical protein	116.1	-0.33	1.23E-01
FTL_1760	-	hypothetical protein	4.9	-0.13	NA
FTL_1761	-	hypothetical protein	1.1	-0.03	NA
FTL_1762	<i>qseC</i>	sensor histidine kinase	898.3	-0.32	8.04E-03
FTL_1763	-	hypothetical protein	266.0	-0.33	6.09E-02
FTL_1764	-	-	103.8	-0.24	2.42E-01
FTL_1765	-	cytochrome oxidase bd-II subunit II	133.1	-0.35	9.34E-02

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1766	-	hypothetical protein	14.8	-0.37	2.00E-01
FTL_1767	-	-	2.6	-0.09	NA
FTL_1768	-	-	0.5	-0.03	NA
FTL_1769	-	-	8.0	0.10	6.65E-01
FTL_1770	-	Type IV pili nucleotide-binding protein	32.9	0.29	2.71E-01
FTL_1771	-	twitching motility protein PilT	324.1	0.58	3.10E-04
FTL_1772	-	aconitate hydratase	48976.9	0.07	5.54E-01
FTL_1773	-	hypothetical protein	1095.2	-0.60	5.63E-06
FTL_1774	-	hypothetical protein	20.0	0.12	6.43E-01
FTL_1775	-	oxygen-independent coproporphyrinogen III	709.7	-0.66	2.19E-07
FTL_1776	-	hypothetical protein	393.0	0.49	1.99E-03
FTL_1777	-	-	62.5	0.94	2.40E-04
FTL_1778	-	-	207.4	1.66	8.16E-23
FTL_1779	<i>secG</i>	preprotein translocase subunit SecG	924.0	0.09	6.72E-01
FTL_1780	-	triosephosphate isomerase	4777.6	0.00	9.76E-01
FTL_1781	<i>glmM</i>	phosphoglucosamine mutase	5690.3	0.03	8.52E-01
FTL_1782	<i>apt</i>	adenine phosphoribosyltransferase	3456.7	-0.25	9.04E-03
FTL_1783	<i>sucB</i>	dihydrolipoamide succinyltransferase compo	25161.8	-0.38	1.24E-06
FTL_1784	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 componen	27205.1	-0.26	1.82E-04
FTL_1785	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	16883.0	-0.18	3.11E-02
FTL_1786	-	succinate dehydrogenase, catalytic and NAD	29071.8	-0.15	2.30E-01
FTL_1787	-	succinate dehydrogenase hydrophobic mem	5205.3	-0.02	8.75E-01
FTL_1788	-	succinate dehydrogenase, cytochrome b556	3474.0	-0.37	4.22E-05

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1789	-	citrate synthase	40094.3	0.47	2.50E-05
FTL_1790	<i>ampG</i>	major facilitator superfamily transporter	8086.1	-0.96	5.31E-13
FTL_1791	-	superoxide dismutase	7993.5	-0.29	2.70E-03
FTL_1792	-	glutaredoxin-like protein	1422.0	-0.87	2.68E-03
FTL_1793	-	hypothetical protein	3592.6	-0.45	6.17E-06
FTL_1794	<i>atpC</i>	F0F1 ATP synthase subunit epsilon	4626.4	-0.13	3.50E-01
FTL_1795	-	F0F1 ATP synthase subunit beta	24052.7	-0.34	1.92E-03
FTL_1796	-	F0F1 ATP synthase subunit gamma	8164.2	-0.05	7.16E-01
FTL_1797	-	F0F1 ATP synthase subunit alpha	23318.4	-0.15	1.44E-01
FTL_1798	-	F0F1 ATP synthase subunit delta	3732.3	-0.67	4.30E-17
FTL_1799	-	F0F1 ATP synthase subunit B	7437.5	-0.69	7.41E-07
FTL_1800	-	F0F1 ATP synthase subunit C	8798.5	-0.50	3.03E-05
FTL_1801	-	F0F1 ATP synthase subunit A	4603.0	0.16	2.40E-01
FTL_1802	-	hypothetical protein	83.7	-0.47	6.57E-02
FTL_1803	<i>ileP</i>	major facilitator transporter, isoleucine trans	2272.9	0.20	2.75E-02
FTL_1804	-	ribosomal large subunit pseudouridine synth	825.2	0.10	4.45E-01
FTL_1805	-	ATPase	872.8	0.82	3.09E-10
FTL_1806	<i>fptD</i>	major facilitator transporter, member of Fpt	1081.5	0.49	1.21E-08
FTL_1807	<i>hisS</i>	histidyl-tRNA synthetase	3953.6	0.44	2.55E-05
FTL_1808	-	ribosome-binding factor A	2819.1	0.29	7.94E-03
FTL_1809	<i>infB</i>	translation initiation factor IF-2	39326.3	-0.04	7.97E-01
FTL_1810	<i>nusA</i>	transcription elongation factor NusA	10651.5	-0.23	2.20E-01
FTL_1811	-	hypothetical protein	1687.6	0.54	1.76E-05

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1812	<i>hemE</i>	uroporphyrinogen decarboxylase	775.3	-0.08	6.47E-01
FTL_1813	-	-	0.1	0.00	NA
FTL_1814	-	-	78.5	0.62	2.68E-03
FTL_1815	<i>isftu1</i>	transposase	551.7	0.09	6.88E-01
FTL_1816	-	-	174.6	0.22	2.39E-01
FTL_1817	-	NADH dehydrogenase I subunit N	7348.1	-0.09	4.99E-01
FTL_1818	-	NADH dehydrogenase I subunit M	5793.7	-0.53	3.03E-10
FTL_1819	-	NADH dehydrogenase I subunit L	9614.0	-0.64	5.45E-11
FTL_1820	-	NADH dehydrogenase I subunit K	536.1	-0.73	8.87E-11
FTL_1821	-	NADH dehydrogenase I subunit J	1250.7	-0.38	1.12E-03
FTL_1822	-	NADH dehydrogenase subunit I	1208.4	-0.38	3.44E-03
FTL_1823	-	NADH dehydrogenase I subunit H	6491.3	-0.10	4.34E-01
FTL_1824	-	NADH dehydrogenase subunit G	19792.1	-0.09	3.51E-01
FTL_1825	-	NADH dehydrogenase I subunit F	6366.8	-1.02	2.15E-12
FTL_1826	-	NADH dehydrogenase I subunit E	1723.9	-0.48	2.29E-03
FTL_1827	-	NADH dehydrogenase subunit D	5808.9	-0.52	9.55E-05
FTL_1828	-	NADH dehydrogenase I	4955.8	-0.24	1.46E-02
FTL_1829	-	NADH dehydrogenase subunit B	5194.6	-0.48	2.62E-03
FTL_1830	-	NADH dehydrogenase I subunit A	920.6	-0.35	1.79E-01
FTL_1831	<i>fur</i>	ferric uptake regulation protein	647.3	-0.56	1.79E-05
FTL_1832	<i>fsIA</i>	hypothetical protein	4494.7	1.36	1.31E-26
FTL_1833	<i>fsIB</i>	hypothetical protein	692.5	1.74	4.67E-20
FTL_1834	<i>fsIC</i>	diaminopimelate decarboxylase	801.9	1.51	4.03E-27

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1835	<i>fsID</i>	hypothetical protein	593.0	1.39	8.90E-30
FTL_1836	<i>fsIE</i>	hypothetical protein	128.2	1.06	6.38E-09
FTL_1837	<i>fsIF</i>	hypothetical protein	18.5	0.61	6.88E-02
FTL_1838	-	hypothetical protein	5.2	0.03	NA
FTL_1839	-	lipase/acyltransferase	0.9	0.07	NA
FTL_1840	-	hypothetical protein	1124.3	-0.57	9.66E-05
FTL_1841	<i>gatB</i>	aspartyl/glutamyl-tRNA amidotransferase su	3990.9	-0.30	9.60E-04
FTL_1842	<i>gatA</i>	aspartyl/glutamyl-tRNA amidotransferase su	5156.5	-0.28	2.60E-04
FTL_1843	-	Glu-tRNA ^{Gln} amidotransferase C subunit	354.7	-0.41	3.82E-03
FTL_1844	-	secretion protein	33.1	0.43	1.17E-01
FTL_1845	-	RND efflux membrane fusion protein	31.6	0.10	7.19E-01
FTL_1846	-	hypothetical protein	14.3	0.17	5.35E-01
FTL_1847	-	toxin secretion ABC transporter ATP-binding	88.1	0.17	4.68E-01
FTL_1848	-	hypothetical protein	514.0	-0.31	3.96E-02
FTL_1849	-	hypothetical protein	600.4	0.27	7.08E-02
FTL_1850	<i>purB</i>	adenylosuccinate lyase	3891.9	-0.46	4.69E-09
FTL_1851	<i>isftu2</i>	transposase	55.6	0.04	8.90E-01
FTL_1852	-	hypothetical protein	970.1	-0.76	5.84E-10
FTL_1853	-	lipoprotein	21.2	0.22	4.21E-01
FTL_1854	-	hypothetical protein	645.2	0.11	5.54E-01
FTL_1855	-	-	51.1	0.10	7.12E-01
FTL_1856	-	-	0.9	0.03	NA
FTL_1857	-	-	10.3	1.07	1.94E-02

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1858	-	-	40.6	0.89	2.47E-03
FTL_1859	-	-	40.2	0.13	6.30E-01
FTL_1860	<i>purL</i>	phosphoribosylformylglycinamide synthase	11796.9	0.10	3.62E-01
FTL_1861	<i>purF</i>	amidophosphoribosyltransferase	4398.9	-0.28	6.08E-03
FTL_1862	-	hypothetical protein	20.7	-0.20	4.59E-01
FTL_1863	-	glutamate decarboxylase	640.6	-0.33	7.09E-03
FTL_1864	-	hypothetical protein	502.7	-0.04	7.65E-01
FTL_1865	-	outer membrane protein tolC	4281.4	-0.01	9.21E-01
FTL_1866	-	protein-L-isoaspartate O-methyltransferase	4145.7	-0.22	1.96E-02
FTL_1867	-	protease yegQ	6253.5	-0.65	4.62E-16
FTL_1868	-	multidrug resistance protein, membrane loca	5489.9	-0.51	7.79E-11
FTL_1869	-	Na ⁺ /H ⁺ antiporter	3778.5	-0.68	1.35E-16
FTL_1870	-	-	11.0	0.02	9.41E-01
FTL_1871	-	-	63.1	0.72	6.34E-03
FTL_1872	-	-	110.0	0.84	5.30E-05
FTL_1873	-	amino acid transporter	2397.5	0.56	6.67E-15
FTL_1874	<i>obgE</i>	GTPase ObgE	3591.4	0.20	1.87E-02
FTL_1875	-	aromatic amino acid HAAP transporter	583.3	-0.46	5.85E-04
FTL_1876	-	outer membrane associated protein, fragme	332.6	0.83	2.29E-11
FTL_1877	-	-	23.5	0.43	1.54E-01
FTL_1878	-	two component sensor protein kdpD	242.0	0.01	9.63E-01
FTL_1879	-	osmosensitive K ⁺ channel His kinase sensor	2982.6	-0.17	1.07E-01
FTL_1880	-	potassium-transporting ATPase C chain	153.0	-0.88	7.07E-05

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1881	-	haloacid dehalogenase-like hydrolase	879.2	-0.64	2.38E-07
FTL_1882	-	potassium-transporting ATPase B chain	4046.0	-0.91	7.79E-19
FTL_1883	-	potassium-transporting ATPase subunit A	6927.7	-1.14	1.24E-44
FTL_1884	-	hypothetical protein	11.2	0.19	4.72E-01
FTL_1885	<i>isftu2</i>	transposase	80.9	0.32	1.51E-01
FTL_1886	<i>isftu1</i>	transposase	544.2	0.07	6.96E-01
FTL_1887	-	3-isopropylmalate dehydrogenase	2.2	0.00	NA
FTL_1888	<i>leuD</i>	isopropylmalate isomerase small subunit	17.1	-0.06	8.12E-01
FTL_1889	-	isopropylmalate isomerase large subunit	33.6	0.20	4.67E-01
FTL_1890	-	-	0.3	0.01	NA
FTL_1891	<i>isftu1</i>	transposase	536.8	0.05	7.75E-01
FTL_1892	-	hypothetical protein	7084.9	0.03	8.30E-01
FTL_1893	-	-	0.1	-0.01	NA
FTL_1894	-	transposase	53.9	0.13	6.21E-01
FTL_1895	-	-	53.3	-0.88	7.02E-04
FTL_1896	-	hypothetical protein	767.8	-0.96	3.01E-20
FTL_1897	-	outer membrane lipoprotein	509.0	-0.32	6.66E-03
FTL_1898	-	DNA polymerase III subunit delta	888.3	-0.22	6.45E-02
FTL_1899	-	glutamine synthetase	12205.4	-0.19	3.48E-02
FTL_1900	-	L-glutaminase	4948.7	0.06	6.19E-01
FTL_1901	-	hypothetical protein	412.8	0.14	6.00E-01
FTL_1902	-	hypothetical protein	1820.0	-0.84	3.18E-19
FTL_1903	-	lysyl-tRNA synthetase	5540.6	-0.20	1.64E-02

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1904	-	peptide chain release factor 2	1283.5	-0.26	3.79E-02
FTL_1905	-	DNA polymerase III subunit gamma and tau	1935.3	-0.23	2.43E-02
FTL_1906	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylgluco	18010.8	0.05	7.29E-01
FTL_1907	-	cell division protein FtsZ	33625.6	-0.27	4.23E-02
FTL_1908	-	cell division protein FtsA	9890.9	0.14	2.00E-01
FTL_1909	-	cell division protein FtsQ	898.1	1.19	6.27E-39
FTL_1910	-	D-alanyl-alanine synthetase A	4682.1	0.30	1.37E-04
FTL_1911	<i>tadA</i>	zinc-binding domain-containing protein (likel	587.1	-0.04	8.38E-01
FTL_1912	<i>rpsA</i>	30S ribosomal protein S1	89670.1	-0.51	1.22E-05
FTL_1913	-	Sua5/YciO/YrdC family protein	422.0	-0.33	2.50E-02
FTL_1914	<i>ripA</i>	hypothetical protein	10434.5	-0.41	9.51E-05
FTL_1915	-	putative acyltransferase	600.4	-0.26	6.73E-02
FTL_1916	-	competence-like protein	211.5	0.55	1.15E-03
FTL_1917	-	30S ribosomal protein S6	1168.3	-0.98	3.69E-13
FTL_1918	-	30S ribosomal protein S6 modification protei	80.1	-0.84	4.77E-04
FTL_1919	-	-	17.2	-0.28	3.02E-01
FTL_1920	-	-	4.4	0.06	NA
FTL_1921	-	ABC transporter ATP-binding protein	214.4	-1.24	1.94E-11
FTL_1922	-	YggT family protein	253.6	-1.15	6.30E-13
FTL_1923	-	hypothetical protein	3216.1	-1.23	2.52E-42
FTL_1924	-	-	4.8	0.18	NA
FTL_1925	<i>isftu1</i>	transposase	537.7	-0.02	9.21E-01
FTL_1926	<i>isftu2</i>	transposase	44.9	-0.23	3.71E-01

				LVS Δ rpsU2 pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1927	-	-	19.5	0.18	5.17E-01
FTL_1928	-	-	23.4	0.18	5.29E-01
FTL_1929	<i>purH</i>	bifunctional phosphoribosylaminoimidazole	4316.5	-0.59	1.00E-07
FTL_1930	<i>purA</i>	adenylosuccinate synthetase	7115.6	-0.94	1.00E-30
FTL_1931	-	hypoxanthine-guanine phosphoribosyltransf	2036.9	-0.83	5.03E-16
FTL_1932	-	-	13.6	-1.25	1.39E-02
FTL_1933	-	-	998.4	-0.30	5.10E-03
FTL_1934	-	ABC transporter permease	1432.6	-0.28	9.96E-03
FTL_1935	-	ABC transporter ATP-binding protein	1271.3	-0.67	1.32E-07
FTL_1936	-	periplasmic solute binding family protein	7922.4	-0.80	1.76E-24
FTL_1937	-	-	21.0	0.07	8.12E-01
FTL_1938	-	-	944.0	-0.31	1.28E-02
FTL_1939	-	outer membrane lipoprotein	350.6	-0.20	2.65E-01
FTL_1940	-	trp repressor binding protein	974.9	0.23	1.12E-01
FTL_1941	-	tRNA processing ribonuclease BN	601.3	-1.02	2.22E-18
FTL_1942	-	transporter	440.8	-0.04	7.83E-01
FTL_1943	-	primosomal protein N'	622.8	-0.10	4.74E-01
FTL_1944	<i>isftu1</i>	transposase	511.7	0.16	3.77E-01
FTL_1945	-	hypothetical protein	21.9	-0.03	9.13E-01
FTL_1946	-	hypothetical protein	795.6	-0.68	1.65E-06
FTL_1947	-	putative ABC transporter ATP-binding protei	9297.7	-0.69	3.05E-13
FTL_1948	-	major facilitator transporter	368.0	-0.26	7.72E-02
FTL_1949	-	hypothetical protein	1.3	0.04	NA

				LVS Δ <i>rpsU2</i> pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_1950	-	hypothetical protein	308.5	-0.17	3.05E-01
FTL_1951	-	amino acid transporter LysE	6.0	0.25	3.04E-01
FTL_1952	-	-	30.2	0.06	8.38E-01
FTL_1953	-	-	6.0	0.07	7.59E-01
FTL_1954	-	hypothetical protein	4.1	0.08	NA
FTL_1955	-	-	39.2	0.76	1.75E-02
FTL_1956	<i>pepN</i>	aminopeptidase N	5477.8	-0.38	4.09E-04
FTL_1957	-	heat shock protein	2392.5	-0.59	6.03E-02
FTL_1958	-	bifunctional indole-3-glycerol phosphate syn	2656.3	-0.12	3.00E-01
FTL_1959	-	hypothetical protein	1.7	0.06	NA
FTL_1960	-	peptide methionine sulfoxide reductase Msr	768.0	-0.04	7.85E-01
FTL_1961	-	hypothetical protein	370.0	-0.79	4.06E-08
FTL_1962	-	hypothetical protein	289.0	-0.73	6.72E-07
FTL_1963	-	hypothetical protein	145.6	0.09	6.85E-01
FTL_1964	-	-	3418.6	0.62	5.19E-11
FTL_1965	-	-	3790.4	0.52	2.83E-09
FTL_1966	-	anthranilate synthase component I	10703.6	0.38	4.18E-07
FTL_1967	-	trp operon repressor	368.4	0.32	9.51E-02
FTL_1968	-	ribonuclease G	178.2	-0.20	3.16E-01
FTL_R0001	<i>ssrA</i>	-	498240.7	0.29	1.92E-02
FTL_R0002	-	-	25.0	-0.08	7.67E-01
FTL_R0003	-	16S ribosomal RNA	1029861.4	-0.25	3.17E-01
FTL_R0004	tRNA-Ile1	Ile tRNA	0.3	0.00	NA

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_R0005	tRNA-Ala1	Ala tRNA	0.5	-0.03	NA
FTL_R0006	-	23S ribosomal RNA	218578.4	-0.46	1.12E-01
FTL_R0007	-	5S ribosomal RNA	11.1	-0.29	1.77E-01
FTL_R0008	tRNA-Gln1	Gln tRNA	1.3	0.04	NA
FTL_R0009	tRNA-Glu1	Glu tRNA	3.3	-0.07	NA
FTL_R0010	<i>rnpB</i>	-	52098.8	0.55	9.07E-05
FTL_R0013	tRNA-Ser1	Ser tRNA	1.1	-0.08	NA
FTL_R0014	tRNA-Ser2	Ser tRNA	20.2	-0.10	7.09E-01
FTL_R0015	tRNA-Val1	Val tRNA	0.1	0.00	NA
FTL_R0016	-	16S ribosomal RNA	1029547.8	-0.25	3.18E-01
FTL_R0017	tRNA-Ile2	Ile tRNA	0.2	0.00	NA
FTL_R0018	tRNA-Ala2	Ala tRNA	1.3	-0.11	NA
FTL_R0019	-	23S ribosomal RNA	218416.3	-0.46	1.13E-01
FTL_R0020	-	5S ribosomal RNA	9.4	-1.17	2.50E-02
FTL_R0022	tRNA-Leu1	Leu tRNA	0.7	0.05	NA
FTL_R0024	tRNA-Gly1	Gly tRNA	0.3	-0.01	NA
FTL_R0025	tRNA-Cys1	Cys tRNA	0.4	-0.03	NA
FTL_R0026	tRNA-Leu2	Leu tRNA	1.5	0.06	NA
FTL_R0027	-	-	2.9	-0.11	NA
FTL_R0028	-	16S ribosomal RNA	1029690.3	-0.25	3.16E-01
FTL_R0029	tRNA-Ile3	Ile tRNA	0.4	-0.02	NA
FTL_R0030	tRNA-Ala3	Ala tRNA	1.0	-0.05	NA
FTL_R0031	-	23S ribosomal RNA	218290.3	-0.47	1.08E-01

				LVS $\Delta rpsU2$ pF vs LVS pF	
Locus	Gene Name	Product Name	baseMean	log2FoldChange	padj
FTL_R0032	-	5S ribosomal RNA	13.1	-0.39	1.51E-01
FTL_R0033	tRNA-Val2	Val tRNA	0.2	0.00	NA
FTL_R0034	tRNA-Ser3	Ser tRNA	0.7	-0.04	NA
FTL_R0042	tRNA-Met1	Met tRNA	0.4	-0.02	NA
FTL_R0043	tRNA-Arg1	Arg tRNA	0.0	NA	NA
FTL_R0053	-	5S ribosomal RNA	22.2	-1.12	1.65E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0001	0.12	2.98E-01	0.06	6.54E-01
FTL_0002	0.08	5.68E-01	0.18	3.95E-01
FTL_0003	0.02	NA	-0.12	6.20E-01
FTL_0004	-0.12	3.88E-01	-0.26	1.75E-01
FTL_0005	-0.01	NA	-0.83	4.74E-02
FTL_0006	0.02	8.54E-01	-0.97	3.22E-04
FTL_0007	0.03	8.59E-01	0.23	3.27E-01
FTL_0008	0.05	7.30E-01	1.13	4.59E-28
FTL_0009	0.02	9.19E-01	0.63	9.09E-06
FTL_0010	0.03	8.64E-01	0.07	5.84E-01
FTL_0011	-0.13	3.00E-01	0.24	8.97E-02
FTL_0012	-0.13	2.60E-01	0.19	1.09E-01
FTL_0013	-0.02	8.71E-01	-0.19	2.81E-01
FTL_0014	0.12	3.35E-01	1.05	7.34E-20
FTL_0015	0.16	1.77E-01	0.64	2.69E-08
FTL_0016	0.20	3.49E-02	0.61	2.43E-11
FTL_0017	0.15	1.57E-01	0.48	2.27E-06
FTL_0018	-0.18	1.89E-01	-0.29	8.35E-02
FTL_0019	-0.12	3.46E-01	-0.27	2.72E-01
FTL_0020	-0.03	8.56E-01	0.09	4.27E-01
FTL_0021	-0.04	7.01E-01	-2.12	5.68E-11
FTL_0022	-0.01	NA	-0.06	8.17E-01
FTL_0023	-0.09	5.19E-01	-0.27	1.68E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0024	0.09	4.68E-01	-0.06	7.18E-01
FTL_0025	0.00	NA	-0.02	NA
FTL_0026	0.78	4.76E-06	1.30	1.20E-13
FTL_0027	0.62	2.65E-03	1.24	1.04E-08
FTL_0028	-0.06	6.78E-01	1.43	3.15E-23
FTL_0029	-0.07	5.58E-01	1.29	5.45E-43
FTL_0030	-0.01	9.57E-01	1.59	1.31E-51
FTL_0031	-0.02	9.19E-01	0.78	4.09E-09
FTL_0032	-0.08	5.54E-01	0.00	9.95E-01
FTL_0033	0.02	8.77E-01	0.41	1.68E-04
FTL_0034	-0.01	9.31E-01	-0.70	7.39E-07
FTL_0035	-0.01	NA	-0.11	NA
FTL_0036	0.01	9.31E-01	0.26	2.58E-01
FTL_0037	-0.46	5.03E-06	-0.07	6.24E-01
FTL_0038	-0.51	9.88E-04	0.44	7.76E-03
FTL_0039	-0.06	6.42E-01	-0.03	9.14E-01
FTL_0040	-0.02	8.90E-01	0.12	5.30E-01
FTL_0041	0.00	NA	-0.35	2.40E-01
FTL_0042	0.00	9.61E-01	-0.07	8.03E-01
FTL_0043	0.05	7.17E-01	0.40	4.87E-02
FTL_0044	-0.03	8.55E-01	-0.06	7.11E-01
FTL_0045	-0.25	1.21E-02	0.95	4.89E-22
FTL_0046	-0.13	3.44E-01	0.96	1.66E-11

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0047	0.00	NA	0.10	6.87E-01
FTL_0048	-0.11	4.11E-01	0.35	3.97E-02
FTL_0049	-0.01	9.26E-01	0.15	4.92E-01
FTL_0050	-0.02	NA	-0.30	2.73E-01
FTL_0051	-0.03	NA	0.00	9.98E-01
FTL_0052	-0.01	NA	-0.21	4.10E-01
FTL_0053	-0.04	NA	-0.13	6.60E-01
FTL_0054	-0.08	5.39E-01	-0.22	2.84E-01
FTL_0055	0.03	NA	-0.08	7.84E-01
FTL_0056	-0.03	8.40E-01	0.37	1.12E-02
FTL_0057	-0.12	3.76E-01	0.46	1.20E-02
FTL_0058	0.08	4.91E-01	0.51	8.67E-07
FTL_0059	0.07	6.13E-01	0.21	2.34E-01
FTL_0060	0.07	5.73E-01	0.28	3.30E-02
FTL_0061	0.08	4.93E-01	0.27	3.29E-01
FTL_0062	-0.01	NA	-0.16	5.69E-01
FTL_0063	-0.05	6.94E-01	0.33	1.30E-01
FTL_0064	0.00	NA	-0.15	NA
FTL_0065	0.03	NA	0.13	6.55E-01
FTL_0066	0.02	NA	0.54	1.17E-01
FTL_0067	0.54	2.65E-03	1.37	1.40E-12
FTL_0068	-0.06	5.73E-01	0.32	5.70E-04
FTL_0069	-0.20	1.85E-01	0.00	9.98E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0070	-0.21	1.22E-01	0.10	5.84E-01
FTL_0071	0.01	9.43E-01	0.41	1.22E-08
FTL_0072	0.00	9.79E-01	-0.26	2.63E-02
FTL_0073	0.20	3.01E-02	1.09	1.60E-34
FTL_0074	-0.24	6.19E-02	0.28	5.59E-02
FTL_0075	-0.21	1.04E-01	0.33	2.35E-02
FTL_0076	-0.31	1.03E-03	0.11	3.64E-01
FTL_0077	-0.06	6.50E-01	-0.39	5.76E-02
FTL_0078	-0.16	2.33E-01	-0.81	8.15E-09
FTL_0079	-0.03	8.10E-01	-0.30	2.81E-01
FTL_0080	-0.16	2.56E-01	-0.42	1.95E-02
FTL_0081	-0.07	NA	-0.26	3.73E-01
FTL_0082	0.03	8.63E-01	1.00	2.69E-12
FTL_0083	0.00	NA	-0.19	5.08E-01
FTL_0084	-0.05	7.15E-01	0.44	3.72E-04
FTL_0085	0.12	3.53E-01	0.42	7.51E-04
FTL_0086	0.18	1.93E-01	0.45	4.03E-03
FTL_0087	-0.15	2.32E-01	-0.25	6.27E-02
FTL_0088	0.02	9.03E-01	0.14	2.60E-01
FTL_0089	-0.28	8.39E-02	0.26	1.88E-01
FTL_0090	-0.02	8.90E-01	0.65	5.18E-06
FTL_0091	-0.08	5.24E-01	0.35	1.13E-01
FTL_0092	0.12	3.10E-01	0.98	1.07E-18

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0093	0.20	2.83E-02	0.51	8.42E-09
FTL_0094	0.56	3.25E-06	1.31	7.14E-27
FTL_0095	-0.28	4.62E-02	-0.21	2.16E-01
FTL_0096	-0.21	1.75E-01	-0.19	4.12E-01
FTL_0097	0.05	5.50E-01	0.61	6.90E-02
FTL_0098	0.09	5.09E-01	1.21	4.03E-17
FTL_0099	0.24	3.15E-02	1.23	7.83E-28
FTL_0100	0.19	1.01E-01	0.83	8.58E-13
FTL_0101	-0.07	6.15E-01	-0.36	1.33E-02
FTL_0102	0.02	9.13E-01	0.21	2.47E-01
FTL_0103	-0.18	1.95E-01	0.34	3.65E-02
FTL_0104	-0.07	5.71E-01	0.36	3.23E-04
FTL_0105	-0.13	2.19E-01	0.47	7.16E-07
FTL_0106	0.07	NA	0.07	8.18E-01
FTL_0107	-0.06	6.51E-01	-0.20	3.59E-01
FTL_0108	0.01	NA	0.12	NA
FTL_0109	-0.03	NA	-0.28	NA
FTL_0110	-0.02	NA	-0.06	NA
FTL_0111 / FTL	0.56	1.06E-04	1.56	9.74E-26
FTL_0112 / FTL	0.53	6.94E-05	0.94	3.79E-12
FTL_0113 / FTL	0.75	3.69E-07	1.12	2.43E-14
FTL_0114 / FTL	0.59	7.26E-05	0.29	7.28E-02
FTL_0115 / FTL	0.76	4.36E-06	1.01	1.68E-09

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0116 / FTL	0.84	3.76E-07	1.47	1.62E-18
FTL_0117 / FTL	0.61	1.36E-02	1.45	5.30E-08
FTL_0118 / FTL	0.68	4.36E-06	1.78	5.73E-32
FTL_0119 / FTL	0.65	6.32E-06	1.46	1.45E-22
FTL_0120 / FTL	0.94	8.13E-07	1.65	2.89E-17
FTL_0121 / FTL	0.39	4.37E-05	1.52	2.33E-54
FTL_0122 / FTL	0.89	3.33E-05	0.93	1.87E-05
FTL_0123 / FTL	0.69	8.55E-06	1.07	1.89E-11
FTL_0124 / FTL	1.07	2.64E-04	1.33	7.76E-06
FTL_0125 / FTL	0.75	5.72E-09	1.70	1.20E-37
FTL_0126 / FTL	0.83	6.44E-07	1.58	1.30E-20
FTL_0127	-0.08	4.58E-01	0.42	4.84E-07
FTL_0128	-0.10	4.48E-01	-0.21	2.99E-01
FTL_0129	0.13	2.84E-01	0.69	8.37E-09
FTL_0130	0.22	1.31E-01	0.95	2.02E-09
FTL_0131	0.38	4.83E-04	0.95	4.31E-18
FTL_0132	0.05	7.13E-01	0.85	5.31E-17
FTL_0133	-0.16	6.44E-02	-1.09	8.72E-44
FTL_0134	-0.03	NA	-0.79	5.87E-02
FTL_0135	-0.06	6.39E-01	-0.20	2.75E-01
FTL_0136	0.08	4.68E-01	-0.10	7.25E-01
FTL_0137	-0.10	4.21E-01	0.29	2.10E-02
FTL_0138	-0.11	3.06E-01	0.11	3.47E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0139	-0.23	6.46E-02	-0.38	3.92E-03
FTL_0140	-0.13	3.54E-01	0.01	9.63E-01
FTL_0141	-0.04	7.30E-01	0.02	9.37E-01
FTL_0142	-0.16	2.46E-01	0.20	4.23E-01
FTL_0143	0.04	NA	-0.21	4.75E-01
FTL_0144	-0.53	7.91E-03	0.13	5.72E-01
FTL_0145	-0.23	6.36E-02	0.89	1.31E-12
FTL_0146	-0.21	2.83E-02	0.89	1.66E-22
FTL_0147	0.70	4.62E-07	0.91	1.42E-10
FTL_0148	0.02	8.63E-01	0.10	4.10E-01
FTL_0149	0.05	6.57E-01	0.19	5.59E-02
FTL_0150	-0.01	9.47E-01	-0.01	9.73E-01
FTL_0151	-0.17	2.24E-01	-0.14	4.58E-01
FTL_0152	-0.04	7.36E-01	0.08	5.90E-01
FTL_0153	-0.16	2.39E-01	-0.24	1.39E-01
FTL_0154	0.02	NA	-0.07	7.83E-01
FTL_0155	0.02	8.98E-01	0.80	1.24E-05
FTL_0156	-0.39	9.26E-05	-0.09	4.71E-01
FTL_0157	-0.28	3.65E-02	0.48	8.01E-04
FTL_0158	0.02	8.63E-01	0.76	2.82E-16
FTL_0159	0.29	4.16E-02	0.15	4.06E-01
FTL_0160	0.47	1.30E-05	0.25	3.16E-02
FTL_0161	0.37	1.49E-02	0.02	9.07E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0162	0.02	8.89E-01	-0.69	6.75E-03
FTL_0163	0.01	NA	0.04	NA
FTL_0164	-0.14	3.33E-01	-0.25	2.07E-01
FTL_0165	-0.11	NA	0.00	9.95E-01
FTL_0166	0.19	1.02E-01	1.12	1.66E-22
FTL_0167	-0.08	5.20E-01	-0.62	1.35E-02
FTL_0168	0.01	9.31E-01	-0.55	6.72E-03
FTL_0169	-0.13	3.50E-01	0.11	5.59E-01
FTL_0170	0.05	7.01E-01	0.64	2.25E-02
FTL_0171	0.09	4.82E-01	0.40	4.59E-03
FTL_0172	0.04	7.02E-01	0.07	5.75E-01
FTL_0173	0.05	7.01E-01	0.17	2.22E-01
FTL_0174	-0.07	6.20E-01	0.69	9.35E-07
FTL_0175	-0.10	3.10E-01	0.41	1.78E-01
FTL_0176	-0.26	7.50E-02	0.35	2.48E-02
FTL_0177	-0.37	6.36E-02	0.17	4.90E-01
FTL_0178	-0.20	1.14E-01	0.53	1.60E-04
FTL_0179	-0.51	8.81E-06	-0.02	9.15E-01
FTL_0180	-0.05	6.77E-01	0.02	8.92E-01
FTL_0181	-0.03	8.48E-01	-0.11	6.23E-01
FTL_0182	-0.05	7.04E-01	0.49	1.09E-03
FTL_0183	-0.24	1.02E-02	0.59	7.85E-10
FTL_0184	-0.17	NA	-0.37	2.36E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0185	-0.13	3.39E-01	-0.20	3.23E-01
FTL_0186	-0.41	6.41E-02	-1.36	3.77E-07
FTL_0187	-0.01	9.61E-01	-1.21	7.78E-14
FTL_0188	-0.09	3.66E-01	-0.08	4.33E-01
FTL_0189	-0.05	6.71E-01	0.11	4.27E-01
FTL_0190	0.02	8.77E-01	0.60	1.60E-04
FTL_0191	-0.17	1.18E-01	0.15	1.99E-01
FTL_0192	-0.20	4.42E-02	0.42	9.40E-05
FTL_0193	-0.14	2.84E-01	0.25	9.75E-02
FTL_0194	-0.45	2.94E-04	0.01	9.67E-01
FTL_0195	-0.39	7.01E-03	-0.61	5.63E-05
FTL_0196	0.00	1.00E+00	0.80	4.85E-14
FTL_0197	-0.19	1.29E-01	-0.21	1.35E-01
FTL_0198	-0.36	3.47E-04	0.00	9.85E-01
FTL_0199	-0.01	9.61E-01	0.42	1.66E-02
FTL_0200	-0.02	8.77E-01	0.24	1.50E-02
FTL_0201	-0.03	8.23E-01	0.08	6.91E-01
FTL_0202	0.01	9.26E-01	0.06	8.36E-01
FTL_0203	-0.06	6.68E-01	0.15	4.90E-01
FTL_0204	0.05	7.01E-01	0.48	5.27E-02
FTL_0205	-0.19	1.29E-01	0.30	3.07E-01
FTL_0206	-0.28	2.84E-02	0.42	1.95E-03
FTL_0207	0.40	2.66E-05	-0.25	1.38E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0208	0.77	5.88E-07	0.12	5.44E-01
FTL_0209	0.34	2.03E-02	-0.02	9.40E-01
FTL_0210	0.00	9.67E-01	0.59	7.19E-16
FTL_0211	0.03	8.46E-01	0.48	4.50E-03
FTL_0212	-0.12	3.92E-01	-0.34	3.81E-02
FTL_0213	-0.15	3.12E-01	-0.07	7.96E-01
FTL_0214	0.18	1.29E-01	0.68	3.47E-09
FTL_0215	0.19	1.04E-01	0.96	1.03E-15
FTL_0216	-0.05	6.66E-01	0.21	4.54E-01
FTL_0217	0.27	1.22E-02	0.58	1.17E-07
FTL_0218	-0.09	4.12E-01	0.42	1.99E-05
FTL_0219	0.01	9.51E-01	-0.31	1.36E-01
FTL_0220	0.02	8.93E-01	-0.15	5.89E-01
FTL_0221	0.30	1.44E-02	0.27	4.09E-02
FTL_0222	0.16	1.14E-01	0.75	4.12E-15
FTL_0223	0.11	2.86E-01	0.82	1.12E-18
FTL_0224	-0.16	9.71E-02	0.09	4.50E-01
FTL_0225	-0.17	1.64E-01	-0.21	1.17E-01
FTL_0226	-0.05	6.96E-01	-0.69	1.01E-06
FTL_0227	-0.08	5.24E-01	-0.32	1.72E-01
FTL_0228	-0.03	8.32E-01	-0.10	6.50E-01
FTL_0229	-0.11	4.17E-01	0.59	2.11E-04
FTL_0230	-0.06	6.15E-01	0.37	1.68E-03

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0231	0.01	9.29E-01	0.22	7.38E-02
FTL_0232	-0.01	9.61E-01	0.32	7.32E-02
FTL_0233	-0.17	1.82E-01	0.21	4.83E-01
FTL_0234	-0.44	2.83E-03	0.09	6.21E-01
FTL_0235	-0.10	4.30E-01	0.32	2.45E-02
FTL_0236	-0.25	7.83E-02	0.10	6.28E-01
FTL_0237	-0.24	5.30E-02	0.63	1.83E-07
FTL_0238	-0.08	3.01E-01	0.62	7.68E-02
FTL_0239	-0.27	9.55E-02	0.60	1.93E-03
FTL_0240	-0.49	2.45E-04	0.39	5.99E-03
FTL_0241	-0.49	4.65E-03	0.32	9.48E-02
FTL_0242	-0.42	9.70E-03	0.33	7.24E-02
FTL_0243	-0.37	2.61E-03	0.07	6.95E-01
FTL_0244	-0.60	3.30E-04	-0.06	7.76E-01
FTL_0245	-0.33	6.18E-03	-0.02	8.91E-01
FTL_0246	-0.13	2.25E-01	0.00	9.99E-01
FTL_0247	-0.23	1.21E-01	0.09	6.86E-01
FTL_0248	-0.06	6.63E-01	-0.10	5.71E-01
FTL_0249	-0.11	4.24E-01	-0.07	6.91E-01
FTL_0250	0.01	9.43E-01	0.07	7.05E-01
FTL_0251	-0.15	2.50E-01	0.11	5.28E-01
FTL_0252	-0.26	6.79E-02	0.07	7.22E-01
FTL_0253	-0.26	3.95E-02	0.32	1.85E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0254	-0.17	1.97E-01	0.34	2.17E-02
FTL_0255	-0.14	1.57E-01	0.19	7.24E-02
FTL_0256	-0.14	2.44E-01	-0.19	1.67E-01
FTL_0257	-0.08	5.49E-01	0.30	5.97E-02
FTL_0258	-0.17	8.30E-02	-0.13	2.57E-01
FTL_0259	-0.19	4.11E-02	-0.23	1.82E-02
FTL_0260	-0.24	2.68E-02	0.12	3.42E-01
FTL_0261	-0.08	5.21E-01	0.01	9.84E-01
FTL_0262	-0.63	1.65E-11	0.52	1.51E-07
FTL_0263	-0.07	6.15E-01	-0.19	3.59E-01
FTL_0264	-0.08	5.11E-01	-0.46	8.25E-02
FTL_0265	0.39	1.95E-03	0.35	9.79E-03
FTL_0266	-0.09	5.24E-01	-0.26	1.99E-01
FTL_0267	0.19	2.00E-01	1.30	2.23E-14
FTL_0268	-0.09	5.26E-01	-0.23	1.65E-01
FTL_0269	-0.17	1.16E-01	0.46	5.63E-05
FTL_0270	-0.07	5.41E-01	-0.12	6.56E-01
FTL_0271	0.07	5.53E-01	-0.12	6.60E-01
FTL_0272	0.03	8.41E-01	-0.09	7.47E-01
FTL_0273	-0.04	7.71E-01	0.14	5.31E-01
FTL_0274	0.06	6.42E-01	0.25	3.34E-01
FTL_0275	-0.03	8.54E-01	0.23	3.41E-01
FTL_0276	0.02	8.92E-01	0.81	2.70E-05

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0277	0.21	7.43E-02	0.66	3.69E-09
FTL_0278	0.12	3.68E-01	0.66	8.57E-03
FTL_0279	0.15	2.61E-01	0.70	1.87E-06
FTL_0280	0.14	2.84E-01	1.12	1.77E-18
FTL_0281	0.07	5.89E-01	0.81	3.20E-04
FTL_0282	0.50	4.14E-05	1.29	1.21E-24
FTL_0283	-0.01	9.46E-01	-0.07	7.54E-01
FTL_0284	-0.04	8.09E-01	0.16	4.12E-01
FTL_0285	0.06	6.21E-01	-0.18	9.42E-02
FTL_0286	-0.24	1.14E-01	0.49	6.80E-03
FTL_0287	-0.02	8.89E-01	0.30	2.60E-01
FTL_0288	0.08	5.42E-01	0.66	2.70E-03
FTL_0289	-0.02	8.89E-01	0.12	6.01E-01
FTL_0290	-0.03	8.63E-01	0.74	3.03E-10
FTL_0291	0.07	6.10E-01	0.75	2.01E-08
FTL_0292	-0.12	3.40E-01	-0.42	1.10E-01
FTL_0293	-0.05	6.84E-01	0.57	2.41E-04
FTL_0294	0.14	2.29E-01	0.82	1.72E-14
FTL_0295	0.12	1.79E-01	0.80	1.02E-24
FTL_0296	0.05	6.99E-01	0.69	3.05E-05
FTL_0297	0.03	8.47E-01	0.28	2.86E-02
FTL_0298	-0.06	6.63E-01	-0.37	4.86E-03
FTL_0299	-0.20	1.24E-01	0.20	2.13E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0300	-0.06	6.51E-01	0.80	9.60E-06
FTL_0301	0.02	NA	-0.81	2.85E-02
FTL_0302	0.03	7.64E-01	0.01	9.89E-01
FTL_0303	0.01	NA	-0.05	NA
FTL_0304	0.10	4.30E-01	0.42	4.08E-04
FTL_0305	-0.09	4.28E-01	-0.14	2.56E-01
FTL_0306	0.12	2.14E-01	0.23	1.53E-02
FTL_0307	-0.18	7.12E-02	0.35	3.39E-04
FTL_0308	-0.01	9.54E-01	-0.45	1.34E-03
FTL_0309	-0.07	5.37E-01	0.24	4.65E-02
FTL_0310	-0.21	8.18E-02	0.22	9.91E-02
FTL_0311	-0.17	2.10E-01	0.18	2.88E-01
FTL_0312	NA	NA	NA	NA
FTL_0313	NA	NA	NA	NA
FTL_0314	-0.07	6.06E-01	-0.26	1.59E-01
FTL_0315	-0.08	5.24E-01	0.44	6.19E-04
FTL_0316	-0.16	2.70E-01	0.26	1.96E-01
FTL_0317	-0.15	2.22E-01	0.71	6.10E-09
FTL_0318	-0.22	1.68E-01	0.30	2.15E-01
FTL_0319	-0.26	1.15E-02	0.53	1.22E-07
FTL_0320	0.02	8.82E-01	-0.01	9.62E-01
FTL_0321	-0.01	NA	-0.05	NA
FTL_0322	-0.03	8.32E-01	-0.25	2.62E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0323	0.00	NA	-0.73	1.86E-02
FTL_0324	0.03	5.65E-01	0.04	8.66E-01
FTL_0325	0.36	9.48E-03	0.95	2.73E-11
FTL_0326	-0.03	8.54E-01	0.37	6.33E-02
FTL_0327	-0.07	5.83E-01	0.29	2.97E-02
FTL_0328	-0.12	3.33E-01	-0.07	6.67E-01
FTL_0329	-0.15	1.81E-01	0.18	1.26E-01
FTL_0330	-0.07	5.51E-01	0.16	5.68E-01
FTL_0331	-0.05	7.02E-01	0.28	3.45E-02
FTL_0332	-0.12	3.58E-01	0.22	1.44E-01
FTL_0333	-0.27	9.82E-02	-0.55	5.24E-03
FTL_0334	-0.19	1.10E-01	0.45	1.85E-04
FTL_0335	-0.14	2.95E-01	0.35	1.55E-01
FTL_0336	-0.01	9.62E-01	0.47	1.98E-04
FTL_0337	-0.11	2.42E-01	0.08	4.25E-01
FTL_0338	0.06	6.63E-01	0.09	7.26E-01
FTL_0339	-0.07	6.03E-01	-0.29	1.29E-01
FTL_0340	-0.01	NA	-0.14	NA
FTL_0341	-0.02	8.63E-01	-0.14	6.25E-01
FTL_0342	0.02	NA	-0.52	1.27E-01
FTL_0343	0.00	9.74E-01	-0.12	6.68E-01
FTL_0344	0.00	NA	0.04	NA
FTL_0345	-0.10	4.45E-01	0.57	1.17E-04

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0346	0.01	9.25E-01	0.22	4.09E-01
FTL_0347	-0.02	8.92E-01	0.15	5.53E-01
FTL_0348	0.45	8.29E-04	1.44	1.48E-24
FTL_0349	-0.01	NA	1.71	1.92E-04
FTL_0350	-0.07	NA	-0.08	8.06E-01
FTL_0351	0.00	NA	-0.06	NA
FTL_0352	-0.02	NA	-0.23	4.07E-01
FTL_0353	-0.07	6.03E-01	-0.32	1.16E-01
FTL_0354	0.04	7.54E-01	0.60	9.94E-05
FTL_0355	-0.04	8.13E-01	0.31	5.27E-02
FTL_0356	0.15	2.43E-01	0.49	2.60E-04
FTL_0357	-0.25	7.30E-02	0.81	2.75E-08
FTL_0358	0.05	7.38E-01	0.25	9.39E-02
FTL_0359	-0.08	5.38E-01	-0.40	2.00E-03
FTL_0360	0.15	2.36E-01	1.23	5.08E-22
FTL_0361	0.11	3.65E-01	1.49	2.91E-39
FTL_0362	0.02	NA	-0.42	1.88E-01
FTL_0363	-0.11	4.33E-01	-0.05	8.07E-01
FTL_0364	0.03	NA	0.06	8.27E-01
FTL_0365	-0.09	4.05E-01	-0.81	7.96E-03
FTL_0366	-0.02	NA	-0.26	3.65E-01
FTL_0367	-0.01	9.35E-01	-0.23	3.99E-01
FTL_0368	-0.22	1.64E-01	-0.27	2.21E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0369	0.01	9.28E-01	0.19	4.27E-01
FTL_0370	-0.11	4.19E-01	0.02	9.52E-01
FTL_0371	-0.35	2.99E-02	0.50	6.66E-03
FTL_0372	-0.05	6.74E-01	0.51	2.29E-07
FTL_0373	-0.11	3.81E-01	-0.50	3.66E-02
FTL_0374	-0.24	4.14E-02	-0.29	2.11E-02
FTL_0375	-0.07	5.87E-01	0.13	4.44E-01
FTL_0376	0.08	5.32E-01	0.29	3.27E-02
FTL_0377	0.03	8.32E-01	0.38	1.66E-04
FTL_0378	0.11	4.45E-01	0.26	1.90E-01
FTL_0379	0.21	1.06E-01	1.06	6.70E-15
FTL_0380	0.02	8.55E-01	0.07	7.25E-01
FTL_0381	0.11	3.90E-01	-0.03	8.53E-01
FTL_0382	0.01	9.68E-01	1.48	2.03E-44
FTL_0383	-0.17	2.12E-01	1.06	2.45E-04
FTL_0384	0.22	6.46E-02	1.17	1.68E-23
FTL_0385	0.19	1.99E-01	1.13	6.04E-09
FTL_0386	0.02	8.66E-01	0.57	5.42E-02
FTL_0387	0.01	9.24E-01	0.88	1.95E-26
FTL_0388	-0.02	8.87E-01	0.08	7.07E-01
FTL_0389	0.08	5.24E-01	0.82	3.23E-13
FTL_0390	-0.17	2.19E-01	-0.54	1.60E-03
FTL_0391	-0.09	5.17E-01	-0.08	7.49E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0392	-0.92	2.30E-03	0.27	3.34E-01
FTL_0393	-0.22	6.21E-02	0.23	7.58E-02
FTL_0394	-0.06	5.55E-01	0.57	5.18E-11
FTL_0395	-0.05	6.42E-01	0.98	1.12E-21
FTL_0396	-0.01	8.96E-01	0.53	3.53E-09
FTL_0397	-0.20	1.46E-01	0.01	9.63E-01
FTL_0398	-0.07	6.13E-01	0.55	2.69E-05
FTL_0399	-0.06	6.12E-01	0.44	5.66E-05
FTL_0400	-0.07	5.45E-01	-0.05	8.83E-01
FTL_0401	0.11	4.09E-01	0.14	5.81E-01
FTL_0402	-0.13	3.61E-01	0.31	1.07E-01
FTL_0403	-0.01	8.92E-01	-0.06	8.37E-01
FTL_0404	-0.09	4.45E-01	0.23	7.52E-02
FTL_0405	0.04	8.10E-01	0.29	3.15E-02
FTL_0406	0.01	9.56E-01	0.23	1.27E-01
FTL_0407	0.01	9.50E-01	0.42	6.45E-06
FTL_0408	-0.25	1.17E-01	0.01	9.67E-01
FTL_0409	-0.04	7.81E-01	0.09	7.47E-01
FTL_0410	0.04	8.15E-01	0.50	1.34E-03
FTL_0411	0.06	6.59E-01	0.28	2.11E-02
FTL_0412	0.16	2.22E-01	0.13	4.26E-01
FTL_0413	-0.04	7.02E-01	0.05	6.58E-01
FTL_0414	0.03	7.63E-01	0.66	1.41E-17

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0415	0.01	NA	-0.28	3.42E-01
FTL_0416	-0.06	6.18E-01	-0.29	2.68E-01
FTL_0417	-0.09	5.11E-01	-0.20	3.37E-01
FTL_0418	-0.03	8.40E-01	0.21	3.37E-01
FTL_0419	0.08	5.18E-01	0.61	9.34E-09
FTL_0420	0.11	4.19E-01	0.65	1.55E-06
FTL_0421	-0.01	9.43E-01	0.48	5.58E-06
FTL_0422	0.03	8.63E-01	-0.38	1.74E-02
FTL_0423	-0.08	5.62E-01	0.92	7.94E-10
FTL_0424	0.03	8.19E-01	0.13	3.83E-01
FTL_0425	0.44	6.32E-06	1.38	6.02E-45
FTL_0426	0.19	6.18E-02	0.12	3.37E-01
FTL_0427	-0.20	1.40E-01	0.07	7.05E-01
FTL_0428	-0.07	5.11E-01	0.15	1.14E-01
FTL_0429	-0.20	1.43E-01	-0.16	3.77E-01
FTL_0430	-0.14	2.41E-01	0.04	7.84E-01
FTL_0431	-0.10	4.30E-01	-0.09	7.46E-01
FTL_0432	0.01	NA	-0.22	4.58E-01
FTL_0433	-0.24	9.00E-02	0.16	3.68E-01
FTL_0434	0.05	7.28E-01	0.65	6.59E-08
FTL_0435	0.08	5.80E-01	-0.05	8.28E-01
FTL_0436	-0.02	8.92E-01	0.16	1.53E-01
FTL_0437	-0.15	1.43E-01	0.45	4.51E-06

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0438	0.02	9.10E-01	0.01	9.45E-01
FTL_0439	-0.03	8.13E-01	-0.07	6.32E-01
FTL_0440	-0.12	3.49E-01	-0.30	1.63E-01
FTL_0441	0.08	5.23E-01	-0.30	2.23E-01
FTL_0442	0.18	2.32E-01	-0.46	2.52E-02
FTL_0443	-0.35	5.85E-04	-0.38	3.19E-04
FTL_0444	-0.10	3.31E-01	0.34	1.68E-04
FTL_0445	-0.05	7.20E-01	0.65	1.98E-03
FTL_0446	-0.08	NA	-0.41	2.04E-01
FTL_0447	0.02	8.92E-01	-0.25	2.07E-01
FTL_0448	0.10	4.51E-01	0.90	3.78E-13
FTL_0449	0.38	2.22E-03	0.60	1.55E-06
FTL_0450	-0.05	6.73E-01	0.64	3.52E-12
FTL_0451	-0.01	9.40E-01	0.30	8.84E-03
FTL_0452	-0.02	8.56E-01	0.20	6.80E-02
FTL_0453	-0.15	2.01E-01	0.34	2.85E-03
FTL_0454	-0.10	3.19E-01	0.35	2.65E-04
FTL_0455	-0.34	1.76E-02	0.17	3.20E-01
FTL_0456	-0.05	7.15E-01	0.37	4.16E-02
FTL_0457	0.06	6.27E-01	0.30	1.23E-02
FTL_0458	0.04	7.52E-01	0.85	4.16E-03
FTL_0459	0.01	9.63E-01	0.61	5.23E-05
FTL_0460	-0.03	8.52E-01	0.02	9.06E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0461	-0.07	6.15E-01	-0.93	4.33E-07
FTL_0462	0.02	9.07E-01	0.48	3.28E-08
FTL_0463	-0.02	8.92E-01	0.95	4.40E-14
FTL_0464	0.19	2.12E-01	0.67	2.41E-04
FTL_0465	0.04	7.44E-01	0.36	3.29E-03
FTL_0466	0.27	7.51E-03	0.77	3.16E-15
FTL_0467	0.00	NA	-0.14	NA
FTL_0468	-0.03	7.90E-01	-0.13	6.36E-01
FTL_0469	0.01	NA	-0.05	NA
FTL_0470	0.05	6.98E-01	0.35	1.15E-01
FTL_0471	0.03	NA	0.06	8.30E-01
FTL_0472	0.03	8.54E-01	0.40	2.21E-05
FTL_0473	0.37	1.22E-04	1.53	3.00E-54
FTL_0474	-0.03	8.56E-01	0.24	4.23E-02
FTL_0475	0.04	7.18E-01	0.15	2.27E-01
FTL_0476	0.15	1.28E-01	0.90	3.47E-23
FTL_0477	0.12	2.84E-01	0.92	1.83E-20
FTL_0478	0.06	6.26E-01	0.80	3.91E-09
FTL_0479	0.04	8.19E-01	1.06	2.90E-18
FTL_0480	0.02	9.20E-01	0.48	8.59E-05
FTL_0481	-0.15	2.73E-01	-0.38	7.05E-03
FTL_0482	-0.14	2.34E-01	-0.23	6.31E-02
FTL_0483	-0.04	7.18E-01	0.08	5.06E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0484	-0.09	4.13E-01	0.46	8.39E-06
FTL_0485	-0.27	3.40E-02	0.65	3.77E-07
FTL_0486	-0.27	1.21E-02	0.25	3.14E-02
FTL_0487	-0.08	5.25E-01	0.26	4.11E-02
FTL_0488	-0.34	1.22E-02	0.11	5.22E-01
FTL_0489	-0.04	7.38E-01	0.20	4.44E-02
FTL_0490	0.05	7.02E-01	0.03	8.78E-01
FTL_0491	0.34	6.12E-02	0.93	6.06E-06
FTL_0492	-0.04	7.40E-01	0.37	2.91E-04
FTL_0493	-0.04	7.42E-01	0.73	2.15E-16
FTL_0494	0.01	NA	-0.06	NA
FTL_0495	0.02	NA	-0.03	NA
FTL_0496	0.00	NA	-0.02	NA
FTL_0497	-0.01	NA	-0.05	NA
FTL_0498	0.00	NA	0.00	9.95E-01
FTL_0499	0.22	6.19E-02	0.57	1.26E-06
FTL_0500	0.20	1.27E-01	-0.15	3.45E-01
FTL_0501	0.01	NA	-0.10	7.39E-01
FTL_0502	-0.09	3.64E-01	-0.06	8.40E-01
FTL_0503	-0.06	6.40E-01	-0.20	3.33E-01
FTL_0504	0.00	NA	0.02	NA
FTL_0505	0.02	NA	0.17	5.10E-01
FTL_0506	0.04	7.67E-01	0.10	6.19E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0507	-0.06	6.13E-01	0.09	5.59E-01
FTL_0508	0.08	4.28E-01	0.89	3.49E-22
FTL_0509	-0.15	2.37E-01	0.59	1.88E-06
FTL_0510	-0.12	3.95E-01	-0.23	2.10E-01
FTL_0511	-0.20	1.85E-01	0.26	2.53E-01
FTL_0512	-0.14	3.22E-01	0.28	1.65E-01
FTL_0513	-0.05	7.01E-01	-0.01	9.82E-01
FTL_0514	-0.17	1.75E-01	0.45	7.48E-04
FTL_0515	-0.30	2.70E-02	0.05	7.69E-01
FTL_0516	-0.27	7.74E-02	-0.22	2.34E-01
FTL_0517	-0.40	7.76E-03	-0.23	1.88E-01
FTL_0518	-0.23	6.16E-02	0.02	9.11E-01
FTL_0519	-0.06	6.12E-01	0.37	2.23E-04
FTL_0520	-0.15	9.55E-02	0.13	1.99E-01
FTL_0521	-0.05	7.12E-01	0.30	1.40E-01
FTL_0522	-0.12	2.98E-01	0.15	2.00E-01
FTL_0523	-0.08	5.42E-01	0.60	2.33E-06
FTL_0524	0.32	2.07E-03	0.46	1.86E-05
FTL_0525	0.02	8.59E-01	0.32	7.18E-03
FTL_0526	-0.06	6.84E-01	-0.21	3.37E-01
FTL_0527	0.01	NA	-0.17	5.47E-01
FTL_0528	0.03	8.19E-01	-0.36	4.04E-02
FTL_0529	0.09	5.11E-01	0.10	6.84E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0530	0.02	NA	0.24	NA
FTL_0531	0.01	NA	0.06	NA
FTL_0532	0.00	NA	1.06	5.03E-03
FTL_0533	0.12	1.95E-01	0.57	7.77E-12
FTL_0534	0.15	1.67E-01	0.23	3.38E-02
FTL_0535	-0.06	6.03E-01	-0.30	7.48E-03
FTL_0536	0.08	4.49E-01	0.41	1.64E-05
FTL_0537	-0.11	4.24E-01	0.32	8.55E-02
FTL_0538	0.03	8.63E-01	0.24	9.30E-02
FTL_0539	-0.02	8.96E-01	0.04	7.84E-01
FTL_0540	-0.07	5.34E-01	-0.18	9.30E-02
FTL_0541	-0.10	3.87E-01	0.27	1.63E-02
FTL_0542	-0.09	5.24E-01	-0.20	2.81E-01
FTL_0543	0.22	3.30E-02	0.53	1.96E-07
FTL_0544	0.01	9.43E-01	0.44	3.28E-03
FTL_0545	-0.10	4.51E-01	0.34	3.32E-02
FTL_0546	-0.09	5.11E-01	-0.45	4.09E-04
FTL_0547	-0.14	1.36E-01	0.05	6.44E-01
FTL_0548	-0.02	8.66E-01	0.61	1.65E-06
FTL_0549	-0.10	4.29E-01	0.21	1.48E-01
FTL_0550	-0.01	NA	0.02	9.36E-01
FTL_0551	0.00	9.71E-01	-1.24	3.40E-07
FTL_0552	-0.10	4.35E-01	0.14	4.67E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0553	-0.12	3.76E-01	-0.15	3.86E-01
FTL_0554	-0.25	8.39E-02	-0.84	3.87E-08
FTL_0555	-0.19	1.60E-01	-0.48	4.76E-04
FTL_0556	0.07	5.11E-01	-0.05	6.36E-01
FTL_0557	0.00	NA	-0.04	8.64E-01
FTL_0558	-0.06	5.33E-01	0.27	3.54E-01
FTL_0559	-0.04	NA	0.48	1.42E-01
FTL_0560	-0.01	NA	-0.30	NA
FTL_0561	-0.02	NA	-0.67	3.38E-02
FTL_0562	0.04	7.11E-01	1.17	3.07E-04
FTL_0563	-0.01	NA	-0.20	4.13E-01
FTL_0564	0.02	NA	-0.16	NA
FTL_0565	0.05	NA	-0.21	4.20E-01
FTL_0566	0.00	9.93E-01	-0.15	5.97E-01
FTL_0567	0.01	NA	0.13	NA
FTL_0568	0.01	9.61E-01	-0.13	6.26E-01
FTL_0569	0.36	9.26E-05	1.12	8.21E-34
FTL_0570	0.28	1.21E-01	0.55	1.92E-02
FTL_0571	0.16	1.88E-01	0.95	6.40E-14
FTL_0572	0.07	5.66E-01	1.08	1.18E-21
FTL_0573	0.04	7.11E-01	0.60	4.06E-11
FTL_0574	-0.16	1.92E-01	-0.98	3.40E-16
FTL_0575	-0.06	5.60E-01	-0.12	6.70E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0576	-0.02	NA	-0.34	2.66E-01
FTL_0577	0.00	NA	0.00	NA
FTL_0578	0.26	2.11E-03	-0.19	4.31E-02
FTL_0579	0.04	7.97E-01	0.38	6.95E-04
FTL_0580	0.05	7.16E-01	0.68	5.54E-04
FTL_0581	0.05	7.25E-01	-0.36	1.43E-02
FTL_0582	0.16	2.17E-01	0.42	2.54E-03
FTL_0583	0.12	3.70E-01	0.36	1.50E-02
FTL_0584	0.23	4.20E-02	0.53	3.82E-06
FTL_0585	0.33	5.69E-03	0.57	2.34E-06
FTL_0586	-0.07	4.83E-01	0.42	2.45E-07
FTL_0587	0.16	2.84E-01	0.59	2.94E-03
FTL_0588	0.04	8.22E-01	0.63	9.61E-07
FTL_0589	-0.08	5.23E-01	0.33	2.62E-03
FTL_0590	0.00	9.67E-01	-0.84	1.64E-24
FTL_0591	-0.02	8.93E-01	-0.02	9.43E-01
FTL_0592	-0.01	9.61E-01	0.27	2.87E-02
FTL_0593	-0.14	3.25E-01	0.36	8.59E-02
FTL_0594	-0.10	3.49E-01	0.42	7.05E-06
FTL_0595	0.08	5.84E-01	0.39	1.85E-02
FTL_0596	-0.01	9.11E-01	0.50	1.21E-08
FTL_0597	-0.07	5.84E-01	0.50	1.18E-02
FTL_0598	0.04	7.86E-01	-0.59	3.91E-04

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0599	0.08	5.39E-01	-0.18	3.95E-01
FTL_0600	-0.06	5.87E-01	0.51	2.68E-08
FTL_0601	-0.17	1.18E-01	-0.16	1.81E-01
FTL_0602	-0.01	9.62E-01	0.11	4.79E-01
FTL_0603	-0.17	1.59E-01	-0.22	1.21E-01
FTL_0604	-0.02	9.01E-01	0.18	2.92E-01
FTL_0605	-0.18	8.79E-02	-0.08	5.28E-01
FTL_0606	-0.02	9.13E-01	0.10	4.77E-01
FTL_0607	-0.05	7.46E-01	-0.28	1.74E-01
FTL_0608	-0.02	8.64E-01	0.56	2.91E-08
FTL_0609	0.00	9.94E-01	0.49	5.56E-07
FTL_0610	-0.22	1.98E-02	0.02	8.65E-01
FTL_0611	-0.13	2.69E-01	0.01	9.58E-01
FTL_0612	-0.06	7.01E-01	0.16	3.75E-01
FTL_0613	-0.15	2.29E-01	-0.42	1.28E-01
FTL_0614	-0.01	NA	-0.12	NA
FTL_0615	0.02	NA	0.16	5.80E-01
FTL_0616	-0.13	3.29E-01	-0.86	3.26E-08
FTL_0617	0.08	5.44E-01	0.20	2.78E-01
FTL_0618	-0.04	8.03E-01	0.00	9.95E-01
FTL_0619	0.01	NA	-0.06	8.56E-01
FTL_0620	0.07	6.20E-01	-0.06	7.54E-01
FTL_0621	-0.08	5.68E-01	-0.07	7.12E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0622	-0.05	6.33E-01	-0.05	8.56E-01
FTL_0623	-0.12	3.59E-01	0.26	1.27E-01
FTL_0624	-0.10	4.27E-01	0.32	6.76E-03
FTL_0625	-0.01	9.59E-01	0.63	6.04E-09
FTL_0626	-0.13	2.65E-01	-0.63	4.61E-08
FTL_0627	0.10	4.68E-01	1.15	6.31E-13
FTL_0628	-0.02	8.82E-01	0.26	8.18E-02
FTL_0629	0.18	1.43E-01	0.64	6.90E-07
FTL_0630	-0.02	NA	-0.17	5.08E-01
FTL_0631	-0.08	5.80E-01	-0.20	2.84E-01
FTL_0632	-0.18	NA	-0.13	6.64E-01
FTL_0633	-0.13	3.27E-01	-0.61	7.36E-03
FTL_0634	0.00	NA	-0.05	NA
FTL_0635	-0.04	7.41E-01	-0.72	4.33E-03
FTL_0636	-0.21	NA	-0.27	3.69E-01
FTL_0637	-0.01	9.30E-01	0.22	7.34E-02
FTL_0638	0.20	1.29E-01	-0.06	7.07E-01
FTL_0639	0.11	4.17E-01	0.68	1.16E-05
FTL_0640	-0.17	1.64E-01	0.06	6.76E-01
FTL_0641	-0.01	NA	-0.07	NA
FTL_0642	0.04	NA	0.25	3.92E-01
FTL_0643	0.01	9.46E-01	0.35	2.39E-03
FTL_0644	-0.04	7.64E-01	0.56	4.59E-05

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0645	-0.13	3.65E-01	0.12	5.30E-01
FTL_0646	0.02	NA	0.13	6.54E-01
FTL_0647	-0.04	NA	-0.42	1.68E-01
FTL_0648	0.03	8.52E-01	0.75	2.06E-05
FTL_0649	-0.09	4.58E-01	0.69	4.50E-08
FTL_0650	0.01	9.26E-01	0.07	5.79E-01
FTL_0651	-0.02	NA	-0.50	1.35E-01
FTL_0652	-0.12	3.19E-01	0.94	1.45E-14
FTL_0653	-0.03	8.15E-01	-0.11	4.33E-01
FTL_0654	-0.12	3.76E-01	-0.17	3.61E-01
FTL_0655	0.03	8.63E-01	0.44	3.87E-03
FTL_0656	-0.05	6.62E-01	0.62	2.11E-09
FTL_0657	-0.01	9.55E-01	-0.09	5.51E-01
FTL_0659	-0.06	6.44E-01	0.57	7.12E-06
FTL_0660	0.07	5.35E-01	0.92	1.61E-03
FTL_0661	-0.01	9.55E-01	0.70	1.71E-12
FTL_0662	-0.38	6.18E-03	-0.83	1.01E-09
FTL_0663	0.04	6.52E-01	-0.25	3.84E-01
FTL_0664	0.51	9.05E-03	0.96	2.94E-06
FTL_0665	0.07	5.46E-01	0.61	1.72E-07
FTL_0666	0.23	2.08E-02	0.77	3.57E-15
FTL_0667	0.11	4.17E-01	0.70	2.46E-03
FTL_0668	0.13	2.65E-01	0.62	5.55E-08

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0669	0.07	5.66E-01	0.38	4.55E-04
FTL_0670	0.12	3.38E-01	0.16	2.52E-01
FTL_0671	-0.30	4.08E-04	0.52	7.29E-10
FTL_0672	-0.29	5.41E-02	0.40	1.97E-02
FTL_0673	-0.20	8.75E-02	0.57	1.03E-06
FTL_0674	-0.15	2.97E-01	0.87	1.30E-05
FTL_0675	-0.05	7.30E-01	0.54	5.67E-04
FTL_0676	-0.13	1.46E-01	-0.15	8.15E-02
FTL_0677	-0.02	8.77E-01	-0.06	8.42E-01
FTL_0678	-0.06	6.39E-01	-0.17	4.24E-01
FTL_0679	-0.16	2.37E-01	0.75	3.20E-07
FTL_0680	-0.07	6.08E-01	0.58	1.32E-06
FTL_0681	-0.01	9.26E-01	0.73	7.36E-16
FTL_0682	-0.09	5.07E-01	-0.25	1.65E-01
FTL_0683	-0.02	NA	0.20	4.91E-01
FTL_0684	-0.23	7.90E-02	0.27	7.35E-02
FTL_0685	-0.05	6.71E-01	-0.04	7.46E-01
FTL_0686	-0.04	7.15E-01	-0.19	9.39E-02
FTL_0687	0.01	9.32E-01	0.19	8.09E-02
FTL_0688	0.07	5.45E-01	-0.10	3.70E-01
FTL_0689	-0.06	6.45E-01	0.20	2.62E-01
FTL_0690	0.00	9.91E-01	0.33	5.16E-04
FTL_0691	0.33	4.23E-04	0.44	3.01E-06

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0692	0.11	4.19E-01	0.27	2.48E-01
FTL_0693	-0.03	8.31E-01	0.03	9.15E-01
FTL_0694	0.06	6.47E-01	1.51	2.32E-15
FTL_0695	0.05	7.03E-01	1.33	1.60E-16
FTL_0696	0.04	7.71E-01	0.65	1.76E-09
FTL_0697	0.05	7.13E-01	0.58	1.78E-07
FTL_0698	0.06	6.47E-01	-0.03	8.66E-01
FTL_0699	-0.11	3.84E-01	0.10	5.47E-01
FTL_0700	0.31	4.37E-02	0.49	3.71E-03
FTL_0701	-0.01	9.43E-01	0.24	7.52E-02
FTL_0702	0.07	6.12E-01	-0.36	2.29E-02
FTL_0703	0.03	8.90E-01	0.61	6.50E-09
FTL_0704	0.21	1.78E-01	0.19	3.95E-01
FTL_0705	0.04	7.77E-01	-0.06	8.31E-01
FTL_0706	-0.01	9.40E-01	-0.32	8.97E-02
FTL_0707	0.09	5.19E-01	0.90	1.41E-11
FTL_0708	0.33	1.15E-02	0.59	1.54E-05
FTL_0709	-0.07	6.15E-01	0.29	1.10E-01
FTL_0710	-0.02	NA	-0.19	4.44E-01
FTL_0711	0.13	2.99E-01	-0.13	6.26E-01
FTL_0712	-0.02	NA	-0.10	NA
FTL_0713	-0.13	3.54E-01	-0.59	6.77E-05
FTL_0714	-0.11	3.86E-01	0.38	2.90E-03

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0715	-0.13	2.95E-01	-0.03	8.37E-01
FTL_0716	-0.08	5.39E-01	-0.19	1.60E-01
FTL_0717	0.03	8.54E-01	-0.42	3.64E-05
FTL_0718	-0.03	8.32E-01	0.63	7.86E-07
FTL_0719	0.02	9.19E-01	0.52	1.11E-02
FTL_0720	0.01	9.60E-01	0.67	1.27E-03
FTL_0721	-0.18	1.47E-01	0.23	1.00E-01
FTL_0722	0.09	5.24E-01	-0.20	2.07E-01
FTL_0723	0.17	2.55E-01	0.07	7.62E-01
FTL_0724	0.44	6.99E-04	0.18	2.22E-01
FTL_0725	-0.04	7.64E-01	0.20	3.32E-01
FTL_0726	-0.02	9.14E-01	-0.36	2.06E-03
FTL_0727	-0.03	8.44E-01	-0.29	1.79E-03
FTL_0728	0.07	5.84E-01	0.19	3.65E-01
FTL_0729	-0.16	2.34E-01	0.37	1.11E-02
FTL_0730	-0.10	4.49E-01	0.13	4.95E-01
FTL_0731	-0.13	3.26E-01	1.02	1.91E-14
FTL_0732	-0.05	6.84E-01	0.29	1.85E-01
FTL_0733	-0.05	7.24E-01	-0.09	6.74E-01
FTL_0734	0.00	9.80E-01	-0.62	9.32E-03
FTL_0735	0.00	NA	-0.04	NA
FTL_0736	0.12	2.24E-01	0.19	5.63E-02
FTL_0737	0.01	9.31E-01	0.25	2.72E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0738	-0.14	3.10E-01	-0.19	2.63E-01
FTL_0739	0.01	9.56E-01	0.20	7.40E-02
FTL_0740	0.08	5.77E-01	-0.12	5.74E-01
FTL_0741	-0.04	7.95E-01	-0.03	9.01E-01
FTL_0742	-0.02	NA	-0.01	9.87E-01
FTL_0743	0.09	5.02E-01	0.87	1.65E-12
FTL_0744	0.11	2.70E-01	0.35	6.67E-05
FTL_0745	-0.01	9.26E-01	0.14	3.34E-01
FTL_0746	-0.04	8.03E-01	0.08	7.31E-01
FTL_0747	0.07	6.11E-01	-0.20	2.81E-01
FTL_0748	0.06	6.78E-01	0.37	1.08E-02
FTL_0749	-0.12	3.19E-01	-0.12	6.66E-01
FTL_0750	-0.26	9.12E-02	-0.48	5.57E-03
FTL_0751	-0.22	1.35E-01	-1.51	7.39E-22
FTL_0752	0.07	6.51E-01	0.19	2.51E-01
FTL_0753	0.05	7.02E-01	0.48	3.57E-02
FTL_0754	0.08	5.24E-01	0.17	1.52E-01
FTL_0755	-0.29	9.05E-03	-0.76	2.75E-12
FTL_0756	-0.34	2.50E-02	-0.63	6.45E-05
FTL_0757	-0.21	1.47E-01	-0.89	3.72E-09
FTL_0758	0.07	5.35E-01	-0.23	3.75E-01
FTL_0759	0.08	5.15E-01	1.63	3.01E-09
FTL_0760	-0.14	2.69E-01	0.06	7.31E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0761	-0.06	6.63E-01	0.33	2.90E-02
FTL_0762	-0.08	5.22E-01	0.39	4.04E-03
FTL_0763	-0.17	2.21E-01	-0.06	7.84E-01
FTL_0764	-0.24	6.36E-02	-0.62	2.64E-06
FTL_0765	0.13	3.19E-01	0.42	1.98E-03
FTL_0766	0.41	4.92E-04	0.39	1.50E-03
FTL_0767	0.34	7.76E-03	0.99	1.90E-14
FTL_0768	0.03	7.96E-01	0.56	2.95E-09
FTL_0769	-0.03	NA	-0.97	1.31E-02
FTL_0770	0.05	NA	0.24	NA
FTL_0771	-0.05	6.50E-01	-0.35	2.22E-01
FTL_0772	-0.01	NA	-0.07	NA
FTL_0773	-0.01	NA	-0.03	NA
FTL_0774	0.00	NA	0.00	NA
FTL_0775	0.00	NA	-0.02	NA
FTL_0776	0.21	NA	0.69	3.09E-02
FTL_0777	0.01	NA	0.02	NA
FTL_0778	-0.01	NA	-0.14	6.37E-01
FTL_0779	-0.03	NA	-0.10	7.48E-01
FTL_0780	-0.05	NA	-1.01	1.55E-02
FTL_0781	0.07	5.84E-01	-0.11	6.77E-01
FTL_0782	0.05	NA	0.11	6.63E-01
FTL_0783	-0.11	4.19E-01	-0.31	1.27E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0784	0.04	7.67E-01	0.25	1.97E-02
FTL_0785	-0.09	5.17E-01	0.33	2.37E-02
FTL_0786	0.12	2.39E-01	0.37	4.45E-05
FTL_0787	0.08	5.20E-01	0.33	1.38E-02
FTL_0788	0.03	8.19E-01	0.34	9.58E-03
FTL_0789	0.07	5.50E-01	0.72	1.23E-13
FTL_0790	0.02	8.63E-01	1.03	1.00E-20
FTL_0791	0.04	NA	0.21	4.31E-01
FTL_0792	0.02	9.19E-01	0.17	2.05E-01
FTL_0793	-0.01	9.25E-01	-0.23	2.48E-01
FTL_0794	-0.01	NA	-0.04	NA
FTL_0795	-0.10	4.41E-01	0.75	2.68E-09
FTL_0796	-0.01	9.44E-01	-0.44	1.06E-03
FTL_0797	-0.08	5.41E-01	-0.51	9.55E-04
FTL_0798	-0.16	2.32E-01	-0.55	5.25E-04
FTL_0799	-0.12	3.78E-01	-0.66	3.36E-04
FTL_0800	-0.26	1.26E-03	-0.85	1.68E-28
FTL_0801	-0.08	4.47E-01	-0.39	4.82E-05
FTL_0802	-0.07	5.46E-01	-0.18	8.79E-02
FTL_0803	-0.29	1.00E-03	0.14	1.86E-01
FTL_0804	0.11	4.06E-01	0.95	6.04E-09
FTL_0805	0.07	6.08E-01	0.44	1.68E-04
FTL_0806	0.20	8.75E-02	1.07	2.69E-21

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0807	0.38	1.81E-03	0.31	1.91E-02
FTL_0808	0.25	2.83E-02	0.25	3.93E-02
FTL_0809	0.20	5.63E-02	0.42	4.75E-05
FTL_0810	0.02	NA	1.27	7.74E-03
FTL_0811	0.00	NA	-0.03	NA
FTL_0812	2.00	NA	0.47	1.41E-01
FTL_0813	0.66	9.11E-03	1.17	1.51E-05
FTL_0814	0.08	5.11E-01	1.96	7.97E-12
FTL_0815	0.01	NA	0.24	NA
FTL_0816	0.10	NA	2.32	3.12E-05
FTL_0817	-0.01	NA	-0.10	NA
FTL_0818	0.01	NA	0.06	NA
FTL_0819	0.00	NA	-0.01	NA
FTL_0820	-0.06	5.86E-01	-0.08	7.94E-01
FTL_0821	0.06	6.42E-01	0.24	9.29E-02
FTL_0822	-0.12	3.79E-01	0.46	3.69E-02
FTL_0823	0.10	3.39E-01	0.08	7.80E-01
FTL_0824	-0.01	9.51E-01	0.05	7.73E-01
FTL_0825	-0.14	3.10E-01	-0.36	2.05E-02
FTL_0826	-0.03	NA	-0.35	2.53E-01
FTL_0827	-0.23	7.36E-03	0.40	3.52E-06
FTL_0828	-0.07	4.85E-01	0.40	1.12E-06
FTL_0829	0.08	5.84E-01	-0.23	1.83E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0830	-0.01	9.55E-01	0.31	4.11E-02
FTL_0831	-0.07	5.24E-01	0.34	1.71E-03
FTL_0832	-0.08	4.25E-01	0.46	3.57E-08
FTL_0833	0.29	1.25E-02	0.77	7.14E-11
FTL_0834	0.28	6.64E-03	1.02	2.36E-23
FTL_0835	0.09	NA	-1.34	2.86E-04
FTL_0836	-0.33	6.79E-02	-1.00	7.21E-07
FTL_0837	0.05	7.11E-01	0.68	2.02E-09
FTL_0838	0.22	3.15E-02	0.92	1.25E-19
FTL_0839	0.13	2.95E-01	0.82	2.94E-12
FTL_0840	-0.15	2.70E-01	0.11	5.69E-01
FTL_0841	-0.14	3.10E-01	0.01	9.56E-01
FTL_0842	-0.02	NA	-0.66	NA
FTL_0843	-0.12	2.82E-01	0.26	1.24E-02
FTL_0844	0.19	2.02E-01	-1.05	1.01E-05
FTL_0845	-0.01	NA	0.04	8.87E-01
FTL_0846	0.35	9.30E-03	0.86	5.65E-10
FTL_0847	-0.06	6.77E-01	0.70	9.01E-07
FTL_0848	0.12	3.05E-01	0.25	2.63E-02
FTL_0849	-0.02	8.83E-01	0.24	1.53E-02
FTL_0850	0.08	5.80E-01	0.73	2.61E-07
FTL_0851	0.04	6.78E-01	0.85	3.60E-33
FTL_0852	0.00	9.93E-01	-0.10	4.83E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0853	0.08	5.45E-01	-0.38	1.60E-02
FTL_0854	0.14	3.10E-01	0.11	6.65E-01
FTL_0855	0.00	9.95E-01	0.20	8.93E-02
FTL_0856	0.01	9.53E-01	0.36	6.68E-04
FTL_0857	0.21	1.78E-01	0.37	1.50E-01
FTL_0858	0.04	8.12E-01	-0.02	9.12E-01
FTL_0859	0.02	8.84E-01	0.34	6.47E-02
FTL_0860	0.05	6.57E-01	0.11	6.58E-01
FTL_0861	-0.01	9.47E-01	0.01	9.75E-01
FTL_0862	-0.02	9.25E-01	0.06	7.82E-01
FTL_0863	0.04	7.67E-01	0.58	8.64E-06
FTL_0864	0.22	6.79E-02	0.81	3.71E-11
FTL_0865	-0.04	7.71E-01	0.83	8.77E-15
FTL_0866	-0.05	7.02E-01	0.26	2.91E-01
FTL_0867	0.03	8.54E-01	-0.89	2.75E-10
FTL_0868	-0.01	9.61E-01	-0.09	7.49E-01
FTL_0869	0.00	NA	0.04	NA
FTL_0870	0.00	NA	0.00	NA
FTL_0871	0.00	NA	-0.04	NA
FTL_0872	0.00	NA	-0.07	NA
FTL_0873	-0.02	NA	-0.34	2.36E-01
FTL_0874	0.04	NA	0.25	3.91E-01
FTL_0875	-0.08	3.68E-01	-1.30	3.60E-83

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0876	-0.01	9.56E-01	-0.26	1.17E-02
FTL_0877	0.24	1.76E-02	0.64	2.37E-10
FTL_0878	0.20	8.25E-02	0.26	3.40E-02
FTL_0879	0.57	4.48E-07	1.63	1.24E-45
FTL_0880	0.52	3.80E-03	1.07	1.06E-08
FTL_0881	0.09	1.35E-01	0.73	6.21E-02
FTL_0882	-0.22	6.75E-02	-0.67	1.67E-08
FTL_0883	-0.27	2.74E-02	-0.39	1.89E-03
FTL_0884	-0.05	7.18E-01	-0.58	4.98E-05
FTL_0885	-0.28	1.37E-02	-0.69	7.24E-10
FTL_0886	-0.03	8.19E-01	-0.17	1.46E-01
FTL_0887	-0.44	8.29E-04	-1.10	9.37E-18
FTL_0888	0.00	NA	-0.44	1.69E-01
FTL_0889	0.01	NA	-0.06	NA
FTL_0890	-0.03	8.32E-01	-0.13	5.32E-01
FTL_0891	0.08	5.73E-01	0.45	4.76E-03
FTL_0892	0.18	1.35E-01	0.61	2.81E-07
FTL_0893	0.19	5.57E-02	0.43	5.88E-06
FTL_0894	0.16	1.08E-01	0.40	7.05E-06
FTL_0895	-0.03	8.60E-01	0.89	2.61E-07
FTL_0896	0.04	8.19E-01	0.48	2.25E-03
FTL_0897	-0.02	8.64E-01	-0.16	2.10E-01
FTL_0898	-0.10	3.51E-01	-0.98	7.42E-21

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0899	-0.42	1.32E-05	-0.58	3.69E-09
FTL_0900	0.02	NA	-1.32	1.34E-02
FTL_0901	0.28	9.08E-02	-0.23	2.59E-01
FTL_0902	-0.04	7.06E-01	0.29	3.08E-01
FTL_0903	-0.13	2.18E-01	0.07	6.21E-01
FTL_0904	-0.05	7.01E-01	-0.05	7.32E-01
FTL_0905	-0.08	5.24E-01	-0.28	5.35E-02
FTL_0906	-0.11	3.31E-01	-0.50	7.76E-06
FTL_0907	-0.25	3.97E-02	0.04	8.37E-01
FTL_0908	-0.18	1.35E-01	-0.41	1.17E-03
FTL_0909	-0.10	NA	-1.59	1.26E-02
FTL_0910	0.00	NA	0.02	NA
FTL_0911	-0.01	NA	-0.12	6.19E-01
FTL_0912	-0.25	1.32E-01	-0.77	2.23E-03
FTL_0913	-0.08	5.11E-01	-0.40	4.14E-04
FTL_0914	-0.29	2.52E-02	-0.62	3.01E-06
FTL_0915	-0.01	9.32E-01	-0.18	4.12E-01
FTL_0916	-0.38	1.62E-04	0.00	9.99E-01
FTL_0917	0.07	5.11E-01	-0.32	1.09E-02
FTL_0918	0.07	5.45E-01	0.50	1.05E-05
FTL_0919	0.08	5.41E-01	-0.57	2.38E-02
FTL_0920	0.03	8.54E-01	0.14	4.62E-01
FTL_0921	-0.14	2.84E-01	-0.12	4.87E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0922	0.15	1.65E-01	0.60	5.30E-09
FTL_0923	0.30	2.94E-02	0.86	1.29E-09
FTL_0924	0.52	2.50E-02	0.68	5.87E-03
FTL_0925	0.05	7.02E-01	0.18	5.09E-01
FTL_0926	-0.08	5.33E-01	1.05	1.56E-12
FTL_0927	0.03	8.63E-01	0.06	6.91E-01
FTL_0928	-0.05	7.01E-01	-0.03	8.24E-01
FTL_0929	-0.06	6.01E-01	0.17	1.97E-01
FTL_0930	-0.02	8.89E-01	-0.10	5.25E-01
FTL_0931	-0.01	9.26E-01	0.58	1.78E-07
FTL_0932	0.04	7.64E-01	0.30	8.37E-02
FTL_0933	0.00	9.94E-01	0.45	3.24E-03
FTL_0934	-0.02	NA	-0.10	6.75E-01
FTL_0935	-0.08	5.11E-01	0.37	1.76E-01
FTL_0936	0.00	NA	-0.04	NA
FTL_0937	0.63	5.70E-04	0.96	3.21E-07
FTL_0938	0.05	7.40E-01	0.24	9.97E-02
FTL_0939	0.00	1.00E+00	0.63	1.25E-05
FTL_0940	-0.06	5.66E-01	0.47	1.10E-01
FTL_0941	0.17	1.57E-01	0.75	1.77E-10
FTL_0942	0.34	7.51E-03	0.59	6.85E-06
FTL_0943	0.01	9.47E-01	0.58	2.20E-03
FTL_0944	0.04	NA	-0.31	2.94E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0945	0.12	3.91E-01	0.21	3.41E-01
FTL_0946	0.01	9.24E-01	0.15	5.95E-01
FTL_0947	0.03	NA	-0.94	2.98E-02
FTL_0948	-0.02	9.03E-01	0.16	4.57E-01
FTL_0949	-0.05	6.83E-01	0.56	2.43E-06
FTL_0950	-0.11	3.68E-01	0.04	8.19E-01
FTL_0951	0.11	4.02E-01	0.18	2.70E-01
FTL_0952	0.00	NA	-2.20	NA
FTL_0953	0.78	1.12E-04	0.12	6.21E-01
FTL_0954	-0.02	8.81E-01	0.20	4.26E-01
FTL_0955	0.02	8.79E-01	0.59	3.68E-11
FTL_0956	-0.01	9.43E-01	0.02	9.15E-01
FTL_0957	-0.09	5.14E-01	-0.09	5.85E-01
FTL_0958	-0.10	4.46E-01	0.28	9.27E-02
FTL_0959	-0.10	4.45E-01	-0.10	5.04E-01
FTL_0960	0.03	8.72E-01	0.39	1.13E-02
FTL_0961	-0.05	6.66E-01	0.15	6.01E-01
FTL_0962	0.04	6.50E-01	0.33	2.69E-01
FTL_0963	0.34	6.62E-03	1.54	7.70E-32
FTL_0964	0.24	3.43E-02	1.70	4.62E-48
FTL_0965	0.16	2.50E-01	1.24	2.90E-13
FTL_0966	-0.13	3.43E-01	0.37	9.03E-02
FTL_0967	0.02	8.97E-01	0.63	1.37E-04

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0968	-0.04	7.85E-01	0.45	4.65E-04
FTL_0969	-0.17	2.23E-01	-0.30	9.52E-02
FTL_0970	0.00	NA	0.10	7.34E-01
FTL_0971	-0.03	8.33E-01	-1.37	4.15E-14
FTL_0972	-0.08	5.22E-01	-0.60	5.72E-03
FTL_0973	0.07	6.06E-01	-0.10	6.26E-01
FTL_0974	-0.02	8.89E-01	0.52	6.67E-05
FTL_0975	-0.06	6.26E-01	0.11	5.18E-01
FTL_0976	0.05	7.01E-01	-0.14	5.65E-01
FTL_0977	0.03	NA	-0.09	7.06E-01
FTL_0978	0.03	NA	0.20	4.69E-01
FTL_0979	0.00	NA	-0.03	NA
FTL_0980	0.00	NA	-0.05	8.75E-01
FTL_0981	-0.01	9.55E-01	-0.15	4.26E-01
FTL_0982	0.04	7.60E-01	0.08	7.07E-01
FTL_0983	0.02	9.19E-01	0.47	8.65E-05
FTL_0984	0.00	9.36E-01	0.15	1.58E-01
FTL_0985	0.05	7.12E-01	0.36	5.90E-03
FTL_0986	0.01	9.51E-01	0.48	9.03E-09
FTL_0987	0.01	9.39E-01	0.61	5.63E-08
FTL_0988	-0.02	8.96E-01	0.10	6.66E-01
FTL_0989	-0.16	1.42E-01	0.20	9.41E-02
FTL_0990	0.00	9.88E-01	0.09	7.76E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_0991	-0.01	NA	0.01	NA
FTL_0992	-0.04	7.67E-01	-0.20	3.25E-01
FTL_0993	-0.26	1.31E-01	-0.19	4.56E-01
FTL_0994	0.07	5.42E-01	0.15	2.31E-01
FTL_0995	0.09	4.74E-01	0.41	1.66E-03
FTL_0996	-0.06	6.79E-01	-0.56	8.16E-05
FTL_0997	0.03	NA	-0.18	4.67E-01
FTL_0998	-0.01	NA	-0.14	5.51E-01
FTL_0999	-0.24	1.29E-01	0.18	3.92E-01
FTL_1000	0.00	9.55E-01	-0.27	2.21E-01
FTL_1001	-0.56	1.40E-02	-0.57	1.61E-02
FTL_1002	-0.01	NA	-0.08	7.69E-01
FTL_1003	0.16	1.51E-01	0.35	1.45E-03
FTL_1004	0.06	7.11E-01	0.45	6.65E-03
FTL_1005	-0.06	6.50E-01	0.24	3.69E-02
FTL_1006	-0.09	5.19E-01	0.11	5.70E-01
FTL_1007	-0.10	3.67E-01	-0.10	7.14E-01
FTL_1008	-0.04	NA	-0.20	3.86E-01
FTL_1009	-0.06	NA	-0.89	3.01E-02
FTL_1010	-0.05	NA	-1.17	1.18E-02
FTL_1011	0.01	NA	0.02	NA
FTL_1012	0.10	5.05E-01	1.37	2.15E-16
FTL_1013	0.21	1.15E-01	0.92	1.67E-11

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1014	0.03	8.79E-01	0.41	3.71E-03
FTL_1015	0.13	2.17E-01	0.94	2.65E-22
FTL_1016	0.33	7.03E-03	0.76	1.72E-09
FTL_1017	-0.03	8.66E-01	0.36	7.96E-03
FTL_1018	0.12	3.90E-01	0.28	1.03E-01
FTL_1019	NA	NA	NA	NA
FTL_1020	-0.10	4.47E-01	-0.29	1.18E-01
FTL_1021	-0.22	8.30E-02	-0.12	4.69E-01
FTL_1022	-0.08	4.84E-01	0.49	8.67E-07
FTL_1023	-0.02	8.67E-01	-0.30	2.07E-01
FTL_1024	-0.35	9.05E-03	0.12	4.91E-01
FTL_1025	-0.28	6.16E-02	0.01	9.76E-01
FTL_1026	-0.29	2.10E-02	-0.01	9.41E-01
FTL_1027	-0.21	6.05E-02	-0.41	1.68E-04
FTL_1028	-0.10	3.71E-01	-0.02	8.50E-01
FTL_1029	-0.18	4.77E-02	0.21	3.19E-02
FTL_1030	-0.34	1.26E-02	-0.38	8.89E-03
FTL_1031	-0.04	7.17E-01	-0.27	3.29E-01
FTL_1032	0.01	8.51E-01	-0.35	2.17E-01
FTL_1033	0.07	NA	-0.45	1.30E-01
FTL_1034	-0.12	3.18E-01	0.38	1.54E-03
FTL_1035	-0.17	2.40E-01	-0.01	9.81E-01
FTL_1036	-0.04	6.95E-01	-0.39	1.69E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1037	-0.11	3.53E-01	0.29	2.32E-02
FTL_1038	-0.09	5.19E-01	-0.12	6.22E-01
FTL_1039	0.03	NA	-0.09	7.79E-01
FTL_1040	0.01	9.43E-01	-0.10	5.66E-01
FTL_1041	-0.01	9.65E-01	-0.32	1.28E-02
FTL_1042	0.01	9.43E-01	0.86	1.56E-14
FTL_1043	-0.06	6.48E-01	0.58	2.91E-08
FTL_1044	0.09	5.24E-01	0.84	1.35E-07
FTL_1045	0.08	5.56E-01	0.83	1.67E-11
FTL_1046	0.28	1.28E-02	0.78	2.24E-12
FTL_1047	4.39	2.01E-23	17.28	1.97E-25
FTL_1048	-0.98	5.04E-16	-3.62	8.43E-190
FTL_1049	-0.99	1.78E-39	-2.19	4.96E-171
FTL_1050	-0.28	4.82E-03	0.32	2.48E-03
FTL_1051	0.51	3.69E-07	0.50	7.33E-07
FTL_1052	0.00	NA	-0.02	NA
FTL_1053	0.02	NA	-0.49	1.30E-01
FTL_1054	-0.03	7.69E-01	0.04	9.02E-01
FTL_1055	0.03	8.22E-01	0.51	7.77E-03
FTL_1056	0.03	NA	0.41	1.99E-01
FTL_1057	0.46	6.18E-03	1.32	7.23E-14
FTL_1058	0.01	9.61E-01	-0.42	3.65E-03
FTL_1059	0.12	3.92E-01	-0.55	4.49E-04

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1060	0.18	1.07E-01	0.28	1.41E-02
FTL_1061	-0.08	4.64E-01	0.49	1.55E-07
FTL_1062	0.01	9.47E-01	-0.01	9.43E-01
FTL_1063	0.10	4.49E-01	-0.25	1.28E-01
FTL_1064	-0.08	5.33E-01	-0.11	4.62E-01
FTL_1065	-0.14	3.20E-01	-0.06	8.06E-01
FTL_1066	-0.06	6.63E-01	0.31	7.41E-02
FTL_1067	0.06	6.05E-01	0.33	3.48E-03
FTL_1068	0.03	8.63E-01	0.08	6.65E-01
FTL_1069	-0.02	8.82E-01	0.15	4.27E-01
FTL_1070	-0.01	NA	-0.06	NA
FTL_1071	0.02	8.57E-01	0.21	4.56E-02
FTL_1072	-0.10	2.66E-01	0.22	1.05E-02
FTL_1073	0.01	9.44E-01	0.73	5.37E-06
FTL_1074	-0.17	1.77E-01	0.10	5.36E-01
FTL_1075	-0.01	9.54E-01	0.57	4.95E-06
FTL_1076	0.02	9.16E-01	0.41	1.44E-03
FTL_1077	0.02	8.93E-01	0.43	3.04E-04
FTL_1078	0.10	4.84E-01	-0.28	1.97E-01
FTL_1079	0.09	NA	0.23	4.31E-01
FTL_1080	0.18	1.96E-01	0.36	1.85E-01
FTL_1081	0.03	NA	-0.02	9.26E-01
FTL_1082	0.02	NA	0.07	NA

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1083	0.00	NA	-0.01	NA
FTL_1084	0.00	NA	0.01	NA
FTL_1085	0.00	NA	-0.06	NA
FTL_1086	0.10	4.22E-01	-0.02	9.42E-01
FTL_1087	0.00	9.64E-01	0.05	8.64E-01
FTL_1088	0.06	6.49E-01	0.64	9.29E-04
FTL_1089	-0.10	3.69E-01	0.78	5.74E-13
FTL_1090	-0.07	5.95E-01	0.42	1.10E-02
FTL_1091	0.68	1.78E-03	1.29	1.60E-08
FTL_1092	0.04	NA	0.38	2.13E-01
FTL_1093	0.02	8.89E-01	0.62	1.51E-09
FTL_1094	0.15	2.86E-01	0.26	2.35E-01
FTL_1095	0.16	2.84E-01	0.81	4.09E-04
FTL_1096	-0.06	6.03E-01	0.71	7.07E-12
FTL_1097	-0.03	8.54E-01	1.00	3.09E-19
FTL_1098	-0.03	NA	-0.74	4.26E-02
FTL_1099	-0.04	7.95E-01	0.16	3.55E-01
FTL_1100	-0.01	9.39E-01	0.48	1.02E-03
FTL_1101	0.14	3.25E-01	0.28	2.18E-01
FTL_1102	-0.09	4.88E-01	0.20	4.22E-01
FTL_1103	0.04	NA	-0.63	7.89E-02
FTL_1104	0.01	NA	-1.06	1.77E-02
FTL_1105	-0.08	5.24E-01	0.51	9.29E-05

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1106	0.07	5.24E-01	0.26	1.53E-02
FTL_1107	0.09	4.49E-01	0.06	6.92E-01
FTL_1108	-0.11	3.88E-01	0.61	3.28E-08
FTL_1109	0.04	6.91E-01	0.62	1.06E-16
FTL_1110	-0.13	3.07E-01	0.78	2.33E-09
FTL_1111	-0.01	NA	-0.33	NA
FTL_1112	-0.04	7.40E-01	-0.22	4.16E-01
FTL_1113	0.05	5.99E-01	-0.95	6.60E-03
FTL_1114	0.00	9.69E-01	-1.79	3.58E-11
FTL_1115	0.19	1.16E-01	0.69	1.95E-08
FTL_1116	0.01	9.55E-01	0.40	6.38E-04
FTL_1117	0.10	4.03E-01	0.55	3.24E-07
FTL_1118	-0.15	1.79E-01	0.50	4.06E-07
FTL_1119	0.11	3.49E-01	0.53	4.46E-06
FTL_1120	-0.01	9.58E-01	0.26	2.17E-01
FTL_1121	0.05	7.08E-01	0.91	1.51E-09
FTL_1122	0.01	NA	0.31	3.03E-01
FTL_1123	-0.05	6.40E-01	0.45	1.41E-01
FTL_1124	0.00	NA	0.24	4.10E-01
FTL_1125	0.01	9.54E-01	-0.04	8.79E-01
FTL_1126	-0.03	NA	-0.11	6.91E-01
FTL_1127	-0.05	6.98E-01	-0.17	3.55E-01
FTL_1128	NA	NA	NA	NA

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1129	0.07	6.13E-01	0.32	5.59E-02
FTL_1130	-0.02	NA	-0.08	NA
FTL_1131	-0.02	8.92E-01	-0.05	8.43E-01
FTL_1132	-0.07	5.66E-01	0.25	3.13E-02
FTL_1133	-0.07	5.87E-01	0.38	5.03E-03
FTL_1134	0.16	1.74E-01	0.75	3.37E-11
FTL_1135	0.45	1.81E-03	1.02	5.53E-12
FTL_1136	-0.27	5.18E-02	-0.33	3.37E-02
FTL_1137	-0.11	3.54E-01	-0.28	3.04E-02
FTL_1138	-0.20	1.09E-01	0.12	4.24E-01
FTL_1139	-0.03	8.14E-01	0.27	3.69E-02
FTL_1140	0.04	8.10E-01	0.18	2.60E-01
FTL_1141	0.05	6.84E-01	0.14	2.81E-01
FTL_1142	-0.21	2.65E-02	-0.08	4.77E-01
FTL_1143	-0.12	3.87E-01	0.16	3.73E-01
FTL_1144	-0.10	4.81E-01	0.22	2.57E-01
FTL_1145	0.08	5.20E-01	0.77	6.21E-12
FTL_1146	0.14	2.32E-01	0.66	1.66E-09
FTL_1147	0.04	8.12E-01	0.44	1.68E-03
FTL_1148	-0.03	8.33E-01	0.46	1.78E-02
FTL_1149	-0.02	8.79E-01	0.41	1.21E-03
FTL_1150	0.00	NA	0.06	NA
FTL_1151	0.02	NA	-0.03	9.22E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1152	0.00	NA	0.00	NA
FTL_1153	-0.08	5.59E-01	-0.25	2.35E-01
FTL_1154	0.02	NA	0.03	NA
FTL_1155	-0.02	NA	-0.16	NA
FTL_1156	0.02	NA	0.09	NA
FTL_1173	-0.18	1.84E-01	0.57	2.69E-05
FTL_1174	0.47	1.44E-04	1.40	9.17E-29
FTL_1175	0.03	NA	0.30	2.38E-01
FTL_1176	0.09	4.68E-01	0.14	5.91E-01
FTL_1177	0.18	1.40E-01	0.37	4.98E-03
FTL_1178	0.00	NA	-0.03	NA
FTL_1179	-0.06	6.15E-01	0.29	4.20E-03
FTL_1180	-0.01	9.11E-01	-0.17	1.45E-01
FTL_1181	-0.09	4.07E-01	-0.64	1.00E-11
FTL_1182	-0.09	4.77E-01	-0.47	6.06E-05
FTL_1183	-0.11	4.16E-01	-0.78	2.61E-05
FTL_1184	-0.09	4.49E-01	-0.10	5.09E-01
FTL_1185	-0.02	8.79E-01	0.00	9.95E-01
FTL_1186	-0.20	2.10E-02	0.33	1.07E-04
FTL_1187	-0.12	3.33E-01	0.58	2.63E-06
FTL_1188	-0.03	8.63E-01	0.11	4.33E-01
FTL_1189	0.10	3.95E-01	0.00	9.95E-01
FTL_1190	0.03	8.13E-01	0.52	9.97E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1191	0.49	1.13E-03	0.94	4.68E-10
FTL_1192	0.18	1.84E-01	0.26	8.60E-02
FTL_1193	0.00	NA	0.03	NA
FTL_1194	-0.01	NA	-0.09	NA
FTL_1195	-0.11	4.43E-01	-0.23	2.35E-01
FTL_1196	0.13	3.01E-01	-0.02	9.55E-01
FTL_1197	0.03	8.54E-01	0.29	6.75E-02
FTL_1198	0.06	6.49E-01	-0.08	5.54E-01
FTL_1199	-0.07	6.20E-01	-0.04	8.16E-01
FTL_1200	-0.20	1.46E-01	-0.22	2.09E-01
FTL_1201	-0.06	6.68E-01	-0.30	1.53E-01
FTL_1202	-0.06	6.83E-01	0.87	2.44E-10
FTL_1203	-0.01	9.35E-01	0.58	5.67E-07
FTL_1204	-0.01	9.51E-01	1.22	4.01E-18
FTL_1205	0.00	NA	-0.08	NA
FTL_1206	0.03	7.98E-01	-0.09	7.54E-01
FTL_1207	-0.16	1.57E-01	-1.02	2.76E-20
FTL_1208	-0.06	6.15E-01	0.08	4.72E-01
FTL_1209	0.03	NA	-0.01	9.62E-01
FTL_1210	0.01	7.82E-01	0.00	9.95E-01
FTL_1211	0.03	8.67E-01	0.77	3.20E-10
FTL_1212	0.06	5.75E-01	0.43	2.21E-05
FTL_1213	0.57	1.49E-04	1.51	1.66E-22

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1214	0.03	NA	0.27	NA
FTL_1215	-0.43	1.81E-03	-0.31	3.69E-02
FTL_1216	-0.18	9.85E-02	-0.02	9.13E-01
FTL_1217	0.88	2.68E-02	1.41	1.26E-03
FTL_1218	0.28	5.68E-02	0.61	9.55E-05
FTL_1219	0.63	2.11E-11	0.89	1.97E-20
FTL_1220	0.06	6.84E-01	0.17	4.35E-01
FTL_1221	0.03	NA	-0.31	2.93E-01
FTL_1222	-0.12	NA	-0.46	1.49E-01
FTL_1223	0.21	1.57E-01	0.96	1.75E-07
FTL_1224	0.20	6.53E-02	1.10	1.17E-26
FTL_1225	0.49	1.17E-04	1.49	8.62E-31
FTL_1226	0.38	4.87E-02	0.51	1.76E-02
FTL_1227	0.09	5.27E-01	1.11	5.68E-10
FTL_1228	-0.01	9.54E-01	0.39	3.21E-02
FTL_1229	-0.22	4.70E-02	0.19	1.26E-01
FTL_1230	-0.20	1.29E-01	0.25	9.03E-02
FTL_1231	-0.38	3.30E-02	-0.14	5.22E-01
FTL_1232	-0.03	8.43E-01	0.20	1.34E-01
FTL_1233	0.02	8.78E-01	0.52	1.33E-05
FTL_1234	0.06	1.88E-01	0.08	7.39E-01
FTL_1235	0.03	8.19E-01	0.28	2.66E-01
FTL_1236	-0.32	2.74E-02	-0.25	1.29E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1237	-0.01	9.26E-01	0.50	4.14E-04
FTL_1238	0.03	NA	0.18	NA
FTL_1239	-0.05	6.94E-01	0.09	4.12E-01
FTL_1240	-0.09	4.31E-01	0.23	1.89E-02
FTL_1241	-0.07	5.73E-01	-0.22	3.03E-01
FTL_1242	0.03	8.54E-01	0.64	3.76E-03
FTL_1243	0.28	4.17E-03	0.71	1.91E-13
FTL_1244	-0.04	7.60E-01	0.42	6.37E-04
FTL_1245	0.02	9.27E-01	0.52	6.33E-05
FTL_1246	-0.07	6.15E-01	0.48	1.15E-03
FTL_1247	0.00	9.77E-01	1.02	2.38E-12
FTL_1248	0.02	8.81E-01	0.56	2.54E-07
FTL_1249	-0.04	7.94E-01	0.54	1.50E-03
FTL_1250	-0.35	8.63E-02	-0.27	3.42E-01
FTL_1251	0.14	2.24E-01	1.02	7.89E-21
FTL_1252	-0.05	6.47E-01	0.45	3.89E-06
FTL_1253	0.03	8.19E-01	-0.10	4.78E-01
FTL_1254	-0.01	9.49E-01	-0.21	4.27E-01
FTL_1255	0.02	8.51E-01	-0.30	2.94E-01
FTL_1256	0.09	5.14E-01	0.71	4.18E-06
FTL_1257	0.02	8.83E-01	0.25	3.61E-01
FTL_1258	-0.16	1.75E-01	-0.04	8.06E-01
FTL_1259	-0.04	7.31E-01	-0.55	1.83E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1260	0.00	NA	-0.53	1.03E-01
FTL_1261	-0.09	5.24E-01	-0.15	4.60E-01
FTL_1262	-0.05	6.73E-01	-0.15	2.42E-01
FTL_1263	0.12	3.61E-01	0.32	4.18E-02
FTL_1264	-0.03	8.18E-01	0.11	6.11E-01
FTL_1265	0.34	1.31E-02	0.57	6.67E-05
FTL_1266	0.21	7.01E-02	1.08	1.03E-20
FTL_1267	0.14	2.60E-01	0.53	1.94E-05
FTL_1268	0.11	NA	1.26	1.32E-02
FTL_1269	0.07	4.37E-01	0.52	1.13E-01
FTL_1270	0.00	9.78E-01	-0.15	5.68E-01
FTL_1271	0.00	9.84E-01	0.33	1.66E-03
FTL_1272	0.24	7.01E-02	0.42	2.88E-03
FTL_1273	0.24	6.87E-02	-0.15	3.43E-01
FTL_1274	0.08	3.50E-01	-0.13	6.58E-01
FTL_1275	-0.03	8.54E-01	0.17	3.14E-01
FTL_1276	-0.03	8.54E-01	0.20	2.69E-01
FTL_1277	-0.01	9.28E-01	0.17	3.44E-01
FTL_1278	0.05	7.29E-01	0.15	4.33E-01
FTL_1279	0.03	8.40E-01	0.21	2.72E-01
FTL_1280	-0.03	NA	-0.09	NA
FTL_1281	-0.08	4.69E-01	-0.47	8.97E-02
FTL_1282	0.03	8.52E-01	0.21	2.31E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1283	-0.15	1.29E-01	-0.04	7.46E-01
FTL_1284	-0.08	4.19E-01	-0.06	6.00E-01
FTL_1285	-0.11	3.79E-01	-0.01	9.48E-01
FTL_1286	0.12	3.01E-01	0.51	4.13E-06
FTL_1287	0.27	4.29E-03	0.90	4.21E-22
FTL_1288	0.07	3.59E-01	0.52	1.24E-01
FTL_1289	-0.01	NA	-0.14	5.03E-01
FTL_1290	-0.10	4.79E-01	-0.19	3.64E-01
FTL_1291	0.01	NA	-0.12	NA
FTL_1292	0.03	NA	0.08	NA
FTL_1293	-0.14	1.95E-01	0.04	7.85E-01
FTL_1294	-0.03	8.56E-01	0.43	7.46E-05
FTL_1295	0.03	8.32E-01	-2.03	1.93E-32
FTL_1296	0.28	1.24E-01	0.11	6.95E-01
FTL_1297	-0.05	7.11E-01	0.18	4.25E-01
FTL_1298	-0.09	5.29E-01	-0.18	3.26E-01
FTL_1299	0.10	4.34E-01	0.56	6.93E-03
FTL_1300	0.06	NA	0.41	1.71E-01
FTL_1301	-0.08	4.97E-01	-0.25	3.62E-01
FTL_1302	0.03	8.19E-01	0.63	1.00E-11
FTL_1303	-0.06	5.24E-01	0.45	1.41E-01
FTL_1304	0.20	2.74E-02	0.47	7.90E-08
FTL_1305	0.14	3.06E-01	-0.02	9.12E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1306	0.06	6.23E-01	0.72	1.82E-14
FTL_1307	-0.16	2.63E-01	-0.51	1.70E-03
FTL_1308	-0.04	7.48E-01	-0.21	3.61E-02
FTL_1309	-0.06	5.75E-01	0.19	4.98E-02
FTL_1310	-0.10	3.97E-01	0.49	1.60E-05
FTL_1311	-0.18	1.41E-01	0.59	7.47E-07
FTL_1312	0.35	1.81E-03	1.47	5.15E-37
FTL_1313	0.22	1.14E-01	0.81	6.91E-08
FTL_1314	-0.02	NA	-0.40	1.93E-01
FTL_1315	0.00	NA	-0.86	5.07E-02
FTL_1316	-0.05	7.54E-01	-0.20	3.42E-01
FTL_1317	0.36	7.18E-03	0.36	1.10E-02
FTL_1318	0.00	NA	-0.01	NA
FTL_1319	-0.09	3.96E-01	-0.30	2.88E-01
FTL_1320	-0.05	NA	-0.24	3.86E-01
FTL_1321	0.01	NA	0.09	NA
FTL_1322	-0.05	NA	-1.94	8.31E-03
FTL_1323	0.02	NA	0.22	4.35E-01
FTL_1324	NA	NA	NA	NA
FTL_1325	0.01	9.58E-01	-0.20	4.54E-01
FTL_1326	0.02	NA	-0.51	1.17E-01
FTL_1327	0.00	9.92E-01	-0.15	3.18E-01
FTL_1328	0.10	4.14E-01	0.33	4.38E-03

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1329	-0.09	5.11E-01	-0.36	5.26E-02
FTL_1330	0.00	9.94E-01	-0.27	1.98E-01
FTL_1331	-0.19	2.03E-01	-0.20	3.20E-01
FTL_1332	-0.18	1.68E-01	-0.17	3.09E-01
FTL_1333	-0.10	4.24E-01	-0.15	2.61E-01
FTL_1334	0.04	7.30E-01	0.08	6.24E-01
FTL_1335	0.07	6.05E-01	0.16	4.79E-01
FTL_1336	0.06	6.25E-01	0.54	1.46E-06
FTL_1337	0.01	9.61E-01	0.39	7.75E-03
FTL_1338	-0.02	8.90E-01	0.84	3.38E-07
FTL_1339	0.08	5.46E-01	0.49	8.68E-03
FTL_1340	0.01	9.32E-01	0.96	2.24E-18
FTL_1341	0.09	5.29E-01	0.38	3.96E-02
FTL_1342	0.03	8.39E-01	0.89	2.32E-15
FTL_1343	-0.12	1.95E-01	-0.26	3.73E-01
FTL_1344	0.01	9.26E-01	0.85	9.62E-06
FTL_1345	0.27	2.50E-02	0.63	1.62E-07
FTL_1346	0.01	NA	-0.10	NA
FTL_1347	0.04	NA	0.06	NA
FTL_1348	-0.04	7.60E-01	-0.12	6.58E-01
FTL_1349	-0.02	9.01E-01	-0.11	6.24E-01
FTL_1350	0.02	8.54E-01	0.15	1.08E-01
FTL_1351	0.10	4.51E-01	0.42	2.87E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1352	-0.04	7.62E-01	-0.12	6.24E-01
FTL_1353	-0.01	NA	-0.19	NA
FTL_1354	0.02	9.16E-01	0.43	1.02E-03
FTL_1355	-0.04	7.82E-01	0.12	5.71E-01
FTL_1356	-0.09	4.64E-01	0.28	2.48E-02
FTL_1357	-0.02	9.10E-01	0.72	3.97E-12
FTL_1358	-0.01	9.50E-01	1.22	1.05E-28
FTL_1359	-0.25	1.14E-01	-0.09	6.92E-01
FTL_1360	0.33	4.54E-02	0.08	7.21E-01
FTL_1361	0.12	3.97E-01	0.18	4.27E-01
FTL_1362	-0.08	5.65E-01	-0.30	5.60E-02
FTL_1363	-0.02	9.21E-01	0.18	2.34E-01
FTL_1364	-0.02	9.15E-01	0.71	1.57E-10
FTL_1365	0.00	9.65E-01	0.01	9.63E-01
FTL_1366	-0.10	4.27E-01	-0.60	7.71E-03
FTL_1367	-0.03	8.39E-01	-0.36	1.98E-02
FTL_1368	0.01	9.24E-01	-0.30	2.34E-01
FTL_1369	-0.04	7.82E-01	-0.15	4.69E-01
FTL_1370	0.02	8.93E-01	0.59	5.29E-07
FTL_1371	-0.30	7.11E-02	-1.05	1.59E-08
FTL_1372	-0.13	3.61E-01	-0.63	2.87E-03
FTL_1373	-0.03	NA	-1.78	1.48E-07
FTL_1374	0.08	5.68E-01	-0.27	6.21E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1375	-0.05	NA	0.57	1.09E-01
FTL_1376	0.15	2.32E-01	0.71	1.57E-07
FTL_1377	0.00	NA	-0.34	2.63E-01
FTL_1378	0.00	NA	-0.04	NA
FTL_1379	0.07	5.79E-01	0.09	6.98E-01
FTL_1380	-0.03	NA	-0.28	NA
FTL_1381	-0.02	NA	-0.14	6.22E-01
FTL_1382	-0.11	4.45E-01	0.23	2.67E-01
FTL_1383	-0.01	9.37E-01	0.99	2.49E-10
FTL_1384	0.01	9.28E-01	0.60	3.07E-02
FTL_1385	0.59	NA	0.52	1.25E-01
FTL_1386	-0.03	7.67E-01	-0.22	4.14E-01
FTL_1387	-0.40	7.43E-02	-0.69	1.67E-02
FTL_1388	-0.37	4.04E-04	-0.04	7.79E-01
FTL_1389	-0.18	1.32E-01	0.02	9.15E-01
FTL_1390	-0.07	5.43E-01	0.19	1.18E-01
FTL_1391	0.01	9.26E-01	0.40	2.71E-04
FTL_1392	-0.20	5.17E-02	0.33	1.16E-03
FTL_1393	-0.37	3.29E-02	-0.18	3.86E-01
FTL_1394	-0.11	3.52E-01	-0.01	9.70E-01
FTL_1395	0.10	4.47E-01	0.51	8.88E-05
FTL_1396	0.07	5.19E-01	0.36	2.11E-04
FTL_1397	-0.08	5.15E-01	0.23	3.72E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1398	0.06	6.59E-01	-0.25	4.84E-02
FTL_1399	0.21	5.39E-02	-0.28	1.49E-02
FTL_1400	0.15	3.01E-01	0.03	8.90E-01
FTL_1401	-0.02	NA	-0.05	8.85E-01
FTL_1402	-0.05	7.27E-01	-0.13	5.24E-01
FTL_1403	0.02	8.67E-01	-0.37	1.25E-01
FTL_1404	-0.31	1.80E-02	0.37	1.05E-02
FTL_1405	-0.31	6.72E-02	0.03	8.90E-01
FTL_1406	-0.05	6.98E-01	-0.61	9.07E-04
FTL_1407	-0.02	9.14E-01	0.40	7.48E-05
FTL_1408	0.01	9.61E-01	-0.09	6.40E-01
FTL_1409	-0.29	9.11E-03	0.75	1.79E-11
FTL_1410	0.02	9.15E-01	0.19	1.25E-01
FTL_1411	0.09	5.11E-01	0.83	1.40E-07
FTL_1412	0.06	6.36E-01	0.53	4.35E-06
FTL_1413	0.07	4.88E-01	0.47	8.24E-09
FTL_1414	-0.16	1.40E-01	0.94	3.55E-21
FTL_1415	-0.02	8.77E-01	1.17	3.09E-19
FTL_1416	-0.15	1.88E-01	0.90	1.55E-16
FTL_1417	0.01	9.46E-01	0.01	9.47E-01
FTL_1418	-0.12	3.54E-01	0.09	5.69E-01
FTL_1419	-0.28	7.82E-03	0.12	3.49E-01
FTL_1420	0.06	6.21E-01	0.40	4.40E-05

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1421	0.03	8.56E-01	-0.14	4.31E-01
FTL_1422	0.08	5.45E-01	-0.34	5.00E-02
FTL_1423	0.06	6.51E-01	-0.41	1.37E-02
FTL_1424	0.03	8.22E-01	-0.39	4.73E-02
FTL_1425	0.00	9.75E-01	0.16	3.92E-01
FTL_1426	0.05	7.36E-01	0.14	4.77E-01
FTL_1427	0.00	9.61E-01	0.05	7.94E-01
FTL_1428	0.05	6.91E-01	0.00	9.81E-01
FTL_1429	0.19	1.44E-01	0.03	8.53E-01
FTL_1430	0.08	4.43E-01	0.21	3.23E-02
FTL_1431	-0.03	8.54E-01	-0.26	5.02E-02
FTL_1432	-0.21	9.46E-02	0.24	8.14E-02
FTL_1433	-0.07	5.71E-01	0.33	5.71E-03
FTL_1434	0.01	NA	-0.07	8.07E-01
FTL_1435	-0.02	NA	-0.15	NA
FTL_1436	0.00	NA	0.00	NA
FTL_1437	0.00	NA	0.16	5.68E-01
FTL_1438	0.00	NA	-0.07	NA
FTL_1439	0.01	NA	0.05	8.43E-01
FTL_1440	0.00	NA	-0.05	8.74E-01
FTL_1441	-0.02	8.94E-01	0.05	8.84E-01
FTL_1442	-0.25	6.49E-03	0.20	5.34E-02
FTL_1443	-0.24	8.62E-03	-0.36	1.10E-04

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1444	-0.12	3.39E-01	-0.07	8.11E-01
FTL_1445	-0.04	7.67E-01	-0.31	2.34E-01
FTL_1446	-0.08	5.51E-01	-0.21	3.07E-01
FTL_1447	0.02	NA	0.20	4.37E-01
FTL_1448	-0.07	5.81E-01	-0.12	4.33E-01
FTL_1449	-0.01	9.59E-01	-0.10	5.84E-01
FTL_1450	0.15	1.29E-01	0.47	3.70E-07
FTL_1451	-0.01	9.52E-01	0.40	7.40E-03
FTL_1452	-0.08	5.51E-01	0.07	6.58E-01
FTL_1453	-0.26	1.30E-01	-0.09	6.98E-01
FTL_1454	-0.12	NA	0.11	7.17E-01
FTL_1455	0.05	6.59E-01	0.42	1.18E-01
FTL_1456	0.00	NA	-0.22	4.27E-01
FTL_1457	-0.03	NA	-0.26	3.80E-01
FTL_1458	0.12	2.67E-01	0.25	1.81E-02
FTL_1459	0.03	8.54E-01	0.70	6.76E-06
FTL_1460	-0.06	6.84E-01	0.34	3.65E-02
FTL_1461	0.03	8.52E-01	0.92	7.46E-20
FTL_1462	-0.09	5.19E-01	-0.15	4.29E-01
FTL_1463	-0.01	9.30E-01	0.05	8.80E-01
FTL_1464	-0.20	1.49E-01	0.03	8.93E-01
FTL_1465	-0.05	NA	0.20	4.92E-01
FTL_1466	-0.04	NA	-0.28	3.45E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1467	-0.05	6.69E-01	-0.04	9.03E-01
FTL_1468	-0.17	2.39E-01	0.01	9.60E-01
FTL_1469	-0.08	NA	0.13	6.58E-01
FTL_1470	-0.05	NA	-0.56	1.09E-01
FTL_1471	-0.11	3.01E-01	-0.23	4.22E-01
FTL_1472	0.00	9.61E-01	0.10	7.49E-01
FTL_1473	-0.07	5.11E-01	-0.40	1.57E-06
FTL_1474	-0.04	7.30E-01	0.35	1.07E-03
FTL_1475	0.11	2.84E-01	0.23	2.49E-02
FTL_1476	0.01	9.46E-01	0.38	4.42E-04
FTL_1477	0.10	4.68E-01	0.17	3.61E-01
FTL_1478	-0.23	6.06E-02	-0.11	4.45E-01
FTL_1479	0.08	5.75E-01	0.74	1.67E-08
FTL_1480	0.07	5.72E-01	0.26	7.38E-02
FTL_1481	-0.05	7.18E-01	0.29	1.23E-02
FTL_1482	0.08	5.16E-01	0.57	6.51E-07
FTL_1483	0.08	5.27E-01	0.45	1.18E-04
FTL_1484	-0.01	9.41E-01	0.11	6.56E-01
FTL_1485	-0.16	2.27E-01	-0.84	3.69E-09
FTL_1486	-0.06	6.36E-01	0.03	8.34E-01
FTL_1487	-0.01	9.32E-01	0.54	7.05E-06
FTL_1488	-0.09	5.24E-01	0.58	8.76E-05
FTL_1489	0.01	9.46E-01	0.26	1.39E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1490	0.11	3.40E-01	0.78	3.86E-14
FTL_1491	0.01	9.60E-01	0.40	1.61E-04
FTL_1492	0.23	1.72E-02	0.76	1.24E-16
FTL_1493	-0.05	7.16E-01	0.19	2.07E-01
FTL_1494	0.18	8.84E-02	1.14	8.26E-30
FTL_1495	0.00	9.67E-01	0.37	9.46E-05
FTL_1496	0.05	7.20E-01	0.35	2.98E-03
FTL_1497	0.10	4.32E-01	0.72	6.46E-09
FTL_1498	-0.12	3.29E-01	0.26	6.07E-02
FTL_1499	0.00	1.00E+00	-0.13	3.27E-01
FTL_1500	-0.11	NA	-0.07	8.11E-01
FTL_1501	0.00	NA	0.00	NA
FTL_1502	0.02	8.46E-01	-0.12	6.82E-01
FTL_1503	0.47	3.76E-07	0.93	4.47E-23
FTL_1504	-0.47	2.94E-04	0.49	3.83E-04
FTL_1505	-0.02	8.83E-01	-0.15	4.08E-01
FTL_1506	0.01	9.46E-01	0.70	2.65E-05
FTL_1507	0.00	9.91E-01	0.80	1.56E-06
FTL_1508	0.04	NA	0.13	NA
FTL_1509	0.26	6.32E-02	1.04	7.39E-13
FTL_1510	0.12	2.72E-01	0.68	4.19E-13
FTL_1511	0.28	4.86E-03	0.99	1.02E-24
FTL_1512	0.09	5.11E-01	-0.06	8.36E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1513	-0.01	NA	-0.05	8.77E-01
FTL_1514	0.01	NA	-0.06	8.11E-01
FTL_1515	0.02	NA	0.00	NA
FTL_1516	-0.01	9.20E-01	0.02	9.45E-01
FTL_1517	-0.09	4.62E-01	-0.86	8.92E-04
FTL_1518	-0.18	2.26E-01	-0.30	1.66E-01
FTL_1519	-0.02	8.55E-01	0.26	3.21E-01
FTL_1520	-0.21	1.37E-01	0.55	4.19E-04
FTL_1521	-0.05	7.18E-01	0.13	3.82E-01
FTL_1522	0.18	1.14E-01	0.97	3.87E-18
FTL_1523	0.02	8.81E-01	0.84	1.16E-11
FTL_1524	0.05	7.15E-01	0.57	1.41E-03
FTL_1525	0.02	8.79E-01	-0.28	8.67E-02
FTL_1526	0.06	6.33E-01	-0.07	6.58E-01
FTL_1527	0.07	5.59E-01	0.33	6.30E-04
FTL_1528	0.15	2.84E-01	-0.12	5.04E-01
FTL_1529	0.10	4.29E-01	-0.47	5.61E-02
FTL_1530	-0.08	5.24E-01	-0.25	3.21E-01
FTL_1531	0.11	3.74E-01	0.03	8.37E-01
FTL_1532	-0.11	3.97E-01	0.51	1.81E-04
FTL_1533	-0.14	3.07E-01	-0.12	5.40E-01
FTL_1534	-0.30	7.92E-03	-0.94	3.53E-17
FTL_1535	-0.11	3.15E-01	-0.24	2.17E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1536	-0.02	8.55E-01	-0.14	6.23E-01
FTL_1537	-0.29	3.30E-02	-0.11	5.44E-01
FTL_1538	-0.14	2.14E-01	0.10	4.38E-01
FTL_1539	-0.13	3.12E-01	-0.14	3.13E-01
FTL_1540	0.09	4.54E-01	0.19	4.67E-01
FTL_1541	-0.07	5.66E-01	0.20	1.26E-01
FTL_1542	-0.01	9.51E-01	0.50	5.87E-08
FTL_1543	0.07	5.84E-01	0.46	2.47E-04
FTL_1544	-0.12	3.74E-01	-0.20	3.32E-01
FTL_1545	-0.05	5.84E-01	0.38	2.17E-01
FTL_1546	0.08	5.24E-01	0.69	1.45E-08
FTL_1547	0.00	9.76E-01	0.06	6.21E-01
FTL_1548	-0.15	2.09E-01	0.18	1.86E-01
FTL_1549	-0.22	4.47E-02	-0.01	9.48E-01
FTL_1550	0.04	7.51E-01	0.55	1.52E-07
FTL_1551	-0.04	NA	-0.10	NA
FTL_1552	-0.02	8.54E-01	0.75	6.35E-18
FTL_1553	-0.21	2.47E-02	0.47	2.30E-07
FTL_1554	-0.19	1.11E-01	0.32	1.26E-02
FTL_1555	-0.46	1.70E-02	-0.34	1.09E-01
FTL_1556	0.13	3.38E-01	0.20	2.72E-01
FTL_1557	-0.18	2.03E-01	0.34	1.89E-01
FTL_1558	0.00	9.80E-01	0.94	4.63E-04

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1559	0.24	1.29E-01	-0.46	7.40E-03
FTL_1560	0.00	NA	0.01	NA
FTL_1561	0.00	NA	-0.05	NA
FTL_1562	-0.01	9.58E-01	0.27	2.27E-01
FTL_1563	-0.03	NA	-0.24	3.84E-01
FTL_1564	-0.01	NA	-0.19	NA
FTL_1565	0.03	8.19E-01	-0.05	8.66E-01
FTL_1566	0.03	8.67E-01	0.46	1.88E-04
FTL_1567	0.06	6.96E-01	-0.34	4.11E-02
FTL_1568	0.28	7.20E-02	0.33	6.86E-02
FTL_1569	-0.04	7.63E-01	0.20	2.00E-01
FTL_1570	-0.05	7.11E-01	0.39	7.88E-04
FTL_1571	0.01	9.41E-01	0.61	4.79E-13
FTL_1572	-0.02	8.55E-01	-0.03	9.35E-01
FTL_1573	0.09	NA	-0.01	9.71E-01
FTL_1574	-0.01	NA	-0.15	NA
FTL_1575	0.00	9.76E-01	-0.24	2.34E-01
FTL_1576	0.13	2.39E-01	0.19	1.18E-01
FTL_1577	-0.02	8.83E-01	0.28	2.66E-01
FTL_1578	-0.08	5.66E-01	0.24	1.73E-01
FTL_1579	0.12	2.64E-01	0.22	5.11E-02
FTL_1580	0.05	6.89E-01	0.25	7.42E-02
FTL_1581	-0.31	4.14E-02	-0.27	1.27E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1582	-0.01	9.61E-01	1.02	3.11E-25
FTL_1583	-0.08	3.95E-01	-0.03	7.74E-01
FTL_1584	0.07	5.70E-01	0.20	1.58E-01
FTL_1585	-0.01	9.43E-01	-0.39	1.30E-05
FTL_1586	-0.08	5.45E-01	-0.63	2.98E-05
FTL_1587	-0.18	1.57E-01	-0.16	2.86E-01
FTL_1588	0.05	NA	-0.23	4.27E-01
FTL_1589	-0.07	5.30E-01	-0.21	4.38E-01
FTL_1590	0.02	9.26E-01	0.20	1.66E-01
FTL_1591	-0.03	8.19E-01	0.08	5.06E-01
FTL_1592	-0.02	8.97E-01	0.21	2.01E-01
FTL_1593	0.06	6.47E-01	0.49	7.83E-04
FTL_1594	0.05	7.30E-01	0.22	2.08E-01
FTL_1595	-0.19	2.00E-01	-0.58	1.36E-03
FTL_1596	-0.18	1.53E-01	-0.88	1.39E-11
FTL_1597	0.00	9.73E-01	-0.18	1.69E-01
FTL_1598	-0.07	4.47E-01	0.47	1.83E-09
FTL_1599	0.00	9.74E-01	-0.25	2.40E-01
FTL_1600	0.17	2.39E-01	-0.24	2.36E-01
FTL_1601	0.29	5.97E-03	0.44	3.78E-05
FTL_1602	0.13	2.45E-01	0.51	6.19E-07
FTL_1603	-0.07	5.73E-01	0.17	4.52E-01
FTL_1604	0.13	1.73E-01	0.19	4.95E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1605	0.12	2.84E-01	0.83	6.58E-20
FTL_1606	0.11	3.39E-01	0.62	2.66E-09
FTL_1607	-0.10	4.49E-01	-0.21	3.01E-01
FTL_1608	-0.15	2.56E-01	0.56	6.97E-05
FTL_1609	0.02	8.89E-01	0.41	9.67E-04
FTL_1610	-0.03	8.54E-01	-0.21	2.57E-01
FTL_1611	-0.04	7.54E-01	0.34	5.27E-04
FTL_1612	0.01	9.54E-01	0.02	9.29E-01
FTL_1613	-0.01	9.67E-01	-0.05	7.86E-01
FTL_1614	0.06	5.91E-01	0.30	4.76E-03
FTL_1615	-0.11	3.12E-01	0.68	4.19E-11
FTL_1616	-0.24	1.75E-03	-0.04	7.15E-01
FTL_1617	-0.09	3.50E-01	0.23	5.24E-03
FTL_1618	0.00	9.98E-01	-0.16	5.73E-01
FTL_1619	0.00	NA	0.03	NA
FTL_1620	-0.10	4.59E-01	0.36	2.55E-02
FTL_1621	-0.02	8.47E-01	0.47	1.72E-08
FTL_1622	-0.04	7.35E-01	0.46	1.44E-04
FTL_1623	-0.01	9.60E-01	0.22	1.99E-01
FTL_1624	-0.06	6.27E-01	-0.44	5.72E-02
FTL_1625	0.01	NA	0.04	8.81E-01
FTL_1626	0.00	NA	0.02	NA
FTL_1627	-0.07	5.87E-01	-0.24	2.34E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1628	0.02	NA	-0.15	5.98E-01
FTL_1629	0.01	9.56E-01	-0.09	7.39E-01
FTL_1630	-0.03	8.32E-01	-0.11	5.85E-01
FTL_1631	0.03	NA	-0.29	3.33E-01
FTL_1632	0.01	NA	0.15	NA
FTL_1633	0.14	3.22E-01	0.14	5.78E-01
FTL_1634	-0.04	8.13E-01	0.21	2.60E-01
FTL_1635	-0.08	5.58E-01	-0.27	6.27E-02
FTL_1636	0.01	NA	0.10	NA
FTL_1637	-0.25	2.74E-02	0.16	2.36E-01
FTL_1638	-0.06	6.15E-01	0.25	6.83E-02
FTL_1639	0.04	7.65E-01	0.14	5.22E-01
FTL_1640	0.47	1.40E-05	1.46	1.14E-39
FTL_1641	0.14	1.32E-01	0.20	4.86E-01
FTL_1642	0.00	NA	-0.01	NA
FTL_1643	-0.08	5.66E-01	-0.22	2.51E-01
FTL_1644	-0.12	3.25E-01	0.56	3.29E-06
FTL_1645	-0.12	3.86E-01	0.83	4.02E-08
FTL_1646	-0.47	1.25E-03	0.43	6.56E-03
FTL_1647	-0.01	NA	-0.19	5.25E-01
FTL_1648	0.03	NA	0.03	9.29E-01
FTL_1649	-0.05	NA	-0.02	9.46E-01
FTL_1650	0.02	NA	0.20	4.05E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1651	-0.01	NA	-0.15	6.12E-01
FTL_1652	-0.01	NA	-0.06	NA
FTL_1653	-0.04	NA	-0.68	7.85E-02
FTL_1654	-0.01	NA	-0.90	1.11E-02
FTL_1655	0.00	9.86E-01	-0.08	7.84E-01
FTL_1656	0.30	3.60E-03	0.91	1.98E-19
FTL_1657	0.01	9.31E-01	0.52	1.60E-04
FTL_1658	0.06	5.83E-01	0.41	8.45E-05
FTL_1659	-0.15	1.66E-01	0.14	2.57E-01
FTL_1660	-0.10	4.14E-01	0.31	9.70E-03
FTL_1661	-0.07	5.95E-01	-0.21	1.02E-01
FTL_1662	0.04	7.98E-01	-0.20	1.41E-01
FTL_1663	0.10	4.14E-01	-0.02	9.11E-01
FTL_1664	0.03	7.90E-01	0.09	4.02E-01
FTL_1665	0.04	7.90E-01	-0.05	7.67E-01
FTL_1666	0.08	4.27E-01	-0.02	8.99E-01
FTL_1667	-0.15	2.40E-01	-0.97	7.88E-16
FTL_1668	-0.03	7.91E-01	0.13	2.10E-01
FTL_1669	0.05	6.78E-01	0.42	4.30E-03
FTL_1670	-0.03	8.41E-01	0.37	7.89E-02
FTL_1671	-0.22	1.75E-02	0.35	3.19E-04
FTL_1672	-0.32	2.47E-03	0.10	4.62E-01
FTL_1673	0.01	9.38E-01	0.52	1.94E-08

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1674	-0.02	NA	-0.10	7.31E-01
FTL_1675	0.00	NA	-0.01	NA
FTL_1676	0.01	NA	0.00	NA
FTL_1677	0.04	NA	0.00	9.95E-01
FTL_1678	0.33	7.51E-03	-0.08	6.13E-01
FTL_1679	0.02	NA	-0.12	NA
FTL_1680	0.01	9.51E-01	-0.02	9.42E-01
FTL_1681	-0.16	2.44E-01	-0.38	2.49E-02
FTL_1682	-0.01	NA	-0.11	NA
FTL_1683	-0.04	7.18E-01	0.53	1.57E-09
FTL_1684	0.00	9.63E-01	0.24	1.92E-02
FTL_1685	0.20	1.68E-01	1.03	2.33E-10
FTL_1686	0.11	4.17E-01	0.11	5.80E-01
FTL_1687	-0.13	3.40E-01	-0.27	1.39E-01
FTL_1688	0.00	NA	-0.22	3.96E-01
FTL_1689	-0.12	3.54E-01	-0.36	7.78E-03
FTL_1690	0.05	6.94E-01	-0.53	3.81E-02
FTL_1691	-0.08	NA	-1.27	1.00E-03
FTL_1692	-0.09	4.68E-01	-1.02	9.13E-06
FTL_1693	0.00	1.00E+00	-0.28	2.65E-01
FTL_1694	-0.50	9.54E-03	-0.65	8.96E-04
FTL_1695	-0.25	1.35E-01	-1.01	1.54E-07
FTL_1696	-0.16	2.63E-01	-0.82	1.59E-04

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1697	0.01	NA	0.01	NA
FTL_1698	-0.01	NA	-0.13	NA
FTL_1699	-0.13	2.61E-01	-0.08	5.83E-01
FTL_1700	0.06	6.36E-01	0.95	2.32E-20
FTL_1701	-0.40	1.40E-05	0.12	3.18E-01
FTL_1702	-0.24	2.68E-02	-0.43	9.29E-05
FTL_1703	-0.23	1.31E-02	0.09	4.67E-01
FTL_1704	-0.14	2.64E-01	0.41	2.42E-03
FTL_1705	0.02	8.63E-01	0.05	7.69E-01
FTL_1706	-0.05	7.40E-01	0.24	2.77E-01
FTL_1707	0.02	8.93E-01	0.28	5.59E-02
FTL_1708	-0.13	1.95E-01	-0.92	4.04E-23
FTL_1709	0.10	4.47E-01	0.57	1.27E-04
FTL_1710	-0.14	2.95E-01	-0.01	9.63E-01
FTL_1711	-0.01	NA	-0.23	NA
FTL_1712	0.00	NA	-0.12	6.31E-01
FTL_1713	-0.09	5.11E-01	-0.29	1.32E-01
FTL_1714	0.00	9.99E-01	0.50	4.39E-03
FTL_1715	-0.05	5.90E-01	-0.07	8.39E-01
FTL_1716	-0.02	NA	0.27	3.42E-01
FTL_1717	0.06	6.68E-01	0.62	1.00E-06
FTL_1718	-0.08	5.35E-01	-0.17	4.02E-01
FTL_1719	0.00	NA	0.07	NA

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1720	-0.02	9.26E-01	-0.43	3.01E-03
FTL_1721	-0.21	1.34E-01	0.20	2.55E-01
FTL_1722	-0.02	9.11E-01	-0.07	5.66E-01
FTL_1723	-0.04	8.15E-01	0.71	2.31E-06
FTL_1724	-0.08	5.17E-01	0.33	1.67E-03
FTL_1725	-0.09	5.11E-01	-0.24	8.19E-02
FTL_1726	0.17	6.19E-02	0.54	5.13E-10
FTL_1727	0.01	9.65E-01	0.50	3.94E-03
FTL_1728	0.01	9.32E-01	0.29	1.44E-01
FTL_1729	0.01	9.55E-01	0.22	9.89E-02
FTL_1730	0.03	NA	-0.30	2.35E-01
FTL_1731	0.03	8.19E-01	0.43	5.29E-02
FTL_1732	-0.10	4.45E-01	0.20	2.60E-01
FTL_1733	0.04	6.84E-01	0.53	3.71E-11
FTL_1734	-0.11	3.33E-01	-0.94	4.03E-19
FTL_1735	0.10	4.88E-01	-0.35	1.21E-02
FTL_1736	0.01	9.47E-01	-0.31	3.14E-02
FTL_1737	-0.08	5.22E-01	-0.16	3.18E-01
FTL_1738	-0.23	1.29E-01	0.21	2.60E-01
FTL_1739	0.44	5.68E-05	1.17	2.25E-25
FTL_1740	0.07	5.63E-01	1.19	7.91E-35
FTL_1741	-0.13	2.43E-01	0.03	8.36E-01
FTL_1742	0.04	5.35E-01	0.06	8.43E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1743	-0.11	2.61E-01	-0.07	5.47E-01
FTL_1744	-0.12	1.61E-01	-0.38	1.04E-06
FTL_1745	-0.26	1.21E-01	0.23	2.92E-01
FTL_1746	-0.19	1.35E-01	-0.22	1.32E-01
FTL_1747	-0.13	2.99E-01	0.03	8.72E-01
FTL_1748	-0.14	2.60E-01	0.33	1.69E-02
FTL_1749	-0.07	5.92E-01	0.53	9.07E-03
FTL_1750	-0.05	6.83E-01	0.05	7.67E-01
FTL_1751	-0.10	3.76E-01	0.35	1.45E-03
FTL_1752	-0.07	5.66E-01	-0.47	4.58E-02
FTL_1753	-0.05	7.09E-01	0.08	7.31E-01
FTL_1754	0.43	1.81E-02	-0.08	7.14E-01
FTL_1755	0.09	5.02E-01	0.28	3.57E-02
FTL_1756	0.17	6.16E-02	0.46	9.98E-08
FTL_1757	-0.15	2.71E-01	-0.43	1.02E-02
FTL_1758	0.01	NA	0.09	7.55E-01
FTL_1759	-0.08	5.24E-01	0.12	6.33E-01
FTL_1760	0.00	NA	0.11	NA
FTL_1761	-0.01	NA	-0.06	NA
FTL_1762	-0.01	9.54E-01	0.30	2.63E-02
FTL_1763	-0.02	9.26E-01	0.29	1.44E-01
FTL_1764	0.02	8.93E-01	0.29	2.10E-01
FTL_1765	0.13	3.54E-01	0.65	4.23E-03

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1766	0.01	NA	0.42	1.82E-01
FTL_1767	0.00	NA	0.06	NA
FTL_1768	0.00	NA	0.04	NA
FTL_1769	0.02	NA	0.02	9.32E-01
FTL_1770	-0.12	NA	-0.91	9.13E-03
FTL_1771	0.02	8.75E-01	-0.52	3.86E-03
FTL_1772	-0.06	6.21E-01	-0.14	2.30E-01
FTL_1773	-0.06	6.70E-01	0.50	7.66E-04
FTL_1774	0.05	NA	0.12	6.65E-01
FTL_1775	0.04	8.10E-01	0.72	2.28E-07
FTL_1776	0.09	5.18E-01	-0.31	9.12E-02
FTL_1777	-0.03	8.06E-01	-1.07	2.04E-04
FTL_1778	-0.06	6.47E-01	-1.81	9.52E-22
FTL_1779	-0.24	1.30E-01	-0.45	2.84E-02
FTL_1780	-0.21	2.83E-02	-0.23	2.48E-02
FTL_1781	-0.28	1.43E-02	-0.34	5.31E-03
FTL_1782	-0.09	4.27E-01	0.14	2.60E-01
FTL_1783	-0.10	2.97E-01	0.25	4.86E-03
FTL_1784	-0.25	9.00E-04	0.00	9.95E-01
FTL_1785	-0.19	2.83E-02	-0.03	8.01E-01
FTL_1786	-0.23	5.68E-02	-0.11	4.50E-01
FTL_1787	-0.31	1.82E-02	-0.32	2.63E-02
FTL_1788	-0.22	2.79E-02	0.12	3.02E-01

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1789	-0.08	5.35E-01	-0.58	1.48E-06
FTL_1790	0.44	2.32E-03	1.45	8.79E-24
FTL_1791	-0.04	7.25E-01	0.23	3.98E-02
FTL_1792	-0.09	4.28E-01	0.43	1.44E-01
FTL_1793	0.09	4.18E-01	0.58	8.70E-08
FTL_1794	-0.37	3.60E-03	-0.27	6.33E-02
FTL_1795	-0.22	5.25E-02	0.07	6.24E-01
FTL_1796	-0.31	6.89E-03	-0.29	2.15E-02
FTL_1797	-0.40	3.55E-05	-0.27	1.49E-02
FTL_1798	-0.45	2.47E-07	0.20	4.24E-02
FTL_1799	-0.55	1.90E-04	0.10	6.05E-01
FTL_1800	-0.31	1.50E-02	0.14	3.62E-01
FTL_1801	-0.27	3.30E-02	-0.48	3.15E-04
FTL_1802	0.03	8.44E-01	0.57	4.41E-02
FTL_1803	0.08	5.05E-01	-0.10	3.53E-01
FTL_1804	-0.13	3.02E-01	-0.26	3.88E-02
FTL_1805	-0.26	6.53E-02	-1.16	7.58E-16
FTL_1806	-0.14	1.78E-01	-0.67	2.24E-12
FTL_1807	-0.21	6.73E-02	-0.69	7.06E-10
FTL_1808	-0.04	7.54E-01	-0.35	3.82E-03
FTL_1809	-0.07	6.42E-01	-0.05	7.80E-01
FTL_1810	-0.06	6.20E-01	0.09	6.82E-01
FTL_1811	0.03	8.32E-01	-0.47	5.73E-04

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1812	0.24	9.89E-02	0.38	1.72E-02
FTL_1813	0.00	NA	0.02	NA
FTL_1814	-0.02	8.92E-01	-0.67	3.92E-03
FTL_1815	-0.10	4.64E-01	-0.28	1.92E-01
FTL_1816	-0.06	6.51E-01	-0.35	8.37E-02
FTL_1817	-0.17	1.43E-01	-0.11	4.07E-01
FTL_1818	-0.26	4.78E-03	0.24	1.86E-02
FTL_1819	-0.28	9.48E-03	0.33	4.68E-03
FTL_1820	-0.07	6.10E-01	0.62	4.49E-07
FTL_1821	-0.12	3.65E-01	0.22	1.22E-01
FTL_1822	-0.20	1.40E-01	0.12	4.71E-01
FTL_1823	-0.20	8.79E-02	-0.13	3.44E-01
FTL_1824	-0.13	1.66E-01	-0.06	5.84E-01
FTL_1825	-0.30	5.41E-02	0.63	9.56E-05
FTL_1826	-0.13	3.74E-01	0.26	1.66E-01
FTL_1827	-0.13	3.44E-01	0.32	3.71E-02
FTL_1828	-0.07	5.56E-01	0.15	2.17E-01
FTL_1829	-0.17	2.35E-01	0.20	2.96E-01
FTL_1830	-0.08	4.43E-01	0.07	8.28E-01
FTL_1831	0.00	9.65E-01	0.54	1.43E-04
FTL_1832	0.07	6.17E-01	-1.24	5.03E-19
FTL_1833	-0.03	8.56E-01	-1.81	3.30E-18
FTL_1834	-0.06	6.63E-01	-1.62	7.88E-26

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1835	-0.28	3.76E-02	-1.75	1.50E-37
FTL_1836	-0.06	6.37E-01	-1.23	2.56E-09
FTL_1837	0.00	NA	-0.58	1.02E-01
FTL_1838	0.01	NA	0.04	NA
FTL_1839	0.01	NA	-0.02	NA
FTL_1840	-0.07	5.87E-01	0.43	9.18E-03
FTL_1841	-0.07	5.49E-01	0.22	4.79E-02
FTL_1842	-0.09	3.68E-01	0.17	5.59E-02
FTL_1843	-0.06	6.49E-01	0.30	7.32E-02
FTL_1844	-0.02	NA	-0.53	8.37E-02
FTL_1845	-0.04	NA	-0.36	2.32E-01
FTL_1846	-0.02	NA	-0.29	3.08E-01
FTL_1847	0.01	9.56E-01	-0.15	5.78E-01
FTL_1848	0.04	7.63E-01	0.39	1.89E-02
FTL_1849	0.11	4.22E-01	-0.10	6.11E-01
FTL_1850	0.05	6.20E-01	0.53	8.76E-10
FTL_1851	-0.15	2.35E-01	-0.42	1.23E-01
FTL_1852	0.01	9.31E-01	0.78	6.31E-09
FTL_1853	-0.04	NA	-0.48	1.44E-01
FTL_1854	0.14	3.22E-01	0.10	6.18E-01
FTL_1855	0.00	9.65E-01	-0.11	7.05E-01
FTL_1856	0.00	NA	-0.03	NA
FTL_1857	-0.04	NA	-1.99	2.38E-03

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1858	-0.03	NA	-1.07	1.50E-03
FTL_1859	-0.03	NA	-0.32	2.75E-01
FTL_1860	0.00	1.00E+00	-0.10	4.23E-01
FTL_1861	-0.04	7.38E-01	0.23	6.47E-02
FTL_1862	-0.01	NA	0.12	6.70E-01
FTL_1863	-0.05	6.85E-01	0.24	9.09E-02
FTL_1864	0.04	7.74E-01	0.10	5.04E-01
FTL_1865	0.04	7.11E-01	0.06	5.83E-01
FTL_1866	-0.04	7.56E-01	0.17	1.29E-01
FTL_1867	-0.39	5.16E-06	0.23	1.55E-02
FTL_1868	-0.04	7.20E-01	0.45	1.29E-07
FTL_1869	0.10	3.12E-01	0.81	1.53E-19
FTL_1870	-0.03	NA	-0.21	3.52E-01
FTL_1871	-0.52	5.25E-02	-1.58	1.22E-06
FTL_1872	-0.13	3.12E-01	-1.20	3.54E-07
FTL_1873	-0.05	6.84E-01	-0.62	8.77E-15
FTL_1874	0.02	8.66E-01	-0.18	8.16E-02
FTL_1875	0.14	2.90E-01	0.67	2.90E-06
FTL_1876	0.12	3.74E-01	-0.64	3.12E-06
FTL_1877	0.03	NA	-0.18	5.36E-01
FTL_1878	-0.01	9.37E-01	-0.03	8.85E-01
FTL_1879	-0.01	9.58E-01	0.16	1.88E-01
FTL_1880	-0.10	4.50E-01	0.58	1.67E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1881	-0.45	5.88E-04	0.14	3.87E-01
FTL_1882	-0.35	1.81E-03	0.52	7.04E-06
FTL_1883	-0.24	7.01E-03	0.86	6.31E-22
FTL_1884	0.00	NA	-0.18	5.03E-01
FTL_1885	0.02	8.89E-01	-0.25	3.17E-01
FTL_1886	-0.11	4.38E-01	-0.25	1.77E-01
FTL_1887	0.00	NA	-0.01	NA
FTL_1888	0.04	NA	0.27	3.44E-01
FTL_1889	0.02	NA	-0.10	7.26E-01
FTL_1890	0.00	NA	-0.02	NA
FTL_1891	-0.12	3.88E-01	-0.24	1.84E-01
FTL_1892	0.32	1.92E-02	0.31	3.30E-02
FTL_1893	0.00	NA	0.00	NA
FTL_1894	-0.03	8.15E-01	-0.22	4.18E-01
FTL_1895	-0.10	4.00E-01	0.48	7.93E-02
FTL_1896	-0.22	5.17E-02	0.68	2.71E-09
FTL_1897	-0.07	6.11E-01	0.22	1.20E-01
FTL_1898	0.15	2.19E-01	0.42	7.28E-04
FTL_1899	-0.10	3.76E-01	0.08	5.09E-01
FTL_1900	0.03	8.32E-01	-0.02	8.83E-01
FTL_1901	0.06	3.09E-01	0.15	5.65E-01
FTL_1902	-0.04	7.53E-01	0.78	2.30E-14
FTL_1903	0.02	8.82E-01	0.22	1.64E-02

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1904	-0.11	3.82E-01	0.10	5.24E-01
FTL_1905	0.14	2.05E-01	0.39	1.57E-04
FTL_1906	0.06	6.15E-01	0.04	8.11E-01
FTL_1907	-0.07	6.12E-01	0.16	3.12E-01
FTL_1908	-0.15	1.54E-01	-0.32	2.65E-03
FTL_1909	-0.07	5.46E-01	-1.29	2.94E-37
FTL_1910	0.01	9.46E-01	-0.29	1.07E-03
FTL_1911	-0.05	7.42E-01	-0.04	8.51E-01
FTL_1912	0.02	8.79E-01	0.55	2.13E-05
FTL_1913	-0.04	8.10E-01	0.26	1.28E-01
FTL_1914	0.17	1.38E-01	0.63	2.96E-08
FTL_1915	-0.24	8.62E-02	-0.03	8.64E-01
FTL_1916	0.02	8.79E-01	-0.49	1.04E-02
FTL_1917	0.58	3.74E-05	1.62	1.29E-28
FTL_1918	0.26	1.30E-01	1.35	1.72E-07
FTL_1919	0.03	NA	0.48	1.48E-01
FTL_1920	0.02	NA	0.07	NA
FTL_1921	0.12	3.92E-01	1.48	8.63E-14
FTL_1922	0.05	7.29E-01	1.25	6.07E-13
FTL_1923	0.06	6.33E-01	1.31	4.07E-40
FTL_1924	0.00	NA	-0.18	NA
FTL_1925	-0.13	3.53E-01	-0.20	3.50E-01
FTL_1926	-0.03	8.23E-01	0.13	6.58E-01

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1927	-0.01	NA	-0.22	4.33E-01
FTL_1928	0.07	NA	0.09	7.69E-01
FTL_1929	0.00	9.78E-01	0.59	1.73E-06
FTL_1930	-0.08	4.27E-01	0.83	1.46E-20
FTL_1931	-0.16	1.54E-01	0.61	5.70E-08
FTL_1932	-0.02	NA	0.75	6.70E-02
FTL_1933	-0.06	6.47E-01	0.21	8.79E-02
FTL_1934	-0.21	7.45E-02	0.04	8.18E-01
FTL_1935	-0.17	1.81E-01	0.42	3.92E-03
FTL_1936	-0.01	9.24E-01	0.78	6.69E-20
FTL_1937	-0.01	NA	-0.13	6.52E-01
FTL_1938	-0.17	1.82E-01	0.09	6.03E-01
FTL_1939	-0.15	2.86E-01	-0.04	8.62E-01
FTL_1940	-0.02	8.96E-01	-0.26	1.03E-01
FTL_1941	0.06	6.20E-01	1.12	7.46E-19
FTL_1942	-0.05	6.96E-01	-0.04	8.45E-01
FTL_1943	-0.14	2.94E-01	-0.08	6.43E-01
FTL_1944	-0.12	3.96E-01	-0.35	4.99E-02
FTL_1945	0.04	NA	0.21	4.62E-01
FTL_1946	-0.03	8.56E-01	0.62	6.99E-05
FTL_1947	0.01	9.74E-01	0.69	4.81E-11
FTL_1948	-0.05	7.42E-01	0.18	3.05E-01
FTL_1949	-0.01	NA	-0.08	NA

	LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS pF		LVS $\Delta rpsU2$ pF-rpsU2 -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_1950	-0.16	2.70E-01	-0.06	7.86E-01
FTL_1951	0.00	NA	-0.20	NA
FTL_1952	0.06	NA	0.18	5.44E-01
FTL_1953	-0.02	NA	-0.19	NA
FTL_1954	-0.01	NA	-0.12	NA
FTL_1955	0.01	NA	-0.63	6.02E-02
FTL_1956	0.41	2.84E-04	0.82	4.52E-13
FTL_1957	0.13	1.55E-01	1.55	3.31E-04
FTL_1958	0.05	7.01E-01	0.18	1.33E-01
FTL_1959	0.00	NA	-0.05	NA
FTL_1960	-0.05	7.28E-01	-0.03	8.84E-01
FTL_1961	-0.01	9.61E-01	0.78	8.98E-07
FTL_1962	-0.07	5.91E-01	0.59	3.00E-04
FTL_1963	0.00	9.92E-01	-0.09	7.28E-01
FTL_1964	0.08	5.17E-01	-0.51	1.02E-06
FTL_1965	0.13	2.40E-01	-0.36	2.45E-04
FTL_1966	0.12	1.93E-01	-0.24	6.46E-03
FTL_1967	0.04	7.92E-01	-0.22	3.07E-01
FTL_1968	0.07	6.10E-01	0.35	9.82E-02
FTL_R0001	0.41	1.60E-03	0.13	4.04E-01
FTL_R0002	-0.02	NA	-0.03	9.17E-01
FTL_R0003	-0.02	8.63E-01	0.17	5.46E-01
FTL_R0004	0.00	NA	-0.01	NA

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_R0005	0.00	NA	0.03	NA
FTL_R0006	0.02	8.64E-01	0.57	8.79E-02
FTL_R0007	-0.01	NA	0.17	4.34E-01
FTL_R0008	0.01	NA	0.01	NA
FTL_R0009	-0.01	NA	-0.01	NA
FTL_R0010	0.34	1.94E-02	-0.14	4.27E-01
FTL_R0013	-0.01	NA	0.01	NA
FTL_R0014	0.01	NA	0.14	6.19E-01
FTL_R0015	0.00	NA	0.00	NA
FTL_R0016	-0.02	8.63E-01	0.17	5.47E-01
FTL_R0017	0.00	NA	0.02	NA
FTL_R0018	-0.01	NA	0.04	NA
FTL_R0019	0.02	8.65E-01	0.57	8.90E-02
FTL_R0020	-0.06	NA	0.06	7.89E-01
FTL_R0022	0.00	NA	-0.03	NA
FTL_R0024	0.00	NA	0.00	NA
FTL_R0025	0.00	NA	0.00	NA
FTL_R0026	0.00	NA	-0.03	NA
FTL_R0027	-0.01	NA	0.05	NA
FTL_R0028	-0.02	8.63E-01	0.17	5.46E-01
FTL_R0029	0.00	NA	0.00	NA
FTL_R0030	-0.01	NA	-0.02	NA
FTL_R0031	0.02	8.67E-01	0.57	8.66E-02

	LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS pF		LVS $\Delta rpsU2$ pF- <i>rpsU2</i> -V vs LVS $\Delta rpsU2$ pF	
Locus	log2FoldChange	padj	log2FoldChange	padj
FTL_R0032	-0.02	NA	0.17	4.91E-01
FTL_R0033	0.00	NA	0.02	NA
FTL_R0034	0.00	NA	0.05	NA
FTL_R0042	0.00	NA	0.00	NA
FTL_R0043	NA	NA	NA	NA
FTL_R0053	-0.05	NA	0.22	4.12E-01

Table S4. Comparison of *in vitro* and intramacrophage growth rates for strains used in this study. *In vitro* growth was assessed during early exponential phase by measuring OD600. *In vitro* generation times for LVS pF, LVS $\Delta rpsU2$ pF, and LVS $\Delta rpsU2$ pF-bS21-2-V were calculated from three independent experiments, others were calculated from two. Generation times for intramacrophage growth are averages across three independent experiments and were determined by comparison of CFU recovered after 2 versus 24 hours. +/- values indicate SD.

Cells	Growth environment		Generation time difference (intramacrophage - <i>in vitro</i>)
	<i>in vitro</i>	Intramacrophage	
LVS pF	135.1 +/- 4.7	144.8 +/- 7.1	9.7
LVS $\Delta rpsU2$ pF	172.8 +/- 4.5	210.7 +/- 29.5	37.9
LVS $\Delta rpsU2$ pF-bS21-1-V	145.1 +/- 3.9	179.3 +/- 8.2	34.2
LVS $\Delta rpsU2$ pF-bS21-2-V	150.6 +/- 1.9	144.5 +/- 5.0	-6.1
LVS $\Delta rpsU2$ pF-bS21-2-V	181.2 +/- 7.6	263.1 +/- 20.3	81.9

CHAPTER 3

Manuscript 2

Ribosome heterogeneity results in leader sequence-mediated regulation of protein synthesis in *Francisella tularensis*

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**Ribosome heterogeneity results in leader sequence-mediated
regulation of protein synthesis in *Francisella tularensis***

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Abstract

While the impacts of ribosomes are generally examined in bulk, there is accumulating evidence that heterogeneity in ribosome composition may lead to altered function and provide ribosomes the capacity to regulate protein synthesis. Ribosome heterogeneity in *F. tularensis* results from incorporation of one of three homologs of bS21, a small ribosomal protein demonstrated to regulate protein synthesis in other bacteria. Loss of one homolog, bS21-2, results in genome-wide post-transcriptional changes in protein abundance. This suggests that bS21-2 can, either directly or indirectly, lead to preferential translation of particular mRNAs. In this study, we examine the potential for bS21-2 to function indirectly (via Hfq) and in a leader sequence-dependent manner. We found that loss of bS21-2 leads to increased abundance of the RNA chaperone Hfq and both Hfq and bS21-2 impact expression of key virulence genes, but these two proteins influence protein abundance via distinct mechanisms. In contrast, the 5' untranslated region (UTR) of some bS21-2 responsive genes, including key virulence genes, is sufficient to lead to changes in translation in cells lacking bS21-2. Focusing on a particular 5' UTR, we identified key elements critical for responsiveness to bS21-2. Specifically, we found that the 5' UTR must have an imperfect Shine-Dalgarno sequence and, in at least one 5' UTR, a specific 6-nucleotide sequence for bS21-2-responsive translation. Our results are consistent with a model in which a bS21 homolog improves translation initiation through interactions with specific leader sequences. Together, we determined that ribosome composition in *F. tularensis* regulates

translation in a leader sequence-dependent manner, a finding which may extend to many other bacteria.

Importance

Ribosome heterogeneity is common in bacteria and there is mounting evidence that ribosome composition plays a regulatory role in protein synthesis. However, mechanisms of ribosome-driven gene regulation are not well understood. In the human pathogen *Francisella tularensis*, which encodes multiple homologs for one ribosomal protein, bS21, loss of one homolog impacts protein synthesis and virulence. Here, we explore the mechanism behind the changes in protein synthesis and find that the ribosomal protein bS21-2 does not function coordinately with the RNA chaperone Hfq. Rather, changes in protein synthesis ~~are~~ ^{can be} linked to a specific ~~6 nucleotide~~ ^S sequence in the leader of transcripts in the absence of strong mRNA-ribosome interactions. Our data support a model in which ribosome composition regulates gene expression through translation, a strategy that may be conserved in diverse organisms with various source of ribosome heterogeneity.

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Introduction

Ribosomes, the molecular machines that synthesize proteins, can be heterogeneous in structure (Genuth & Barna, 2018). As bacterial ribosomes are composed of 3 ribosomal RNA molecules (rRNAs) and ~ 50 ribosomal proteins (r-proteins), heterogeneity can arise from differences in rRNA ~~or~~ ^{modifications,} ~~and~~ post-transcriptional or post-translational modifications of rRNA and r-proteins (Byrgazov et al., 2013). The consequences of ribosome heterogeneity are incompletely understood, and much debate surrounds the hypothesis that distinct classes of ribosomes can have specialized functions by preferentially translating subsets of mRNA (Ferretti & Karbstein, 2019). The 30S subunit r-protein bS21 is one of the last assembled proteins in the ribosome and is easily exchanged among ribosomes (Mizushima & Nomura, 1970; Robertson et al., 1977), allowing bS21 to be a source of ribosomal heterogeneity.

In *E. coli*, bS21 is involved in translation initiation (van Duin & Wijnands, 1981; Chang & Craven, 1977), and multiple studies have suggested that bS21 might play a regulatory role in gene expression (Trautmann & Ramsey, 2022; Jha et al., 2020; Mizuno et al., 2019; Chen et al., 2022). Recent work in the Bacteroidia species *Flavobacterium johnsoniae* clearly demonstrated that bS21 controls gene expression. In this organism, incorporation of bS21 into the ribosome contributes to sequestration of the anti-Shine Dalgarno (ASD) (Jha et al., 2020). The mRNA encoding bS21, *rpsU*, is one of the few *F. johnsoniae* mRNAs with a strong Shine-Dalgarno (SD) sequence. Depletion of bS21 ^{removal of} ~~or~~ the region of bS21 necessary for ASD sequestration results in increased translation from the *rpsU* mRNA and

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mRNAs engineered to have a strong SD (McNutt et al., 2023). These studies unambiguously demonstrate that ribosomes lacking bS21 have altered specificity for particular mRNAs in translation initiation, providing evidence that bS21 functions as a bona fide regulator of gene expression (McNutt et al, 2023).

Francisella tularensis, a human pathogen that requires a type VI secretion system (T6SS) to cause disease, encodes three distinct homologs of bS21. We have shown that all three homologs can be incorporated into ribosomes, and loss of one of the homologs, bS21-2, leads to changes in protein abundance of most T6SS-encoding genes that cannot be explained by changes in transcript abundance or protein stability. Loss of bS21-2 also results in defective intramacrophage replication in cells that can be complemented by restoration of bS21-2, but not the other two homologs. This indicates that bS21-2 specifically governs virulence genes, including those that encode the T6SS (Trautmann & Ramsey, 2022).

While our results support a model in which bS21 proteins in *F. tularensis* regulate gene expression at the level of translation, it is clear that bS21 homologs in Gammaproteobacteria exert their effects in a manner distinct from bS21 homologs in Bacteroidia. The bS21 proteins in *F. tularensis* and *F. johnsoniae* differ significantly at the amino acid level, particularly in the variable C-terminal (Jha et al., 2020). In Bacteroidia, there are multiple conserved C-terminal residues required for bS21 to interact with the ASD that are not conserved in other bacterial lineages, including the Gammaproteobacteria. Thus, in the current study we aim to understand the mechanisms by which bS21-2 affects translation in *F. tularensis*.

Using qPCR and immunoblot analyses, we show that bS21-2 and the RNA-binding protein Hfq both influence T6SS proteins, but do not act in a coordinated manner and function via distinct pathways. Through reporter assays using translational fusions, we see that the 5' untranslated region (5' UTR) of some transcripts is sufficient to cause differences in protein production if bS21-2 is lost, indicating that these 5' UTRs are responsive to bS21-2. By mutagenizing the sequences of bS21-2-responsive 5' UTRs, we also found that transcripts with ideal SD sequences do not require bS21-2 for efficient translation. In an attempt to identify which component of the 5' UTR is driving the responsiveness to bS21-2, we concluded that the secondary structure of the leader sequence does not play a clear role and two STREME-identified motifs that are enriched in bS21-2-impacted genes are not needed to cause changes in protein abundance. Finally, we identified a short nucleotide sequence in the 5' UTR of *mraY* that is critical for bS21-2-mediated translation. Our findings reveal that an r-protein homolog, bS21-2, governs protein abundance by influencing translation from mRNA species with specific leader sequences.

Results

bS21-2 and Hfq influence T6SS protein abundance via different mechanisms

While the small subunit ribosomal protein bS21-2 post-transcriptionally governs the abundance of many genes, including those that encode T6SS proteins, the mechanism by which this occurs is unknown (Trautmann & Ramsey, 2022). In considering the control of the T6SS proteins, we first hypothesized that bS21-2 may be exerting its effects indirectly, by modifying the abundance of a regulator that directly controls production of the T6SS proteins. The regulatory RNA-binding protein Hfq is known to control gene expression post-transcriptionally in many organisms and has been shown to impact the expression of T6SS proteins in *F. tularensis* (Meibom et al., 2009; Lenco et al., 2014). Our proteomics analysis identified increased Hfq in cells lacking bS21-2 compared to wild-type (5.9-fold), although substantial variation in biological replicates precluded the differences from reaching statistical significance (adj p=0.066; Trautmann & Ramsey, 2022). Additionally, many of the genes impacted by bS21-2 have AU-rich 5' UTRs that resemble ARN-motifs, known targets of Hfq (Link et al., 2009). This led us to hypothesize that Hfq may play a role in bS21-2-mediated regulation of T6SS proteins.

To validate the previous proteomics data and confirm that cells lacking bS21-2 do have increased Hfq, we added DNA specifying a C-terminal vesicular stomatitis virus ^{no higher}glycoprotein (VSV-G) epitope tag to *hfq* in cells with (WT) and without ($\Delta rpsU2$) bS21-2 and determined relative protein abundance by

quantitative immunoblotting. We found a moderate increase in Hfq (about 30%, **Fig 1A**) in cells lacking bS21-2 compared to wild-type; this is consistent with our proteomics findings, including that it is not a difference that would have reached our significance threshold.

Yet given the detectable increase in Hfq in cells lacking bS21-2, we sought to determine if this is due to increased translation of the *hfq* mRNA. Using a translational fusion in a GFP reporter assay (described in more detail below), we assessed the relative translation of mRNAs containing the *hfq* 5' UTR. Briefly, reporters expressing either the 5' UTR of *hfq* or a control 5' UTR (*tu14*) fused to *gfp* were introduced into cells with and without bS21-2. We found that there is approximately 1.88-fold more GFP produced from the 5' UTR of *hfq* in cells lacking bS21-2, indicating this UTR leads to more efficient translation by ribosomes without bS21-2 (**Fig 1B**). This suggests that the observed increase in Hfq in cells lacking bS21-2 is likely due to increase translation initiation.

If the moderate increase in Hfq leads to the observed reduction in T6SS proteins when bS21-2 is absent, Hfq must be acting as a repressor of the T6SS. However, inconsistent results have been reported with respect to the role of *F. tularensis* Hfq in regulating the T6SS genes. A transcriptomic analysis of cells lacking Hfq found that one of the two Francisella Pathogenicity Island (FPI) operons encoding the T6SS, the *pdpA* operon, was upregulated in *hfq* mutant cells (Meibom et al., 2009). A proteomics study of *hfq* mutant cells determined that proteins encoded by the other FPI operon, the *iglA* operon, are less abundant and

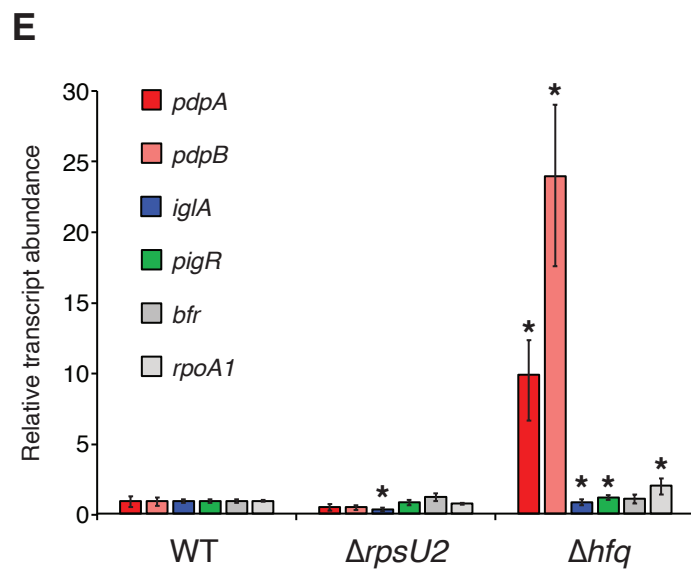
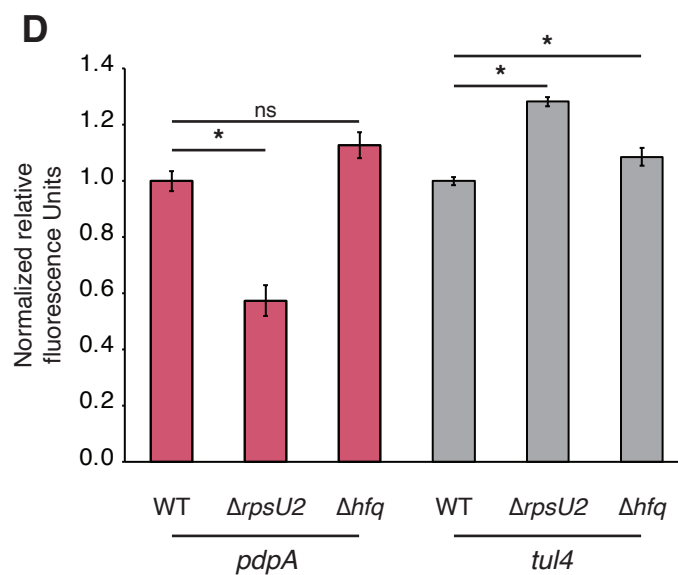
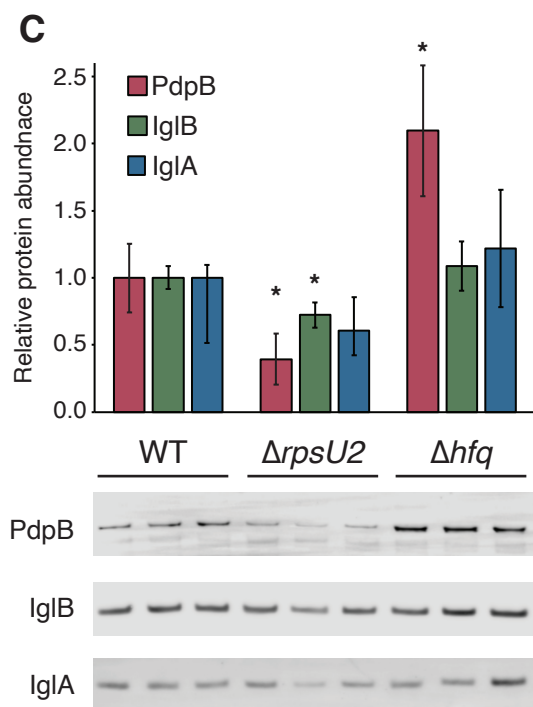
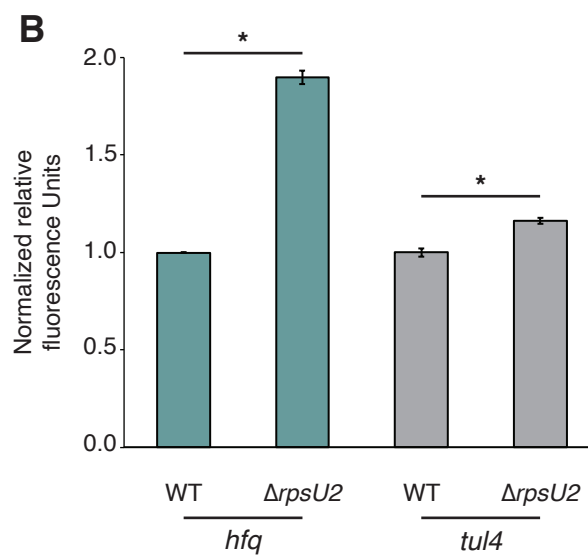
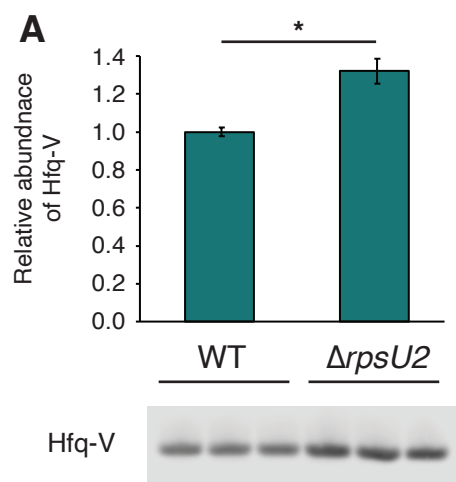


Figure 1. Hfq and bS21-2 influence production of T6SS proteins via different pathways. (A) Cells lacking bS21-2 have more Hfq. Bottom: Immunoblots probed with anti-VSV-G antibody. Whole cell lysates from bacteria containing Hfq-VSV-G and either with (WT) or without ($\Delta rpsU2$) bS21-2, in biological triplicate. Top: Quantification of immunoblots. Band intensities for each protein were normalized to total protein per lane on the membrane. **(B)** Loss of bS21-2 leads to more *hfq* translation. Relative fluorescence is reported for translational fusion reporters containing the 5' UTR of either *hfq* or *tul4* fused to *gfp* in cells with (WT) or without ($\Delta rpsU2$) bS21-2, in biological triplicate. Values relative to WT for each 5' UTR are shown. **(C)** Only some of the T6SS proteins are influenced by loss of Hfq. Bottom: Immunoblots probed with antibodies to indicated T6SS proteins in lysates of WT cells, cells lacking bS21-2 ($\Delta rpsU2$), or cells lacking Hfq (Δhfq). Top: Quantification of immunoblots. Band intensities for each protein were normalized to total protein per lane on the membrane. **(D)** Hfq does not influence translation of the T6SS protein PdpA. Relative fluorescence is reported for translational fusion reporters containing the 5' UTR of either *pdpA* or *tul4* fused to *gfp* in WT cells, cells lacking bS21-2 ($\Delta rpsU2$), or cells lacking Hfq (Δhfq), in biological triplicate. **(E)** Hfq is a negative regulator of T6SS gene transcript abundance. Quantitative real-time PCR was used to determine the relative transcript abundance for indicated FPI-encoded genes in WT cells, cells lacking bS21-2 ($\Delta rpsU2$), or cells lacking Hfq (Δhfq), normalized to the *tul4* gene. The *rpoA1* and *bfr* genes are included as additional negative controls, as their expression is not meaningfully influenced by bS21-2. (A-E) Error bars represent 1 SD. Experiments were repeated at least twice and data from a representative experiment are shown. (A-D) * $p < 0.05$ after Bonferroni correction. (E) * $p < 0.005$ after Bonferroni correction.

found no change in the abundance of proteins encoded by the *pdpA* operon (Lenco et al., 2014). To clarify the impact of Hfq on T6SS protein abundance, we determined the abundance of several T6SS proteins encoded on both FPI operons in cells with and without Hfq by quantitative immunoblotting (**Fig 1C**) (Trautmann & Ramsey, 2022). PdpB, encoded in the *pdpA* operon, was more abundant in cells without Hfq compared to wild-type (>2-fold; $p < 0.01$), while IglB and IglA, encoded on the *iglA* operon, were not impacted by the loss of Hfq (**Fig 1C**). This is in contrast to cells lacking bS21-2, which contained reduced amounts of all three proteins (**Fig 1C**; Trautmann & Ramsey, 2022). These data suggest that Hfq regulates expression of proteins encoded by the *pdpA* operon, but not the *iglA* operon, consistent with Meibom et al. (2009).

Hfq can exert its effects through a variety of mechanisms, some of which result in changes in translation initiation. To determine if the presence of *F. tularensis* Hfq impacts the translation of T6SS proteins (like bS21-2), we analyzed the ability of cells lacking Hfq to translate mRNAs containing either the 5' UTRs of the T6SS protein gene *pdpA* or control gene *tul4* fused to *gfp*. We found that translation of mRNAs with the *pdpA* or *tul4* 5' UTRs are not altered when Hfq is absent compared to wild-type, while *pdpA* translation decreases if bS21-2 is absent (**Fig 1D**). Thus, Hfq-associated changes in T6SS proteins are not due to changes in translation initiation.

As work from the Charbit lab indicates that Hfq represses *pdpA* operon transcript abundance (Meibom et al., 2009) and we found that Hfq does not impact

translation of the *pdpA* 5' UTR, we hypothesized that cells lacking Hfq might have increased PdpB due to increased *pdpB* (and *pdpA* operon) transcript abundance. We compared mRNA isolated from wild-type cells as well as those lacking bS21-2 ($\Delta rpsU2$) or Hfq (Δhfq) cells by qPCR, and found that *pdpA* and *pdpB* transcripts have large, statistically significant increases when Hfq is not present (42-fold and 69-fold, respectively) but the relative impact on *iglA* transcript is minor (2.5-fold increased) (**Fig 1E**); neither *pdpA*, *pdpB*, nor *iglA* transcripts are meaningfully impacted by the loss of bS21-2.

If bS21-2 influences the abundance of T6SS proteins indirectly, through another post-transcriptional regulator, we expect that regulator would influence translation of essentially all the T6SS proteins without impacting transcript abundance. We have demonstrated that bS21-2 represses Hfq production and Hfq functions as a negative regulator of T6SS proteins; so this network could in theory lead to increased T6SS proteins in cells lacking bS21-2. But critically, Hfq only represses T6SS proteins encoded on the *pdpA* operon, and does so by reducing transcript abundance. Thus, our results suggest two distinct pathways of regulation for the genes encoding the T6SS: one in which bS21-2 improves efficiency of translation initiation from both operons, and one in which Hfq represses transcript abundance of only the *pdpA* operon.

bS21-2 promotes translation of specific genes in a 5' UTR-dependent manner

In *E. coli*, bS21 has been implicated in sequence-dependent translation initiation and is located adjacent to the 5' untranslated region (UTR) of mRNAs

I think this
needs re-working in
a future
version -
not now!

during translation initiation (Kaledhonkar et al., 2019; van Duin & Wijnands, 1981). Loss of bS21-2 in *F. tularensis* leads to changes in abundance for a subset of the proteome (Trautmann & Ramsey, 2022). This led us to hypothesize that bS21-2 may directly impact protein abundance by modulating translation initiation in a 5' UTR-dependent manner. In order to test this hypothesis, our goal was to assess the role of 5' UTR sequences in bS21-2-mediated translation of particular genes. Thus, we developed a series of reporter constructs that consisted of the experimentally determined or predicted 5' UTR with the first 6 codons of the gene of interest, fused to a reporter gene (*lacZ* or *gfp*) (**Fig 2a**; also as in **Fig 1B** and **1D**). Reporter constructs were expressed by the *tul4* promoter, which is unaffected by the presence or absence of bS21-2 (Trautmann & Ramsey, 2022). This design allows for comparable transcription of reporter genes in both genotypes so that we can compare relative translation initiation. The reporter constructs were introduced into *F. tularensis* cells with (WT) or without bS21-2 ($\Delta rpsU2$). Some experiments were completed using β -galactosidase reporters incorporated into the chromosome at the Tn7 site. Toxicity of plasmids that produce high levels of β -galactosidase in *E. coli* during plasmid production led us to use a GFP-based reporter system for some constructs. Reporter constructs using *gfp* were cloned into a multi-copy plasmid that is retained at essentially the same copy number in *F. tularensis* cells with and without bS21-2 (**Fig S1**).

These reporter assays evaluated the relative efficiency of translation initiation of specific 5' UTRs in cells with or without bS21-2. We chose to assess the 5' UTRs corresponding to proteins with significant changes only in protein

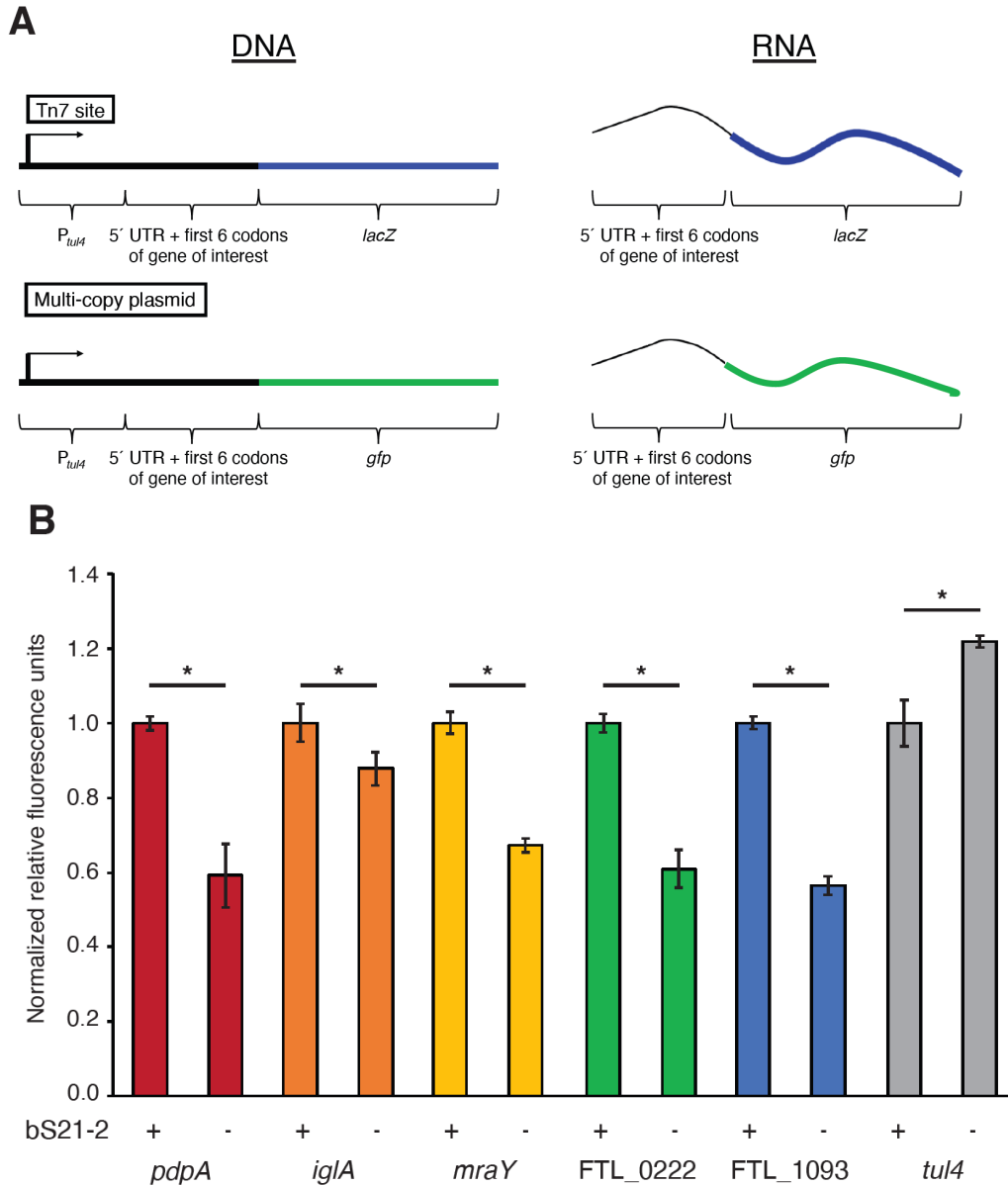


Figure 2. 5' UTRs are sufficient to lead to bS21-2-mediated changes in translation. (A) Diagrams of the translational reporter fusions used. Reporters used the *tul4* promoter to drive expression of the tested 5' UTR, including the first 6 codons of the gene, and are in frame with either *lacZ* at the Tn7 site of the genome or *gfp* on a multi-copy plasmid. **(B)** Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2 in biological triplicate. The *tul4* reporter serves as a control. 5' UTR sequences can be found in Table 1. Error bars represent 1 SD. * $p < 0.05$ by t-test. Experiments were repeated at least twice and data from a representative experiment are shown.

abundance in cells lacking bS21-2 (Trautmann & Ramsey, 2022). Consistent with the observed changes in protein abundance being due to changes in translation initiation, we found that the 5' UTRs of *pdpA*, *iglA*, *mraY*, FTL_0222, or FTL_1093 genes fused to GFP led to significantly less fluorescence in cells lacking bS21-2 compared to wild-type (**Fig 2B**). In contrast, the 5' UTR of *tul4*, a gene not differentially expressed in cells lacking bS21-2, did not lead to a significant decrease in fluorescence in cells lacking bS21-2 (**Fig 2B**). These data reveal that the 5' UTR of a gene is sufficient for bS21-2 to affect translation and is consistent with the idea that bS21 may be regulating translation initiation. We will refer to 5' UTRs that result in altered protein abundance in the presence of bS21-2 as “bS21-2-responsive.” We also found that the 5' UTRs of some genes impacted by bS21-2 in our proteomics analysis did not lead to reporter gene differences in cells lacking bS21-2, including FTL_0881 and FTL_0215 (**Fig S2**). We do not have experimentally determined transcription start sites for these genes, so it is possible the lack of regulation is due to inaccurate 5' UTR predictions. Other possibilities, including indirect regulation of these particular genes, are described in the discussion.

An ideal Shine-Dalgarno sequence masks the positive effects of bS21-2 on translation

Given that the FPI gene *pdpA* has a bS21-2-responsive 5' UTR (**Fig 1D and 2A**), we further examined features of the *pdpA* 5' UTR that may lead to preferential translation from ribosomes containing bS21-2. Based on structures of

the *E. coli* ribosome during translation initiation, the bS21 residue R17 is close enough to directly contact the 16S rRNA nucleotide C1529, which is part of the anti-Shine Dalgarno (ASD) sequence (Kaledhonkar et al., 2019; **Fig 3A**). R17 is conserved in all three *F. tularensis* bS21 homologs and the rRNA-encoded ASD is identical in *F. tularensis* and *E. coli*. Thus, we hypothesized that bS21 homologs in *F. tularensis* may also contact the ASD and influence Shine-Dalgarno (SD)-ASD binding during translation initiation. To test this possibility, we developed β -galactosidase translational reporters with altered SD sequences in the *pdpA* 5' UTR (**Fig 3B**). 5' UTRs with mutations that retained imperfect base-pairing between the ASD and SD (*badSD*, *tul4SD*) were still bS21-2-responsive. However, introducing an ideal SD, in two different positions (*idealSD*, *ideal_movedSD*), led to similar reporter gene expression in cells with and without bS21-2, indicating that these 5' UTRs are no longer bS21-2-responsive (**Fig 3B**).

We replicated the impact of a perfect SD on the bS21-2 responsive 5' UTR of another gene, *mraY*. Modification of the imperfect *mraY* SD to an ideal SD resulted in no significant difference in GFP production in cells with or without bS21-2 (**Fig 3C**). It is worth noting that in each of these cases, the addition of a perfect SD in the correct location (separated from the start codon by 6 to 8 nt) leads to increased total reporter production (**Fig S3**). These data suggest that genes with perfect SD sequences do not require bS21-2 for efficient translation; in other words, an ideal SD may lead to such efficient translation that any response to bS21-2 becomes negligible.

Figure 3. Genes with ideal Shine-Dalgarno (SD) sequences are not responsive to bS21-2. (A) bS21 interacts with the anti-Shine Dalgarno (ASD) sequence. In *E. coli*, the amino acid R17 of the sole bS21 protein (green) directly interacts with nt C1539 of the 16S, which is part of the ASD (blue). Measured distance is 2.7Å distance (PDB 6o7k visualized on PyMol v2.4; Kaledhonkar et al. 2019). **(B)** Introduction of an ideal SD in the *pdpA* leader leads to loss of bS21-2 responsiveness. Top: Relative β -galactosidase activity from modified or wild-type *pdpA* 5' UTRs in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. Bottom: Alignment of modifications to *pdpA* 5' UTR. Nucleotides altered from WT are capitalized; ideal SD sequences are in bold. **(C)** Introduction of an ideal SD in the *mraY* leader leads to loss of bS21-2 responsiveness. Top: Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. Bottom: Alignment of indicated 5' UTRs; ideal SD sequences are in bold. Value in parenthesis indicates the number of identical nts omitted from 5' end of the UTRs. (B-C) Error bars represent 1 SD. * $p < 0.05$ by t-test. Ns = not significant. Experiments were repeated at least twice and data from a representative experiment are shown. **(D)** The absence of strong SD-ASD interactions is correlated with bS21-2 influencing translation. Fraction of genes that are positively-impacted (n=74), negatively-impacted (n=84), or unaffected (n=82) by bS21-2, categorized by strength of SD. "Strong" SD indicates 4 or more nts complementary to ASD; "weak" SD indicates 3 or fewer complementary nts.

Because perfect SD sequences mask the impacts of bS21-2, we hypothesized that genes with weaker SD sequences may require bS21-2 for efficient translation. We compared predicted SDs for genes whose proteins are positively affected (n=74), negatively affected (n=84), or unaffected (n=82) by bS21-2 (Trautmann & Ramsey, 2022). We found that the genes positively affected generally have weaker SD sequences, with only 39% having strong SD sequences (defined by 4 or more nucleotides [nt] complementary to the ASD), compared to 54% or 69% strong SDs in negatively affected or unaffected genes, respectively (**Fig 3D**). These data are consistent with a model in which bS21-2 influences translation initiation predominately in the absence of strong SD-ASD interactions. However, given that many genes have weak or non-perfect SDs and are not affected by bS21-2, there is an unidentified component of the 5' UTR that results in responsiveness to bS21-2.

Sequence-specific motifs found in the 5' UTR of genes governed by bS21-2 do not alter bS21-2 responsiveness

We reasoned that 5' UTRs may be responsive to bS21-2 because they harbor a common sequence-specific element that may mediate an altered interaction with bS21-2 or bS21-2-containing ribosomes. To identify such an element, we compiled 5' UTR sequences including 100 nts upstream of the start codon and the first six codons of the gene for all proteins that were significantly less abundant in cells lacking bS21-2 compared to wild-type (n=74; 100 nt was arbitrarily chosen because most *F. tularensis* transcription start sites have not been

identified). As a control, we also compiled 5' UTR sequences from 82 genes that were not impacted by bS21-2 presence. Using the motif-finding algorithm STREME, which identifies ungapped motifs enriched in large data sets (Bailey, 2021), we identified sequence motifs enriched in the 5' UTRs of the 20 genes most positively governed by bS21-2 (Trautmann & Ramsey, 2022). The motifs we identified were enriched compared to shuffled sequences and were not found to be enriched in the control sequences. Two motifs, which we refer to as Motif 1 and Motif 2, are AU-rich and are found in 19 and 18 of the 20 sequences assessed, respectively (**Fig 4A**). Targeted mutations were made to modify these motifs in the *mraY* 5' UTR and assess their impact on responsiveness to bS21-2. Mutations 1 and 2 modified Motif 1 from AAAAUAAC to CCCC GCCG, which altered the AU-content of the entire motif, and AAAUAUACA, which altered the three most conserved nt in the motif. When assessed using the GFP reporter assay, neither of these modifications altered the responsiveness of the 5' UTR to bS21-2 (**Fig 4B**). To assess the contribution of Motif 2, we created mutation 5, a truncation of the 5' end of the *mraY* 5' UTR that removed 25 nt including motif 2. Similarly, this 5' UTR also remained responsive to bS21-2 (**Fig 6**). Together, these data indicate that neither of the two STREME-predicted AU-rich motifs are necessary for the positive impact of bS21-2 on translation of the *mraY* 5' UTR.

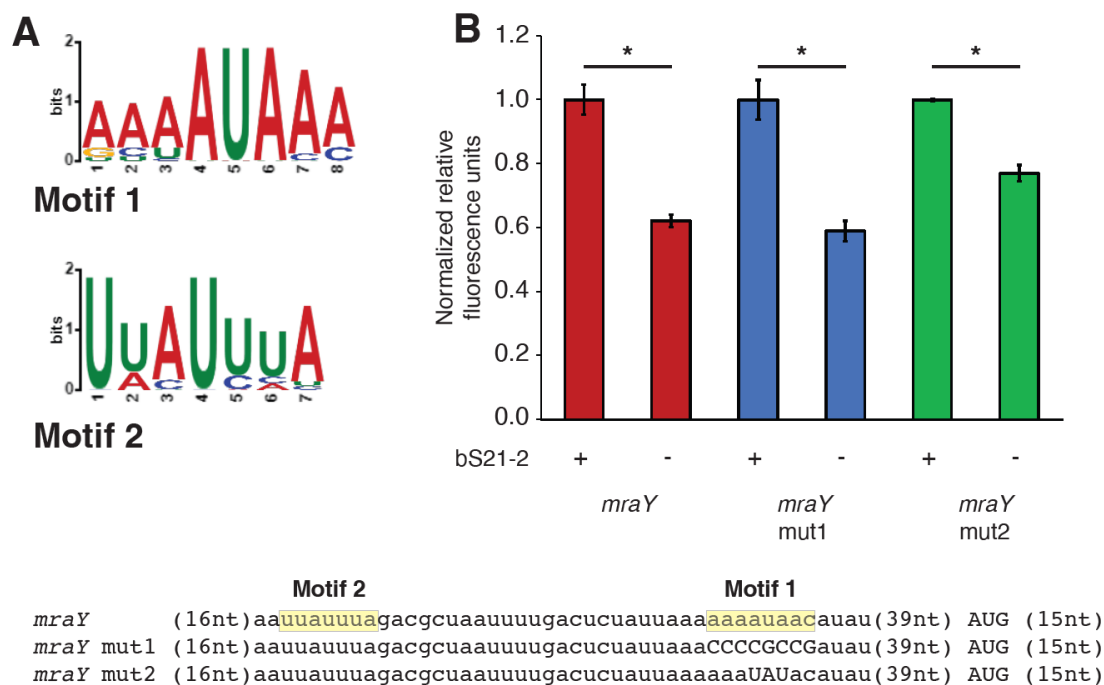


Figure 4. STREME-detected motifs are not necessary for bS21-2-responsive translation in the *mraY* 5' UTR. (A) Logos of two sequence motifs generated by STREME, found to be enriched in the 5' UTRs of the 20 most bS21-2-responsive genes compared to shuffled sequences. Motif 1 was detected in 19/20 input sequences; Motif 2 was detected in 18/20 input sequences. (B) Top: Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. Error bars represent 1 SD. * $p < 0.05$ by t-test. Experiments were repeated twice and data from a representative experiment are shown. Bottom: Alignment of modifications to *mraY* 5' UTR. Nucleotides altered from WT are capitalized. Motifs are highlighted in yellow. Values in parenthesis indicates the number of identical nts omitted from the ends of the UTRs.

Predicted secondary structures of 5' UTRs are not responsible for bS21-2 responsiveness

The secondary structure of mRNA molecules is an important determinant of translation initiation efficiency (Hall et al., 1982; de Smit & van Duin, 1994). We hypothesized that the secondary structure of mRNAs ~~that are differentially expressed in cells with or without bS21-2~~ *bS21-mediated* may play a role in ~~altered~~ translation. We predicted the secondary structure of the *pdpA* 5' UTR using MXfold2 (**Fig S4**), made targeted mutations to disrupt the predicted stem-loop structure (*pdpA* mut1), and generated β -galactosidase reporters at the Tn7 site in cells with (WT) and without ($\Delta rpsU2$) bS21-2 (**Fig 5A**). We also made complementary mutations to restore the original predicted secondary structure without maintaining the original sequence (*pdpA* mut2). In designing each mutation, we ensured that there was no significant disruption to the Shine-Dalgarno or start codon. Neither of these variants that altered the *pdpA* 5' UTR structure affected responsiveness to bS21-2, indicating that the secondary structure of this 5' UTR does not play a role in translation modulation by bS21-2.

We then looked at the secondary structure of a longer 5' UTR, *mraY*, which was predicted using MXFold2 to contain a large stem-loop (**Fig 5B**). We mutated a region that was predicted to form the stem closest to the loop, thereby disrupting the structure (*mraY* mut3). We also made complementary mutations to restore the structure (*mraY* mut4) and assessed these 5' UTRs in a GFP reporter assay. We found that the disruption to the predicted secondary structure (*mraY* mut3) did not

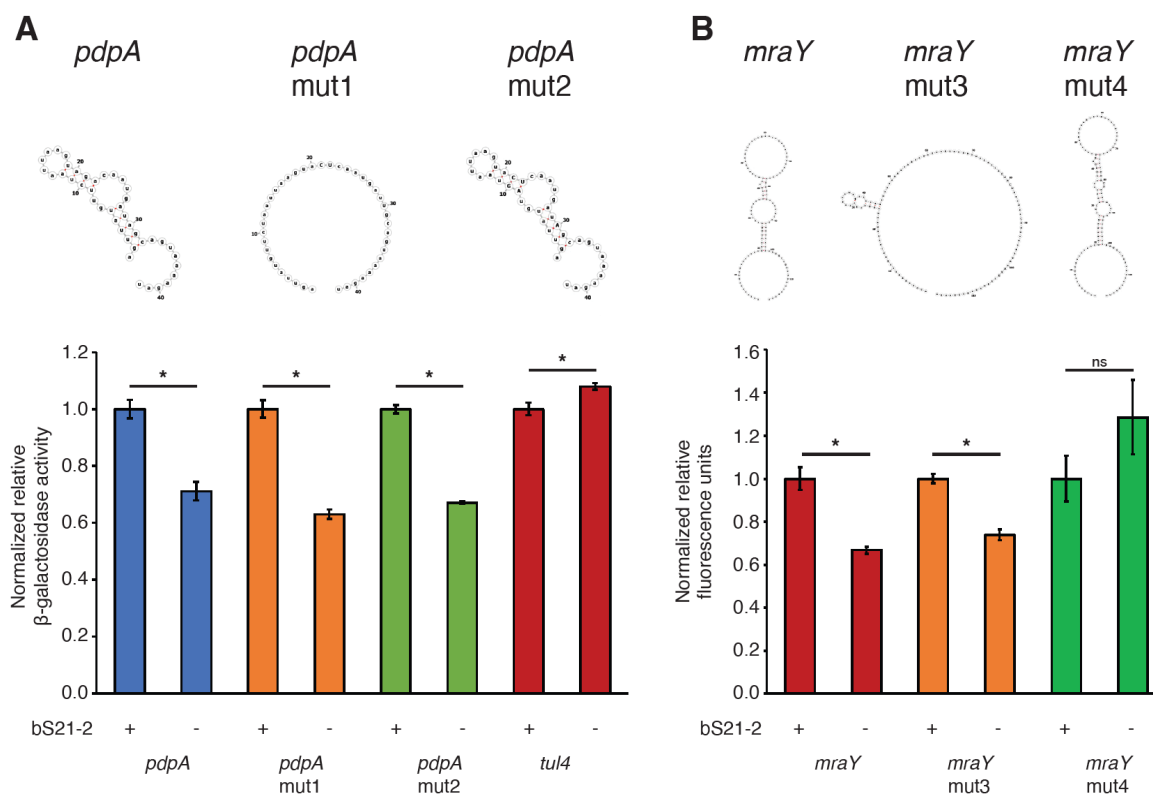


Figure 5. Predicted secondary structure plays no clear role in bS21-2-responsive translation. (A) Changing the *pdpA* secondary structure does not impact responsiveness to bS21-2. Top: Predicted secondary structures for wild-type and modified *pdpA* 5' UTRs, from MXFold2. Sequence modification can be found in Table 1. Bottom: Relative β -galactosidase activity from indicated 5' UTR fused to *lacZ*, in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. *tul4* is included as a control. **(B)** Changing the *mraY* secondary structure does not impact responsiveness to bS21-2. Top: Secondary structure predictions of wild-type and modified *mraY* 5' UTRs, from MXFold2. Sequence modification can be found in Table 1. Bottom: Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. (A-B) Error bars represent 1 SD. * $p < 0.05$ by t-test. Experiments were repeated twice and data from a representative experiment are shown.

affect bS21-2 responsiveness. In contrast, the complementary mutation that restored the stem-loop structure was no longer responsive to bS21-2 (**Fig 5B**). In our studies of two different bS21-2 responsive 5' UTRs, we did not find a specific secondary structure that is necessary for bS21-2-responsive translation.

A 6-nucleotide region of the *mraY* 5' UTR is critical for bS21-2-responsiveness

While testing the importance of the *mraY* 5' UTR structure to bS21-2 responsiveness, we identified a 5' UTR variant that was no longer responsive to bS21-2 (*mraY* mut4). This variant included mutations in nt 58-63 upstream of the initiation codon. To further clarify the sequence necessary for bS21-2-responsiveness in the *mraY* 5' UTR, we made a series of truncations and modifications from the 5' end of the leader sequence. Truncating the 5' UTR to 75 nt (*mraY* mut5) did not impact bS21-2-responsiveness, nor did modifying the AU-rich region located 64-70 nt from the initiation codon (*mraY* mut8) (**Fig 6**). But truncating the 5' UTR to 57 nt (*mraY* mut6) led to loss of bS21-2-responsiveness, further implicating the nt 58-63 upstream of the initiation codon, GACUCU, in responsiveness to bS21-2, as suggested by *mraY* mut4 (**Fig 5B**). We further assessed the importance of the GACUCU sequence using *mraY* mut7 (truncating the 5' UTR to 60 nt and changing the first three nt to AGA) and *mraY* mut9 (truncating the 5' UTR to 63 and mutating nt 58-63 to AGUGAG), and found neither was responsive to bS21-2. These data allow us to conclude that the nt 58-63 upstream of the *mraY* initiation codon, GACUCU, are critical for bS21-2-responsive translation of the

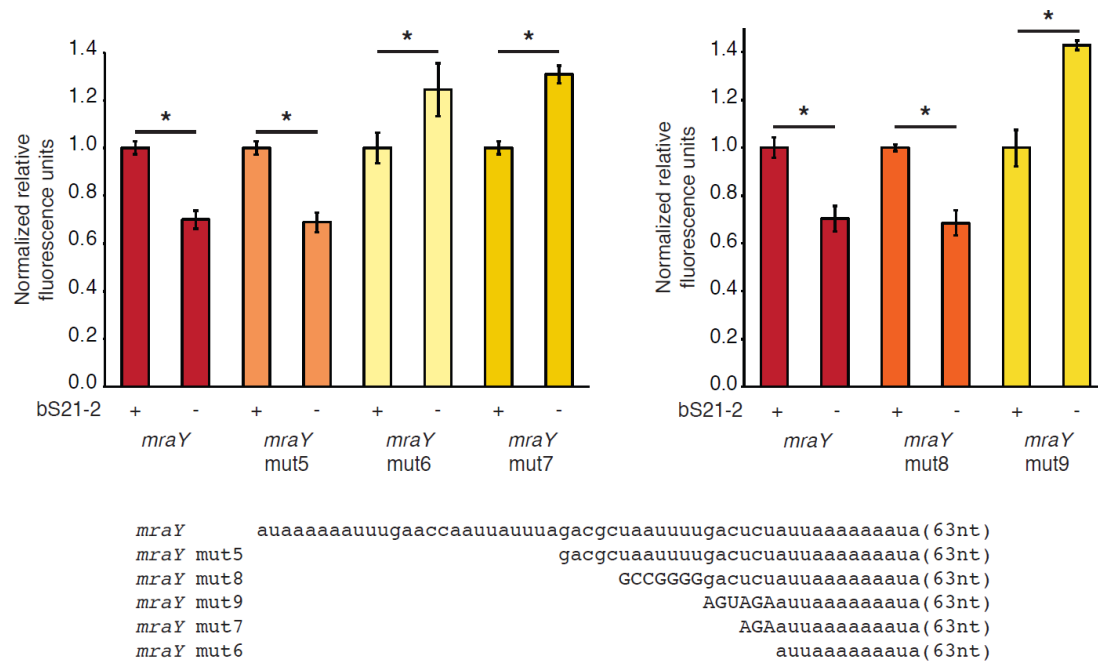


Figure 6. GACUCU is critical for bS21-2-mediated translation in the *mraY* 5' UTR. Top: Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2, in biological triplicate. Error bars represent 1 SD. * $p < 0.05$ by t-test. Experiments were repeated twice and data from a representative experiment are shown. Bottom: Alignment of modifications to *mraY* 5' UTR. Nucleotides altered from WT are capitalized. Values in parenthesis indicates the number of identical nts omitted from the 3' ends of the UTRs.

mraY 5' UTR. This is consistent with a model in which bS21-2-containing ribosomes interact directly or indirectly with a specific element of the leader sequence to facilitate efficient translation initiation of some transcripts.

Discussion

In this work, we addressed two hypotheses regarding how bS21-2 exerts its effects on protein synthesis. In the first, we suggested that the effects of bS21-2 on the T6SS proteins may be mediated by Hfq, a known regulator of T6SS proteins. However, since there have been conflicting reports regarding the impacts of Hfq on the T6SS, we also examined the effects of Hfq on T6SS protein and transcript abundance. Our work clearly demonstrates that Hfq is a negative regulator of one of the FPI two operons encoding T6SS proteins and that this regulation influences transcript abundance rather than translation, consistent with and building upon, a prior study (Meibom et al., 2009). In contrast, the positive effects of bS21-2 on essentially all T6SS proteins can be attributed to differences in protein synthesis. Thus, we conclude that Hfq and bS21-2 function in independent pathways to regulate the T6SS proteins. The second hypothesis we addressed is that ribosomes containing bS21-2 may influence translation initiation of specific transcripts in a leader sequence-dependent manner. Using reporter assays, we determined that specific 5' UTR sequences are sufficient to lead to altered translation in cells with or without bS21-2. In a comprehensive assessment of 5' UTR elements, we found that bS21-2 responsive 5' UTRs have imperfect SD

sequences and, in a specific responsive 5' UTR, the presence of a particular six nucleotide sequence. Together, these results suggest that bS21-2 impacts protein synthesis by altering translation initiation on mRNAs with specific leader sequences.

In *F. tularensis*, loss of the RNA chaperone Hfq results in defective intramacrophage replication, which is essential for virulence. Yet how Hfq promotes *F. tularensis* intramacrophage replication remains poorly-understood. Few small RNAs have been identified in *F. tularensis* and none have been identified that are Hfq-dependent (Postic et al., 2010; Postic et al., 2012). Two prior studies identified that cells without Hfq have altered expression of the T6SS genes, encoded on the FPI (Meibom et al., 2009; Lenco et al., 2014). One study reported increased transcript abundance of only the *pdpA* operon genes, while the other identified decreased abundance of proteins encoded by the *iglA* operon (Meibom et al., 2009; Lenco et al., 2014). Our results corroborate the former report and we additionally demonstrate a concordant increase in protein abundance for a *pdpA*-operon encoded gene. Finally, using a translational reporter fusion, we show that changes in protein abundance for genes in the *pdpA* operon are not due to changes in translation efficiency. These results demonstrate that Hfq acts to repress *pdpA* operon transcript abundance but does not appear to influence T6SS protein synthesis. The molecular mechanism by which Hfq exerts its effects on this operon, and if it involves a small RNA, remain unclear. Regardless, the change in production of T6SS components is consistent with the observed intramacrophage

growth defect, as *F. tularensis* cells overproducing the T6SS are defective for intramacrophage survival (Rohlfing et al., 2018).

This work demonstrates that bS21-2 exerts its effects on protein synthesis in a leader sequence-dependent manner and is validated in a subset of bS21-2-responsive 5' UTRs (**Fig 2**). While loss of bS21-2 results in altered abundance for about 160 proteins (Trautmann & Ramsey, 2022), we expect that changes in protein abundance for at least some of these may not be due leader-sequence dependent effects, but rather due to downstream or secondary effects. For example, bS21-2 may directly impact synthesis of proteins that influence the abundance of other proteins. Several proteases and peptidases were found to be differentially abundant in cells lacking bS21-2. Thus, proteins like those encoded by FTL_0881 and FTL_0215 may have altered abundance in bS21-2 mutant cells due to changes in the abundance of proteases or protein processing genes.

In our search for an element responsible for leader sequences to be responsive to bS21-2, we found that ideal SD sequences prevent responsiveness. These leader sequences with perfect SDs also lead to much higher translation. This suggests to us that perfect SD-ASD complementarity leads to such efficient translation that any contribution of bS21-2 to translation are minor and effectively masked. It is perhaps unsurprising that other regulators of translation, such as H-NS in *E. coli*, similarly function to regulate translation of mRNAs with imperfect SDs (Park et al., 2010).

While we were unsuccessful at identifying a common element across all bS21-2 responsive leader sequences, we were able to hone in on the 6 nt sequence in the *mraY* 5' UTR that leads to bS21-2 responsiveness, GACUCU. It is notable that this 6 nt sequence, which is found 58-63 nt away from the initiation codon, is predicted to form a stem-loop complementary to sequence 3 nt away from the SD. Yet disruption of that structure by mutating the complementary sequence does not impact the response to bS21-2, implicating the 6 nt sequence alone. Further work will be necessary to determine if this sequence is sufficient for bS21-2 responsiveness, to identify the commonalities among bS21-2 responsive 5' UTRs, and to determine how bS21-2 influences translation initiation on specific leader sequences.

Materials and Methods

Bacterial strains and growth conditions

Unless otherwise noted, bacterial strains were grown as indicated. *Francisella tularensis* subsp. *holarctica* Live Vaccine Strain (LVS) cells were grown in Mueller-Hinton broth (BD Difco) supplemented with 0.025% iron pyrophosphate, 0.1% glucose, and 2% Isovitalex (sMHB), shaking aerobically or on cystine heart agar (BD Difco or prepared in house) plates with 1% hemoglobin (CHA-H) at 37°C. *Escherichia coli* XL1-Blue, DH5 α (New England Biolabs), and DH5 α λ -pir cells were grown in lysogeny broth (LB) shaking aerobically or on LB agar plates at 37°C. Kanamycin was used at concentrations of 5 μ g/mL (*F. tularensis*) or 50 μ g/mL (*E. coli*); hygromycin B was used at concentrations of 200 μ g/mL. *Saccharomyces cerevisiae* cells were grown in synthetic defined (SD) broth without uracil (-ura) shaking aerobically or on SD-ura agar plates at 30°C.

Vector construction

Tn7:*lacZ* plasmids

Mini-Tn7 plasmids for each β -galactosidase reporter were created from a plasmid derived from pMP749 (LoVullo et al. 2009). *E. coli lacZ* was amplified from pEX-*pigR::lacZ* (Charity et al., 2009) using a 5' primer specifying a NotI site and alanine linker (5'-GCGGCCGCT-3') and a 3' primer specifying a BamHI site. The amplified *lacZ* gene was cloned into NotI/BamHI digested pMP749, resulting in pKR68 (Tn7-*lacZ*). Subsequently, two fragments were amplified from LVS genomic DNA (gDNA): (1) the *tul4* promoter with a 5' primer specifying a KpnI site

and a 3' primer overlapping the second fragment; and (2) either modified or wild-type UTRs from genes of interest, along with the first six codons of the corresponding gene, with a 3' primer specifying a NotI site and a 5' primer overlapping the first fragment. Overlap extension PCR was then conducted on the two fragments and the PCR product was cloned into KpnI/NotI digested pKR68 such that *lacZ* was in-frame with the first six codons of the gene of interest. The resulting plasmids are all indicated in **Table 1** below. Modifications to wild-type UTRs were encoded on primers for PCR amplification.

Some reporter plasmids with the high-copy pUC *ori* produced enough β -galactosidase in *E. coli* to be toxic, so cloning required one of two alternate approaches. In one approach, the origin of the pMP749 plasmid was replaced by a low-copy R6Ky origin, amplified from pKL91 (Ramsey et al., 2020) using primers that encode an NspI site. The digested product was cloned into NspI-digested pMP749, resulting in pKR88 (Mini_Tn7_R6Kg), which was propagated in DH5 α λ -pir cells. Subsequently, the *tul4* promoter and 5' UTR was amplified from LVS gDNA using a 5' primer specifying a KpnI and a 3' primer specifying a NotI site; *lacZ* was amplified from pKR68 using a 5' primer specifying a NotI site and alanine linker (5'-GCGGCCGCT-3') and a 3' primer specifying a BamHI site. The two fragments were cloned into BamHI/KpnI-digested pKR88 using a three-way ligation, resulting in pKR89 (Tn7_P*tul4*_tul4UTR_*lacZ*_R6Kg; **Table 1**).

In a second approach, *lacZ* plasmids were cloned using *Saccharomyces cerevisiae*. The 2 μ origin and *URA3* gene were isolated from pYES2 (Invitrogen) by digestion with PstI, then cloned into DraI-digested pKR68, disrupting the β -

lactamase gene. The resulting plasmid, pKR128 pYES2 Tn7-*lacZ*, was used for subsequent cloning of 5' UTRs using alanine linkers and NotI sites, as described above and detailed in **Table 1** below. pYES2-based plasmids were purified from overnight cultures of *S. cerevisiae* using the Zymoprep Yeast Plasmid Miniprep III kit.

pF-GFP plasmids

Multicopy GFP reporter plasmids were created from a previously described shuttle vector, pFNLTP6 (Maier et al. 2004). A fragment containing the promoter, 5' UTR, and first six codons of *tul4* was digested from pKR89 with KpnI/NotI. sfGFP codon-optimized for expression in *F. tularensis* LVS was purchased as a gBlock (IDT) and digested with NotI/BamHI. Fragment were cloned into KpnI/BamHI-digested pF such that GFP was in-frame with the first six codons of *tul4*, resulting in pKR145 (pF-*tul4* UTR-GFP). The plasmid pKR146 (pF-*pdpA* UTR-GFP) was constructed similarly, after amplification from pKR74 of the *tul4* promoter and *pdpA* 5' UTR and first six codons and digestion of the PCR product with Kpn/NotI. Subsequent constructs were cloned into pKR145 to replace the *tul4* 5' UTR using the endogenously encoded PacI site in the *tul4* promoter (**Table 1** for details). For genes in which a transcription start site had not been annotated at the time of plasmid design, 100 nucleotides upstream of the start codon were included as the 5' UTR (**Table 1** for details). Known transcription start sites for *tul4*, *iglA*, and *pdpA* were previously published by Ramsey et al. (2015); the transcription start site for *hfq* was experimentally determined by Meibom et al. (2009) and Chambers & Bender (2011).

Allelic exchange plasmid

The plasmid pEX18kan was modified to create the in-frame deletion construct for deletion of *hfq* as previously described (Charity et al. 2007). Flanking regions of ~1000 base pairs from both sides of the *hfq* gene were amplified by PCR. Primers amplifying the DNA adjacent to *hfq* included the first three or last three codons of the open reading frame and DNA specifying a NotI site, which also encodes an alanine linker (5'-GCGGCCGCT-3'). The two fragments were cloned into BamHI/KpnI-digested pEX18kan, yielding pKL111 pEXΔ*hfq*.

VSV-G tagging integration vector

A single-integration vector for VSV-G tagging of *hfq* was made by modifying pKL02 (Ramsey et al., 2015). The final 200 nucleotides of the 3' end of *hfq* was amplified using a 5' primer specifying a KpnI site and a 3' primer that lacked the native stop codon and included DNA specifying a NotI site. The fragment was cloned into KpnI/NotI digested pKL02 such that the 3' end of *hfq* is in frame with the codons specifying three alanine residues followed by the VSV-G epitope, resulting in pKR158 (pEX-*hfq*-V).

Table 1: Plasmids used in this study.

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
Tn7:<i>lacZ</i> constructs						
pKR68	Tn7_ <i>lacZ</i>	pMP749	BamHI/ HindIII	PCR of <i>lacZ</i> from pEX-pigR:: <i>lacZ</i>	-	-
pKR74	Tn7_ <i>Ptul4</i> _pdpA UTR_ <i>lacZ</i>	pKR68	KpnI/NotI	Overlap extension PCR. Both <i>pdpA</i> 5'UTR and <i>tul4</i> promoter amplified from LVS gDNA	<i>pdpA</i>	agttatgttctaattaagtagacaat gatagcagtaaaagat
pKR84	Tn7_ <i>Ptul4</i> _pdpA UTR_mut1_ <i>lacZ</i>	pKR68	KpnI/NotI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgttctaattaagtaCTcaat gatTgcagtaaaagat
pKR85	Tn7_ <i>Ptul4</i> _pdpA UTR_mut2_ <i>lacZ</i>	pKR68	KpnI/NotI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgtActGattaagtagacaa tgatagcagtaaaagat
pKR98	Tn7_ <i>Ptul4</i> _pdpA UTR_badSD- <i>lacZ</i>	pKR68	KpnI/NotI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgttctCcttCCATCAac aatgatagcagtaaaagat
pKR99	Tn7_ <i>Ptul4</i> _pdpA UTR_ideal_movedSD- <i>lacZ</i>	pKR68	KpnI/NotI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgAAGGAGGTCCAT CAacaatgatagcagtaaaagat
Tn7:<i>lacZ</i> with R6ky origin						
pKR88	Mini_Tn7_R6Kg	pKR55	Nspl	R6K λ origin from pKL91	-	

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
pKR89	Tn7_ <i>Ptul4_tul4</i> UTR_ <i>lacZ</i> _R6Kg	pKR88	BamHI/KpnI / NotI	PCR of <i>tul4</i> promoter and 5'UTR from LVS gDNA; <i>lacZ</i> amplified from pKR68; three-way ligation	<i>tul4</i>	gagtatatgtgaatattttaaaaatag gagtatctatatgaaaaaataatt aag
Tn7:<i>lacZ</i> with 2μ origin						
pKR128	pYES2_Tn7_ <i>lacZ</i>	pKR68	DraI/ PstI	<i>ura3</i> gene and 2μ origin digested from pYES2	-	
pKR129	pYES2_Tn7_ <i>Ptul4_pdpA</i> UTR_idealS D- <i>lacZ</i>	pKR128	NotI/KpnI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgttctAAGGAGGTCA acaatgatagcagtaaaagat
pKR130	pYES2_Tn7_ <i>Ptul4_pdpA</i> UTR_ <i>tul4</i> S D- <i>lacZ</i>	pKR128	NotI/KpnI	PCR of <i>pdpA</i> 5'UTR from pKR74; modifications encoded on primers	<i>pdpA</i>	agttatgttctaAGGAGTATCa caatgatagcagtaaaagat
pF-GFP constructs						
pKR145	pF- <i>tul4</i> UTR-GFP	pF	KpnI/BamHI / NotI	PCR of <i>tul4</i> promoter and 5'UTR from pKR89; PCR of <i>gfp</i> from IDT gBlock of super-folder GFP codon-optimized for LVS; three-way ligation	<i>tul4</i>	gagtatatgtgaatattttaaaaatag gagtatctatatgaaaaaataatt aag

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
pKR146	pF- <i>pdpA</i> UTR-GFP	pF	KpnI/BamHI / NotI	PCR of <i>tul4</i> promoter and <i>pdpA</i> 5'UTR from pKR74; PCR of <i>gfp</i> from IDT gBlock of super-folder GFP codon-optimized for LVS; three-way ligation	<i>pdpA</i>	agttatgttctaattaagtagacaat gatagcagtaaaagat
pKR151	pF- <i>mraY</i> UTR-GFP	pKR145	PacI/NotI	PCR of <i>mraY</i> 5'UTR from LVS gDNA	<i>mraY</i>	ataaaaaattgaaccaattatttag acgctaatttgactctataaaaaa ataacatatctattataactccaa ggtcattaaacattttaatatatgct gatttatctttt
pKR152	pF-FTL_0215 UTR-	pKR145	PacI/NotI	PCR of FTL_0215 5'UTR from LVS gDNA	FTL_0215	ataattacaaaaaataaaaatat ctctagcctaataaacattgttgaa aaatttttataaaatatactgattga aacctttaagatttttttattatgaa tatagttgactac
pKR156	pF- <i>mraY</i> UTR_mut1-GFP	pKR145	PacI/NotI	Overlap extension PCR of <i>mraY</i> 5'UTR from pKR151; modifications encoded on primers	<i>mraY</i>	ataaaaaattgaaccaattatttag acgctaatttgactctataaaCC CCGCCGatctctattataatactc caaggtcattaaacattttaatatata tgctgatttatctttt

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
pKR157	pF- <i>mraY</i> UTR_mut2-GFP	pKR145	PacI/NotI	Overlap extension PCR of <i>mraY</i> 5'UTR from pKR151; modifications encoded on primers	<i>mraY</i>	ataaaaaaattgaaccaattatttag acgctaatttgactctattataaaaa TATacatatctattataaatactcca aggctattaacattttaatatatg ctgattatctttt
pKR160	pF- <i>iglA</i> UTR-GFP	pKR151	KpnI/NotI	PCR of <i>iglA</i> 5'UTR from LVS gDNA	<i>iglA</i>	aagggtgtgtgaaaaaaggaca ataagatggcaaaaaataaaatc
pKR161	pF-FTL_0222UTR-GFP	pKR151	PacI/NotI	PCR of FTL_0222 5'UTR from LVS gDNA	FTL_0222	aaaaaataaaaatttgtaatttagtc agaccatttaagtagaatttgagta atcataatgtagatttaattacaca gaatattaaatttttaataccaatgctc agctcaagtcctca
pKR162	pF-FTL_0881 UTR	pKR151	PacI/NotI	PCR of FTL_0881 5'UTR from LVS gDNA	FTL_0881	aaaatttttactggataaaaaagttt catgcagatgtttttatttactatttag attttaacaacataaaacaataa tagtaaatgaaggagaaaaaatg aaaaagataattaca
pKR163	pF-FTL_1093 UTR-GFP	pKR151	PacI/NotI	PCR of FTL_1093 5'UTR from LVS gDNA	FTL_1093	ccttcaatttagactagatatgttag attagaataatacttttctaagtttat atcataattattaacaattatttaaca aattaataaggtaagtagatgctaa aaactaagagc

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
pKR179	pF- <i>mraY</i> -mut8-UTR-GFP	pKR151	NotI/PacI	PCR of portion of <i>mraY</i> 5'UTR from pKR165; modifications encoded on primers	<i>mraY</i>	<div>_____GCCGGGGgac</div> <div>tctattaaaaaataacatatctatt</div> <div>ataatactccaaggtcattaaacatt</div> <div>ttaatatatgctgatttatctttt</div>
pKR180	pF- <i>mraY</i> -mut9-UTR-GFP	pKR151	NotI/PacI	PCR of portion of <i>mraY</i> 5'UTR from pKR165; modifications encoded on primers	<i>mraY</i>	<div>_____AGTG</div> <div>AGattaaaaaataacatatctatt</div> <div>ataatactccaaggtcattaaacatt</div> <div>ttaatatatgctgatttatctttt</div>
pKR182	pF- <i>mraY</i> -mut3-UTR-GFP	pKR151	NotI/PacI	PCR of <i>mraY</i> 5'UTR from LVS gDNA; modifications encoded on primers	<i>mraY</i>	<div>ataaaaaatttgaaccaattatttag</div> <div>acgctaattttagactctattaaaaa</div> <div>ataacatatctattataatactccaC</div> <div>TACTattaaacattttaatatatg</div> <div>ctgatttatctttt</div>
pKR183	pF- <i>mraY</i> -mut4-UTR-GFP	pKR151	NotI/PacI	Overlap extension PCR of <i>mraY</i> 5'UTR from LVS gDNA; modifications encoded on primers	<i>mraY</i>	<div>ataaaaaatttgaaccaattatttag</div> <div>acgctaatttAGTGAGattaaa</div> <div>aaaataacatatctattataatactc</div> <div>caCTACTattaaacattttaaata</div> <div>tatgctgatttatctttt</div>
Allelic exchange vector						

Plasmid Name	Descriptive Name	Backbone	Enzymes	Insert construction/PCR description	5' UTR	5' UTR Sequence (Modification from WT indicated by capital letters or dashes to represent deletions)
pKL111	pEXΔ <i>hfq</i>	pEX	BamHI/KpnI / NotI	PCR of regions flanking <i>hfq</i> from LVS gDNA; three-way ligation	-	-
VSV-G tagging integration vector						
pKR158	pEX- <i>hfq</i> -V	pKL02	KpnI/NotI	PCR of 3' end of <i>hfq</i> gene from LVS gDNA	-	-

Strain construction

β -galactosidase reporter strains (**Table 2**) were constructed by site- and orientation-specific single chromosome integration using the Tn7 transposon as previously described (LoVullo et al. 2009). Helper plasmid pMP720 was electroporated into either wild-type (LVS) or bS21-2 mutant ($\Delta rpsU2$) competent cells in 0.2 cm cuvettes with a 2.5 kV pulse and hygromycin-resistant cells were selected by plating on CHA-H with hygromycin. Cells with the helper plasmid were electroporated with the appropriate mini-Tn7 plasmid and selected for on CHA-H with kanamycin. Colonies were screened for plasmid integration at the *attTn7* site using PCR. Candidate strains were confirmed by amplification of genomic DNA outside of the *attTn7* site and Sanger sequencing (Rhode Island INBRE Molecular Informatics Core).

Reporter constructs encoded on pF plasmids were electroporated into LVS, LVS $\Delta rpsU2$, or LVS Δhfq cells as described above and selected for on CHA-H with kanamycin (**Table 2**).

The Hfq deletion strain was constructed by allelic exchange as previously described (Trautmann & Ramsey 2022). Briefly, at least 1 μ g of allelic exchange plasmid pEX Δhfq was electroporated into competent cells as above. Cells in which a single integration event occurred were selected for on CHA-H-kanamycin. Counter-selection for the vector was accomplished by plating on CHA-H (BD Difco) containing 10% sucrose. Sucrose-resistant, kanamycin-sensitive colonies were screened for deletions using PCR. Candidate strains were confirmed by

amplification of genomic DNA outside of the flanking regions on each side of the deletion and Sanger sequencing, validating LVS Δhfq .

Cells with VSV-G-tagged Hfq were made as previously described (Ramsey et al., 2015). Briefly, at least 1 μ g of pKR158 pEX-*hfq*-V was electroporated into LVS and $\Delta rpsU2$ cells and transformants were selected on CHA-H-with kanamycin. Cells were confirmed to have a single integration by PCR amplification of DNA across the integration site and subsequent Sanger sequencing of the PCR product (RI-INBRE CRCF).

Table 2: Strains used in this study

Strain Number	Description	Background Strain	Plasmid Name
β-galactosidase reporter strains			
KRLVS96	LVS Tn7::Ptul4-pdpA 5'UTR-lacZ <i>aphA</i>	LVS	pKR74
KRLVS97	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR74
KRLVS102	LVS Tn7::Ptul4-pdpA 5'UTR-mut1-lacZ <i>aphA</i>	LVS	pKR84
KRLVS106	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-mut1-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR84
KRLVS110	LVS Tn7::Ptul4-pdpA 5'UTR-mut2-lacZ <i>aphA</i>	LVS	pKR85
KRLVS107	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-mut2-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR85
KRLVS114	LVS Tn7::Ptul4-pdpA 5'UTR-badSD-lacZ <i>aphA</i>	LVS	pKR98
KRLVS117	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-badSD-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR98
KRLVS115	LVS Tn7::Ptul4-pdpA 5'UTR-ideal_movedSD-lacZ <i>aphA</i>	LVS	pKR99
KRLVS118	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-ideal_movedSD-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR99
KRLVS112	LVS Tn7::Ptul4-tul4 5'UTR-lacZ <i>aphA</i>	LVS	pKR89
KRLVS111	LVS $\Delta rpsU2$ Tn7::Ptul4-tul4 5'UTR-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR89
KRLVS158	LVS Tn7::Ptul4-pdpA 5'UTR-idealSD-lacZ <i>aphA</i>	LVS	pKR129
KRLVS160	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-idealSD-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR129
KRLVS159	LVS Tn7::Ptul4-pdpA 5'UTR-tul4SD-lacZ <i>aphA</i>	LVS	pKR130
KRLVS161	LVS $\Delta rpsU2$ Tn7::Ptul4-pdpA 5'UTR-tul4SD-lacZ <i>aphA</i>	$\Delta rpsU2$	pKR130
pF-GFP reporter strains			
KRLVS180	LVS pF-tul4UTR-GFP	LVS	pKR145
KRLVS182	LVS $\Delta rpsU2$ pF-tul4UTR-GFP	$\Delta rpsU2$	pKR145

Strain Number	Description	Background Strain	Plasmid Name
KRLVS234	LVS Δhfq pF- <i>tuI4</i> UTR-GFP	Δhfq	pKR145
KRLVS181	LVS pF- <i>pdp</i> AUTR-GFP	LVS	pKR146
KRLVS183	LVS $\Delta rpsU2$ pF- <i>pdp</i> AUTR-GFP	$\Delta rpsU2$	pKR146
KRLVS236	LVS Δhfq pF- <i>pdpA</i> UTR-GFP	Δhfq	pKR146
KRLVS188	LVS pF- <i>mra</i> YUTR-GFP	LVS	pKR151
KRLVS189	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR-GFP	$\Delta rpsU2$	pKR151
KRLVS190	LVS pF-FTL_0215UTR-GFP	LVS	pKR152
KRLVS191	LVS $\Delta rpsU2$ pF-FTL_0215UTR-GFP	$\Delta rpsU2$	pKR152
KRLVS199	LVS pF- <i>mra</i> YUTR_mut1-GFP	LVS	pKR156
KRLVS200	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut1-GFP	$\Delta rpsU2$	pKR156
KRLVS201	LVS pF- <i>mra</i> YUTR_mut2-GFP	LVS	pKR157
KRLVS202	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut2-GFP	$\Delta rpsU2$	pKR157
KRLVS206	LVS pF- <i>igl</i> AUTR-GFP	LVS	pKR160
KRLVS207	LVS $\Delta rpsU2$ pF- <i>igl</i> AUTR-GFP	$\Delta rpsU2$	pKR160
KRLVS208	LVS pF-FTL_0222UTR-GFP	LVS	pKR161
KRLVS209	LVS $\Delta rpsU2$ pF-FTL_0222UTR-GFP	$\Delta rpsU2$	pKR161
KRLVS210	LVS pF-FTL_0881UTR-GFP	LVS	pKR162
KRLVS211	LVS $\Delta rpsU2$ pF-FTL_0881UTR-GFP	$\Delta rpsU2$	pKR162
KRLVS212	LVS pF-FTL_1093UTR-GFP	LVS	pKR163
KRLVS213	LVS $\Delta rpsU2$ pF-FTL_1093UTR-GFP	$\Delta rpsU2$	pKR163
KRLVS214	LVS pF- <i>mra</i> YUTR_mut5-GFP	LVS	pKR165
KRLVS215	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut5-GFP	$\Delta rpsU2$	pKR165
KRLVS222	LVS pF- <i>mra</i> YUTR_idealSD-GFP	LVS	pKR169
KRLVS223	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_idealSD-GFP	$\Delta rpsU2$	pKR169
KRLVS228	LVS pF- <i>hfq</i> UTR-GFP	LVS	pKR172

Strain Number	Description	Background Strain	Plasmid Name
KRLVS229	LVS $\Delta rpsU2$ pF- <i>hfq</i> UTR-GFP	$\Delta rpsU2$	pKR172
KRLVS243	LVS pF- <i>mra</i> YUTR_mut6-GFP	LVS	pKR175
KRLVS244	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut6-GFP	$\Delta rpsU2$	pKR175
KRLVS247	LVS pF- <i>mra</i> YUTR_mut7-GFP	LVS	pKR177
KRLVS248	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut7-GFP	$\Delta rpsU2$	pKR177
KRLVS252	LVS pF- <i>mra</i> YUTR_mut8-GFP	LVS	pKR179
KRLVS253	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut8-GFP	$\Delta rpsU2$	pKR179
KRLVS260	LVS pF- <i>mra</i> YUTR_mut9-GFP	LVS	pKR180
KRLVS261	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut9-GFP	$\Delta rpsU2$	pKR180
KRLVS262	LVS pF- <i>mra</i> YUTR_mut3-GFP	LVS	pKR182
KRLVS263	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut3-GFP	$\Delta rpsU2$	pKR182
KRLVS264	LVS pF- <i>mra</i> YUTR_mut4-GFP	LVS	pKR183
KRLVS265	LVS $\Delta rpsU2$ pF- <i>mra</i> YUTR_mut4-GFP	$\Delta rpsU2$	pKR183
Deletion strains			
KMLFT97	LVS Δhfq	LVS	pKL111
VSV-G tagged strains			
KRLVS194	LVS <i>hfq</i> -VSVG	LVS	pKR158
KRLVS195	LVS $\Delta rpsU2$ <i>hfq</i> -VSVG	$\Delta rpsU2$	pKR158

β-galactosidase assays

β-galactosidase assays using *F. tularensis* LVS or *ΔrpsU2* cells containing indicated reporter constructs were conducted as previously described (Charity et al., 2009). If significant yellow color was not produced within two hours, reactions were stopped at 120 minutes. Experiments were conducted at least twice in biological triplicate.

GFP assays

F. tularensis LVS, *ΔrpsU2*, or *Δhfq* reporter constructs were grown in sMHB to mid-log phase in biological triplicate. Cells were pelleted and resuspended in PBS. A₆₀₀ and fluorescence with excitation of 495 nm and emission of 535 nm were determined using ID3 plate reader (RI-INBRE CRCF), in technical triplicate. Fluorescence readings were normalized to A₆₀₀ and fluorescence of LVS cells (lacking any GFP reporter) was subtracted from each reading to account for basal level fluorescence of the cells. Experiments were conducted at least twice in biological triplicate.

Plasmid copy number qPCR

Wild-type LVS or LVS *ΔrpsU2* cells with pF plasmids were grown to mid-log (OD₆₀₀ = 0.3-0.4). Total DNA was extracted from 1 mL culture using the MasterPure Complete DNA purification kit (Lucigen). qRT-PCR was performed using PowerUp SYBR Green Master Mix (Applied Biosystems) and a Roche LightCycler 480 (RI-INBRE CRCF) essentially as described (Charity et al., 2007) with 0.05 ng of DNA. DNA abundances were calculated for an opening reading frame (ORF3) on the plasmid and relative abundance is reported compared to a

chromosomally-encoded control gene, *tul4*. Experiments comparing wild-type and *rpsU2* mutant cells were performed three times in biological triplicate.

5' UTR secondary structure prediction

Secondary structures reported above were predicted using the MXfold2 web server (Sato et al., 2021). Cross-algorithm comparison of predictions (Figure S4) were conducted to validate findings using the ViennaRNA 2.0 package via Snapgene v6.2 (Lorenz et al., 2011), the MXFold2 server, and Ufold v1.2 webserver (Fu et al., 2022).

5' UTR motif analyses

The 5' UTRs of genes that have decreases in protein, but not transcript, abundance in cells lacking bS21-2 compared to wild-type (Trautmann & Ramsey, 2022) were analyzed. As there is insufficient annotation of transcriptional start sites in *F. tularensis* LVS, 100 nucleotides upstream of the start codon along with the first six codons were chosen for analysis.

STREME software (MEME suite) was used to analyze the 5' UTRs of the 20 genes with the largest fold decreases in protein in $\Delta rpsU2$ cells compared to LVS. These were compared to shuffled sequences to find two candidate motifs. As a control, the same parameters were used to compare the predicted 5' UTRs of 20 genes not differentially expressed in LVS and $\Delta rpsU2$.

Shine-Dalgarno predictions were made by highest similarity to the reverse complement of the anti-Shine-Dalgarno (5'-AGGAGG-3') within 20 nucleotides of the start codon.

Immunoblotting

Immunoblotting was completed as previously described (Trautmann & Ramsey, 2022). Briefly, cell lysates were separated by SDS-PAGE, transferred to PVDF, and analyzed for total protein with the Invitrogen No-Stain Protein labeling reagent for normalization. Membranes were probed with indicated monoclonal antibodies (BEI Resources, diluted 1:250 for PdpB, 1:1000 for IgIB, and 1:1000 for IgIA) or the VSV-G epitope tag (Sigma, diluted 1:2222) in blocking buffer. Proteins were detected using IRDye 800 CW donkey anti-mouse IgG or donkey anti-rabbit IgG secondary antibodies (Li-Cor, diluted 1:10,000). Protein abundance was calculated as fluorescence of protein bands relative to total protein in each lane. Experiments were performed at least twice in biological triplicate.

RNA purification and qRT-PCR

Total RNA was purified according to the RNAsnap™ protocol (Stead et al., 2012). *F. tularensis* LVS was grown in biological triplicate to mid-log phase. Pelleted cells (10 mL) were resuspended in 100 µl of fresh RES (95% formamide, 18 mM EDTA, 0.025% SDS, 1% BME), then incubated at 95°C for 7 minutes. Cell debris were pelleted by centrifugation and the supernatant was preserved. Total nucleic acid was recovered with 0.3M sodium acetate (pH 5.2) and 3x volumes 100% ethanol. Samples were stored at -80°C for 1 hour, then nucleic acid was pelleted by centrifugation at 4°C for 30 minutes. The pellet was washed with 75% ethanol and resuspended in water. Purified nucleic acids were treated with RQ1 DNase (Promega) for 1 hour at 37°C and RNA was purified again with sodium acetate/ethanol precipitation.

cDNA was synthesized using Superscript III reverse transcriptase (Life Technologies) as previously described (Charity et al., 2007). qRT-PCR was performed with the PowerUP SYBR Green Master Mix (Applied Biosystems) and the Roche Lightcycler 480 (RI-INBRE CRCF). Transcript abundances of *pdpA*, *pdpB*, *iglA*, *pigR*, *rpoA1*, and *bfr* were normalized to a control gene, *tul4*. Experiments were conducted twice in biological triplicate.

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Supplemental Figures

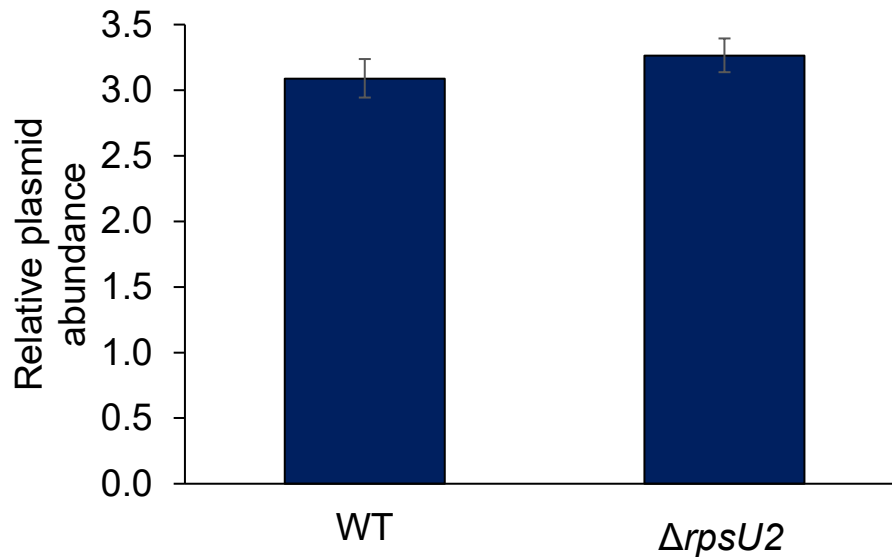


Figure S1. pF plasmid copy number is not affected by presence of bS21-2. Quantitative real-time PCR of total DNA from wild-type (WT) cells and cells lacking bS21-2 ($\Delta rpsU2$) was used to assess the relative abundance of the multi-copy pF plasmid used in GFP experiments. An opening reading frame on the plasmid, ORF3, was amplified and normalized to chromosomally-encoded *tul4*. Error bars represent 1 SD from the mean value (calculated using the mean threshold cycle). Experiments were repeated three times and data from a representative experiment are shown.

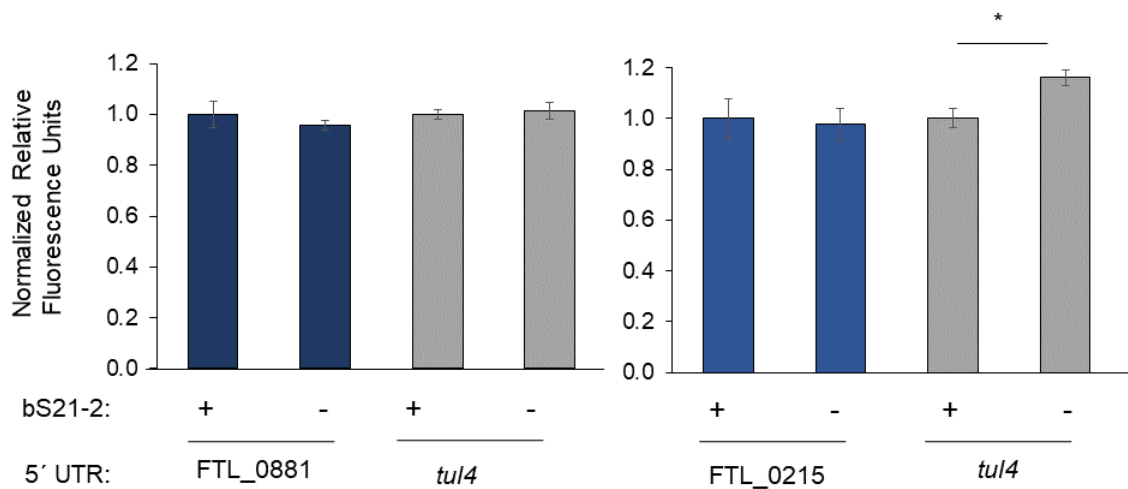


Figure S2. Some 5' UTRs do not lead to bS21-2-mediated changes in translation. Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; $\Delta rpsU2$) bS21-2. FTL_0881 and FTL_0215 were found to be less abundant at the protein level in cells lacking bS21-2 in a proteomics screen (Trautmann & Ramsey, 2022). The *tul4* 5' UTR is included as a control. Error bars represent 1 SD. Experiments were repeated twice and data from representative experiments are shown. * $p < 0.05$

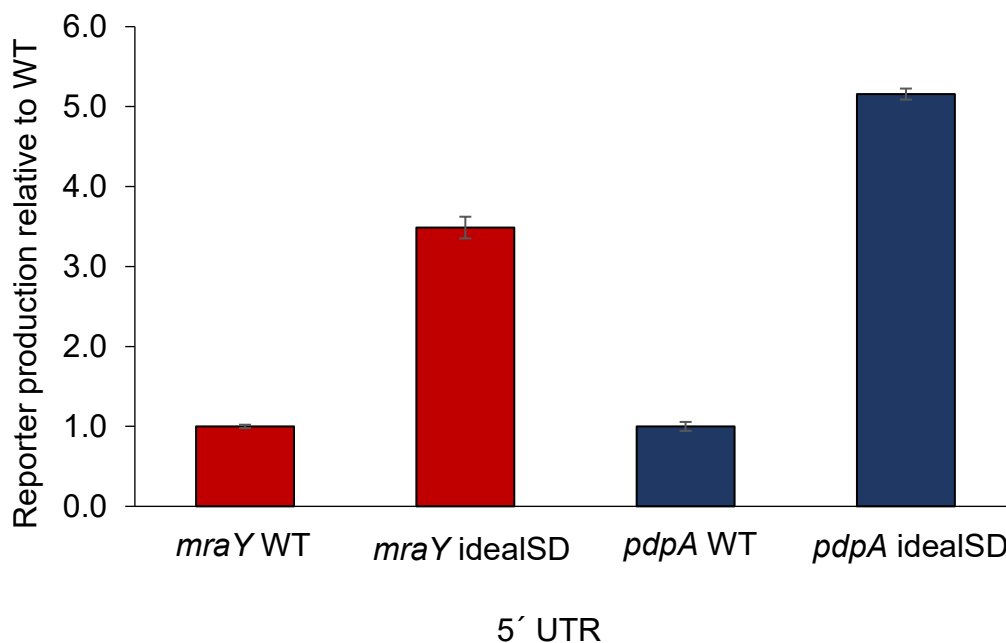











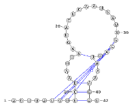



Figure S3. Addition of an ideal Shine-Dalgarno sequence increases reporter protein production relative to unmodified 5' UTRs. Relative β -galactosidase activity or fluorescence of *pdpA* or *mraY* 5' UTRs, respectively, in cells with bS21-2, compared to unmodified (WT) 5' UTR for each gene. Error bars represent 1 SD. Experiments were repeated twice and data from representative experiments are shown.

5' UTR	Sequence	MXFold2	Ufold	ViennaRNA
<i>mraY</i> WT	auaaaaaaauugaaccaauuauu uagacgcuaauuuugacucuaau aaaaaaaauaacauaucuaauua auacuccaaggucuuuaacauu uuaaaauauAUGcugauuuaucu uuuu			
<i>mraY</i> mut3	auaaaaaaauugaaccaauuauu uagacgcuaauuuugacucuaau aaaaaaaauaacauaucuaauua auacuccaCUACUauuaaacau uuuaaaau AUG cugauuuaucuuuuu		Server unavailable	
<i>mraY</i> mut4	auaaaaaaauugaaccaauuauu uagacgcuaauuuuAGUGAGa uuaaaaaaaaaacauaucuaaua uaauacuccaCUACUauuaaac auuuuaaaau AUG cugauuuaucuuuuu		Server unavailable	
<i>pdpA</i> WT	aguuauguucuaauuaaguagac aaugauagcaguaaaaagau			
<i>pdpA</i> mut1	aguuauguucuaauuaaguaCU caaugauUgcaguaaaaagau			


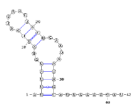

5' UTR	Sequence	MXFold2	Ufold	ViennaRNA
<i>pdpA</i> mut2	aguuauguAGuaauuaaguaCU caaugauAgcaguaaaagau			

Figure S4. Comparison of secondary structure prediction software.

Predicted structures of wild-type or modified *mraY* and *pdpA* 5' UTRs from three secondary structure prediction programs: MxFold2 (Sato et al. 2021), Ufold (Fu et al. 2022), and ViennaRNA (Lorenz et al. 2011).

CHAPTER 4

CONCLUSIONS AND OPEN QUESTIONS

BACKGROUND SUMMARY

Francisella tularensis is an intracellular human pathogen that can cause the fatal disease tularemia. Regulation of gene expression is critical to this bacteria's ability to survive in diverse environments and infect hosts. However, our understanding of gene regulation in this organism is limited (reviewed in Dai et al., 2011 & Spidlova et al., 2020). An area of gene regulation that had been unexplored in *F. tularensis* is the possibility of ribosome heterogeneity that leads to altered ribosome activity, or “specialized ribosomes,” contributing to regulation of translation.

The model that ribosomes may have specialized functions has been explored in eukaryotes and some species of bacteria. Ribosomes are commonly heterogeneous with respect to ribosomal RNA content, ribosomal protein content, and post-transcriptional and post-translational modifications. The functional consequences of this heterogeneity on translation and gene expression remains incompletely understood (Genuth & Barna, 2018; Xue & Barna, 2012; Sauert et al., 2015).

Previous research suggested that the small ribosomal protein bS21 serves a regulatory role in bacterial translation. In the most direct example, in *Flavobacterium johnsoniae* bS21 sequesters the anti-Shine-Dalgarno (ASD) of the 16S rRNA. When ribosomes lack bS21, the ASD is available to bind with

transcripts containing strong Shine-Dalgarno sequences, including the transcript encoding bS21 (Jha et al., 2020; McNutt et al., 2023). Loss of bS21 also leads to specific phenotypes in other organisms (Metselaar et al., 2015; Basco et al., 2019; Blake & O'Neill, 2013; Friedman et al., 2006; Takada et al., 2014). Together, this literature suggests that bS21 may be involved in gene regulation in diverse species of bacteria.

This led us to hypothesize that the incorporation of one of the three homologs of bS21 into ribosomes in *F. tularensis* may influence translation initiation and regulate gene expression. Specifically, we proposed a model in which a particular bS21 homolog directly or indirectly leads to preferential translation initiation of a subset of transcripts, leading to changes in protein abundance. To assess this, we asked how loss of one bS21 homolog, bS21-2, impacts the transcriptome and/or proteome of *F. tularensis* cells, whether known virulence genes are impacted, and how this affected intramacrophage replication. Once we had found bS21-2 affects genes at the protein level, we then focused in on the mechanism behind these impacts, looking at what component of bS21-2-responsive 5' UTRs are critical for efficient protein production. This research is significant not only in that it may help improve our understanding of pathogenicity in *F. tularensis*, but also it may reveal a conserved pathway of bS21-driven translation regulation in diverse bacteria.

CHAPTER 2 SUMMARY

Our initial research into bS21 in *F. tularensis* revealed that this organism, despite its small genome, encodes three distinct copies of bS21: bS21-1,

bS21-2, and bS21-3. This led us to hypothesize that ribosomes may create a source of ribosome heterogeneity. Through mass spectrometry, we found that wild-type ribosomes contain more than one bS21 homolog. Using ectopically expressed bS21 homologs, we confirmed that each bS21 homolog could be incorporated into ribosomes. Specifically, our sucrose sedimentation profiles combined with immunoblot analyses identified that each bS21 homolog can be found in 30S, 70S, and polysome particles. This demonstrated that *F. tularensis* wild-type ribosomes can be heterogeneous with respect to bS21 content, and all three bS21 homologs can associate with ribosomes throughout translation.

We subsequently looked at the genome-wide impacts on the transcriptome and proteome when bS21 homologs were lost. While deletion of bS21-1 and bS21-3 had no significant impact on protein abundance, cells lacking bS21-2 had significant changes in 165 proteins that were not explained by changes in transcript abundance. These data support the hypothesis that bS21-2 may impact expression of some genes at the level of translation.

Amongst the genes that were governed by bS21-2 at the level of translation were genes encoding the type VI secretion system (T6SS) in *F. tularensis*, known as FPI genes. The T6SS proteins were less abundant in cells lacking bS21-2, as confirmed by immunoblot analysis, and there was no significant difference in transcript abundance of the FPI genes, as detected by qPCR of purified RNA. Ectopic expression of bS21-2 and bS21-3 restored T6SS protein abundance, but expression of bS21-1 did not. This indicates that more than one bS21 homolog impacts translation of T6SS proteins. Finally,

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intramacrophage replication assays revealed that bS21-2 is important for virulence. Loss of bS21-2 led to an intramacrophage growth defect that could be restored by complementation with bS21-2, but not with expression of bS21-1 or bS21-3.

Altogether, the research described in Chapter 2 showed us that bS21-2 modulates expression of many genes at the protein level, including key virulence genes encoding the T6SS, and promotes intramacrophage replication. These data support our model that bS21-2 specifically impacts expression of some genes, either directly or indirectly, during translation initiation. Combined with other recent findings of bS21 impacting translation of subsets of mRNA in different bacterial species, our work supports a new model of bS21-driven gene regulation at the level of translation. Further research into this field may reveal that other types of heterogeneous ribosomes can impact different stages of translation to rapidly alter bacteria's proteome. However, the mechanism by which bS21-2 impacts some genes in *F. tularensis* remained an open question.

CHAPTER 3 SUMMARY

In the next chapter of my research, we investigated the mechanism that leads to altered protein abundance for bS21-2-responsive genes. We validated that there is an increase in abundance RNA-binding protein Hfq in cells lacking bS21-2. Together with the fact that Hfq is known to impact FPI gene expression, this raised the possibility that impacts of bS21-2 on the FPI could be due to Hfq. If so, would expect that Hfq acts as a negative regulator of all FPI genes during protein synthesis. While we validated that Hfq negatively regulates the FPI, we

found that this was only true of a subset of genes, and that it does so by regulating transcript abundance, not protein synthesis. These data indicate that Hfq and bS21-2 ~~both~~ impact expression of genes encoded by the FPI, via distinct mechanisms.

The position of bS21 in *E. coli* ribosomes, close to the mRNA exit channel, led us to hypothesize that bS21-2 may interact with the 5' UTR of some transcripts. In at least five bS21-2-responsive genes identified in the proteomics screen in Chapter 2, the 5' UTR was sufficient to cause positive impacts by bS21-2. Our next goal was to identify the aspect of the bS21-2-responsive 5' UTRs that drives the altered protein production, by testing multiple elements of leader sequences: ~~the~~ Shine-Dalgarno, ~~sequence~~ secondary structure, and enriched sequence motifs. While we did not find specific influence of secondary structure ~~or~~ ~~or~~ STREME-identified motifs on bS21-2-responsive translation, we did find that perfect SD sequences (5'-AGGAGG-3'), regardless of position, led to no difference in protein production between wild-type and bS21-2 mutants. We thereby concluded that ideal SD sequences masked the impacts of bS21-2 on protein production. Then, by making a series of truncations of the *mraY* 5' UTR, we identified a 6-nucleotide sequence, GACUCU, that was important for efficient translation by bS21-2.

Our research reveals a specific component of a bS21-2-responsive 5' UTR that is necessary for efficient translation in ribosomes with bS21-2. One other study in the literature that identifies specific changes in translation related to bS21 presence in *Flavobacterium johnsoniae* (McNutt et al., 2023). However,

in this species the mechanism of bS21-mediated gene regulation is dependent on characteristics of bS21 proteins unique to the Bacteroidia phylum (Jha et al., 2020), so unsurprisingly differs from the mechanism we are describing in *F. tularensis*. Our work is a stepping stone for the investigation of bS21-mediated translation in species with similar bS21 homologs and the finding that distinct r-protein homologs control gene expression may be more broadly applied to other r-proteins. Still, significant work is needed to determine whether the mechanism identified in *mraY* is applicable to other bS21-2-responsive 5' UTRs and to uncover alternate mechanisms that lead to changes in protein production from cells lacking bS21-2.

OPEN QUESTIONS

Open Question 1: Is the mechanism of the *mraY* 5' UTR conserved across all bS21-2-responsive 5' UTRs?

In Chapter 3, we identified the element of the *mraY* 5' UTR that leads to responsiveness to bS21-2: the short sequence of nucleotides, GACUCU. The analyses we have done indicate that this sequence, GACUCU, is necessary for efficient translation by bS21-2-containing ribosomes, but it does not indicate whether this sequence is sufficient to cause changes in translation. In the future, we will add the GACUCU sequence to the 5' UTR of a gene not responsive to bS21-2, choosing a 5' UTR that has a weak Shine-Dalgarno to allow bS21-2 to exert its effects. If addition of the GACUCU sequence allows the 5' UTR to respond to bS21-2, it would suggest this sequence is both necessary and sufficient to cause changes in translation efficiency based on bS21-2 presence.

GACUCU was not found in the predicted 5' UTR of any other bS21-2-responsive genes, suggesting this finding may be limited to the *mraY* 5' UTR. We do find marginal enrichment of a portion of this sequence, CUCU, in bS21-2-responsive 5' UTRs with weak SDs (31.1%, n=45) compared to genes negatively- or not-affected by bS21-2 (26.9%, n=67 combined). It may be that some of these bS21-2-responsive 5' UTRs are regulated in different ways, making it difficult to find a single sequence motif that is broadly applicable. Alternatively, this may be because our recent approach to identifying key elements of bS21-2-responsive 5' UTRs was limited by the poor annotation of transcription start sites in the *F. tularensis* genome. ^{For the} The majority of 5' UTRs that ^{we} we have analyzed in our motif analyses and reporter assays have arbitrarily chosen the 100 nts upstream of the start codon to represent the 5' UTR. Previously published transcription start site (TSS) mapping of 110 high-quality TSSs found that 19% were located more than 100 nucleotides upstream of the translation start site (Ramsey et al., 2015). Thus, ^{are} it is likely that, of our estimated 5' UTRs, ^{are} a significant portion is shorter than the native 5' UTRs. We plan to collaborate with other researchers to complete comprehensive TSS-mapping through specialized RNA-Seq. We hope that a larger number of TSSs will be identified and provide us with more accurate data about 5' UTR sequences.

With well-defined 5' UTRs across the genome, we hope to have more statistical power in our descriptive analyses of bS21-2-responsive 5' UTRs. Specifically, we can compare the 5' UTR length, GC content, and purine content of genes impacted by bS21-2 or not impacted, based on the proteomics screen

from Chapter 2. This may reveal trends that have so far been masked due to our inaccurate predictions. Additionally, while we did not find GACUCU in other bS21-2-impacted 5' UTRs, it is possible we could find enrichment of this sequence, or a portion of it, in full-length 5' UTRs once they are known. Otherwise, we can re-run the motif-finding analyses described in Chapter 3 with a more comprehensive list of known 5' UTRs to reveal new motifs that may be more broadly conserved among bS21-2-impacted 5' UTRs. Additionally, some of the 5' UTRs may be affected indirectly, so separating 5' UTRs directly affected from those indirectly affected would improve the analysis (see discussion below).

Open Question 2: What transcripts are directly regulated by bS21-2?

Though we have identified proteins across the genome that are impacted by loss of bS21-2 (Chapter 2, Figure 2), it is likely that only a portion of those genes are regulated by bS21-2 in a leader sequence-dependent manner. Abundance of some proteins may be influenced by downstream effects of bS21-2 loss (as discussed further below). It would be beneficial to identify those genes regulated in a leader sequence-dependent manner, as it would facilitate our understanding of which elements of a leader sequence lead to bS21-2 responsiveness. To identify directly-regulated genes, we could use ribosome profiling (also known as Ribo-Seq), a technique that assesses which mRNA molecules are actively translated by ribosomes at a given time (Ingolia et al., 2009). In brief, actively-translating ribosomes are isolated and incubated with RNases to degrade free mRNA molecules, so that only transcripts protected by

ribosomes are isolated and sequenced. By tagging bS21-2 and conducting immunoprecipitation in conjunction with ribosome profiling, we could isolate transcripts that are specifically bound by ribosomes containing bS21-2. The bS21-2-bound transcripts could be compared to total ribosome profiles, revealing which genes are preferentially translated by bS21-2-containing ribosomes. While this protocol is technically nontrivial, the data could provide clear evidence of direct regulation by bS21-2. Further, the technique may be used with the other two bS21 homologs to determine transcripts that are preferentially translated by bS21-1 or bS21-3.

Open Question 3: What other mechanisms contribute to changes in protein expression in cells lacking bS21-2?

Our investigation into the mechanism by which bS21-2 governs protein abundance focused on the 5' UTRs of bS21-2-responsive genes. Indeed, we found that the 5' UTRs of several genes were sufficient to cause changes in protein production (Chapter 3, Figure 1B). However, some genes, including FTL_0881 and FTL_0215, were found to be different at the protein level in the proteomics screen (Chapter 2, Figure 2; Supplemental Table 2), but their 5' UTRs were not responsive to bS21-2 in our reporter assays (Chapter 3, Supplemental Figure 2). One possible explanation is that their estimated 5' UTRs are inaccurate and missing a regulatory element. As mentioned, we plan to map transcription start sites across the genome to get more accurate predictions of 5' UTRs. It is possible that with correct FTL_0881 and FTL_0215

5' UTRs, we will see impacts from bS21-2 that are consistent with the proteomics screen.

Alternatively, the lack of response of some 5' UTRs to bS21-2 may suggest there are other regulatory mechanisms that impact expression of these genes. Specifically, bS21-2 may directly impact synthesis of proteins that influence the abundance of other proteins, leading to indirect effects. With respect to protein stability, we only assessed the half-life of PdpB, determining it was unaffected by loss of bS21-2 (Chapter 2, Figure S5). ~~Given that the 5'~~

~~UTR of *pdpB* is responsive to bS21-2, we interpret this to mean that the~~ expression of *pdpB* is governed by bS21-2 during translation initiation. Other proteins, like FTL_0881 and FTL_0215, may have altered abundance in bS21-2 mutant cells as the result of changes in the abundance of proteases or protein processing genes. Several proteases and peptidases were found to have altered abundance in our genome-wide analyses of cells lacking bS21-2 at either the transcript or protein level. These include pyrrolidone-carboxylate peptidase (FTL_0207), an uncharacterized peptidase (FTL_0008), peptidase M16 family protein (FTL_1482) and ATP-dependent proteases HslU (FTL_0964) all of which could impact protein stability and function. Further analyses of protein stability of more genes may reveal secondary impacts of loss of bS21-2. This could be achieved by comparing protein stability in the context of a protease knockout if the protease is more abundant in cells lacking bS21-2, or by ectopically expressing the protease if it is less abundant in cells lacking

Oops! You didn't test this UTR specifically, did you?

This suggests

bS21-2. If protein stability returns to wild-type levels, we would conclude that the protease is responsible for changes in protein abundance.

In addition to proteases, there may be other regulators governed by bS21-2 that lead to indirect effects. For instance, we have documented changes in abundance of the RNA chaperone Hfq in bS21-2 mutant cells. While our Hfq analyses focused on impacts on the FPI genes, there may be Hfq-mediated effects on other transcripts that impact translation initiation. A study in *Pseudomonas aureginosa* identified that Hfq functions co-transcriptionally in regulating some genes (Kambara et al., 2018). By performing a similar study in *F. tularensis* wild-type and the bS21-2 mutant cells, we could identify Hfq-mediated effects that are bS21-2-dependent.

Though our focus has been on proteins with decreased abundance, it is worth noting that loss of bS21-2 results in increased translation of some genes in a 5' UTR-dependent manner. For instance, protein production from mRNAs with the *tul4* 5' UTR is slightly but significantly higher in the bS21-2 mutant than in wild-type cells (Chapter 3, Figure 1B, 2B, 2C). We hypothesize that the loss of bS21-2-mediated preferential translation initiation for certain transcripts allows ribosomes to initiate on transcripts less favored by bS21-2-containing ribosomes more frequently. This shift would lead to an increase in protein synthesis of genes that are less preferred, or possibly effectively excluded, by bS21-2-containing ribosomes. Additionally, it is possible that in cells without bS21-2, ribosomes incorporate either bS21-1 or bS21-3 more frequently and these two bS21 homologs positively influence translation initiation for specific

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transcripts. Thus, we hypothesize that many of the proteins that are more abundant in bS21-2-mutant cells (top half of Chapter 2, Figure 2) may be indirectly impacted by bS21-2 due to this shifting balance of translation initiation. To address this hypothesis, we could utilize an *in vitro* assay (described below) where we can control the ratio of bS21-2-containing ribosomes, and detect if production of *tul4* is impacted as this ratio shifts.

Open Question 4: Does bS21-2 directly interact with bS21-2-responsive leader sequences?

We propose that bS21-2 is impacting translation initiation of specific genes through interaction, directly or indirectly, with the 5' UTR of these genes. To address the question of whether this interaction is direct, we could use a commercially-available *in vitro* protein synthesis system to assess whether purified ribosomes, outside of the context of the cell, are sufficient to cause changes in protein production. Using purified ribosomes either with or without bS21-2 and DNA encoding the bS21-2-responsive 5' UTRs under control of a T7 promoter, we can assess protein production of reporters. If a difference is detected in the protein production between ribosomes with bS21-2 and those without, it would suggest bS21-2 is sufficient to cause these changes. If no difference is detected, bS21-2 is likely functioning on translation initiation indirectly, raising the possibility that an intermediary protein interacts with the 5' UTRs of bS21-2-responsive genes to mediate initiation.

During my PhD work, I piloted use of this *in vitro* protein synthesis system in the lab, but was limited by the activity of ribosomes purified from *F. tularensis* and the sensitivity of the output. Additional work in the lab has already improved the sensitivity, by using luciferase as a reporter. To address ribosome activity, the ribosome concentration could be increased, the current purification protocol could be optimized, or other purification strategies could be used.

If the *in vitro* assay suggests bS21-2 is functioning indirectly, we could identify potential intermediary proteins using a co-immunoprecipitation strategy. Specifically, biotinylated mRNAs could be immunoprecipitated after crosslinking, and proteins co-purified could be identified via mass spectrometry. Proteins associated with bS21-2-responsive mRNAs, but not other mRNAs, would be candidate intermediary proteins that facilitate preferential translation in cells with bS21-2.

If the *in vitro* assay indicates that bS21-2 directly affects translation initiation for particular leader sequences, we could then ask if this is due to direct bS21-2-mRNA interactions. To assess the potential for bS21-2 to bind directly to mRNA, we could use an electrophoretic mobility shift assay (EMSA), which is based on the principle that RNA-protein complexes move more slowly during gel electrophoresis than free RNA. We could use purified bS21-2, bS21-2-containing ribosomes, and ribosomes without bS21-2 together with the bS21-2-responsive *mraY* mRNA to determine if bS21-2 alone or in the context of the ribosome can bind directly to the mRNA. If we find that bS21-2 does interact directly, we could then look to identify what residues of the mRNA are protected

by bS21-2 occupancy using RNA footprinting. Given the identification of GACUCU as critical for bS21-2-responsive translation in *mraY* (Chapter 3), we would hypothesize that bS21-2 may directly bind this 6-nt sequence of the mRNA.

Alternatively, if pure bS21-2 does not interact directly with the *mraY* mRNA but ribosomes containing bS21-2 do, it would suggest that bS21-2 impacts the structure of the ribosome in such a way that it allows interaction of the transcript with other ribosomal components (r-proteins or rRNA). Comprehensive structural studies of ribosomes with and without bS21-2, via cryoEM, could allow us to understand this dynamic.

If we find bS21-2 directly alters translation initiation on particular 5' UTRs, it would raise the possibility that the other *F. tularensis* bS21 homologs function similarly by preferentially initiating translation on ~~the same~~ ^{some} mRNAs. We report in Chapter 2 that bS21-3 (and to some extent bS21-1) may also impact production of the T6SS proteins. We could look to see if bS21-3 causes increased protein production from 5' UTRs encoding the T6SS by including bS21-3-containing ribosomes in the *in vitro* assay described above, and assessing complementation with bS21-1 and bS21-3 in the reporter assays from Chapter 3. If we find that production of GFP from the bS21-2-responsive 5' UTRs is not restored with increased amounts of bS21-1 and bS21-3, we can conclude that bS21-2 alone is sufficient to cause these effects. We have previously shown that these homologs function differently (Chapter 2), so we would expect that they are unlikely to affect all the same genes. We could

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identify specific genes impacted by bS21-1 and bS21-3 using Ribo-Seq, as described above.

Open Question 5: Does bS21-2-mediated translation modify transcript stability?

Why is this weird? → **in** cells without bS21-2 compared to wild-type cells, without significant changes in corresponding transcript abundance (Figure 2, yellow dots). However, there is a moderate shift in transcript abundance in many of these genes that did not reach our statistical significance cutoff (≥ 2 -fold change, adjusted $P < 0.05$). One explanation for this trend could be that occupancy by ribosomes protects mRNAs and increases transcript stability. On the other hand, transcripts with reduced translation are degraded more rapidly. In bacteria, translating or stalled ribosomes can protect mRNAs by masking cleavage sites, thereby improving stability of the transcript (Lopez et al., 1998; Bechhofer & Zen, 1989; Hui et al., 2014).

To explicitly test the impact of bS21-2-mediated translation on transcript stability and degradation, we could compare mRNA stability in cells with and without bS21-2. To do so, we must assess RNA abundance without novel production via transcription, which is accomplished by inhibiting RNA polymerase ~~via~~ **by** adding rifampicin to actively growing cultures and taking samples at several time points after treatment. Purified RNA from each time point can be analyzed by RNA-Seq or qPCR of specific target genes to determine rates of degradation. The half-lives of mRNAs in cells with and

without bS21-2 can be compared to determine if there is a correlation between protein abundance (as a proxy for translation) and transcript stability.

Open Question 6: How does Hfq control production of the T6SS?

While the RNA chaperone Hfq is known to impact expression of *F. tularensis* T6SS proteins, there are inconsistencies in the literature about which genes are impacted and if they are positively- or negatively-regulated. Our findings are consistent with previous research published by Meibom et al. (2009), that transcript abundance of the *pdpA* operon, but not the *iglA* operon, is negatively impacted by Hfq. We also found that at least one T6SS protein encoded on the *pdpA* operon is more abundant, suggesting that Hfq exerts its effects on the T6SS proteins by regulating transcript abundance rather than post-transcriptionally. These findings are in contrast to Lenco et al. (2014), which found all the proteins encoded on the *iglA* operon and one of the twelve encoded on the *pdpA* operon, are less abundant if Hfq is absent. A possible explanation for this discrepancy could be the use of different methodologies. We used immunoblotting of whole cell lysates, while Lenco et al. (2014) used two mass spectrometry-based approaches: iTRAQ analysis and LC-SRM. While there have been advances in the sensitivity of various mass spectrometry protocols in recent years, these analyses depend on the ability to detect fractionated peptides and often have limited sensitivity. Given that our results validate a previous study (Meibom et al., 2009) and the RNA and protein levels are concordant in our data, we have ~~faith~~ in the validity of our findings.

confidence

The mechanism by which Hfq impacts transcript abundance of the genes encoding the T6SS remains an open question. Hfq is well-documented to work in conjunction with small RNAs to impact translation initiation and RNA stability (e.g. Geissmann & Touati, 2004). If an sRNA is acting as a regulator of FPI genes, the sRNA has not yet been discovered; we could identify that sRNA using a strategy like RIL-seq (Melamed et al., 2018). Hfq may also recruit RNases to mRNA to promote degradation (Morita et al., 2005), a model which would be supported by our data. One way to identify RNases associated with Hfq would be through co-immunoprecipitation, either purifying Hfq and assessing if any RNases are co-purified, or purifying RNase E (a common interactor of Hfq) to detect if Hfq co-purifies. Co-immunoprecipitation of any RNase with Hfq would suggest coordinate function between the two proteins.

Open Question 7: Why is bS21-2 controlling virulence?

In Chapter 2, we concluded that bS21-2 is likely regulating genes important for virulence in addition to the T6SS, because ectopic expression of bS21-3 restores T6SS protein abundance but does not restore intramacrophage replication. To determine what these other virulence genes may be, we compared data from a study that used Tn-Seq to identify genes important for replication of *F. tularensis* in macrophage with our proteomics data from Chapter 2. This revealed seven genes that are less abundant at the protein level but not the transcript level when bS21-2 is absent *and* are important for virulence, excluding genes encoding the T6SS. While all seven should be

Tn-Seq
citation

investigated, two genes in particular stand out as likely candidates: FTL_1216 which may encode a YqgE/AlgH family protein that may function as a regulatory factor and *potG* which encodes a putrescine transport protein shown to act as a virulence factor in other species (Shi et al., 2019; Sturgill & Rather, 2004; Kurihara et al., 2013).

Candidates for what?
we know they are important for virulence

It is worth reflecting on why *F. tularensis* is using bS21-2 to control its virulence in this way. bS21 is one of the last proteins assembled into the ribosome and is easily exchanged in *E. coli* (Mizushima & Nomura, 1970). *F. tularensis* may be able to switch which bS21 homolog is in ribosomes to rapidly adapt their proteome based on changing conditions (i.e. when in a host vacuole). This strategy may be faster than impacting transcription. If virulence genes are always transcribed but poorly translated, they can be “turned on” by switching out bS21 homologs and improving translation initiation. *F. tularensis* has three bS21 homologs which may allow the bacteria to change the proteome with this mechanism during several life cycle changes, and may indeed be the reason why the three homologs evolved.

Open Question 8: How do changes to the 5' UTRs impact overall protein production?

Throughout our 5' UTR reporter analyses in Chapter 3, we focused our attention on the relative protein production in cells without bS21-2 compared to those with bS21-2. This allowed a clear comparison of translation from the same 5' UTR while changing only bS21-2 presence. However, there were significant

differences in overall protein production between 5' UTRs. Looking first at the wild-type 5' UTRs, the *tul4* 5' UTR fused to *gfp* produced 51-fold more fluorescence than the *mraY* 5' UTR fused to *gfp*, with all other UTRs somewhere between (Chapter 3, Figure 1B and Suppl. Fig. 2). While we considered presence of an unstructured 5' tail, nucleotide frequency, GC content, and codon rarity, the factor that clearly correlates to high protein production is presence of a strong SD. Indeed, the 5' UTRs with the lowest overall fluorescence all had SDs with less than 4 nt complementary to the aSD. Further, of all the mutations we made to the *mraY* and *pdpA* 5' UTRs, the most significant changes in overall protein production were modifications improving Shine-Dalgarno sequences, in an optimal position (-12) relative to the start codon (i.e. *moved_idealSD* was not highly translated despite perfect complementarity with the aSD; Chapter 3, Figure 2B).

Open Question 9: How does Shine-Dalgarno strength correlate with bS21 across species?

The Shine-Dalgarno is well-documented to play an important role in translation initiation in bacteria such as *E. coli* and *B. subtilis*, with better complementarity between the Shine-Dalgarno and anti-Shine-Dalgarno improving translation efficiency in these species (Vellanworth & Rabinowitz, 1992; Saito et al., 2020). However, there is great diversity of SD presence and strength both within and across species. In some species, as few as 11% of mRNAs have SD sequences, while in other species it can be as high as 90%

(Wen et al., 2020). In *F. tularensis* LVS, we reviewed upstream sequences of 240 genes and found that about 53% have SD sequences that match at least 4 nucleotides to the aSD sequence. Less than 1% have a perfect SD sequence (5'-AGGAGG-3'). Based on this analysis, *F. tularensis* has fewer SDs than the average of gamma proteobacteria (64%) but is considered to have moderate to high SD content compared to prokaryotes more broadly (Nakagawa et al., 2010).

mRNA that do not have canonical SD sequences may be translated less efficiently, but can utilize other portions of the leader sequence to facilitate translation initiation. Our data suggests that bS21 may play a role in translation initiation of mRNA with non-ideal SD sequences. In our review of the literature, there does not appear to be a clear trend between bS21 presence and low SD-content. For instance, *B. subtilis* encodes a bS21 homolog, but 78% of mRNAs have a Shine-Dalgarno sequence (Nakagawa et al., 2010). That said, any correlation between SD content and bS21 may be obscured because of additional components of the leader sequence and interacting proteins that impact translation initiation in other species (Saito et al., 2020). For instance, bS1 plays a key role in translation initiation without SD-binding and leaderless mRNA can be translated by 70S ribosomes (Kolb et al., 1977; Leiva & Katz, 2022). Nonetheless, our research suggests that bS21-moderated translation initiation may be an adaptive pathway for species containing significant numbers of mRNAs with poor SD sequences, a problem that is faced by a wide diversity of bacteria.

Saito only
looks at
E. coli!

significant advances?

Through the data shown in this dissertation, we have made ~~big strides~~ in understanding that bS21 homologs provides a source of ribosome heterogeneity in the human pathogen *Francisella tularensis* and impact protein production. Yet, there are many aspects of bS21 regulation, generally and specifically, that remain to be understood. These contributions provide a springboard for future research on ribosome heterogeneity with regards to bS21.

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