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MrvR, a Group B *Streptococcus* Transcription Factor that Controls Multiple Virulence Traits

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Abstract

Streptococcus agalactiae (group B *Streptococcus*; GBS) remains a dominant cause of serious neonatal infections. One aspect of GBS that renders it particularly virulent during the perinatal period is its ability to invade the chorioamniotic membranes and persist in amniotic fluid, which is nutritionally deplete and rich in fetal immunologic factors such as antimicrobial peptides. We used next-generation sequencing of transposon-genome junctions (Tn-seq) to identify five GBS genes that promote survival in the presence of human amniotic fluid. We confirmed our Tn-seq findings using a novel CRISPR inhibition (CRISPRi) gene expression knockdown system. This analysis showed that one gene, which encodes a GntR-class transcription factor that we named MrvR, conferred a significant fitness benefit to GBS in amniotic fluid. We generated an isogenic targeted knockout of the *mrvR* gene, which we found to have a growth defect in amniotic fluid relative to the wild type parent strain. In addition to growing poorly in amniotic fluid, the knockout also showed a significant biofilm defect *in vitro*. Subsequent *in vivo* studies showed that, while the knockout was able to cause persistent murine vaginal colonization, pregnant mice colonized with the knockout strain did not develop preterm labor despite consistent GBS invasion of the uterus and the fetoplacental units. In contrast, pregnant mice colonized with wild type GBS consistently deliver prematurely. Similarly, in a sepsis model in which 87% of mice infected with wild type GBS died within three days, none of the mice infected with the knockout strain died. In order to better understand the mechanism by which this newly identified transcription factor controls GBS virulence, we performed electrophoresis mobility

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shift assays with recombinant MrvR and whole-genome transcriptomic analysis on the knockout and wild type strains. We show that MrvR binds to its own promoter region, suggesting likely self-regulation. RNA-seq revealed that the transcription factor affects expression of a wide range of genes across the GBS chromosome. Nucleotide biosynthesis and salvage pathways were highly represented among the set of differentially expressed genes, suggesting a linkage between purine or pyrimidine availability and activity of MrvR in multiple GBS virulence traits.

Introduction

Streptococcus agalactiae (group B *Streptococcus*; GBS) is a cause of chorioamnionitis, stillbirth, and neonatal infections including bacteremia, pneumonia, and meningitis (1–10). GBS is a common commensal of the intestinal and reproductive tracts in healthy adults, among whom invasive disease is rare (11, 12). In the pregnant or neonatal host, however, GBS can be highly invasive, breaching anatomic and immunologic barriers with potentially severe consequences (13, 14).

GBS is known to express a number of virulence factors such as adhesins (15–17), IgA binding proteins (18–20), and the cytotoxic ornithine-rhamnopolyene β-hemolysin/cytolysin (13, 21–30). Many of these are regulated by transcription factors, some of which have been studied and described in detail (31–40), yet many of the predicted transcription factors encoded by GBS remain minimally characterized.

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We have previously described development of a GBS saturated transposon mutant library and its use in Tn-seq experiments to identify essential and conditionally essential genes (41, 42). In this study, we performed Tn-seq on GBS grown in human amniotic fluid in order to identify bacterial genes that promote survival in the nutrient-poor, unhospitable growth conditions of the amniotic sac.

Among the candidate genes was a transcription factor with domain features marking it as a member of the GntR protein superfamily. We named this GntR-class transcription factor MrvR (multiple regulator of virulence). Here we describe the role of MrvR in several GBS virulence-related phenotypes, including survival in human amniotic fluid, *in vitro* biofilm formation, and invasive bacteremia and preterm labor in murine models. We also use transcriptomic data and electrophoresis mobility shift assay results to demonstrate autoregulation of MrvR expression and its significant role in modifying expression of genes integral to nucleotide metabolism.

Results

Five GBS genes are conditionally essential for GBS survival in human amniotic fluid

Using a previously described transposon mutant library in an A909 (serotype Ia) background (41), we performed Tn-seq after growth challenge in eight human amniotic fluid samples from amniocentesis (two to three technical replicates in three separate biological samples). Prior to

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use for Tn-seq, the amniotic fluid was filter sterilized to remove any contaminating microorganisms and host cells that may have been present. The same mutant library was grown in rich media as an input control.

We used ESSENTIALS, a publicly available Tn-seq bioinformatics package, to analyze sequencing data from the Tn-seq experiment. This analysis revealed five candidate conditionally essential genes (**Figure 1 and Table 1**).

One of the candidate genes, SAK_RS10120, which we termed *mrvR*, had conserved functional domains suggesting its membership in the GntR superfamily of transcriptional regulators. The other candidate genes encoded an expected DeoR family transcriptional regulator (SAK_RS09545), a predicted membrane-spanning protein of unknown function (SAK_RS05160), an ABC-class transporter (SAK_RS09890), and one protein (SAK_RS02930) with a single domain of unknown function whose cellular localization and role are also unknown.

CRISPRi knockdown and targeted knockout competition assays validate Tn-seq findings

To further validate the five candidate genes conditionally essential for GBS survival in amniotic fluid, we developed a CRISPRi gene expression knockdown system, which uses natively expressed, catalytically inactive Cas9 (dCas9) encoded on the GBS chromosome along with a single guide RNA (sgRNA) expression plasmid to generate efficient and flexible gene expression inhibition in GBS. We competed knockdowns of the five candidate conditionally essential genes

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against a sham targeting control dCas9 strain in human amniotic fluid and assayed survival using quantitative PCR analysis of knockdown and control strain persistence.

Development of a GBS CRISPRi system was aided by the fact that the GBS *cas9* gene shows high sequence similarity to the canonical *cas9* endonuclease first described in *Streptococcus pyogenes* (43–46) (**Supplemental Figure 1**). This homology allowed us to predict the two missense mutations that would establish a catalytically inactive isoform in GBS: D10A and H840A. The high level of homology between *S. pyogenes* Cas9 and the GBS homolog also suggested that the protospacer adjacent motif (PAM) necessary for Cas9 genomic target recognition likely followed the same NGG pattern as in *S. pyogenes*. We used a previously described sucrose-counterselectable mutagenesis plasmid, pMBsacB, to generate point mutations within the coding sequence of the *cas9* gene in GBS strain CNCTC 10/84 (serotype V) (47), which is the strain with which our animal models of vaginal colonization and ascending chorioamnionitis have been optimized.

We developed a sgRNA expression shuttle plasmid, p3015b, into which we cloned 20-bp protospacers against two genomic targets for each of the five candidate genes. We used the Broad Institute's Genetic Perturbation Platform sgRNA design tool (https://portals.broadinstitute.org/gpp/public/analysis-tools/sgrna-design) to select optimized protospacers, then cloned synthetic oligonucleotide DNA into p3015b (48, 49). After confirming successful protospacer cloning, the targeting plasmids were purified and transformed into competent 10/84 modified to express dCas9.

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To establish proof-of-concept for this approach we knocked down the first open reading frame (*cylX*) in the *cyl* operon that encodes genes responsible for synthesis of the pigmented cytotoxin β-hemolysin/cytolysin (50). p3015b encoding anti-*cylX* sgRNA could not be transformed into wild type GBS, presumably because Cas9 targeting to the chromosome resulted in lethal double-stranded DNA cleavage. The dCas9 strain, however, had high transformation efficiency and generated non-pigmented, non-hemolytic knockdowns when transformed with plasmid expressing anti-*cylX* sgRNA (**Figure 2A**).

Next, we created plasmids targeting two different sites in each of the five candidate amniotic fluid conditionally essential genes **(Figure 2B**) and transformed dCas9-expressing 10/84. As in previously described CRISPRi systems, we found optimal performance when the sgRNA targeting sequence matched sites within the open reading frame but on the non-template strand (51).

The resulting knockdown strains, plus a control dCas9 strain transformed with p3015b bearing a sham protospacer, were used to inoculate amniotic fluid and control broth. Plasmid DNA was purified at 24 hours of outgrowth. We used protospacer-specific quantitative PCR primers to characterize persistent GBS as targeting or non-targeting control. **Figure 2C** shows the results of these competition assays and demonstrates an expected competition defect in amniotic fluid for the five candidate knockdown strains.

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As with CRISPRi knockdown systems in other organisms, the extent of the knockdown effect varied depending on the exact sequence targeted within the gene. In general, targets closer to the start codon showed more significant effects, which is consistent with other studies (51).

A targeted knockout of mrvR shows a growth defect in human amniotic fluid

MrvR showed a consistent CRISPRi knockdown pattern, where both targeting protospacers generated a pronounced fitness defect in amniotic fluid. We selected this gene for further study based on these results and the hypothesis that this transcription factor may bridge microenvironmental changes associated with exposure to amniotic fluid and gene expression responses that promote amniotic fluid survival and possibly other GBS virulence traits.

Using pMBsacB, we generated an isogenic knockout of W903_RS09645, the *mrvR* ortholog in 10/84. We also complemented the gene deletion by cloning the full coding sequence of W903_RS09645 and its upstream promoter sequence into the shuttle vector pBSU101 (replacing the green fluorescent protein and *cfb* promoter sequence originally cloned into pBSU101) (52) and transforming the knockout with this plasmid.

We tested the knockout and complemented strains for survival defects in human amniotic fluid and in broth. **Figure 2D** shows growth curves of the wild type and knockout strains in tryptic soy broth, indicating that growth kinetics between the two strains in rich media are identical. **Figure 2E** shows results of competition assays in which amniotic fluid and broth were inoculated with a

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mixture of wild type 10/84 and the knockout strain or its complement. After 24 hours of outgrowth, these mixtures were plated for CFU enumeration on selective and nonselective media, permitting determination of the relative survival of the strains in competition.

We observed that in broth the knockout strain had a mild growth defect relative to wild type, but that the defect was more severe in amniotic fluid, and that both defects could be complemented through expression of the full-length *mrvR* gene.

MrvR controls GBS biofilm formation

We observed phenotypic differences in growth of the *mrvR* knockout as compared to wild type 10/84. In liquid media, the mutant seemed to aggregate in clumps with less coating of the outgrowth vessel. We suspected that the knockout was biofilm deficient, which we confirmed using a biofilm assay. The biofilm index is the ratio of crystal-violet stained biofilm (following overnight growth in a multi-well plate) divided by the planktonic-phase optical density from the same sample. **Figure 2F** confirms that the knockout mutant is biofilm deficient compared to wild type 10/84, and that the biofilm phenotype is restored in the complemented strain.

MrvR activity does not affect vaginal colonization

To test whether *mrvR* is necessary for persistent vaginal colonization, we colonized healthy adult female mice with knockout GBS or wild type control and performed serial surveillance

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swabs using an established protocol (13). We did not include the complemented knockout in this experiment because of past observations that, without ongoing *in vivo* antibiotic selection, plasmid DNA is rapidly cured by colonizing GBS.

While there was a trend toward earlier clearance among the mice colonized with the mutant strain, neither initial colonization density nor eventual clearance among the two groups differed significantly (**Figure 3**).

The MrvR knockout causes chorioamnionitis without preterm delivery in a mouse model

To test the effect of *mrvR* in ascending chorioamnionitis, we used an established mouse model, vaginally colonizing pregnant female mice on pregnancy day 13 with either wild type 10/84 or the *mrvR* knockout.

Colonized pregnant mice were monitored through pregnancy day 17. Preterm delivery between day 13 and day 17 by a colonized mouse was one experimental endpoint, while animals that remained pregnant on day 17 were sacrificed and assessed for persistent vaginal colonization and ascending chorioamnionitis. Chorioamnionitis was established based on any of the following: GBS present in placental homogenates, GBS present in fetal homogenates, or GBS present in amniotic fluid. Data from mice that were no longer vaginally colonized on day 17 were not included in the analysis; none of the mice who cleared their vaginal colonization had chorioamnionitis.

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There was a significant difference between pregnancy outcomes for mice colonized with wild type GBS and those colonized with the knockout. Whereas eight of eleven mice colonized with wild type GBS delivered preterm, none of the eleven mice colonized with the knockout strain did. However, all of the knockout colonized mice had chorioamnionitis with widespread GBS dissemination throughout the placentas, fetuses, and amniotic fluid. Of the mice colonized with wild type GBS, two of the three that carried their pregnancies through day 17 had chorioamnionitis (**Figure 4A-4B**).

Colony counts from tissue and amniotic fluid samples collected at laparotomy showed a significant difference between wild type and knockout GBS density in amniotic fluid but not placental or fetal tissue. Bacterial density was higher in placental homogenates than in fetal tissue homogenates and amniotic fluid for both GBS strains, suggesting the placenta as the portal of infection (**Figure 4C**).

MrvR is necessary for lethal invasive bacteremia in a murine sepsis model

To assess the role of the transcription factor in bloodstream invasion and systemic infection, we performed intraperitoneal injections of knockout and wild type GBS in healthy adult BALB-c mice. Both bacterial strains were transformed with a toxin-antitoxin stabilized plasmid expression system that generates constitutive luciferase, permitting *in vivo* monitoring of bacterial spread upon bacterial exposure to luciferin cofactor.

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The infected mice were photographed using an IVIS *in vivo* imaging system at the time of initial intraperitoneal infection, then daily afterward until either death or complete clearance of the luciferase signal. Surviving mice that had cleared their infection based on imaging were subsequently observed for the following five days, and all remained well-appearing with normal behavior, eating, and stable weights throughout this post-imaging observation period.

This experiment revealed a significant difference in the ability of infected mice to clear mutant and wild type GBS. Whereas 87% of mice infected with wild type GBS died of the infection within three days, none of the mice infected with the knockout strain died. *In vivo* imaging showed that the mice were able to contain and clear the knockout strain, while the wild type strain tended to invade beyond the peritoneum such as into the thorax, a finding that was invariably followed by death (**Figure 5**).

Whole-genome transcriptomics shows that MrvR affects a widespread genetic network including multiple operons involved in nucleotide metabolism

We performed whole-genome RNA-seq on wild type GBS and the *mrvR* knockout in order to gain a preliminary understanding of the transcription factor's regulon. We purified RNA from liquid cultures of the two strains at three growth time points: early log phase, late log phase, and stationary phase.

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Comparing gene expression between the knockout and wild type GBS demonstrated that a substantial fraction of GBS transcription is controlled directly or indirectly by MrvR (**Figure 5A**). 16.8 percent of genes showed at least a 2-fold change in expression in the knockout relative to wild type during early logarithmic growth. This total increased to 35.7 percent in late logarithmic phase before dropping to 19.9 percent in stationary phase. Notably, a prophage island from W903_RS03075 through W903_RS03520 showed significant downregulation in the knockout at all three phases of growth. In order to confirm that this prophage DNA remained present in the knockout and had not undergone lysogeny, we performed PCR amplification of three prophage regions using genomic DNA template from the wild type and mutant GBS strains (**Supplemental Figure 2**).

We used a publicly available gene set enrichment search tool (53) to assess the differential gene expression data for functional patterns. This analysis revealed that genes involved in purine and pyrimidine metabolism were significantly enriched among the set of differentially expressed genes and that these nucleotide metabolism genes showed differential expression across all three growth phases. Other functional categories that showed significant differential expression tended to only be affected in one or, at most, two phases of growth (**Figure 5B-F**).

The *mrvR* gene is located next to a uridine phosphorylase gene (W903_RS09640), which encodes the Udp enzyme that converts uridine to uracil. The *udp* gene appears coregulated by MrvR, based on RNA-seq data. Intriguingly, the arrangement of MrvR adjacent to nucleotide

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metabolic genes— particularly uridine phosphorylase genes—is highly conserved across Gram-positive bacteria (**Supplemental Figure 3**).

An electrophoresis mobility shift assay shows that the GntR transcription factor binds the intergenic region between its own coding sequence and the udp gene

Based on our transcriptomics data, we suspected that the transcription factor auto-regulates its own expression. To test this hypothesis, we used a *Brevibacillus*-based expression system to purify recombinant MrvR. We then used this recombinant sample to test DNA binding to the common promoter region between the coding region for MrvR and the adjacent *udp* gene using electrophoresis mobility shift assays. This experiment demonstrated a greater shift when the recombinant transcription factor was combined with the target DNA sequence as compared to a scrambled control DNA sequence with identical nucleotide ratios (**Figure 5G**), indicating autoregulation through binding of MrvR to its own promoter, which also coregulates *udp* expression.

Discussion

GBS can survive and grow in diverse environments within the human host. It can persist in the intestine, in the male and female reproductive tracts, within the placenta, the amniotic fluid, human blood, joint spaces, the neonatal lung, and the central nervous system (1, 9, 12, 33, 54–

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58). This environmental tolerance contributes to GBS virulence, allowing it to invade and grow within compartments that are prohibitive to other bacteria.

This study began with a Tn-seq examination of genes that promote GBS fitness in amniotic fluid. GBS survival within human amniotic fluid contributes to its ability to cause ascending chorioamnionitis, which can lead to preterm labor and early-onset sepsis, sometimes in combination—a circumstance that can result in delivery of a severely infected preterm newborn with multi-organ system dysfunction (14, 59–62). Intraamniotic infection can also result in stillbirth (10). Amniotic fluid has chemical and immunological characteristics that are antimicrobial. The fetus and membranes produce antimicrobial peptides that inhibit bacterial survival, and amniotic fluid is intrinsically poor in nutrients required for bacterial proliferation (63–71).

We identified five GBS genes required for survival in human amniotic fluid. Two of these were predicted to encode transcriptional regulators, two encode surface-associated proteins, and one remains uncharacterized. A previous study that used a proteomic approach to evaluate differential gene expression in GBS strain A909 (the same background used for our Tn-seq library) during conditions associated with colonization and fetal invasion did not identify any of the same genes (72). Intriguingly, however, that investigation found two differentially expressed proteins (encoded by SAK_RS10135 and SAK_RS09535) whose genes are both two loci away from members of our set.

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This study introduces a novel CRISPRi gene expression knockdown system, which we paired with qPCR to further interrogate the candidates suggested by our Tn-seq screen. Our approach builds on prior knockdown systems in other microorganisms and demonstrates some of the same findings, including the requirement that the DNA sequence targeted by the dCas9 enzyme must be on the antisense strand of the coding region and decreasing knockdown potency as the target region gets further from the start codon (51, 73, 74).

Our GBS CRISPRi system—which permits flexible and rapid phenotypic discovery without the challenge associated with generating gene deletions on the chromosome—could be used for diverse experimental purposes. In this case, it allowed us to validate Tn-seq results and to decide which candidate gene to further study. We envision additional uses, however, including rapid generation of knockdown libraries for multiplex testing of gene contributions to fitness in GBS and exploration of the roles of essential genes whose expression cannot be eliminated entirely.

In this study, the CRISPRi screen pointed our attention to a GntR-class transcription factor that seemed to play an important role in bacterial fitness in amniotic fluid. While GntR transcription factors are widely distributed throughout the bacterial kingdom, and some have been shown to play a role in virulence (75–83), this gene's role in GBS host-pathogen interactions has not been explored. Interestingly, an orthologous gene was previously shown to influence group A *Streptococcus* susceptibility to the mouse cathelicidin CRAMP during murine skin infection (84). We investigated whether our knockout GBS had altered CRAMP sensitivity, but did not observe

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an effect. Instead we focused on various GBS phenotypic features that are regulated by this transcription factor.

We confirmed our CRISPRi knockdown findings with survival assays in broth and human amniotic fluid, using an in-frame deletion of the transcription factor, which we competed against the wild type parent strain. Unexpectedly, the MrvR knockout was visibly deficient at forming biofilms, which we subsequently confirmed with formal biofilm assays. GBS biofilms have been posited to influence colonization and host immune evasion in GBS and other bacteria (16, 85–87).

In a murine model of chorioamnionitis, absence of MrvR had a major impact on the ability of GBS to trigger preterm birth, with mice colonized on pregnancy day 13 showing consistent carriage of their pregnancies through day 17, despite extensive uterine invasion of the knockout strain. This is in contrast to the high rates of preterm delivery seen when pregnant mice are vaginally colonized with wild type GBS, which was observed in this study and in prior work (13) and has been documented in other animal models and clinical practice (14, 29).

This finding adds to accumulating evidence that GBS invasion of the fetoplacental unit is not, in itself, sufficient to trigger preterm delivery. A previous study demonstrated similar findings in an examination of the role of β-hemolysin/cytolysin in chorioamnionitis and preterm birth (13). Several others have shown that consequential inflammatory cascades are triggered in the choriodecidua following GBS invasion (14, 24, 30, 88). We hypothesize that these inflammatory

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cascades are enhanced by expression of virulence factors regulated by MrvR, such that its absence ameliorates the inflammation that leads to preterm birth without preventing tissue invasion; this hypothesis will be the focus of additional future work.

Our work also shows that pathways regulated by MrvR are critical for bloodstream invasion and host immune evasion. In an adult mouse model of sepsis, dramatic differences were seen between wild type and knockout GBS in terms of systemic spread and eventual mortality.

Our transcriptomic analysis of the *mrvR* knockout suggests that this transcription factor is involved in mediating nucleotide metabolism. Purine and pyrimidine sensing, biosynthesis, and salvage all play key roles in modulation of virulence traits in other bacterial pathogens (89–91). Furthermore, intracellular nucleotide homeostasis is highly regulated through diverse signaling pathways (89, 92, 93), lending plausibility to the prospect that the transcription factor under study here also participates in maintaining nucleotide concentrations. Our electrophoresis mobility shift assay results suggest that the transcription factor binds its own promoter region, which is also adjacent to the *udp* gene involved in purine metabolism—further suggesting a link between this signaling molecule and nucleotide availability. Future work will also focus on deeper characterization of the exact binding sites of this transcription factor across the GBS genome.

In conclusion, this study applied genome-wide screens, novel and established molecular techniques, and multiple murine models of GBS colonization and invasive disease to identify

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and characterize a GntR-class transcription factor, MrvR, with key roles in multiple virulence-related phenotypes. This newly described transcription factor presents an appealing subject for further mechanistic study and may be a target for novel pharmaceutical approaches to limit GBS virulence through modulation of this molecule's activities.

Methods

Ethics statement

Animal experiments were performed under approved IACUC protocols at NYU and University of Pittsburgh. Adult phlebotomy for hemolysis assays was conducted under a University of Pittsburgh approved IRB protocol. Collection of anonymous, discarded amniotic fluid was conducted under an approved exemption from the NYU IRB.

Statistical analyses

Statistics for Tn-seq were determined with ESSENTIALS software (94) and RNA-seq statistical tests were performed with DESeq (95). Remaining statistics for figures were calculated using Prism for macOS v. 8.4.3 (Graphpad Software, San Diego, CA).

Bacterial strains and growth conditions

GBS strains A909 (serotype Ia, sequence type 7) and CNCTC 10/84 (serotype V, sequence type 26) and their derivatives were grown at 37°C (or 28°C when the temperature-sensitive pMBsacB plasmid was present and extrachromosomal) under stationary conditions in tryptic soy (TS)

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428 medium (Fisher Scientific cat. # DF0370-17-3), supplemented with 5 µg/ml erythromycin, 150
429 µg/ml spectinomycin, or rifampin 10 µg/ml as needed for selection. *Escherichia coli* was grown
430 at 37°C (or 28°C with extrachromosomal pMBsacB present) with shaking in Luria-Bertani (LB)
431 medium (Fisher Scientific cat. # DF9446-07-5) supplemented with 300 µg/ml erythromycin and
432 150 µg/ml spectinomycin as needed for selection. *Brevibacillus choshinensis* for expression of
433 recombinant MrvR was grown at 28°C in TM or 2SY media supplemented with neomycin 50
434 µg/mL according to the recommendations of Takara Bio.
435
436 *Tn-seq on GBS grown in human amniotic fluid*
437 Discarded, anonymous amniotic fluid from amniocentesis was obtained from the NYU-Langone
438 Medical Center Department of Obstetrics and Gynecology. Samples were stored frozen at -
439 20°C, then thawed on ice. Before use in outgrowth experiments, the amniotic fluid was passed
440 through a 0.2 µm sterile filter.
441
442 A previously described saturated transposon mutant library in an A909 background (41) was
443 thawed from frozen stock. The library was washed twice in sterile PBS to remove glycerol
444 cryoprotectant, then resuspended in 3 mL PBS and seeded into 100 mL of TS broth with
445 erythromycin selection. After overnight outgrowth, 20 mL of the library was seeded into fresh
446 TS broth with erythromycin and allowed to grow to mid-log phase (OD_{600}=1). 120 mL of this
447 culture was then pelleted and washed twice with PBS, then resuspended in 1 mL of PBS.
448

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50 µL of this concentrated library was then used to seed either 5 mL of amniotic fluid pre-warmed to 37°C or control TS broth. The seeded amniotic fluid and TS was allowed to grow overnight. Unseeded control amniotic fluid samples were also incubated and plated the following morning to ensure that there was no contamination present.

After overnight outgrowth, the TS and amniotic fluid samples were transferred into 250 mL aliquots of TS. These were grown overnight, then genomic DNA was purified from 90 mL of each culture using the MoBio Powersoil DNA Extraction Kit (cat. # 128888) according to manufacturer instructions. Purified DNA was subsequently digested with MmeI and used for barcoded terminal adapter ligation, PCR, and sequencing on a 150-nt paired-end run of the Illumina (San Diego, CA, USA) HiSeq 4000 platform, with a target number of reads per library of 50 million and subsequent demultiplexing as previously described (41, 42).

We used ESSENTIALS, a publicly available Tn-seq analysis server, to analyze our data (94). ESSENTIALS generates a plot of genome-wide $\log_2$ fold-change values for actual-versus-expected transposon detection. Bimodality in this plot indicates separate gene populations—those with approximately the expected number of transposon insertions detected in the experimental condition, and those with fewer than expected detected insertions. The latter group represents the set of conditionally essential genes, and the local minimum between the two modal peaks can be used to generate a cutoff value between nonessential and conditionally essential genes. In the case of our amniotic fluid Tn-seq experiment, the local

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minimum was at a $\log_2$ fold-change value of -3.22. The five candidate genes evaluated had $\log_2$ fold-change values below this cutoff (**Supplemental Data 1**).

Development of a GBS CRISPRi system for gene expression knockdown

To generate GBS expressing dCas9, we used the mutagenesis plasmid pMBsacB in GBS strain 10/84 as previously described (47). Two separate synthetic, double-stranded DNA fragments, 800 to 1000 nt in length, were designed and ordered from Genscript (Piscataway, NJ, USA). The fragments matched the native 10/84 *cas9* coding sequence except for the two missense mutations, D10A and H840A, needed to render the enzyme catalytically inactive. These fragments were cloned into pMBsacB using Gibson assembly and used to transform chemically competent DH5α *E. coli* (New England Biolabs, Ipswich, MA, USA) according to manufacturer instructions. We confirmed proper cloning by Sanger sequencing of miniprepped plasmid DNA, which we then used to transform electrocompetent GBS as previously described (47, 96, 97). We performed the C-terminal (H840A) mutagenesis first, following the protocol we have described previously (47). Once this mutation was generated and confirmed by Sanger sequencing, we made those GBS competent and created the second mutation using identical techniques.

p3015b is a shuttle vector originally derived from pVPL3004 (98). We used PCR, synthetic DNA, and Gibson assembly approaches to make multiple changes to this plasmid for use in GBS. The kanamycin resistance cassette was changed to the erythromycin resistance gene; the *cas9* gene from *S. pyogenes* was removed; and the tracrRNA sequence downstream of the dual BsaI

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restriction sites used for protospacer introduction was replaced with a new sequence that conforms to the predicted folding structure of the native GBS tracrRNA sequence (**Supplemental Figure 1**). We also sought to introduce anhydrotetracycline inducibility of sgRNA expression by cloning a *tetR* coding sequence and a 2x tetO inducible promoter upstream of the sgRNA coding sequence. Despite extensive efforts, however, we could not suppress baseline sgRNA expression in GBS to the point that gene knockdown was inducible (data not shown), so the plasmid was used for constitutive sgRNA expression in GBS without anhydrotetracycline addition.

Targeting protospacers were designed using the Broad Institute's online sgRNA design tool (48, 49). Target sequences were selected based on their antisense orientation and, where possible, position in the first half of the coding sequence. Protospacer oligonucleotide sequences were ordered from Integrated DNA Technologies (Coralville, IA, USA) and cloned into BsaI-digested 3015b as originally described by Jiang et al. in their description of pCas9, from which pVPL3004 was developed (99).

CRISPRi multiplex competition assay

Cultures of 10/84 dCas9 transformed with p3015b plasmid bearing targeting protospacers against candidate conditionally essential genes were grown overnight in selective broth. A control strain with p3015b plasmid containing a sham protospacer with no matching sequence in the GBS chromosome was grown as a control. The 11 cultures were spun down and washed twice in PBS, then resuspended and normalized to an OD_{600} of 0.8. These suspensions were

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514 then plated as serial dilutions to confirm that the starting CFU concentrations were
515 approximately equal.
516
517 500 μL from each of the 11 normalized GBS suspensions were then combined to make a
518 starting mixed culture. A sample of this mixed culture was used for plasmid DNA purification
519 using the Thermo MagJET plasmid DNA Kit (cat. # K2791) according to manufacturer
520 instructions.
521
522 Amniotic fluid or TS broth containing erythromycin for continued plasmid selection was pre-
523 warmed to 37°C and seeded 1:50 with the mixed culture, then allowed to grow stationary
524 overnight. 24 hours after seeding, plasmid DNA was extracted from the amniotic fluid and TS
525 samples.
526
527 At both the starting and 24-hour timepoints, prior to purification, DNA from dead bacteria was
528 removed using ethidium monoazide using techniques described by Soejima et al. (100).
529 Ethidium monoazide—which binds to extracellular DNA or DNA within dead bacteria, but not to
530 DNA within live cells—was added to a final concentration of 10 μg/mL, after which the cultures
531 were allowed to incubate at 4°C for five minutes. They were then placed under a high intensity
532 white light source, which destroys DNA bound to ethidium monoazide. The treated samples
533 were then spun down, washed once in PBS, then used for plasmid purification.
534

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qPCR on purified plasmid samples from the initial and 24-hour timepoints was performed using Applied Biosystems Power SYBR Green Master Mix (Thermo cat. #4368577) on a BioRad (Hercules, CA, USA) CFX384 real-time PCR thermocycler. The different plasmids present were detected using a conserved reverse primer and a forward primer complementary to either one of the targeting protospacer sequences or the sham protospacer sequence. We also used a pair of normalization primers complementary to plasmid sequences distant from the protospacer cloning site. This strategy allowed determination of relative abundances of each of the targeting protospacers (and the sham control) relative to the total plasmid concentration in each sample.

Competition indices for each knockdown strain were calculated using the formula: $\ln((NE^{target}_{T24}/NE^{target}_{T0})/(NE^{sham}_{T24}/NE^{sham}_{T0}))$ where NE is normalized expression scaled to total plasmid quantity, target and sham reflect targeting and control plasmids, and T0 and T24 represent samples from the initial mixed culture or from the 24-hour timepoint, respectively. qPCR was performed twice, with two to three technical replicates per primer pair. Competition indices for the knockdown strains were normalized to survival for each strain in TS broth.

Generation of the mrvR knockout and its complemented control strain

A synthetic double-stranded DNA fragment was designed to contain the chloramphenicol acetyltransferase gene surrounded by 500-nt homology arms that match upstream and downstream sequences flanking the *mrvR* open reading frame in 10/84. This mutagenesis cassette was cloned into pMBsacB using Gibson assembly, then used to transform

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electrocompetent wild type 10/84. Temperature- and sucrose-based selection and counterselection were used to isolate single-cross and double-cross plasmid insertion and excision mutants, which were confirmed using targeted PCR and Sanger sequencing as previously described (47).

To complement the gene deletion, the wild type 10/84 *mrvR* gene and 75 nt of upstream promoter sequence were amplified using PCR and cloned into pBSU101 in place of the *cfb* promoter and green fluorescent protein gene present in the original plasmid (52). This plasmid was then used to transform the knockout strain, using spectinomycin for positive selection.

Amniotic fluid competition assays with CFU quantification

Amniotic fluid or TS broth was seeded with either a) a 10/84 strain with a defined mutation in the *rpoB* gene that confers rifampin resistance (101) and a spontaneous streptomycin-resistant knockout clone or b) the rifampin-resistant 10/84 strain transformed with empty pBSU101 (for spectinomycin resistance) and the complemented, streptomycin-resistant knockout strain. After 24 hours of outgrowth, these mixtures were plated for CFU enumeration on nonselective media, rifampin-containing media, and streptomycin-containing media. This permitted determination of total growth and allowed discrimination between the knockout and wild type strains.

Competition indices were calculated using colony forming unit (CFU) density per mL, where competition index=$\ln((CFU^{expt}_{T24}/CFU^{expt}_{T0})/(CFU^{WT}_{T24}/CFU^{WT}_{T0}))$; here, expt represents the

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experimental strain (either knockout or control) and WT is wild type 10/84. Assays were performed in triplicate and the experiment was repeated twice.

Hemolysis assays

Whole cell GBS was used in hemolysis assays on washed human erythrocytes as previously described (42).

Growth curve analysis

Wild type and *mrvR* knockout GBS were grown to late logarithmic phase in TS broth. The two cultures were then normalized to an OD_{600} of 1.0, then diluted 1:50 in broth. Triplicate samples were then instilled into a clear, flat-bottom 96-well plate, the lid of which had been treated with sterile defogging solution. OD_{600} absorbance readings were taken every 10 minutes, with a brief shaking step before each read, using a Molecular Devices (San Jose, CA, USA) SpectraMax M4 plate reader set to 37°C.

Biofilm assays

10 μL of stationary-phase GBS was used to seed 1 mL of fresh broth with appropriate antibiotic selection and 5% glucose supplementation in a 12-well, clear-bottom plate, which was then allowed to grow for 24 hours at 37°C. The plate was rocked gently on an orbital shaker for 1 minute to resuspend non-adherent bacteria, then the media was carefully removed and transferred to a fresh plate. OD_{600} absorbance readings of the planktonic phase bacteria were recorded.

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The plate that grew overnight was then used to stain the residual biofilms. 500 μL of 1% crystal violet was carefully added to each well, being cautious not to disturb the biofilm. After 10 minutes of gentle shaking at room temperature, the stain was removed and each well was washed three times in 1 mL of sterile PBS. After the final wash, the stained biofilm was allowed to dry, then solubilized with 1 mL of a 20% acetone/80% ethanol solution. Absorbance at 550 nm was measured. Biofilm indices were calculated as OD_{550}/OD_{600}. The experiment was performed three times with three technical replicates for each condition.

Murine vaginal colonization model

Vaginal colonization of nonpregnant C57BL/6J mice was performed as previously described by Randis et al. (13) with minor modifications.

6- to 8-week old mice were injected subcutaneously with 0.5 mg β-estradiol on two successive days to synchronize estrus. On the third day, stationary phase GBS was pelleted and resuspended in a 1:1 mixture of PBS and a sterile 10% gelatin solution to enhance viscosity. The mixtures were diluted and plated for CFU enumeration. Mice were vaginally colonized with 50 μL, corresponding to 10^7 CFU.

Following colonization, mice were single-housed. After 48 hours, an initial swab to detect colonization was performed. A sterile nasopharyngeal swab was moistened in 300 μL sterile PBS, then inserted into the murine vagina and rotated three times, after which it was replaced

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in the PBS and swirled to release adherent GBS. The PBS was diluted and plated for CFU enumeration on GBS-specific Chromagar plates (Chromagar, Paris, France, cat. # SB282), which were then grown overnight at 37°C.

Mice with established vaginal colonization, based on the 48-hour swab, were then swabbed three times weekly (Monday, Wednesday, and Friday) following the above protocol. Colonization clearance was defined as two sequential swabs with no detectable GBS.

Chorioamnionitis and preterm delivery model

The murine chorioamnionitis/early-onset sepsis model was performed as previously described (13) with minor modifications. Two- to four-month old BALB/c mice were mated and plug-positive female mice were monitored for pregnancy by physical examination and serial weights.

On pregnancy day 13, mice were vaginally colonized with either wild type 10/84 or the *mrvR* knockout as in the vaginal colonization model (without the preceding estradiol injections). Following colonization, they were single-housed and monitored daily for preterm delivery. If delivery occurred prior to day 17, this outcome was considered chorioamnionitis with preterm birth. Mice that remained pregnant on day 17 were sacrificed and dissected. Each fetus was examined for signs of intrauterine fetal demise (significant pallor or hyperemia, visible skin sloughing or purulence, or evidence of ongoing fetal resorption). An insulin needle was used to withdraw amniotic fluid from within the fetal membranes, after which placentas and fetuses were isolated and homogenized.

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Amniotic fluid and tissue homogenates were diluted and plated on Chromagar plates for CFU enumeration, which was performed after overnight plate growth at 37°C.

Generation of luciferase reporter GBS

A toxin-antitoxin stabilized shuttle vector expressing the firefly luciferase gene, pLZ12Km2-P23R:TA:ffluc, was a gift from Thomas Proft (Addgene plasmid # 88900 ; http://n2t.net/addgene:88900 ; RRID:Addgene_88900). We used Gibson assembly techniques to excise the kanamycin resistance marker on pLZ12Km2-P23R:TA:Ffluc and replace it with an erythromycin resistance gene. The new plasmid, called pFfluc-Erm, was purified from *E. coli* and used to transform electrocompetent wild type 10/84 and the *mrvR* knockout.

In order to fluoresce, GBS bearing the pFfluc-Erm plasmid must be exposed to the cofactor D-luciferin (Millipore Sigma cat. # L9504), which was prepared in a filter-sterilized stock solution at a concentration of 28 mg/mL in water. We performed *in vitro* imaging of serial dilutions of liquid cultures of GBS transformed with pFfluc-Erm combined 1:1 with D-luciferin stock and determined the level of fluorescence detection at 290,000 CFU/mL.

Adult mouse sepsis model with in vivo imaging

Six- to eight-week old female BALB/c mice were injected intraperitoneally under general anesthesia with 10^8 CFU of PBS-washed, stationary phase WT 10/84 or *mrvR* knockout 10/84 bearing the pFfluc-Erm plasmid and 500 µg of D-luciferin in 500 µL PBS. Immediately after the

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injection, mice were imaged on a Perkin-Elmer (Waltham, MA, USA) IVIS Lumina Series II imaging instrument with a 1-minute exposure time.

On subsequent days, surviving mice were injected intraperitoneally with 560 µg D-luciferin in sterile water then imaged after 10-15 minutes using a 1-minute exposure time. Mice that cleared their luciferase signal were subsequently observed for five days.

Whole-genome RNA-seq transcriptomic analyses

Wild type 10/84 and the *mrvR* knockout 10/84 strain were grown in TS broth overnight. 13-mL overnight culture samples were used for stationary phase RNA extraction. This culture was also used to seed pre-warmed broth, which was then grown to an OD_{600} 0.3-0.6 (early log phase) or 0.9-1.1 (late log phase), at which point RNA extraction was performed.

We used the Ribopure Bacteria RNA Purification Kit (Thermo cat. # AM1925) according to manufacturer specifications with the following exceptions: the initial bead beating step was performed for 20 minutes; the early log bacterial RNA was extracted from an 85-mL starting culture while late log and stationary phases were extracted from 13-mL cultures. RNA samples were then treated with the DNase and DNase inactivation reagents supplied with the kit.

Sequencing library preparation was conducted with the Illumina TruSeq total RNA kit according to manufacturer instructions. rRNA depletion was performed using the Ribo-Zero Plus rRNA Depletion Illumina. Next, random primers initiated first and second strand cDNA synthesis.

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Adenylation of 3' ends was followed by adapter ligation and library amplification with indexing. Sequencing was performed on an Illumina NextSeq500 platform with paired-end 75-nt reads over 150 cycles.

Trimmed and demultiplexed reads were aligned to the 10/84 genome using Bowtie 2 (102). These alignments were then used for statistical analysis using DESeq (95), which allowed determination of expression fold-change and p values. Gene set enrichment analyses were performed with Genome2D (53).

Purification of recombinant MrvR

The coding sequence for MrvR was PCR amplified from 10/84 genomic DNA using primers optimized for subsequent cloning into the four supplied BIC *Brevibacillus* expression system pBIC plasmids (Takara cat. # HB300/HB310) in order to generate secreted, N-terminus poly-His tagged recombinant MrvR. PCR, cloning, and transformation steps were carried out in accordance with manufacturer recommendations. Resultant colonies were PCR screened and Sanger sequenced for successful cloning. Optimal secretion of recombinant protein was observed in *Brevibacillus* bearing the pBIC3 plasmid construct. This strain was then grown in 2SY medium supplemented with neomycin for 72 hours at 28 °C.

His-tag affinity purification was performed with Takara Capturem maxiprep columns (cat. # 635713) according to manufacturer instructions. Following protein elution through the column,

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the product was concentrated and buffer exchanged into 1x PBS pH 7.4 using a Pierce protein concentrator column (Thermo cat. # 88527).

SDS-PAGE was performed under denaturing conditions using Thermo Scientific Bolt 4-12% Bis-Tris precast gels (cat. # NW04120BOX) and recommended reagents. For Coomassie staining, purified His-tagged MrvR was analyzed along with unprocessed supernatant before and after passage through a 0.2 μm filter to remove any planktonic cells, flow-through, and the final membrane wash flowthrough (**Supplemental Figure 4A**). For Western blot, three separate purifications of MrvR were run with a His-tagged human CD4 protein as a positive control (**Supplemental Figure 4B**). Following transfer to a PVDF membrane, Rabbit anti-His tag monoclonal IgG (Fisher cat. # TA591008S) was used to probe the blot, followed by chemiluminescent detection using the Pierce Fast Western Blotting Kit with SuperSignal Rabbit West Pico reagents (Thermo cat. #35061).

Electrophoresis mobility shift assay

Electrophoresis mobility shift assay was performed with the Thermo Lightshift Chemiluminescent EMSA Kit (cat. # 20148) according to manufacturer instructions with the following details. The 153-nt *mrvR* and *udp* promoter region was PCR amplified using a biotinylated forward primer and gel purified. A scrambled biotinylated DNA fragment of the same length and with the same nucleotide ratios was used as a control. Mixtures of undiluted, purified recombinant MrvR (20 mg/mL) and four 2-fold dilutions were combined with promoter

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DNA at a fixed concentration, while only undiluted rMrvR was combined with the scrambled control fragment. All reactions included poly (dI•dC) as a nonspecific blocking reagent, as well as 1x binding buffer included with the kit. Additional negative controls were performed in which no rMrvR was present. Coincubation continued for 20 minutes at room temperature, after which the reactions were run on a 4-6% polyacrylamide gel under native conditions. Blotting and detection of the labeled DNA fragments was performed in accordance with instructions with the EMSA kit.

Acknowledgements

We are grateful to the University of Pittsburgh Center for Research Computing, which maintains the HTC cluster used for bioinformatic analysis of RNA-seq data. William MacDonald and Rania Elbakri in the University of Pittsburgh Health Sciences Sequencing Center assisted with next-generation sequencing of RNA-seq samples. Staff at the University of Maryland Genomic Resource Center assisted with sequencing for Tn-seq. Thomas Proft kindly made the plasmid pLZ12Km2-P23R:TA:ffluc available through Addgene. We thank Thomas Diacovo and Jeffrey Weiser, who shared equipment for multiple experiments in this study.

Funding

This work was supported by NIH/NIAID grants K08AI132555 to T.A.H., R21AI147511 to T.A.H. and A.J.R., and R01AI143290 to A.J.R.; the Pittsburgh Children's Foundation Children's Trust Young Investigator Award (T.A.H.); the Richard King Mellon Institute for Pediatric Research Pilot Award (T.A.H.); and the i4Kids Pilot Award (T.A.H.).

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Data availability

Tn-seq and RNA-seq reads available on SRA.

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Table 1: GBS genes conditionally essential for survival in human amniotic fluid

Gene locus	$\log_2$ Fold-Change[a]	Expected product
SAK_RS09545	-4.3690439	DeoR family transcriptional regulator
SAK_RS02930	-4.3341605	hypothetical protein
SAK_RS09890	-4.1865043	ABC-class transporter
SAK_RS10120	-3.8123495	GntR family transcriptional regulator (mrvR)
SAK_RS05160	-3.7270772	membrane-spanning protein of unknown function

[a] Fold-change between expected and observed transposon insertions in amniotic fluid experimental outgrowth conditions

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Figure Captions

Figure 1. Tn-seq screening of GBS grown in human amniotic fluid revealed 5 conditionally essential genes. GBS transposon library in a background of strain A909 was grown in eight human amniotic fluid samples, then subjected to Tn-seq analysis. Each ring of the Circos plot shows a different representation of the A909 circular chromosome. From the center of the plot, rings 1-8 show transposon insertion density detected in the eight amniotic fluid outgrowth samples (lowest detection: red; highest detection: blue). Ring 9 shows essential genes (red), nonessential genes (green), intermediate genes (yellow), and those for which baseline fitness cannot be determined (white; see reference (41)). The outermost ring shows $\log_2$ fold-change values for each gene in amniotic fluid outgrowth as determined by ESSENTIALS. Genes with inward-pointing peaks had fewer than expected transposon insertions. Outward-pointing peaks had more than expected transposon insertions. The peaks are color coded for statistical significance (low adjusted p value: red; high adjusted p value: green). The five labeled peaks are described in the text and are listed in **Table 1**. Peak 4 is the GntR-class transcription factor, *mrvR*.

Figure 2. CRISPRi knockdowns of candidate genes and phenotypic characterization of GBS lacking MrvR in amniotic fluid, rich media, and biofilm-promoting growth conditions. Two CRISPRi targeting protospacers (targeting nucleotides 112 and 213 of *cylx*, the first gene in the operon) against the *cyl* operon were developed to knockdown expression of β-hemolysin/cytolysin. The resultant knockdown strains (in a 10/84 background) were compared

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786 to wild type in a human erythrocyte hemolysis assay (**A**). Targeting protospacers against the five
787 candidate conditionally essential genes from amniotic fluid Tn-seq. For each gene, the number
788 indicates the targeted nucleotide; the protospacer sequence is shown in parentheses (**B**). A
789 qPCR-based multiplex CRISPRi screen using knockdowns of all five candidate genes revealed
790 decreased fitness in amniotic fluid compared to tryptic soy (TS) broth (**C**); black columns show
791 the competition index of strains bearing individual targeting protospacer plasmids, while red
792 columns show pooled results from both targeting plasmids for each gene. Statistical significance
793 of each knockdown phenotype was determined relative to growth of the knockdowns in TS
794 broth. Growth curves of the Δ*mrvR* and wild type (WT) 10/84 in broth (**D**). Colony forming unit
795 enumeration-based competition assays between Δ*mrvR* and Δ*mrvR*+pBSU101::*mrvR* in TS broth
796 (TSB) and amniotic fluid (AF); **E**). Biofilm assay results comparing WT 10/84, Δ*mrvR*, and
797 Δ*mrvR*+pBSU101::*mrvR*. *p<0.05, ** p<0.01, *** p<0.005, **** p<0.001; t test. Error bars
798 show SEM surrounding mean.
799
800 **Figure 3. MrvR does not affect establishment or maintenance of vaginal colonization.** Adult
801 nonpregnant C57/BLJ mice were vaginally colonized with wild type (WT) 10/84 or Δ*mrvR*.
802 Neither the colonization density at the initial swab 48 hours after inoculation (**A**) nor duration
803 of colonization (**B**) showed significant differences (CFU: colony forming units, NS: not
804 significant).
805
806 **Figure 4. MrvR has a significant effect on the outcome of chorioamnionitis.** Pregnant BALB/c
807 mice were vaginally colonized with wild type (WT) or knockout (KO) 10/84 on pregnancy day 13.

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Pregnancies were monitored until day 17 or preterm delivery, whichever came first. On day 17, mice that remained pregnant were dissected and evaluated for vaginal colonization and chorioamnionitis. While none of the KO-colonized mice with chorioamnionitis delivered preterm, 8 of 11 WT-colonized mice delivered early. One WT-colonized mouse did not develop chorioamnionitis (**A-B**; *** $p<0.005$; Mantel-Cox test). Dissected pregnancy tissue was homogenized and quantified, showing a difference in invasion density in amniotic fluid (AF) but not in fetal or placental tissue (**C**, ** $p<0.01$; t test, error bars show interquartile ranges surrounding medians).

Figure 5. MrvR affects GBS invasiveness and lethality in a sepsis model. BALB/c mice were infected intraperitoneally with wild type (WT) 10/84 or Δ*mrvR*, both bearing a plasmid to allow in vivo tracking of a luciferase signal. There was a significant difference in outcome between the two strains (**A**, **** $p<0.001$ Mantel-Cox test) Mice were imaged daily (**B**) until they either died (red boxes) or completely cleared the luciferase signal (green circles). Mice that cleared the luciferase signal were monitored for the following five days and remained well.

Figure 6. Analysis of the MrvR regulon reveals widespread effects with emphasis on genes involved in nucleotide metabolism. RNA-seq analysis of wild type (WT) and Δ*mrvR* 10/84 at three growth timepoints showed extensive regulation across the chromosome in all phases of growth (**A**, expression $\log_2$ fold-change shown relative to WT). A phage island (Φ) with significant differences from WT is noted. Gene set enrichment analysis showed that, across all three bacterial growth phases tested, the KEGG pathways most influenced by the presence of

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MrvR were pyrimidine and purine metabolism (**B**), which is also shown in volcano plots (**C-E**). Panel **F** shows specific genes of the de novo and salvage pathways of pyrimidine metabolism in GBS whose expression is significantly affected by the presence of MrvR. An electrophoresis mobility shift assay (EMSA) with recombinant MrvR (rMrvR) transcription factor combined with the shared promoter region between the *mrvR* and *udp* suggested increased protein binding (**G**) compared to a sequence scrambled control (sc). rMrvR had a maximal concentration of 20 mg/mL (+); in the experimental coincubation, each subsequent dilution was 2-fold in the same sterile PBS as the original suspension.

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Supplemental Data Files

Supplemental Data 1: GBS amniotic fluid conditionally essential gene analysis

Output from ESSENTIALS analysis of eight A909 library aliquots grown in human amniotic fluid. The table is sorted by $\log_2$ fold-change (D), and the five conditionally essential genes described in the main text are highlighted in yellow. The index (column A) allows sorting by gene locus if set from smallest to largest.

Supplemental Data 2: RNA-seq comparing Δ*mrvR* with wild type 10/84 genome-wide gene expression

Output from DESeq analysis of RNA-seq read alignments. Log_2 fold-change and adjusted p values are provided for three growth phases as described in the text.

Supplemental Figure 1: GBS CRISPRi sequence data

Alignments of GBS and *S. pyogenes* genomic DNA regions encoding CRISPR-Cas complex components (**A-C**). Predicted folding of gRNA complexes (**D**) generated using the mfold server (103). Sequence of sgRNA complex used to target candidate genes using GBS CRISPRi system (**E**). Sanger sequence showing the two targeted mutations used to generate dCas9 on the 10/84 chromosome (**F**).

Supplemental Figure 2: PCR targeting three regions within the prophage island found to be downregulated in Δ*mrvR*

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Three regions within the prophage island spanning gene loci W903_RS03075 through W903_RS03520 were amplified from wild type and *mrvR* knockout GBS genomic DNA. The PCR products from the two strains were the same size when assessed by gel electrophoresis (**A**). The bottom schematic shows the three amplified regions of the chromosome in red (**B**).

Supplemental Figure 3: *mrvR* gene neighborhood alignments in other bacteria

Gene synteny plot showing orthologs of the GBS *mrvR* gene in 16 other bacterial species. The plot was generated using the Integrated Microbial Genomes & Microbiomes server on the JGI genome portal (https://img.jgi.doe.gov). Genes are color coded by COG functional prediction. COG categories related to nucleotide metabolism present on the diagram are noted.

Supplemental Figure 4: Recombinant MrvR purification

Coomassie stained PAGE gel (**A**) and Western blot (**B**) probed with anti-His tag antibody. Lanes 1-6 in panel A are: Thermo PageRuler Plus prestained protein ladder (cat. # 26620); supernatant from the *Brevibacillus* outgrowth media; supernatant after passage through a 0.2 µm sterilization filter; initial flowthrough from the Takara Capturem his tag purification unit; flowthrough following sequential washes of the purification unit; elution of the purified protein with expected MW=29 kDa.

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Figure 1

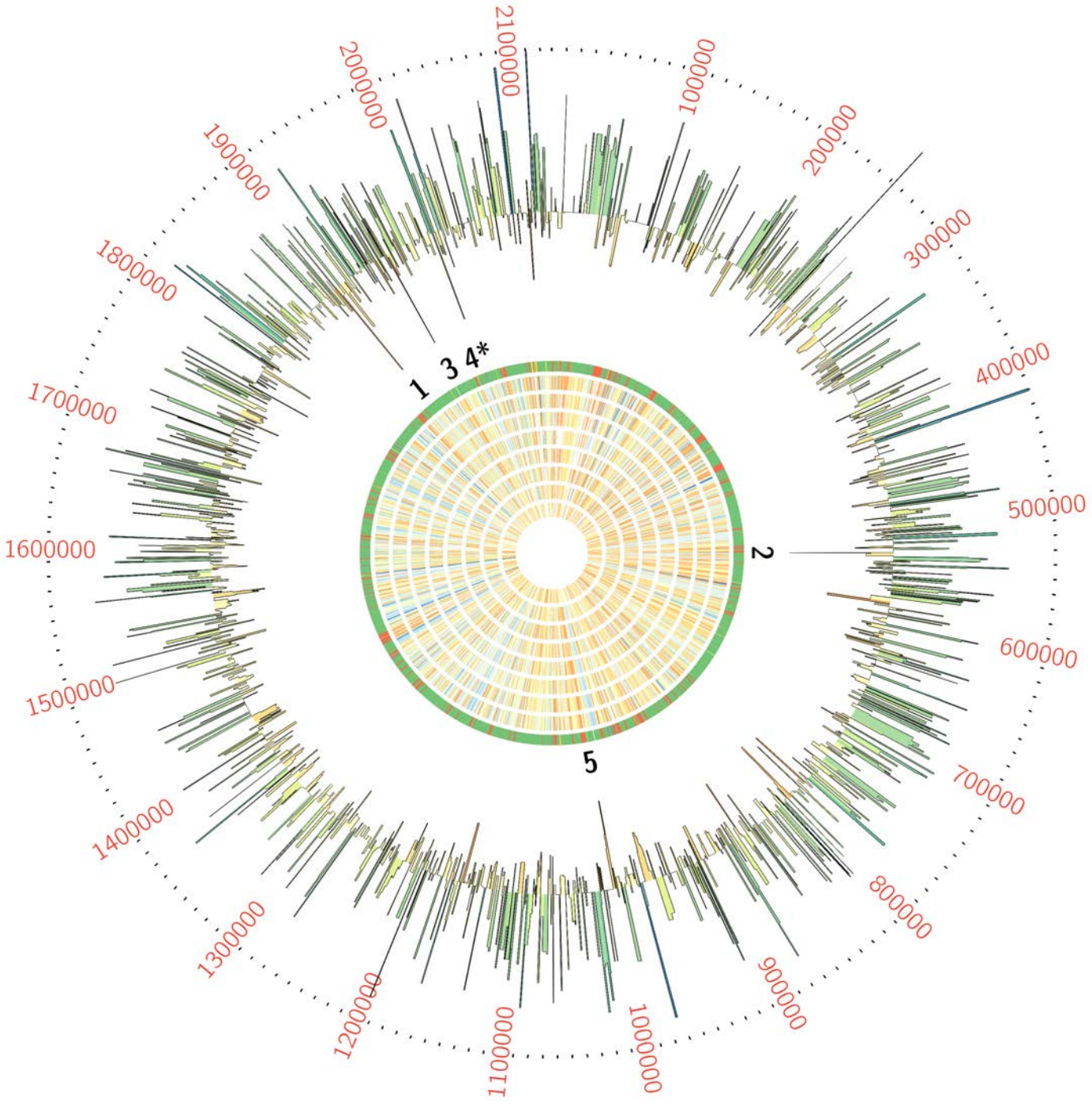

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Figure 2

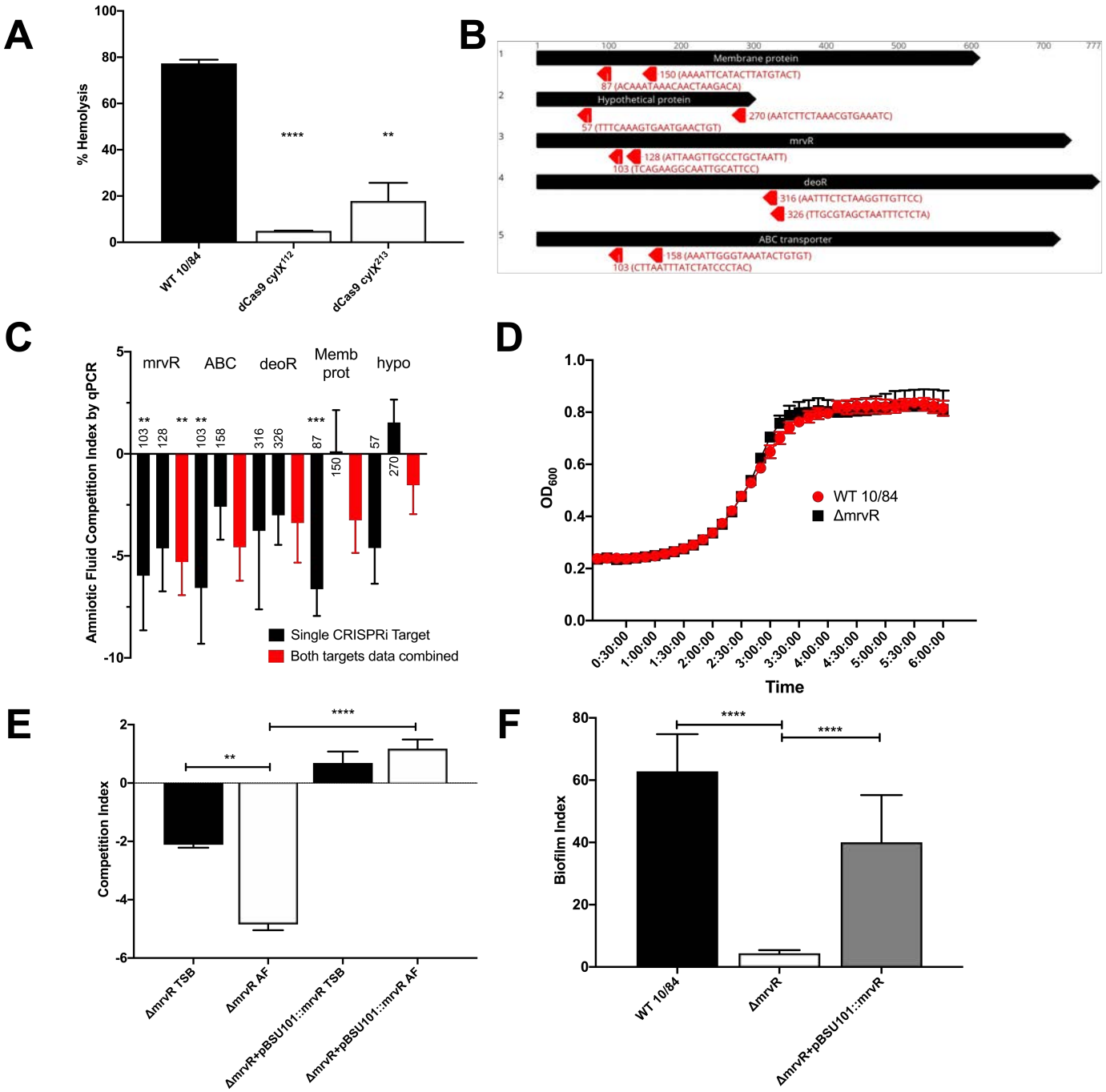

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Figure 3

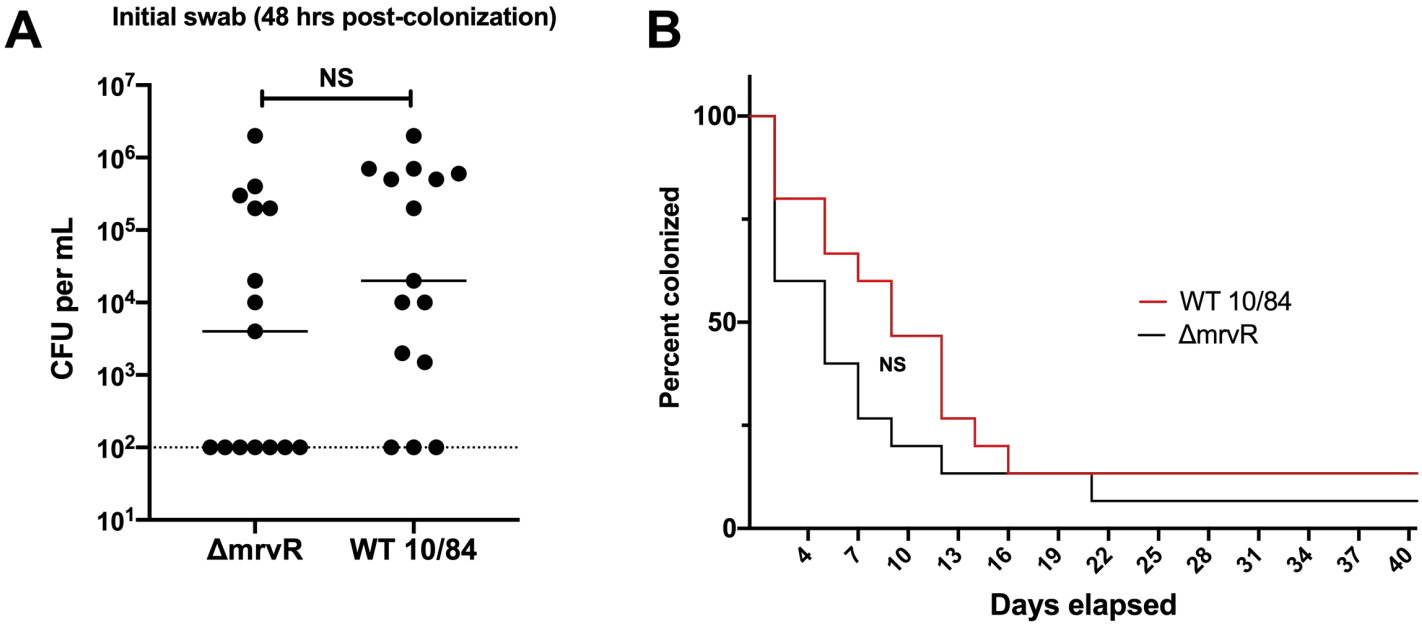

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Figure 4

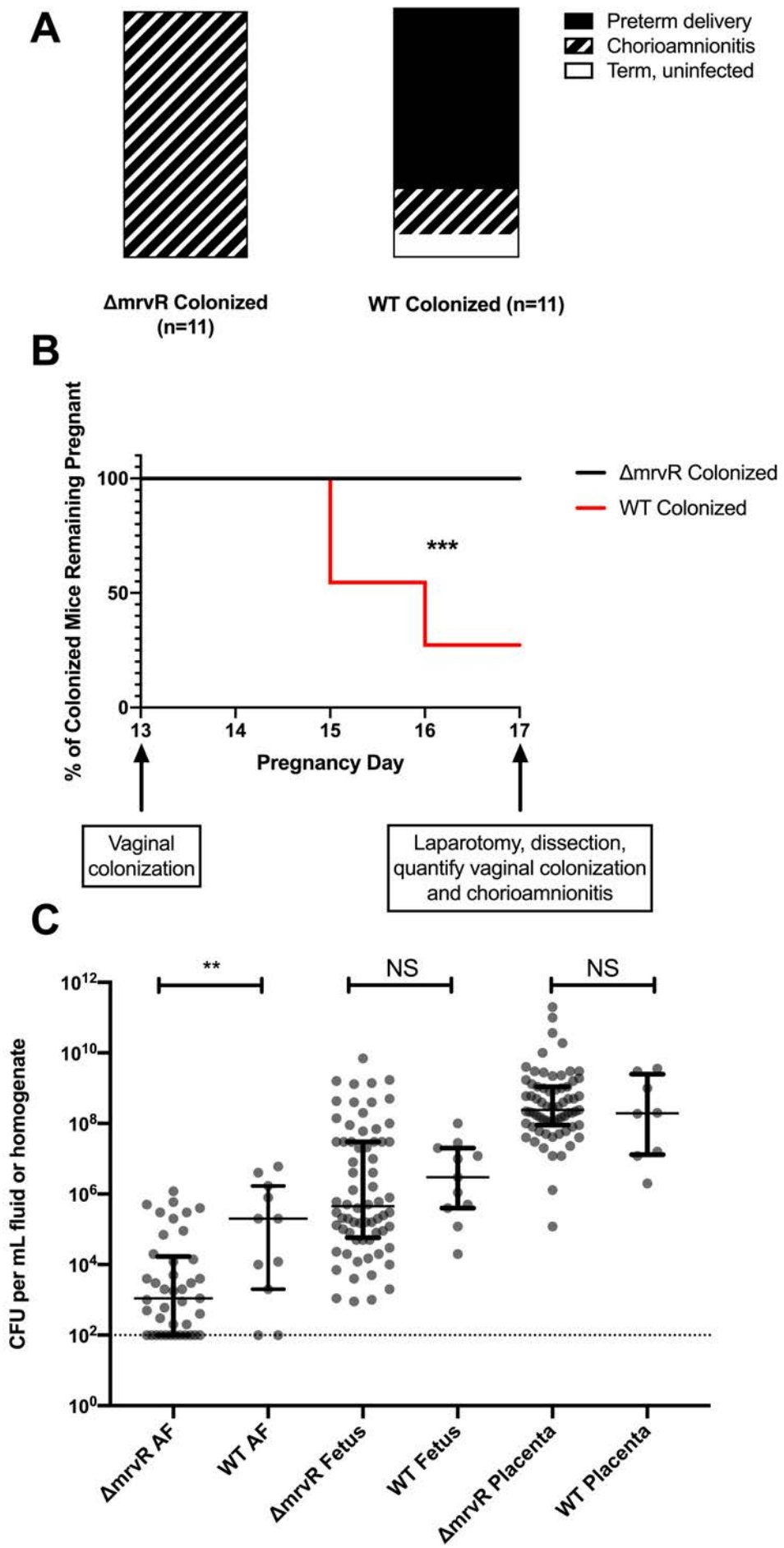

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Figure 5

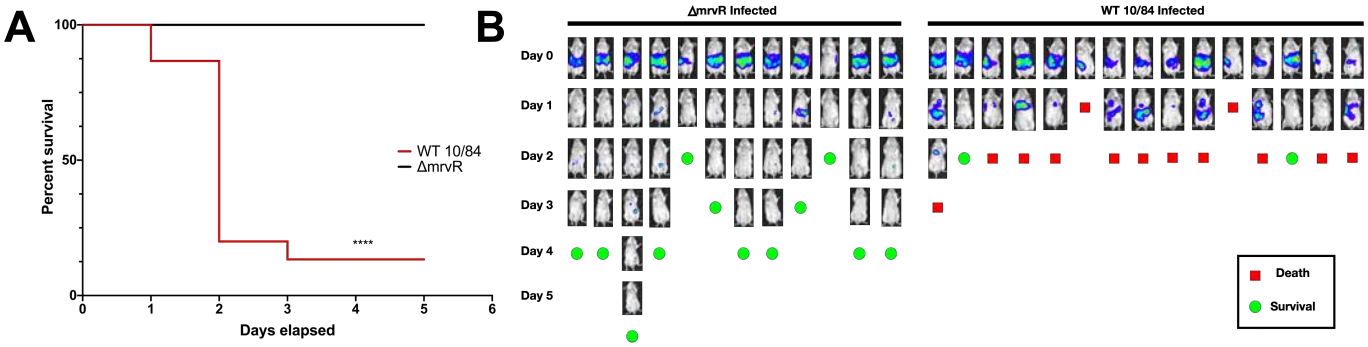

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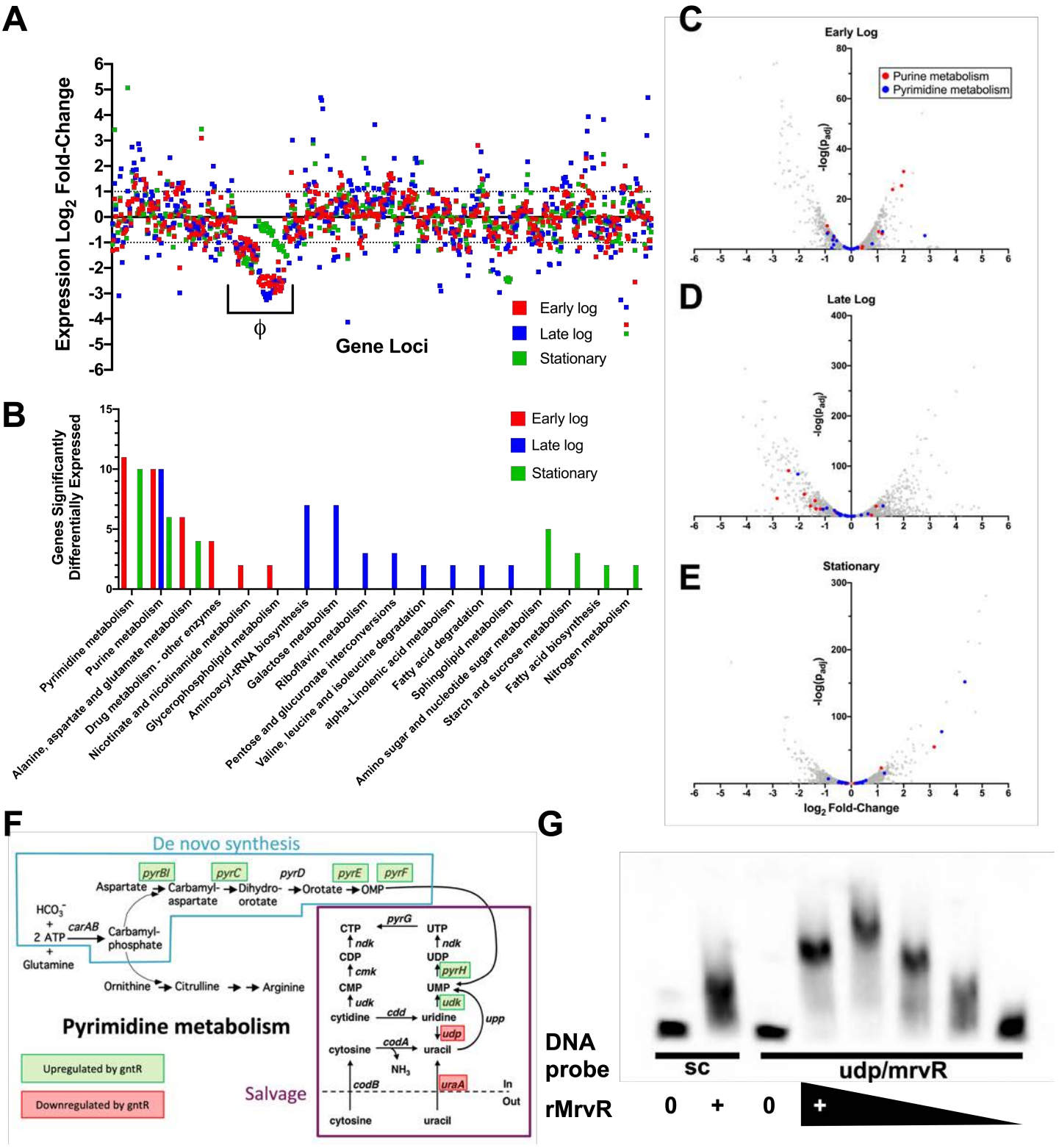
Figure 6



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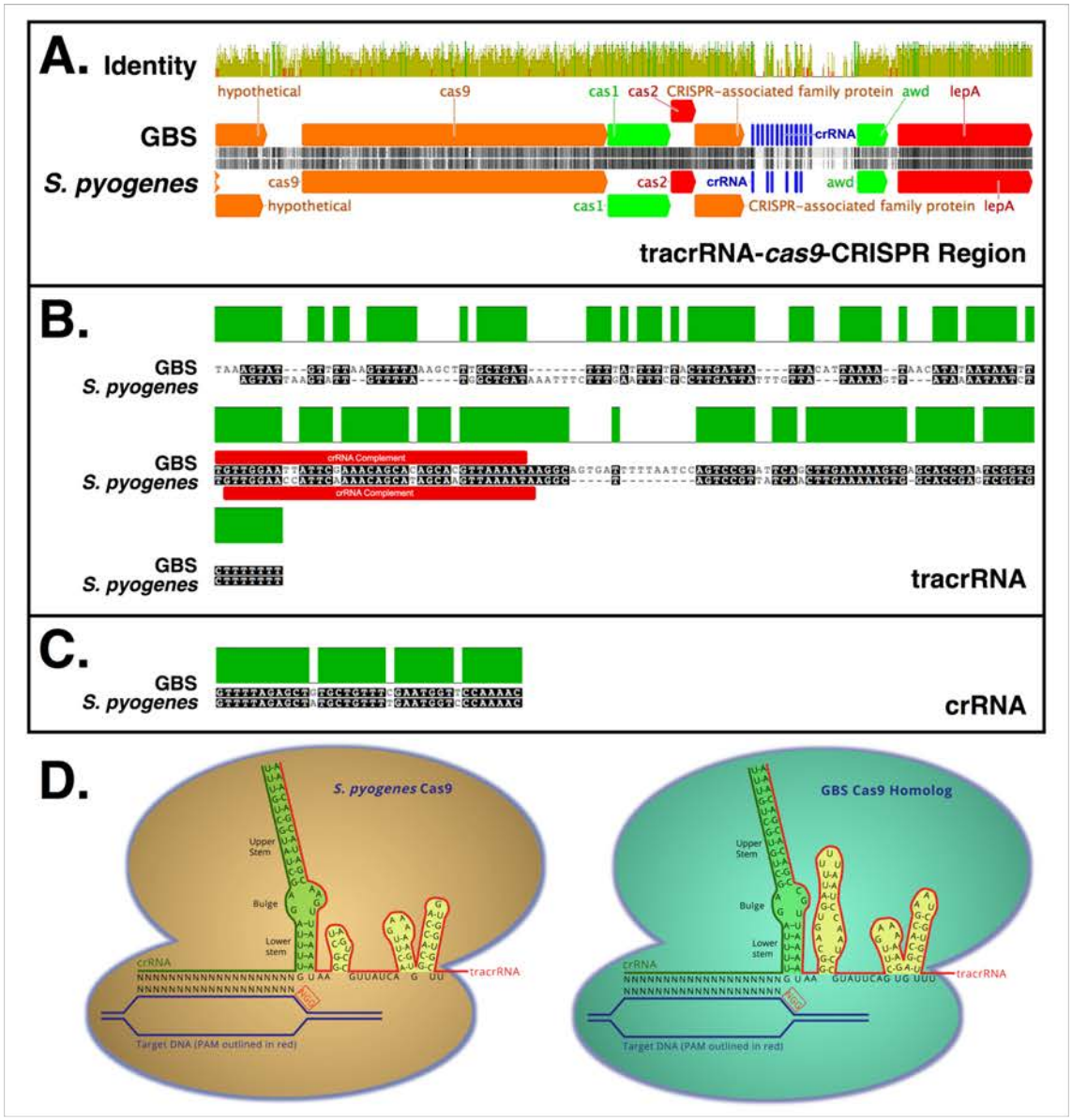
Supplemental Figure 1



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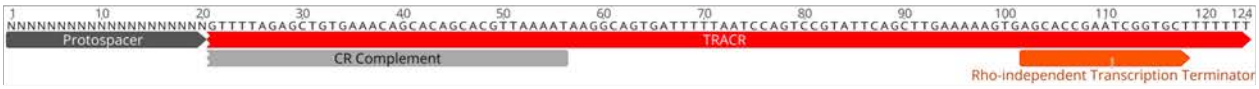

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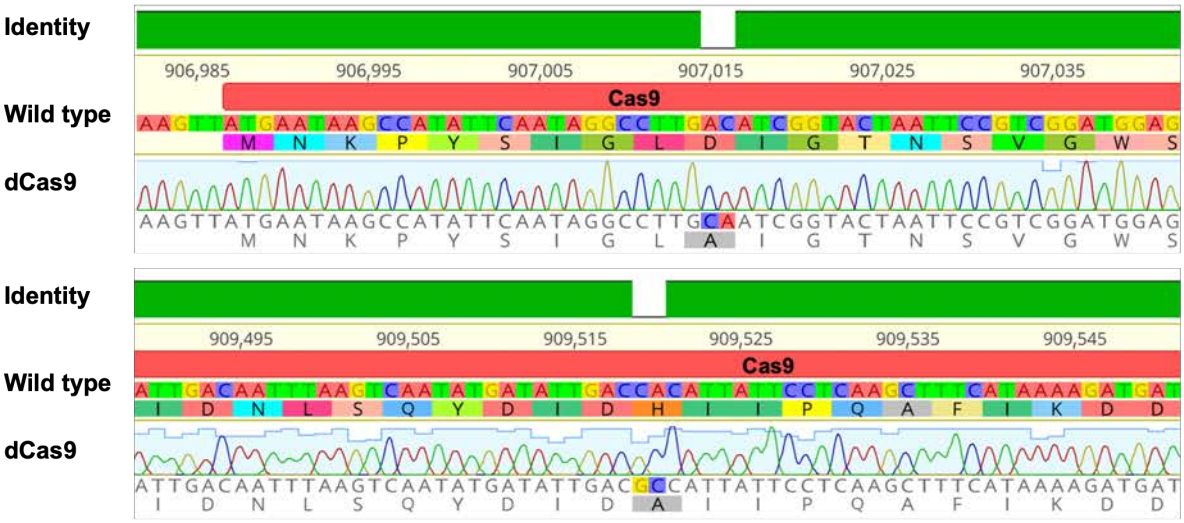

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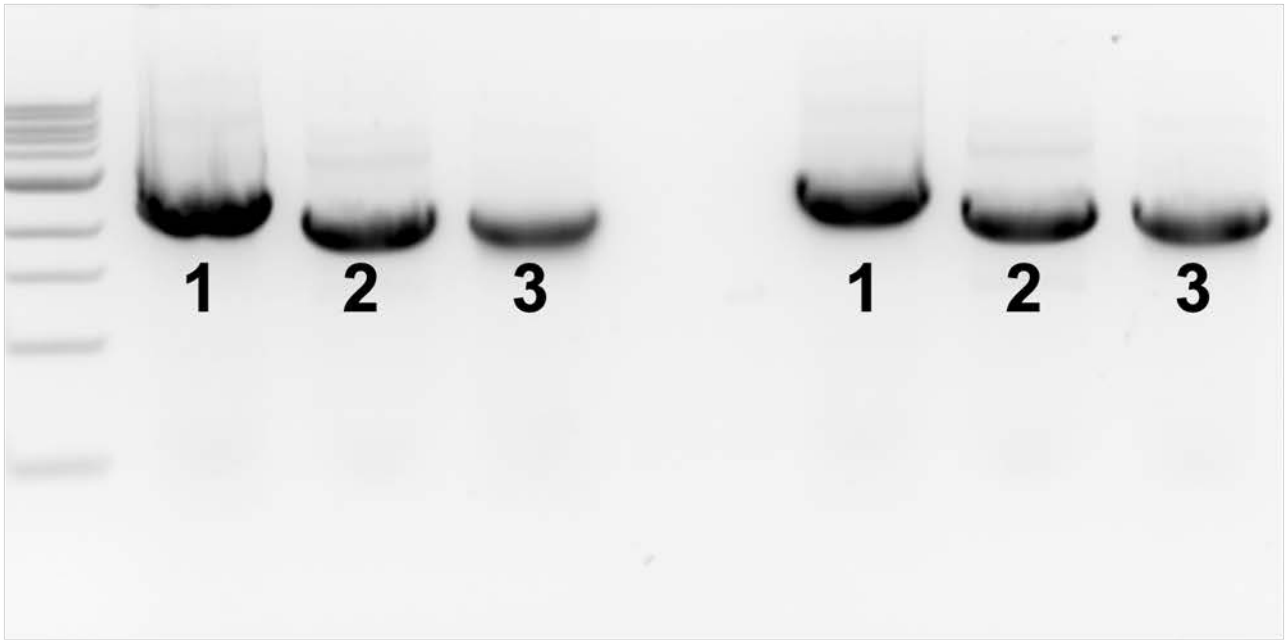
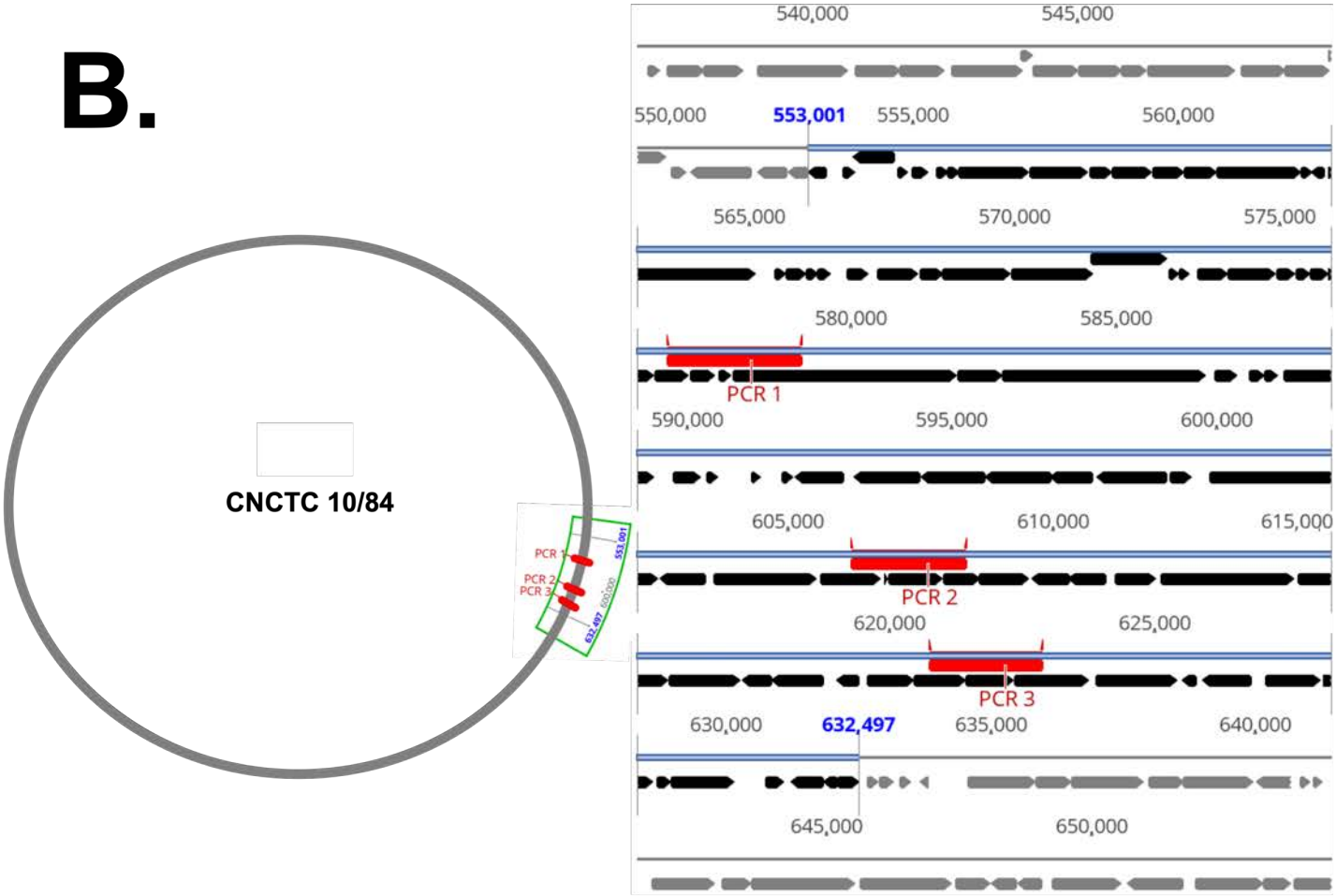
Supplemental Figure 2

A.



B.



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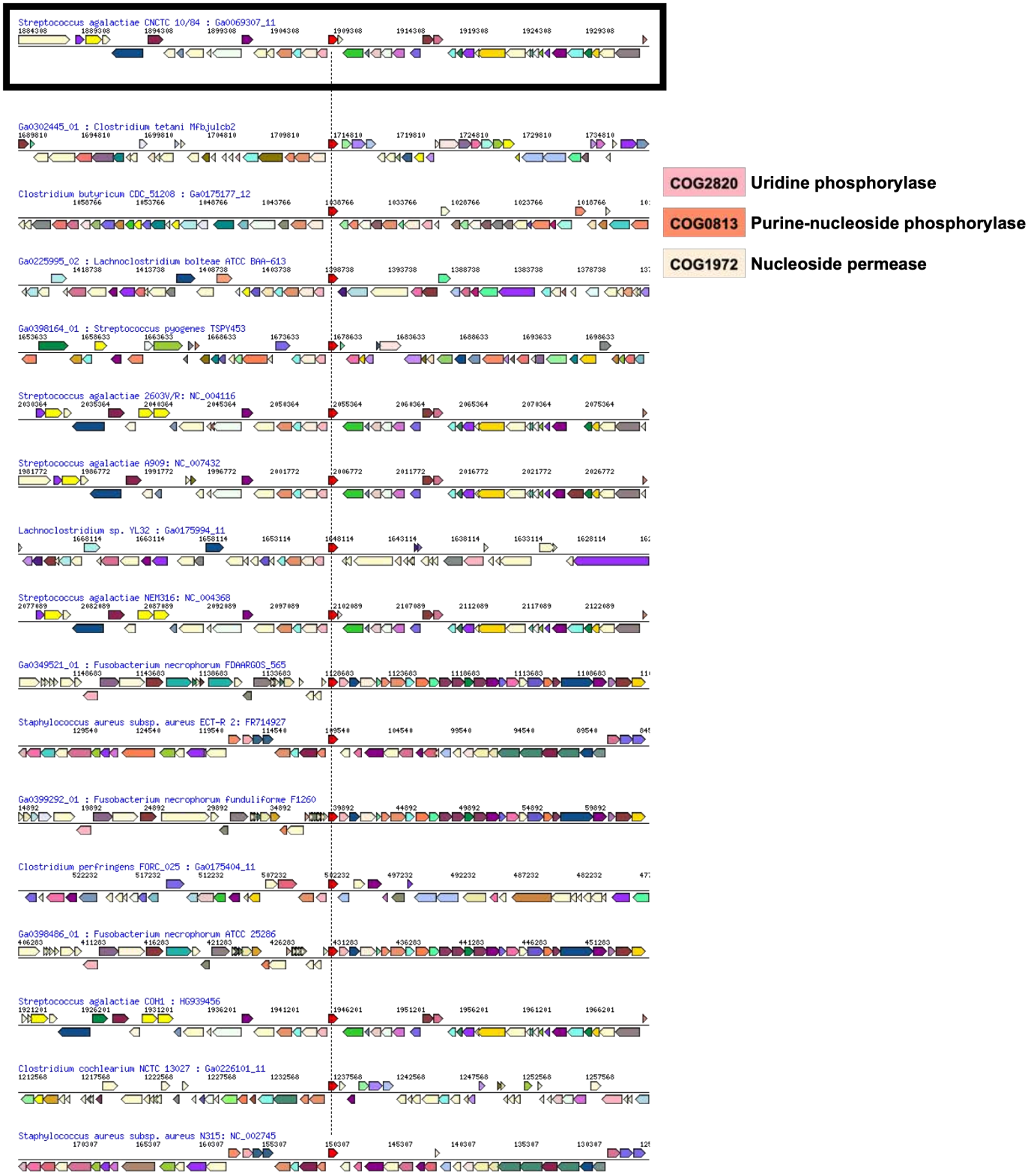
Supplemental Figure 3



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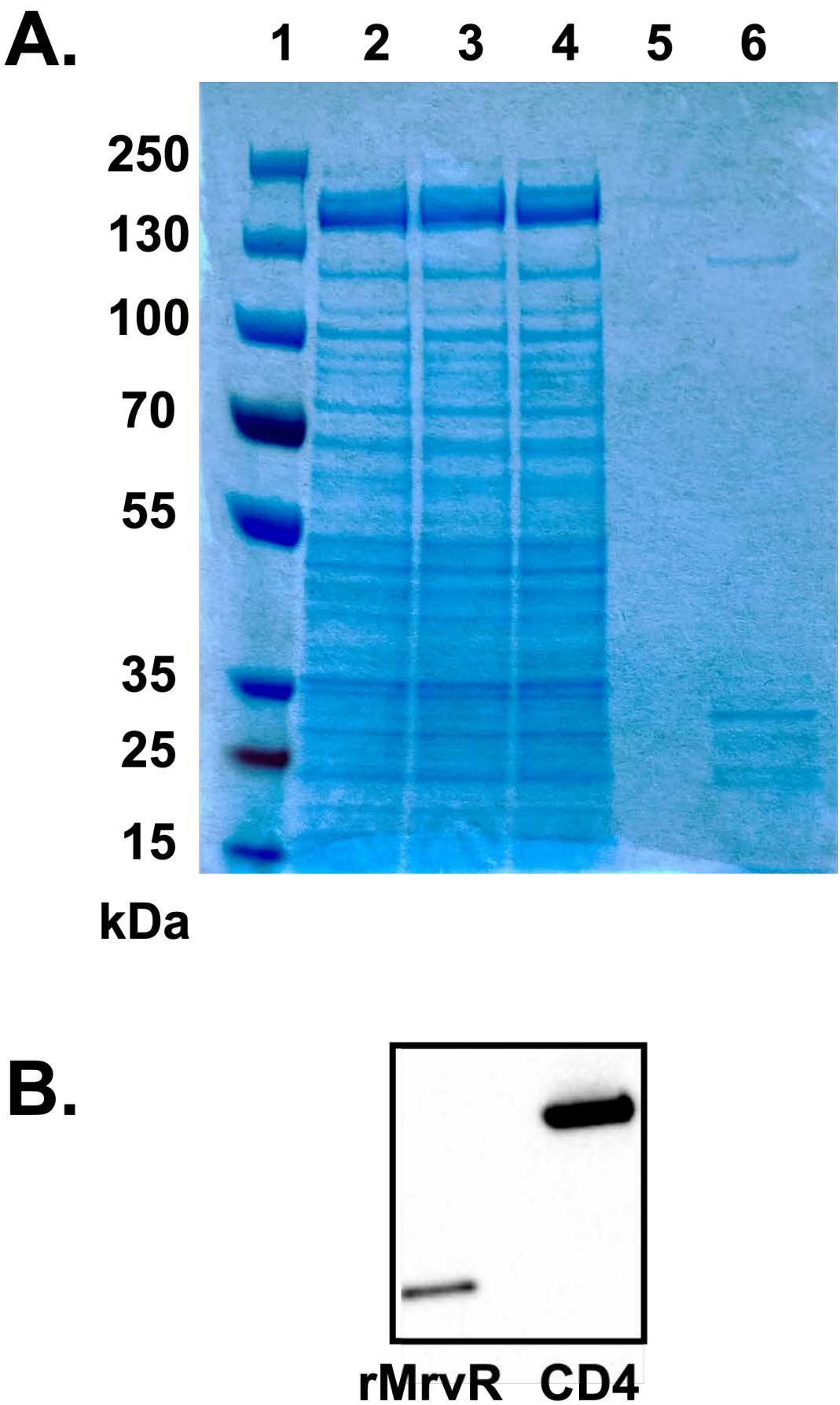
Supplemental Figure 4



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Supplemental Data 1

Index	New Locus Tag	Old Locus Tag	logFC	adj.P.Val	Start	Stop	Strand	Length	Gene
1896	SAK_RS09545	SAK_1896	-4.369043935	2.07E-14	1896329	1897105	+	777	-
588	SAK_RS02930	SAK_0588	-4.334160498	6.17E-14	531495	531797	-	303	-
1965	SAK_RS09890	SAK_1965	-4.186504256	1.08E-11	1955676	1956398	-	723	-
2012	SAK_RS10120	SAK_2012	-3.812349482	1.39E-11	2006402	2007139	+	738	mrvR
1031	SAK_RS05160	SAK_1031	-3.727077207	7.04E-10	1000406	1001017	+	612	-
853	SAK_RS04270	SAK_0853	-2.914281284	0.001172189	800893	802503	+	1611	ftsY
2114	SAK_RS10650	SAK_2114	-2.814015133	0.008276941	2104985	2106094	+	1110	recF
835	SAK_RS04180	SAK_0835	-2.750161096	0.010132895	780699	781697	+	999	-
914	SAK_RS04570	SAK_0914	-2.646573421	0.005020334	864068	864919	+	852	-
648	SAK_RS03245	SAK_0648	-2.625489661	0.005894511	580503	582506	+	2004	-
1774	SAK_RS08930	SAK_1774	-2.5803376	0.001172189	1767695	1768231	-	537	-
1175	SAK_RS05880	SAK_1175	-2.575797821	0.000190588	1152800	1154800	-	2001	-
840	SAK_RS04205	SAK_0840	-2.471913997	0.005020334	787644	788210	+	567	-
1032	SAK_RS05165	SAK_1032	-2.310372707	0.001924826	1001054	1001836	-	783	-
1795	SAK_RS09035	SAK_1795	-2.267894167	0.005048137	1787967	1788908	-	942	-
1900	SAK_RS09565	SAK_1900	-2.230948465	0.005894511	1901627	1903843	-	2217	relA
1556	SAK_RS07845	SAK_1556	-2.16980131	0.008276941	1553936	1554862	-	927	mtsA
1004	SAK_RS05025	SAK_1004	-2.098788616	0.016106467	967197	968954	+	1758	-
85	SAK_RS00420	SAK_0085	-2.038812798	0.049204984	66913	68691	+	1779	-
290	SAK_RS01430	SAK_0290	-2.00828642	0.095981098	250257	250547	+	291	-
84	SAK_RS00415	SAK_0084	-1.950174441	0.082269681	66536	66916	+	381	-
1003	SAK_RS05020	SAK_1003	-1.925319292	0.049887517	965749	967137	+	1389	-
1554	SAK_RS07835	SAK_1554	-1.908204399	0.032039909	1552214	1553047	-	834	mtsC
1510	SAK_RS07605	SAK_1510	-1.88165868	0.036861887	1506407	1507795	+	1389	cycA
1240	SAK_RS06220	SAK_1240	-1.845243257	0.054129749	1210062	1210292	-	231	-
1743	SAK_RS08765	SAK_1743	-1.819369789	0.053769112	1732904	1733563	+	660	-
1306	SAK_RS06550	SAK_1306	-1.791049337	0.104483905	1283629	1284231	-	603	-
1688	SAK_RS08500	SAK_1688	-1.785016451	0.053769112	1674328	1675539	-	1212	-
901	SAK_RS04505	SAK_0901	-1.774037861	0.054129749	850398	851228	+	831	-
1102	SAK_RS05510	SAK_1102	-1.758512696	0.096516319	1075382	1076410	-	1029	-
1033	SAK_RS05170	SAK_1033	-1.707120157	0.082269681	1001848	1002546	-	699	-
1094	SAK_RS05470	SAK_1094	-1.650490124	0.11149771	1065277	1065708	-	432	-
2022	SAK_RS10175	SAK_2022	-1.641370227	0.118937627	2016537	2017028	-	492	-
1555	SAK_RS07840	SAK_1555	-1.631320049	0.114092804	1553049	1553765	-	717	mtsB
303	SAK_RS01495	SAK_0303	-1.629874464	0.11149771	258189	259334	-	1146	-
222	SAK_RS01100	SAK_0222	-1.62701866	0.095981098	186394	188691	+	2298	-
583	SAK_RS02905	SAK_0583	-1.589920056	0.104483905	525869	526474	+	606	-
955	SAK_RS04785	SAK_0955	-1.589056744	0.115099042	910378	912639	+	2262	-
1945	SAK_RS09795	SAK_1945	-1.583339386	0.11297899	1942416	1943444	-	1029	-
301	SAK_RS01485	SAK_0301	-1.577807802	0.11149771	256625	257551	-	927	-
1091	SAK_RS05455	SAK_1091	-1.574983149	0.11149771	1062900	1063313	-	414	spxA
536	#N/A	SAK_0536	-1.568116314	0.104483905	479378	480550	+	1173	galK
688	SAK_RS03440	SAK_0688	-1.545420919	0.104483905	623359	624381	+	1023	add
1002	SAK_RS05015	SAK_1002	-1.542737172	0.13513782	964624	965622	+	999	-
1585	SAK_RS07995	SAK_1585	-1.519661637	0.130362767	1581422	1581970	-	549	-
1524	SAK_RS07680	SAK_1524	-1.505296991	0.127312727	1521303	1521704	-	402	-
1195	SAK_RS05980	SAK_1195	-1.495883658	0.129734883	1173488	1174282	-	795	potB
512	#N/A	SAK_0512	-1.490199363	0.125726808	454032	455068	-	1037	-
1373	SAK_RS06910	SAK_1373	-1.480486043	0.12947717	1359488	1360336	-	849	-
691	SAK_RS03455	SAK_0691	-1.453113846	0.129734883	625228	626424	+	1197	-
1414	SAK_RS07115	SAK_1414	-1.452580096	0.138762275	1397171	1399315	+	2145	-
2076	SAK_RS10445	SAK_2076	-1.436390507	0.145369724	2071253	2071876	-	624	-
1264	#N/A	SAK_1264	-1.433785776	0.145369724	1235051	1235818	-	768	-
154	SAK_RS00760	SAK_0154	-1.412145687	0.138762275	112295	113137	-	843	-
1105	SAK_RS05525	SAK_1105	-1.410911863	0.132975096	1078201	1079163	-	963	-
993	SAK_RS04970	SAK_0993	-1.407315552	0.132975096	948079	948600	+	522	-
65	SAK_RS00320	SAK_0065	-1.396142377	0.138762275	47331	48635	+	1305	sip
302	SAK_RS01490	SAK_0302	-1.395074447	0.129734883	257554	258189	-	636	-
1001	SAK_RS05010	SAK_1001	-1.39054359	0.169868628	963581	964549	+	969	-
989	SAK_RS04950	SAK_0989	-1.387343564	0.138762275	944268	945539	+	1272	murA
1611	SAK_RS08125	SAK_1611	-1.385300118	0.138762275	1604407	1605147	-	741	xerD
679	SAK_RS03395	SAK_0679	-1.375483102	0.138762275	614037	615020	-	984	-
1661	#N/A	SAK_1661	-1.375376509	0.157720711	1652015	1652128	+	114	-
1367	SAK_RS06880	SAK_1367	-1.336590789	0.155716174	1351616	1352125	+	510	-
83	SAK_RS00410	SAK_0083	-1.335647016	0.145369724	66092	66529	+	438	-
1432	SAK_RS07205	SAK_1432	-1.329171331	0.140920456	1414035	1415369	-	1335	-
1913	SAK_RS09635	SAK_1913	-1.328895211	0.145369724	1916590	1917498	-	909	-
1222	SAK_RS06130	SAK_1222	-1.327673464	0.145369724	1196121	1196318	-	198	-
506	SAK_RS02525	SAK_0506	-1.324230925	0.14117843	451781	452239	-	459	-
1794	SAK_RS09030	SAK_1794	-1.319824945	0.145369724	1787058	1787870	-	813	purR
369	SAK_RS01830	SAK_0369	-1.313874938	0.155716174	316472	317806	+	1335	pepC
1828	SAK_RS09205	SAK_1828	-1.301603797	0.155716174	1823461	1824444	-	984	-
1123	SAK_RS05615	SAK_1123	-1.294141396	0.143058407	1093406	1097815	-	4410	-
772	SAK_RS03850	SAK_0772	-1.28865065	0.147719162	707515	708264	-	750	-
1005	SAK_RS05030	SAK_1005	-1.286361828	0.145369724	969052	970041	+	990	lplA
153	SAK_RS00755	SAK_0153	-1.285290027	0.145369724	111689	112258	+	570	-
2101	SAK_RS10585	SAK_2101	-1.28322615	0.145369724	2093487	2094098	-	612	-
1935	SAK_RS09745	SAK_1935	-1.277596245	0.163741103	1935837	1936145	-	309	-
662	SAK_RS03310	SAK_0662	-1.272689115	0.161487887	592426	593742	-	1317	-
1983	SAK_RS09980	SAK_1983	-1.269780026	0.147719162	1969227	1969994	-	768	cfb
2098	SAK_RS10570	SAK_2098	-1.253585144	0.155716174	2088909	2089361	-	453	rplI
188	SAK_RS00935	SAK_0188	-1.238722344	0.155716174	149900	151240	-	1341	-
1234	SAK_RS06190	SAK_1234	-1.236544174	0.147719162	1206716	1207411	+	696	-
1886	SAK_RS09495	SAK_1886	-1.22914635	0.156913217	1887081	1887977	-	897	-
74	SAK_RS00365	SAK_0074	-1.227833141	0.172669706	55716	56693	+	978	-
1015	SAK_RS05080	SAK_1015	-1.226034318	0.169956616	978499	979269	+	771	-
998	SAK_RS04995	SAK_0998	-1.224611449	0.155716174	959067	959984	+	918	-
1128	SAK_RS05640	SAK_1128	-1.224099198	0.180357604	1102906	1103196	-	291	-
1718	SAK_RS08640	SAK_1718	-1.218348031	0.155716174	1708250	1708921	-	672	-
1233	SAK_RS06185	SAK_1233	-1.209787289	0.17074747	1206343	1206735	+	393	-
1728	SAK_RS08690	SAK_1728	-1.203076224	0.158610161	1717491	1718033	-	543	-
1437	SAK_RS07230	SAK_1437	-1.199255996	0.156818512	1418626	1419225	-	600	-

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341	SAK_RS01690	SAK_0341	-1.197657247	0.180357604	284801	285442	+	642	-
1326	SAK_RS06660	SAK_1326	-1.186879183	0.166416628	1309068	1310249	-	1182	-
1612	SAK_RS08130	SAK_1612	-1.184829731	0.172669706	1605137	1605610	-	474	-
437	SAK_RS02170	SAK_0437	-1.182643563	0.163741103	384996	385580	+	585	-
1046	SAK_RS05230	SAK_1046	-1.180964844	0.163741103	1014769	1015689	-	921	coaA
576	SAK_RS02870	SAK_0576	-1.175383376	0.170990433	518281	518526	+	246	-
1145	SAK_RS05725	SAK_1145	-1.173348688	0.17239133	1123189	1124208	-	1020	lplA
1893	SAK_RS09530	SAK_1893	-1.170228205	0.169868628	1893852	1895300	-	1449	-
1651	SAK_RS08320	SAK_1651	-1.169306253	0.174705686	1642475	1643530	+	1056	-
397	SAK_RS01970	SAK_0397	-1.162120599	0.170990433	346258	347241	+	984	-
1660	SAK_RS08365	SAK_1660	-1.156826013	0.17239133	1651415	1651951	-	537	-
1435	SAK_RS07220	SAK_1435	-1.155240109	0.166416628	1417136	1417777	-	642	-
1440	SAK_RS07245	SAK_1440	-1.152859258	0.169868628	1420792	1422300	-	1509	-
553	SAK_RS02750	SAK_0553	-1.151510975	0.17239133	496116	496565	-	450	-
469	SAK_RS02335	SAK_0469	-1.150848116	0.163741103	414492	415232	-	741	-
1184	SAK_RS05925	SAK_1184	-1.150267809	0.184091563	1162110	1162457	+	348	-
590	SAK_RS02940	SAK_0590	-1.143942923	0.17239133	532502	534763	-	2262	clpE
1409	SAK_RS07090	SAK_1409	-1.141324963	0.18748101	1392455	1392790	-	336	-
1496	SAK_RS07530	SAK_1496	-1.138127261	0.169868628	1491473	1492393	-	921	-
609	SAK_RS03035	SAK_0609	-1.137617049	0.169868628	550495	550875	-	381	-
1442	#N/A	SAK_1442	-1.136796835	0.184091563	1425799	1426641	-	843	-
140	SAK_RS00690	SAK_0140	-1.13343611	0.174968901	99890	100309	+	420	-
389	SAK_RS01930	SAK_0389	-1.123348852	0.18958454	338179	340134	+	1956	stk1
2134	SAK_RS10750	SAK_2134	-1.113379892	0.189174312	2124951	2125430	-	480	-
1586	#N/A	SAK_1586	-1.105354361	0.174968901	1582038	1583130	-	1093	serC
1067	SAK_RS05335	SAK_1067	-1.105307905	0.174968901	1037659	1038147	-	489	-
328	SAK_RS01620	SAK_0328	-1.10483702	0.187140104	273285	273863	+	579	-
163	SAK_RS00805	SAK_0163	-1.101632964	0.184091563	121207	122526	+	1320	-
173	SAK_RS00855	SAK_0173	-1.096695269	0.184091563	132770	133456	+	687	-
1752	SAK_RS08810	SAK_1752	-1.0947966	0.174968901	1744576	1745475	-	900	-
703	SAK_RS03515	SAK_0703	-1.091863331	0.188667224	636258	636845	-	588	-
1354	SAK_RS06815	SAK_1354	-1.090156487	0.184091563	1336645	1337640	-	996	fni
379	SAK_RS01880	SAK_0379	-1.089565725	0.189335928	328345	329085	+	741	-
1487	SAK_RS07480	SAK_1487	-1.088966164	0.180357604	1476583	1477779	-	1197	-
1709	SAK_RS08605	SAK_1709	-1.085206833	0.174309267	1699638	1699868	-	231	-
564	SAK_RS02810	SAK_0564	-1.084425328	0.186437602	507187	508677	-	1491	-
339	SAK_RS01680	SAK_0339	-1.082649715	0.196880977	283032	283574	+	543	-
1623	SAK_RS08185	SAK_1623	-1.082491255	0.21112807	1612031	1612963	+	933	-
1441	#N/A	SAK_1441	-1.082009324	0.184091563	1422341	1425622	-	3282	-
1383	SAK_RS06960	SAK_1383	-1.081106469	0.178270806	1369959	1371029	-	1071	-
186	SAK_RS00925	SAK_0186	-1.074681808	0.180357604	145690	149184	-	3495	bag
1903	SAK_RS09580	SAK_1903	-1.073363903	0.184091563	1907128	1908165	+	1038	-
1714	#N/A	SAK_1714	-1.070949133	0.189062541	1701570	1702637	-	1068	pepP
826	SAK_RS04135	SAK_0826	-1.068332409	0.209867819	769867	770484	+	618	eda
1146	SAK_RS05730	SAK_1146	-1.06704191	0.189335928	1124235	1125113	-	879	-
1951	#N/A	SAK_1951	-1.066891121	0.203123056	1947346	1948100	-	755	-
2053	SAK_RS10325	SAK_2053	-1.063074959	0.198989025	2045239	2046654	+	1416	-
2126	SAK_RS10710	SAK_2126	-1.053113469	0.198989025	2117043	2118068	-	1026	trpS
1203	SAK_RS06020	SAK_1203	-1.047111918	0.196880977	1180017	1180904	-	888	rarD
478	SAK_RS02385	SAK_0478	-1.043994059	0.189062541	422216	423259	+	1044	-
582	SAK_RS02900	SAK_0582	-1.043168221	0.186437602	525183	525857	+	675	-
948	SAK_RS04740	SAK_0948	-1.04175284	0.186437602	901887	903140	+	1254	-
1392	SAK_RS07005	SAK_1392	-1.03685998	0.189335928	1376017	1377264	-	1248	-
2017	SAK_RS10150	SAK_2017	-1.036401097	0.202067542	2011446	2012408	-	963	-
1549	SAK_RS07810	SAK_1549	-1.033551836	0.196880977	1545552	1546088	+	537	-
1967	SAK_RS09900	SAK_1967	-1.032438849	0.202774204	1957698	1958552	-	855	-
604	SAK_RS03010	SAK_0604	-1.030342034	0.197739438	547082	547921	+	840	-
1096	SAK_RS05480	SAK_1096	-1.030251319	0.186437602	1067026	1067616	-	591	-
1044	SAK_RS05220	SAK_1044	-1.029882045	0.200328935	1013550	1014383	+	834	-
1011	SAK_RS05060	SAK_1011	-1.028757386	0.186437602	975759	976130	+	372	-
977	SAK_RS04890	SAK_0977	-1.026951523	0.189335928	933565	934704	+	1140	glgC
1748	SAK_RS08790	SAK_1748	-1.024161428	0.189335928	1739087	1740805	-	1719	cydD
1823	SAK_RS09180	SAK_1823	-1.021982338	0.198989025	1817089	1818606	-	1518	-
682	#N/A	SAK_0682	-1.021492125	0.196880977	616918	617694	+	777	-
1904	SAK_RS09585	SAK_1904	-1.014205176	0.193916283	1908165	1908662	+	498	-
1469	SAK_RS07385	SAK_1469	-1.013945972	0.19854204	1451297	1452283	-	987	-
461	SAK_RS02295	SAK_0461	-1.010371101	0.196408987	405695	406309	+	615	-
470	SAK_RS02340	SAK_0470	-1.005653859	0.198989025	415419	416561	+	1143	tgt
353	SAK_RS01750	SAK_0353	-1.005178603	0.197046947	298513	300117	+	1605	-
1366	SAK_RS06875	SAK_1366	-1.00371058	0.198989025	1350099	1351448	-	1350	gdhA
1877	SAK_RS09450	SAK_1877	-1.003321104	0.204619869	1875572	1877041	-	1470	-
183	SAK_RS00905	SAK_0183	-1.002783792	0.198989025	142732	143616	+	885	-
671	SAK_RS03355	SAK_0671	-1.001472151	0.204619869	604247	605695	-	1449	-
1405	SAK_RS07070	SAK_1405	-1.000091083	0.210300662	1387827	1389041	-	1215	thiI
300	SAK_RS01480	SAK_0300	-0.999664559	0.198981738	255974	256624	-	651	-
504	SAK_RS02515	SAK_0504	-0.998394239	0.199504128	450375	450911	+	537	-
354	SAK_RS01755	SAK_0354	-0.995522938	0.210934582	300325	301710	-	1386	-
1235	SAK_RS06195	SAK_1235	-0.994315897	0.203643304	1207480	1208103	+	624	-
1242	SAK_RS06230	SAK_1242	-0.993676405	0.208367958	1211510	1213969	-	2460	parC
1508	SAK_RS07595	SAK_1508	-0.992604573	0.198989025	1504831	1505223	+	393	gloA
1836	SAK_RS09245	SAK_1836	-0.991688972	0.201357963	1830094	1830711	-	618	-
941	SAK_RS04705	SAK_0941	-0.989538239	0.209510112	892696	894147	+	1452	-
958	SAK_RS04795	SAK_0958	-0.983282249	0.216258089	913647	914213	+	567	-
1698	SAK_RS08550	SAK_1698	-0.983191902	0.198989025	1686150	1687157	-	1008	-
320	SAK_RS01580	SAK_0320	-0.98157816	0.21112807	265841	267331	+	1491	-
233	SAK_RS01150	SAK_0233	-0.980792039	0.212001013	200981	201955	+	975	-
1151	SAK_RS05755	SAK_1151	-0.975675075	0.203643304	1128433	1129266	-	834	-
1042	SAK_RS05210	SAK_1042	-0.975574751	0.21112807	1012256	1012897	+	642	-
1223	SAK_RS06135	SAK_1223	-0.974333911	0.210934582	1196365	1196907	-	543	-
1948	SAK_RS09810	SAK_1948	-0.97374758	0.254233211	1944822	1945316	+	495	-
1158	SAK_RS05795	SAK_1158	-0.970834959	0.202774204	1136826	1137428	-	603	-
1313	SAK_RS06585	SAK_1313	-0.970134093	0.221542766	1291572	1292168	+	597	-
2015	SAK_RS10140	SAK_2015	-0.967239187	0.212456086	2009726	2010529	-	804	-

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1194	SAK_RS05975	SAK_1194	-0.965471448	0.209510112	1172715	1173491	-	777	potC
1750	SAK_RS08800	SAK_1750	-0.963000806	0.21112807	1741825	1743252	-	1428	cydA
1140	SAK_RS05700	SAK_1140	-0.962293089	0.210538919	1116194	1116532	-	339	-
1700	SAK_RS08560	SAK_1700	-0.959242989	0.212001013	1689920	1690867	-	948	manA
1621	SAK_RS08175	SAK_1621	-0.958516777	0.215204656	1610893	1611636	-	744	-
327	SAK_RS01615	SAK_0327	-0.955141792	0.209510112	272625	273185	+	561	-
1629	SAK_RS08215	SAK_1629	-0.953594313	0.209510112	1618877	1619380	-	504	-
613	SAK_RS03055	SAK_0613	-0.949566937	0.212213114	552166	552501	-	336	-
1168	SAK_RS05845	SAK_1168	-0.948260891	0.21519047	1144913	1146148	+	1236	-
867	SAK_RS04335	SAK_0867	-0.946926844	0.215204656	812037	812948	+	912	-
1861	#N/A	SAK_1861	-0.945730012	0.227732614	1857986	1859126	-	1141	-
1382	SAK_RS06955	SAK_1382	-0.945542347	0.215204656	1369023	1369946	-	924	panE
1188	SAK_RS05945	SAK_1188	-0.944467876	0.21112807	1165263	1166699	-	1437	arb
2070	SAK_RS10415	SAK_2070	-0.941784451	0.255198773	2063651	2066191	-	2541	-
854	SAK_RS04275	SAK_0854	-0.9414358	0.21112807	802540	803352	-	813	-
812	SAK_RS04065	SAK_0812	-0.941047485	0.242071372	754648	755319	+	672	-
1684	SAK_RS08480	SAK_1684	-0.940978962	0.217198349	1670972	1671469	-	498	-
1213	SAK_RS06075	SAK_1213	-0.939186988	0.248542053	1189245	1189931	-	687	-
885	SAK_RS04425	SAK_0885	-0.939077126	0.21112807	829735	832530	+	2796	ppc
329	SAK_RS01625	SAK_0329	-0.938642934	0.214828534	273906	274586	+	681	-
1747	SAK_RS08785	SAK_1747	-0.935501195	0.215204656	1737346	1739094	-	1749	cydC
589	SAK_RS02935	SAK_0589	-0.935135603	0.212001013	531861	532316	-	456	-
404	SAK_RS02005	SAK_0404	-0.927871077	0.239137121	354031	354957	-	927	-
1635	SAK_RS08240	SAK_1635	-0.927729497	0.266994845	1626200	1627102	-	903	dnaI
142	SAK_RS00700	SAK_0142	-0.927687216	0.230277253	101110	101802	+	693	-
1352	SAK_RS06805	SAK_1352	-0.92582636	0.218821478	1335459	1336313	+	855	-
1756	SAK_RS08830	SAK_1756	-0.921056476	0.220157415	1751340	1753325	-	1986	tkt
919	SAK_RS04595	SAK_0919	-0.918974967	0.230277253	870721	871977	+	1257	-
352	SAK_RS01745	SAK_0352	-0.918754947	0.217175681	297775	298509	+	735	-
257	SAK_RS01265	SAK_0257	-0.918159049	0.230277253	220089	222119	+	2031	-
206	SAK_RS01020	SAK_0206	-0.915798258	0.227290649	169047	170702	+	1656	-
1553	SAK_RS07830	SAK_1553	-0.912557755	0.219354656	1551359	1552162	+	804	-
939	SAK_RS04695	SAK_0939	-0.905236451	0.240729169	890955	891713	+	759	-
1336	SAK_RS06725	SAK_1336	-0.905150307	0.227290649	1320422	1322530	+	2109	clpL
1268	SAK_RS06360	SAK_1268	-0.904619043	0.217383842	1238627	1239034	-	408	arsC
1644	SAK_RS08285	SAK_1644	-0.90064557	0.229172068	1634280	1635659	+	1380	-
923	SAK_RS04615	SAK_0923	-0.898464737	0.239137121	874902	875582	+	681	-
2093	SAK_RS10545	SAK_2093	-0.897888466	0.230277253	2083694	2084659	+	966	-
393	SAK_RS01950	SAK_0393	-0.895876626	0.230277253	342682	344082	+	1401	-
715	SAK_RS03575	SAK_0715	-0.892861874	0.237386666	648187	649470	+	1284	aroA
537	SAK_RS02670	SAK_0537	-0.889269215	0.239137121	480563	482044	+	1482	galT
2033	SAK_RS10230	SAK_2033	-0.888006739	0.233731862	2025345	2026604	-	1260	cinA
326	SAK_RS01610	SAK_0326	-0.885524489	0.247354993	271834	272052	+	219	-
1353	SAK_RS06810	SAK_1353	-0.884730477	0.244276007	1336359	1336577	-	219	-
1365	SAK_RS06870	SAK_1365	-0.884557017	0.230277253	1349619	1350029	-	411	def
1771	SAK_RS08915	SAK_1771	-0.882332999	0.23112401	1764952	1766142	+	1191	cfa
1842	SAK_RS09275	SAK_1842	-0.88144307	0.244627648	1837633	1838451	+	819	-
1157	SAK_RS05790	SAK_1157	-0.881052515	0.231453519	1135096	1136814	-	1719	-
940	SAK_RS04700	SAK_0940	-0.880600276	0.227732614	891798	892361	-	564	-
1749	SAK_RS08795	SAK_1749	-0.871249202	0.242022895	1740805	1741824	-	1020	cydB
2007	SAK_RS10095	SAK_2007	-0.870412499	0.242071899	2000452	2002092	-	1641	-
1535	SAK_RS07735	SAK_1535	-0.870225923	0.263815242	1530741	1531595	-	855	-
1280	SAK_RS06420	SAK_1280	-0.86662199	0.266164941	1252098	1253324	-	1227	-
1029	SAK_RS05155	SAK_1029	-0.866256576	0.243200988	999057	999695	-	639	-
1193	SAK_RS05970	SAK_1193	-0.860825259	0.249943584	1171649	1172722	-	1074	potD
1768	SAK_RS08905	SAK_1768	-0.859684222	0.266063731	1763152	1763562	-	411	-
355	SAK_RS01760	SAK_0355	-0.857944162	0.242286709	301851	302654	+	804	proB
1784	SAK_RS08980	SAK_1784	-0.851754357	0.24114476	1776787	1777296	-	510	-
1733	SAK_RS08715	SAK_1733	-0.851237382	0.249909389	1722624	1723106	+	483	-
1219	#N/A	SAK_1219	-0.851155293	0.255198773	1193976	1194738	-	763	-
560	SAK_RS02790	SAK_0560	-0.850260699	0.244627648	502296	502811	+	516	-
387	SAK_RS01920	SAK_0387	-0.846099177	0.242504335	336082	337404	+	1323	sun
1178	SAK_RS05895	SAK_1178	-0.845726209	0.257690003	1156776	1157660	-	885	-
1763	#N/A	SAK_1763	-0.840726104	0.264006972	1759082	1759565	-	484	-
460	SAK_RS02290	SAK_0460	-0.839169584	0.244627648	405379	405585	+	207	-
786	SAK_RS03920	SAK_0786	-0.834667929	0.298535565	723252	724403	+	1152	-
79	SAK_RS00390	SAK_0079	-0.825737631	0.253003725	60969	62360	+	1392	-
927	SAK_RS04635	SAK_0927	-0.82369308	0.258110751	878350	879501	+	1152	-
1699	SAK_RS08555	SAK_1699	-0.823669798	0.263815242	1687283	1689811	-	2529	secA
929	SAK_RS04645	SAK_0929	-0.823668576	0.258110751	880516	882321	+	1806	pepB
1646	SAK_RS08295	SAK_1646	-0.822846717	0.263815942	1636378	1637208	-	831	-
518	#N/A	SAK_0518	-0.820077185	0.278581315	462673	463375	+	703	-
1846	SAK_RS09295	SAK_1846	-0.819664164	0.255364611	1841801	1842442	+	642	-
1103	SAK_RS05515	SAK_1103	-0.817712172	0.261634673	1076472	1077233	-	762	-
647	SAK_RS03240	SAK_0647	-0.817022343	0.266063731	576381	580502	+	4122	-
1012	SAK_RS05065	SAK_1012	-0.816315293	0.266063731	976155	976535	+	381	-
805	SAK_RS04015	SAK_0805	-0.815315688	0.292945589	743195	746419	+	3225	-
1557	SAK_RS07850	SAK_1557	-0.814813085	0.263815242	1555029	1555676	+	648	-
1080	SAK_RS05400	SAK_1080	-0.814350899	0.271605064	1051800	1052480	-	681	ciaR
1821	SAK_RS09170	SAK_1821	-0.81324603	0.258110751	1814563	1816170	-	1608	-
597	SAK_RS02975	SAK_0597	-0.810494293	0.260062546	540785	542125	+	1341	xseA
1789	SAK_RS09005	SAK_1789	-0.808653108	0.274842775	1781408	1782277	-	870	-
1928	SAK_RS09710	SAK_1928	-0.803547385	0.266063731	1931360	1931920	-	561	-
1138	SAK_RS05690	SAK_1138	-0.803537277	0.266063731	1113250	1114470	-	1221	-
904	SAK_RS04520	SAK_0904	-0.798574004	0.279696141	853493	854257	-	765	-
1847	SAK_RS09300	SAK_1847	-0.798050839	0.279696141	1842456	1842947	+	492	-
1655	SAK_RS08340	SAK_1655	-0.797900471	0.283096027	1646841	1647665	-	825	-
1624	SAK_RS08190	SAK_1624	-0.794870942	0.266063731	1613163	1613828	-	666	-
1739	SAK_RS08745	SAK_1739	-0.793880519	0.266063731	1729021	1729980	+	960	-
599	SAK_RS02985	SAK_0599	-0.792829788	0.278581315	542318	543190	+	873	-
673	SAK_RS03365	SAK_0673	-0.792128065	0.282108519	606547	607245	-	699	-
1317	#N/A	SAK_1317	-0.790163413	0.293571626	1293992	1295098	+	1107	-
1478	SAK_RS07430	SAK_1478	-0.789639724	0.279696141	1463653	1465125	+	1473	-

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1931	#N/A	SAK_1931	-0.787463467	0.283723286	1933607	1934065	-	459	-
1745	SAK_RS08775	SAK_1745	-0.78559312	0.280903297	1735876	1736235	+	360	-
1613	SAK_RS08135	SAK_1613	-0.780467171	0.300124568	1605607	1606128	-	522	-
1081	SAK_RS05405	SAK_1081	-0.779959802	0.279696141	1052642	1055191	-	2550	pepN
1991	SAK_RS10020	SAK_1991	-0.779901745	0.294807681	1979631	1984346	+	4716	cspA
1479	SAK_RS07435	SAK_1479	-0.777624506	0.296193317	1465170	1465634	-	465	-
1908	SAK_RS09610	SAK_1908	-0.777338429	0.280903297	1912497	1913324	-	828	-
150	SAK_RS00740	SAK_0150	-0.776607578	0.296680325	109721	110497	+	777	truA
1020	SAK_RS05105	SAK_1020	-0.776080481	0.291985895	985611	986276	+	666	-
2128	SAK_RS10720	SAK_2128	-0.77530512	0.278501194	2119225	2119983	+	759	-
375	SAK_RS01860	SAK_0375	-0.774239612	0.282428037	323367	324830	+	1464	-
1528	SAK_RS07700	SAK_1528	-0.771606472	0.283723286	1524153	1524959	-	807	-
1116	SAK_RS05580	SAK_1116	-0.769853315	0.312810888	1088829	1089479	-	651	-
1891	SAK_RS09520	SAK_1891	-0.769453109	0.280116719	1891163	1893316	-	2154	-
1729	SAK_RS08695	SAK_1729	-0.768336841	0.280903297	1718036	1718347	-	312	-
1147	SAK_RS05735	SAK_1147	-0.76579255	0.281628814	1125082	1125900	-	819	-
378	SAK_RS01875	SAK_0378	-0.761649492	0.325649365	327462	328358	+	897	-
1115	SAK_RS05575	SAK_1115	-0.755394176	0.289155078	1088525	1088818	-	294	-
1843	SAK_RS09280	SAK_1843	-0.753606976	0.300124568	1838448	1839704	+	1257	-
382	SAK_RS01895	SAK_0382	-0.751074466	0.296680325	330809	331513	+	705	-
724	SAK_RS03620	SAK_0724	-0.750904169	0.314120856	663365	663934	+	570	-
1596	SAK_RS08050	SAK_1596	-0.746167708	0.309186324	1590704	1591657	-	954	livM
1079	SAK_RS05395	SAK_1079	-0.742754162	0.302376522	1050503	1051816	-	1314	ciaH
1309	SAK_RS06565	SAK_1309	-0.736866454	0.306331783	1288166	1288933	+	768	-
1628	SAK_RS08210	SAK_1628	-0.733796386	0.337156514	1616988	1618790	-	1803	-
468	SAK_RS02330	SAK_0468	-0.733746373	0.307124171	413441	414478	+	1038	-
1331	SAK_RS06700	SAK_1331	-0.7329157	0.302376522	1313445	1314650	-	1206	-
771	SAK_RS03845	SAK_0771	-0.732060269	0.312810888	707062	707394	+	333	-
569	SAK_RS02835	SAK_0569	-0.731301673	0.329037947	512072	513301	+	1230	-
1192	SAK_RS05965	SAK_1192	-0.727292985	0.314120856	1170008	1171540	-	1533	-
1104	SAK_RS05520	SAK_1104	-0.726441149	0.314120856	1077230	1078204	-	975	-
882	SAK_RS04410	SAK_0882	-0.726269797	0.311620626	826771	827295	+	525	-
1972	SAK_RS09925	SAK_1972	-0.724902685	0.307885744	1961014	1961349	-	336	-
2001	SAK_RS10070	SAK_2001	-0.721126878	0.309186324	1995471	1995860	+	390	-
1370	SAK_RS06895	SAK_1370	-0.719966195	0.314120856	1355746	1356219	-	474	-
855	SAK_RS04280	SAK_0855	-0.719387825	0.310271221	803352	804254	-	903	-
1406	SAK_RS07075	SAK_1406	-0.71822779	0.332109337	1389043	1390188	-	1146	-
967	SAK_RS04840	SAK_0967	-0.715351071	0.316713977	921200	921772	+	573	-
1438	SAK_RS07235	SAK_1438	-0.712344399	0.318368259	1419218	1419889	-	672	-
467	SAK_RS02325	SAK_0467	-0.711345077	0.322082233	412753	413439	+	687	-
1150	SAK_RS05750	SAK_1150	-0.711272108	0.318368259	1127237	1128436	-	1200	-
1226	SAK_RS06150	SAK_1226	-0.710271786	0.324383904	1197763	1198011	-	249	-
674	SAK_RS03370	SAK_0674	-0.705722931	0.334457577	607413	608177	+	765	-
356	SAK_RS01765	SAK_0356	-0.700604602	0.319858607	302664	303917	+	1254	proA
1546	SAK_RS07790	SAK_1546	-0.700382778	0.333925851	1541300	1542682	-	1383	-
775	SAK_RS03865	SAK_0775	-0.700290374	0.319858607	709858	711066	-	1209	-
1572	SAK_RS07930	SAK_1572	-0.699587642	0.333925851	1567338	1568771	-	1434	-
1061	SAK_RS05305	SAK_1061	-0.69863221	0.320325033	1031449	1031838	+	390	-
8	SAK_RS00035	SAK_0008	-0.695579084	0.322082233	6244	9741	+	3498	mfd
1980	SAK_RS09965	SAK_1980	-0.694161135	0.333925851	1966867	1967427	+	561	-
1095	SAK_RS05475	SAK_1095	-0.693132957	0.333925851	1065721	1066992	-	1272	-
1433	SAK_RS07210	SAK_1433	-0.689800949	0.338891996	1415549	1416115	-	567	-
1529	SAK_RS07705	SAK_1529	-0.688289198	0.348691911	1525281	1525757	-	477	-
80	SAK_RS00395	SAK_0080	-0.68822025	0.337156514	62382	63680	+	1299	purB
602	SAK_RS03000	SAK_0602	-0.68450704	0.357672905	544482	546140	+	1659	recN
1160	SAK_RS05805	SAK_1160	-0.684006505	0.338371963	1138412	1139668	-	1257	glyA
1303	SAK_RS06535	SAK_1303	-0.683256693	0.331194488	1280746	1281480	-	735	-
920	SAK_RS04600	SAK_0920	-0.683205712	0.347745702	872078	873142	+	1065	-
1968	#N/A	SAK_1968	-0.679506048	0.337156514	1958731	1959282	-	552	-
1208	SAK_RS06045	SAK_1208	-0.677703241	0.333925851	1184888	1185277	-	390	-
1064	SAK_RS05320	SAK_1064	-0.675272067	0.338891996	1034491	1035825	+	1335	gid
2120	SAK_RS10680	SAK_2120	-0.673635147	0.361401132	2110786	2111490	+	705	-
495	SAK_RS02470	SAK_0495	-0.67103416	0.350222564	436296	437060	+	765	-
516	SAK_RS02565	SAK_0516	-0.670855655	0.341207848	457819	459012	-	1194	-
717	SAK_RS03585	SAK_0717	-0.670698671	0.337371643	650032	651405	+	1374	-
2062	SAK_RS10375	SAK_2062	-0.670361186	0.355988703	2053828	2055192	+	1365	-
190	SAK_RS00945	SAK_0190	-0.670061689	0.337865636	152094	152483	-	390	-
768	SAK_RS03825	SAK_0768	-0.668210589	0.359463977	704649	705386	+	738	aphA
541	SAK_RS02690	SAK_0541	-0.663957788	0.341207848	484457	484846	+	390	-
401	SAK_RS01990	SAK_0401	-0.662659197	0.35618514	349589	352045	+	2457	-
2060	#N/A	SAK_2060	-0.661923631	0.359463977	2052557	2053087	+	531	-
1804	SAK_RS09080	SAK_1804	-0.66185982	0.34235069	1795257	1796039	-	783	-
1463	SAK_RS07355	SAK_1463	-0.660697693	0.348691911	1446539	1446916	+	378	mscL
933	SAK_RS04665	SAK_0933	-0.660684845	0.348691911	885155	885640	+	486	-
189	SAK_RS00940	SAK_0189	-0.660354347	0.353715599	151237	151890	-	654	-
723	SAK_RS03615	SAK_0723	-0.659662279	0.349408151	661088	662956	+	1869	-
505	SAK_RS02520	SAK_0505	-0.658203008	0.347724174	450887	451720	+	834	-
857	SAK_RS04290	SAK_0857	-0.654696797	0.357672905	804521	805564	+	1044	-
1888	SAK_RS09505	SAK_1888	-0.649058133	0.361849546	1889010	1889942	-	933	lacC
1477	SAK_RS07425	SAK_1477	-0.64890957	0.359463977	1462586	1463422	+	837	-
1864	SAK_RS09385	SAK_1864	-0.648173087	0.363265583	1860646	1861647	-	1002	-
1230	SAK_RS06170	SAK_1230	-0.645166309	0.369303033	1201619	1202944	-	1326	uraA
1503	SAK_RS07570	SAK_1503	-0.644789007	0.36260743	1499232	1499810	-	579	-
299	SAK_RS01475	SAK_0299	-0.642744321	0.355988703	254731	255912	+	1182	-
1547	SAK_RS07795	SAK_1547	-0.642539881	0.359463977	1542690	1543904	-	1215	-
502	SAK_RS02505	SAK_0502	-0.640575723	0.359836159	446733	449900	+	3168	-
1767	SAK_RS08900	SAK_1767	-0.640112622	0.36260743	1762351	1763142	-	792	-
273	SAK_RS01345	SAK_0273	-0.638621021	0.359871121	238007	238525	+	519	-
2112	SAK_RS10640	SAK_2112	-0.637267996	0.377045864	2103146	2104390	-	1245	-
1737	SAK_RS08735	SAK_1737	-0.63720527	0.360887437	1727278	1728207	-	930	-
1969	SAK_RS09910	SAK_1969	-0.634815025	0.359463977	1959323	1959712	-	390	-
158	SAK_RS00780	SAK_0158	-0.634525409	0.362173577	117327	118253	+	927	-
1614	SAK_RS08140	SAK_1614	-0.633177489	0.359836159	1606110	1607084	-	975	rdgB

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584	SAK_RS02910	SAK_0584	-0.632272785	0.392230658	526477	526731	+	255	-	
823	SAK_RS04120	SAK_0823	-0.630518862	0.363265583	766209	767234	+	1026	-	
1109	SAK_RS05545	SAK_1109	-0.62609849	0.38710259	1081846	1082418	-	573	-	
2043	SAK_RS10275	SAK_2043	-0.625036454	0.370243472	2036653	2036961	+	309	-	
1139	SAK_RS05695	SAK_1139	-0.624582176	0.36260743	1114522	1116063	-	1542	-	
653	SAK_RS03270	SAK_0653	-0.62368496	0.374613962	583718	585049	+	1332	-	
2039	SAK_RS10255	SAK_2039	-0.622573389	0.363265583	2031322	2031525	+	204	-	
175	SAK_RS00865	SAK_0175	-0.621695071	0.369303033	134151	135221	+	1071	-	
1885	SAK_RS09490	SAK_1885	-0.620111081	0.369303033	1886135	1886986	-	852	-	
820	SAK_RS04105	SAK_0820	-0.619788369	0.389673739	762322	763380	+	1059	-	
220	SAK_RS01090	SAK_0220	-0.616222284	0.389673739	183414	184445	-	1032	-	
1550	SAK_RS07815	SAK_1550	-0.615147105	0.373480294	1546064	1546897	+	834	-	
907	SAK_RS04535	SAK_0907	-0.612002675	0.381308016	855869	858106	+	2238	-	
1468	SAK_RS07380	SAK_1468	-0.611669171	0.374613962	1450133	1451260	+	1128	-	
769	SAK_RS03830	SAK_0769	-0.611283531	0.374364869	705707	706225	+	519	-	
1949	SAK_RS09815	SAK_1949	-0.610752176	0.383912208	1945603	1946553	-	951	-	
1118	SAK_RS05590	SAK_1118	-0.606816742	0.380758797	1090513	1090827	-	315	-	
1985	SAK_RS09990	SAK_1985	-0.603617691	0.389673739	1971503	1972588	+	1086	-	
1962	SAK_RS09875	SAK_1962	-0.602425957	0.389503316	1953613	1953921	+	309	-	
895	SAK_RS04475	SAK_0895	-0.602217441	0.386708435	844282	844968	+	687	-	
1610	SAK_RS08120	SAK_1610	-0.601491542	0.383424343	1603700	1604407	-	708	scpA	
1143	SAK_RS05715	SAK_1143	-0.60042731	0.437406181	1119716	1121191	-	1476	-	
144	SAK_RS00710	SAK_0144	-0.600397352	0.383424343	102548	103123	+	576	-	
2016	SAK_RS10145	SAK_2016	-0.599408083	0.389673739	2010534	2011430	-	897	-	
1870	SAK_RS09415	SAK_1870	-0.599079494	0.393182791	1868987	1869571	-	585	-	
1349	SAK_RS06790	SAK_1349	-0.597160448	0.397705743	1333259	1333708	+	450	-	
139	SAK_RS00685	SAK_0139	-0.594337662	0.393182791	99119	99670	+	552	-	
444	SAK_RS02205	SAK_0444	-0.591693241	0.396827784	390584	391003	-	420	-	
672	SAK_RS03360	SAK_0672	-0.5907607	0.397050486	605840	606550	-	711	-	
1564	SAK_RS07885	SAK_1564	-0.590138611	0.390415625	1559774	1560730	-	957	-	
1241	SAK_RS06225	SAK_1241	-0.589909957	0.389673739	1210375	1211397	-	1023	ilvE	
143	SAK_RS00705	SAK_0143	-0.589465028	0.386719411	101799	102551	+	753	-	
1647	SAK_RS08300	SAK_1647	-0.589160674	0.389673739	1637201	1638877	-	1677	-	
1302	SAK_RS06530	SAK_1302	-0.587503882	0.389673739	1276819	1280577	-	3759	-	
1666	SAK_RS08390	SAK_1666	-0.587115484	0.389894774	1655092	1655496	-	405	-	
1702	SAK_RS08570	SAK_1702	-0.585428079	0.393182791	1691934	1693853	-	1920	-	
439	SAK_RS02180	SAK_0439	-0.584893825	0.390415625	386573	387805	+	1233	-	
1389	SAK_RS06990	SAK_1389	-0.584399105	0.389673739	1373721	1375232	-	1512	-	
376	SAK_RS01865	SAK_0376	-0.581750894	0.391880121	325055	325537	-	483	luxS	
76	SAK_RS00375	SAK_0076	-0.581552861	0.393261066	57802	59064	+	1263	purD	
1484	SAK_RS07465	SAK_1484	-0.580954714	0.392230658	1472120	1473604	-	1485	asp2	
1266	SAK_RS06350	SAK_1266	-0.580681628	0.393261066	1236521	1237777	-	1257	-	
1075	SAK_RS05375	SAK_1075	-0.580513209	0.392230658	1046983	1047756	-	774	-	
1368	SAK_RS06885	SAK_1368	-0.579611443	0.393046772	1352166	1353935	-	1770	-	
1519	SAK_RS07645	SAK_1519	-0.578573152	0.403729819	1515703	1516524	-	822	mutM	
464	SAK_RS02310	SAK_0464	-0.577672507	0.402048856	409921	410361	+	441	-	
1551	SAK_RS07820	SAK_1551	-0.574046929	0.397322395	1546946	1548661	-	1716	pabB	
1606	SAK_RS08100	SAK_1606	-0.568159074	0.397322395	1600693	1602132	+	1440	-	
1351	SAK_RS06800	SAK_1351	-0.567833994	0.397322395	1334444	1335358	+	915	-	
666	SAK_RS03330	SAK_0666	-0.566554521	0.407384536	598289	600220	+	1932	fbp	
1166	SAK_RS05835	SAK_1166	-0.564757289	0.40553778	1143322	1144269	+	948	-	
852	SAK_RS04265	SAK_0852	-0.563971454	0.403729819	800069	800893	+	825	-	
238	SAK_RS01170	SAK_0238	-0.563075512	0.404184446	204299	204964	+	666	-	
184	SAK_RS00915	SAK_0184	-0.562822619	0.404184446	144017	145039	+	1023	-	
540	SAK_RS02685	SAK_0540	-0.560818283	0.402048856	484041	484424	+	384	-	
1070	SAK_RS05350	SAK_1070	-0.560067074	0.399828584	1040055	1042010	+	1956	-	
2059	SAK_RS10360	SAK_2059	-0.557643169	0.401016245	2050792	2052057	+	1266	-	
395	SAK_RS01960	SAK_0395	-0.556280724	0.410665403	344487	345263	-	777	-	
2000	SAK_RS10065	SAK_2000	-0.553401009	0.409530285	1995055	1995438	+	384	-	
1381	SAK_RS06950	SAK_1381	-0.55261246	0.406829589	1367177	1368811	-	1635	-	
325	SAK_RS01605	SAK_0325	-0.551466546	0.407384536	271250	271831	+	582	-	
66	SAK_RS00325	SAK_0066	-0.550513087	0.42275996	48882	49580	+	699	-	
1548	SAK_RS07800	SAK_1548	-0.548546121	0.416134775	1544162	1545067	+	906	-	
284	SAK_RS01400	SAK_0284	-0.545655962	0.409530285	245277	246152	+	876	-	
630	#N/A	SAK_0630	-0.545493232	0.412963943	563613	563987	+	375	-	
252	SAK_RS01240	SAK_0252	-0.544952303	0.416126638	214845	216473	+	1629	-	
513	SAK_RS02550	SAK_0513	-0.544749143	0.418555119	455178	456020	-	843	-	
716	SAK_RS03580	SAK_0716	-0.543790983	0.412963943	649463	649975	+	513	aroK	
949	SAK_RS04745	SAK_0949	-0.543212372	0.428155813	903173	904255	-	1083	-	
274	SAK_RS01350	SAK_0274	-0.54169843	0.419985019	238618	239478	+	861	-	
191	SAK_RS00950	SAK_0191	-0.540019138	0.418901076	152516	152899	-	384	-	
725	SAK_RS03625	SAK_0725	-0.539782899	0.4426257	663973	665928	-	1956	-	
1970	SAK_RS09915	SAK_1970	-0.539437224	0.419109253	1959745	1960128	-	384	-	
1780	SAK_RS08960	SAK_1780	-0.53469351	0.416126638	1773382	1773789	-	408	rimI	
438	SAK_RS02175	SAK_0438	-0.529277039	0.429366831	385670	386281	+	612	-	
1504	SAK_RS07575	SAK_1504	-0.5274548	0.419985019	1499920	1501962	-	2043	-	
1255	SAK_RS06295	SAK_1255	-0.52737341	0.437268869	1226719	1227858	-	1140	cpsH	
1060	SAK_RS05300	SAK_1060	-0.526059142	0.428215382	1031033	1031416	+	384	-	
1587	SAK_RS08005	SAK_1587	-0.523932544	0.42491063	1583263	1583898	+	636	-	
1618	SAK_RS08160	SAK_1618	-0.523593802	0.434509782	1609051	1609572	-	522	-	
974	SAK_RS04875	SAK_0974	-0.521221017	0.453339242	928126	929145	+	1020	-	
2040	SAK_RS10260	SAK_2040	-0.518728843	0.437406181	2031582	2034158	-	2577	hexA	
746	SAK_RS03725	SAK_0746	-0.518246189	0.428155813	682200	683489	+	1290	-	
1295	SAK_RS06495	SAK_1295	-0.513044123	0.437406181	1270846	1271607	-	762	-	
685	SAK_RS03425	SAK_0685	-0.509967613	0.437406181	620156	621676	+	1521	adcA	
1133	SAK_RS05665	SAK_1133	-0.50988279	0.437406181	1108212	1109288	-	1077	carA	
1806	SAK_RS09090	SAK_1806	-0.508384342	0.444472343	1796512	1796904	-	393	-	
1289	SAK_RS06465	SAK_1289	-0.507607277	0.437406181	1262931	1263719	-	789	-	
1332	SAK_RS06705	SAK_1332	-0.507030146	0.443650852	1314702	1315193	-	492	-	
164	SAK_RS00810	SAK_0164	-0.50621638	0.437406181	122833	123999	-	1167	-	
975	SAK_RS04880	SAK_0975	-0.504013449	0.438924756	929149	931449	+	2301	pulA	
1058	SAK_RS05290	SAK_1058	-0.503350144	0.437406181	1028621	1029583	+	963	-	
1668	SAK_RS08400	SAK_1668	-0.502470628	0.440310941	1656441	1657550	-	1110	-	

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1883	SAK_RS09480	SAK_1883	-0.501454142	0.437406181	1883165	1884772	-	1608	dexB
1755	SAK_RS08825	SAK_1755	-0.501419557	0.437406181	1749430	1751202	-	1773	-
865	SAK_RS04325	SAK_0865	-0.501321193	0.45236022	810935	811366	+	432	-
1272	SAK_RS06380	SAK_1272	-0.50127168	0.441295796	1242062	1242850	-	789	estA
1394	SAK_RS07015	SAK_1394	-0.499770544	0.444703166	1377992	1379236	-	1245	-
1209	SAK_RS06050	SAK_1209	-0.498814544	0.444703166	1185310	1185693	-	384	-
707	SAK_RS03535	SAK_0707	-0.496686398	0.450634609	639241	639801	+	561	-
1592	SAK_RS08030	SAK_1592	-0.491572243	0.450520948	1587120	1588286	+	1167	-
868	SAK_RS04340	SAK_0868	-0.491127979	0.444703166	813078	814364	+	1287	-
405	SAK_RS02010	SAK_0405	-0.490976031	0.452216367	355048	355692	-	645	-
915	SAK_RS04575	SAK_0915	-0.490197193	0.457529636	864912	866780	+	1869	bglF
1901	SAK_RS09570	SAK_1901	-0.489444292	0.453116083	1904103	1906505	+	2403	cpdB
2071	SAK_RS10420	SAK_2071	-0.48882584	0.453435595	2066175	2066918	-	744	-
1333	SAK_RS06710	SAK_1333	-0.487624677	0.450520948	1315207	1318818	-	3612	-
1486	SAK_RS07475	SAK_1486	-0.485654589	0.458649575	1475230	1476459	-	1230	secY
574	SAK_RS02860	SAK_0574	-0.4851891	0.463008407	515783	516163	+	381	-
1393	SAK_RS07010	SAK_1393	-0.482800246	0.45733362	1377279	1377989	-	711	-
804	SAK_RS04010	SAK_0804	-0.482281831	0.450634609	740435	743092	+	2658	-
1480	SAK_RS07445	SAK_1480	-0.479641794	0.463008407	1465917	1467242	-	1326	-
1907	SAK_RS09605	SAK_1907	-0.47823809	0.45733362	1910710	1912359	-	1650	-
970	SAK_RS04855	SAK_0970	-0.475630722	0.458649575	923933	924853	+	921	-
264	SAK_RS01300	SAK_0264	-0.475370506	0.45733362	229768	231027	+	1260	-
1807	SAK_RS09095	SAK_1807	-0.471464986	0.461785074	1796895	1798187	-	1293	-
1027	SAK_RS05145	SAK_1027	-0.47079102	0.466148493	995041	997833	+	2793	-
931	SAK_RS04655	SAK_0931	-0.467370715	0.466148493	883252	883923	+	672	-
1293	SAK_RS06485	SAK_1293	-0.465782007	0.460483732	1265935	1268499	-	2565	-
1545	SAK_RS07785	SAK_1545	-0.465519568	0.463008407	1539800	1540966	+	1167	-
462	SAK_RS02300	SAK_0462	-0.465396936	0.469526376	406324	407136	+	813	-
442	SAK_RS02195	SAK_0442	-0.464733635	0.463008407	388920	390227	+	1308	-
1565	#N/A	SAK_1565	-0.461982394	0.475217088	1560727	1561178	-	452	-
739	SAK_RS03685	SAK_0739	-0.461804711	0.468042129	677023	678276	+	1254	-
605	SAK_RS03015	SAK_0605	-0.459978642	0.480237822	547896	548498	+	603	-
832	SAK_RS04165	SAK_0832	-0.459150723	0.471980658	776757	777842	-	1086	pepQ
884	SAK_RS04420	SAK_0884	-0.457649032	0.469042005	827727	829526	-	1800	pepF
2130	SAK_RS10730	SAK_2130	-0.456955861	0.468042129	2121791	2124370	+	2580	-
1171	SAK_RS05860	SAK_1171	-0.455886711	0.472597599	1148404	1148985	-	582	xpt
1695	SAK_RS08535	SAK_1695	-0.455754547	0.468042129	1683038	1684576	-	1539	-
567	#N/A	SAK_0567	-0.455502949	0.485252851	510460	510954	+	495	-
1017	SAK_RS05090	SAK_1017	-0.452664652	0.468042129	980303	984415	+	4113	-
258	SAK_RS01270	SAK_0258	-0.450690381	0.490942785	222341	223966	+	1626	-
1641	SAK_RS08270	SAK_1641	-0.447881305	0.471521343	1631959	1632849	-	891	htpX
2005	SAK_RS10085	SAK_2005	-0.44660197	0.476356331	1997178	1999499	-	2322	pbp2A
813	SAK_RS04070	SAK_0813	-0.446195835	0.480237822	755376	756794	-	1419	-
1288	SAK_RS06460	SAK_1288	-0.44289733	0.476488284	1261819	1262922	-	1104	-
1602	SAK_RS08080	SAK_1602	-0.437776831	0.486830579	1595755	1596924	-	1170	-
1712	#N/A	SAK_1712	-0.435544956	0.486583435	1700640	1700804	-	165	-
254	SAK_RS01250	SAK_0254	-0.434997999	0.489124242	217560	218381	+	822	-
2116	SAK_RS10660	SAK_2116	-0.433505977	0.487863691	2107028	2107690	-	663	-
385	SAK_RS01910	SAK_0385	-0.432659805	0.497852608	332720	335110	+	2391	priA
1341	SAK_RS06750	SAK_1341	-0.431647401	0.489124242	1326482	1327111	+	630	-
766	SAK_RS03815	SAK_0766	-0.428373444	0.489124242	702564	704069	+	1506	-
1772	SAK_RS08920	SAK_1772	-0.428031702	0.487863691	1766212	1766937	-	726	-
1472	SAK_RS07400	SAK_1472	-0.424582132	0.493924087	1454694	1456958	-	2265	glgP
819	SAK_RS04100	SAK_0819	-0.422827072	0.497962232	761245	762129	-	885	-
449	SAK_RS02235	SAK_0449	-0.421932723	0.524571353	394760	395395	+	636	trmB
1149	SAK_RS05745	SAK_1149	-0.421751771	0.493966213	1126254	1127240	-	987	-
995	SAK_RS04980	SAK_0995	-0.418922229	0.499498032	951128	952030	-	903	-
370	SAK_RS01835	SAK_0370	-0.41820611	0.497962232	317852	320098	-	2247	-
680	SAK_RS03400	SAK_0680	-0.417072075	0.497962232	615266	615679	-	414	-
1782	SAK_RS08970	SAK_1782	-0.416077419	0.5009368	1774662	1774892	+	231	-
1422	SAK_RS07155	SAK_1422	-0.415187668	0.497962232	1402873	1404093	-	1221	pepT
1897	SAK_RS09550	SAK_1897	-0.414061411	0.497880737	1897387	1899969	-	2583	-
1443	SAK_RS07255	SAK_1443	-0.41360975	0.497962232	1426660	1427229	-	570	lepB
1475	SAK_RS07415	SAK_1475	-0.412523316	0.497962232	1459871	1461118	+	1248	-
458	SAK_RS02280	SAK_0458	-0.412228291	0.497962232	402675	403091	+	417	copY
936	SAK_RS04680	SAK_0936	-0.411867996	0.497962232	889160	889978	+	819	-
1686	SAK_RS08490	SAK_1686	-0.411519678	0.49758321	1672802	1673350	-	549	-
1515	SAK_RS07625	SAK_1515	-0.409951044	0.497962232	1511293	1512462	-	1170	-
1217	SAK_RS06100	SAK_1217	-0.408765481	0.497962232	1192750	1193244	-	495	tpx
1793	SAK_RS09025	SAK_1793	-0.404801998	0.532636863	1786426	1786839	-	414	rpsL
149	SAK_RS00735	SAK_0149	-0.403570493	0.499584173	108403	109650	+	1248	-
2023	SAK_RS10180	SAK_2023	-0.402972969	0.499205114	2017037	2017969	-	933	-
1021	SAK_RS05115	SAK_1021	-0.402621577	0.501545822	987960	988376	+	417	ndk
573	SAK_RS02855	SAK_0573	-0.399885648	0.503657759	514803	515771	+	969	-
1088	SAK_RS05440	SAK_1088	-0.398904726	0.501545822	1060494	1061804	-	1311	-
1787	SAK_RS08995	SAK_1787	-0.398432083	0.502682512	1779275	1779814	-	540	-
1820	SAK_RS09165	SAK_1820	-0.397947719	0.506137551	1813155	1814246	-	1092	-
2006	SAK_RS10090	SAK_2006	-0.396454375	0.501778249	1999543	2000427	+	885	-
1218	SAK_RS06105	SAK_1218	-0.394174809	0.509985189	1193317	1193976	-	660	-
1936	SAK_RS09750	SAK_1936	-0.391194235	0.509402173	1936188	1936658	-	471	-
2061	SAK_RS10370	SAK_2061	-0.390348572	0.506587663	2053173	2053844	+	672	-
1560	SAK_RS07865	SAK_1560	-0.386893333	0.513600141	1556684	1557238	-	555	-
2135	SAK_RS10755	SAK_2135	-0.385574149	0.513600141	2125631	2126860	+	1230	htrA
1625	SAK_RS08195	SAK_1625	-0.382202099	0.514353126	1613852	1614709	-	858	-
1310	SAK_RS06570	SAK_1310	-0.379220511	0.516188383	1288992	1290332	-	1341	-
1532	SAK_RS07720	SAK_1532	-0.378493111	0.515435879	1527953	1529725	-	1773	-
678	SAK_RS03390	SAK_0678	-0.377438514	0.518575552	613483	614040	-	558	-
1575	SAK_RS07945	SAK_1575	-0.376166232	0.519259366	1570565	1571902	-	1338	brnQ
965	SAK_RS04830	SAK_0965	-0.375290759	0.519259366	919059	919730	+	672	thiE
1862	SAK_RS09375	SAK_1862	-0.375281463	0.519259366	1859250	1859894	+	645	-
1259	SAK_RS06315	SAK_1259	-0.374976252	0.518449108	1230310	1231008	-	699	cpsD
821	SAK_RS04110	SAK_0821	-0.371172559	0.520767451	763394	764386	+	993	ldhA
1000	SAK_RS05005	SAK_1000	-0.370180249	0.520859367	961521	963431	+	1911	-

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294	SAK_RS01450	SAK_0294	-0.368875666	0.523208403	252254	252640	+	387	-
1490	SAK_RS07495	SAK_1490	-0.367794018	0.521763611	1479882	1481123	-	1242	-
620	SAK_RS03100	SAK_0620	-0.36773083	0.527759204	558375	559244	+	870	-
972	SAK_RS04865	SAK_0972	-0.359329456	0.528012075	925507	926016	+	510	-
1107	SAK_RS05535	SAK_1107	-0.358974695	0.52891986	1079971	1080732	-	762	rnhB
1227	SAK_RS06155	SAK_1227	-0.357509399	0.53366742	1198059	1198304	-	246	-
1380	SAK_RS06945	SAK_1380	-0.357182696	0.533783615	1365798	1367033	-	1236	-
1838	SAK_RS09255	SAK_1838	-0.354117328	0.532636863	1831366	1832658	-	1293	purA
1271	SAK_RS06375	SAK_1271	-0.346124368	0.539716597	1241262	1241972	-	711	-
1506	SAK_RS07585	SAK_1506	-0.345176269	0.542197233	1502960	1503802	-	843	-
517	SAK_RS02570	SAK_0517	-0.34458493	0.542197233	459256	462318	+	3063	-
1723	SAK_RS08665	SAK_1723	-0.343202217	0.542285989	1712228	1713352	+	1125	mutY
1678	SAK_RS08450	SAK_1678	-0.342142084	0.544008878	1663081	1663968	-	888	-
1989	SAK_RS10010	SAK_1989	-0.341779716	0.545689223	1978303	1978626	-	324	-
938	SAK_RS04690	SAK_0938	-0.338491393	0.54890596	890737	890952	+	216	-
1187	SAK_RS05940	SAK_1187	-0.336709464	0.547151512	1164039	1165172	-	1134	-
1369	SAK_RS06890	SAK_1369	-0.334841913	0.550221141	1353940	1355679	-	1740	-
195	SAK_RS00965	SAK_0195	-0.327337447	0.554895886	155947	157821	+	1875	-
799	SAK_RS03985	SAK_0799	-0.318648488	0.561984187	735195	737390	+	2196	cylI
1800	SAK_RS09060	SAK_1800	-0.314342479	0.567346933	1792496	1793347	-	852	-
1744	SAK_RS08770	SAK_1744	-0.312307349	0.568216735	1733587	1735872	+	2286	pepX
161	SAK_RS00795	SAK_0161	-0.310099844	0.570306978	119056	120420	+	1365	radA
1404	SAK_RS07065	SAK_1404	-0.307232424	0.573476498	1386547	1387725	-	1179	-
1802	SAK_RS09070	SAK_1802	-0.306595293	0.573503238	1794251	1794700	-	450	-
570	SAK_RS02840	SAK_0570	-0.305580492	0.573476498	513414	514046	+	633	nth
556	SAK_RS02770	SAK_0556	-0.303425751	0.575797889	498010	499083	+	1074	-
1019	SAK_RS05100	SAK_1019	-0.302988015	0.575797889	985283	985624	+	342	-
400	SAK_RS01985	SAK_0400	-0.302888205	0.575797889	348107	349408	+	1302	-
1583	SAK_RS07985	SAK_1583	-0.30004237	0.578408334	1579647	1580123	-	477	-
2106	SAK_RS10610	SAK_2106	-0.296707189	0.579666834	2097997	2098536	-	540	-
1817	SAK_RS09150	SAK_1817	-0.293582404	0.581973303	1807342	1809069	-	1728	proWX
2034	SAK_RS10235	SAK_2034	-0.292502849	0.5814861	2026693	2027244	-	552	tag
1261	SAK_RS06325	SAK_1261	-0.29187914	0.582872033	1231720	1232451	-	732	cpsB
1375	SAK_RS06920	SAK_1375	-0.289999572	0.584622965	1360788	1361321	-	534	-
338	SAK_RS01675	SAK_0338	-0.288747312	0.584927671	281765	282913	+	1149	nagA
634	SAK_RS03170	SAK_0634	-0.288141795	0.587220305	566972	567160	+	189	-
837	SAK_RS04190	SAK_0837	-0.287974171	0.616490813	783490	785433	+	1944	thrS
2026	SAK_RS10195	SAK_2026	-0.285957228	0.587100557	2020496	2021983	-	1488	-
2037	SAK_RS10250	SAK_2037	-0.285277015	0.587220305	2029123	2031096	-	1974	mutL
1705	SAK_RS08585	SAK_1705	-0.279769562	0.607926001	1696528	1696962	-	435	nusB
1224	SAK_RS06140	SAK_1224	-0.270800047	0.61265392	1196963	1197157	-	195	-
1225	SAK_RS06145	SAK_1225	-0.269419035	0.601167844	1197167	1197748	-	582	-
667	SAK_RS03335	SAK_0667	-0.26460897	0.606149569	600310	601434	+	1125	-
1541	SAK_RS07765	SAK_1541	-0.263693166	0.60341954	1535384	1536328	-	945	nikB
784	#N/A	SAK_0784	-0.261637861	0.607926001	721133	721803	+	671	-
1566	SAK_RS07900	SAK_1566	-0.261248473	0.607926001	1561417	1562115	-	699	fabG
1493	#N/A	SAK_1493	-0.261091311	0.608091239	1483672	1487448	-	3777	-
697	#N/A	SAK_0697	-0.259901455	0.595259316	629936	630097	-	162	-
1854	SAK_RS09335	SAK_1854	-0.259738399	0.608859416	1849628	1851160	+	1533	ahpF
735	#N/A	SAK_0735	-0.258299749	0.600771152	673376	673477	+	102	-
445	SAK_RS02210	SAK_0445	-0.254528514	0.612067594	391339	391842	+	504	-
1410	SAK_RS07095	SAK_1410	-0.252906902	0.61268019	1392874	1394040	-	1167	aroC
477	SAK_RS02380	SAK_0477	-0.252643877	0.61268019	421413	422084	+	672	-
1657	SAK_RS08350	SAK_1657	-0.250255502	0.613572805	1648741	1649430	-	690	-
1507	SAK_RS07590	SAK_1507	-0.246420175	0.613572805	1504069	1504743	+	675	-
414	SAK_RS02055	SAK_0414	-0.240871457	0.622226103	363873	365225	-	1353	-
702	SAK_RS03510	SAK_0702	-0.239282902	0.621791	634905	636206	+	1302	-
690	SAK_RS03450	SAK_0690	-0.236403453	0.626520219	624960	625235	+	276	-
1253	SAK_RS06285	SAK_1253	-0.232926255	0.618316546	1224764	1225711	-	948	-
1065	SAK_RS05325	SAK_1065	-0.231357681	0.629771049	1035903	1036646	+	744	-
208	SAK_RS01030	SAK_0208	-0.230825613	0.63032143	171745	172776	+	1032	-
1626	SAK_RS08200	SAK_1626	-0.229290592	0.63047464	1614870	1616330	-	1461	-
1398	SAK_RS07035	SAK_1398	-0.228887831	0.598337748	1382915	1383805	-	891	-
1307	SAK_RS06555	SAK_1307	-0.224921736	0.633311761	1284549	1286183	+	1635	-
1538	SAK_RS07750	SAK_1538	-0.224297806	0.636817348	1533135	1533815	-	681	nikE
665	#N/A	SAK_0665	-0.222104407	0.633388531	597277	598137	-	861	-
1135	SAK_RS05675	SAK_1135	-0.221649503	0.633388531	1110390	1111682	-	1293	pyrC
1170	SAK_RS05855	SAK_1170	-0.221221404	0.633388531	1147130	1148404	-	1275	pbuX
1024	SAK_RS05130	SAK_1024	-0.221091991	0.633283275	993347	993982	+	636	-
1016	SAK_RS05085	SAK_1016	-0.220633867	0.634665719	979244	979915	+	672	-
1994	SAK_RS10035	SAK_1994	-0.220498069	0.633311761	1986743	1987351	+	609	-
1619	SAK_RS08165	SAK_1619	-0.219721577	0.633388531	1609640	1610329	-	690	-
1439	SAK_RS07240	SAK_1439	-0.219241792	0.633388531	1419879	1420754	-	876	-
1742	SAK_RS08760	SAK_1742	-0.218785495	0.633283275	1731546	1732748	-	1203	-
374	SAK_RS01855	SAK_0374	-0.218353816	0.63374025	322200	323354	+	1155	-
2045	SAK_RS10285	SAK_2045	-0.215645972	0.634665719	2037968	2038912	-	945	-
756	SAK_RS03770	SAK_0756	-0.21498597	0.634665719	687988	691107	+	3120	-
431	SAK_RS02140	SAK_0431	-0.211822806	0.63897958	379501	380493	+	993	-
872	SAK_RS04360	SAK_0872	-0.206693872	0.642932998	817571	818680	+	1110	ribD
1278	SAK_RS06410	SAK_1278	-0.206630472	0.639571324	1249573	1250292	-	720	budA
1654	SAK_RS08335	SAK_1654	-0.20652259	0.64350579	1645331	1646707	-	1377	-
1495	SAK_RS07525	SAK_1495	-0.204180632	0.64350579	1489421	1491412	-	1992	uvrB
1860	SAK_RS09365	SAK_1860	-0.202570216	0.64350579	1856957	1857940	+	984	-
676	SAK_RS03380	SAK_0676	-0.199224809	0.646971279	610883	612076	+	1194	-
1631	SAK_RS08225	SAK_1631	-0.198328915	0.647978304	1620807	1621424	-	618	-
1204	SAK_RS06025	SAK_1204	-0.197207931	0.647978304	1180891	1181757	-	867	thrB
1325	SAK_RS06655	SAK_1325	-0.196552079	0.647031011	1307631	1308866	+	1236	-
1026	SAK_RS05140	SAK_1026	-0.195282518	0.649850644	994455	994889	+	435	msrB
1530	SAK_RS07710	SAK_1530	-0.19393147	0.650369234	1525949	1526752	+	804	-
1872	SAK_RS09425	SAK_1872	-0.191915932	0.650587689	1871641	1872900	-	1260	-
351	SAK_RS01740	SAK_0351	-0.191511054	0.649850644	297450	297755	+	306	-
463	SAK_RS02305	SAK_0463	-0.19128827	0.647978304	407249	409891	+	2643	polA
443	SAK_RS02200	SAK_0443	-0.190103363	0.647978304	390291	390587	-	297	-

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776	SAK_RS03870	SAK_0776	-0.189646196	0.648432892	711448	713112	+	1665	-
1704	SAK_RS08580	SAK_1704	-0.189302214	0.650587689	1695479	1696441	+	963	scrR
1751	SAK_RS08805	SAK_1751	-0.18899753	0.647978304	1743355	1744563	-	1209	-
1481	SAK_RS07450	SAK_1481	-0.187007074	0.653554576	1467235	1468743	-	1509	-
1766	SAK_RS08895	SAK_1766	-0.186520652	0.650720644	1761779	1762309	-	531	-
1284	SAK_RS06440	SAK_1284	-0.184074381	0.654578158	1255748	1258993	+	3246	hylB
559	SAK_RS02785	SAK_0559	-0.184064775	0.654578158	501190	502296	+	1107	-
493	SAK_RS02460	SAK_0493	-0.182899316	0.653637317	433797	434573	-	777	recX
494	SAK_RS02465	SAK_0494	-0.181391548	0.653554576	434672	436027	+	1356	rumA
801	SAK_RS03995	SAK_0801	-0.181283749	0.653554576	738614	739150	+	537	cylK
1717	SAK_RS08635	SAK_1717	-0.178827609	0.654578158	1705290	1708118	-	2829	uvrA
1841	SAK_RS09270	SAK_1841	-0.178630812	0.656245803	1835257	1837509	+	2253	-
681	SAK_RS03405	SAK_0681	-0.177069102	0.656245803	615833	616723	+	891	-
636	SAK_RS03180	SAK_0636	-0.176033319	0.656453622	568764	569228	+	465	-
1853	SAK_RS09330	SAK_1853	-0.175596478	0.650587689	1849050	1849610	+	561	ahpC
243	SAK_RS01195	SAK_0243	-0.174746928	0.650369234	207758	208081	+	324	-
1542	SAK_RS07770	SAK_1542	-0.174434391	0.658832859	1536315	1537931	-	1617	nikA
782	SAK_RS03900	SAK_0782	-0.172876688	0.659404293	719698	720303	+	606	-
1304	SAK_RS06540	SAK_1304	-0.172559995	0.659260455	1281495	1282079	-	585	-
501	SAK_RS02500	SAK_0501	-0.170390388	0.660223813	444502	446670	+	2169	-
714	SAK_RS03570	SAK_0714	-0.16898553	0.660430834	646894	647958	-	1065	-
1413	SAK_RS07110	SAK_1413	-0.168977855	0.660223813	1395879	1397036	-	1158	-
1260	SAK_RS06320	SAK_1260	-0.165767582	0.659404293	1231019	1231711	-	693	cpsC
1996	SAK_RS10045	SAK_1996	-0.162858194	0.668875802	1990319	1991566	+	1248	-
1429	SAK_RS07190	SAK_1429	-0.159485582	0.670007976	1411414	1412067	-	654	-
269	SAK_RS01325	SAK_0269	-0.159462407	0.667446107	235251	235433	+	183	-
711	SAK_RS03555	SAK_0711	-0.156213856	0.670007976	644328	644813	-	486	-
1298	SAK_RS06510	SAK_1298	-0.155780266	0.67138155	1273220	1274458	-	1239	-
1966	SAK_RS09895	SAK_1966	-0.154432884	0.670007976	1956402	1957019	-	618	-
207	SAK_RS01025	SAK_0207	-0.150677798	0.676716444	170821	171735	+	915	oppD
1489	SAK_RS07490	SAK_1489	-0.149301317	0.67138155	1478708	1479892	-	1185	-
1305	SAK_RS06545	SAK_1305	-0.146687291	0.6772854	1282176	1283582	-	1407	pepV
850	SAK_RS04255	SAK_0850	-0.141114127	0.668875802	795642	799181	+	3540	smc
1436	SAK_RS07225	SAK_1436	-0.138844243	0.650587689	1417758	1418342	-	585	-
1567	SAK_RS07905	SAK_1567	-0.13867276	0.688848576	1562108	1562344	-	237	-
1670	SAK_RS08410	SAK_1670	-0.135681102	0.669650812	1657821	1658555	-	735	-
1320	SAK_RS06630	SAK_1320	-0.133634627	0.691219602	1298934	1302386	-	3453	scpB
523	SAK_RS02600	SAK_0523	-0.133228676	0.656453622	465273	467333	+	2061	-
1212	SAK_RS06070	SAK_1212	-0.133132197	0.691902938	1188130	1189137	-	1008	-
913	SAK_RS04565	SAK_0913	-0.132237908	0.685080408	863122	863730	+	609	sodA
89	SAK_RS00440	SAK_0089	-0.130780633	0.686174933	74513	75793	+	1281	-
598	SAK_RS02980	SAK_0598	-0.126178293	0.71158824	542103	542318	+	216	xseB
881	SAK_RS04405	SAK_0881	-0.122619469	0.694814146	825766	826614	-	849	-
2036	SAK_RS10245	SAK_2036	-0.121341476	0.682297755	2027859	2029091	-	1233	-
210	SAK_RS01040	SAK_0210	-0.118843404	0.697497622	173835	174767	+	933	oppF
897	SAK_RS04485	SAK_0897	-0.118547687	0.695032281	846862	848406	+	1545	prfC
1574	SAK_RS07940	SAK_1574	-0.118343406	0.695507173	1569505	1570200	-	696	-
1022	SAK_RS05120	SAK_1022	-0.116025769	0.701437319	988512	990344	+	1833	lepA
2087	#N/A	SAK_2087	-0.114254372	0.702908417	2079069	2079638	-	570	-
1599	SAK_RS08065	SAK_1599	-0.113236608	0.698411751	1593956	1594201	-	246	-
951	SAK_RS04755	SAK_0951	-0.111485388	0.697322328	905116	905613	+	498	-
773	SAK_RS03855	SAK_0773	-0.109257252	0.703892491	708384	708659	-	276	-
906	SAK_RS04530	SAK_0906	-0.098608024	0.716779715	855232	855885	+	654	-
858	SAK_RS04295	SAK_0858	-0.096322328	0.720840527	805669	807831	+	2163	-
1921	SAK_RS09675	SAK_1921	-0.093488055	0.717597902	1924888	1926543	-	1656	-
1584	SAK_RS07990	SAK_1584	-0.088249627	0.725150213	1580178	1581359	-	1182	-
1588	SAK_RS08010	SAK_1588	-0.08320107	0.725010628	1584168	1585031	-	864	-
930	SAK_RS04650	SAK_0930	-0.079695503	0.725612393	882516	883142	+	627	-
848	SAK_RS04245	SAK_0848	-0.076327632	0.735891975	794404	794772	+	369	-
1865	SAK_RS09390	SAK_1865	-0.072150841	0.729509685	1861727	1862671	-	945	-
1173	SAK_RS05870	SAK_1173	-0.066935743	0.720597296	1150426	1151766	-	1341	-
1919	SAK_RS09665	SAK_1919	-0.061908763	0.725612393	1921678	1922508	-	831	rgfB
767	SAK_RS03820	SAK_0767	-0.058411758	0.725010628	704319	704531	+	213	-
1043	SAK_RS05215	SAK_1043	-0.053842209	0.746216659	1012907	1013536	+	630	-
1337	SAK_RS06730	SAK_1337	-0.049261157	0.756013166	1322624	1323568	-	945	mmuM
12	SAK_RS00055	SAK_0012	-0.049175939	0.729830767	10799	12085	+	1287	-
1156	SAK_RS05785	SAK_1156	-0.047044112	0.744868906	1133362	1135095	-	1734	-
88	SAK_RS00435	SAK_0088	-0.04571302	0.755394479	72918	74408	+	1491	thrC
330	SAK_RS01630	SAK_0330	-0.045265404	0.749248104	274846	275793	-	948	-
1732	SAK_RS08710	SAK_1732	-0.043261158	0.756013166	1720089	1722509	+	2421	-
1997	SAK_RS10050	SAK_1997	-0.042511239	0.75494372	1991609	1992418	-	810	-
1066	SAK_RS05330	SAK_1066	-0.042220739	0.759935601	1036779	1037627	+	849	-
498	SAK_RS02485	SAK_0498	-0.040236728	0.758261297	441613	442521	+	909	-
1167	SAK_RS05840	SAK_1167	-0.036690912	0.762004457	1144287	1144889	+	603	-
2111	SAK_RS10635	SAK_2111	-0.036559653	0.75494372	2101861	2103144	-	1284	-
496	SAK_RS02475	SAK_0496	-0.03483266	0.742144265	437094	437522	+	429	-
535	SAK_RS02660	SAK_0535	-0.03422256	0.754165972	477087	479288	+	2202	-
847	SAK_RS04240	SAK_0847	-0.032870371	0.767716542	793592	794401	+	810	-
899	SAK_RS04495	SAK_0899	-0.028108489	0.768457736	848993	849727	+	735	-
2094	SAK_RS10550	SAK_2094	-0.027652743	0.75494372	2084998	2086164	+	1167	-
1494	#N/A	SAK_1494	-0.023576462	0.758489942	1487831	1489323	+	1493	-
718	SAK_RS03590	SAK_0718	-0.018710185	0.768846129	651506	652861	+	1356	rumA
1292	SAK_RS06480	SAK_1292	-0.018048786	0.758608044	1265294	1265812	-	519	apt
1172	SAK_RS05865	SAK_1172	-0.015632779	0.768466917	1149240	1150223	-	984	guaC
1483	SAK_RS07460	SAK_1483	-0.014744646	0.77734695	1471131	1472123	-	993	asp3
1622	SAK_RS08180	SAK_1622	-0.014274868	0.774224194	1611668	1611946	+	279	-
1990	SAK_RS10015	SAK_1990	-0.008448113	0.783946375	1978616	1979308	-	693	-
1920	SAK_RS09670	SAK_1920	-0.005466183	0.790842059	1922547	1924730	-	2184	-
1053	SAK_RS05265	SAK_1053	-0.000783161	0.767716542	1022111	1023481	+	1371	nox
827	SAK_RS04140	SAK_0827	0.006778494	0.803281809	770501	771901	+	1401	uxaC
1690	SAK_RS08510	SAK_1690	0.009496105	0.768535779	1676314	1677696	-	1383	-
737	SAK_RS03670	SAK_0737	0.013246374	0.790842059	674690	675055	+	366	-
722	#N/A	SAK_0722	0.013491596	0.80123095	654904	660228	+	5325	-

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218	SAK_RS01080	SAK_0218	0.014173891	0.801399041	181691	182401	+	711	adcC
1269	SAK_RS06365	SAK_1269	0.016561348	0.798575081	1239085	1240296	-	1212	deoB
362	SAK_RS01795	SAK_0362	0.016615119	0.790842059	310141	310953	+	813	-
1205	SAK_RS06030	SAK_1205	0.017902944	0.808557912	1181759	1183042	-	1284	hom
1431	SAK_RS07200	SAK_1431	0.023907149	0.754165972	1413179	1413967	-	789	pflA
1211	SAK_RS06065	SAK_1211	0.024530554	0.813648074	1186680	1188056	-	1377	-
710	SAK_RS03550	SAK_0710	0.031296895	0.806112633	643666	644307	+	642	serB
1598	#N/A	SAK_1598	0.031491128	0.809601261	1592635	1593801	-	1167	livK
482	SAK_RS02405	SAK_0482	0.034581454	0.820363131	425814	426629	+	816	-
660	SAK_RS03300	SAK_0660	0.034987949	0.815439636	590323	591543	-	1221	-
324	SAK_RS01600	SAK_0324	0.038688395	0.787363092	270039	270389	+	351	-
1014	SAK_RS05075	SAK_1014	0.04172686	0.815439636	977761	978498	+	738	-
1207	#N/A	SAK_1207	0.043482882	0.813648074	1184129	1184866	-	738	-
1912	SAK_RS09630	SAK_1912	0.045764087	0.808018227	1915327	1916379	-	1053	-
1653	SAK_RS08330	SAK_1653	0.045784301	0.823482079	1644268	1645338	-	1071	-
457	SAK_RS02275	SAK_0457	0.050593189	0.824716875	401507	402511	-	1005	-
1358	SAK_RS06835	SAK_1358	0.058038438	0.824716875	1340542	1341771	-	1230	-
1321	SAK_RS06635	SAK_1321	0.05864016	0.813710336	1302923	1303948	-	1026	-
244	SAK_RS01200	SAK_0244	0.058645393	0.831771161	208114	208740	+	627	-
1283	SAK_RS06435	SAK_1283	0.059978048	0.813759978	1255047	1255529	-	483	mutX
1727	SAK_RS08685	SAK_1727	0.06058739	0.837397003	1715067	1717406	-	2340	-
1559	SAK_RS07860	SAK_1559	0.063681056	0.768846129	1556415	1556684	-	270	-
209	SAK_RS01035	SAK_0209	0.065684913	0.813710336	172789	173835	+	1047	oppD
2069	SAK_RS10410	SAK_2069	0.067996187	0.842249492	2062058	2063572	+	1515	-
1933	SAK_RS09735	SAK_1933	0.069105753	0.837987743	1934944	1935414	-	471	-
1656	SAK_RS08345	SAK_1656	0.071651311	0.835884371	1647806	1648639	-	834	-
1601	SAK_RS08075	SAK_1601	0.072715782	0.824716875	1595016	1595645	-	630	upp
1652	SAK_RS08325	SAK_1652	0.072844969	0.836057263	1643579	1644271	-	693	metI
546	SAK_RS02715	SAK_0546	0.073168196	0.791821529	486768	487460	+	693	-
2122	SAK_RS10690	SAK_2122	0.075768657	0.837987743	2113016	2113426	+	411	-
877	SAK_RS04385	SAK_0877	0.077470491	0.843925747	822747	823649	+	903	-
1301	SAK_RS06525	SAK_1301	0.080402841	0.844224164	1275768	1276685	-	918	-
950	SAK_RS04750	SAK_0950	0.080665286	0.813648074	904400	905029	+	630	udk
511	SAK_RS02540	SAK_0511	0.081493685	0.837987743	453701	454016	-	316	-
1777	SAK_RS08945	SAK_1777	0.084486755	0.824716875	1770522	1770791	+	270	rpsN
1274	SAK_RS06390	SAK_1274	0.089467652	0.852242343	1244864	1245625	-	762	-
1191	SAK_RS05960	SAK_1191	0.101062103	0.844026277	1169022	1169951	+	930	-
1713	SAK_RS08615	SAK_1713	0.105131823	0.86485475	1701106	1701558	-	453	-
531	SAK_RS02640	SAK_0531	0.107578594	0.866941123	472910	473740	-	831	-
687	SAK_RS03435	SAK_0687	0.108798334	0.868220847	622158	623093	-	936	-
1875	SAK_RS09440	SAK_1875	0.111782044	0.857851698	1874658	1874999	-	342	yajC
194	SAK_RS00960	SAK_0194	0.117512411	0.871012075	154261	155811	-	1551	-
990	SAK_RS04955	SAK_0990	0.117855872	0.744868906	945541	945732	+	192	-
822	SAK_RS04115	SAK_0822	0.121695069	0.880862072	764592	766142	+	1551	-
1427	SAK_RS07180	SAK_1427	0.128199326	0.844224164	1409362	1410387	+	1026	fhuB
1491	SAK_RS07500	SAK_1491	0.128771989	0.868220847	1481120	1482325	-	1206	-
9	SAK_RS00040	SAK_0009	0.130201961	0.877799791	10032	10304	+	273	-
261	SAK_RS01285	SAK_0261	0.130243916	0.878494612	226518	227873	+	1356	ulaA
1923	SAK_RS09685	SAK_1923	0.13094789	0.865709617	1927213	1927869	-	657	phoU
2008	SAK_RS10100	SAK_2008	0.131508246	0.884241512	2002262	2003473	-	1212	deoB
2075	SAK_RS10440	SAK_2075	0.133054552	0.813648074	2070494	2070790	-	297	-
1169	SAK_RS05850	SAK_1169	0.136237429	0.844026277	1146247	1147035	+	789	-
1938	SAK_RS09760	SAK_1938	0.139422529	0.884166911	1937468	1938736	+	1269	-
497	#N/A	SAK_0497	0.144050382	0.893244474	437701	441403	+	3703	scpA
1013	SAK_RS05070	SAK_1013	0.145103661	0.882439255	976627	977757	+	1131	-
2115	SAK_RS10655	SAK_2115	0.146474027	0.893244474	2106106	2106972	-	867	-
1258	SAK_RS06310	SAK_1258	0.14859937	0.874294761	1228909	1230297	-	1389	cpsE
2079	SAK_RS10455	SAK_2079	0.148740463	0.875889185	2072866	2073252	-	387	-
1256	SAK_RS06300	SAK_1256	0.149557676	0.865801714	1227954	1228436	-	483	-
1796	SAK_RS09040	SAK_1796	0.15176649	0.871012075	1788898	1790172	-	1275	-
878	SAK_RS04390	SAK_0878	0.151790988	0.870973876	823685	824326	-	642	-
1183	SAK_RS05920	SAK_1183	0.152700909	0.871167183	1160993	1162108	+	1116	-
86	SAK_RS00425	SAK_0086	0.153231056	0.725612393	68961	71603	+	2643	-
1294	SAK_RS06490	SAK_1294	0.154663053	0.893244474	1268651	1270849	-	2199	recJ
262	SAK_RS01290	SAK_0262	0.154730201	0.871919603	227876	228733	+	858	-
237	SAK_RS01165	SAK_0237	0.159764971	0.890748321	203775	204230	+	456	-
1074	SAK_RS05370	SAK_1074	0.162748148	0.888249397	1045289	1046950	+	1662	-
1813	SAK_RS09130	SAK_1813	0.172426136	0.882439255	1803206	1804393	-	1188	dltS
1642	SAK_RS08275	SAK_1642	0.177320394	0.879569896	1632870	1633424	-	555	-
81	SAK_RS00400	SAK_0081	0.177333208	0.899028989	63833	64741	+	909	-
2051	SAK_RS10315	SAK_2051	0.180120041	0.890748321	2044224	2044838	+	615	cadD
935	SAK_RS04675	SAK_0935	0.180940165	0.87602693	888356	889072	+	717	-
205	SAK_RS01015	SAK_0205	0.181888614	0.871167183	167571	168806	-	1236	-
1978	SAK_RS09955	SAK_1978	0.188528322	0.917868692	1965725	1966339	-	615	-
962	SAK_RS04815	SAK_0962	0.190743806	0.910846078	916794	917474	+	681	-
1858	SAK_RS09355	SAK_1858	0.191286009	0.888249397	1853911	1854864	+	954	-
552	SAK_RS02745	SAK_0552	0.199219037	0.932749146	495079	496071	+	993	asnA
193	SAK_RS00955	SAK_0193	0.200715698	0.910846078	153511	154251	-	741	-
1419	SAK_RS07140	SAK_1419	0.203369236	0.922003891	1401599	1402123	-	525	-
1930	SAK_RS09720	SAK_1930	0.205032118	0.899028989	1932657	1933610	-	954	prmA
1474	SAK_RS07410	SAK_1474	0.205971008	0.922888442	1458587	1459615	-	1029	-
5	#N/A	SAK_0005	0.206834276	0.922888442	4113	4229	+	117	-
1773	SAK_RS08925	SAK_1773	0.209114726	0.940662421	1767064	1767651	-	588	-
1137	SAK_RS05685	SAK_1137	0.210888485	0.930371688	1112336	1113037	-	702	pyrF
1633	SAK_RS08230	SAK_1633	0.213318173	0.899028989	1621589	1624687	-	3099	-
1465	SAK_RS07365	SAK_1465	0.214212726	0.935910013	1447293	1447796	-	504	-
1275	SAK_RS06395	SAK_1275	0.216122026	0.930371688	1245625	1246488	-	864	-
216	SAK_RS01070	SAK_0216	0.216358469	0.922985095	180308	181159	+	852	ipk
1819	SAK_RS09160	SAK_1819	0.221060494	0.860634817	1810687	1813065	-	2379	xpkA
1279	SAK_RS06415	SAK_1279	0.226845972	0.938026098	1250306	1251988	-	1683	budB
1482	SAK_RS07455	SAK_1482	0.227688247	0.899977066	1468757	1471144	-	2388	secA
1775	SAK_RS08935	SAK_1775	0.229998032	0.946168569	1768366	1769538	+	1173	-
1411	SAK_RS07100	SAK_1411	0.230417915	0.956185751	1394041	1395108	-	1068	aroB

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1512	SAK_RS07615	SAK_1512	0.249320982	0.930566507	1508349	1510754	-	2406	rnr
1502	SAK_RS07565	SAK_1502	0.251221827	0.939960034	1497956	1499197	+	1242	pepS
777	SAK_RS03875	SAK_0777	0.256796733	0.958727998	713201	714124	+	924	-
1159	SAK_RS05800	SAK_1159	0.264329642	0.97211807	1137430	1138407	-	978	-
1360	SAK_RS06845	SAK_1360	0.270887129	0.956185751	1342459	1343085	-	627	-
1257	SAK_RS06305	SAK_1257	0.271763938	0.899028989	1228436	1228885	-	450	cpsF
1569	SAK_RS07915	SAK_1569	0.273458005	0.979664465	1562880	1563380	-	501	-
337	SAK_RS01670	SAK_0337	0.278756491	0.958703294	280780	281487	+	708	-
251	SAK_RS01235	SAK_0251	0.279187056	0.983877718	213874	214602	+	729	-
1232	SAK_RS06180	SAK_1232	0.292846306	0.998271181	1204949	1206184	+	1236	-
2104	SAK_RS10600	SAK_2104	0.302569038	0.965660819	2096180	2097052	+	873	sdhA
1231	SAK_RS06175	SAK_1231	0.305380234	0.997385155	1203540	1204886	+	1347	-
843	SAK_RS04220	SAK_0843	0.313045587	0.905796423	789629	790429	-	801	-
1206	SAK_RS06035	SAK_1206	0.314496131	0.965660819	1183219	1184106	+	888	-
1018	SAK_RS05095	SAK_1018	0.314747076	0.991984176	984417	985286	+	870	cas1
705	SAK_RS03525	SAK_0705	0.3148114	0.902602462	637304	637492	+	189	-
656	SAK_RS03280	SAK_0656	0.317298108	0.967027568	586485	586682	+	198	-
796	SAK_RS03970	SAK_0796	0.322325784	0.888511869	731370	732248	+	879	cylB
1814	SAK_RS09135	SAK_1814	0.32541865	0.992070522	1804393	1805067	-	675	dltr
1246	SAK_RS06250	SAK_1246	0.326522086	0.982904517	1217594	1218079	-	486	-
1818	SAK_RS09155	SAK_1818	0.331202029	0.998356824	1809088	1810311	-	1224	proV
1922	SAK_RS09680	SAK_1922	0.332489594	0.977018403	1926536	1927213	-	678	-
1210	#N/A	SAK_1210	0.335156839	0.899028989	1185698	1186537	-	840	-
1164	SAK_RS05825	SAK_1164	0.33674133	0.96381863	1142293	1142862	-	570	tdk
1759	SAK_RS08845	SAK_1759	0.33919626	0.983695175	1754737	1755840	-	1104	-
1981	SAK_RS09970	SAK_1981	0.340814035	0.971385761	1967732	1968595	+	864	-
2030	SAK_RS10215	SAK_2030	0.348638631	0.836057263	2023050	2023316	-	267	-
256	SAK_RS01260	SAK_0256	0.348705436	0.975266079	219180	219806	+	627	-
249	SAK_RS01225	SAK_0249	0.360351174	0.998271181	212507	213247	+	741	-
991	SAK_RS04960	SAK_0991	0.365309586	0.962349065	945807	946664	+	858	endA
1434	SAK_RS07215	SAK_1434	0.369921442	0.940662421	1416108	1417043	-	936	-
1028	SAK_RS05150	SAK_1028	0.370128866	0.940662421	997833	998936	+	1104	-
834	SAK_RS04175	SAK_0834	0.373676764	0.965660819	779188	780654	+	1467	-
838	SAK_RS04195	SAK_0838	0.374930517	1	785655	786359	+	705	-
797	SAK_RS03975	SAK_0797	0.386555381	0.956185751	732245	734248	+	2004	cylE
248	SAK_RS01220	SAK_0248	0.389329462	0.946168569	210781	212526	+	1746	-
380	SAK_RS01885	SAK_0380	0.390517908	0.946168569	329082	330167	+	1086	-
236	#N/A	SAK_0236	0.393014153	0.935910013	203597	203734	+	138	-
1805	SAK_RS09085	SAK_1805	0.395032805	0.941025278	1796221	1796493	-	273	-
922	SAK_RS04610	SAK_0922	0.39735452	0.949139564	873721	874749	-	1029	queA
1245	SAK_RS06245	SAK_1245	0.402066689	0.956185751	1216842	1217495	-	654	ung
794	SAK_RS03960	SAK_0794	0.405969146	0.925643667	729982	730458	+	477	cylZ
1516	SAK_RS07630	SAK_1516	0.413850719	0.930157007	1512658	1514304	-	1647	-
87	SAK_RS00430	SAK_0087	0.420003928	0.946168569	71782	72798	+	1017	adhA
1122	SAK_RS05610	SAK_1122	0.425643421	0.916316381	1093058	1093393	-	336	-
1485	SAK_RS07470	SAK_1485	0.430265981	0.977594383	1473686	1475230	-	1545	asp1
52	SAK_RS00255	SAK_0052	0.431563812	0.905796423	31399	32574	+	1176	-
1190	SAK_RS05955	SAK_1190	0.436166114	0.928467796	1167577	1168398	-	822	-
1982	SAK_RS09975	SAK_1982	0.437224339	0.897979654	1968752	1969054	-	303	-
472	SAK_RS02350	SAK_0472	0.443136378	0.998027208	416986	417525	+	540	-
1117	SAK_RS05585	SAK_1117	0.449994092	0.945372619	1089485	1090321	-	837	-
558	SAK_RS02780	SAK_0558	0.450831664	0.902044497	500561	501139	+	579	-
349	SAK_RS01730	SAK_0349	0.471544444	0.883480502	293697	295127	+	1431	-
167	SAK_RS00825	SAK_0167	0.471729245	0.893244474	126800	127732	-	933	rbsC
10	SAK_RS00045	SAK_0010	0.476455647	0.954369217	10291	10662	+	372	-
1578	SAK_RS07960	SAK_1578	0.480452507	0.888511869	1575271	1575966	-	696	-
1609	SAK_RS08115	SAK_1609	0.480548542	0.868220847	1603119	1603703	-	585	scpB
1892	SAK_RS09525	SAK_1892	0.491959076	0.889086844	1893377	1893652	-	276	-
607	SAK_RS03025	SAK_0607	0.492126964	0.86485475	548964	550106	-	1143	-
1106	SAK_RS05530	SAK_1106	0.492465278	0.905796423	1079402	1079950	-	549	-
1940	SAK_RS09770	SAK_1940	0.498519984	0.87602693	1939326	1940435	-	1110	-
1311	SAK_RS06575	SAK_1311	0.50132566	0.866653114	1290433	1290843	-	411	-
800	SAK_RS03990	SAK_0800	0.502941736	0.999769997	737395	738606	+	1212	cylJ
1577	SAK_RS07955	SAK_1577	0.518675713	0.874412315	1574238	1575113	+	876	-
219	SAK_RS01085	SAK_0219	0.522725571	0.864807312	182391	183203	+	813	adcB
483	SAK_RS02410	SAK_0483	0.525687622	0.897979654	426637	427458	+	822	-
1636	SAK_RS08245	SAK_1636	0.529470459	0.893244474	1627099	1628274	-	1176	-
1531	SAK_RS07715	SAK_1531	0.534283565	0.868220847	1526843	1527829	-	987	-
1281	SAK_RS06425	SAK_1281	0.538214062	0.899028989	1253314	1254504	-	1191	-
1047	SAK_RS05235	SAK_1047	0.539966789	0.852176022	1015795	1016385	+	591	-
1059	SAK_RS05295	SAK_1059	0.543622645	0.837987743	1029646	1030773	-	1128	-
3	SAK_RS00015	SAK_0003	0.546222411	0.877513756	2823	3704	+	882	-
611	SAK_RS03045	SAK_0611	0.54815175	0.871012075	551413	551631	+	219	-
1263	SAK_RS06335	SAK_1263	0.549481319	0.87602693	1234103	1235026	+	924	cpsY
1734	SAK_RS08720	SAK_1734	0.557578534	0.820363131	1723177	1724271	-	1095	dinB
271	SAK_RS01335	SAK_0271	0.568121871	0.893244474	236766	237152	+	387	-
1643	SAK_RS08280	SAK_1643	0.569401948	0.824162512	1633552	1634265	+	714	gidB
675	SAK_RS03375	SAK_0675	0.569925493	0.866914988	608290	610797	+	2508	-
1581	SAK_RS07975	SAK_1581	0.572052581	0.85476476	1578422	1579249	+	828	xth
1262	SAK_RS06330	SAK_1262	0.572916305	0.831771161	1232457	1233914	-	1458	-
657	SAK_RS03285	SAK_0657	0.581722995	0.816677979	586726	587658	-	933	pyrD
1121	SAK_RS05605	SAK_1121	0.583047473	0.844026277	1092693	1093049	-	357	-
1676	SAK_RS08440	SAK_1676	0.585561243	0.893244474	1661319	1662437	-	1119	-
817	SAK_RS04090	SAK_0817	0.591406641	0.842249492	759453	760226	+	774	-
2103	SAK_RS10595	SAK_2103	0.592207888	0.824716875	2095497	2096165	+	669	sdhB
170	SAK_RS00840	SAK_0170	0.593082767	0.824716875	129610	130521	-	912	rbsK
890	SAK_RS04450	SAK_0890	0.593519504	0.830553415	837389	839434	+	2046	-
909	SAK_RS04545	SAK_0909	0.595715251	0.796388389	859052	859996	+	945	-
1282	SAK_RS06430	SAK_1282	0.598550946	0.946168569	1254596	1255057	-	462	-
179	SAK_RS00885	SAK_0179	0.599813939	0.937198569	139079	139996	-	918	-
1316	SAK_RS06600	SAK_1316	0.600166739	0.822652106	1293687	1293977	+	291	-
1880	SAK_RS09465	SAK_1880	0.600841045	0.790842059	1879853	1881379	+	1527	-
1650	#N/A	SAK_1650	0.600852289	0.824716875	1640995	1642361	+	1367	brnQ

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1778	SAK_RS08950	SAK_1778	0.60571468	0.834926041	1771152	1772177	-	1026	ltaE
2065	SAK_RS10390	SAK_2065	0.611720824	0.822089608	2057885	2058883	-	999	argF
1971	SAK_RS09920	SAK_1971	0.626145487	0.813648074	1960419	1961027	-	609	-
1379	SAK_RS06940	SAK_1379	0.626363543	0.837987743	1364924	1365667	-	744	-
978	SAK_RS04895	SAK_0978	0.636068943	0.779316833	934694	935827	+	1134	glgD
554	SAK_RS02755	SAK_0554	0.64209237	0.835884371	496697	497236	+	540	-
706	SAK_RS03530	SAK_0706	0.646146725	0.833442828	637917	639122	+	1206	-
1604	SAK_RS08090	SAK_1604	0.657255992	0.77734695	1597781	1599133	-	1353	-
1119	SAK_RS05595	SAK_1119	0.659105949	0.790842059	1090856	1091401	-	546	-
757	SAK_RS03775	SAK_0757	0.660119851	0.869641502	691104	691829	+	726	-
197	SAK_RS00975	SAK_0197	0.6603321	0.803895886	158826	159581	+	756	-
979	SAK_RS04900	SAK_0979	0.666051959	0.843762494	935824	937254	+	1431	glgA
902	SAK_RS04510	SAK_0902	0.666635335	0.758261297	851463	853049	+	1587	-
432	SAK_RS02145	SAK_0432	0.67224345	0.864453578	380531	380833	-	303	-
1025	SAK_RS05135	SAK_1025	0.673077612	0.802526818	993991	994455	+	465	-
1252	SAK_RS06280	SAK_1252	0.676625069	0.765550026	1223724	1224680	-	957	-
788	SAK_RS03930	SAK_0788	0.67964261	0.884453236	725598	726416	+	819	-
487	#N/A	SAK_0487	0.681275326	0.791177397	432606	432721	+	116	rrfG
754	SAK_RS03765	SAK_0754	0.684575264	0.893244474	687274	687693	+	420	-
846	SAK_RS04235	SAK_0846	0.688288725	0.785157832	792239	793588	+	1350	-
19	#N/A	SAK_0019	0.689040649	0.768846129	21206	21321	+	116	rrfA
1844	SAK_RS09285	SAK_1844	0.689451793	0.732136333	1839844	1840719	+	876	hslO
988	SAK_RS04945	SAK_0988	0.69162582	0.994537468	943969	944205	+	237	-
1918	#N/A	SAK_1918	0.694812656	0.861852711	1921118	1921462	-	345	-
596	SAK_RS02970	SAK_0596	0.708017991	0.747348133	539823	540659	+	837	-
1738	SAK_RS08740	SAK_1738	0.724561823	0.724726709	1728204	1728959	-	756	-
810	SAK_RS04045	SAK_0810	0.728335105	0.756013166	751971	753200	+	1230	-
32	#N/A	SAK_0032	0.733515846	0.756013166	27038	27153	+	116	rrfB
816	SAK_RS04085	SAK_0816	0.738030992	0.755394479	758800	759456	+	657	-
2073	SAK_RS10430	SAK_2073	0.753875947	0.756859352	2067475	2069793	-	2319	-
548	SAK_RS02725	SAK_0548	0.754628792	0.701437319	490372	491301	-	930	-
1038	SAK_RS05195	SAK_1038	0.757035669	0.77734695	1008989	1009546	+	558	lepB
911	SAK_RS04555	SAK_0911	0.766715213	0.725010628	861223	861951	+	729	-
75	SAK_RS00370	SAK_0075	0.768712291	0.725747584	56716	57519	-	804	-
1679	SAK_RS08455	SAK_1679	0.771515624	0.824716875	1664125	1665567	-	1443	gatB
1694	SAK_RS08530	SAK_1694	0.773471552	0.691219602	1680943	1682958	-	2016	recG
798	SAK_RS03980	SAK_0798	0.773978485	0.691219602	734245	735198	+	954	cylF
371	SAK_RS01840	SAK_0371	0.775508033	0.748284612	320085	320684	-	600	recU
1248	SAK_RS06260	SAK_1248	0.775920211	0.718575521	1219445	1220074	-	630	neuD
180	SAK_RS00890	SAK_0180	0.778537356	0.729830767	140235	140423	+	189	rpmB
1984	SAK_RS09985	SAK_1984	0.785375883	0.713411063	1970763	1971302	+	540	-
415	SAK_RS02060	SAK_0415	0.794205675	0.748284612	365319	365969	+	651	-
107	SAK_RS00530	SAK_0107	0.802177002	0.925086882	84000	84356	+	357	rplR
510	SAK_RS02535	SAK_0510	0.806231491	0.67138155	453222	453617	-	396	-
1857	SAK_RS09350	SAK_1857	0.807587258	0.740554071	1853508	1853744	-	237	-
1229	SAK_RS06165	SAK_1229	0.807775352	0.765569942	1201100	1201486	-	387	-
1089	SAK_RS05445	SAK_1089	0.80947129	0.654578158	1061872	1062603	-	732	-
1816	SAK_RS09145	SAK_1816	0.812000461	0.790762022	1805741	1807096	-	1356	-
239	SAK_RS01175	SAK_0239	0.814015364	0.668248292	204985	205755	-	771	proC
1110	SAK_RS05550	SAK_1110	0.819627701	0.67138155	1082619	1084103	-	1485	cstA
1308	SAK_RS06560	SAK_1308	0.819689076	0.660223813	1286225	1288006	-	1782	uvrC
259	SAK_RS01275	SAK_0259	0.828418384	0.700957184	224182	226218	+	2037	-
1881	SAK_RS09470	SAK_1881	0.834742767	0.656453622	1881381	1882061	+	681	-
412	#N/A	SAK_0412	0.835158064	0.72096857	363463	363578	+	116	rrfF
968	SAK_RS04845	SAK_0968	0.835314012	0.647978304	921765	923048	+	1284	-
521	SAK_RS02590	SAK_0521	0.83672504	0.735731221	463959	464297	-	339	-
1364	SAK_RS06865	SAK_1364	0.844627986	0.820363131	1347510	1349582	+	2073	-
2072	SAK_RS10425	SAK_2072	0.850708392	0.649850644	2067052	2067408	-	357	-
1973	SAK_RS09930	SAK_1973	0.852311645	0.716481238	1961878	1962366	-	489	-
1247	SAK_RS06255	SAK_1247	0.855102314	0.656245803	1218193	1219434	-	1242	neuA
695	SAK_RS03475	SAK_0695	0.856275145	0.725612393	628380	628784	+	405	-
795	SAK_RS03965	SAK_0795	0.856346478	0.660430834	730448	731377	+	930	cylA
2002	SAK_RS10075	SAK_2002	0.860509176	0.650587689	1995857	1996456	-	600	-
335	SAK_RS01660	SAK_0335	0.868233673	0.630738135	279573	280256	-	684	-
1859	SAK_RS09360	SAK_1859	0.871459778	0.638611901	1854914	1856809	-	1896	pepO
1182	SAK_RS05915	SAK_1182	0.881931142	0.697497622	1160015	1160989	+	975	prs
357	SAK_RS01770	SAK_0357	0.887387333	0.633283275	304000	304947	+	948	mraW
322	SAK_RS01590	SAK_0322	0.892210771	0.620735109	268104	269738	+	1635	-
2117	SAK_RS10665	SAK_2117	0.900218595	0.627395082	2107765	2109246	-	1482	guaB
1856	SAK_RS09345	SAK_1856	0.901723181	0.609411175	1851437	1853506	-	2070	-
1667	SAK_RS08395	SAK_1667	0.904751942	0.639978426	1655635	1656348	-	714	-
1740	SAK_RS08750	SAK_1740	0.907683613	0.804292535	1730059	1730886	-	828	-
1509	SAK_RS07600	SAK_1509	0.91698521	0.616657046	1505352	1506278	+	927	-
1100	SAK_RS05500	SAK_1100	0.917412516	0.691219602	1072187	1074307	-	2121	topA
266	SAK_RS01310	SAK_0266	0.920332063	0.612990002	231765	233894	+	2130	pnp
1839	SAK_RS09260	SAK_1839	0.925417134	0.743336033	1833029	1834051	-	1023	pfoR
204	SAK_RS01010	SAK_0204	0.931039699	0.608091239	166231	167418	-	1188	-
793	SAK_RS03955	SAK_0793	0.937986298	0.623514367	729693	729998	+	306	-
562	SAK_RS02800	SAK_0562	0.944904904	0.630738135	504742	506481	+	1740	-
447	SAK_RS02225	SAK_0447	0.949126697	0.62967992	392878	393912	+	1035	-
1848	SAK_RS09305	SAK_1848	0.95074918	0.578877528	1843167	1845614	-	2448	clpC
2077	SAK_RS10450	SAK_2077	0.951873469	0.720324263	2071866	2072372	-	507	-
1576	SAK_RS07950	SAK_1576	0.953229772	0.683437921	1572098	1574095	-	1998	metG
1520	SAK_RS07650	SAK_1520	0.954759894	0.716481238	1516673	1517521	-	849	-
121	#N/A	SAK_0121	0.955520599	0.640637297	95729	95844	+	116	rrfC
436	SAK_RS02165	SAK_0436	0.95596499	0.635320124	384095	384907	-	813	-
1399	SAK_RS07040	SAK_1399	0.956365548	0.656245803	1383789	1384253	-	465	lspA
635	SAK_RS03175	SAK_0635	0.957482687	0.750527819	567268	568683	+	1416	-
2068	SAK_RS10405	SAK_2068	0.957862878	0.848884859	2061333	2062055	+	723	-
561	SAK_RS02795	SAK_0561	0.96803594	0.584927671	503007	504752	+	1746	-
1830	SAK_RS09215	SAK_1830	0.970356601	0.712332252	1825266	1825982	-	717	araD
629	SAK_RS03145	SAK_0629	0.973367839	0.61268019	562613	563041	+	429	-
921	#N/A	SAK_0921	0.974706465	0.582090748	873197	873640	-	444	-

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1523	#N/A	SAK_1523	0.978833485	0.579666834	1520319	1520573	-	255	-
241	SAK_RS01185	SAK_0241	0.987506079	0.636071861	207077	207316	-	240	-
1746	SAK_RS08780	SAK_1746	0.991545073	0.644989952	1736281	1737261	+	981	-
694	#N/A	SAK_0694	1.001162657	0.56517131	627496	628380	-	885	-
1692	SAK_RS08520	SAK_1692	1.001818297	0.547943296	1678762	1679640	-	879	aroE
2136	SAK_RS10760	SAK_2136	1.004227517	0.676716444	2126958	2127731	+	774	-
1362	SAK_RS06855	SAK_1362	1.005505872	0.595976611	1344937	1346754	-	1818	-
1009	SAK_RS05050	SAK_1009	1.006177808	0.661481534	973271	974230	+	960	-
1620	SAK_RS08170	SAK_1620	1.033895912	0.581973303	1610352	1610855	-	504	-
1492	SAK_RS07505	SAK_1492	1.035989658	0.61191597	1482334	1483341	-	1008	-
550	SAK_RS02735	SAK_0550	1.047164131	0.573649839	492838	493740	+	903	-
2009	SAK_RS10105	SAK_2009	1.047279775	0.553727419	2003540	2004211	-	672	deoC
288	SAK_RS01420	SAK_0288	1.061418727	0.514964712	249138	249473	-	336	-
1408	SAK_RS07085	SAK_1408	1.066056776	0.509402173	1390931	1392280	-	1350	gor
519	#N/A	SAK_0519	1.069745521	0.668875802	463511	463581	-	71	-
1505	SAK_RS07580	SAK_1505	1.075426042	0.591281446	1502047	1502769	-	723	-
700	SAK_RS03500	SAK_0700	1.078218909	0.501778249	632782	634158	+	1377	-
1648	SAK_RS08305	SAK_1648	1.078276729	0.591281446	1638894	1639442	-	549	-
1153	SAK_RS05765	SAK_1153	1.086011298	0.546293936	1130099	1130641	+	543	coaC
1165	SAK_RS05830	SAK_1165	1.088279185	0.519259366	1143000	1143182	+	183	-
1395	SAK_RS07020	SAK_1395	1.088454926	0.499498032	1379445	1381043	-	1599	-
214	#N/A	SAK_0214	1.09097673	0.56517131	179974	180089	+	116	rrfD
1318	SAK_RS06620	SAK_1318	1.093757333	0.530560764	1295297	1297765	-	2469	-
331	SAK_RS01635	SAK_0331	1.096413696	0.52891986	275790	276281	-	492	-
346	SAK_RS01715	SAK_0346	1.102465147	0.522873182	289742	291571	+	1830	glpO
1072	SAK_RS05360	SAK_1072	1.102915036	0.66722164	1042785	1043723	+	939	-
1344	#N/A	SAK_1344	1.111935985	0.501778249	1328986	1329132	+	147	-
1376	SAK_RS06925	SAK_1376	1.126215388	0.513085097	1361372	1361866	-	495	-
1359	SAK_RS06840	SAK_1359	1.148925155	0.519259366	1341771	1342457	-	687	-
1956	SAK_RS09855	SAK_1956	1.15287761	0.635320124	1951499	1951789	+	291	-
1964	SAK_RS09885	SAK_1964	1.153386894	0.633388531	1955121	1955522	-	402	-
446	SAK_RS02220	SAK_0446	1.154216049	0.729509685	392151	392876	+	726	ecsA
1277	SAK_RS06405	SAK_1277	1.16690793	0.49735054	1247864	1249519	+	1656	fbpA
1073	SAK_RS05365	SAK_1073	1.167327039	0.687351986	1043766	1044836	-	1071	xerS
1476	SAK_RS07420	SAK_1476	1.197789376	0.479647524	1461216	1462586	+	1371	-
272	SAK_RS01340	SAK_0272	1.201062082	0.56030962	237255	238010	+	756	-
62	SAK_RS00305	SAK_0062	1.214706172	0.444703166	43773	44525	+	753	-
698	SAK_RS03490	SAK_0698	1.218306423	0.576174127	630839	632116	+	1278	-
1488	SAK_RS07485	SAK_1488	1.220464891	0.49518538	1477840	1478715	-	876	-
2064	SAK_RS10385	SAK_2064	1.225330238	0.494427487	2056947	2057873	-	927	arcC
307	#N/A	SAK_0307	1.240718322	0.501778249	264561	264676	+	116	rrfE
1377	SAK_RS06930	SAK_1377	1.241268187	0.444703166	1362055	1364019	-	1965	-
1837	#N/A	SAK_1837	1.246676493	0.472597599	1830888	1831343	+	456	-
1093	SAK_RS05465	SAK_1093	1.251765361	0.471521343	1064301	1065185	-	885	truB
879	SAK_RS04395	SAK_0879	1.251780294	0.460347135	824348	824821	-	474	-
155	SAK_RS00765	SAK_0155	1.252413636	0.595965164	113294	114577	+	1284	tig
240	SAK_RS01180	SAK_0240	1.255086632	0.499498032	205825	206892	-	1068	pepA
1993	SAK_RS10030	SAK_1993	1.257569182	0.497962232	1985262	1986650	+	1389	-
1144	SAK_RS05720	SAK_1144	1.263526499	0.467722354	1121430	1123100	-	1671	fhs
910	SAK_RS04550	SAK_0910	1.269625683	0.435308424	860055	861047	-	993	-
863	SAK_RS04315	SAK_0863	1.272490202	0.519259366	809752	810525	+	774	lgt
1249	SAK_RS06265	SAK_1249	1.274316461	0.475217088	1220071	1221225	-	1155	neuC
953	SAK_RS04770	SAK_0953	1.281052688	0.609978251	907541	908476	-	936	-
1683	SAK_RS08475	SAK_1683	1.284667559	0.437406181	1670131	1670961	-	831	-
966	SAK_RS04835	SAK_0966	1.288261642	0.635320124	919857	921116	+	1260	murA
1071	SAK_RS05355	SAK_1071	1.293710127	0.450634609	1042120	1042788	+	669	-
247	SAK_RS01215	SAK_0247	1.297489863	0.557645418	210110	210754	+	645	-
1884	SAK_RS09485	SAK_1884	1.3080423	0.463008407	1884901	1886034	-	1134	msmK
551	SAK_RS02740	SAK_0551	1.327081691	0.393261066	493900	494964	+	1065	-
1329	#N/A	SAK_1329	1.328071024	0.466148493	1311820	1312896	-	1077	-
1339	SAK_RS06740	SAK_1339	1.329489702	0.437406181	1325079	1325729	-	651	-
1959	SAK_RS09865	SAK_1959	1.330227965	0.523407731	1952530	1952913	+	384	-
1397	SAK_RS07030	SAK_1397	1.340598837	0.463008407	1382218	1382739	-	522	pyrR
815	SAK_RS04080	SAK_0815	1.342479724	0.452966568	757945	758583	-	639	-
434	SAK_RS02155	SAK_0434	1.353379212	0.852242343	381938	382750	-	813	-
2044	SAK_RS10280	SAK_2044	1.356310634	0.393261066	2036988	2037860	-	873	-
2113	SAK_RS10645	SAK_2113	1.361312198	0.635320124	2104629	2104982	+	354	-
53	SAK_RS00260	SAK_0053	1.361506775	0.475217088	32564	33325	+	762	recO
1992	SAK_RS10025	SAK_1992	1.365611141	0.394720246	1984579	1985265	+	687	-
1340	SAK_RS06745	SAK_1340	1.37523863	0.520767451	1325887	1326210	-	324	-
2127	SAK_RS10715	SAK_2127	1.375383927	0.374613962	2118176	2118868	-	693	-
1176	SAK_RS05885	SAK_1176	1.387085666	0.49327433	1154935	1155696	-	762	-
1371	SAK_RS06900	SAK_1371	1.399202795	0.497962232	1356216	1358084	-	1869	-
2063	SAK_RS10380	SAK_2063	1.411929827	0.466148493	2055300	2056853	-	1554	-
918	SAK_RS04590	SAK_0918	1.436699683	0.47814981	869554	870696	+	1143	-
1130	SAK_RS05650	SAK_1130	1.439679883	0.453775717	1103770	1104552	-	783	-
1131	SAK_RS05655	SAK_1131	1.450865533	0.404184446	1104549	1104872	-	324	-
1710	#N/A	SAK_1710	1.45216392	0.513600141	1699881	1700051	-	171	-
1937	SAK_RS09755	SAK_1937	1.454064101	0.537718916	1936894	1937475	+	582	-
1905	SAK_RS09595	SAK_1905	1.460174471	0.389673739	1908884	1909921	-	1038	-
1111	SAK_RS05555	SAK_1111	1.469474951	0.36599435	1084259	1084993	-	735	-
1425	SAK_RS07170	SAK_1425	1.47232507	0.369303033	1407596	1408390	+	795	fhuC
459	SAK_RS02285	SAK_0459	1.472927783	0.729509685	403104	405338	+	2235	copA
1363	SAK_RS06860	SAK_1363	1.474231392	0.451489799	1346801	1347241	-	441	-
765	SAK_RS03810	SAK_0765	1.474805565	0.424994396	701777	702550	+	774	-
1466	SAK_RS07370	SAK_1466	1.477724424	0.527759204	1447879	1448685	-	807	-
321	SAK_RS01585	SAK_0321	1.485129579	0.393261066	267582	268040	+	459	-
803	SAK_RS04005	SAK_0803	1.488579593	0.530560764	739868	740383	+	516	-
278	SAK_RS01365	SAK_0278	1.493460745	0.377688025	241346	242500	-	1155	-
896	SAK_RS04480	SAK_0896	1.508736172	0.345542684	845147	846685	+	1539	-
407	SAK_RS02020	SAK_0407	1.526530837	0.55204352	357037	357702	+	666	-
345	SAK_RS01710	SAK_0345	1.538167991	0.389503316	288221	289729	+	1509	glpK
1976	SAK_RS09945	SAK_1976	1.545892667	0.314120856	1964192	1964398	-	207	-

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522	SAK_RS02595	SAK_0522	1.558483933	0.321467013	464318	465082	-	765	-
964	SAK_RS04825	SAK_0964	1.563201562	0.497962232	918275	919045	+	771	thiM
396	SAK_RS01965	SAK_0396	1.567026371	0.893244474	345384	346139	+	756	-
348	SAK_RS01725	SAK_0348	1.567923223	0.391345805	292369	293706	+	1338	-
1999	#N/A	SAK_1999	1.573584992	0.319858607	1993337	1995052	-	1716	-
585	SAK_RS02915	SAK_0585	1.580226444	0.445352595	526733	527521	+	789	-
996	SAK_RS04985	SAK_0996	1.592047946	0.45733362	952208	955441	+	3234	rexB
2090	SAK_RS10525	SAK_2090	1.59839187	0.489124242	2081211	2081813	-	603	-
1250	SAK_RS06270	SAK_1250	1.608363955	0.300816021	1221302	1222327	-	1026	neuB
1946	SAK_RS09800	SAK_1946	1.610921478	0.418434995	1943447	1943866	-	420	-
1582	SAK_RS07980	SAK_1582	1.613345257	0.337156514	1579289	1579645	-	357	-
1845	SAK_RS09290	SAK_1845	1.621781414	0.371866911	1840703	1841680	+	978	-
408	SAK_RS02025	SAK_0408	1.622605717	0.359871121	357779	358333	+	555	yfiA
549	SAK_RS02730	SAK_0549	1.629050975	0.312810888	491718	492677	+	960	-
571	SAK_RS02845	SAK_0571	1.634082666	0.397322395	514047	514436	-	390	-
1338	SAK_RS06735	SAK_1338	1.635388329	0.704047122	1323573	1324949	-	1377	-
719	SAK_RS03595	SAK_0719	1.642839645	0.359463977	653383	653901	+	519	-
1497	SAK_RS07535	SAK_1497	1.681481817	0.36599435	1492576	1494759	+	2184	-
1693	SAK_RS08525	SAK_1693	1.686397485	0.320325033	1679738	1680652	-	915	-
1181	SAK_RS05910	SAK_1181	1.692789953	0.346946656	1159249	1159839	+	591	-
1276	SAK_RS06400	SAK_1276	1.696487646	0.36260743	1246501	1247505	-	1005	-
253	SAK_RS01245	SAK_0253	1.716649823	0.320171411	216586	217563	+	978	-
1254	SAK_RS06290	SAK_1254	1.736444506	0.480237822	1225745	1226719	-	975	cpsI
874	SAK_RS04370	SAK_0874	1.745782323	0.242286709	819329	820522	+	1194	ribBA
1957	SAK_RS09860	SAK_1957	1.747157176	0.370250573	1951890	1952264	+	375	-
1327	SAK_RS06670	SAK_1327	1.750213897	0.450520948	1310504	1311070	-	567	-
435	SAK_RS02160	SAK_0435	1.753408635	0.682297755	382783	383793	-	1011	-
1889	SAK_RS09510	SAK_1889	1.754277476	0.278581315	1889953	1890468	-	516	lacB
1708	SAK_RS08600	SAK_1708	1.75812841	0.391345805	1698921	1699220	-	300	-
780	SAK_RS03890	SAK_0780	1.762122348	0.333925851	715933	718605	+	2673	-
1963	#N/A	SAK_1963	1.768111618	0.314986183	1954690	1954893	-	204	-
1906	SAK_RS09600	SAK_1906	1.797201302	0.244276007	1909933	1910706	-	774	-
2031	SAK_RS10220	SAK_2031	1.801813303	0.428215382	2023518	2023916	-	399	spxA
1426	SAK_RS07175	SAK_1426	1.813092635	0.59736893	1408414	1409346	+	933	fhuD
997	SAK_RS04990	SAK_0997	1.837741785	0.356220247	955431	959054	+	3624	rexA
1803	SAK_RS09075	SAK_1803	1.839383567	0.36260743	1794704	1795270	-	567	-
225	SAK_RS01115	SAK_0225	1.847391711	0.322082233	196671	197036	+	366	-
1941	SAK_RS09775	SAK_1941	1.849431986	0.409953467	1940575	1940784	-	210	-
2018	SAK_RS10155	SAK_2018	1.861923157	0.307885744	2012873	2013670	-	798	-
245	SAK_RS01205	SAK_0245	1.86296088	0.340397624	208794	209510	-	717	-
1715	SAK_RS08625	SAK_1715	1.865813522	0.217383842	1702737	1703453	-	717	-
1412	SAK_RS07105	SAK_1412	1.879805063	0.419985019	1395202	1395879	-	678	aroD
1251	SAK_RS06275	SAK_1251	1.880126531	0.232234038	1222327	1223727	-	1401	cpsL
515	SAK_RS02560	SAK_0515	1.916488653	0.230277253	457100	457624	+	525	-
1608	SAK_RS08110	SAK_1608	1.920360921	0.254454943	1602407	1603129	-	723	rluB
1754	SAK_RS08820	SAK_1754	1.923847228	0.314120856	1747226	1748806	+	1581	hsdM
971	SAK_RS04860	SAK_0971	1.938055333	0.36260743	924870	925325	-	456	-
1760	SAK_RS08850	SAK_1760	1.950255724	0.274842775	1755853	1756302	-	450	-
1987	SAK_RS10000	SAK_1987	1.956885061	0.226079692	1973807	1975651	-	1845	-
633	SAK_RS03165	SAK_0633	1.957473361	0.230277253	565752	566972	+	1221	-
886	SAK_RS04430	SAK_0886	1.969177749	0.355988703	832636	833904	+	1269	-
344	SAK_RS01705	SAK_0344	1.9742165	0.306614774	287843	288106	+	264	-
789	SAK_RS03935	SAK_0789	1.982943569	0.243942227	726418	727203	+	786	-
824	SAK_RS04125	SAK_0824	1.985728541	0.359836159	767251	769050	+	1800	-
347	SAK_RS01720	SAK_0347	1.986886787	0.269276372	291583	292281	+	699	glpF
1324	SAK_RS06650	SAK_1324	2.004997097	0.238330535	1305401	1307215	-	1815	-
2083	SAK_RS10475	SAK_2083	2.006616092	0.212001013	2075461	2076903	-	1443	-
1605	SAK_RS08095	SAK_1605	2.014368007	0.332599435	1599339	1600688	+	1350	trkA
733	SAK_RS03655	SAK_0733	2.01525575	0.397050486	671392	672768	+	1377	-
696	#N/A	SAK_0696	2.016831797	0.202774204	628946	629428	+	483	-
473	SAK_RS02355	SAK_0473	2.017813875	0.198989025	417664	418440	+	777	-
2032	SAK_RS10225	SAK_2032	2.019567341	0.325649365	2024132	2025229	-	1098	recA
508	#N/A	SAK_0508	2.022735976	0.289486263	452633	452794	-	162	-
712	SAK_RS03560	SAK_0712	2.026550076	0.404184446	644826	645281	-	456	-
433	SAK_RS02150	SAK_0433	2.029229405	0.700754622	381012	381923	-	912	-
255	SAK_RS01255	SAK_0255	2.031606927	0.220443657	218393	219196	+	804	-
1428	SAK_RS07185	SAK_1428	2.048596131	0.241295652	1410384	1411385	+	1002	-
1460	SAK_RS07340	SAK_1460	2.049664332	0.213939594	1442974	1443315	-	342	-
2084	SAK_RS10480	SAK_2084	2.060986069	0.222864927	2076983	2077840	-	858	-
1757	SAK_RS08835	SAK_1757	2.078646735	0.254233211	1753374	1754018	-	645	-
2066	SAK_RS10395	SAK_2066	2.087522466	0.312810888	2058986	2060281	+	1296	-
1568	SAK_RS07910	SAK_1568	2.103900266	0.406289713	1562434	1562682	-	249	-
1216	SAK_RS06095	SAK_1216	2.10623917	0.389673739	1192141	1192674	+	534	-
1765	#N/A	SAK_1765	2.108402417	0.212001013	1760509	1761370	+	862	-
263	SAK_RS01295	SAK_0263	2.112438312	0.210300662	228730	229659	+	930	-
1498	SAK_RS07540	SAK_1498	2.116292048	0.216258089	1494759	1495499	+	741	-
839	SAK_RS04200	SAK_0839	2.128799175	0.184091563	786457	787476	+	1020	-
1112	SAK_RS05560	SAK_1112	2.129498823	0.21112807	1085005	1086744	-	1740	-
1579	SAK_RS07965	SAK_1579	2.130160752	0.175018813	1576302	1577519	+	1218	-
2118	SAK_RS10670	SAK_2118	2.141156416	0.768510042	2109403	2109888	-	486	-
646	SAK_RS03235	SAK_0646	2.144138781	0.220443657	574848	576380	+	1533	-
174	SAK_RS00860	SAK_0174	2.150581095	0.199504128	133487	134158	+	672	-
818	SAK_RS04095	SAK_0818	2.150756787	0.21112807	760390	761208	+	819	-
563	SAK_RS02805	SAK_0563	2.151898027	0.264006972	506609	507175	+	567	-
1638	SAK_RS08255	SAK_1638	2.160504324	0.219683069	1628902	1630407	-	1506	-
1180	SAK_RS05905	SAK_1180	2.163652655	0.219354656	1158468	1159139	-	672	-
924	SAK_RS04620	SAK_0924	2.17236957	0.173440403	875733	876434	+	702	nagB
372	SAK_RS01845	SAK_0372	2.191024529	0.181755726	320759	321277	+	519	-
2089	SAK_RS10520	SAK_2089	2.196017298	0.198989025	2080337	2080975	-	639	-
1711	#N/A	SAK_1711	2.202390815	0.239137121	1700504	1700629	-	126	-
916	SAK_RS04580	SAK_0916	2.21651681	0.21519047	866797	868224	+	1428	-
298	SAK_RS01470	SAK_0298	2.217632209	0.196880977	253798	254658	+	861	-
1977	SAK_RS09950	SAK_1977	2.219454877	0.184091563	1964400	1965476	-	1077	-

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829	SAK_RS04150	SAK_0829	2.222309702	0.245811457	773089	773928	+	840	-
230	SAK_RS01135	SAK_0230	2.232218961	0.261607823	199803	200102	+	300	-
229	SAK_RS01130	SAK_0229	2.234374052	0.359463977	199493	199831	+	339	-
1361	SAK_RS06850	SAK_1361	2.234744737	0.173440403	1343193	1344947	-	1755	-
1162	SAK_RS05815	SAK_1162	2.235663743	0.244276007	1140349	1141179	-	831	-
1835	SAK_RS09240	SAK_1835	2.242582044	0.244439264	1828487	1829926	-	1440	ulaA
2025	SAK_RS10190	SAK_2025	2.249180491	0.264042606	2018200	2020371	-	2172	nrdD
917	SAK_RS04585	SAK_0917	2.249541642	0.198989025	868293	869387	-	1095	-
628	SAK_RS03140	SAK_0628	2.251305984	0.266063731	561959	562225	+	267	-
171	SAK_RS00845	SAK_0171	2.257862826	0.202774204	130514	131500	-	987	rbsR
1136	SAK_RS05680	SAK_1136	2.257926459	0.212001013	1111694	1112323	-	630	pyrE
1521	SAK_RS07655	SAK_1521	2.259477094	0.173440403	1517738	1519330	+	1593	-
1228	SAK_RS06160	SAK_1228	2.272084019	0.212001013	1198715	1200994	-	2280	pcrA
78	SAK_RS00385	SAK_0078	2.274431154	0.186437602	59825	60916	+	1092	purK
224	SAK_RS01110	SAK_0224	2.28084457	0.307885744	192907	196557	+	3651	rpoC
908	SAK_RS04540	SAK_0908	2.287822312	0.185392775	858232	859041	+	810	-
655	SAK_RS03275	SAK_0655	2.29696406	0.299007809	585900	586079	+	180	-
1396	SAK_RS07025	SAK_1396	2.298397542	0.222864927	1381099	1382169	-	1071	carA
1952	SAK_RS09835	SAK_1952	2.302302562	0.199504128	1948097	1948483	-	387	-
1125	SAK_RS05625	SAK_1125	2.303290505	0.291985895	1099099	1099341	-	243	-
291	SAK_RS01435	SAK_0291	2.3090944	0.174968901	250649	251056	+	408	-
976	SAK_RS04885	SAK_0976	2.311711632	0.189199204	931655	933523	+	1869	glgB
663	SAK_RS03315	SAK_0663	2.312447916	0.198989025	593818	594204	+	387	-
586	SAK_RS02920	SAK_0586	2.319848295	0.341207848	527531	528301	+	771	-
217	SAK_RS01075	SAK_0217	2.325501936	0.36260743	181245	181688	+	444	adcR
1975	SAK_RS09940	SAK_1975	2.329146978	0.174968901	1963293	1964195	-	903	-
260	SAK_RS01280	SAK_0260	2.337973527	0.19938339	226221	226505	+	285	-
619	SAK_RS03095	SAK_0619	2.340175126	0.21112807	556553	558106	+	1554	-
1236	#N/A	SAK_1236	2.341334627	0.231453519	1208372	1208443	-	72	-
391	SAK_RS01940	SAK_0391	2.342183903	0.184091563	340987	342006	+	1020	-
870	SAK_RS04350	SAK_0870	2.345977678	0.283096027	814827	815447	+	621	-
1898	SAK_RS09555	SAK_1898	2.347417927	0.244638428	1899996	1900919	-	924	-
1099	SAK_RS05495	SAK_1099	2.352723804	0.219683069	1071349	1072050	-	702	-
791	SAK_RS03945	SAK_0791	2.35978842	0.170990433	728133	728981	+	849	cylD
1943	SAK_RS09785	SAK_1943	2.362539194	0.186437602	1941036	1942166	-	1131	-
292	SAK_RS01440	SAK_0292	2.367287743	0.17239133	251056	251616	+	561	-
1724	SAK_RS08670	SAK_1724	2.367600962	0.17239133	1713529	1714122	+	594	-
814	SAK_RS04075	SAK_0814	2.369292356	0.279696141	757082	757867	+	786	-
402	SAK_RS01995	SAK_0402	2.373410609	0.199504128	352055	352723	+	669	-
1068	SAK_RS05340	SAK_1068	2.37430831	0.202774204	1038313	1039275	+	963	-
1840	SAK_RS09265	SAK_1840	2.38280305	0.189335928	1834413	1835087	+	675	-
1098	SAK_RS05490	SAK_1098	2.389659589	0.206957978	1068707	1071337	-	2631	-
1762	SAK_RS08860	SAK_1762	2.398510643	0.239137121	1756641	1758530	-	1890	-
1142	SAK_RS05710	SAK_1142	2.398554399	0.390415625	1117985	1119025	-	1041	-
928	SAK_RS04640	SAK_0928	2.399031689	0.254454943	879553	880500	+	948	-
1801	SAK_RS09065	SAK_1801	2.413914015	0.174265958	1793351	1794223	-	873	ksgA
2054	SAK_RS10330	SAK_2054	2.417977003	0.21112807	2046975	2047424	+	450	-
1974	SAK_RS09935	SAK_1974	2.424337512	0.165179892	1962535	1963296	-	762	-
1706	SAK_RS08590	SAK_1706	2.425951364	0.256553996	1696955	1697344	-	390	-
1132	SAK_RS05660	SAK_1132	2.428373758	0.174968901	1104999	1108181	-	3183	carB
1300	SAK_RS06520	SAK_1300	2.430363195	0.264888798	1275550	1275726	+	177	-
1517	SAK_RS07635	SAK_1517	2.437188856	0.174705686	1514294	1514995	-	702	-
1917	SAK_RS09655	SAK_1917	2.440007996	0.173440403	1919379	1920713	-	1335	rgfC
390	SAK_RS01935	SAK_0390	2.444065158	0.188667224	340295	340990	+	696	-
1924	SAK_RS09690	SAK_1924	2.445241783	0.221203875	1927866	1928615	-	750	pstB
72	SAK_RS00355	SAK_0072	2.447296213	0.17239133	53893	54810	+	918	-
557	SAK_RS02775	SAK_0557	2.455513855	0.170990433	499158	500492	+	1335	-
1662	SAK_RS08370	SAK_1662	2.456058486	0.17239133	1652125	1653114	+	990	-
963	SAK_RS04820	SAK_0963	2.45642816	0.219487391	917476	918273	+	798	thiD
1809	SAK_RS09105	SAK_1809	2.45668794	0.244276007	1798754	1800016	-	1263	dltD
1267	SAK_RS06355	SAK_1267	2.466041591	0.199821077	1237779	1238588	-	810	punA
297	SAK_RS01460	SAK_0297	2.467243187	0.256553996	253572	253676	+	105	-
608	SAK_RS03030	SAK_0608	2.467922755	0.221436801	550234	550443	-	210	-
287	SAK_RS01415	SAK_0287	2.471493708	0.213939594	248363	248833	+	471	-
1685	SAK_RS08485	SAK_1685	2.472316699	0.170990433	1671622	1672755	+	1134	-
572	SAK_RS02850	SAK_0572	2.47919324	0.209510112	514597	514806	+	210	-
894	SAK_RS04470	SAK_0894	2.485349496	0.258110751	842933	844153	+	1221	-
617	SAK_RS03085	SAK_0617	2.48577218	0.199504128	554684	556048	+	1365	-
60	SAK_RS00295	SAK_0060	2.486865879	0.155716174	42012	43034	+	1023	purM
1097	SAK_RS05485	SAK_1097	2.489260388	0.266063731	1067723	1068601	-	879	-
2024	SAK_RS10185	SAK_2024	2.499936688	0.184091563	2017982	2018125	-	144	-
1953	SAK_RS09840	SAK_1953	2.514240277	0.169868628	1948590	1949162	-	573	-
2019	SAK_RS10160	SAK_2019	2.529049756	0.184091563	2013856	2014716	+	861	-
1573	SAK_RS07935	SAK_1573	2.544736433	0.306331783	1568776	1569453	-	678	-
71	SAK_RS00350	SAK_0071	2.546885593	0.198989025	53234	53896	+	663	-
1343	SAK_RS06760	SAK_1343	2.561039737	0.188442309	1327699	1328925	-	1227	clpX
830	SAK_RS04155	SAK_0830	2.561067899	0.264339605	774081	774893	+	813	-
187	SAK_RS00930	SAK_0187	2.561419815	0.21423225	149264	149791	-	528	-
2067	SAK_RS10400	SAK_2067	2.563704137	0.17239133	2060278	2061111	+	834	-
1141	SAK_RS05705	SAK_1141	2.572473088	0.173809905	1116702	1117778	-	1077	asd
1471	SAK_RS07395	SAK_1471	2.575062884	0.202067542	1452906	1454279	-	1374	-
787	SAK_RS03925	SAK_0787	2.575866945	0.163741103	724603	725595	+	993	-
403	SAK_RS02000	SAK_0403	2.576257188	0.163741103	352791	353879	+	1089	gldA
250	SAK_RS01230	SAK_0250	2.578352142	0.198989025	213417	213872	+	456	-
1649	SAK_RS08310	SAK_1649	2.581309298	0.145369724	1639611	1640819	-	1209	ygjU
932	SAK_RS04660	SAK_0932	2.585154108	0.660223813	883984	884913	+	930	prsA
1669	SAK_RS08405	SAK_1669	2.586239634	0.189335928	1657547	1657798	-	252	-
1562	SAK_RS07875	SAK_1562	2.598676073	0.169868628	1558882	1559295	-	414	-
2013	SAK_RS10130	SAK_2013	2.609922117	0.198989025	2007549	2009171	-	1623	groEL
661	SAK_RS03305	SAK_0661	2.612959226	0.312810888	591543	592355	-	813	-
2125	SAK_RS10705	SAK_2125	2.613192078	0.184091563	2115966	2116922	+	957	arcC
177	SAK_RS00875	SAK_0177	2.614577026	0.145369724	136584	137972	+	1389	argH
790	SAK_RS03940	SAK_0790	2.617115951	0.241501982	727828	728133	+	306	cylX

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176	SAK_RS00870	SAK_0176	2.624849894	0.145369724	135375	136565	+	1191	argG
1850	SAK_RS09315	SAK_1850	2.625269795	0.173632464	1846248	1846709	+	462	-
1932	SAK_RS09730	SAK_1932	2.627158558	0.145369724	1934189	1934905	+	717	-
59	SAK_RS00290	SAK_0059	2.63111072	0.170990433	40530	41984	+	1455	purF
514	SAK_RS02555	SAK_0514	2.633847816	0.145369724	456105	456968	-	864	-
1189	SAK_RS05950	SAK_1189	2.642094444	0.184091563	1166862	1167476	-	615	-
1887	SAK_RS09500	SAK_1887	2.648598305	0.189335928	1888031	1889008	-	978	lacD
166	SAK_RS00820	SAK_0166	2.653278895	0.184091563	125779	126747	-	969	rbsB
1214	#N/A	SAK_1214	2.658505261	0.186437602	1190350	1191693	+	1344	-
763	SAK_RS03800	SAK_0763	2.668865658	0.22553654	699217	700458	+	1242	-
1265	SAK_RS06345	SAK_1265	2.679939215	0.175018813	1235827	1236537	-	711	deoD
1986	SAK_RS09995	SAK_1986	2.681415212	0.199504128	1972753	1973460	-	708	-
781	#N/A	SAK_0781	2.685154308	0.198989025	718636	719449	+	814	-
758	SAK_RS03780	SAK_0758	2.68580473	0.200140125	691829	694744	+	2916	-
579	SAK_RS02885	SAK_0579	2.688180609	0.21112807	521094	522230	+	1137	divIB
727	SAK_RS03630	SAK_0727	2.69009331	0.21112807	666159	666722	-	564	-
2129	SAK_RS10725	SAK_2129	2.690501201	0.159466405	2120049	2121668	+	1620	-
1911	SAK_RS09625	SAK_1911	2.691584012	0.184091563	1914655	1915080	-	426	-
807	SAK_RS04030	SAK_0807	2.699558641	0.220443657	748666	749697	+	1032	-
1054	SAK_RS05270	SAK_1054	2.708268742	0.282938996	1023602	1024591	-	990	ldh
526	SAK_RS02615	SAK_0526	2.712729045	0.23648522	468206	469543	+	1338	-
871	SAK_RS04355	SAK_0871	2.717543837	0.161699253	815502	816842	-	1341	-
638	SAK_RS03190	SAK_0638	2.720027271	0.312810888	570130	570345	+	216	-
1716	SAK_RS08630	SAK_1716	2.720172849	0.161699253	1703455	1704954	-	1500	-
333	SAK_RS01650	SAK_0333	2.736663656	0.169868628	277493	278590	-	1098	-
828	SAK_RS04145	SAK_0828	2.736689468	0.170990433	771919	772965	+	1047	uxuA
67	SAK_RS00330	SAK_0067	2.744712723	0.166416628	49627	50943	+	1317	-
1988	SAK_RS10005	SAK_1988	2.748370258	0.145369724	1975696	1977933	-	2238	metE
701	SAK_RS03505	SAK_0701	2.749034502	0.188143552	634255	634908	+	654	vncR
465	SAK_RS02315	SAK_0465	2.764333961	0.170990433	410443	410922	+	480	-
293	SAK_RS01445	SAK_0293	2.766366834	0.140920456	251589	252269	+	681	-
2028	SAK_RS10205	SAK_2028	2.77021259	0.157497934	2022288	2022605	-	318	-
684	SAK_RS03420	SAK_0684	2.773434315	0.147719162	618617	620014	+	1398	pepDA
1594	SAK_RS08040	SAK_1594	2.775909301	0.167893773	1589229	1589939	-	711	livF
1925	SAK_RS09695	SAK_1925	2.783219444	0.153054468	1928608	1929486	-	879	pstA
455	SAK_RS02265	SAK_0455	2.783485383	0.186437602	398181	400964	+	2784	infB
1063	SAK_RS05315	SAK_1063	2.783767367	0.138762275	1033679	1034377	+	699	-
1127	SAK_RS05635	SAK_1127	2.791443327	0.145369724	1099807	1102824	-	3018	-
632	SAK_RS03160	SAK_0632	2.792443406	0.199504128	564491	565759	+	1269	-
1534	SAK_RS07730	SAK_1534	2.795404031	0.18748101	1530094	1530603	-	510	msrA
761	#N/A	SAK_0761	2.795639162	0.18704725	697031	698041	+	1011	-
1374	SAK_RS06915	SAK_1374	2.804761669	0.151534397	1360336	1360716	-	381	-
1890	SAK_RS09515	SAK_1890	2.806278276	0.153272897	1890489	1890914	-	426	lacA
534	SAK_RS02655	SAK_0534	2.806755336	0.17239133	476244	477077	+	834	-
1595	SAK_RS08045	SAK_1595	2.807212826	0.138762275	1589939	1590703	-	765	livG
1879	SAK_RS09460	SAK_1879	2.808748935	0.17239133	1878362	1879699	-	1338	-
1129	SAK_RS05645	SAK_1129	2.811506847	0.215204656	1103363	1103653	-	291	-
566	SAK_RS02820	SAK_0566	2.816589962	0.205408608	509343	510335	-	993	bioB
748	SAK_RS03735	SAK_0748	2.819503186	0.183472396	684194	685402	+	1209	-
226	SAK_RS10775	SAK_0226	2.826690434	0.186437602	197209	198180	+	972	comGA
2121	SAK_RS10685	SAK_2121	2.833350747	0.21112807	2111757	2112989	+	1233	arcA
499	SAK_RS02490	SAK_0499	2.835785491	0.146980978	443076	444086	+	1011	nrdF
172	SAK_RS00850	SAK_0172	2.842118752	0.158546106	131682	132770	+	1089	-
760	SAK_RS03790	SAK_0760	2.854424474	0.263815942	696631	697029	+	399	-
130	#N/A	SAK_0130	2.85690147	0.203767353	96542	96615	+	74	-
1825	SAK_RS09190	SAK_1825	2.861127822	0.155716174	1819683	1821134	-	1452	-
744	SAK_RS03715	SAK_0744	2.866432158	0.167893773	681525	681830	+	306	-
1758	SAK_RS08840	SAK_1758	2.871005483	0.169868628	1754036	1754725	-	690	-
859	SAK_RS04300	SAK_0859	2.871764511	0.184091563	807824	808252	+	429	-
232	SAK_RS01145	SAK_0232	2.879928929	0.205747703	200495	200866	+	372	-
809	SAK_RS04040	SAK_0809	2.882399921	0.21112807	750786	751847	+	1062	-
45	#N/A	SAK_0045	2.890318997	0.189199204	28215	28288	+	74	-
738	SAK_RS03680	SAK_0738	2.894551613	0.187140104	675788	677026	+	1239	-
568	SAK_RS02830	SAK_0568	2.898781015	0.174705686	510964	512079	+	1116	-
1701	SAK_RS08565	SAK_1701	2.900234463	0.21112807	1690985	1691866	-	882	scrK
169	SAK_RS00835	SAK_0169	2.900606234	0.155716174	129237	129635	-	399	rbsD
873	SAK_RS04365	SAK_0873	2.900813388	0.138762275	818661	819311	+	651	ribE
332	SAK_RS01645	SAK_0332	2.90221838	0.145369724	276861	277469	-	609	-
476	SAK_RS02375	SAK_0476	2.906315118	0.151534397	420889	421416	+	528	-
1467	SAK_RS07375	SAK_1467	2.908579878	0.186437602	1449010	1450029	-	1020	-
1570	SAK_RS07920	SAK_1570	2.910531185	0.156913217	1563620	1565032	-	1413	-
1603	SAK_RS08085	SAK_1603	2.924267525	0.189335928	1597060	1597608	-	549	-
64	SAK_RS00315	SAK_0064	2.937942747	0.142383873	46285	47184	+	900	zooA
2057	SAK_RS10345	SAK_2057	2.939783334	0.14117843	2049045	2049650	+	606	-
645	SAK_RS03230	SAK_0645	2.945573329	0.174968901	572842	574854	+	2013	-
168	SAK_RS00830	SAK_0168	2.945591738	0.134569919	127743	129221	-	1479	rbsA
1664	SAK_RS08380	SAK_1664	2.965103601	0.197739438	1653730	1654104	+	375	-
1120	SAK_RS05600	SAK_1120	2.966706291	0.158546106	1091407	1092693	-	1287	-
1445	SAK_RS07265	SAK_1445	2.967398586	0.175018813	1427724	1428872	-	1149	-
196	SAK_RS00970	SAK_0196	2.968529394	0.271103117	157867	158706	+	840	uppP
228	SAK_RS01125	SAK_0228	2.968692013	0.19854204	199114	199443	+	330	-
286	SAK_RS01410	SAK_0286	2.971379126	0.170990433	246939	248195	+	1257	pre
1950	SAK_RS09820	SAK_1950	2.971525707	0.208367958	1946624	1947214	+	591	-
1328	#N/A	SAK_1328	2.972439319	0.189335928	1311205	1311818	-	614	-
1039	#N/A	SAK_1039	2.977960265	0.174968901	1009560	1009703	-	144	-
1041	SAK_RS05205	SAK_1041	2.982635552	0.180357604	1011792	1012121	+	330	phnA
1691	SAK_RS08515	SAK_1691	2.993795088	0.13610747	1677765	1678727	+	963	-
70	SAK_RS00345	SAK_0070	2.996278257	0.163741103	52771	53214	+	444	-
529	SAK_RS02630	SAK_0529	2.998787092	0.173440403	471008	472339	+	1332	-
1050	SAK_RS05250	SAK_1050	3.000128279	0.138762275	1018359	1019894	+	1536	-
528	SAK_RS02625	SAK_0528	3.005430995	0.198989025	470531	470995	+	465	-
1319	SAK_RS06625	SAK_1319	3.00918625	0.189335928	1297778	1298698	-	921	lmb
898	SAK_RS04490	SAK_0898	3.009785451	0.202333988	848492	848872	+	381	-

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730	SAK_RS03645	SAK_0730	3.017270423	0.145369724	668561	670846	+	2286	-
1607	SAK_RS08105	SAK_1607	3.017892578	0.184091563	1602156	1602407	-	252	-
137	SAK_RS00680	SAK_0137	3.01961608	0.220443657	97532	97963	+	432	-
642	SAK_RS03215	SAK_0642	3.020017524	0.163741103	571654	572211	+	558	-
1735	SAK_RS08725	SAK_1735	3.024024691	0.142383873	1724456	1726768	+	2313	pflB
1909	SAK_RS09615	SAK_1909	3.029827278	0.201513422	1913321	1914130	-	810	-
851	SAK_RS04260	SAK_0851	3.033300367	0.48494263	799272	800069	+	798	-
82	SAK_RS00405	SAK_0082	3.038119928	0.436170801	64942	65940	+	999	ruvB
1764	#N/A	SAK_1764	3.044320498	0.26500319	1759685	1760503	+	819	-
759	SAK_RS03785	SAK_0759	3.048435753	0.170990433	694757	696613	+	1857	-
1663	SAK_RS08375	SAK_1663	3.054888624	0.162222213	1653152	1653730	+	579	-
808	SAK_RS04035	SAK_0808	3.062525317	0.156913217	749732	750751	+	1020	-
2081	SAK_RS10465	SAK_2081	3.077543212	0.138762275	2073989	2074477	-	489	-
825	SAK_RS04130	SAK_0825	3.082306463	0.145369724	769079	769750	+	672	-
1849	SAK_RS09310	SAK_1849	3.083811468	0.271103117	1845611	1846075	-	465	ctsR
869	SAK_RS04345	SAK_0869	3.091093616	0.198989025	814491	814703	+	213	-
503	SAK_RS02510	SAK_0503	3.091289101	0.179638018	449913	450302	+	390	-
1954	SAK_RS09845	SAK_1954	3.098200234	0.208367958	1949164	1949496	-	333	-
734	SAK_RS03660	SAK_0734	3.108717491	0.166416628	672761	673258	+	498	-
1899	SAK_RS09560	SAK_1899	3.110225586	0.169868628	1901174	1901617	-	444	dtd
720	#N/A	SAK_0720	3.110937477	0.222864927	654026	654124	-	99	-
601	SAK_RS02995	SAK_0601	3.112811493	0.138762275	543997	544470	+	474	-
1910	SAK_RS09620	SAK_1910	3.116864922	0.21112807	1914146	1914637	-	492	-
1675	SAK_RS08435	SAK_1675	3.12170216	0.199504128	1660909	1661226	-	318	-
381	SAK_RS01890	SAK_0381	3.125272738	0.138762275	330169	330759	+	591	-
1444	SAK_RS07260	SAK_1444	3.135428115	0.169868628	1427213	1427485	-	273	-
533	SAK_RS02650	SAK_0533	3.139122933	0.170990433	475340	476230	+	891	-
1078	SAK_RS05390	SAK_1078	3.144433187	0.201780026	1050082	1050390	-	309	-
1051	SAK_RS05255	SAK_1051	3.144884289	0.114092804	1019887	1020948	+	1062	-
592	SAK_RS02950	SAK_0592	3.146932978	0.130158907	535433	536125	+	693	-
538	SAK_RS02675	SAK_0538	3.15431797	0.181924349	482046	483041	+	996	galE
792	SAK_RS03950	SAK_0792	3.156114395	0.142383873	728978	729700	+	723	cylG
1023	SAK_RS05125	SAK_1023	3.159508158	0.147719162	991064	993223	+	2160	-
1979	SAK_RS09960	SAK_1979	3.160764994	0.17239133	1966553	1966870	+	318	-
69	SAK_RS00340	SAK_0069	3.161068357	0.138762275	51928	52758	+	831	-
1672	SAK_RS08420	SAK_1672	3.1681725	0.160327046	1658979	1659500	-	522	-
242	SAK_RS01190	SAK_0242	3.169169865	0.170990433	207477	207761	+	285	-
742	SAK_RS03705	SAK_0742	3.174650676	0.145369724	679575	681167	+	1593	-
1407	SAK_RS07080	SAK_1407	3.175846746	0.145369724	1390435	1390887	+	453	-
313	#N/A	SAK_0313	3.176060654	0.170990433	265134	265207	+	74	-
1682	SAK_RS08470	SAK_1682	3.183403875	0.145369724	1667473	1670118	-	2646	ppdK
1895	SAK_RS09540	SAK_1895	3.209706747	0.155716174	1895647	1896111	-	465	-
429	SAK_RS02130	SAK_0429	3.210733943	0.145369724	377180	377812	+	633	-
1134	SAK_RS05670	SAK_1134	3.218777034	0.18704725	1109302	1110225	-	924	pyrB
542	SAK_RS02695	SAK_0542	3.220394278	0.155716174	484866	485060	+	195	-
2123	SAK_RS10695	SAK_2123	3.222873124	0.138762275	2113442	2114455	+	1014	argF
670	SAK_RS03350	SAK_0670	3.231868473	0.589033218	603296	604225	+	930	-
1776	SAK_RS08940	SAK_1776	3.233180483	0.169868628	1769581	1770363	-	783	-
1868	SAK_RS09405	SAK_1868	3.23477503	0.184091563	1863906	1864331	-	426	-
1832	SAK_RS09225	SAK_1832	3.242518111	0.17429977	1826851	1827516	-	666	ulaD
1824	SAK_RS09185	SAK_1824	3.266386348	0.163918506	1818672	1819661	-	990	-
61	SAK_RS00300	SAK_0061	3.280736076	0.108384563	43202	43753	+	552	purN
2124	SAK_RS10700	SAK_2124	3.282496823	0.555188193	2114518	2115945	+	1428	-
2082	SAK_RS10470	SAK_2082	3.283726866	0.145369724	2074551	2075096	-	546	-
957	#N/A	SAK_0957	3.289141132	0.198989025	913411	913539	+	129	-
68	SAK_RS00335	SAK_0068	3.289559717	0.138762275	51031	51918	+	888	-
1808	SAK_RS09100	SAK_1808	3.295835385	0.174968901	1798187	1798579	-	393	-
544	SAK_RS02705	SAK_0544	3.30392563	0.13513782	485614	485925	+	312	-
1637	SAK_RS08250	SAK_1637	3.310969196	0.172717352	1628274	1628753	-	480	nrdR
856	SAK_RS04285	SAK_0856	3.313487975	0.196648029	804260	804388	-	129	-
1770	SAK_RS08910	SAK_1770	3.322344741	0.145369724	1764492	1764791	+	300	-
762	#N/A	SAK_0762	3.341816249	0.169868628	697996	698436	+	441	-
58	SAK_RS00285	SAK_0058	3.346746511	0.11297899	36685	40296	+	3612	-
1448	SAK_RS07280	SAK_1448	3.369228385	0.303440104	1431131	1432495	-	1365	-
54	SAK_RS00265	SAK_0054	3.37786828	0.134569919	33415	34266	+	852	-
246	SAK_RS01210	SAK_0246	3.380616398	0.148556245	209591	209986	+	396	ssb2
1929	SAK_RS09715	SAK_1929	3.381003852	0.147719162	1931917	1932657	-	741	-
2058	SAK_RS10350	SAK_2058	3.387647641	0.132975096	2049856	2050461	+	606	-
2020	SAK_RS10165	SAK_2020	3.387761514	0.132543065	2014759	2015490	+	732	-
1934	SAK_RS09740	SAK_1934	3.390303112	0.145369724	1935386	1935844	-	459	-
1299	SAK_RS06515	SAK_1299	3.392048112	0.11149771	1274549	1275439	-	891	miaA
532	SAK_RS02645	SAK_0532	3.393399928	0.147719162	473979	475256	+	1278	-
365	SAK_RS01810	SAK_0365	3.395403046	0.186437602	312716	312940	+	225	-
1645	SAK_RS08290	SAK_1645	3.396554223	0.122319158	1635672	1636343	+	672	-
811	#N/A	SAK_0811	3.40329892	0.138762275	753210	754436	+	1227	-
466	SAK_RS02320	SAK_0466	3.413776887	0.138762275	411075	412640	+	1566	-
406	SAK_RS02015	SAK_0406	3.427588768	0.163741103	355748	357037	+	1290	-
900	SAK_RS04500	SAK_0900	3.43528724	0.118691185	849720	850382	+	663	-
1048	SAK_RS05240	SAK_1048	3.454514877	0.103346728	1016711	1017100	+	390	cdd
227	SAK_RS01120	SAK_0227	3.456852807	0.145369724	198215	199117	+	903	-
683	SAK_RS03415	SAK_0683	3.458988125	0.11149771	617691	618602	+	912	-
2099	SAK_RS10575	SAK_2099	3.465557534	0.143058407	2089367	2091349	-	1983	-
1665	SAK_RS08385	SAK_1665	3.465724793	0.123356837	1654114	1654827	+	714	glpF
520	SAK_RS02585	SAK_0520	3.467248478	0.138762275	463652	463957	-	306	-
1961	SAK_RS09870	SAK_1961	3.474096757	0.175018813	1953193	1953537	+	345	-
527	SAK_RS02620	SAK_0527	3.474890987	0.155716174	469566	470396	+	831	rhaD
1894	SAK_RS09535	SAK_1894	3.486060837	0.145369724	1895340	1895645	-	306	-
2074	SAK_RS10435	SAK_2074	3.499991667	0.145369724	2069932	2070471	+	540	-
2056	SAK_RS10340	SAK_2056	3.504276064	0.158610161	2047948	2049048	+	1101	-
1597	SAK_RS08055	SAK_1597	3.507646804	0.118937627	1591660	1592529	-	870	livH
441	SAK_RS02190	SAK_0441	3.515797339	0.160561618	388390	388911	+	522	-
1539	SAK_RS07755	SAK_1539	3.517439287	0.173440403	1533802	1534590	-	789	nikD
875	SAK_RS04375	SAK_0875	3.526573517	0.104483905	820537	821007	+	471	ribH

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704	SAK_RS03520	SAK_0704	3.533652257	0.138762275	637083	637262	+	180	-
152	SAK_RS00750	SAK_0152	3.542933407	0.163741103	111228	111692	+	465	-
1726	#N/A	SAK_1726	3.543565494	0.138762275	1714563	1714949	-	387	-
745	SAK_RS03720	SAK_0745	3.544360241	0.138762275	681847	682119	+	273	-
1571	SAK_RS07925	SAK_1571	3.545275619	0.138762275	1565172	1567331	-	2160	-
806	#N/A	SAK_0806	3.569689302	0.105722142	746690	748634	+	1945	-
500	SAK_RS02495	SAK_0500	3.569953466	0.142383873	444087	444500	+	414	nrdI
1312	SAK_RS06580	SAK_1312	3.582717245	0.132543065	1290853	1291350	-	498	-
1867	SAK_RS09400	SAK_1867	3.586399012	0.140920456	1863159	1863773	-	615	-
779	SAK_RS03885	SAK_0779	3.587227489	0.132543065	715000	715851	+	852	-
883	SAK_RS04415	SAK_0883	3.603198474	0.138762275	827279	827668	+	390	-
594	SAK_RS02960	SAK_0594	3.61816072	0.105722142	537139	538833	+	1695	-
1196	SAK_RS05985	SAK_1196	3.621998717	0.134569919	1174266	1175420	-	1155	potA
509	SAK_RS02530	SAK_0509	3.625867301	0.186169556	452881	453198	-	318	-
639	SAK_RS03195	SAK_0639	3.629810952	0.134569919	570359	570790	+	432	-
1753	SAK_RS10780	SAK_1753	3.631812955	0.116292066	1745884	1746807	-	924	-
1124	SAK_RS05620	SAK_1124	3.651601645	0.138762275	1097822	1099099	-	1278	-
1540	SAK_RS07760	SAK_1540	3.668218456	0.138762275	1534578	1535339	-	762	nikC
1659	#N/A	SAK_1659	3.671347515	0.104483905	1650419	1651207	-	789	-
764	SAK_RS03805	SAK_0764	3.684187095	0.123356837	700361	701707	+	1347	-
545	SAK_RS02710	SAK_0545	3.684205458	0.115099042	486193	486771	+	579	-
1101	SAK_RS05505	SAK_1101	3.692950235	0.13513782	1074402	1075244	-	843	-
192	#N/A	SAK_0192	3.702152482	0.138762275	153000	153170	-	171	-
637	SAK_RS03185	SAK_0637	3.717725618	0.138762275	569231	570133	+	903	-
728	SAK_RS03635	SAK_0728	3.728476084	0.169868628	666727	667848	-	1122	-
1458	SAK_RS07330	SAK_1458	3.731866027	0.145369724	1440759	1441913	-	1155	rgpAc
1878	SAK_RS09455	SAK_1878	3.738515026	0.142383873	1877174	1878337	-	1164	-
1876	SAK_RS09445	SAK_1876	3.740965856	0.145369724	1875076	1875420	-	345	-
961	SAK_RS04810	SAK_0961	3.743015443	0.123175947	916042	916710	+	669	-
283	SAK_RS01390	SAK_0283	3.759354677	0.158610161	244336	244977	+	642	-
880	SAK_RS04400	SAK_0880	3.764463295	0.158610161	825116	825733	+	618	-
63	SAK_RS00310	SAK_0063	3.767487991	0.145369724	44545	46092	+	1548	purH
1470	SAK_RS07390	SAK_1470	3.775794318	0.118937627	1452446	1452751	+	306	-
1388	#N/A	SAK_1388	3.780318988	0.140920456	1373542	1373613	-	72	-
956	SAK_RS04790	SAK_0956	3.780451529	0.122319158	912706	913251	+	546	-
1831	SAK_RS09220	SAK_1831	3.78220027	0.114045074	1825984	1826847	-	864	-
234	SAK_RS01155	SAK_0234	3.78807494	0.095981098	201987	203180	+	1194	ackA
1533	SAK_RS07725	SAK_1533	3.821469833	0.151534397	1529882	1530070	-	189	-
282	SAK_RS01385	SAK_0282	3.822138606	0.142383873	244006	244332	+	327	-
450	#N/A	SAK_0450	3.828125246	0.138762275	395439	395526	+	88	-
1330	SAK_RS06695	SAK_1330	3.832363498	0.145369724	1312896	1313210	-	315	-
1926	SAK_RS09700	SAK_1926	3.841757274	0.104483905	1929488	1930333	-	846	pstC
1736	SAK_RS08730	SAK_1736	3.851411948	0.13513782	1726869	1727243	+	375	-
925	SAK_RS04625	SAK_0925	3.866511882	0.142383873	876506	877462	-	957	-
740	SAK_RS03695	SAK_0740	3.879565502	0.123356837	678619	679068	+	450	-
2011	SAK_RS10115	SAK_2011	3.906303198	0.053769112	2005464	2006243	-	780	udp
669	SAK_RS03345	SAK_0669	3.932986106	0.64350579	602620	603312	+	693	ftsE
593	SAK_RS02955	SAK_0593	3.935776438	0.145369724	536118	536852	+	735	-
699	SAK_RS03495	SAK_0699	3.944713043	0.118937627	632126	632782	+	657	-
778	SAK_RS03880	SAK_0778	3.98471269	0.138762275	714126	715043	+	918	-
1593	SAK_RS08035	SAK_1593	3.990506508	0.174388443	1588551	1589210	-	660	-
864	SAK_RS04320	SAK_0864	3.99617556	0.140920456	810540	810938	+	399	-
1914	SAK_RS09640	SAK_1914	4.000139805	0.11149771	1917464	1917742	-	279	-
1083	#N/A	SAK_1083	4.015058598	0.237386666	1056024	1056581	-	558	-
1421	SAK_RS07150	SAK_1421	4.026165339	0.147719162	1402353	1402844	-	492	-
1689	SAK_RS08505	SAK_1689	4.042822368	0.145369724	1675806	1676258	+	453	-
860	SAK_RS04305	SAK_0860	4.101656474	0.11149771	808333	808596	+	264	-
73	SAK_RS00360	SAK_0073	4.106913945	0.11149771	54827	55708	+	882	-
1927	SAK_RS09705	SAK_1927	4.115992335	0.130362767	1930348	1931229	-	882	-
2055	#N/A	SAK_2055	4.127798593	0.129734883	2047627	2047833	+	207	-
866	SAK_RS04330	SAK_0866	4.130012168	0.146980978	811407	811682	-	276	-
774	SAK_RS03860	SAK_0774	4.154658601	0.130362767	709317	709664	-	348	-
747	SAK_RS03730	SAK_0747	4.15736791	0.132975096	683482	684180	+	699	-
2041	SAK_RS10265	SAK_2041	4.193107476	0.145369724	2034215	2034652	-	438	argR
831	SAK_RS04160	SAK_0831	4.215961278	0.104483905	774909	776699	+	1791	-
1617	SAK_RS08155	SAK_1617	4.237678465	0.104483905	1608447	1608989	-	543	-
721	SAK_RS03600	SAK_0721	4.266638529	0.130362767	654203	654733	-	531	-
631	SAK_RS03155	SAK_0631	4.27295764	0.123361093	564138	564494	+	357	-
1154	SAK_RS05770	SAK_1154	4.338350311	0.11297899	1130687	1131259	+	573	-
1297	SAK_RS06505	SAK_1297	4.340702029	0.093228622	1272580	1273227	-	648	-
575	SAK_RS02865	SAK_0575	4.358175161	0.095981098	516395	518236	+	1842	typA
1827	SAK_RS09200	SAK_1827	4.451111289	0.116292066	1822207	1823226	-	1020	-
1580	SAK_RS07970	SAK_1580	4.482156412	0.11297899	1577503	1578345	+	843	-
1186	SAK_RS05935	SAK_1186	4.498893647	0.16335217	1163263	1163943	-	681	radC
1090	SAK_RS05450	SAK_1090	4.518260285	0.095981098	1062626	1062907	-	282	-
1671	SAK_RS08415	SAK_1671	4.526852902	0.11149771	1658621	1658977	-	357	-
141	SAK_RS00695	SAK_0141	4.531193932	0.11297899	100509	100988	+	480	comX
959	SAK_RS04800	SAK_0959	4.543129435	0.097120997	914210	914764	+	555	-
285	SAK_RS01405	SAK_0285	4.552053848	0.155716174	246188	246622	+	435	-
2080	SAK_RS10460	SAK_2080	4.562076644	0.082269681	2073227	2073589	-	363	-
1049	SAK_RS05245	SAK_1049	4.587827647	0.115099042	1017165	1018214	+	1050	-
539	SAK_RS02680	SAK_0539	4.617071287	0.123175947	483167	484036	+	870	-
2010	SAK_RS10110	SAK_2010	4.635932619	0.006747214	2004241	2005443	-	1203	-
1514	#N/A	SAK_1514	4.662414336	0.104483905	1511150	1511293	-	144	rpmG1
377	SAK_RS01870	SAK_0377	4.700361977	0.11149771	325726	327333	+	1608	-
1501	SAK_RS07560	SAK_1501	4.73873366	0.145369724	1497650	1497778	-	129	-
1113	SAK_RS05570	SAK_1113	4.768508687	0.145369724	1087720	1088094	-	375	-
600	SAK_RS02990	SAK_0600	4.828824767	0.138762275	543183	544010	+	828	tlyA
1687	SAK_RS08495	SAK_1687	4.865983993	0.104483905	1673417	1674202	-	786	codY
2078	#N/A	SAK_2078	4.876618416	0.145369724	2072646	2072756	-	111	-
11	SAK_RS00050	SAK_0011	4.892444244	0.14117843	10665	10799	+	135	-
1378	SAK_RS06935	SAK_1378	4.901927333	0.138762275	1364016	1364927	-	912	-
1563	SAK_RS07880	SAK_1563	4.918911112	0.054129749	1559308	1559685	-	378	-

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1052	SAK_RS05260	SAK_1052	5.060122638	0.051933248	1020950	1021906	+	957	-
1826	SAK_RS09195	SAK_1826	5.132035039	0.082269681	1821232	1822188	-	957	-
1915	#N/A	SAK_1915	5.428309724	0.036877032	1917748	1918595	-	848	-
926	SAK_RS04630	SAK_0926	5.446231406	0.11149771	877558	878277	+	720	-
1822	SAK_RS09175	SAK_1822	5.550707512	0.11149771	1816308	1817069	-	762	-
1221	SAK_RS06125	SAK_1221	5.741589625	0.082269681	1195548	1196099	-	552	-
2021	SAK_RS10170	SAK_2021	5.770760919	0.087192822	2015847	2016464	-	618	nrdG
1010	SAK_RS05055	SAK_1010	5.7979383	0.174265958	974284	975636	+	1353	glmM
2097	SAK_RS10565	SAK_2097	6.137811167	0.184091563	2087511	2088866	-	1356	dnaC
2119	SAK_RS10675	SAK_2119	6.689581231	0.369303033	2109898	2110578	-	681	-
475	SAK_RS02370	SAK_0475	6.766968361	0.155716174	419218	420567	+	1350	pgi
295	SAK_RS01455	SAK_0295	8.515919513	0.497962232	252674	252955	+	282	-
1	SAK_RS00005	SAK_0001	NA	NA	101	1462	+	1362	dnaA
2	SAK_RS00010	SAK_0002	NA	NA	1617	2753	+	1137	dnaN
4	SAK_RS00020	SAK_0004	NA	NA	3714	3911	+	198	-
6	SAK_RS00025	SAK_0006	NA	NA	4473	5588	+	1116	ychF
7	SAK_RS00030	SAK_0007	NA	NA	5672	6247	+	576	pth
13	SAK_RS00060	SAK_0013	NA	NA	12087	13361	+	1275	tilS
14	SAK_RS00065	SAK_0014	NA	NA	13366	13908	+	543	hpt
15	SAK_RS00070	SAK_0015	NA	NA	13931	15907	+	1977	ftsH
16	#N/A	SAK_0016	NA	NA	16406	17912	+	1507	rrsA
17	#N/A	SAK_0017	NA	NA	18002	18074	+	73	-
18	#N/A	SAK_0018	NA	NA	18229	21131	+	2903	rrlA
20	#N/A	SAK_0020	NA	NA	21325	21397	+	73	-
21	#N/A	SAK_0021	NA	NA	21400	21472	+	73	-
22	#N/A	SAK_0022	NA	NA	21475	21547	+	73	-
23	#N/A	SAK_0023	NA	NA	21557	21638	+	82	-
24	#N/A	SAK_0024	NA	NA	21649	21721	+	73	-
25	#N/A	SAK_0025	NA	NA	21755	21826	+	72	-
26	#N/A	SAK_0026	NA	NA	21835	21919	+	85	-
27	#N/A	SAK_0027	NA	NA	21931	22004	+	74	-
28	#N/A	SAK_0028	NA	NA	22012	22085	+	74	-
29	#N/A	SAK_0029	NA	NA	22238	23744	+	1507	rrsB
30	#N/A	SAK_0030	NA	NA	23834	23906	+	73	-
31	#N/A	SAK_0031	NA	NA	24061	26963	+	2903	rrlB
33	#N/A	SAK_0033	NA	NA	27157	27229	+	73	-
34	#N/A	SAK_0034	NA	NA	27232	27304	+	73	-
35	#N/A	SAK_0035	NA	NA	27307	27379	+	73	-
36	#N/A	SAK_0036	NA	NA	27389	27470	+	82	-
37	#N/A	SAK_0037	NA	NA	27481	27553	+	73	-
38	#N/A	SAK_0038	NA	NA	27587	27658	+	72	-
39	#N/A	SAK_0039	NA	NA	27667	27751	+	85	-
40	#N/A	SAK_0040	NA	NA	27763	27836	+	74	-
41	#N/A	SAK_0041	NA	NA	27844	27917	+	74	-
42	#N/A	SAK_0042	NA	NA	27933	28006	+	74	-
43	#N/A	SAK_0043	NA	NA	28026	28099	+	74	-
44	#N/A	SAK_0044	NA	NA	28115	28204	+	90	-
46	#N/A	SAK_0046	NA	NA	28291	28363	+	73	-
47	#N/A	SAK_0047	NA	NA	28383	28453	+	71	-
48	#N/A	SAK_0048	NA	NA	28488	28561	+	74	-
49	#N/A	SAK_0049	NA	NA	28575	28662	+	88	-
50	SAK_RS00245	SAK_0050	NA	NA	28898	30199	+	1302	pcsB
51	SAK_RS00250	SAK_0051	NA	NA	30323	31291	+	969	prs
55	SAK_RS00270	SAK_0055	NA	NA	34344	35336	+	993	plsX
56	SAK_RS00275	SAK_0056	NA	NA	35347	35586	+	240	-
57	SAK_RS00280	SAK_0057	NA	NA	35710	36417	+	708	purC
77	SAK_RS00380	SAK_0077	NA	NA	59350	59838	+	489	purE
90	SAK_RS00445	SAK_0090	NA	NA	75998	76306	+	309	rpsJ
91	SAK_RS00450	SAK_0091	NA	NA	76411	77037	+	627	rplC
92	SAK_RS00455	SAK_0092	NA	NA	77061	77684	+	624	rplD
93	SAK_RS00460	SAK_0093	NA	NA	77684	77980	+	297	rplW
94	SAK_RS00465	SAK_0094	NA	NA	77998	78831	+	834	rplB
95	SAK_RS00470	SAK_0095	NA	NA	78930	79208	+	279	rpsS
96	SAK_RS00475	SAK_0096	NA	NA	79224	79568	+	345	rplV
97	SAK_RS00480	SAK_0097	NA	NA	79581	80234	+	654	rpsC
98	SAK_RS00485	SAK_0098	NA	NA	80238	80651	+	414	rplP
99	SAK_RS00490	SAK_0099	NA	NA	80661	80867	+	207	rpmC
100	SAK_RS00495	SAK_0100	NA	NA	80893	81153	+	261	rpsQ
101	SAK_RS00500	SAK_0101	NA	NA	81178	81546	+	369	rplN
102	SAK_RS00505	SAK_0102	NA	NA	81626	81931	+	306	rplX
103	SAK_RS00510	SAK_0103	NA	NA	81955	82497	+	543	rplE
104	SAK_RS00515	SAK_0104	NA	NA	82515	82700	+	186	rpsN
105	SAK_RS00520	SAK_0105	NA	NA	82855	83253	+	399	rpsH
106	SAK_RS00525	SAK_0106	NA	NA	83363	83899	+	537	rplF
108	SAK_RS00535	SAK_0108	NA	NA	84375	84869	+	495	rpsE
109	SAK_RS00540	SAK_0109	NA	NA	84884	85063	+	180	rpmD
110	SAK_RS00545	SAK_0110	NA	NA	85188	85628	+	441	rplO
111	SAK_RS00550	SAK_0111	NA	NA	85649	86953	+	1305	secY
112	SAK_RS00555	SAK_0112	NA	NA	87048	87686	+	639	adk
113	SAK_RS00560	SAK_0113	NA	NA	87802	88020	+	219	infA
114	SAK_RS00565	SAK_0114	NA	NA	88180	88545	+	366	rpsM
115	SAK_RS00570	SAK_0115	NA	NA	88563	88946	+	384	rpsK
116	SAK_RS00575	SAK_0116	NA	NA	88996	89934	+	939	rpoA
117	SAK_RS00580	SAK_0117	NA	NA	89949	90335	+	387	rplQ
118	#N/A	SAK_0118	NA	NA	90927	92433	+	1507	rrsC
119	#N/A	SAK_0119	NA	NA	92523	92595	+	73	-
120	#N/A	SAK_0120	NA	NA	92752	95654	+	2903	rrlC
122	#N/A	SAK_0122	NA	NA	95848	95920	+	73	-
123	#N/A	SAK_0123	NA	NA	95923	95995	+	73	-
124	#N/A	SAK_0124	NA	NA	95998	96070	+	73	-
125	#N/A	SAK_0125	NA	NA	96080	96161	+	82	-
126	#N/A	SAK_0126	NA	NA	96172	96244	+	73	-
127	#N/A	SAK_0127	NA	NA	96273	96349	+	77	-

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128	#N/A	SAK_0128	NA	NA	96357	96428	+	72	-
129	#N/A	SAK_0129	NA	NA	96442	96531	+	90	-
131	#N/A	SAK_0131	NA	NA	96618	96690	+	73	-
132	#N/A	SAK_0132	NA	NA	96702	96782	+	81	-
133	#N/A	SAK_0133	NA	NA	96789	96859	+	71	-
134	#N/A	SAK_0134	NA	NA	96874	96946	+	73	-
135	#N/A	SAK_0135	NA	NA	96953	97024	+	72	-
136	#N/A	SAK_0136	NA	NA	97035	97118	+	84	-
138	#N/A	SAK_0138	NA	NA	98033	98203	+	171	-
145	SAK_RS00715	SAK_0145	NA	NA	103266	104300	+	1035	hrcA
146	SAK_RS00720	SAK_0146	NA	NA	104342	104875	+	534	grpE
147	SAK_RS00725	SAK_0147	NA	NA	105056	106885	+	1830	dnaK
148	SAK_RS00730	SAK_0148	NA	NA	107174	108289	+	1116	dnaJ
151	SAK_RS00745	SAK_0151	NA	NA	110460	111218	+	759	-
156	SAK_RS00770	SAK_0156	NA	NA	114766	115341	+	576	rpoE
157	SAK_RS00775	SAK_0157	NA	NA	115614	117218	+	1605	pyrG
159	#N/A	SAK_0159	NA	NA	118300	118385	+	86	-
160	SAK_RS00790	SAK_0160	NA	NA	118448	118894	+	447	dut
162	SAK_RS00800	SAK_0162	NA	NA	120556	121053	+	498	-
165	SAK_RS00815	SAK_0165	NA	NA	124303	125739	+	1437	gltX
178	SAK_RS00880	SAK_0178	NA	NA	138113	138994	+	882	fba
181	SAK_RS00895	SAK_0181	NA	NA	140555	140920	+	366	-
182	SAK_RS00900	SAK_0182	NA	NA	140953	142584	+	1632	-
185	SAK_RS00920	SAK_0185	NA	NA	145294	145512	-	219	-
198	SAK_RS00980	SAK_0198	NA	NA	159583	160743	+	1161	-
199	SAK_RS00985	SAK_0199	NA	NA	160908	161678	+	771	sufC
200	SAK_RS00990	SAK_0200	NA	NA	161715	162977	+	1263	sufD
201	SAK_RS00995	SAK_0201	NA	NA	162979	164211	+	1233	sufS
202	SAK_RS01000	SAK_0202	NA	NA	164198	164641	+	444	-
203	SAK_RS01005	SAK_0203	NA	NA	164741	166159	+	1419	sufB
211	#N/A	SAK_0211	NA	NA	175172	176678	+	1507	rrsD
212	#N/A	SAK_0212	NA	NA	176768	176840	+	73	-
213	#N/A	SAK_0213	NA	NA	176997	179899	+	2903	rrlD
215	#N/A	SAK_0215	NA	NA	180095	180168	+	74	-
221	SAK_RS01095	SAK_0221	NA	NA	185024	186283	-	1260	tyrS
223	SAK_RS01105	SAK_0223	NA	NA	189215	192790	+	3576	rpoB
231	SAK_RS01140	SAK_0231	NA	NA	200125	200517	+	393	-
235	SAK_RS01160	SAK_0235	NA	NA	203332	203538	+	207	-
265	SAK_RS01305	SAK_0265	NA	NA	231115	231384	+	270	rpsO
267	SAK_RS01315	SAK_0267	NA	NA	233896	234648	+	753	-
268	SAK_RS01320	SAK_0268	NA	NA	234657	235241	+	585	cysE
270	SAK_RS01330	SAK_0270	NA	NA	235430	236773	+	1344	cysS
275	#N/A	SAK_0275	NA	NA	239823	239942	+	120	-
276	SAK_RS01355	SAK_0276	NA	NA	240359	240805	+	447	rplM
277	SAK_RS01360	SAK_0277	NA	NA	240826	241218	+	393	rpsI
279	SAK_RS01370	SAK_0279	NA	NA	242569	243120	-	552	-
280	SAK_RS01375	SAK_0280	NA	NA	243285	243578	+	294	-
281	SAK_RS01380	SAK_0281	NA	NA	243719	244000	+	282	-
289	SAK_RS01425	SAK_0289	NA	NA	249463	249750	-	288	-
296	#N/A	SAK_0296	NA	NA	253046	253144	+	99	-
304	#N/A	SAK_0304	NA	NA	259761	261267	+	1507	rrsE
305	#N/A	SAK_0305	NA	NA	261357	261429	+	73	-
306	#N/A	SAK_0306	NA	NA	261584	264486	+	2903	rrlE
308	#N/A	SAK_0308	NA	NA	264680	264752	+	73	-
309	#N/A	SAK_0309	NA	NA	264758	264828	+	71	-
310	#N/A	SAK_0310	NA	NA	264865	264941	+	77	-
311	#N/A	SAK_0311	NA	NA	264949	265020	+	72	-
312	#N/A	SAK_0312	NA	NA	265034	265123	+	90	-
314	#N/A	SAK_0314	NA	NA	265210	265282	+	73	-
315	#N/A	SAK_0315	NA	NA	265294	265374	+	81	-
316	#N/A	SAK_0316	NA	NA	265381	265451	+	71	-
317	#N/A	SAK_0317	NA	NA	265466	265538	+	73	-
318	#N/A	SAK_0318	NA	NA	265545	265616	+	72	-
319	#N/A	SAK_0319	NA	NA	265627	265710	+	84	-
323	SAK_RS01595	SAK_0323	NA	NA	269757	270029	+	273	-
334	SAK_RS01655	SAK_0334	NA	NA	278593	279309	-	717	-
336	SAK_RS01665	SAK_0336	NA	NA	280277	280588	-	312	-
340	SAK_RS01685	SAK_0340	NA	NA	283887	284801	+	915	glyQ
342	SAK_RS01695	SAK_0342	NA	NA	285446	287485	+	2040	glyS
343	SAK_RS01700	SAK_0343	NA	NA	287497	287754	+	258	-
350	SAK_RS01735	SAK_0350	NA	NA	295252	297237	+	1986	tkt
358	SAK_RS01775	SAK_0358	NA	NA	304962	305288	+	327	-
359	SAK_RS01780	SAK_0359	NA	NA	305397	307550	+	2154	pbpX
360	SAK_RS01785	SAK_0360	NA	NA	307552	308562	+	1011	mraY
361	SAK_RS01790	SAK_0361	NA	NA	308660	310003	+	1344	-
363	SAK_RS01800	SAK_0363	NA	NA	311048	311851	+	804	-
364	SAK_RS01805	SAK_0364	NA	NA	311851	312594	+	744	-
366	SAK_RS01815	SAK_0366	NA	NA	313009	313923	+	915	trxB
367	SAK_RS01820	SAK_0367	NA	NA	314081	315541	+	1461	-
368	SAK_RS01825	SAK_0368	NA	NA	315538	316359	+	822	nadE
373	SAK_RS01850	SAK_0373	NA	NA	321398	321730	+	333	-
383	SAK_RS01900	SAK_0383	NA	NA	331680	332309	+	630	gmk
384	SAK_RS01905	SAK_0384	NA	NA	332332	332646	+	315	rpoZ
386	SAK_RS01915	SAK_0386	NA	NA	335157	336092	+	936	fmt
388	SAK_RS01925	SAK_0388	NA	NA	337442	338179	+	738	stp1
392	SAK_RS01945	SAK_0392	NA	NA	341999	342640	+	642	-
394	SAK_RS01955	SAK_0394	NA	NA	344066	344440	+	375	-
398	SAK_RS01975	SAK_0398	NA	NA	347445	347768	+	324	-
399	SAK_RS01980	SAK_0399	NA	NA	347785	348105	+	321	-
409	#N/A	SAK_0409	NA	NA	358663	360169	+	1507	rrsF
410	#N/A	SAK_0410	NA	NA	360259	360331	+	73	-
411	#N/A	SAK_0411	NA	NA	360486	363388	+	2903	rrlF
413	#N/A	SAK_0413	NA	NA	363584	363657	+	74	-

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416	SAK_RS02065	SAK_0416	NA	NA	366106	366897	+	792	-
417	SAK_RS02070	SAK_0417	NA	NA	366993	367427	+	435	-
418	SAK_RS02075	SAK_0418	NA	NA	367427	368398	+	972	fabH
419	SAK_RS02080	SAK_0419	NA	NA	368456	368680	+	225	acpP
420	SAK_RS02085	SAK_0420	NA	NA	368835	369794	+	960	fabK
421	SAK_RS02090	SAK_0421	NA	NA	369814	370740	+	927	fabD
422	SAK_RS02095	SAK_0422	NA	NA	370749	371483	+	735	fabG
423	SAK_RS02100	SAK_0423	NA	NA	371499	372731	+	1233	fabF
424	SAK_RS02105	SAK_0424	NA	NA	372733	373233	+	501	accB
425	SAK_RS02110	SAK_0425	NA	NA	373230	373652	+	423	fabZ
426	SAK_RS02115	SAK_0426	NA	NA	373690	375060	+	1371	accC
427	SAK_RS02120	SAK_0427	NA	NA	375069	375944	+	876	accD
428	SAK_RS02125	SAK_0428	NA	NA	375937	376710	+	774	accA
430	SAK_RS02135	SAK_0430	NA	NA	377858	379135	-	1278	serS
440	SAK_RS02185	SAK_0440	NA	NA	387888	388397	+	510	-
448	SAK_RS02230	SAK_0448	NA	NA	393970	394770	+	801	-
451	SAK_RS02245	SAK_0451	NA	NA	395978	396361	+	384	-
452	SAK_RS02250	SAK_0452	NA	NA	396397	397548	+	1152	nusA
453	SAK_RS02255	SAK_0453	NA	NA	397570	397866	+	297	ylxR
454	SAK_RS02260	SAK_0454	NA	NA	397859	398161	+	303	-
456	SAK_RS02270	SAK_0456	NA	NA	401073	401423	+	351	rbfA
471	SAK_RS02345	SAK_0471	NA	NA	416668	416979	+	312	-
474	SAK_RS02360	SAK_0474	NA	NA	418440	418946	+	507	-
479	SAK_RS02390	SAK_0479	NA	NA	423350	424249	-	900	galU
480	SAK_RS02395	SAK_0480	NA	NA	424286	425302	-	1017	gpsA
481	SAK_RS02400	SAK_0481	NA	NA	425472	425801	+	330	rnpA
484	#N/A	SAK_0484	NA	NA	427806	429312	+	1507	rrsG
485	#N/A	SAK_0485	NA	NA	429402	429474	+	73	-
486	#N/A	SAK_0486	NA	NA	429629	432531	+	2903	rrlG
488	#N/A	SAK_0488	NA	NA	432725	432797	+	73	-
489	#N/A	SAK_0489	NA	NA	432803	432873	+	71	-
490	#N/A	SAK_0490	NA	NA	432910	432986	+	77	-
491	#N/A	SAK_0491	NA	NA	432994	433065	+	72	-
492	SAK_RS02455	SAK_0492	NA	NA	433180	433713	-	534	-
507	#N/A	SAK_0507	NA	NA	452511	452633	-	123	-
524	SAK_RS02605	SAK_0524	NA	NA	467448	467897	+	450	-
525	SAK_RS02610	SAK_0525	NA	NA	467916	468194	+	279	-
530	SAK_RS02635	SAK_0530	NA	NA	472341	472625	+	285	-
543	SAK_RS02700	SAK_0543	NA	NA	485251	485505	+	255	-
547	SAK_RS02720	SAK_0547	NA	NA	487482	490136	+	2655	valS
555	SAK_RS02765	SAK_0555	NA	NA	497535	498020	+	486	coaD
565	SAK_RS02815	SAK_0565	NA	NA	508803	509342	-	540	-
577	SAK_RS02875	SAK_0577	NA	NA	518656	520011	+	1356	murD
578	SAK_RS02880	SAK_0578	NA	NA	520014	521090	+	1077	murG
580	SAK_RS02890	SAK_0580	NA	NA	522502	523875	+	1374	ftsA
581	SAK_RS02895	SAK_0581	NA	NA	523897	525177	+	1281	ftsZ
587	SAK_RS02925	SAK_0587	NA	NA	528586	531378	+	2793	ileS
591	SAK_RS02945	SAK_0591	NA	NA	535061	535291	+	231	-
595	SAK_RS02965	SAK_0595	NA	NA	538972	539826	+	855	folD
603	SAK_RS03005	SAK_0603	NA	NA	546253	547089	+	837	-
606	SAK_RS03020	SAK_0606	NA	NA	548601	548876	+	276	hup
610	SAK_RS03040	SAK_0610	NA	NA	550862	551221	-	360	-
612	SAK_RS03050	SAK_0612	NA	NA	551729	552061	+	333	-
614	#N/A	SAK_0614	NA	NA	553227	553376	+	150	-
615	SAK_RS03075	SAK_0615	NA	NA	553649	553939	+	291	-
616	SAK_RS03080	SAK_0616	NA	NA	553926	554609	+	684	-
618	SAK_RS03090	SAK_0618	NA	NA	556053	556535	+	483	-
621	SAK_RS03105	SAK_0621	NA	NA	559264	559545	+	282	-
622	SAK_RS03110	SAK_0622	NA	NA	559624	559920	+	297	-
623	#N/A	SAK_0623	NA	NA	560174	560338	+	165	-
624	#N/A	SAK_0624	NA	NA	560608	560751	+	144	-
625	SAK_RS03125	SAK_0625	NA	NA	560748	561260	+	513	-
626	SAK_RS03130	SAK_0626	NA	NA	561281	561580	+	300	-
627	SAK_RS03135	SAK_0627	NA	NA	561768	561962	+	195	-
640	SAK_RS03200	SAK_0640	NA	NA	570741	571079	+	339	-
641	SAK_RS03210	SAK_0641	NA	NA	571309	571644	+	336	-
643	SAK_RS03220	SAK_0643	NA	NA	572211	572456	+	246	-
644	SAK_RS03225	SAK_0644	NA	NA	572471	572842	+	372	-
649	SAK_RS03250	SAK_0649	NA	NA	582518	582910	+	393	-
650	#N/A	SAK_0650	NA	NA	582933	583061	+	129	-
651	SAK_RS03260	SAK_0651	NA	NA	583070	583372	+	303	-
652	SAK_RS03265	SAK_0652	NA	NA	583365	583592	+	228	-
654	#N/A	SAK_0654	NA	NA	585311	585514	-	204	-
658	SAK_RS03290	SAK_0658	NA	NA	587845	589080	-	1236	fibB
659	SAK_RS03295	SAK_0659	NA	NA	589099	590310	-	1212	-
664	SAK_RS03320	SAK_0664	NA	NA	594548	597232	+	2685	-
668	#N/A	SAK_0668	NA	NA	601503	602601	+	1099	prfB
677	SAK_RS03385	SAK_0677	NA	NA	612097	613443	+	1347	asnC
686	SAK_RS03430	SAK_0686	NA	NA	621789	622049	-	261	rpmE2
689	SAK_RS03445	SAK_0689	NA	NA	624440	624883	+	444	-
692	SAK_RS03460	SAK_0692	NA	NA	627004	627351	+	348	rplS
693	#N/A	SAK_0693	NA	NA	627462	627533	+	72	-
708	SAK_RS03540	SAK_0708	NA	NA	639802	641754	+	1953	gyrB
709	SAK_RS03545	SAK_0709	NA	NA	641848	643572	+	1725	ezrA
713	SAK_RS03565	SAK_0713	NA	NA	645479	646786	+	1308	eno
726	#N/A	SAK_0726	NA	NA	665978	666142	-	165	-
729	SAK_RS03640	SAK_0729	NA	NA	667841	668164	-	324	-
731	#N/A	SAK_0731	NA	NA	670867	670971	+	105	-
732	SAK_RS03650	SAK_0732	NA	NA	671130	671411	+	282	-
736	SAK_RS03665	SAK_0736	NA	NA	673651	674688	+	1038	metK
741	SAK_RS03700	SAK_0741	NA	NA	679165	679578	+	414	-
743	SAK_RS03710	SAK_0743	NA	NA	681223	681525	+	303	-
749	SAK_RS03740	SAK_0749	NA	NA	685399	685656	+	258	-

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750	SAK_RS03745	SAK_0750	NA	NA	685656	685994	+	339	-	
751	SAK_RS03750	SAK_0751	NA	NA	685987	686355	+	369	-	
752	SAK_RS03755	SAK_0752	NA	NA	686364	686690	+	327	-	
753	SAK_RS03760	SAK_0753	NA	NA	686693	687262	+	570	-	
755	#N/A	SAK_0755	NA	NA	687762	687857	+	96	-	
770	#N/A	SAK_0770	NA	NA	706354	706590	-	237	-	
783	#N/A	SAK_0783	NA	NA	720824	720916	+	93	-	
785	SAK_RS03915	SAK_0785	NA	NA	722922	723191	+	270	-	
802	SAK_RS04000	SAK_0802	NA	NA	739493	739834	+	342	-	
833	SAK_RS04170	SAK_0833	NA	NA	778052	779056	+	1005	ccpA	
836	SAK_RS04185	SAK_0836	NA	NA	781699	783033	+	1335	-	
841	SAK_RS04210	SAK_0841	NA	NA	788259	788909	-	651	-	
842	SAK_RS04215	SAK_0842	NA	NA	788921	789616	-	696	-	
844	SAK_RS04225	SAK_0844	NA	NA	790441	791196	-	756	-	
845	SAK_RS04230	SAK_0845	NA	NA	791536	792246	+	711	-	
849	SAK_RS04250	SAK_0849	NA	NA	794948	795634	+	687	rnc	
861	#N/A	SAK_0861	NA	NA	808574	808708	+	135	-	
862	SAK_RS04310	SAK_0862	NA	NA	808824	809759	+	936	hprK	
876	SAK_RS04380	SAK_0876	NA	NA	821082	822572	-	1491	lysS	
887	SAK_RS04435	SAK_0887	NA	NA	834256	835452	+	1197	tuf	
888	SAK_RS04440	SAK_0888	NA	NA	835633	836391	+	759	tpiA	
889	SAK_RS04445	SAK_0889	NA	NA	836568	837260	+	693	gpmA	
891	SAK_RS04455	SAK_0891	NA	NA	839449	840045	+	597	recR	
892	SAK_RS04460	SAK_0892	NA	NA	840186	841232	+	1047	ddl	
893	SAK_RS04465	SAK_0893	NA	NA	841379	842746	+	1368	murF	
903	SAK_RS04515	SAK_0903	NA	NA	853234	853500	-	267	-	
905	SAK_RS04525	SAK_0905	NA	NA	854392	855132	+	741	-	
912	SAK_RS04560	SAK_0912	NA	NA	862005	863042	+	1038	holA	
934	SAK_RS04670	SAK_0934	NA	NA	885656	888274	+	2619	alaS	
937	SAK_RS04685	SAK_0937	NA	NA	890399	890692	+	294	-	
942	SAK_RS04710	SAK_0942	NA	NA	894163	895122	-	960	nrdF	
943	SAK_RS04715	SAK_0943	NA	NA	895325	897484	-	2160	-	
944	SAK_RS04720	SAK_0944	NA	NA	897562	897786	-	225	-	
945	SAK_RS04725	SAK_0945	NA	NA	898169	898432	+	264	ptsH	
946	SAK_RS04730	SAK_0946	NA	NA	898437	900170	+	1734	ptsI	
947	SAK_RS04735	SAK_0947	NA	NA	900320	901747	+	1428	gapN	
952	SAK_RS04760	SAK_0952	NA	NA	905613	907277	+	1665	dnaX	
954	SAK_RS04775	SAK_0954	NA	NA	908661	909857	+	1197	metK	
960	SAK_RS04805	SAK_0960	NA	NA	914768	916054	+	1287	-	
969	SAK_RS04850	SAK_0969	NA	NA	923071	923931	+	861	map	
973	SAK_RS04870	SAK_0973	NA	NA	926156	928114	+	1959	ligA	
980	SAK_RS04905	SAK_0980	NA	NA	937586	937786	+	201	atpE	
981	SAK_RS04910	SAK_0981	NA	NA	937819	938535	+	717	atpB	
982	SAK_RS04915	SAK_0982	NA	NA	938553	939050	+	498	atpF	
983	SAK_RS04920	SAK_0983	NA	NA	939050	939586	+	537	atpH	
984	SAK_RS04925	SAK_0984	NA	NA	939602	941107	+	1506	atpA	
985	SAK_RS04930	SAK_0985	NA	NA	941123	942004	+	882	atpG	
986	SAK_RS04935	SAK_0986	NA	NA	942078	943484	+	1407	atpD	
987	SAK_RS04940	SAK_0987	NA	NA	943497	943910	+	414	atpC	
992	SAK_RS04965	SAK_0992	NA	NA	946956	947996	+	1041	pheS	
994	SAK_RS04975	SAK_0994	NA	NA	948654	951059	+	2406	pheT	
999	SAK_RS05000	SAK_0999	NA	NA	960017	961393	-	1377	trmE	
1006	SAK_RS05035	SAK_1006	NA	NA	970149	970934	-	786	-	
1007	SAK_RS05040	SAK_1007	NA	NA	970934	972277	-	1344	-	
1008	SAK_RS05045	SAK_1008	NA	NA	972417	973268	+	852	-	
1030	#N/A	SAK_1030	NA	NA	999967	1000313	-	347	-	
1034	SAK_RS05175	SAK_1034	NA	NA	1002547	1002915	-	369	-	
1035	SAK_RS05180	SAK_1035	NA	NA	1003060	1006164	+	3105	dnaE	
1036	SAK_RS05185	SAK_1036	NA	NA	1006245	1007267	+	1023	pfkA	
1037	SAK_RS05190	SAK_1037	NA	NA	1007316	1008818	+	1503	pyk	
1040	SAK_RS05200	SAK_1040	NA	NA	1009815	1011629	+	1815	glmS	
1045	SAK_RS05225	SAK_1045	NA	NA	1014467	1014700	-	234	rpsT	
1055	SAK_RS05275	SAK_1055	NA	NA	1024830	1027289	+	2460	gyrA	
1056	SAK_RS05280	SAK_1056	NA	NA	1027296	1028039	+	744	-	
1057	SAK_RS05285	SAK_1057	NA	NA	1028055	1028468	+	414	-	
1062	SAK_RS05310	SAK_1062	NA	NA	1031904	1033466	-	1563	guaA	
1069	SAK_RS05345	SAK_1069	NA	NA	1039301	1040053	+	753	-	
1076	SAK_RS05380	SAK_1076	NA	NA	1047746	1048432	-	687	satD	
1077	SAK_RS05385	SAK_1077	NA	NA	1048499	1050064	-	1566	ffh	
1082	SAK_RS05410	SAK_1082	NA	NA	1055337	1055990	-	654	phoU	
1084	SAK_RS05420	SAK_1084	NA	NA	1056794	1057597	-	804	pstB	
1085	SAK_RS05425	SAK_1085	NA	NA	1057609	1058496	-	888	pstA	
1086	SAK_RS05430	SAK_1086	NA	NA	1058486	1059403	-	918	pstC	
1087	SAK_RS05435	SAK_1087	NA	NA	1059449	1060309	-	861	-	
1092	SAK_RS05460	SAK_1092	NA	NA	1063356	1064288	-	933	ribF	
1108	SAK_RS05540	SAK_1108	NA	NA	1080719	1081570	-	852	rbgA	
1114	#N/A	SAK_1114	NA	NA	1088185	1088328	-	144	-	
1126	SAK_RS05630	SAK_1126	NA	NA	1099325	1099798	-	474	-	
1148	SAK_RS05740	SAK_1148	NA	NA	1125893	1126225	-	333	-	
1152	SAK_RS05760	SAK_1152	NA	NA	1129405	1130106	+	702	coaB	
1155	SAK_RS05775	SAK_1155	NA	NA	1131369	1133087	+	1719	-	
1161	SAK_RS05810	SAK_1161	NA	NA	1139760	1140356	-	597	-	
1163	SAK_RS05820	SAK_1163	NA	NA	1141179	1142258	-	1080	prfA	
1174	SAK_RS05875	SAK_1174	NA	NA	1152058	1152729	+	672	-	
1177	SAK_RS05890	SAK_1177	NA	NA	1155758	1156750	-	993	eutD	
1179	SAK_RS05900	SAK_1179	NA	NA	1157657	1158484	-	828	ppnK	
1185	SAK_RS05930	SAK_1185	NA	NA	1162618	1163250	+	633	-	
1197	SAK_RS05990	SAK_1197	NA	NA	1175469	1176371	-	903	murB	
1198	SAK_RS05995	SAK_1198	NA	NA	1176515	1177003	-	489	folK	
1199	SAK_RS06000	SAK_1199	NA	NA	1177000	1177362	-	363	folB	
1200	SAK_RS06005	SAK_1200	NA	NA	1177364	1178167	-	804	folP	
1201	SAK_RS06010	SAK_1201	NA	NA	1178171	1178734	-	564	folE	
1202	SAK_RS06015	SAK_1202	NA	NA	1178753	1180015	-	1263	folC	

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1215	SAK_RS06090	SAK_1215	NA	NA	1191853	1192041	+	189	-
1220	SAK_RS06120	SAK_1220	NA	NA	1194743	1195384	-	642	-
1237	SAK_RS06205	SAK_1237	NA	NA	1208516	1209718	-	1203	rpsA
1238	#N/A	SAK_1238	NA	NA	1209841	1209915	-	75	-
1239	#N/A	SAK_1239	NA	NA	1209921	1210001	-	81	-
1243	SAK_RS06235	SAK_1243	NA	NA	1214103	1216031	-	1929	parE
1244	SAK_RS06240	SAK_1244	NA	NA	1216181	1216804	+	624	-
1270	SAK_RS06370	SAK_1270	NA	NA	1240353	1241024	-	672	rpiA
1273	SAK_RS06385	SAK_1273	NA	NA	1242907	1244568	-	1662	-
1285	SAK_RS06445	SAK_1285	NA	NA	1259045	1260091	-	1047	rfbB
1286	SAK_RS06450	SAK_1286	NA	NA	1260298	1260891	-	594	rmlC
1287	SAK_RS06455	SAK_1287	NA	NA	1260891	1261760	-	870	rfbA
1290	SAK_RS06470	SAK_1290	NA	NA	1263709	1264392	-	684	-
1291	SAK_RS06475	SAK_1291	NA	NA	1264496	1265176	-	681	-
1296	SAK_RS06500	SAK_1296	NA	NA	1271609	1272538	-	930	rnz
1314	SAK_RS06590	SAK_1314	NA	NA	1292358	1292648	+	291	-
1315	SAK_RS06595	SAK_1315	NA	NA	1292684	1293463	+	780	-
1322	SAK_RS06640	SAK_1322	NA	NA	1304188	1304478	+	291	-
1323	SAK_RS06645	SAK_1323	NA	NA	1304514	1305275	+	762	-
1334	SAK_RS06715	SAK_1334	NA	NA	1319059	1319424	-	366	rplL
1335	SAK_RS06720	SAK_1335	NA	NA	1319488	1319988	-	501	rplJ
1342	SAK_RS06755	SAK_1342	NA	NA	1327092	1327688	-	597	engB
1345	SAK_RS06770	SAK_1345	NA	NA	1329143	1329637	-	495	folA
1346	SAK_RS06775	SAK_1346	NA	NA	1329717	1330556	-	840	thyA
1347	SAK_RS06780	SAK_1347	NA	NA	1330710	1331882	+	1173	-
1348	SAK_RS06785	SAK_1348	NA	NA	1331884	1333167	+	1284	-
1350	SAK_RS06795	SAK_1350	NA	NA	1333713	1334357	+	645	-
1355	SAK_RS06820	SAK_1355	NA	NA	1337637	1338629	-	993	-
1356	SAK_RS06825	SAK_1356	NA	NA	1338622	1339566	-	945	mvaD
1357	SAK_RS06830	SAK_1357	NA	NA	1339548	1340426	-	879	mvk
1372	SAK_RS06905	SAK_1372	NA	NA	1358095	1359288	-	1194	papS
1384	SAK_RS06965	SAK_1384	NA	NA	1371166	1372158	-	993	-
1385	SAK_RS06970	SAK_1385	NA	NA	1372139	1372894	-	756	trmD
1386	SAK_RS06975	SAK_1386	NA	NA	1372881	1373399	-	519	rimM
1387	#N/A	SAK_1387	NA	NA	1373462	1373533	-	72	-
1390	SAK_RS06995	SAK_1390	NA	NA	1375364	1375606	-	243	-
1391	SAK_RS07000	SAK_1391	NA	NA	1375616	1375888	-	273	rpsP
1400	SAK_RS07045	SAK_1400	NA	NA	1384262	1385167	-	906	-
1401	SAK_RS07050	SAK_1401	NA	NA	1385383	1385676	-	294	rpmA
1402	SAK_RS07055	SAK_1402	NA	NA	1385698	1386036	-	339	-
1403	SAK_RS07060	SAK_1403	NA	NA	1386043	1386357	-	315	rplU
1415	SAK_RS07120	SAK_1415	NA	NA	1399557	1399916	-	360	rplT
1416	SAK_RS07125	SAK_1416	NA	NA	1399974	1400174	-	201	rpmI
1417	SAK_RS07130	SAK_1417	NA	NA	1400214	1400744	-	531	infC
1418	SAK_RS07135	SAK_1418	NA	NA	1400905	1401588	-	684	cmk
1420	SAK_RS07145	SAK_1420	NA	NA	1402169	1402366	+	198	-
1423	SAK_RS07160	SAK_1423	NA	NA	1404228	1405862	-	1635	-
1424	SAK_RS07165	SAK_1424	NA	NA	1405986	1407440	+	1455	murE
1430	SAK_RS07195	SAK_1430	NA	NA	1412127	1413062	-	936	ppaC
1446	SAK_RS07270	SAK_1446	NA	NA	1428862	1429710	-	849	-
1447	SAK_RS07275	SAK_1447	NA	NA	1429707	1431131	-	1425	-
1449	SAK_RS07285	SAK_1449	NA	NA	1432497	1433444	-	948	-
1450	SAK_RS07290	SAK_1450	NA	NA	1433453	1434388	-	936	-
1451	SAK_RS07295	SAK_1451	NA	NA	1434390	1435445	-	1056	-
1452	SAK_RS07300	SAK_1452	NA	NA	1435448	1436167	-	720	ispD
1453	SAK_RS07305	SAK_1453	NA	NA	1436170	1436994	-	825	licD2
1454	SAK_RS07310	SAK_1454	NA	NA	1437019	1438752	-	1734	-
1455	SAK_RS07315	SAK_1455	NA	NA	1438745	1439098	-	354	-
1456	SAK_RS07320	SAK_1456	NA	NA	1439095	1439823	-	729	-
1457	SAK_RS07325	SAK_1457	NA	NA	1439828	1440769	-	942	-
1459	SAK_RS07335	SAK_1459	NA	NA	1442030	1442884	-	855	rfbD
1461	SAK_RS07345	SAK_1461	NA	NA	1443424	1444533	-	1110	rpoD
1462	SAK_RS07350	SAK_1462	NA	NA	1444541	1446322	-	1782	dnaG
1464	SAK_RS07360	SAK_1464	NA	NA	1447013	1447189	-	177	rpsU
1473	SAK_RS07405	SAK_1473	NA	NA	1456970	1458466	-	1497	malQ
1499	SAK_RS07550	SAK_1499	NA	NA	1496083	1496250	-	168	-
1500	SAK_RS07555	SAK_1500	NA	NA	1496276	1497583	-	1308	obgE
1511	SAK_RS07610	SAK_1511	NA	NA	1507879	1508346	-	468	smpB
1513	SAK_RS07620	SAK_1513	NA	NA	1510867	1511103	-	237	secG
1518	SAK_RS07640	SAK_1518	NA	NA	1515119	1515706	-	588	coaE
1522	#N/A	SAK_1522	NA	NA	1519986	1520084	-	99	-
1525	SAK_RS07685	SAK_1525	NA	NA	1521941	1522840	-	900	era
1526	SAK_RS07690	SAK_1526	NA	NA	1522882	1523280	-	399	dgkA
1527	SAK_RS07695	SAK_1527	NA	NA	1523261	1523746	-	486	-
1536	SAK_RS07740	SAK_1536	NA	NA	1531713	1532270	-	558	frr
1537	SAK_RS07745	SAK_1537	NA	NA	1532286	1533014	-	729	pyrH
1543	SAK_RS07775	SAK_1543	NA	NA	1538320	1539009	-	690	rplA
1544	SAK_RS07780	SAK_1544	NA	NA	1539113	1539538	-	426	rplK
1552	SAK_RS07825	SAK_1552	NA	NA	1548743	1551184	-	2442	ftsK
1558	SAK_RS07855	SAK_1558	NA	NA	1555716	1556405	-	690	pfs
1561	SAK_RS07870	SAK_1561	NA	NA	1557259	1558638	-	1380	glmU
1589	SAK_RS08015	SAK_1589	NA	NA	1585037	1585363	-	327	-
1590	SAK_RS08020	SAK_1590	NA	NA	1585393	1586256	-	864	holB
1591	SAK_RS08025	SAK_1591	NA	NA	1586276	1586911	-	636	tmk
1600	SAK_RS08070	SAK_1600	NA	NA	1594301	1594891	-	591	clpP
1615	SAK_RS08145	SAK_1615	NA	NA	1607081	1607875	-	795	murI
1616	SAK_RS08150	SAK_1616	NA	NA	1608050	1608289	-	240	-
1627	SAK_RS08205	SAK_1627	NA	NA	1616433	1616915	-	483	greA
1630	SAK_RS08220	SAK_1630	NA	NA	1619466	1620797	-	1332	murC
1632	#N/A	SAK_1632	NA	NA	1621429	1621527	-	99	-
1634	SAK_RS08235	SAK_1634	NA	NA	1624842	1626152	-	1311	engA
1639	SAK_RS08260	SAK_1639	NA	NA	1630397	1631086	-	690	csrR
1640	SAK_RS08265	SAK_1640	NA	NA	1631321	1631854	-	534	-

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1658	SAK_RS08355	SAK_1658	NA	NA	1649585	1650301	-	717	-
1673	SAK_RS08425	SAK_1673	NA	NA	1659563	1660150	-	588	-
1674	SAK_RS08430	SAK_1674	NA	NA	1660147	1660779	-	633	nadD
1677	SAK_RS08445	SAK_1677	NA	NA	1662437	1662970	-	534	-
1680	SAK_RS08460	SAK_1680	NA	NA	1665567	1667033	-	1467	gatA
1681	SAK_RS08465	SAK_1681	NA	NA	1667033	1667335	-	303	gatC
1696	SAK_RS08540	SAK_1696	NA	NA	1684669	1685769	-	1101	alr
1697	SAK_RS08545	SAK_1697	NA	NA	1685766	1686125	-	360	acpS
1703	SAK_RS08575	SAK_1703	NA	NA	1694038	1695477	+	1440	scrB
1707	SAK_RS08595	SAK_1707	NA	NA	1697433	1697993	-	561	efp
1719	SAK_RS08645	SAK_1719	NA	NA	1708946	1709890	-	945	-
1720	SAK_RS08650	SAK_1720	NA	NA	1710060	1710299	-	240	rpsR
1721	SAK_RS08655	SAK_1721	NA	NA	1710344	1710835	-	492	ssb1
1722	SAK_RS08660	SAK_1722	NA	NA	1710847	1711134	-	288	rpsF
1725	SAK_RS08675	SAK_1725	NA	NA	1714168	1714482	-	315	trx
1730	SAK_RS08700	SAK_1730	NA	NA	1718458	1719351	+	894	rnhC
1731	SAK_RS08705	SAK_1731	NA	NA	1719367	1719960	+	594	lepB
1741	SAK_RS08755	SAK_1741	NA	NA	1731076	1731528	-	453	-
1761	SAK_RS08855	SAK_1761	NA	NA	1756316	1756627	-	312	-
1769	#N/A	SAK_1769	NA	NA	1763970	1764068	-	99	-
1779	SAK_RS08955	SAK_1779	NA	NA	1772296	1773306	-	1011	gcp
1781	SAK_RS08965	SAK_1781	NA	NA	1773791	1774483	-	693	-
1783	SAK_RS08975	SAK_1783	NA	NA	1774946	1776625	+	1680	-
1785	SAK_RS08985	SAK_1785	NA	NA	1777444	1778790	-	1347	glnA
1786	SAK_RS08990	SAK_1786	NA	NA	1778824	1779195	-	372	glnR
1788	SAK_RS09000	SAK_1788	NA	NA	1780077	1781273	-	1197	pgk
1790	SAK_RS09010	SAK_1790	NA	NA	1782486	1783496	-	1011	gap
1791	SAK_RS09015	SAK_1791	NA	NA	1783701	1785779	-	2079	fusA
1792	SAK_RS09020	SAK_1792	NA	NA	1785934	1786404	-	471	rpsG
1797	SAK_RS09045	SAK_1797	NA	NA	1790174	1790806	-	633	-
1798	SAK_RS09050	SAK_1798	NA	NA	1790799	1791461	-	663	rpe
1799	SAK_RS09055	SAK_1799	NA	NA	1791468	1792340	-	873	-
1810	SAK_RS09110	SAK_1810	NA	NA	1800009	1800248	-	240	dltC
1811	SAK_RS09115	SAK_1811	NA	NA	1800263	1801528	-	1266	dltB
1812	SAK_RS09120	SAK_1812	NA	NA	1801525	1803060	-	1536	dltA
1815	SAK_RS09140	SAK_1815	NA	NA	1805423	1805557	-	135	rpmH
1829	SAK_RS09210	SAK_1829	NA	NA	1824608	1825255	-	648	-
1833	SAK_RS09230	SAK_1833	NA	NA	1827629	1828114	-	486	-
1834	SAK_RS09235	SAK_1834	NA	NA	1828181	1828459	-	279	-
1851	SAK_RS09320	SAK_1851	NA	NA	1846869	1847909	-	1041	tsf
1852	SAK_RS09325	SAK_1852	NA	NA	1848003	1848773	-	771	rpsB
1855	#N/A	SAK_1855	NA	NA	1851295	1851365	+	71	-
1863	SAK_RS09380	SAK_1863	NA	NA	1859960	1860574	+	615	def
1866	SAK_RS09395	SAK_1866	NA	NA	1862739	1862987	+	249	-
1869	SAK_RS09410	SAK_1869	NA	NA	1864458	1868864	-	4407	polC
1871	SAK_RS09420	SAK_1871	NA	NA	1869696	1871549	-	1854	proS
1873	SAK_RS09430	SAK_1873	NA	NA	1872931	1873725	-	795	cdsA
1874	SAK_RS09435	SAK_1874	NA	NA	1873740	1874492	-	753	uppS
1882	SAK_RS09475	SAK_1882	NA	NA	1882082	1883077	-	996	galE
1902	SAK_RS09575	SAK_1902	NA	NA	1906662	1907117	+	456	nrdI
1916	SAK_RS09650	SAK_1916	NA	NA	1919126	1919308	+	183	-
1939	#N/A	SAK_1939	NA	NA	1939018	1939093	+	76	-
1942	SAK_RS09780	SAK_1942	NA	NA	1940873	1941013	-	141	-
1944	SAK_RS09790	SAK_1944	NA	NA	1942170	1942355	-	186	-
1947	#N/A	SAK_1947	NA	NA	1944192	1944365	-	174	-
1955	#N/A	SAK_1955	NA	NA	1950930	1951058	+	129	-
1958	#N/A	SAK_1958	NA	NA	1952333	1952458	+	126	-
1960	#N/A	SAK_1960	NA	NA	1952910	1953014	+	105	-
1995	SAK_RS10040	SAK_1995	NA	NA	1987441	1989942	-	2502	leuS
1998	SAK_RS10055	SAK_1998	NA	NA	1992592	1993131	-	540	nusG
2003	SAK_RS10080	SAK_2003	NA	NA	1996768	1996941	-	174	secE
2004	#N/A	SAK_2004	NA	NA	1996977	1997123	-	147	rpmGB
2014	SAK_RS10135	SAK_2014	NA	NA	2009267	2009551	-	285	groES
2027	SAK_RS10200	SAK_2027	NA	NA	2022083	2022205	-	123	-
2029	SAK_RS10210	SAK_2029	NA	NA	2022631	2023041	-	411	-
2035	SAK_RS10240	SAK_2035	NA	NA	2027267	2027857	-	591	ruvA
2038	#N/A	SAK_2038	NA	NA	2031227	2031328	-	102	-
2042	SAK_RS10270	SAK_2042	NA	NA	2034874	2036565	+	1692	argS
2046	SAK_RS10290	SAK_2046	NA	NA	2038902	2040653	-	1752	aspS
2047	SAK_RS10295	SAK_2047	NA	NA	2040746	2042026	-	1281	hisS
2048	SAK_RS10300	SAK_2048	NA	NA	2042246	2042428	+	183	rpmF
2049	SAK_RS10305	SAK_2049	NA	NA	2042444	2042593	+	150	rpmG
2050	SAK_RS10310	SAK_2050	NA	NA	2042762	2043970	-	1209	-
2052	SAK_RS10320	SAK_2052	NA	NA	2044850	2045188	+	339	cadX
2085	SAK_RS10490	SAK_2085	NA	NA	2078116	2078445	-	330	-
2086	SAK_RS10500	SAK_2086	NA	NA	2078648	2078980	-	333	-
2088	SAK_RS10510	SAK_2088	NA	NA	2079662	2079835	-	174	-
2091	SAK_RS10535	SAK_2091	NA	NA	2082243	2082857	+	615	-
2092	#N/A	SAK_2092	NA	NA	2083250	2083354	-	105	-
2095	SAK_RS10555	SAK_2095	NA	NA	2086271	2086882	-	612	rpsD
2096	SAK_RS10560	SAK_2096	NA	NA	2087212	2087499	-	288	-
2100	SAK_RS10580	SAK_2100	NA	NA	2091416	2093317	-	1902	gidA
2102	SAK_RS10590	SAK_2102	NA	NA	2094130	2095251	-	1122	mnmA
2105	SAK_RS10605	SAK_2105	NA	NA	2097187	2097864	-	678	-
2107	SAK_RS10615	SAK_2107	NA	NA	2098752	2099546	-	795	-
2108	SAK_RS10620	SAK_2108	NA	NA	2099539	2100381	-	843	cbiO
2109	SAK_RS10625	SAK_2109	NA	NA	2100357	2101196	-	840	cbiO
2110	SAK_RS10630	SAK_2110	NA	NA	2101196	2101738	-	543	pgsA
2131	#N/A	SAK_2131	NA	NA	2124438	2124511	-	74	-
2132	#N/A	SAK_2132	NA	NA	2124541	2124612	-	72	-
2133	#N/A	SAK_2133	NA	NA	2124805	2124878	+	74	-

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Supplemental Data 2

	new_locus_tag	old_locus_ta	start	end	name	description	log2FoldChange_earlyLog	padj_EarlyLog	log2FoldChange_lateLog	padj_lateLog	log2FoldChange_stat	padj_stat
1	W903_RS00005	W903_0001	54	1463	dnaA	chromosomal replication initiator protein DnaA	-0.192067193	0.272179322	-0.30511719	0.007573575	-0.30511719	0.007573575
2	W903_RS00010	W903_0002	1618	2754	dnaN	DNA polymerase III, beta subunit	-0.088169456	0.629611169	-0.856579541	6.62975E-13	-0.856579541	6.62975E-13
3	W903_RS00015	W903_0003	2812	3705	NA	diacylglycerol kinase catalytic catalytic domain protein	-0.806137191	8.1301E-07	0.391108678	0.005227457	0.391108678	0.005227457
4	W903_RS00020	W903_0004	3715	3912	NA	hypothetical protein	-1.31569835	9.20913E-13	-0.259427933	0.100153884	-0.259427933	0.100153884
5	NA	W903_0005	4037	4177	NA	helix-turn-helix family protein	-0.152996563	0.566833212	0.275656155	0.098943389	0.275656155	0.098943389
6	W903_RS00030	W903_0006	4535	5650	NA	50S ribosome-binding GTPase family protein	-0.547306916	0.001019086	-1.170317955	7.36474E-32	-1.170317955	7.36474E-32
7	W903_RS00035	W903_0007	5734	6309	pth	peptidyl-tRNA hydrolase	-0.648196454	0.006565025	-1.397500868	1.65455E-21	-1.397500868	1.65455E-21
8	W903_RS00040	W903_0008	6306	9803	mfd	transcription-repair coupling factor	-0.812046428	2.16187E-05	-1.812506544	2.81494E-54	-1.812506544	2.81494E-54
9	W903_RS00045	W903_0009	10094	10366	NA	S4 domain protein	-0.931606411	1.20706E-06	-1.075244929	1.19573E-14	-1.075244929	1.19573E-14
10	W903_RS00050	W903_0010	10353	10724	NA	septum formation initiator family protein	-0.812343739	8.9586E-07	-0.726275204	1.67237E-08	-0.726275204	1.67237E-08
11	W903_RS00055	W903_0011	10727	10861	NA	hypothetical protein	-1.457177723	3.378E-13	-1.043231159	1.15849E-08	-1.043231159	1.15849E-08
12	W903_RS00060	W903_0012	10861	12147	NA	D-alanyl-D-alanine carboxypeptidase family protein	-0.899765758	1.17178E-08	-0.732746049	1.42937E-14	-0.732746049	1.42937E-14
13	W903_RS00065	W903_0013	12149	13423	tilS	tRNA(Ile)-lysidine synthetase	-0.595875518	5.69449E-05	0.112876081	0.276457054	0.112876081	0.276457054
14	W903_RS00070	W903_0014	13428	13970	hpt	hypoxanthine phosphoribosyltransferase	0.1156808	0.503809141	-0.964722774	5.17484E-25	-0.964722774	5.17484E-25
15	W903_RS00075	W903_0015	13993	15969	hflB	ATP-dependent metallopeptidase HflB family protein	0.566663928	0.000108051	-0.624648825	9.26956E-12	-0.624648825	9.26956E-12
16	W903_RS00080	W903_0016	16467	18003	rRNA	NA	2.410228946	0.376532116	-4.336131983	0.025327637	-4.336131983	0.025327637
17	W903_RS00085	W903_0017	18063	18135	rRNA	NA	-0.902731633	NA	-0.053706497	0.960968817	-0.053706497	0.960968817
18	W903_RS00090	W903_0018	18292	21192	rRNA	NA	2.788501858	0.238231645	-4.49089962	0.024708989	-4.49089962	0.024708989
19	W903_RS00095	W903_0019	21270	21383	rRNA	NA	-1.530553442	0.014692636	1.291313578	0.011584324	1.291313578	0.011584324
20	W903_RS00100	W903_0020	21386	21458	rRNA	NA	-0.008981392	NA	-1.412224254	0.550598186	-1.412224254	0.550598186
21	W903_RS00105	W903_0021	21461	21533	rRNA	NA	-1.296189788	NA	0.21618932	0.882784086	0.21618932	0.882784086
22	W903_RS00110	W903_0022	21536	21608	rRNA	NA	-0.815028368	NA	1.375629996	0.368438014	1.375629996	0.368438014
23	W903_RS00115	W903_0023	21618	21699	NA	NA	NA	NA	1.048062688	0.86167603	1.048062688	0.86167603
24	W903_RS00120	W903_0024	21710	21782	rRNA	NA	-0.7358948	NA	-0.082981902	0.971479693	-0.082981902	0.971479693
25	W903_RS00125	W903_0025	21816	21887	rRNA	NA	-0.834842062	NA	0.158238201	0.856110387	0.158238201	0.856110387
26	W903_RS00130	W903_0026	21896	21980	rRNA	NA	-0.517943311	NA	-0.08399439	0.945066339	-0.08399439	0.945066339
27	W903_RS00135	W903_0027	21992	22065	rRNA	NA	-2.599052178	NA	2.130341804	0.443677967	2.130341804	0.443677967
28	W903_RS00140	W903_0028	22073	22146	rRNA	NA	0.707266024	NA	1.317858829	0.055468389	1.317858829	0.055468389
29	W903_RS00145	W903_0029	22298	23834	rRNA	NA	2.403759877	0.377928802	-4.329608987	0.025957193	-4.329608987	0.025957193
30	W903_RS00150	W903_0030	23894	23966	rRNA	NA	-0.829079144	NA	-0.411633831	0.749853298	-0.411633831	0.749853298
31	W903_RS00155	W903_0031	24123	27023	rRNA	NA	2.789290799	0.238231645	-4.46934484	0.025180409	-4.46934484	0.025180409
32	W903_RS00160	W903_0032	27101	27214	rRNA	NA	-0.816388837	0.260142929	1.089765495	0.037412149	1.089765495	0.037412149
33	W903_RS00165	W903_0033	27217	27289	rRNA	NA	-2.059390653	NA	1.833398181	0.400871853	1.833398181	0.400871853
34	W903_RS00170	W903_0034	27292	27364	rRNA	NA	-1.228452108	NA	0.596972864	0.765232568	0.596972864	0.765232568
35	W903_RS00175	W903_0035	27367	27439	rRNA	NA	-0.679289454	NA	0.817416983	0.496498369	0.817416983	0.496498369
36	W903_RS00180	W903_0036	27449	27530	rRNA	NA	1.170348617	NA	-1.943554221	0.737862841	-1.943554221	0.737862841
37	W903_RS00185	W903_0037	27541	27613	rRNA	NA	-1.095681031	NA	1.470412164	0.420397259	1.470412164	0.420397259
38	W903_RS00190	W903_0038	27647	27718	rRNA	NA	-1.095309805	NA	0.639745024	0.384515144	0.639745024	0.384515144
39	W903_RS00195	W903_0039	27727	27811	rRNA	NA	0.018741414	NA	0.300571073	0.807643153	0.300571073	0.807643153
40	W903_RS00200	W903_0040	27823	27896	rRNA	NA	-0.088381731	NA	-0.364998529	0.946331025	-0.364998529	0.946331025
41	W903_RS00205	W903_0041	27904	27977	rRNA	NA	-0.257947718	NA	0.910395492	0.402091417	0.910395492	0.402091417
42	W903_RS00210	W903_0042	27993	28066	rRNA	NA	-0.053834414	NA	0.979450433	0.627271987	0.979450433	0.627271987
43	W903_RS00215	W903_0043	28086	28159	rRNA	NA	-0.56930183	0.435886345	1.185054344	0.051335926	1.185054344	0.051335926
44	W903_RS00220	W903_0044	28175	28264	rRNA	NA	-0.284965672	0.733854288	0.636213859	0.401409142	0.636213859	0.401409142
45	W903_RS00225	W903_0045	28275	28348	rRNA	NA	-1.500724356	NA	2.731406411	0.275636328	2.731406411	0.275636328
46	W903_RS00230	W903_0046	28351	28423	tRNA	NA	-1.98032567	NA	1.450158491	0.453048129	1.450158491	0.453048129
47	W903_RS00235	W903_0047	28443	28513	tRNA	NA	-3.751729086	NA	2.731406411	0.275636328	2.731406411	0.275636328
48	W903_RS00240	W903_0048	28548	28621	rRNA	NA	-1.705053102	NA	1.909600748	0.341223627	1.909600748	0.341223627
49	W903_RS00245	W903_0049	28635	28722	tRNA	NA	-4.136760643	NA	-0.040787376	0.986162366	-0.040787376	0.986162366
50	W903_RS00250	W903_0050	28958	30295	NA	CHAP domain protein	-1.270039514	3.50543E-17	-0.946475236	1.14662E-26	-0.946475236	1.14662E-26
51	W903_RS00255	W903_0051	30419	31387	prs	ribose-phosphate diphosphokinase family protein	-0.106069267	0.536398445	-0.015310527	0.8830912	-0.015310527	0.8830912
52	W903_RS00260	W903_0052	31495	32670	NA	aminotransferase class-V family protein	0.022672516	0.909836741	-0.237594713	0.015101179	-0.237594713	0.015101179
53	W903_RS00265	W903_0053	32660	33421	recO	DNA repair protein RecO	-0.346842884	0.058233186	-0.233406788	0.010470242	-0.233406788	0.010470242
54	W903_RS00270	W903_0054	33484	34362	NA	CAAX protease self-immunity family protein	-0.339024387	0.365184946	-0.912893172	9.16251E-05	-0.912893172	9.16251E-05
55	W903_RS00275	W903_0055	34440	35432	plsX	fatty acid/phospholipid synthesis protein PlsX	-0.107411442	0.554005697	-0.43391214	8.80647E-05	-0.43391214	8.80647E-05
56	W903_RS00280	W903_0056	35443	35682	NA	phosphopantetheine attachment site family protein	0.942089407	1.15664E-09	-0.064272295	0.550454629	-0.064272295	0.550454629
57	W903_RS00285	W903_0057	35806	36510	purC	phosphoribosylaminoimidazolesuccinocarboxamide synthase	0.411949036	0.446374739	-2.389249605	1.03297E-26	-2.389249605	1.03297E-26
58	NA	W903_0058	36527	36640	NA	phosphoribosylformylglycinamidine synthase domain protein	-0.21814021	NA	-3.092522068	2.00702E-06	-3.092522068	2.00702E-06
59	W903_RS00290	W903_0059	36633	40358	NA	phosphoribosylformylglycinamidine synthase	1.167106317	2.44698E-06	-2.858703217	1.9143E-131	-2.858703217	1.9143E-131
60	W903_RS00295	W903_0060	40398	40730	NA	glycerophosphoryl diester phosphodiesterase family protein	0.886425574	0.021623854	-2.910061941	5.06554E-53	-2.910061941	5.06554E-53
61	W903_RS00300	W903_0061	40880	42334	purF	amidophosphoribosyltransferase	1.654871277	9.53326E-14	-2.795438952	2.8787E-113	-2.795438952	2.8787E-113
62	W903_RS00305	W903_0062	42362	43384	purM	phosphoribosylformylglycinamidine cyclo-ligase	1.606658336	8.10917E-09	-2.801255502	3.60047E-63	-2.801255502	3.60047E-63
63	W903_RS00310	W903_0063	43552	44100	purN	phosphoribosylglycinamide formyltransferase	1.880321467	3.28879E-11	-3.063149939	8.15491E-79	-3.063149939	8.15491E-79
64	W903_RS00315	W903_0064	44123	44875	NA	acetyltransferase family protein	1.12142573	2.14802E-09	-2.347797941	1.9575E-108	-2.347797941	1.9575E-108
65	W903_RS00320	W903_0065	44895	46442	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.368327432	1.22792E-14	-2.191444446	6.85435E-98	-2.191444446	6.85435E-98
66	W903_RS00325	W903_0066	46635	47534	NA	peptidase M23 family protein	0.641402587	0.031426788	1.592106764	4.29666E-12	1.592106764	4.29666E-12
67	W903_RS00330	W903_0067	47681	48991	NA	lysM domain protein	-1.087298588	2.2691E-13	0.17465421	0.052700956	0.17465421	0.052700956
68	W903_RS00335	W903_0068	49238	49336	rlA	putative N-acetylmannosamine-6-phosphate 2-epimerase	-0.184621958	0.735544957	0.904653999	0.000484969	0.904653999	0.000484969
69	W903_RS00340	W903_0069	49983	51290	NA	bacterial extracellular solute-binding family protein	0.050958373	0.932692932	1.496373303	1.02642E-07	1.496373303	1.02642E-07
70	W903_RS00345	W903_0070	51387	52274	NA	binding--dependent transport system inner membrane component family protein	0.34256847	0.674964304	2.8739743	7.97891E-14	2.8739743	7.97891E-14
71	W903_RS00350	W903_0071	52284	53114	NA	binding--dependent transport system inner membrane component family protein	0.386466145	0.641226111	2.613852952	9.39116E-12	2.613852952	9.39116E-12
72	W903_RS00355	W903_0072	53127	53570	NA	hypothetical protein	0.564434474	0.484301603	1.148142693	0.013645992	1.148142693	0.013645992
73	W903_RS00360	W903_0073	53590	54252	NA	hypothetical protein	-0.265296111	NA	2.039946432	1.83371E-05	2.039946432	1.83371E-05
74	W903_RS00365	W903_0074	54249	55166	NA	dihydrodipicolinate synthetase family protein	0.853048963	0.187598324	1.51316635	0.000104185	1.51316635	0.000104185
75	W903_RS00370	W903_0075	55183	56064	NA	ROK family protein	0.366956753	0.479805785	1.239508771	4.36243E-06	1.239508771	4.36243E-06
76	W903_RS00375	W903_0076	56072	57049	axe1	xylan esterase 1	1.154567504	0.023352457	1.425857305	5.51175E-05	1.425857305	5.51175E-05
77	W903_RS00380	W903_0077	57072	57875	NA	helix-turn-helix domain, rpiR family protein	-0.391298211	0.125079485	0.241257671	0.244943932	0.241257671	0.244943932
78	W903_RS00385	W903_0078	58157	59419	purD	phosphoribosylamine--glycine ligase	1.941536917	1.97424E-20	-1.784649822	4.90521E-21	-1.784649822	4.90521E-21
79	W903_RS00390	W903_0079	60005	60493	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.286587867	7.23174E-10	-1.181116753	1.27614E-05	-1.181116753	1.27614E-05
80	W903_RS00395	W903_0080	60480	61553	purK	phosphoribosylaminoimidazole carboxylase, ATPase subunit	1.944486874	1.16308E-25	-1.684198176	4.6227E-28	-1.684198176	4.6227E-28
81	W903_RS00400	W903_0081	61563	61820	NA	putative phosphoribosylaminoimidazole carboxylase ATPase subunit	0.351526065	0.213132413	-0.915264089	3.94738E-06	-0.915264089	3.94738E-06
82	W903_RS00405	W903_0082	62038	63288	NA	hypothetical protein	0.916899444	3.5071E-10	-0.27064574	0.002969583	-0.27064574	0.002969583
83	W903_RS00410	W903_0083	63374	64672	purB	adenylosuccinate lyase	0.961892979	3.90051E-11	-0.625305584	2.39043E-08	-0.625305584	2.39043E-08
84	W903_RS00415	W903_0084	64825	65736	NA	helix-turn-helix family protein	-1.133285473	3.08363E-11	-0.379904103	0.000692856	-0.379904103	0.000692856
85	W903_RS00420	W903_0085	66033	67031	ruvB	holliday junction DNA helicase RuvB	-0.763387666	2.25231E-05	0.441438706	2.44039E-05	0.441438706	2.44039E-05
86	W903_RS00425	W903_0086	67183	67620	NA	low molecular weight phosphotyrosine phosphatase family protein	-0.281208968	0.11198161	0.063854486	0.639063401	0.063854486	0.639063401
87	W903_RS00430	W903_0087	67627	68007	NA	MORN repeat family protein	0.125206289	0.494839205	0.409891799	2.4831E-05	0.409891799	2.4831E-05
88	W903_RS00435	W903_0088	68004	69782	NA	acyltransferase family protein	0.03928857	0.825599533	-0.006184993	0.955409198	-0.006184993	0.955409198
89	W903_RS00440	W903_0089	70052	72694	NA	aldehyde dehydrogenase family protein	0.091241701	0.717318267	1.889851898	1.11099E-30	1.889851898	1.11099E-30
90	W903_RS00445	W903_0090	72873	73889	NA	zinc-binding dehydrogenase family protein	-0.088017238	0.642192846	1.137431006	2.29547E-18	1.137431006	2.29547E-18
91	W903_RS00450	W903_0091	74009	75499	thrC	threonine synthase	0.212193945	0.240481793	-0.421350922	0.000280243	-0.421350922	0.000280243
92	W903_RS00455	W903_0092	75604	76884	NA	MATE efflux family protein	0.271944086	0.100497184	0.208739721	0.05391016	0.208739721	0.05391016
93	W903_RS00460	W903_0093	77090	77398	rpsJ	ribosomal protein S10	-0.091072933	0.624569854	-1.597909489	1.86253E-31	-1.597909489	1.86253E-31
94	W903_RS00465	W903_0094	77503	78129	rplC	50S ribosomal protein L3	0.270709549	0.123894898	-1.36886168	1.59598E-22	-1.36886168	1.59598E-22
95	W903_RS00470	W903_0095	78153	78776	rplD	50S ribosomal protein L4	0.285810258	0.069411897	-1.307750072	8.65618E-26	-1.307750072	8.65618E-26
96	W903_RS00475	W903_0096	78776	79072	rplW	50S ribosomal protein L23	0.000499452	0.998097116	-1.449227018	2.33608E-20	-1.449227018	2.33608E-20
97	W903_RS00480	W903_0097	79090	79923	rplB	ribosomal protein L2	0.582015638	0.000116877	-1.167571401	4.04429E-21	-1.167571401	4.04429E-21
98	W903_RS00485	W903_0098	80022	80300	rpsS	ribosomal protein S19	0.502299316	0.004164815	-1.306616512	4.92072E-16	-1.306616512	4.92072E-16
99	W903_RS00490	W903_0099	80316	80660	rplV	ribosomal protein L22	0.469094721	0.002162424	-1.245454617	5.24886E-16	-1.245454617	5.24886E-16
100	W903_RS00495	W903_0100	80673	81326	rpsC	ribosomal protein S3	1.044675776	2.19789E-14	-0.938762656	4.13357E-12	-0.938762656	4.13357E-12
101	W903_RS00500	W903_0101	81330	81743	rplP	ribosomal protein L16	1.135350431	5.58782E-16	-0.934759465	3.7845E-17	-0.934759465	3.7845E-17
102	W903_RS00505	W903_0102	81753	81959	rpmC	ribosomal protein L29	0.635784192	9.02419E-06	-1.374764074	6.67953E-21	-1.374764074	6.67953E-21
103	W903_RS00510	W903_0103	81985	82245	rpsQ	30S ribosomal protein S17	1.066145609	4.10223E-14	-1.153399068	3.11651E-19	-1.153399068	3.11651E-19
104	W903_RS00515	W903_0104	82270	82634	rplN	ribosomal protein L14	0.991780034	4.60253E-11	-1.180780036	4.42373E-27	-1.180780036	4.42373E-27
105	W903_RS00520	W903_0105	82718	83023	rplX	ribosomal protein L24	1.208729824	3.50543E-17	-1.133261732	5.64714E-25	-1.133261732	5.64714E-25
106	W903_RS00525	W903_0106	83047	83589	rplE	50S ribosomal protein L5	0.856437639	3.87167E-09	-1.173170007	2.01199E-14	-1.173170007	2.01199E-14
107	W903_RS00530	W903_0107	83607	83792	rpsZ	30S ribosomal protein S14 type Z	0.478816266	0.012507613	-1.54102174	1.27323E-22	-1.54102174	1.27323E-22
108	W903_RS00535	W903_0108	83947	84345	rpsH	30S ribosomal protein S8	0.394070154	0.041698478	-1.451123341	3.00829E-18	-1.451123341	3.00829E-18
109	W903_RS00540	W903_0109	84455	84991	rplF	ribosomal protein L6	0.672410937	0.000197833	-1.474231564	2.1836E-35	-1.474231564	2.1836E-35
110	W903_RS00545	W903_0110	85092	85448	rplR	ribosomal protein L18	0.936234401	8.44101E-09	-1.168946797	1.37604E-25	-1.168946797	1.37604E-25
111	W903_RS00550	W903_0111	85467	85961	rpsE	ribosomal protein S5	1.120680619	5.50993E-14	-1.079756926	8.85838E-15	-1.079756926	8.85838E-15
112	W903_RS00555	W903_0112	85976	86155	rpmD	ribosomal protein L30	0.375931442	0.036890805	-1.700265953	1.93102E-21	-1.700265953	1.93102E-21
113	W903_RS00560	W903_0113	86280	86720	rplO	ribosomal protein L15	0.802834183	1.65981E-08	-1.353079492	8.29163E-16	-1.353079492	8.29163E-16
114	W903_RS00565	W903_0114	86741	88045	secY	preprotein translocase, SecY subunit	0.685891681	8.19376E-07	-1.470320624	1.05527E-25	-1.470320624	1.05527E-25
115	W903_RS00570	W903_0115	88140	88778	adk	adenylate kinase	-1.155177667	3.36045E-10	-1.78134431	2.25015E-36	-1.78134431	2.25015E-36
116	W903_RS00575	W903_0116	88894	89112	infA	translation initiation factor IF-1	-0.897309205	2.73892E-06	-1.265415532	1.46442E-49	-1.265415532	1.46442E-49
117	W903_RS10205	W903_0117	89138	89254	rpmJ	ribosomal protein L36	0.178286822	0.387696786	-0.556024268	1.5094E-08	-0.556024268	1.5094E-08
118	W903_RS00580	W903_0118	89272	89637	rpsM	30S ribosomal protein S13	-0.644901309	0.003758254	-0.994480003	1.95817E-31	-0.994480003	1.95817E-31
119	W903_RS00585	W903_0119	89655	90038	rpsK	30S ribosomal protein S11	-0.1035415	0.568710442	-0.490957213	1.11683E-06	-0.490957213	1.11683E-06
120	W903_RS00590	W903_0120	90088	91026	rpoA	DNA-directed RNA polymerase, alpha subunit	-0.550420971	0.000587297	-0.41762386	9.16559E-06	-0.41762386	9.16559E-06
121	W903_RS00595	W903_0121	91041	91427	rplQ	ribosomal protein L17	-0.475642392	0.003955895	-0.169788124	0.070211636	-0.169788124	0.070211636
122	W903_RS00600	W903_0122	92021	93557	rRNA	NA	2.395692532	0.295806045	-4.317340309	0.026629559	-4.317340309	0.026629559
123	W903_RS00605	W903_0123	93617	93689	rRNA	NA	-0.584801729	0.509464899	1.791107509	0.164699683	1.791107509	0.164699683
124	W903_RS00610	W903_0124	93846	96746	rRNA	NA	2.788151164	0.238231645	-4.489222951	0.024498859	-4.489222951	0.024498859
125	W903_RS00615	W903_0125	96824	96937	rRNA	NA	-1.144082958	0.075629973	1.228334097	0.03701817	1.228334097	0.03701817
126	W903_RS00620	W903_0126	96940	97012	tRNA	NA	-2.236685848	NA	1.333788115	0.608364086	1.333788115	0.608364086
127	W903_RS00625	W903_0127	97015	97087	rRNA	NA	-1.536025336	NA	1.784342926	0.289883319	1.784342926	0.289883319
128	W903_RS00630	W903_0128	97090	97162	rRNA	NA	-0.905761953	NA	1.095913821	0.413819862	1.095913821	0.413819862
129	W903_RS00635	W903_0129	97172	97253	rRNA	NA	-0.968406418	NA	NA	NA	NA	NA
130	W903_RS00640	W903_0130	97264	97336	rRNA	NA	-0.260110015	NA	1.317599062	0.388727127	1.317599062	0.388727127
131	W903_RS00645	W903_0131	97365	97441	rRNA	NA	-0.386621625	0.641226111	0.118167919	0.888036667	0.118167919	0.888036667
132	W903_RS00650	W903_0132	97449	97520	rRNA	NA	0.498974692	NA	1.01511388	0.865322464	1.01511388	0.865322464
133	W903_RS00655	W903_0133	97534	97628	NA	NA	NA	NA	NA	NA	NA	NA
134	W903_RS00660	W903_0134	97639	97712	rRNA	NA	-1.533667816	NA	1.083226579	0.28974592	1.083226579	0.28974592
135	W903_RS00665	W903_0135	97715	97787	rRNA	NA	-0.07327521	NA	1.209131335	0.209207889	1.209131335	0.209207889
136	W903_RS00670	W903_0136	97799	97879	rRNA	NA	0.60090339	NA	0.472748079	0.581516414	0.472748079	0.581516414
137	W903_RS00675	W903_0137	97886	97956	rRNA	NA	-0.51151837	0.560572697	-1.41388743	0.087813097	-1.41388743	0.087813097

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138	W903_RS00680	W903_0139	97971	98043	NA	NA	NA	NA	NA	NA	NA	NA	NA
139	W903_RS00685	W903_0140	98050	98121	rRNA	NA	0.778040693	NA	-0.395632635	0.943602143	-0.395632635	0.943602143	
140	W903_RS00690	W903_0141	98132	98215	tRNA	NA	2.193392017	NA	NA	NA	NA	NA	
141	W903_RS10745	W903_0142	98697	99062	NA	putative lipoprotein BUG3	0.153021213	0.670231561	0.321349463	0.237011352	0.321349463	0.237011352	
142	W903_RS00700	W903_0143	99132	99335	NA	hypothetical protein	-0.865655952	0.015422106	-0.208911871	0.547197575	-0.208911871	0.547197575	
143	W903_RS00705	W903_0144	99552	99926	NA	putative lipoprotein BUG3	-0.306423997	0.170933729	0.190243173	0.276098899	0.190243173	0.276098899	
144	W903_RS00710	W903_0145	100062	100262	NA	hypothetical protein	-0.192534574	0.692379451	0.35765566	0.303911069	0.35765566	0.303911069	
145	W903_RS00715	W903_0146	101052	101648	NA	hypothetical protein	-0.611454993	0.004894732	-0.956318649	6.14803E-09	-0.956318649	6.14803E-09	
146	W903_RS00720	W903_0147	101822	102241	NA	hypothetical protein	-0.249531231	0.239586923	-0.330760324	0.00311575	-0.330760324	0.00311575	
147	W903_RS00725	W903_0148	102441	102920	NA	putative aTP-dependent endopeptidase clp proteolytic subunit clpP	-0.240270593	0.778085155	0.465729155	0.330438231	0.465729155	0.330438231	
148	W903_RS00730	W903_0149	103042	103734	NA	histidine phosphatase super family protein	0.430515804	0.014941801	-0.436939476	0.000117494	-0.436939476	0.000117494	
149	W903_RS00735	W903_0150	103731	104483	NA	D-alanyl-D-alanine carboxypeptidase family protein	0.098536461	0.58566575	-0.497061064	1.26045E-07	-0.497061064	1.26045E-07	
150	W903_RS00740	W903_0151	104480	105055	NA	mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein	0.142240183	0.480806187	-0.793577616	3.54917E-10	-0.793577616	3.54917E-10	
151	W903_RS00745	W903_0152	105198	106232	hrcA	heat-inducible transcription repressor HrcA	0.610437264	5.39739E-05	2.744016781	0.000228381	2.744016781	0.000228381	
152	W903_RS00750	W903_0153	106274	106807	NA	grpE family protein	0.708370123	4.7969E-05	1.834919808	0.004215923	1.834919808	0.004215923	
153	W903_RS00755	W903_0154	106988	108817	dnaK	chaperone protein DnaK	1.186451135	1.94284E-13	2.121288703	0.000343446	2.121288703	0.000343446	
154	W903_RS00760	W903_0155	108933	109283	NA	hypothetical protein	1.329109786	7.73448E-09	1.546623024	7.25289E-07	1.546623024	7.25289E-07	
155	W903_RS00765	W903_0156	109536	110675	dnaJ	chaperone protein DnaJ	1.627959919	5.37888E-27	1.858489175	0.001140041	1.858489175	0.001140041	
156	W903_RS00770	W903_0157	110793	112040	NA	bacterial regulatory s, gntR family protein	0.694135957	0.000342888	0.844556014	3.37411E-06	0.844556014	3.37411E-06	
157	W903_RS00775	W903_0158	112111	112887	truA	tRNA pseudouridine(38-40) synthase	-0.990108749	7.50567E-10	2.524474721	7.8801E-133	2.524474721	7.8801E-133	
158	W903_RS00780	W903_0159	112850	113608	NA	pfkB carbohydrate kinase family protein	-0.663372951	0.000170063	2.299746162	1.4723E-125	2.299746162	1.4723E-125	
159	W903_RS00785	W903_0160	113618	114082	NA	ECF-type riboflavin transporter, S component family protein	0.144681768	0.525444689	2.86943696	2.094E-155	2.86943696	2.094E-155	
160	W903_RS00790	W903_0161	114079	114648	NA	hypothetical protein	0.316970182	0.192577816	2.64700434	2.57282E-90	2.64700434	2.57282E-90	
161	W903_RS00795	W903_0162	114685	115527	NA	mechanosensitive ion channel family protein	0.29817359	0.157715534	1.462170674	1.96258E-38	1.462170674	1.96258E-38	
162	W903_RS00800	W903_0163	115684	116967	tig	trigger factor	-0.983512147	1.87488E-12	-2.299121289	1.2846E-126	-2.299121289	1.2846E-126	
163	W903_RS00805	W903_0164	117156	117740	NA	putative DNA-directed RNA polymerase subunit delta	-1.656692642	1.08554E-31	-0.638816605	1.45923E-10	-0.638816605	1.45923E-10	
164	W903_RS00810	W903_0165	118013	119617	pyrG	CTP synthase	-0.259781785	0.272693386	-0.639427401	4.55012E-08	-0.639427401	4.55012E-08	
165	W903_RS00815	W903_0166	119726	120652	NA	dienelactone hydrolase family protein	-1.084975582	3.87159E-14	-1.489384362	2.17073E-48	-1.489384362	2.17073E-48	
166	W903_RS00820	W903_0167	120699	120784	rRNA	NA	-0.304933837	NA	1.628568963	0.009749001	1.628568963	0.009749001	
167	W903_RS00825	W903_0168	120847	121293	dut	dUTP diphosphatase family protein	-1.389300007	3.61483E-12	0.001549282	0.991802713	0.001549282	0.991802713	
168	W903_RS00830	W903_0169	121455	122819	radA	DNA repair protein RadA	0.460483052	0.003654195	0.646245135	7.83398E-11	0.646245135	7.83398E-11	
169	W903_RS00835	W903_0170	122955	123452	NA	carbonic anhydrase family protein	-0.1639169	0.811226915	0.072471769	0.600400495	0.072471769	0.600400495	
170	W903_RS00840	W903_0171	123606	124925	NA	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	0.311065237	0.057318233	-0.007432704	0.955989916	-0.007432704	0.955989916	
171	W903_RS00845	W903_0172	125134	126588	gltX	glutamate--tRNA ligase	-0.620768072	0.000159371	-1.252706396	2.068166E-44	-1.252706396	2.068166E-44	
172	W903_RS00850	W903_0173	126628	127598	NA	sugar-binding protein	-0.19797975	0.57805903	2.387797925	3.90485E-57	2.387797925	3.90485E-57	
173	W903_RS00855	W903_0174	127649	128590	NA	branched-chain amino acid transport system / permease component family protein	-0.359284778	0.292125033	2.126842351	1.22412E-34	2.126842351	1.22412E-34	
174	W903_RS00860	W903_0175	128592	130070	NA	heme ABC exporter, ATP-binding protein CcmA	0.320790446	0.242243803	2.260404928	6.37762E-53	2.260404928	6.37762E-53	
175	W903_RS00865	W903_0176	130086	130484	rbsD	D-ribose pyranase	-0.056591757	0.92897826	1.778521871	2.95828E-07	1.778521871	2.95828E-07	
176	W903_RS00870	W903_0177	130459	131370	rbsK	ribokinase	-0.506539817	0.057168931	2.139521154	6.47202E-25	2.139521154	6.47202E-25	
177	W903_RS00875	W903_0178	131363	132349	NA	helix-turn-helix family protein	-1.17174469	1.77068E-11	-0.995155433	2.01717E-17	-0.995155433	2.01717E-17	
178	W903_RS00880	W903_0179	132531	133619	NA	ftsX-like permease family protein	-0.297971715	0.546474694	1.19343533	2.32608E-06	1.19343533	2.32608E-06	
179	W903_RS00885	W903_0180	133619	134305	NA	ABC transporter family protein	-0.181079661	0.798433935	0.953281139	0.013366731	0.953281139	0.013366731	
180	W903_RS00890	W903_0181	134336	135007	NA	putative transcriptional activator CadC	-0.176376642	0.486062835	0.822166548	6.72612E-09	0.822166548	6.72612E-09	
181	W903_RS00895	W903_0182	135051	136070	NA	HAMP domain protein	-0.573136291	0.00089004	0.116669597	0.448188674	0.116669597	0.448188674	
182	W903_RS00900	W903_0183	136224	137414	argG	argininosuccinate synthase	1.479789064	8.63451E-13	1.461969137	7.03975E-24	1.461969137	7.03975E-24	
183	W903_RS00905	W903_0184	137433	138821	argH	argininosuccinate lyase	1.086375733	2.5953E-08	0.848519173	1.06867E-07	0.848519173	1.06867E-07	
184	W903_RS00910	W903_0185	138962	139843	fba	fructose-1,6-bisphosphate aldolase, class II	0.250190176	0.105440968	-2.652061832	1.6435E-122	-2.652061832	1.6435E-122	
185	W903_RS00915	W903_0186	139928	140845	NA	L-2-hydroxyisocaproate dehydrogenase	1.29081304	3.24583E-12	1.185991003	5.79017E-26	1.185991003	5.79017E-26	
186	W903_RS00920	W903_0187	141084	141272	rpmB	ribosomal protein L28	-1.110968591	6.02874E-05	-0.239431846	0.239895374	-0.239431846	0.239895374	
187	W903_RS00925	W903_0188	141404	141769	NA	asp23 family protein	-0.082449853	0.633686901	0.245317778	0.042955077	0.245317778	0.042955077	
188	W903_RS00930	W903_0189	141769	143433	NA	DAK2 domain fusion YloV family protein	0.259307454	0.103410495	0.071291925	0.530226734	0.071291925	0.530226734	
189	W903_RS00935	W903_0190	143581	144465	NA	SPFH domain / Band 7 family protein	-0.77372457	5.96994E-05	-1.556519776	5.12678E-22	-1.556519776	5.12678E-22	
190	W903_RS00940	W903_0191	144557	144673	NA	hypothetical protein	-0.499152314	0.125617798	-2.059444407	1.53021E-13	-2.059444407	1.53021E-13	
191	W903_RS00945	W903_0192	145040	145270	NA	hypothetical protein	-0.514539603	0.003758254	-1.591369973	1.92723E-15	-1.591369973	1.92723E-15	
192	W903_RS00950	W903_0193	145612	146352	NA	ABC transporter family protein	-0.117464701	0.504826288	-0.633859036	8.95176E-11	-0.633859036	8.95176E-11	
193	W903_RS00955	W903_0194	146362	147912	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	0.035171064	0.845209685	-0.410401195	3.75344E-05	-0.410401195	3.75344E-05	
194	W903_RS00960	W903_0195	148048	149931	NA	hypothetical protein	-0.283142362	0.080270011	0.513276297	4.54675E-06	0.513276297	4.54675E-06	
195	W903_RS00965	W903_0196	149977	150816	NA	bacitracin resistance BacA family protein	-0.450247365	0.0059542	0.092119821	0.35307081	0.092119821	0.35307081	
196	W903_RS00970	W903_0197	150936	151691	NA	negative regulator of genetic competence family protein	-0.374895131	0.029560975	-0.357431264	0.001924934	-0.357431264	0.001924934	
197	W903_RS00975	W903_0198	151693	152853	NA	glycosyl transferase 4 family protein	-0.157747199	0.423077872	0.260146488	0.007463719	0.260146488	0.007463719	
198	W903_RS00980	W903_0199	153018	153788	sufC	feS assembly ATPase SufC	0.275976945	0.152314871	0.231361442	0.02746427	0.231361442	0.02746427	
199	W903_RS00985	W903_0200	153825	155087	sufD	feS assembly protein SufD	0.47735251	0.006001977	0.698706783	5.12379E-13	0.698706783	5.12379E-13	
200	W903_RS00990	W903_0201	155089	156321	sufS	cysteine desulfurase, SufS family protein	0.569721531	0.001433861	0.98947963	4.94263E-21	0.98947963	4.94263E-21	
201	W903_RS00995	W903_0202	156308	156751	NA	SUF system FeS assembly protein, NifU family	0.440489086	0.016783976	0.833719336	4.56529E-15	0.833719336	4.56529E-15	
202	W903_RS01000	W903_0203	156851	158269	sufB	feS assembly protein SufB	0.332876799	0.058745063	0.542180445	2.63008E-08	0.542180445	2.63008E-08	
203	W903_RS01005	W903_0204	158341	159528	NA	D-alanyl-D-alanine carboxypeptidase family protein	-0.022003079	0.914504482	-0.822324411	1.21046E-14	-0.822324411	1.21046E-14	
204	W903_RS01010	W903_0205	159681	160868	NA	D-alanyl-D-alanine carboxypeptidase family protein	-0.3314335	0.053941558	-0.764371251	8.84332E-12	-0.764371251	8.84332E-12	
205	W903_RS01015	W903_0206	161158	162813	NA	bacterial extracellular solute-binding s, 5 Middle family protein	0.561450697	0.001675972	-1.625201144	3.64534E-36	-1.625201144	3.64534E-36	
206	W903_RS01020	W903_0207	162932	163846	NA	binding--dependent transport system inner membrane component family protein	0.818582033	2.61384E-06	-1.141002593	1.74469E-16	-1.141002593	1.74469E-16	
207	W903_RS01025	W903_0208	163856	164887	NA	N-terminal TM domain of oligopeptide transport permease C family protein	-0.139362786	0.048604072	-1.576489193	1.24623E-26	-1.576489193	1.24623E-26	
208	W903_RS01030	W903_0209	164900	165949	NA	oligopeptide/dipeptide ABC transporter, ATP-binding , C-terminal domain protein	0.32445646	0.043980081	-1.753746219	3.5735E-48	-1.753746219	3.5735E-48	
209	W903_RS01035	W903_0210	165946	166878	NA	ABC transporter family protein	0.056200694	0.78773361	-1.960145966	9.57266E-51	-1.960145966	9.57266E-51	
210	W903_RS01040	W903_0211	167284	168820	rRNA	NA	2.402607004	0.379068928	-4.328438143	0.027268189	-4.328438143	0.027268189	
211	W903_RS01045	W903_0212	168880	168952	rRNA	NA	-0.330808731	NA	0.509805822	0.636247259	0.509805822	0.636247259	
212	W903_RS01050	W903_0213	169109	172009	rRNA	NA	2.786630679	0.238231645	-4.468779074	0.024971458	-4.468779074	0.024971458	
213	W903_RS01055	W903_0214	172087	172200	rRNA	NA	0.119583736	NA	0.746123922	0.185782641	0.746123922	0.185782641	
214	W903_RS01060	W903_0215	172205	172278	tRNA	NA	-1.931519103	NA	0.097279542	0.973133722	0.097279542	0.973133722	
215	W903_RS01065	W903_0216	172418	173269	ispE	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	0.353970911	0.040437657	0.322052667	0.016738406	0.322052667	0.016738406	
216	W903_RS01070	W903_0217	173355	173798	adcR	transcriptional repressor AdcR	0.600272269	0.000328494	0.318364463	0.016838326	0.318364463	0.016838326	
217	W903_RS01075	W903_0218	173801	174511	NA	ABC transporter family protein	0.413094773	0.006604414	-0.009292323	0.946331025	-0.009292323	0.946331025	
218	W903_RS01080	W903_0219	174501	175313	NA	fecCD transport family protein	0.106949561	0.589504886	-0.200399077	0.153425172	-0.200399077	0.153425172	
219	W903_RS01085	W903_0220	175523	176554	NA	DNA/RNA non-specific endonuclease family protein	0.454469628	0.077965777	0.518164246	0.014278265	0.518164246	0.014278265	
220	W903_RS01090	W903_0221	177134	178393	tyrS	tyrosine--tRNA ligase	0.186056661	0.278351491	-0.480891213	2.08747E-06	-0.480891213	2.08747E-06	
221	W903_RS01095	W903_0222	178504	180801	NA	penicillin binding transpeptidase domain protein	0.428521377	0.003758254	0.498169456	3.41243E-08	0.498169456	3.41243E-08	
222	W903_RS01100	W903_0223	181325	184900	rpoB	DNA-directed RNA polymerase, beta subunit	0.79661013	1.80906E-08	0.114502112	0.377485448	0.114502112	0.377485448	
223	W903_RS01105	W903_0224	185044	188667	rpoC	DNA-directed RNA polymerase, beta' subunit	1.030931108	1.63205E-13	-0.118723068	0.352563214	-0.118723068	0.352563214	
224	NA	W903_0225	188624	188758	NA	glycerophosphoryl diester phosphodiesterase family protein	NA	NA	3.619698662	0.263576189	3.619698662	0.263576189	
225	W903_RS01110	W903_0226	188781	189146	NA	hypothetical protein	-0.652632471	0.033233312	2.585289496	6.17735E-55	2.585289496	6.17735E-55	
226	W903_RS01115	W903_0227	189318	190289	NA	ATPase associated with various cellular activities family protein	0.81488714	0.032654149	2.937594061	1.3017E-39	2.937594061	1.3017E-39	
227	W903_RS01120	W903_0228	190354	191226	NA	type II secretion system (T2SS), F family protein	0.231570434	0.680577703	2.226869381	1.09893E-19	2.226869381	1.09893E-19	
228	W903_RS01125	W903_0229	191223	191552	NA	prepilin-type N-terminal cleavage/methylation domain protein	-0.308132563	NA	1.160387342	0.029295295	1.160387342	0.029295295	
229	W903_RS01130	W903_0230	191602	191940	NA	putative competence protein CglD	-0.492708973	NA	1.301855517	0.006234049	1.301855517	0.006234049	
230	W903_RS01135	W903_0231	191966	192211	NA	type II secretory pathway pseudopilin family protein	0.190271476	0.839238676	1.660457576	3.16204E-06	1.660457576	3.16204E-06	
231	NA	W903_0232	192294	192626	NA	putative comG operon protein 6	0.29605043	0.703622167	1.016138098	0.00461068	1.016138098	0.00461068	
232	W903_RS01145	W903_0233	192604	192975	NA	putative competence protein ComGG	0.65974835	NA	1.447621049	0.001566895	1.447621049	0.001566895	
233	W903_RS01150	W903_0234	193090	194064	NA	N-6 DNA Methylase family protein	-0.877323583	2.67929E-07	-1.498201647	3.86487E-24	-1.498201647	3.86487E-24	
234	W903_RS01155	W903_0235	194096	195289	ackA	acetate kinase	-0.305233385	0.04932856	-0.925492021	3.75505E-17	-0.925492021	3.75505E-17	
235	NA	W903_0236	195478	195609	NA	helix-turn-helix family protein	1.718989894	NA	0.056992458	0.960968817	0.056992458	0.960968817	
236	W903_RS10230	W903_0237	195603	195854	NA	putative membrane protein	-0.158879769	NA	-0.567912319	0.384566457	-0.567912319	0.384566457	
237	W903_RS01165	W903_0238	195923	196588	NA	CAAX protease self-immunity family protein	-0.572439722	0.003106036	-1.024210919	7.4477E-14	-1.024210919	7.4477E-14	
238	W903_RS01170	W903_0239	196609	197379	proC	pyrroline-5-carboxylate reductase	0.089357211	0.642158087	-0.505822347	3.28517E-05	-0.505822347	3.28517E-05	
239	W903_RS01175	W903_0240	197449	198516	pepA	glutamyl aminopeptidase	0.613031912	6.88899E-05	0.073720362	0.574644801	0.073720362	0.574644801	
240	W903_RS01180	W903_0241	198696	198935	NA	putative membrane protein	0.724351387	0.003128903	1.021596287	5.15946E-06	1.021596287	5.15946E-06	
241	W903_RS01185	W903_0242	199096	199380	NA	hypothetical protein	-0.922793656	0.022693766	0.124818861	0.475150497	0.124818861	0.475150497	
242	W903_RS01190	W903_0243	199377	199700	NA	thioredoxin family protein	-0.348515959	0.069028379	-0.060601633	0.665501691	-0.060601633	0.665501691	
243	W903_RS01195	W903_0244	199733	200359	NA	putative tRNA binding domain protein	-0.331198056	0.040469854	-0.352786663	0.001024914	-0.352786663	0.001024914	
244	W903_RS01200	W903_0245	200599	201129	NA	methyltransferase domain protein	-0.206351698	0.381549257	-0.245022367	0.049088311	-0.245022367	0.049088311	
245	W903_RS01205	W903_0246	201210	201605	NA	single-stranded DNA-binding family protein	0.975709004	0.020388883	2.227993298	5.37911E-18	2.227993298	5.37911E-18	
246	W903_RS01210	W903_0247	201729	202373	NA	HAD hydrolase, IA, variant 1 family protein	0.71390607	2.66938E-05	0.939163048	7.2982E-13	0.939163048	7.2982E-13	
247	W903_RS01215	W903_0248	202400	204145	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	0.839116777	3.43143E-08	1.221989025	1.22365E-39	1.221989025	1.22365E-39	
248	W903_RS01220	W903_0249	204126	204866	NA	response regulator	0.955813834	5.88535E-05	1.27724907	2.34099E-16	1.27724907	2.34099E-16	
249	W903_RS01225	W903_0250	205036	205491	NA	lrgA family protein	-0.09569392	0.816605926	-0.014207576	0.953178734	-0.014207576	0.953178734	
250	W903_RS01230	W903_0251	205493	206221	lrgB	antiholin-like protein LrgB	0.795971316	0.006282405	0.462319344	0.006673725	0.462319344	0.006673725	
251	W903_RS01235	W903_0252	206464	208092	NA	bacterial extracellular solute-binding s, 5 Middle family protein	-0.507806435	0.03445741	-0.410641105	0.024604229	-0.410641105	0.024604229	
252	W903_RS01240	W903_0253	208277	209182	NA	binding--dependent transport system inner membrane component family protein	1.082592066	0.005898782	0.440077318	0.134906061	0.440077318	0.134906061	
253	W903_RS01245	W903_0254	209179	210000	NA	binding--dependent transport system inner membrane component family protein	1.359694419	0.012886664	0.945287513	0.017440295	0.945287513	0.017440295	
254	W903_RS01250	W903_0255	210012	210815	NA	ABC transporter family protein	1.018620695	0.023654651	0.688056389	0.077274661	0.688056389	0.077274661	
255	W903_RS01255	W903_0256	210799	211425	NA	ABC transporter family protein	0.913746801	0.215830317	0.254967378	0.673886216	0.254967378	0.673886216	
256	W903_RS01260	W903_0257	211708	213738	treP	PTS system, trehalose-specific IIBC component	0.015231679	0.949637452	2.326142501	7.01496E-67	2.326142501	7.01496E-67	
257	W903_RS01265	W903_0258	213960	215585	treC	alpha,alpha-phosphotrehalase	-0.025029543	0.922986202	1.325073147	2.75731E-19	1.325073147	2.75731E-19	
258	W903_RS01270	W903_0259	215801	217837	NA	PRD domain protein	-0.407677428	0.11627191	0.939075186	4.91519E-07	0.939075186	4.91519E-07	
259	W903_RS01275	W903_0260	217840	218124	NA	PTS system, Lactose/Cellobiose specific IIB subunit	1.107348556	0.073197008	2.478812639	1.78033E-11	2.478812639	1.78033E-11	
260	W903_RS01280	W903_0261	218149	219492	NA	PTS system sugar-specific permease component family protein	1.112098227	2.58341E-05	1.471869654	6.50299E-18	1.471869654	6.50299E-18	
261	W903_RS01285	W903_0262	219495	220352	NA	thiamine pyrophosphate enzyme, C-terminal TPP binding domain protein	0.085860168	0.772213125	0.686496139	5.313E-05	0.686496139	5.313E-05	
262	W903_RS01290	W903_0263	220349	221278	NA	transketolase, pyrimidine binding domain protein	0.656454767	0.020946997	1.036467887	1.98101E-09	1.036467887	1.98101E-09	
263	W903_RS01295	W903_0264	221387	222646	NA	oxidoreductase NAD-binding domain protein	0.723420729	1.48561E-05	-1.560490385	2.41928E-21	-1.560490385	2.41928E-21	
264	W903_RS01300	W903_0265	222734	223003	rpsO	ribosomal protein S15	-0.8909876	3.60753E-10	-0.70510929	9.26627E-10	-0.70510929	9.26627E-10	
265	W903_RS01305	W903_0266	223384	225513	pnp	polyribonucleotide nucleotidyltransferase	1.20212224	1.14315E-15	-0.236285793	0.093951661	-0.236285793	0.093951661	
266	W903_RS01310	W903_0267	225515	226267	NA	hypothetical protein	1.26711762	2.46291E-15	0.175580549	0.145036933	0.175580549	0.145036933	
267	W903_RS01315	W903_0268	226276	226860	cysE	serine O-acetyltransferase	0.947813619	3.90391E-08	0.057430285	0.666706745	0.057430285	0.666706745	
268	W903_RS01320	W903_0269	226870	227052	NA	putative membrane protein	0.842105672	0.00133644	-0.024228665	0.922291966	-0.024228665	0.922291966	
269	W903_RS01325	W903_0270	227049	228392	cysS	cysteine--tRNA ligase	0.755354903	9.18723E-07	0.087500605	0.531444645	0.087500605	0.531444645	
270	W903_RS01330	W903_0271	228385	228771	NA	ribonuclease III domain protein	0.506242307	0.010203245	-0.016257946	0.934830964	-0.016257946	0.934830964	
271	W903_RS01335	W903_0272	228880	229629	NA	RNA 2'-O ribose methyltransferase substrate binding family protein	0.513056188	0.0010479	-0.423303985	0.000570048	-0.423303985	0.000570048	
272	W903_RS01340	W903_0273	229626	230144	NA	yacP-like NYN domain protein	0.47532442	0.002888992	-0.390328268	0.000640865	-0.390328268	0.000640865	
273	W903_RS01345	W903_0274	230237	231097	NA	EDD, DegV family domain protein	-0.270627932	0.136367761	0.017465327	-0.363093136	0.017465327	-0.363093136	
274	NA	W903_0275	231200	231328	NA	hypothetical protein	1.282105346	6.82786E-05	1.217263506	0.000278672	1.217263506	0.000278672	
275	NA	W903_0276	231443	231562	NA	putative membrane protein	0.775827451	0.015633271	0.855713705	0.004913527	0.855713705	0.004913527	

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276	W903_RS01350	W903_0277	231635	231757	NA	helix-turn-helix family protein	0.883158209	0.006679815	1.06330298	7.02663E-05	1.06330298	7.02663E-05
277	W903_RS01355	W903_0278	231979	232425	rplM	ribosomal protein L13	-0.418273259	0.006084625	-0.275558357	0.038024879	-0.275558357	0.038024879
278	W903_RS01360	W903_0279	232446	232838	rpsI	30S ribosomal protein S9	0.374677449	0.024139031	-0.361241177	0.009574104	-0.361241177	0.009574104
279	W903_RS01365	W903_0280	233296	233586	NA	virulence factor esxA	-0.771416427	2.55634E-05	-0.238058517	0.102017803	-0.238058517	0.102017803
280	W903_RS01370	W903_0281	233760	234095	NA	hypothetical protein	-0.940520496	2.5318E-08	-1.320281434	3.00473E-34	-1.320281434	3.00473E-34
281	NA	W903_0282	234095	235309	NA	hypothetical protein	0.126663777	0.47998015	-0.641089265	1.25534E-12	-0.641089265	1.25534E-12
282	W903_RS01385	W903_0283	235294	235680	NA	hypothetical protein	-0.524607154	0.005148331	-1.204766872	2.07247E-24	-1.204766872	2.07247E-24
283	W903_RS01390	W903_0284	235714	235995	NA	hypothetical protein	0.115656851	0.536398445	-0.698150881	1.90349E-07	-0.698150881	1.90349E-07
284	NA	W903_0285	236582	236704	NA	hypothetical protein	-1.304738976	NA	-0.211533933	0.73319654	-0.211533933	0.73319654
285	W903_RS01405	W903_0286	236826	237686	NA	transcriptional activator, Rgg/GadR/MutR family, C-terminal domain protein	-0.358972245	0.087957605	-0.253635736	0.060963871	-0.253635736	0.060963871
286	W903_RS01410	W903_0287	237758	238939	NA	major Facilitator Superfamily protein	-0.038795594	0.892105609	0.470319227	0.004651838	0.470319227	0.004651838
287	W903_RS01415	W903_0288	239001	239651	NA	binding--dependent transport system inner membrane component family protein	0.982975101	6.68086E-09	0.444936032	0.000140452	0.444936032	0.000140452
288	W903_RS01420	W903_0289	239652	240578	opuCC	glycine betaine/carnitine/choline-binding protein	0.896766786	2.20645E-09	0.219459113	0.024733716	0.219459113	0.024733716
289	W903_RS01425	W903_0290	240581	241216	NA	binding--dependent transport system inner membrane component family protein	1.135099216	7.66679E-14	0.418125012	6.105E-05	0.418125012	6.105E-05
290	W903_RS01430	W903_0291	241216	242361	NA	glycine betaine/L-proline transport ATP binding subunit	0.566330495	0.00047665	-0.108930869	0.256870419	-0.108930869	0.256870419
291	W903_RS01435	W903_0292	242789	244325	rRNA	NA	2.4052954	0.380602152	-4.32388054	0.026897209	-4.32388054	0.026897209
292	W903_RS01440	W903_0293	244385	244457	rRNA	NA	-0.844621431	NA	0.387279407	0.765272841	0.387279407	0.765272841
293	W903_RS01445	W903_0294	244614	247515	rRNA	NA	2.838236902	0.217098082	-4.028684939	0.034422254	-4.028684939	0.034422254
294	W903_RS01450	W903_0295	247593	247706	rRNA	NA	-1.4469859	0.0426321	0.500192879	0.377625001	0.500192879	0.377625001
295	W903_RS01455	W903_0296	247709	247781	tRNA	NA	-2.96875926	NA	2.024916062	0.699719099	2.024916062	0.699719099
296	W903_RS01460	W903_0297	247787	247857	tRNA	NA	-2.615095903	NA	0.07070075	0.980059476	0.07070075	0.980059476
297	W903_RS01465	W903_0298	247894	247970	rRNA	NA	-0.531150352	0.501170254	1.378076463	0.121735888	1.378076463	0.121735888
298	W903_RS01470	W903_0299	247978	248049	rRNA	NA	-0.419920405	NA	0.297353191	0.899203501	0.297353191	0.899203501
299	W903_RS01475	W903_0300	248063	248152	rRNA	NA	-1.563337395	0.038467454	0.188459699	0.838900429	0.188459699	0.838900429
300	W903_RS01480	W903_0301	248163	248236	NA	NA	NA	NA	NA	NA	NA	NA
301	W903_RS01485	W903_0302	248239	248311	rRNA	NA	-0.595913977	NA	0.456861165	0.605105891	0.456861165	0.605105891
302	W903_RS01490	W903_0303	248323	248403	rRNA	NA	-0.162396429	0.839238676	0.245726274	0.774863441	0.245726274	0.774863441
303	W903_RS01495	W903_0304	248410	248480	rRNA	NA	-0.408814678	0.604754542	-0.883741427	0.173947427	-0.883741427	0.173947427
304	W903_RS01500	W903_0306	248495	248567	rRNA	NA	-0.277184968	NA	0.226621826	0.780618505	0.226621826	0.780618505
305	W903_RS01505	W903_0307	248574	248645	rRNA	NA	0.405466154	NA	-0.364998529	0.946331025	-0.364998529	0.946331025
306	W903_RS01510	W903_0308	248656	248739	NA	NA	NA	NA	NA	NA	NA	NA
307	W903_RS01515	W903_0309	248944	249504	NA	acetyltransferase domain protein	-0.228113903	0.330951294	0.465308775	0.000141032	0.465308775	0.000141032
308	W903_RS01520	W903_0310	249805	250215	NA	acetyltransferase family protein	-0.157278352	0.528875534	0.993699646	2.98824E-11	0.993699646	2.98824E-11
309	W903_RS01525	W903_0311	250205	250912	NA	acetyltransferase domain protein	-0.404864329	0.039475339	0.321094882	0.004215923	0.321094882	0.004215923
310	W903_RS01530	W903_0312	251178	252125	NA	sigma factor regulator C-terminal family protein	-0.889542035	2.0136E-06	-0.469362931	0.000122448	-0.469362931	0.000122448
311	W903_RS01535	W903_0313	252122	252613	NA	RNA polymerase sigma factor, sigma-70 family protein	-0.787681971	0.000285909	-0.762737002	1.86551E-06	-0.762737002	1.86551E-06
312	NA	W903_0314	252773	252895	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.76736975	0.138665132	0.979857005	0.000213975	0.979857005	0.000213975
313	W903_RS01540	W903_0315	252897	253058	NA	putative lipoprotein	0.103255552	0.78773361	1.326162089	1.48752E-09	1.326162089	1.48752E-09
314	W903_RS01545	W903_0316	253193	253801	NA	bacterial regulatory s, tetR family protein	-0.247820553	0.464171074	0.161011305	0.383763582	0.161011305	0.383763582
315	W903_RS01550	W903_0317	253825	254922	NA	ABC-2 type transporter family protein	-0.120005994	0.647719608	0.631332999	8.22248E-05	0.631332999	8.22248E-05
316	W903_RS01555	W903_0318	254925	255641	NA	ABC transporter family protein	-0.317604623	0.30968107	0.55055317	0.003187135	0.55055317	0.003187135
317	W903_RS01560	W903_0319	255904	256587	NA	hypothetical protein	-0.452376318	0.100497184	1.702090204	1.61481E-36	1.702090204	1.61481E-36
318	W903_RS01565	W903_0320	256607	256918	NA	transcriptional regulator PadR-like family protein	-0.710068697	0.009136126	2.497453364	1.54498E-73	2.497453364	1.54498E-73
319	W903_RS01570	W903_0321	257110	257817	NA	hypothetical protein	-1.296567946	3.57153E-19	-1.509323728	2.07548E-59	-1.509323728	2.07548E-59
320	W903_RS01575	W903_0322	258095	259243	nagA	N-acetylglucosamine-6-phosphate deacetylase	0.399373858	0.041146409	0.646032219	1.89313E-11	0.646032219	1.89313E-11
321	W903_RS01580	W903_0323	259362	259904	NA	isoprenylcysteine carboxyl methyltransferase family protein	-1.996014176	1.62365E-46	-2.978437285	3.1349E-138	-2.978437285	3.1349E-138
322	W903_RS01585	W903_0324	260217	261131	glyQ	glycine--tRNA ligase, alpha subunit	0.359440226	0.020363643	-1.849539232	4.70434E-37	-1.849539232	4.70434E-37
323	W903_RS01590	W903_0325	261131	261772	NA	NADPH-dependent FMN reductase family protein	0.193593043	0.243397527	-2.070903011	6.0079E-66	-2.070903011	6.0079E-66
324	W903_RS01595	W903_0326	261776	263815	glyS	glycine--tRNA ligase, beta subunit	0.458355481	0.001743195	-1.963547055	2.64094E-38	-1.963547055	2.64094E-38
325	W903_RS01600	W903_0327	263827	264084	NA	hypothetical protein	1.2923427	5.98477E-14	-1.371007189	6.24028E-23	-1.371007189	6.24028E-23
326	W903_RS01605	W903_0328	264173	264436	NA	hypothetical protein	1.13930424	4.21228E-07	-0.910634714	5.58589E-06	-0.910634714	5.58589E-06
327	W903_RS01610	W903_0329	264551	266059	glpK	glycerol kinase	1.099480945	3.29177E-10	0.042944223	0.801929886	0.042944223	0.801929886
328	W903_RS01615	W903_0330	266072	267901	NA	FAD dependent oxidoreductase family protein	1.172120885	5.99895E-07	0.632104989	0.000176952	0.632104989	0.000176952
329	W903_RS01620	W903_0331	267913	268611	NA	MIP channel s family protein	1.348498922	1.29539E-05	0.934496481	2.17623E-05	0.934496481	2.17623E-05
330	W903_RS01625	W903_0332	268699	270036	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.17141604	0.407712338	1.108007094	1.93094E-17	1.108007094	1.93094E-17
331	W903_RS01630	W903_0333	270027	271457	NA	mga helix-turn-helix domain protein	0.242961527	0.279637146	0.5772429	0.000154982	0.5772429	0.000154982
332	W903_RS01635	W903_0334	271582	273567	tkt	transketolase	0.469851069	0.001199773	-0.730457877	8.27676E-09	-0.730457877	8.27676E-09
333	W903_RS01640	W903_0335	273779	274084	NA	enterocin A Immunity family protein	0.094574186	0.699641117	-1.001254106	6.30747E-17	-1.001254106	6.30747E-17
334	W903_RS01645	W903_0336	274104	274838	NA	ABC transporter family protein	0.348810801	0.046727717	-1.005571055	5.535E-14	-1.005571055	5.535E-14
335	W903_RS01650	W903_0337	274842	276446	NA	putative membrane protein	0.448291208	0.003976592	-0.740291607	2.52419E-09	-0.740291607	2.52419E-09
336	W903_RS01655	W903_0338	276654	278039	NA	PTS system, glucose-like IIB component domain protein	0.27574653	0.247510373	2.384438811	1.86314E-81	2.384438811	1.86314E-81
337	W903_RS01660	W903_0339	278330	278983	proB	glutamate 5-kinase	0.758614067	1.39166E-05	0.558010481	1.86692E-05	0.558010481	1.86692E-05
338	W903_RS01665	W903_0340	278993	280246	proA	glutamate-5-semialdehyde dehydrogenase	0.526459783	0.000479238	0.45174082	2.32431E-05	0.45174082	2.32431E-05
339	W903_RS01670	W903_0341	280380	281276	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase	-0.037872496	0.832460447	0.746066445	5.37115E-15	0.746066445	5.37115E-15
340	W903_RS01675	W903_0342	281291	281617	ftsL	cell division protein FtsL	-0.283763348	0.118232223	-0.129388626	0.404141085	-0.129388626	0.404141085
341	W903_RS01680	W903_0343	281726	283879	NA	penicillin binding transpeptidase domain protein	0.038452741	0.833343489	-0.395324063	0.000135626	-0.395324063	0.000135626
342	W903_RS01685	W903_0344	283881	284891	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	-0.028754419	0.890009272	-0.430214837	8.33598E-05	-0.430214837	8.33598E-05
343	W903_RS01690	W903_0345	284989	286332	NA	helicase domain protein	0.047110785	0.798030544	-1.084909764	8.76801E-34	-1.084909764	8.76801E-34
344	W903_RS01695	W903_0346	286470	287282	NA	bacterial extracellular solute-binding s, 3 family protein	0.014003295	0.947199325	-1.338337849	2.96155E-25	-1.338337849	2.96155E-25
345	W903_RS01700	W903_0347	287377	288180	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	0.415562446	0.005076862	1.046083299	3.78123E-19	1.046083299	3.78123E-19
346	W903_RS01705	W903_0348	288180	288923	NA	ABC transporter family protein	-0.048490509	0.784485464	0.456539149	0.000287317	0.456539149	0.000287317
347	W903_RS01710	W903_0349	289045	289269	NA	hypothetical protein	-0.510381572	0.047875045	0.650477096	0.000505388	0.650477096	0.000505388
348	W903_RS01715	W903_0350	289338	290252	trxB	thioredoxin-disulfide reductase	-0.286110878	0.112947803	-0.00438308	0.968072643	-0.00438308	0.968072643
349	W903_RS01720	W903_0351	290408	291868	NA	nicotinate phosphoribosyltransferase family protein	-0.011737523	0.948583974	-0.715726746	3.54169E-15	-0.715726746	3.54169E-15
350	W903_RS01725	W903_0352	291865	292686	nadE	NAD+ synthetase	0.427111518	0.007606915	-0.340792231	0.001252578	-0.340792231	0.001252578
351	W903_RS01730	W903_0353	292799	294133	NA	papain cysteine protease family protein	0.330117536	0.168307538	-1.013841659	7.52719E-15	-1.013841659	7.52719E-15
352	W903_RS01735	W903_0354	294179	296425	NA	penicillin-binding , 1A family protein	0.437315329	0.002854352	0.243452192	0.031571299	0.243452192	0.031571299
353	W903_RS01740	W903_0355	296412	297011	recU	recombination protein U	0.174665752	0.349244784	1.209367689	1.23222E-28	1.209367689	1.23222E-28
354	W903_RS01745	W903_0356	297086	297604	NA	hypothetical protein	-0.451225073	0.085270842	0.422762609	0.016197645	0.422762609	0.016197645
355	W903_RS01750	W903_0357	297725	298057	NA	divIVA domain protein	-0.79622695	1.46789E-07	-0.499435194	5.81829E-05	-0.499435194	5.81829E-05
356	W903_RS01755	W903_0358	298527	299681	NA	hypothetical protein	0.38258162	0.030932373	0.157632171	0.126115349	0.157632171	0.126115349
357	W903_RS01760	W903_0359	299694	301157	NA	putative holliday junction-specific endonuclease	-0.098642756	0.608738677	-0.423401795	1.18962E-06	-0.423401795	1.18962E-06
358	W903_RS01765	W903_0360	301382	301864	NA	S-Ribosylhomocysteinase family protein	0.044980738	0.816305791	0.381338958	0.003368482	0.381338958	0.003368482
359	W903_RS01770	W903_0361	302053	303660	rny	ribonuclease Y	-0.341737463	0.032371599	-1.227916518	2.11969E-29	-1.227916518	2.11969E-29
360	W903_RS01775	W903_0362	303789	304685	NA	ABC transporter family protein	0.241882234	0.355685142	0.721385851	1.84582E-06	0.721385851	1.84582E-06
361	W903_RS01780	W903_0363	304672	305412	NA	ABC-2 type transporter family protein	0.488485738	0.071010168	0.497128298	0.004547655	0.497128298	0.004547655
362	NA	W903_0364	305799	306494	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-0.031123856	0.892719202	0.920218994	3.92E-12	0.920218994	3.92E-12
363	W903_RS01790	W903_0365	306496	307086	NA	bacterial regulatory s, luxR family protein	-0.523620894	0.003758254	1.050824366	6.97348E-25	1.050824366	6.97348E-25
364	W903_RS01795	W903_0366	307136	307840	NA	hypothetical protein	-0.028397393	0.901111124	1.409838875	1.90964E-37	1.409838875	1.90964E-37
365	W903_RS01800	W903_0367	308007	308636	gmk	guanylate kinase	-0.661165011	8.45352E-05	-0.58386471	1.0408E-05	-0.58386471	1.0408E-05
366	W903_RS01805	W903_0368	308659	308973	rpoZ	DNA-directed RNA polymerase, omega subunit	-0.665653731	6.36821E-05	-1.066960662	1.43033E-12	-1.066960662	1.43033E-12
367	W903_RS01810	W903_0369	309047	311437	priA	primosomal protein N'	0.16926115	0.362916975	0.27972571	0.066115276	0.27972571	0.066115276
368	W903_RS01815	W903_0370	311484	312419	fmt	methionyl-tRNA formyltransferase	0.657758627	1.82019E-05	0.169882582	0.154532248	0.169882582	0.154532248
369	W903_RS01820	W903_0371	312409	313731	sun	ribosomal RNA small subunit methyltransferase B	0.319337467	0.048361682	0.11338541	0.289883319	0.11338541	0.289883319
370	W903_RS01825	W903_0372	313769	314506	NA	phosphatase 2C family protein	0.369798652	0.014692636	0.150175902	0.150892148	0.150175902	0.150892148
371	W903_RS01830	W903_0373	314506	316461	NA	phosphotransferase enzyme family protein	-0.078719312	0.647719608	-0.263668025	0.003799502	-0.263668025	0.003799502
372	W903_RS01835	W903_0374	316622	317317	NA	hypothetical protein	-1.074332559	9.71241E-07	-0.388607182	0.009291667	-0.388607182	0.009291667
373	W903_RS01840	W903_0375	317314	318333	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-0.63100365	0.000299908	-0.379780732	0.00132099	-0.379780732	0.00132099
374	W903_RS01845	W903_0376	318326	318967	NA	bacterial regulatory s, luxR family protein	-0.701895788	1.19037E-05	-0.304518777	0.002068081	-0.304518777	0.002068081
375	W903_RS01850	W903_0377	319009	320409	NA	putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	-0.199467122	0.218113744	-0.509569362	8.22223E-08	-0.509569362	8.22223E-08
376	W903_RS01855	W903_0378	320411	320767	NA	S1 RNA binding domain protein	0.395845804	0.095916955	-0.182640712	0.263082877	-0.182640712	0.263082877
377	W903_RS01860	W903_0379	320814	321590	NA	glycyl-radical enzyme activating family protein	0.566254177	0.021525304	1.104747217	4.5674E-13	1.104747217	4.5674E-13
378	W903_RS01865	W903_0380	321711	322466	NA	deoR C terminal sensor domain protein	0.109346536	0.589504886	0.605526205	4.09962E-06	0.605526205	4.09962E-06
379	W903_RS01870	W903_0381	322585	323568	NA	putative sugar-binding domain protein	0.07129117	0.71314676	0.417781032	0.000227348	0.417781032	0.000227348
380	W903_RS01875	W903_0382	323772	324095	NA	PTS system, Lactose/Cellobiose specific IIA subunit	1.05629019	0.076817593	0.705348223	0.038328853	0.705348223	0.038328853
381	W903_RS01880	W903_0383	324112	324432	NA	PTS system, Lactose/Cellobiose specific IIB subunit	0.124062982	0.858438886	0.676481862	0.134649327	0.676481862	0.134649327
382	W903_RS01885	W903_0384	324434	325735	NA	PTS system, lactose/cellobiose IIC component family protein	0.480933226	0.11315208	1.071144774	2.65308E-09	1.071144774	2.65308E-09
383	W903_RS01890	W903_0385	325916	328372	NA	glycyl radical enzyme, PFL2/glycerol dehydratase family protein	0.79925547	6.09827E-05	0.652835071	6.4858E-06	0.652835071	6.4858E-06
384	W903_RS01895	W903_0386	328382	329050	NA	transaldolase family protein	0.644067667	0.009246904	0.881059801	7.88273E-10	0.881059801	7.88273E-10
385	W903_RS01900	W903_0387	329118	330206	gldA	glycerol dehydrogenase	0.304046398	0.364527265	0.551169194	0.003271423	0.551169194	0.003271423
386	W903_RS01905	W903_0388	330358	331284	cysK	cysteine synthase A	-0.08615722	0.64460116	-0.790308582	2.557E-10	-0.790308582	2.557E-10
387	W903_RS01910	W903_0389	331375	332019	NA	hypothetical protein	0.332796326	0.084095498	0.048134912	0.775345315	0.048134912	0.775345315
388	W903_RS01915	W903_0390	332075	333364	NA	helicase domain protein	0.046254976	0.92288861	1.406160426	2.80568E-05	1.406160426	2.80568E-05
389	W903_RS01920	W903_0391	333493	334029	NA	phosphoribosyl transferase domain protein	-0.034428751	NA	1.560866927	0.006415346	1.560866927	0.006415346
390	W903_RS01925	W903_0392	334106	334660	raiA	ribosomal subunit interface protein	-0.356616931	0.045895244	-0.198271455	0.053199793	-0.198271455	0.053199793
391	W903_RS01930	W903_0393	334991	336527	rRNA	NA	2.668577167	0.226196936	-3.898324137	0.035553265	-3.898324137	0.035553265
392	W903_RS01935	W903_0394	336587	336659	rRNA	NA	-1.15094223	NA	1.679406325	0.228362631	1.679406325	0.228362631
393	W903_RS01940	W903_0395	336816	339716	rRNA	NA	2.78714616	0.238523766	-4.467329348	0.024974968	-4.467329348	0.024974968
394	W903_RS01945	W903_0396	339794	339907	rRNA	NA	0.57966878	0.483069328	0.829343796	0.114633161	0.829343796	0.114633161
395	W903_RS01950	W903_0397	339912	339985	rRNA	NA	-0.968406418	NA	1.048062688	0.86167603	1.048062688	0.86167603
396	W903_RS01955	W903_0398	340201	341553	NA	aspartate kinase domain protein	-1.224013428	4.60599E-17	-1.781623265	1.62488E-55	-1.781623265	1.62488E-55
397	W903_RS01960	W903_0399	341677	342297	NA	beta-phosphoglucomutase, putative	-1.092207528	1.3838E-12	0.024654561	0.024654561	-0.271294026	0.024654561
398	W903_RS01965	W903_0400	342435	343226	NA	enoyl-CoA hydratase/isomerase family protein	0.03865415	0.833008384	-1.540816338	2.38979E-14	-1.540816338	2.38979E-14
399	W903_RS01970	W903_0401	343322	343756	NA	iron dependent repressor, N-terminal DNA binding domain protein	-0.182719651	0.277470661	-0.838229342	1.0477E-06	-0.838229342	1.0477E-06
400	W903_RS01975	W903_0402	343756	344727	fabH	3-oxoacyl-[acyl-carrier-] synthase III family protein	0.126578717	0.476095248	-0.828434146	5.03009E-06	-0.828434146	5.03009E-06
401	W903_RS01980	W903_0403	344785	345009	NA	phosphopantetheine attachment site family protein	-0.333661013	0.02634239	-1.338078728	1.95733E-13	-1.338078728	1.95733E-13
402	W903_RS01985	W903_0404	345163	346122	NA	nitronate monooxygenase family protein	0.932293426	2.06104E-11	-0.866663843	8.14412E-06	-0.866663843	8.14412E-06
403	W903_RS01990	W903_0405	346142	347068	fabD	malonyl CoA-acyl carrier protein transacylase	0.843323813	6.02844E-09	-1.044815067	0.010498995	-1.044815067	0.010498995
404	W903_RS01995	W903_0406	347077	347811	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	0.909315838	3.58569E-11	-1.253170818	0.001026254	-1.253170818	0.001026254
405	W903_RS02000	W903_0407	347827	349059	fabF	beta-ketoacyl-acyl-carrier-protein synthase II	0.593860516	7.32293E-05	-1.589277026	5.63478E-16	-1.589277026	5.63478E-16
406	W903_RS02005	W903_0408	349061	349561	accB	acetyl-CoA carboxylase, biotin carboxyl carrier protein	1.181927085	4.0096E-16	-1.620560291	1.99984E-20	-1.620560291	1.99984E-20
407	W903_RS02010	W903_0409	349558	349980	fabZ	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ	0.801637199	2.25463E-06	-1.829847744	2.14854E-30	-1.829847744	2.14854E-30
408	W903_RS02015	W903_0410	350018	351388	accC	acetyl-CoA carboxylase, biotin carboxylase subunit	1.001484901	2.40058E-11	-1.925057187	4.83193E-34	-1.925057187	4.83193E-34
409	W903_RS02020	W903_0411	351397	352272	accD	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	0.808604069	4.54971E-08	-2.370628542	1.50877E-67	-2.370628542	1.50877E-67
410	W903_RS02025	W903_0412	352277	353038	accA	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	1.13638034	4.87263E-14	-2.29644155	1.02391E-86	-2.29644155	1.02391E-86
411	W903_RS02030	W903_0413	353506	354138	NA	glucose-6-phosphate 1-dehydrogenase family protein	0.432836348	0.043870218	-1.335223846	9.59178E-29	-1.335223846	9.59178E-29
412	W903_RS02035	W903_0414	354184	355461	serS	serine--tRNA ligase	0.765627174	2.53023E-07	-1.972815653	2.51855E-66	-1.972815653	2.51855E-66
413	W903_RS02040	W903_0415	355827	356819	NA	acyltransferase family protein	-0.250846089	0.252500145	1.829073512	1.24499E-73	1.829073512	1.24499E-73

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414	W903_RS02045	W903_0416	356857	357219	NA	hypothetical protein	-0.199184362	0.240481793	-0.830694884	7.49911E-17	-0.830694884	7.49911E-17
415	W903_RS02050	W903_0417	357338	358249	NA	PTS system, mannose/fructose/sorbose , IID component family protein	0.805959492	3.78829E-08	-1.263889754	3.47832E-33	-1.263889754	3.47832E-33
416	W903_RS02055	W903_0418	358264	359076	NA	PTS system sorbose-specific iic component family protein	0.907354986	2.19433E-10	-1.335043314	1.77576E-26	-1.335043314	1.77576E-26
417	W903_RS02060	W903_0419	359109	360119	manX	PTS system mannose-specific EIIAB component	0.117396937	0.52257258	-1.93776494	2.0302E-85	-1.93776494	2.0302E-85
418	W903_RS02065	W903_0420	360422	361234	NA	HAD hydrolase, IIB family protein	-0.685885182	7.44243E-06	-0.361976717	0.00068489	-0.361976717	0.00068489
419	W903_RS02070	W903_0421	361323	361907	NA	putative membrane protein	-0.889570946	1.46769E-08	-0.187319893	0.05050587	-0.187319893	0.05050587
420	W903_RS02075	W903_0422	361997	362608	NA	hypothetical protein	-0.429869219	0.004487954	-0.205901956	0.032057896	-0.205901956	0.032057896
421	W903_RS02080	W903_0423	362711	364132	NA	permease family protein	0.323194554	0.140752343	-0.794075633	5.89751E-15	-0.794075633	5.89751E-15
422	W903_RS02085	W903_0424	364281	364724	NA	tRNA threonylcarbamoyl adenosine modification protein YjeE	-0.460681074	0.011313412	0.364289808	0.002558756	0.364289808	0.002558756
423	W903_RS02090	W903_0425	364717	365238	NA	acetyltransferase family protein	-0.094529286	0.624569854	0.107521264	0.339547959	0.107521264	0.339547959
424	W903_RS02095	W903_0426	365247	366554	brpA	biofilm regulatory protein A	-0.134404325	0.427430056	0.134937268	0.143554214	0.134937268	0.143554214
425	W903_RS02100	W903_0427	366618	366914	NA	hypothetical protein	-0.636554006	0.004850929	-0.151549388	0.367209097	-0.151549388	0.367209097
426	W903_RS02105	W903_0428	366911	367330	NA	HIT domain protein	0.502117402	0.002136569	1.569375276	1.83152E-29	1.569375276	1.83152E-29
427	W903_RS02110	W903_0429	367666	368169	NA	hypothetical protein	-2.167807085	1.47349E-27	-3.629377703	0	-3.629377703	0
428	W903_RS02115	W903_0430	368479	369222	NA	ABC transporter family protein	-0.366247486	0.024133038	-1.194208553	4.98014E-31	-1.194208553	4.98014E-31
429	W903_RS02120	W903_0431	369206	370240	NA	bacterial ABC transporter EcsB family protein	-0.01914786	0.914074262	-0.610640558	4.51752E-08	-0.610640558	4.51752E-08
430	W903_RS02125	W903_0432	370298	371098	NA	phosphotransferase enzyme family protein	-0.213341577	0.196263472	-0.808912416	1.2019E-16	-0.808912416	1.2019E-16
431	W903_RS02130	W903_0433	371088	371723	trmB	tRNA (guanine-N(7)-)-methyltransferase	-0.837659661	2.75984E-08	-0.604082165	2.1851E-08	-0.604082165	2.1851E-08
432	W903_RS02135	W903_0434	371767	371853	tRNA	NA	3.09206873	NA	0.473960349	0.776325669	0.473960349	0.776325669
433	NA	W903_0435	372176	372439	NA	hypothetical protein	0.127386303	NA	0.899345443	0.046369028	0.899345443	0.046369028
434	NA	W903_0436	372929	373042	NA	glycerophosphoryl diester phosphodiesterase family protein	0.753565871	0.367966213	0.755314117	0.036274513	0.755314117	0.036274513
435	NA	W903_0437	373292	373468	NA	glycerophosphoryl diester phosphodiesterase family protein	0.295420677	NA	0.619664968	0.169864073	0.619664968	0.169864073
436	NA	W903_0438	373575	373739	NA	hypothetical protein	-0.283138384	NA	1.191920984	0.040036379	1.191920984	0.040036379
437	W903_RS02150	W903_0439	373741	374775	NA	replication initiator A family protein	-0.443583354	0.296007939	0.591057016	0.020087488	0.591057016	0.020087488
438	W903_RS02155	W903_0440	374769	375458	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.343054637	0.519384764	0.774419109	0.005312801	0.774419109	0.005312801
439	NA	W903_0441	375455	375595	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.378845666	NA	0.900232408	0.460011568	0.900232408	0.460011568
440	W903_RS02160	W903_0442	375592	375789	NA	helix-turn-helix family protein	-1.065965087	0.060639429	0.246498892	0.470001629	0.246498892	0.470001629
441	W903_RS02165	W903_0443	376172	376471	NA	hypothetical protein	-0.362287433	0.468176574	0.489982656	0.04244246	0.489982656	0.04244246
442	W903_RS02170	W903_0444	376488	378752	NA	LPXTG cell wall anchor domain protein	-0.247319078	0.315859247	0.302059246	0.021252642	0.302059246	0.021252642
443	W903_RS02175	W903_0445	378772	379494	NA	LPXTG cell wall anchor domain protein	0.224135161	0.525444689	0.479422146	0.030672411	0.479422146	0.030672411
444	W903_RS02180	W903_0446	379547	382369	NA	putative cross-wall-targeting lipoprotein signal	-0.379643142	0.090008853	-0.086177761	0.504130818	-0.086177761	0.504130818
445	W903_RS02185	W903_0447	382664	382891	NA	putative membrane protein	-0.804988678	0.005621574	-0.357434787	0.066227141	-0.357434787	0.066227141
446	W903_RS02190	W903_0448	382996	383577	NA	hypothetical protein	-0.7551924	1.37849E-05	0.733869599	5.07661E-13	0.733869599	5.07661E-13
447	W903_RS02195	W903_0449	383628	384380	NA	putative membrane protein	-0.556628858	0.143974617	-0.216800211	0.45028242	-0.216800211	0.45028242
448	W903_RS02200	W903_0450	384417	384713	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.294231176	0.083255569	-0.631028613	0.201124848	-0.631028613	0.201124848
449	W903_RS02205	W903_0451	384706	385164	NA	hypothetical protein	-0.214694886	0.711554523	0.577115431	0.078705731	0.577115431	0.078705731
450	W903_RS02210	W903_0452	385226	385585	NA	hypothetical protein	-1.028297839	0.03641127	-1.126034514	0.005168433	-1.126034514	0.005168433
451	W903_RS02215	W903_0453	385566	387926	NA	AAA-like domain protein	0.4514854	0.124473964	-0.209685268	0.250206519	-0.209685268	0.250206519
452	W903_RS02220	W903_0454	387919	388512	NA	hypothetical protein	0.316301403	0.460404359	0.176518068	0.532192284	0.176518068	0.532192284
453	W903_RS02225	W903_0455	388536	388862	NA	glycerophosphoryl diester phosphodiesterase family protein	0.395030205	0.427465018	0.565863559	0.0535035	0.565863559	0.0535035
454	W903_RS02230	W903_0456	388897	391587	NA	peptidase M23 family protein	0.475338649	0.057826884	0.443946164	0.005852891	0.443946164	0.005852891
455	W903_RS02235	W903_0457	391608	392213	NA	putative prgL	0.234821203	0.71409499	-0.75693336	0.087222286	-0.75693336	0.087222286
456	W903_RS02240	W903_0458	392233	392505	NA	hypothetical protein	0.044184452	0.95607518	-0.271425984	0.653083749	-0.271425984	0.653083749
457	W903_RS02245	W903_0459	392505	393290	NA	hypothetical protein	-0.093284633	0.844341147	-0.702844855	0.013091519	-0.702844855	0.013091519
458	W903_RS02250	W903_0460	393312	393803	NA	hypothetical protein	0.275313281	0.50440675	-0.430023707	0.114442897	-0.430023707	0.114442897
459	W903_RS02255	W903_0461	393803	395848	NA	type IV secretory system Conjugative DNA transfer family protein	0.857236638	0.001726505	0.075259658	0.773514954	0.075259658	0.773514954
460	W903_RS02260	W903_0462	395890	396255	NA	glycerophosphoryl diester phosphodiesterase family protein	1.022684016	0.079081585	0.121000325	0.80144881	0.121000325	0.80144881
461	W903_RS02265	W903_0463	396257	399496	NA	hypothetical protein	1.044061535	5.03682E-05	-0.335192262	0.117378053	-0.335192262	0.117378053
462	W903_RS02270	W903_0464	399548	399847	NA	glycerophosphoryl diester phosphodiesterase family protein	0.532599824	0.466957553	-2.618873431	1.10919E-06	-2.618873431	1.10919E-06
463	W903_RS02275	W903_0465	400190	400750	NA	glycerophosphoryl diester phosphodiesterase family protein	0.377413387	0.58319645	1.500314548	8.06384E-06	1.500314548	8.06384E-06
464	W903_RS02280	W903_0466	400753	401127	NA	bacterial mobilization family protein	-0.173907123	NA	1.520443483	0.041037569	1.520443483	0.041037569
465	W903_RS02285	W903_0467	401099	402739	NA	relaxase/mobilization nuclease domain protein	0.409543699	0.402857741	0.910297555	0.005190617	0.910297555	0.005190617
466	NA	W903_0468	402768	402917	NA	glycerophosphoryl diester phosphodiesterase family protein	0.474200736	NA	0.134087957	0.885242075	0.134087957	0.885242075
467	W903_RS02290	W903_0469	402876	403283	NA	hypothetical protein	-0.149682661	0.604754542	0.364706579	0.036828065	0.364706579	0.036828065
468	W903_RS02295	W903_0470	403314	404597	NA	hypothetical protein	0.112436776	0.648392027	0.366905006	0.006241848	0.366905006	0.006241848
469	W903_RS02300	W903_0471	405192	405575	rimP	ribosome maturation factor rimP	0.222693388	0.251844765	-0.21015826	0.312600545	-0.21015826	0.312600545
470	W903_RS02305	W903_0472	405611	406762	nusA	transcription termination factor NusA	0.152571017	0.381549257	-0.565599676	0.010522808	-0.565599676	0.010522808
471	W903_RS02310	W903_0473	406784	407080	NA	hypothetical protein	0.23473817	0.229316616	-0.656103548	0.001894406	-0.656103548	0.001894406
472	W903_RS02315	W903_0474	407073	407375	NA	ribosomal L7Ae/L30e/S12e/Gadd45 family protein	0.011896621	0.950641272	-0.739021243	0.00095757	-0.739021243	0.00095757
473	W903_RS02320	W903_0475	407395	410178	infB	translation initiation factor IF-2	0.600759179	7.43109E-05	-0.299446878	0.090909952	-0.299446878	0.090909952
474	W903_RS02325	W903_0476	410287	410637	rbfA	ribosome-binding factor A	0.373124246	0.059041648	-0.234482131	0.225683105	-0.234482131	0.225683105
475	W903_RS02330	W903_0477	410721	411725	NA	alpha/beta hydrolase fold family protein	0.084288631	0.733854288	-0.901248242	1.56825E-18	-0.901248242	1.56825E-18
476	W903_RS02335	W903_0478	411888	412304	NA	copper transport repressor, CopY/TcrY family	0.239101143	0.513275836	0.921726731	0.000661892	0.921726731	0.000661892
477	W903_RS02340	W903_0479	412317	414551	NA	copper-translocating P-type ATPase	0.059864062	0.769509545	1.462840341	4.84711E-29	1.462840341	4.84711E-29
478	W903_RS02345	W903_0480	414592	414798	NA	heavy-metal-associated domain protein	0.265179109	0.483314144	1.391987013	1.11234E-11	1.391987013	1.11234E-11
479	W903_RS02350	W903_0481	414908	415522	NA	hypothetical protein	0.555106435	0.00033977	0.624647911	1.27873E-07	0.624647911	1.27873E-07
480	W903_RS02355	W903_0482	415537	416349	NA	HAD hydrolase, IIB family protein	-0.128099425	0.466665594	-0.46295342	5.36623E-07	-0.46295342	5.36623E-07
481	W903_RS02360	W903_0483	416462	419104	polA	DNA polymerase I	0.133449737	0.423657793	-0.44027238	7.85377E-07	-0.44027238	7.85377E-07
482	W903_RS02365	W903_0484	419134	419574	NA	coA binding domain protein	-0.142599267	0.403920269	-0.591106209	1.59006E-07	-0.591106209	1.59006E-07
483	W903_RS02370	W903_0485	419656	420135	NA	ferric uptake regulator family protein	-0.333285905	0.048427359	0.254345516	0.017968425	0.254345516	0.017968425
484	W903_RS02375	W903_0486	420287	421852	NA	LPXTG cell wall anchor domain protein	-0.2402247	0.344004389	0.163698322	0.366292005	0.163698322	0.366292005
485	W903_RS02380	W903_0487	421965	422651	NA	putative transcriptional activator CadC	-0.627096062	0.000183797	0.362823079	0.000531942	0.362823079	0.000531942
486	W903_RS02385	W903_0488	422653	423690	NA	HAMP domain protein	-0.849678806	1.97167E-07	-0.350158177	0.00092861	-0.350158177	0.00092861
487	W903_RS02390	W903_0489	423704	424444	NA	hypothetical protein	-0.252360905	0.150816281	0.387112883	0.008468648	0.387112883	0.008468648
488	W903_RS02395	W903_0490	424631	425773	tgt	queuine tRNA-ribosyltransferase	-0.255188264	0.116396909	-1.575725751	4.99882E-36	-1.575725751	4.99882E-36
489	NA	W903_0491	425748	425870	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.089388986	NA	-3.415447656	0.377750863	-3.415447656	0.377750863
490	W903_RS02400	W903_0492	425882	426190	NA	CHY zinc finger family protein	0.373207213	0.38120064	1.155995892	2.28654E-06	1.155995892	2.28654E-06
491	W903_RS02405	W903_0493	426197	426736	NA	biotin transporter BioY	0.496687836	0.179320305	0.6792325	0.006051031	0.6792325	0.006051031
492	W903_RS02410	W903_0494	426875	427651	NA	metallo-beta-lactamase superfamily protein	-0.029587273	0.876832988	-0.802543921	1.49462E-15	-0.802543921	1.49462E-15
493	W903_RS02415	W903_0495	427651	428157	NA	cytidine and deoxycytidylate deaminase zinc-binding region family protein	0.627920361	0.000291063	-0.378217806	0.000229417	-0.378217806	0.000229417
494	NA	W903_0496	428259	428393	NA	glycerophosphoryl diester phosphodiesterase family protein	0.166995372	0.593646859	1.297614852	3.22786E-15	1.297614852	3.22786E-15
495	W903_RS02425	W903_0497	428429	429778	NA	phosphoglucose isomerase family protein	-0.128783892	0.446374739	-0.785248983	4.69363E-18	-0.785248983	4.69363E-18
496	W903_RS02430	W903_0498	430100	430627	NA	5-formyltetrahydrofolate cyclo-ligase	-0.536093312	0.012850849	-0.023346334	0.883933745	-0.023346334	0.883933745
497	W903_RS02435	W903_0499	430618	431295	NA	rhomboid family protein	-0.43246043	0.007514823	-0.02247665	0.882747555	-0.02247665	0.882747555
498	W903_RS02440	W903_0500	431427	432470	NA	basic membrane family protein	-0.738416658	2.82742E-06	-0.253551795	0.030525336	-0.253551795	0.030525336
499	W903_RS02445	W903_0501	432561	433460	galU	UTP-glucose-1-phosphate uridylyltransferase	0.304109152	0.052360454	-0.897709312	1.53658E-20	-0.897709312	1.53658E-20
500	W903_RS02450	W903_0502	433497	434513	gpsA	glycerol-3-phosphate dehydrogenase	0.869688455	5.26544E-09	-0.699928471	3.8949E-13	-0.699928471	3.8949E-13
501	W903_RS02455	W903_0503	434683	435012	rnpA	ribonuclease P protein component	-0.95313514	1.22964E-09	-0.441581856	4.93859E-05	-0.441581856	4.93859E-05
502	W903_RS02460	W903_0504	435025	435840	NA	membrane insertase, YidC/Oxa1 family domain protein	-0.764158037	1.25872E-06	-0.873923697	2.83318E-17	-0.873923697	2.83318E-17
503	W903_RS02465	W903_0505	435848	436669	NA	KH domain protein	-0.765082337	7.75869E-08	-1.222309788	6.44862E-37	-1.222309788	6.44862E-37
504	W903_RS02470	W903_0506	437018	438554	rRNA	NA	2.402121674	0.377928802	-4.309363724	0.025957193	-4.309363724	0.025957193
505	W903_RS02475	W903_0507	438614	438686	rRNA	NA	-0.604774779	NA	-0.082256581	0.960423095	-0.082256581	0.960423095
506	W903_RS02480	W903_0508	438843	441741	rRNA	NA	2.826876075	0.219716273	-4.025499514	0.035237629	-4.025499514	0.035237629
507	W903_RS02485	W903_0509	441819	441932	rRNA	NA	-1.591778373	0.012387597	0.329722515	0.559046211	0.329722515	0.559046211
508	W903_RS02490	W903_0510	441935	442007	rRNA	NA	0.989144927	NA	1.994972911	0.726361185	1.994972911	0.726361185
509	W903_RS02495	W903_0511	442013	442083	rRNA	NA	0.694939672	NA	-0.395563864	0.90981923	-0.395563864	0.90981923
510	W903_RS02500	W903_0512	442120	442196	rRNA	NA	-0.058656773	NA	1.231302304	0.18320809	1.231302304	0.18320809
511	W903_RS02505	W903_0513	442204	442275	NA	NA	NA	NA	NA	NA	NA	NA
512	W903_RS02510	W903_0514	442390	442923	NA	hypothetical protein	0.117071979	0.565005127	1.199422848	1.6836E-16	1.199422848	1.6836E-16
513	W903_RS02515	W903_0515	443007	443783	NA	recX family protein	-1.049954893	1.3009E-09	-0.72290606	5.90109E-08	-0.72290606	5.90109E-08
514	W903_RS02520	W903_0516	443882	445237	NA	23S rRNA (uracil-5-)-methyltransferase RumA	-0.54796748	0.000852337	-0.649655645	7.95523E-11	-0.649655645	7.95523E-11
515	W903_RS02525	W903_0517	445506	446270	NA	phosphorylase superfamily protein	-0.487311042	0.005514122	-1.176989884	5.75311E-30	-1.176989884	5.75311E-30
516	W903_RS02530	W903_0518	446304	446747	NA	acetyltransferase family protein	-0.205035597	0.338526977	-0.763383207	1.46525E-16	-0.763383207	1.46525E-16
517	W903_RS02535	W903_0519	446920	450621	scpA	CSa peptidase	-0.307168352	0.064728237	-1.695548389	1.77611E-46	-1.695548389	1.77611E-46
518	W903_RS02540	W903_0520	450831	451739	NA	glycosyl transferase 2 family protein	-0.724139799	3.39477E-05	-1.271256814	3.17579E-38	-1.271256814	3.17579E-38
519	W903_RS02545	W903_0521	452293	453303	nrdF	ribonucleoside-diphosphate reductase subunit beta	-0.136475949	0.755212804	-0.757714727	5.29993E-05	-0.757714727	5.29993E-05
520	W903_RS02550	W903_0522	453304	453717	NA	nrdl protein	0.011574989	0.981959839	-0.748176992	0.001681175	-0.748176992	0.001681175
521	W903_RS02555	W903_0523	453719	455887	NA	ribonucleoside-diphosphate reductase, alpha subunit	0.091253966	0.705759832	-0.383904543	0.005397271	-0.383904543	0.005397271
522	W903_RS02560	W903_0524	455950	459117	NA	leucine rich repeats family protein	-0.154553388	0.466856237	-0.601985775	2.90751E-07	-0.601985775	2.90751E-07
523	W903_RS02565	W903_0525	459130	459519	NA	pyridoxamine 5'-phosphate oxidase family protein	0.221491709	0.570214659	-0.377847274	0.048593988	-0.377847274	0.048593988
524	W903_RS02570	W903_0526	459563	460054	NA	gyrl-like small molecule binding domain protein	0.890577709	1.31818E-05	1.449419683	5.15521E-30	1.449419683	5.15521E-30
525	W903_RS02575	W903_0527	460293	460577	NA	hypothetical protein	0.266917881	0.31244217	0.882273543	2.07842E-11	0.882273543	2.07842E-11
526	W903_RS02580	W903_0528	460664	460981	NA	carboxymuconolactone decarboxylase family protein	0.706308023	0.002383671	1.190849909	7.90155E-24	1.190849909	7.90155E-24
527	W903_RS02585	W903_0529	461005	461400	NA	cupin domain protein	0.90600684	1.02679E-06	1.280332261	1.77838E-28	1.280332261	1.77838E-28
528	W903_RS02590	W903_0530	461410	461799	adhR	HTH-type transcriptional regulator AdhR	0.767232058	5.80076E-05	1.259549294	1.52867E-25	1.259549294	1.52867E-25
529	W903_RS02595	W903_0531	461815	462852	NA	zinc-binding dehydrogenase family protein	0.704704787	2.50467E-05	1.030476791	6.85182E-29	1.030476791	6.85182E-29
530	W903_RS02600	W903_0532	462962	463816	NA	aldo/keto reductase family protein	0.835020761	0.000354474	1.906719998	3.52541E-50	1.906719998	3.52541E-50
531	W903_RS02605	W903_0533	463901	464764	NA	cation diffusion facilitator transporter family protein	-0.100757303	0.780622309	2.385500714	4.27771E-36	2.385500714	4.27771E-36
532	W903_RS02610	W903_0534	464896	465420	NA	bacterial regulatory s, tetR family protein	-0.270931013	0.231815288	-1.137863751	1.36027E-11	-1.137863751	1.36027E-11
533	NA	W903_0535	465599	465739	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.275545928	0.589912333	-1.003941795	0.024283597	-1.003941795	0.024283597
534	W903_RS02615	W903_0536	465826	466032	NA	putative membrane protein	0.112624999	0.768072746	-0.193179507	0.575919546	-0.193179507	0.575919546
535	W903_RS02620	W903_0537	466129	466353	NA	hypothetical protein	3.271120141	NA	1.152665145	0.459351623	1.152665145	0.459351623
536	W903_RS02625	W903_0538	466451	466521	tRNA	NA	1.666508696	0.000381532	-0.4203245	0.252485891	-0.4203245	0.252485891
537	W903_RS02630	W903_0539	466592	466897	NA	cupin domain protein	0.373715286	0.086558854	-0.880353627	3.62996E-08	-0.880353627	3.62996E-08
538	W903_RS02635	W903_0540	466899	467237	NA	cupin domain protein	0.542105589	0.003976592	-0.786623744	6.62041E-14	-0.786623744	6.62041E-14
539	W903_RS02640	W903_0541	467258	468013	NA	methyltransferase domain protein	-0.384635286	0.028734377	-1.365369977	4.75548E-38	-1.365369977	4.75548E-38
540	W903_RS02645	W903_0542	468213	470273	NA	deoR-like helix-turn-helix domain protein	0.223844595	0.519650659	1.882505833	6.77331E-33	1.882505833	6.77331E-33
541	W903_RS02650	W903_0543	470382	470837	NA	phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein	-0.180488308	0.736276249	-0.032043447	0.94134607	-0.032043447	0.94134607
542	W903_RS02655	W903_0544	470856	471134	NA	PTS system, Lactose/Cellobiose specific IIB subunit	0.672355351	NA	2.135025658	2.43506E-05	2.135025658	2.43506E-05
543	W903_RS02660	W903_0545	471146	472483	NA	PTS system sugar-specific permease component family protein	-0.095603897	0.835816596	2.075917384	2.17729E-14	2.075917384	2.17729E-14
544	W903_RS02665	W903_0546	472506	473336	NA	class II Aldolase and Adducin N-terminal domain protein	0.132861975	0.786454518	1.906729802	1.93094E-17	1.906729802	1.93094E-17
545	W903_RS02670	W903_0547	473471	473935	NA	phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein	-0.092796959	0.844341147	0.241956862	0.435207178	0.241956862	0.435207178
546	W903_RS02675	W903_0548	473948	475279	NA	PTS system sugar-specific permease component family protein	0.685832206	0.066496319	1.649931848	5.87236E-12	1.649931848	5.87236E-12
547	W903_RS02680	W903_0549	475281	475565	NA	PTS system, Lactose/Cellobiose specific IIB subunit	0.526814043	0.302225232	1.630959674	1.88849E-09	1.630959674	1.88849E-09
548	W903_RS02685	W903_0550	475850	476680	NA	bacterial regulatory helix-turn-helix s, AraC family protein	0.768484931	0.000104525	0.102927792	0.51939211	0.102927792	0.51939211
549	W903_RS02695	W903_0553	478280	479170	NA	binding--dependent transport system inner membrane component family protein	0.549729489	0.458894815	2.351053604	7.49184E-12	2.351053604	7.49184E-12
550	W903_RS02700	W903_0554	479184	480017	NA	binding--dependent transport system inner membrane component family protein	0.934600083	0.1233448	1.993391003	1.85437E-13	1.993391003	1.85437E-13
551	W903_RS02705	W903_0555	480027	482228	NA	glycosyl hydrolases 31 family protein	0.797449124	0.012080109	1.651874628	2.29455E-22	1.651874628	2.29455E-22

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552	W903_RS02710	W903_0556	482318	483490	galK	galactokinase	1.007620157	0.006936004	1.643528593	3.30874E-10	1.643528593	3.30874E-10
553	W903_RS02715	W903_0557	483500	484984	galT	galactose-1-phosphate uridylyltransferase	0.812628166	0.039699193	1.432144731	6.76386E-14	1.432144731	6.76386E-14
554	W903_RS02720	W903_0558	484986	485981	NA	UDP-glucose 4-epimerase GalE	0.855810721	0.04827578	1.697373124	2.62894E-14	1.697373124	2.62894E-14
555	W903_RS02725	W903_0559	486107	487108	NA	aldose 1-epimerase family protein	0.380614682	0.41083729	1.117675245	1.63971E-07	1.117675245	1.63971E-07
556	W903_RS02730	W903_0560	487299	487553	NA	hypothetical protein	-1.172838854	1.95216E-09	-1.267690946	5.96489E-17	-1.267690946	5.96489E-17
557	W903_RS02735	W903_0561	487662	487973	NA	hypothetical protein	-1.251948042	1.64751E-14	-1.267267462	5.98618E-24	-1.267267462	5.98618E-24
558	W903_RS02740	W903_0562	488241	488810	NA	acetyltransferase family protein	1.093299541	8.3033E-13	-0.526424401	1.14548E-05	-0.526424401	1.14548E-05
559	W903_RS02745	W903_0563	488908	489492	NA	acetyltransferase family protein	1.017395107	3.09976E-10	-0.474316949	0.000185505	-0.474316949	0.000185505
560	W903_RS02750	W903_0564	489489	490055	NA	AAA domain protein	0.93441373	1.1975E-08	-1.135877994	2.56734E-16	-1.135877994	2.56734E-16
561	W903_RS02755	W903_0565	490055	492706	valS	valine--tRNA ligase	1.15701368	1.17327E-16	-1.389050413	4.69686E-33	-1.389050413	4.69686E-33
562	W903_RS02760	W903_0566	492787	493767	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.020121347	5.65552E-08	0.011081539	0.946381898	0.011081539	0.946381898
563	W903_RS02765	W903_0567	493775	494299	NA	putative membrane protein	-0.646640294	0.018608585	0.395395181	0.024340504	0.395395181	0.024340504
564	NA	W903_0568	494667	494822	NA	hypothetical protein	-0.270237401	0.327552535	0.453368625	0.006871657	0.453368625	0.006871657
565	NA	W903_0569	494842	495009	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.976238392	0.037178662	0.471924617	0.157366473	0.471924617	0.157366473
566	W903_RS02770	W903_0570	495107	496066	NA	oxidoreductase , NAD-binding Rossmann fold family protein	-0.169308088	0.331233356	0.822914889	2.93254E-13	0.822914889	2.93254E-13
567	W903_RS02775	W903_0571	496227	497129	NA	corA-like Mg2+ transporter family protein	-0.170474092	0.445570203	1.771937609	2.42256E-50	1.771937609	2.42256E-50
568	W903_RS02780	W903_0572	497290	498354	NA	hypothetical protein	0.35505758	0.12356904	0.945479938	1.7359E-11	0.945479938	1.7359E-11
569	W903_RS02785	W903_0573	498470	499462	asnA	aspartate--ammonia ligase	0.371984985	0.05130082	-0.253945946	0.011524372	-0.253945946	0.011524372
570	W903_RS02790	W903_0574	499507	499875	NA	hypothetical protein	-0.032936966	0.890009272	0.226214476	0.049102066	0.226214476	0.049102066
571	W903_RS02795	W903_0575	500087	500626	NA	RNA methyltransferase, RsmD family	-0.095768887	0.590511184	-0.048886688	0.643701007	-0.048886688	0.643701007
572	W903_RS02800	W903_0576	500638	500928	NA	putative membrane protein	-0.717602126	3.38407E-05	-0.352883632	0.002157577	-0.352883632	0.002157577
573	W903_RS02805	W903_0577	500925	501410	coaD	pantetheine-phosphate adenylyltransferase	-0.186956506	0.274774767	-0.084159407	0.42755962	-0.084159407	0.42755962
574	W903_RS02810	W903_0578	501400	502473	NA	lon protease (S16) C-terminal proteolytic domain protein	-0.406445943	0.00814957	-0.696240483	6.2004E-13	-0.696240483	6.2004E-13
575	W903_RS02815	W903_0579	502671	503882	NA	5'-nucleotidase, C-terminal domain protein	0.266121231	0.136213354	0.798077074	2.82181E-15	0.798077074	2.82181E-15
576	W903_RS02820	W903_0580	503952	504530	NA	hypothetical protein	0.460165733	0.003153271	0.139541258	0.182229127	0.139541258	0.182229127
577	W903_RS02825	W903_0581	504581	505687	rlmN	23S rRNA methyltransferase	0.603107424	8.61363E-05	-0.233012815	0.059361285	-0.233012815	0.059361285
578	W903_RS02830	W903_0582	505687	506202	NA	vanZ like family protein	0.890224022	4.60839E-05	0.062721694	0.77640213	0.062721694	0.77640213
579	W903_RS02835	W903_0583	506387	508132	NA	ABC transporter family protein	0.362504597	0.138091152	-0.115440514	0.32523653	-0.115440514	0.32523653
580	W903_RS02840	W903_0584	508122	509861	NA	ABC transporter family protein	0.208409961	0.43371711	-0.374629159	0.000425709	-0.374629159	0.000425709
581	W903_RS02845	W903_0585	509989	510555	NA	glutamine amidotransferase of anthranilate synthase/aminodeoxychorismate synthase family protein	-0.014650905	0.961982117	-0.091121581	0.647122672	-0.091121581	0.647122672
582	W903_RS02850	W903_0586	510622	511161	NA	biotin transporter BioY	0.583956098	0.126093455	-0.930597554	0.003772281	-0.930597554	0.003772281
583	W903_RS02855	W903_0587	511162	512154	bioB	biotin synthase	0.463228248	0.14610702	0.045394922	0.879707266	0.045394922	0.879707266
584	W903_RS02860	W903_0588	512279	512794	NA	hypothetical protein	0.794435808	0.027719201	0.605230961	0.037889125	0.605230961	0.037889125
585	W903_RS02865	W903_0589	512784	513899	NA	acetyl-CoA C-acetyltransferase family protein	1.253269125	7.27072E-07	0.372784065	0.065808305	0.372784065	0.065808305
586	W903_RS02870	W903_0590	513892	515121	NA	AMP-binding enzyme family protein	0.561835127	0.069270068	0.654527002	0.000499994	0.654527002	0.000499994
587	W903_RS02875	W903_0591	515234	515866	nth	endonuclease III	0.27836378	0.164668168	1.035464129	7.39198E-13	1.035464129	7.39198E-13
588	W903_RS02880	W903_0592	515867	516256	NA	type IV leader peptidase family protein	-0.803093599	NA	1.255963196	0.111511931	1.255963196	0.111511931
589	W903_RS02885	W903_0593	516417	516626	NA	hypothetical protein	-0.586508533	0.014369568	-0.805524581	1.29422E-06	-0.805524581	1.29422E-06
590	W903_RS02890	W903_0594	516623	517591	NA	ROK family protein	0.271833835	0.088864179	-0.268765431	0.005211136	-0.268765431	0.005211136
591	W903_RS02895	W903_0595	517603	517983	NA	rhodanese-like domain protein	0.60286342	0.000332729	-0.116891469	0.326112248	-0.116891469	0.326112248
592	W903_RS02900	W903_0596	518215	520056	typA	GTP-binding protein TypA/BipA	-0.239096819	0.139982028	-0.905361446	2.72312E-17	-0.905361446	2.72312E-17
593	W903_RS02905	W903_0597	520101	520346	NA	hypothetical protein	0.361487829	0.108402596	-0.651641469	2.02961E-06	-0.651641469	2.02961E-06
594	W903_RS02910	W903_0598	520476	521831	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	0.193201041	0.257219764	-0.443021813	1.72572E-06	-0.443021813	1.72572E-06
595	W903_RS02915	W903_0599	521834	522910	NA	glycosyltransferase family 28 C-terminal domain protein	0.168141993	0.328559663	-0.341098612	0.00101776	-0.341098612	0.00101776
596	W903_RS02920	W903_0600	522914	524053	NA	cell division FtsQ family protein	-0.165581722	0.355685142	-0.530961386	1.22832E-06	-0.530961386	1.22832E-06
597	W903_RS02925	W903_0601	524325	525698	ftsA	cell division protein FtsA	0.188148684	0.252500145	-0.540146346	2.96226E-07	-0.540146346	2.96226E-07
598	W903_RS02930	W903_0602	525720	527000	ftsZ	cell division protein FtsZ	0.545311575	0.000130106	-0.487042783	1.3357E-07	-0.487042783	1.3357E-07
599	W903_RS02935	W903_0603	527009	527680	NA	alanine racemase, N-terminal domain protein	0.269350435	0.087925789	-0.45128445	7.20869E-05	-0.45128445	7.20869E-05
600	W903_RS02940	W903_0604	527692	528297	NA	hypothetical protein	0.439670869	0.005401446	-0.438389057	2.94036E-06	-0.438389057	2.94036E-06
601	W903_RS02950	W903_0605	528556	529344	NA	S4 domain protein	-0.023685241	0.892365276	-0.267090748	0.00320721	-0.267090748	0.00320721
602	W903_RS02955	W903_0606	529354	530124	NA	divIVA domain protein	-0.391331683	0.009367493	-0.890284641	2.19947E-20	-0.890284641	2.19947E-20
603	W903_RS02960	W903_0607	530409	533201	ileS	isoleucine--tRNA ligase	0.484740449	0.000853006	-1.672939204	1.63828E-47	-1.672939204	1.63828E-47
604	W903_RS02965	W903_0608	533318	533620	NA	hypothetical protein	-0.526899286	0.009569687	-0.652128622	2.7883E-11	-0.652128622	2.7883E-11
605	W903_RS02970	W903_0609	533684	534139	NA	NUDIX domain protein	-0.907680946	1.17678E-06	-1.264927942	5.50806E-28	-1.264927942	5.50806E-28
606	W903_RS02975	W903_0610	534325	536586	NA	istB-like ATP binding family protein	0.580895212	0.000275248	1.427800195	1.14165E-18	1.427800195	1.14165E-18
607	W903_RS02980	W903_0611	536884	537114	NA	hypothetical protein	-0.837192979	0.004795017	1.135739379	0.00030638	1.135739379	0.00030638
608	W903_RS02985	W903_0612	537255	537947	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	0.255519279	0.206759631	0.327589497	0.0242945	0.327589497	0.0242945
609	W903_RS02990	W903_0613	537940	538674	NA	ABC transporter family protein	-0.233857557	0.26326899	-0.164672704	0.249518326	-0.164672704	0.249518326
610	W903_RS02995	W903_0614	538960	540654	NA	phosphoglucomutase/phosphomannomutase, C-terminal domain protein	-0.163036657	0.418459993	-0.920938312	4.21822E-10	-0.920938312	4.21822E-10
611	W903_RS03000	W903_0615	540793	541647	NA	tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain protein	-0.184724219	0.293839545	-0.977076865	3.11773E-19	-0.977076865	3.11773E-19
612	W903_RS03005	W903_0616	541644	542480	NA	hypothetical protein	-0.008694322	0.964761157	-0.524874523	5.29168E-06	-0.524874523	5.29168E-06
613	W903_RS03010	W903_0617	542606	543946	xseA	exodeoxyribonuclease VII, large subunit	0.126846395	0.495327691	0.101235359	0.343131155	0.101235359	0.343131155
614	W903_RS03015	W903_0618	543924	544139	xseB	exodeoxyribonuclease VII, small subunit	0.293348488	0.331233356	-0.210451783	0.300594877	-0.210451783	0.300594877
615	W903_RS03020	W903_0619	544139	545011	NA	polyprenyl synthetase family protein	-0.051879243	0.780671567	0.028969135	0.814047485	0.028969135	0.814047485
616	W903_RS03025	W903_0620	545004	545831	NA	hemolysin TlyA family protein	0.078487792	0.705759832	-0.109273596	0.309264296	-0.109273596	0.309264296
617	W903_RS03030	W903_0621	545818	546291	NA	arginine repressor, DNA binding domain protein	-0.360026667	0.037886466	-0.52674463	1.57609E-06	-0.52674463	1.57609E-06
618	W903_RS03035	W903_0622	546303	547961	recN	DNA repair protein RecN	-0.195736737	0.278351491	-0.409264179	2.56312E-05	-0.409264179	2.56312E-05
619	W903_RS03040	W903_0623	548074	548910	NA	degV family protein	-0.115380378	0.549536178	-0.182410587	0.084994463	-0.182410587	0.084994463
620	W903_RS03045	W903_0624	548978	549742	NA	GDSL-like Lipase/Acylhydrolase family protein	-0.194363146	0.300532643	-0.38929555	0.001044907	-0.38929555	0.001044907
621	W903_RS03050	W903_0625	549717	550313	NA	hypothetical protein	-0.155903409	0.549536178	-0.182775579	0.168966153	-0.182775579	0.168966153
622	W903_RS03055	W903_0626	550422	550697	hup	DNA-binding protein HU	-0.821413266	1.21209E-08	-0.875741976	1.8222E-21	-0.875741976	1.8222E-21
623	W903_RS03060	W903_0627	550785	551927	NA	phage integrase family protein	-0.218464876	0.286334644	-0.364387356	0.026161579	-0.364387356	0.026161579
624	W903_RS03065	W903_0628	552042	552593	NA	hypothetical protein	0.551148763	0.004296654	-1.74104652	1.89006E-45	-1.74104652	1.89006E-45
625	W903_RS03070	W903_0629	552611	552997	NA	hypothetical protein	0.245290989	0.357011977	-0.909613962	3.54277E-10	-0.909613962	3.54277E-10
626	W903_RS03075	W903_0630	553001	553348	NA	helix-turn-helix family protein	-0.200750119	0.354573027	-1.000545436	3.08663E-09	-1.000545436	3.08663E-09
627	W903_RS03080	W903_0631	553645	553890	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.046626844	1.32701E-06	-1.186649552	3.71793E-06	-1.186649552	3.71793E-06
628	W903_RS03085	W903_0632	553841	554629	NA	putative phage membrane protein	-1.396524593	4.60599E-17	-1.225567305	2.8338E-25	-1.225567305	2.8338E-25
629	W903_RS03090	W903_0633	554680	554871	NA	cro/C1-type HTH DNA-binding domain protein	-1.854164516	6.18138E-22	-1.746252835	1.45369E-22	-1.746252835	1.45369E-22
630	W903_RS03095	W903_0634	554951	555262	NA	putative excisionase	-1.57173312	4.22581E-19	-1.141913693	7.97507E-15	-1.141913693	7.97507E-15
631	NA	W903_0635	555267	555416	NA	hypothetical protein	-0.802800732	0.105367014	-1.088092283	0.028584335	-1.088092283	0.028584335
632	W903_RS03100	W903_0636	555410	555637	NA	hypothetical protein	-1.247982546	1.07998E-06	-0.842070856	4.60579E-05	-0.842070856	4.60579E-05
633	W903_RS03105	W903_0637	555630	555860	NA	hypothetical protein	-1.466355516	4.73922E-08	-1.443726808	4.14108E-09	-1.443726808	4.14108E-09
634	W903_RS03110	W903_0638	555844	557163	NA	AAA ATPase domain protein	-1.256559904	1.55448E-16	-1.41076039	3.8201E-43	-1.41076039	3.8201E-43
635	W903_RS03115	W903_0639	557178	558272	NA	AAA domain protein	-0.857003873	1.17178E-08	-0.985533914	5.52074E-21	-0.985533914	5.52074E-21
636	W903_RS03120	W903_0640	558312	558734	NA	putative phage protein	-1.20651038	1.17255E-14	-1.203507774	4.49658E-23	-1.203507774	4.49658E-23
637	W903_RS03125	W903_0641	558736	559470	NA	putative phage protein	-1.028808397	2.00645E-10	-1.009525973	1.62849E-17	-1.009525973	1.62849E-17
638	W903_RS03130	W903_0642	559491	560096	NA	hypothetical protein	-0.875157613	2.47168E-07	-0.930058018	7.92515E-14	-0.930058018	7.92515E-14
639	W903_RS03135	W903_0643	560096	560704	NA	hypothetical protein	-1.292145307	5.00108E-17	-1.142106116	2.59777E-18	-1.142106116	2.59777E-18
640	W903_RS03140	W903_0644	560749	562293	NA	DEAD/DEAH box helicase family protein	-0.969479725	9.44787E-10	-1.116865638	3.30637E-26	-1.116865638	3.30637E-26
641	W903_RS03145	W903_0645	562302	562499	NA	glycerophosphoryl diester phosphodiesterase family protein	-2.187713904	1.44649E-07	-1.87222481	0.000329916	-1.87222481	0.000329916
642	W903_RS03150	W903_0646	562492	562743	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.958971195	6.19034E-07	-1.260151765	1.64502E-18	-1.260151765	1.64502E-18
643	W903_RS03155	W903_0647	562814	565093	NA	AAA domain protein	-1.466397549	4.79176E-24	-1.278392067	8.60786E-36	-1.278392067	8.60786E-36
644	W903_RS03160	W903_0648	565455	565673	NA	putative rNA polymerase sigma factor	-1.645399761	1.85767E-11	-1.358994844	1.79581E-07	-1.358994844	1.79581E-07
645	W903_RS03165	W903_0649	565666	566061	NA	endodeoxyribonuclease RusA family protein	-1.134688623	1.38088E-09	-1.210379343	3.40507E-16	-1.210379343	3.40507E-16
646	W903_RS03170	W903_0650	566058	566273	NA	hypothetical protein	-1.066045369	0.04836609	-0.365942849	0.353519471	-0.365942849	0.353519471
647	W903_RS03175	W903_0651	566270	566506	NA	hypothetical protein	-1.667159556	1.56493E-20	-1.554179685	1.6555E-24	-1.554179685	1.6555E-24
648	W903_RS03185	W903_0652	566813	567226	NA	phage transcriptional regulator, RinA family protein	-1.255035874	5.62443E-07	-1.226396242	2.26918E-07	-1.226396242	2.26918E-07
649	W903_RS03190	W903_0653	567401	568153	NA	hypothetical protein	-2.291504639	1.37401E-49	-2.659271226	1.2795E-117	-2.659271226	1.2795E-117
650	W903_RS03195	W903_0654	568207	568638	NA	terminase, small subunit	-2.55348602	2.31427E-25	-2.16844919	5.08707E-30	-2.16844919	5.08707E-30
651	W903_RS03200	W903_0655	568628	569908	NA	phage terminase, large subunit, PBSX family	-2.447463919	9.60013E-43	-2.113661063	6.28822E-44	-2.113661063	6.28822E-44
652	W903_RS03205	W903_0656	569986	571452	NA	phage portal protein, SPP1 family	-2.65852612	1.1325E-57	-2.391251708	9.72425E-92	-2.391251708	9.72425E-92
653	W903_RS03210	W903_0657	571418	572860	NA	phage head morphogenesis , SPP1 gp7 family domain protein	-2.339141739	1.18227E-50	-2.660782904	1.93606E-91	-2.660782904	1.93606E-91
654	NA	W903_0658	572960	573076	NA	putative membrane protein	-0.389123998	NA	0.777477434	0.199593713	0.777477434	0.199593713
655	W903_RS03220	W903_0659	573081	573284	NA	hypothetical protein	-2.710837645	3.37838E-39	-2.940864446	4.57082E-49	-2.940864446	4.57082E-49
656	W903_RS03225	W903_0660	573427	573996	NA	hypothetical protein	-2.362052782	9.98927E-32	-3.020387156	6.0592E-83	-3.020387156	6.0592E-83
657	W903_R10740	W903_0661	574015	574911	NA	putative head protein	-2.403742096	3.53172E-50	-3.135128863	2.4077E-124	-3.135128863	2.4077E-124
658	W903_RS03235	W903_0662	574917	575273	NA	phage gp6-like head-tail connector family protein	-2.625619921	5.92035E-31	-3.254316262	4.2104E-103	-3.254316262	4.2104E-103
659	W903_RS03240	W903_0663	575284	575562	NA	hypothetical protein	-2.322938881	1.39141E-25	-3.021561729	1.38981E-52	-3.021561729	1.38981E-52
660	W903_RS03245	W903_0664	575577	575903	NA	hypothetical protein	-2.573295639	4.7313E-32	-3.038477218	2.32772E-55	-3.038477218	2.32772E-55
661	W903_RS03250	W903_0665	575911	576270	NA	putative phage protein	-2.709893324	6.63388E-47	-3.170578213	4.1075E-112	-3.170578213	4.1075E-112
662	W903_RS03255	W903_0666	576282	576914	NA	phage major tail protein, TP901-1 family	-2.636292389	8.52271E-49	-2.982285768	2.5008E-100	-2.982285768	2.5008E-100
663	W903_RS03260	W903_0667	576965	577420	NA	phage family protein	-2.384059335	6.95819E-32	-2.573189108	1.71489E-73	-2.573189108	1.71489E-73
664	W903_RS03265	W903_0668	577495	577725	NA	hypothetical protein	-2.662628593	5.28866E-46	-2.87263206	3.3373E-128	-2.87263206	3.3373E-128
665	W903_RS03270	W903_0669	577754	581980	NA	tape measure domain protein	-2.315774545	2.02315E-53	-2.411438443	5.0479E-121	-2.411438443	5.0479E-121
666	W903_RS03275	W903_0670	581993	582835	NA	phage tail family protein	-2.965951053	1.9711E-74	-2.785050193	8.9799E-140	-2.785050193	8.9799E-140
667	NA	W903_0671	582848	584356	NA	prophage endopeptidase tail family protein	-2.850566794	7.64589E-75	-2.500190956	3.57751E-92	-2.500190956	3.57751E-92
668	NA	W903_0672	584404	586674	NA	gp58-like family protein	-2.648777944	8.25563E-60	-2.591293641	3.2112E-119	-2.591293641	3.2112E-119
669	NA	W903_0673	586683	586835	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.756736365	2.69457E-11	-2.079138378	1.56751E-20	-2.079138378	1.56751E-20
670	W903_RS03290	W903_0674	586846	587262	NA	hypothetical protein	-2.40319147	5.99265E-36	-2.531051734	2.96133E-51	-2.531051734	2.96133E-51
671	NA	W903_0675	587325	587486	NA	hypothetical protein	-2.907780115	6.52619E-27	-2.83464243	2.04959E-36	-2.83464243	2.04959E-36
672	W903_RS03295	W903_0676	587496	587786	NA	putative phage protein	-2.744560834	3.82561E-35	-2.783670594	1.79593E-93	-2.783670594	1.79593E-93
673	W903_RS03300	W903_0677	587788	588039	NA	holin, phage phi LC3 family	-2.549502832	1.54757E-51	-2.49512233	5.72478E-39	-2.49512233	5.72478E-39
674	W903_RS03310	W903_0678	588159	589352	NA	mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein	-2.07737032	2.47868E-30	-2.492407057	2.7431E-104	-2.492407057	2.7431E-104
675	W903_RS03315	W903_0679	589760	590233	NA	hypothetical protein	-1.205455497	1.98798E-13	0.510095681	1.89487E-06	0.510095681	1.89487E-06
676	W903_RS03320	W903_0680	590360	590560	NA	csbD-like family protein	-0.851895606	0.064799054	0.476874604	0.335698455	0.476874604	0.335698455
677	NA	W903_0681	590601	590771	NA	putative nicotinate phosphoribosyltransferase	-1.17777237	0.067096287	-0.277684316	0.531434549	-0.277684316	0.531434549
678	W903_RS03325	W903_0682	591191	591370	NA	hypothetical protein	-0.938974491	6.49819E-06	0.61196396	0.000821709	0.61196396	0.000821709
679	W903_RS03330	W903_0683	591776	591973	NA	hypothetical protein	-0.949032577	0.206759631	0.145852535	0.739545253	0.145852535	0.739545253
680	W903_RS03335	W903_0684	592017	592949	NA	putative dihydroorotate dehydrogenase	-0.370962377	0.616449631	-2.48248906	1.6064E-116	-2.48248906	1.6064E-116
681	W903_RS03340	W903_0685	593135	594370	NA	femAB family protein	0.436817732	0.01342991	0.519486059	1.27694E-07	0.519486059	1.27694E-07
682	W903_RS03345	W903_0686	594389	595600	NA	femAB family protein	0.384880364	0.015250379	0.586288557	4.81631E-11	0.586288557	4.81631E-11
683	W903_RS03350	W903_0687	595613	596833	NA	femAB family protein	0.233231906	0.160806264	0.71094476	4.55494E-13	0.71094476	4.55494E-13
684	W903_RS03355	W903_0688	596833	597645	NA	putative hydrolase	0.465567121	0.00221873	0.849182492	3.99446E-19	0.849182492	3.99446E-19
685	W903_RS03360	W903_0689	597716	599032	NA	HD domain protein	0.403815851	0.014621274	0.514388812	1.99366E-05	0.514388812	1.99366E-05
686	W903_RS03365	W903_0690	599096	599494	NA	hypothetical protein	-0.99121986	3.50053E-08	0.426572238	0.001065317	0.426572238	0.001065317
687	W903_RS03370	W903_0691	599838	602522	NA	calcium-translocating P-type ATPase, PMCA-type	0.025161919	0.885855408	-0.609864531	7.94272E-06	-0.609864531	7.94272E-06
688	W903_RS03375	W903_0692	602567	603427	NA	phosphoesterase family protein	-0.519636619	0.006633666	1.057764706	1.00056E-19	1.057764706	1.00056E-19
689	W903_RS03380	W903_0693	603579	605510	fbp	fructose-1,6-bisphosphatase class 3	0.130230055	0.578632939	1.777376146	3.3983E-52	1.777376146	3.3983E-52

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690	W903_RS03385	W903_0694	605600	606724	queG	epoxyqueuosine reductase	-0.453716947	0.026176266	1.656159125	8.43291E-62	1.656159125	8.43291E-62
691	W903_RS03390	W903_0695	606911	607891	prfB	peptide chain release factor 2	0.23980682	0.126321509	-0.549603919	8.8808E-10	-0.549603919	8.8808E-10
692	W903_RS03395	W903_0696	607910	608602	ftsE	cell division ATP-binding protein FtsE	0.248088129	0.126747878	-0.379972928	6.3735E-05	-0.379972928	6.3735E-05
693	W903_RS03400	W903_0697	608595	609515	NA	ftsX-like permease family protein	-0.020073371	0.909836741	-0.628579047	3.87196E-09	-0.628579047	3.87196E-09
694	W903_RS03405	W903_0698	609568	610278	NA	alpha/beta hydrolase family protein	0.314815798	0.080799139	1.032660606	2.16697E-29	1.032660606	2.16697E-29
695	W903_RS03410	W903_0699	610275	610910	NA	hypothetical protein	0.34623521	0.065377276	0.823642438	1.71515E-16	0.823642438	1.71515E-16
696	W903_RS03415	W903_0700	611141	611905	NA	acetoin reductases family protein	-0.137064665	0.475889989	0.48908623	1.7155E-06	0.48908623	1.7155E-06
697	W903_RS03420	W903_0701	612055	614520	NA	exonuclease, DNA polymerase III, epsilon subunit family domain protein	0.080224691	0.661507684	-0.15870886	0.125809507	-0.15870886	0.125809507
698	W903_RS03425	W903_0702	614615	615799	NA	degT/Dnrl/EryC1/StrS aminotransferase family protein	0.300395347	0.061982832	-0.101386248	0.308001055	-0.101386248	0.308001055
699	W903_RS03430	W903_0703	615820	617166	asnS	asparagine--tRNA ligase	-0.078298208	0.654620604	-0.803643522	1.00693E-18	-0.803643522	1.00693E-18
700	W903_RS03435	W903_0704	617206	617763	NA	hypothetical protein	-0.41165345	0.027939254	-0.728900043	1.72935E-06	-0.728900043	1.72935E-06
701	W903_RS03440	W903_0705	617760	618743	NA	inosine-uridine preferring nucleoside hydrolase family protein	-0.537363165	0.000250615	-0.743460108	3.65351E-12	-0.743460108	3.65351E-12
702	W903_RS03445	W903_0706	618988	619401	NA	osmC-like family protein	-0.72413227	0.000185571	-0.423172244	0.002341797	-0.423172244	0.002341797
703	W903_RS03450	W903_0707	619555	620445	NA	P-loop ATPase family protein	0.578920819	0.000877752	-0.499784853	1.85188E-05	-0.499784853	1.85188E-05
704	W903_RS03455	W903_0708	620442	621416	NA	hypothetical protein	0.844308418	2.52525E-07	0.075491512	0.547051688	0.075491512	0.547051688
705	W903_RS03460	W903_0709	621413	622324	NA	sporulation Regulator WhiA C terminal domain protein	0.308708459	0.057293238	0.003866388	0.973334254	0.003866388	0.973334254
706	W903_RS03465	W903_0710	622339	623736	pepD	dipeptidase	0.323045155	0.0426321	-0.068121845	0.502091611	-0.068121845	0.502091611
707	W903_RS03470	W903_0711	623878	625398	NA	yodA lipocalin-like domain protein	-0.782828123	1.99237E-05	-1.801895815	2.17638E-17	-1.801895815	2.17638E-17
708	W903_RS03475	W903_0712	625510	625770	rpmE	ribosomal protein L31	-1.05618314	1.48836E-14	-0.852615391	1.01048E-16	-0.852615391	1.01048E-16
709	W903_RS03480	W903_0713	625879	626814	NA	DHHA1 domain protein	0.206899004	0.287022861	0.495590809	1.36574E-05	0.495590809	1.36574E-05
710	W903_RS03485	W903_0714	627080	628102	add	adenosine deaminase	0.075218343	0.806170452	-1.559596434	7.52714E-30	-1.559596434	7.52714E-30
711	W903_RS03490	W903_0715	628161	628604	NA	flavodoxin	-0.956739803	9.10932E-07	-0.437960314	2.40012E-05	-0.437960314	2.40012E-05
712	W903_RS03495	W903_0716	628681	628956	NA	chorismate mutase	-0.863879864	7.49766E-06	0.098116545	0.62029633	0.098116545	0.62029633
713	W903_RS03500	W903_0717	628949	630145	NA	voltage gated chloride channel family protein	-0.294227	0.203693857	0.460251463	0.000154982	0.460251463	0.000154982
714	W903_RS03505	W903_0718	630729	631076	rplS	ribosomal protein L19	-1.18838736	3.17084E-16	-0.766216129	1.05248E-10	-0.766216129	1.05248E-10
715	W903_RS03510	W903_0719	631187	631258	tRNA	NA	1.747111785	NA	0.612434274	0.758020569	0.612434274	0.758020569
716	W903_RS03520	W903_0721	632093	632497	NA	transposase family protein	-0.919783469	1.00413E-06	1.328713583	1.26181E-27	1.328713583	1.26181E-27
717	W903_RS03525	W903_0722	632659	632859	NA	putative integrase	-1.116348073	3.45948E-09	1.29653463	2.5435E-24	1.29653463	2.5435E-24
718	W903_RS03530	W903_0723	632884	633141	tnpSth1	iSSth1, transposase (Orf2), IS3 family	-1.261396398	7.41255E-10	1.592862038	1.82199E-17	1.592862038	1.82199E-17
719	W903_RS10310	W903_0724	633649	633810	NA	TM2 domain protein	0.476858352	0.29098286	3.011610275	2.55488E-41	3.011610275	2.55488E-41
720	W903_RS03535	W903_0725	634553	635830	NA	ftsX-like permease family protein	-1.299598172	7.32005E-14	0.37658312	0.001878773	0.37658312	0.001878773
721	W903_RS03540	W903_0726	635840	636496	NA	ABC transporter family protein	-0.726759213	0.00113149	0.610813801	3.69044E-05	0.610813801	3.69044E-05
722	W903_RS03545	W903_0727	636496	637872	NA	ftsX-like permease family protein	-0.269134833	0.149383746	0.636741836	3.02247E-08	0.636741836	3.02247E-08
723	W903_RS03550	W903_0728	637969	638622	NA	putative transcriptional activator CadC	-0.86417561	0.000118972	-0.348450892	0.0270274	-0.348450892	0.0270274
724	W903_RS03555	W903_0729	638619	639938	NA	HAMP domain protein	-1.174777275	5.00105E-10	-0.754345972	1.37799E-07	-0.754345972	1.37799E-07
725	W903_RS03560	W903_0730	639990	640601	NA	integrase core domain protein	-0.408680777	0.075582676	0.351721995	0.018010755	0.351721995	0.018010755
726	W903_RS03565	W903_0731	640815	641015	NA	csbD-like family protein	0.111134485	0.758765308	0.59730218	0.008090943	0.59730218	0.008090943
727	W903_RS10315	W903_0732	641057	641245	NA	hypothetical protein	-0.526558651	0.17335524	0.338511499	0.077240652	0.338511499	0.077240652
728	W903_RS03570	W903_0733	641670	642875	NA	cell cycle family protein	-0.521779406	0.000700963	0.267438828	0.006754369	0.267438828	0.006754369
729	W903_RS03575	W903_0734	642994	643554	NA	HAD hydrolase, IA, variant 1 family protein	-0.718176083	2.42897E-06	1.403788222	5.20103E-40	1.403788222	5.20103E-40
730	W903_RS03580	W903_0735	643555	645507	gyrB	DNA gyrase, B subunit	-0.246809219	0.116374595	0.059878105	0.558635249	0.059878105	0.558635249
731	W903_RS03585	W903_0736	645601	647325	NA	septation ring formation regulator, EzrA family protein	-0.632784439	1.36352E-05	-0.814740774	1.02301E-16	-0.814740774	1.02301E-16
732	W903_RS03590	W903_0737	647419	648060	serB	phosphoserine phosphatase SerB	0.543730505	0.00230222	-0.441045877	0.000505627	-0.441045877	0.000505627
733	W903_RS03595	W903_0738	648081	648566	NA	NUDIX domain protein	0.237070731	0.412459017	-0.179518295	0.383844701	-0.179518295	0.383844701
734	W903_RS03600	W903_0739	648579	649034	NA	hypothetical protein	-0.084880001	0.705759832	-0.267419265	0.04397493	-0.267419265	0.04397493
735	W903_RS03605	W903_0740	649232	650539	eno	phosphopyruvate hydratase	-0.077209541	0.681248828	-1.252777837	4.2941E-48	-1.252777837	4.2941E-48
736	W903_RS03610	W903_0741	650647	651711	NA	DNA/RNA non-specific endonuclease family protein	-0.199489691	0.337668674	1.716504665	3.60922E-56	1.716504665	3.60922E-56
737	W903_RS03615	W903_0742	651940	653223	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	0.438207322	0.008380055	0.539938503	3.70185E-09	0.539938503	3.70185E-09
738	W903_RS03620	W903_0743	653216	653728	NA	shikimate kinase family protein	-0.226968284	0.311453557	0.219858143	0.060223356	0.219858143	0.060223356
739	W903_RS03625	W903_0744	653785	655158	NA	cell envelope-related function transcriptional attenuator common domain protein	0.029468317	0.873551447	0.179867072	0.093460728	0.179867072	0.093460728
740	W903_RS03630	W903_0745	655259	656620	NA	23S rRNA (uracil-5-)-methyltransferase RumA	-0.725564929	1.92147E-05	-1.144193926	8.89396E-28	-1.144193926	8.89396E-28
741	NA	W903_0746	657718	657894	NA	hypothetical protein	-0.653102255	0.015353759	1.847643387	2.6128E-56	1.847643387	2.6128E-56
742	NA	W903_0747	659098	659292	NA	putative succinyl-diaminopimelate desuccinylase	-0.194062528	NA	1.997429693	0.010902711	1.997429693	0.010902711
743	W903_RS03645	W903_0748	659278	659508	NA	hypothetical protein	0.621183999	NA	2.619475396	0.036458903	2.619475396	0.036458903
744	W903_RS03650	W903_0749	659569	660720	NA	beta-lactamase family protein	-0.346382773	0.083411153	0.498092791	2.02719E-07	0.498092791	2.02719E-07
745	W903_RS03655	W903_0750	660920	661912	NA	ABC transporter family protein	-0.350703235	0.065391433	0.657520336	2.53782E-09	0.657520336	2.53782E-09
746	W903_RS03665	W903_0753	662736	663521	NA	ABC-2 transporter family protein	0.215967823	0.365440383	0.934837602	1.07135E-13	0.934837602	1.07135E-13
747	NA	W903_0754	664317	664451	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.142506179	0.769579939	-0.535063113	0.005184447	-0.535063113	0.005184447
748	W903_RS03675	W903_0755	664451	665299	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.398512326	0.051557722	-1.011052642	2.62201E-17	-1.011052642	2.62201E-17
749	W903_RS03680	W903_0756	665296	666018	NA	short chain dehydrogenase family protein	0.09689937	0.717464977	-0.907942051	1.56032E-19	-0.907942051	1.56032E-19
750	W903_RS03685	W903_0757	666011	666316	NA	phosphopantetheine attachment site family protein	-0.620284562	0.010113378	-1.623338358	6.08856E-57	-1.623338358	6.08856E-57
751	W903_RS03690	W903_0758	666333	666776	NA	fabA-like domain protein	0.529081378	0.010546432	-0.638473044	4.4074E-12	-0.638473044	4.4074E-12
752	W903_RS03695	W903_0759	666766	667695	NA	ABC transporter family protein	0.158517662	0.521627441	-0.928820508	5.48077E-24	-0.928820508	5.48077E-24
753	W903_RS03700	W903_0760	667688	668566	NA	ABC-2 type transporter family protein	0.102962645	0.646585966	-0.922683409	7.41462E-25	-0.922683409	7.41462E-25
754	W903_RS03705	W903_0761	668563	670566	NA	putative cylE	-0.09934888	0.631284966	-0.754945133	1.51003E-19	-0.754945133	1.51003E-19
755	W903_RS03710	W903_0762	670563	671516	NA	aminomethyltransferase folate-binding domain protein	-0.20004506	0.277322139	-0.825166151	1.88214E-21	-0.825166151	1.88214E-21
756	W903_RS03715	W903_0763	671552	673708	NA	beta-ketoacyl synthase, C-terminal domain protein	0.143655038	0.398263862	-0.424951816	1.40947E-05	-0.424951816	1.40947E-05
757	W903_RS03720	W903_0764	673713	674924	NA	UDP-glucoronosyl and UDP-glucosyl transferase family protein	-0.578400574	0.000120828	-0.622065394	1.48752E-09	-0.622065394	1.48752E-09
758	W903_RS03725	W903_0765	674893	675468	NA	hypothetical protein	-0.71587674	4.57745E-06	-0.786115754	1.63938E-15	-0.786115754	1.63938E-15
759	W903_RS03730	W903_0766	675611	676264	NA	ftsX-like permease family protein	0.272057969	0.534175267	1.265309329	8.00323E-11	1.265309329	8.00323E-11
760	W903_RS03735	W903_0767	676274	677296	NA	macB-like periplasmic core domain protein	-0.081040838	0.818227551	0.988266924	7.74687E-08	0.988266924	7.74687E-08
761	W903_RS03745	W903_0770	677711	678382	NA	ABC transporter family protein	0.091237018	0.802265072	0.989184372	4.54647E-07	0.989184372	4.54647E-07
762	W903_RS03755	W903_0773	680145	680930	NA	DNA/RNA non-specific endonuclease family protein	0.134921772	0.632735521	1.116396665	2.4878E-17	1.116396665	2.4878E-17
763	W903_RS03760	W903_0774	681008	681646	NA	hypothetical protein	1.225023928	6.23008E-07	1.839533273	8.68815E-26	1.839533273	8.68815E-26
764	W903_RS03765	W903_0775	681863	682519	NA	ABC transporter family protein	-0.496792185	0.008631153	-1.047670152	1.8382E-29	-1.047670152	1.8382E-29
765	W903_RS03770	W903_0776	682516	683289	NA	hypothetical protein	-0.22221319	0.256969376	-0.781867091	4.14362E-12	-0.781867091	4.14362E-12
766	W903_RS03775	W903_0777	683453	684271	NA	hypothetical protein	-0.061244281	0.870685211	-0.026330781	0.903573839	-0.026330781	0.903573839
767	NA	W903_0778	684308	684877	NA	lysR substrate binding domain protein	0.188966262	0.430272975	1.088266462	9.32371E-18	1.088266462	9.32371E-18
768	NA	W903_0779	685111	685365	NA	hypothetical protein	0.129739315	0.755212804	1.281356784	3.67861E-10	1.281356784	3.67861E-10
769	W903_RS03785	W903_0780	685385	686443	NA	phosphotransferase system, EIIC family protein	0.906720695	6.88E-05	0.875848502	4.56819E-11	0.875848502	4.56819E-11
770	W903_RS03790	W903_0781	686457	687449	ldhD	D-lactate dehydrogenase	1.001049557	0.000314325	0.630648064	0.000240243	0.630648064	0.000240243
771	W903_RS03795	W903_0782	687657	689207	NA	MFS/sugar transport family protein	-0.661796068	0.077950145	-0.356370516	0.258066643	-0.356370516	0.258066643
772	W903_RS03800	W903_0783	689274	690299	NA	pfkB carbohydrate kinase family protein	0.699436377	0.280296301	1.836607117	2.32049E-06	1.836607117	2.32049E-06
773	W903_RS03805	W903_0784	690316	692115	uidA	beta-glucuronidase	0.823984996	0.000141854	0.466734916	0.002212106	0.466734916	0.002212106
774	W903_RS03810	W903_0785	692144	692815	NA	bacterial regulatory s, gntR family protein	0.442216972	0.016899212	-0.808357048	2.73264E-12	-0.808357048	2.73264E-12
775	W903_RS03815	W903_0786	692932	693549	NA	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase family protein	0.158778246	0.648392027	1.823687513	6.01275E-33	1.823687513	6.01275E-33
776	W903_RS03820	W903_0787	693566	694966	NA	glucuronate isomerase family protein	0.503389426	0.039791776	2.192369376	1.55827E-60	2.192369376	1.55827E-60
777	W903_RS03825	W903_0788	694984	696030	uxuA	mannonate dehydratase	0.855734079	0.000331854	1.805694864	3.72262E-37	1.805694864	3.72262E-37
778	W903_RS03830	W903_0789	696153	696992	NA	hypothetical protein	0.783279681	0.028426092	2.175954834	1.6303E-33	2.175954834	1.6303E-33
779	W903_RS03835	W903_0790	697145	697957	NA	HAD hydrolase, IA, variant 1 family protein	1.023801537	0.000104671	1.899649723	1.83187E-38	1.899649723	1.83187E-38
780	W903_RS03840	W903_0791	697973	699763	NA	glycosyl hydrolase family 3 N terminal domain protein	0.731880501	0.000623182	1.657708486	4.1961E-37	1.657708486	4.1961E-37
781	W903_RS03845	W903_0792	699820	700905	NA	metallopeptidase M24 family protein	-0.038148081	0.828736007	0.114912312	0.20883586	0.114912312	0.20883586
782	W903_RS03850	W903_0793	701115	702119	ccpA	catabolite control protein A	0.099689236	0.593049584	-0.088178173	0.549881366	-0.088178173	0.549881366
783	W903_RS03855	W903_0794	702251	703717	NA	alpha amylase, catalytic domain protein	0.595593313	0.000168817	0.416432977	3.1953E-05	0.416432977	3.1953E-05
784	W903_RS03860	W903_0795	703762	704760	NA	glycosyl transferases group 1 family protein	0.086883264	0.643341349	0.86225215	2.35438E-22	0.86225215	2.35438E-22
785	W903_RS03865	W903_0796	704762	706096	NA	glycosyl transferases group 1 family protein	-0.173499561	0.307346492	0.60055029	7.76645E-11	0.60055029	7.76645E-11
786	W903_RS03870	W903_0797	706553	708496	thrS	threonine--tRNA ligase	0.337369096	0.023316963	-1.725054709	4.35731E-30	-1.725054709	4.35731E-30
787	W903_RS03875	W903_0798	708805	709422	NA	putative transcriptional activator CadC	-1.236078467	2.05901E-11	0.352987754	0.001844484	0.352987754	0.001844484
788	W903_RS03880	W903_0799	709520	710539	NA	hypothetical protein	-0.210704637	0.313877608	0.502167488	5.77906E-06	0.502167488	5.77906E-06
789	W903_RS03885	W903_0800	710706	711272	NA	peptidase propeptide and YPEB domain protein	-1.310636317	2.69047E-07	0.707224295	1.16413E-05	0.707224295	1.16413E-05
790	W903_RS03890	W903_0801	711321	711971	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	-1.792446893	1.10415E-29	0.312619128	0.213891993	0.312619128	0.213891993
791	W903_RS03895	W903_0802	711983	712678	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	-1.144944262	1.17178E-08	0.8308668	5.83061E-05	0.8308668	5.83061E-05
792	W903_RS03900	W903_0803	712691	713491	NA	bacterial extracellular solute-binding s, 3 family protein	-1.36812966	2.61125E-11	0.71670879	0.001391575	0.71670879	0.001391575
793	W903_RS03905	W903_0804	713503	714258	NA	ABC transporter family protein	-1.253140059	2.02543E-08	1.089658465	1.8694E-06	1.089658465	1.8694E-06
794	W903_RS03910	W903_0805	714598	715308	rrD2	response regulator	0.408333606	0.018399558	-0.099916111	0.354588167	-0.099916111	0.354588167
795	W903_RS03915	W903_0806	715301	716650	NA	sensory box protein	0.572655208	0.000136573	0.191056779	0.046904711	0.191056779	0.046904711
796	W903_RS03920	W903_0807	716654	717463	NA	metallo-beta-lactamase superfamily protein	0.509386239	0.000947601	0.351538085	0.000469585	0.351538085	0.000469585
797	W903_RS03925	W903_0808	717466	717834	NA	hypothetical protein	1.323994332	8.02534E-12	0.905979416	7.59477E-10	0.905979416	7.59477E-10
798	W903_RS03930	W903_0809	718010	718696	rnc	ribonuclease III	-0.108267318	0.565005127	-0.358375548	0.075744133	-0.358375548	0.075744133
799	W903_RS03935	W903_0810	718704	722243	smc	chromosome segregation protein SMC	-0.239358599	0.137687003	-0.410804088	0.005518727	-0.410804088	0.005518727
800	W903_RS03940	W903_0811	722334	723131	NA	HAD hydrolase, IIB family protein	-0.202563556	0.266437751	0.776613796	1.12844E-06	0.776613796	1.12844E-06
801	W903_RS03945	W903_0812	723131	723955	NA	HAD hydrolase, IIB family protein	0.259591847	0.129946656	1.094944617	4.12414E-27	1.094944617	4.12414E-27
802	W903_RS03950	W903_0813	723955	725565	ftsY	signal recognition particle-docking protein FtsY	0.96214283	3.45372E-11	0.631630672	5.35523E-07	0.631630672	5.35523E-07
803	W903_RS03955	W903_0814	725602	726414	NA	hypothetical protein	0.097296184	0.639428324	-0.266772848	0.008848499	-0.266772848	0.008848499
804	W903_RS03960	W903_0815	726414	727316	NA	putative permease family protein	-0.395039009	0.017118302	0.031566669	0.771729787	0.031566669	0.771729787
805	W903_RS03965	W903_0816	727322	727450	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.447015159	0.073270666	0.326614276	0.075192509	0.326614276	0.075192509
806	W903_RS03970	W903_0817	727583	728626	NA	luciferase-like monooxygenase family protein	0.123671072	0.832394958	3.030838756	2.48687E-37	3.030838756	2.48687E-37
807	W903_RS03975	W903_0818	728732	730894	NA	S1 RNA binding domain protein	0.14705895	0.376532116	0.206120073	0.072190635	0.206120073	0.072190635
808	W903_RS03980	W903_0819	730908	731315	NA	sprT-like family protein	0.197313965	0.348200027	0.224604867	0.124203578	0.224604867	0.124203578
809	W903_RS03985	W903_0820	731396	731659	NA	pspC domain protein	0.690817635	0.000391694	1.368091358	7.6536E-20	1.368091358	7.6536E-20
810	NA	W903_0821	731637	731771	NA	hypothetical protein	0.98260001	4.81653E-05	1.283422732	5.14655E-07	1.283422732	5.14655E-07
811	W903_RS03990	W903_0822	731887	732822	hprK	HPr(Ser) kinase/phosphatase	1.224389838	3.94157E-18	0.923077187	4.23028E-19	0.923077187	4.23028E-19
812	W903_RS03995	W903_0823	732815	733588	lgt	prolipoprotein diacylglyceryl transferase	1.332115349	2.45412E-21	0.898397952	4.77775E-18	0.898397952	4.77775E-18
813	W903_RS04000	W903_0824	733603	734001	NA	hypothetical protein	0.279509218	0.086558854	0.066733835	0.606356145	0.066733835	0.606356145
814	W903_RS04005	W903_0825	733998	734429	NA	hypothetical protein	0.909333008	2.71044E-07	0.086497512	0.655322751	0.086497512	0.655322751
815	W903_RS04010	W903_0826	734470	734745	NA	hypothetical protein	-0.590017163	0.000536344	0.660525091	3.24451E-09	0.660525091	3.24451E-09
816	W903_RS04015	W903_0827	735087	736013	NA	peptidase U32 family protein	-0.026125035	0.914504482	-1.972667569	1.11389E-86	-1.972667569	1.11389E-86
817	W903_RS04020	W903_0828	736143	737429	NA	peptidase U32 family protein	0.169275337	0.46809963	-1.877735728	5.31282E-89	-1.877735728	5.31282E-89
818	W903_RS04025	W903_0829	737556	737768	NA	hypothetical protein	0.624600762	0.052097292	-1.236642408	1.98962E-05	-1.236642408	1.98962E-05
819	W903_RS04030	W903_0830	737892	738689	NA	putative membrane protein	-0.058732406	0.814729644	0.522805268	7.14483E-06	0.522805268	7.14483E-06
820	W903_RS04035	W903_0831	738790	740130	NA	metal ion transporter, metal ion family protein	-0.062874206	0.734062253	0.30911799	0.00165815	0.30911799	0.00165815
821	W903_RS04040	W903_0832	740859	741968	ribD	riboflavin biosynthesis protein RibD	0.316076608	0.252500145	4.685798309	7.9708E-21	4.685798309	7.9708E-21
822	W903_RS04045	W903_0833	741949	742599	ribE	riboflavin synthase, alpha subunit	0.128379263	0.647719608	4.575524935	7.82067E-15	4.575524935	7.82067E-15
823	W903_RS04050	W903_0834	742617	743810	ribA	GTP cyclohydrolase II	0.020971443	0.933659036	4.243515478	3.2909E-19	4.243515478	3.2909E-19
824	W903_RS04055	W903_0835	743825	744295	ribH	6,7-dimethyl-8-ribityllumazine synthase	-0.254003612	0.277470661	4.042901573	3.31815E-24	4.042901573	3.31815E-24
825	W903_RS04060	W903_0836	744370	745860	lysS	lysine--tRNA ligase	0.138108546	0.423657793	-0.969292885	2.12494E-20	-0.969292885	2.12494E-20
826	W903_RS04065	W903_0837	746035	746937	NA	HAD hydrolase, IA, variant 1 family protein	-1.873198941	2.09743E-29	-1.484173793	1.42361E-22	-1.484173793	1.42361E-22
827	W903_RS04070	W903_0838	746973	747614	NA	histidine phosphatase super family protein	0.360503955	0.047678813	0.140206962	0.248191356	0.140206962	0.248191356

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828	W903_RS04075	W903_0839	747636	748109	NA	bacteriocin-type signal sequence domain protein	-0.069897911	0.740170779	-0.106350664	0.482226303	-0.106350664	0.482226303
829	W903_RS04080	W903_0840	748404	749021	NA	NAD dependent epimerase/dehydratase family protein	-0.138080706	0.636323631	2.125776195	1.62578E-55	2.125776195	1.62578E-55
830	W903_RS04085	W903_0841	749054	749902	NA	glycosyl hydrolases 25 family protein	-1.078881742	4.47528E-11	0.454129364	5.22116E-05	0.454129364	5.22116E-05
831	W903_RS04090	W903_0842	750059	750583	NA	ECF-type riboflavin transporter, S component family protein	-0.229341516	0.278195052	0.577325002	5.17211E-05	0.577325002	5.17211E-05
832	W903_RS04095	W903_0843	750567	750956	NA	putative lipoprotein	-0.540334155	0.003170788	-0.17262167	0.324269643	-0.17262167	0.324269643
833	W903_RS04100	W903_0844	751015	752814	NA	oligoendopeptidase F	0.539597295	0.003392532	-0.467447884	3.23259E-07	-0.467447884	3.23259E-07
834	W903_RS04105	W903_0845	753023	755818	NA	phosphoenolpyruvate carboxylase family protein	-0.371528687	0.037371044	0.086128497	0.39265141	0.086128497	0.39265141
835	W903_RS04110	W903_0846	756161	757192	NA	cell cycle family protein	0.121497935	0.549536178	0.180604537	0.106335863	0.180604537	0.106335863
836	W903_RS04115	W903_0847	757544	758740	tuf	translation elongation factor Tu	0.18734885	0.237745726	-1.079988749	2.48687E-37	-1.079988749	2.48687E-37
837	W903_RS04120	W903_0848	758921	759679	tpiA	triose-phosphate isomerase	0.12687315	0.437073844	-1.594378153	3.35753E-67	-1.594378153	3.35753E-67
838	W903_RS04125	W903_0849	759856	760548	NA	phosphoglycerate mutase 1 family protein	0.172219346	0.344073825	-1.717253266	6.46049E-68	-1.717253266	6.46049E-68
839	W903_RS04130	W903_0850	760681	760869	NA	phage integrase family protein	0.766540307	NA	1.5448946	0.057256852	1.5448946	0.057256852
840	W903_RS04135	W903_0851	760984	761376	NA	phage integrase family protein	-2.059390653	NA	1.163522903	0.150585639	1.163522903	0.150585639
841	NA	W903_0852	761549	762157	NA	glycerophosphoryl diester phosphodiesterase family protein	0.859567947	NA	2.395897755	0.002963539	2.395897755	0.002963539
842	NA	W903_0853	762413	762571	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.802842705	NA	1.948360858	0.010470242	1.948360858	0.010470242
843	W903_RS04145	W903_0854	763171	764094	NA	hypothetical protein	-0.794467367	6.80338E-06	-0.679120272	7.86496E-12	-0.679120272	7.86496E-12
844	W903_RS04150	W903_0855	764108	764659	NA	hypothetical protein	-0.697128706	0.004579459	-0.761243495	4.50839E-05	-0.761243495	4.50839E-05
845	W903_RS04155	W903_0856	764974	767016	NA	penicillin binding transpeptidase domain protein	-0.022294801	0.893990343	0.018895362	0.885454913	0.018895362	0.885454913
846	W903_RS04160	W903_0857	767031	767627	recR	recombination protein RecR	-0.011062449	0.955386747	-0.043740952	0.733215929	-0.043740952	0.733215929
847	W903_RS04165	W903_0858	767768	768814	ddl	D-alanine--D-alanine ligase	-0.385742313	0.015980682	-0.320986301	0.000626387	-0.320986301	0.000626387
848	W903_RS04170	W903_0859	768961	770328	murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase family protein	-0.584195997	8.55503E-05	0.291818003	0.002996617	0.291818003	0.002996617
849	W903_RS04175	W903_0860	770516	771736	NA	major Facilitator Superfamily protein	0.267403593	0.274774767	0.35654911	0.009403192	0.35654911	0.009403192
850	W903_RS04180	W903_0861	771865	772551	NA	integral membrane family protein	-1.197555698	3.00819E-14	0.079084883	0.556972826	0.079084883	0.556972826
851	W903_RS04190	W903_0864	774445	775989	prfC	peptide chain release factor 3	0.22198632	0.17915471	0.484481731	5.59505E-08	0.484481731	5.59505E-08
852	W903_RS04195	W903_0865	776075	776455	NA	hypothetical protein	-0.468004993	0.013735518	0.013579824	0.931269524	0.013579824	0.931269524
853	W903_RS04200	W903_0866	776649	777383	NA	ABC transporter family protein	-0.897465825	7.3538E-05	2.801229369	4.7841E-155	2.801229369	4.7841E-155
854	W903_RS04205	W903_0867	777376	778038	NA	binding--dependent transport system inner membrane component family protein	-0.164777807	0.488081032	3.051246079	6.4904E-122	3.051246079	6.4904E-122
855	W903_RS04210	W903_0868	778054	778884	NA	NLPA lipofamily protein	-0.627326089	0.009954694	2.225583009	4.98769E-59	2.225583009	4.98769E-59
856	W903_RS04215	W903_0869	779119	780705	NA	helicase domain protein	-0.35626763	0.03638661	-2.221657152	3.01433E-76	-2.221657152	3.01433E-76
857	W903_RS04220	W903_0870	780890	781156	NA	GIY-YIG catalytic domain protein	0.673216395	0.014979291	0.044917228	0.86230103	0.044917228	0.86230103
858	W903_RS04225	W903_0871	781149	781913	NA	methyltransferase domain protein	0.164390927	0.385202647	-0.612567971	3.01981E-07	-0.612567971	3.01981E-07
859	W903_RS04230	W903_0872	782048	782788	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	-0.343692444	0.067561666	-0.227085308	0.051181591	-0.227085308	0.051181591
860	W903_RS04235	W903_0873	782887	783540	NA	competence ComEA helix-hairpin-helix repeat region domain protein	-0.151434491	NA	2.746797549	3.03472E-09	2.746797549	3.03472E-09
861	W903_RS04240	W903_0874	783524	785761	NA	DNA internalization-related competence protein ComEC/Rec2	-0.259676788	0.285467335	1.088057002	1.92717E-17	1.088057002	1.92717E-17
862	W903_RS04245	W903_0875	785887	786696	NA	HAD hydrolase, IIB family protein	-0.174658391	0.535808713	0.869934357	1.18905E-08	0.869934357	1.18905E-08
863	W903_RS04250	W903_0876	786707	787651	NA	bacterial regulatory s, lacI family protein	0.467369266	0.043896081	1.303932212	3.9727E-17	1.303932212	3.9727E-17
864	W903_RS04255	W903_0877	787710	788702	NA	alpha/beta hydrolase fold family protein	0.952980523	1.35023E-05	2.10511535	3.84806E-87	2.10511535	3.84806E-87
865	W903_RS04260	W903_0878	788877	789605	NA	methyltransferase domain protein	-0.213280693	0.446374739	0.702367382	7.91966E-07	0.702367382	7.91966E-07
866	W903_RS04265	W903_0879	789659	790696	holA	DNA polymerase III, delta subunit	-0.807326836	8.1301E-07	1.02563183	5.41004E-25	1.02563183	5.41004E-25
867	W903_RS04270	W903_0880	790776	791384	sodA	superoxide dismutase	-0.503032389	0.013077952	0.579715028	3.07149E-08	0.579715028	3.07149E-08
868	W903_RS04275	W903_0881	791723	792574	licT	transcription antiterminator LicT	-0.023905541	0.914504482	2.116245743	1.61949E-70	2.116245743	1.61949E-70
869	W903_RS04280	W903_0882	792567	794435	NA	PTS system, beta-glucoside-specific IIABC component family protein	0.676901086	0.002573908	1.43235082	2.34928E-22	1.43235082	2.34928E-22
870	W903_RS04285	W903_0883	794452	795879	NA	cellulase family protein	0.613255951	0.002303312	0.539552857	5.56628E-05	0.539552857	5.56628E-05
871	W903_RS04290	W903_0884	795947	797041	NA	sugar diacid recognition family protein	-0.350068918	0.074564757	0.819806135	2.71834E-12	0.819806135	2.71834E-12
872	W903_RS04295	W903_0885	797208	798350	NA	glycerate kinase family protein	0.307475349	0.346377236	0.915259299	0.000128038	0.915259299	0.000128038
873	W903_RS04300	W903_0886	798375	799631	NA	citrate transporter family protein	0.237934893	0.497265329	0.950785469	9.00721E-05	0.950785469	9.00721E-05
874	NA	W903_0887	800209	800796	NA	D-alanyl-D-alanine carboxypeptidase family protein	-0.644198715	0.000234013	0.137682786	0.389517383	0.137682786	0.389517383
875	W903_RS10360	W903_0888	800851	801288	NA	marR family protein	0.163499842	0.40043987	-0.39131278	6.34074E-05	-0.39131278	6.34074E-05
876	W903_RS04315	W903_0889	801375	802403	queA	tRNA ribosyltransferase-isomerase	0.609026171	8.03639E-05	-0.459513946	7.85122E-05	-0.459513946	7.85122E-05
877	W903_RS04320	W903_0890	802556	803236	NA	VIT family protein	-0.424702931	0.086116923	-1.285226233	0.00219478	-1.285226233	0.00219478
878	W903_RS04325	W903_0891	803387	804088	nagB	glucosamine-6-phosphate deaminase	-0.797368298	1.02679E-06	0.120494924	0.58148367	0.120494924	0.58148367
879	W903_RS04330	W903_0892	804160	805116	NA	glutathione S-transferase, C-terminal domain protein	-0.157013052	0.549536178	0.559716885	0.000460747	0.559716885	0.000460747
880	W903_RS04335	W903_0893	805212	805931	NA	pseudouridine synthase family protein	-0.007294941	0.977276951	1.173978351	7.50621E-16	1.173978351	7.50621E-16
881	W903_RS04340	W903_0894	806004	807155	NA	major Facilitator Superfamily protein	-0.436044761	0.040928658	0.288907958	0.006393623	0.288907958	0.006393623
882	W903_RS04345	W903_0895	807207	808154	NA	competence CoiA-like family protein	0.559269905	0.267008777	1.86488977	7.83398E-11	1.86488977	7.83398E-11
883	W903_RS04350	W903_0896	808170	809975	NA	oligoendopeptidase F	0.679920891	6.37209E-06	-0.911381734	4.85788E-21	-0.911381734	4.85788E-21
884	W903_RS04355	W903_0897	810169	810795	NA	HAD hydrolase, IA, variant 1 family protein	0.206041909	0.323786712	-1.181255899	2.13537E-15	-1.181255899	2.13537E-15
885	W903_RS04360	W903_0898	810869	811576	NA	methyltransferase domain protein	-0.85099831	2.01201E-08	-1.06019632	5.91598E-25	-1.06019632	5.91598E-25
886	W903_RS04365	W903_0899	811637	812566	NA	PPIC-type PPIASE domain protein	-0.291976576	0.069196501	-2.456231671	4.4712E-136	-2.456231671	4.4712E-136
887	W903_RS04370	W903_0900	812808	813293	NA	tubby C 2 family protein	0.319605157	0.05641049	-1.537315698	3.6479E-33	-1.537315698	3.6479E-33
888	W903_RS04375	W903_0901	813309	815927	alaS	alanine--tRNA ligase	0.608483543	1.80157E-05	-1.453017853	1.1199E-40	-1.453017853	1.1199E-40
889	W903_RS04380	W903_0902	816009	816725	NA	hypothetical protein	0.543414317	0.001717206	-0.64635599	3.56919E-06	-0.64635599	3.56919E-06
890	W903_RS04385	W903_0903	816813	817631	NA	glycosyl transferase 8 family protein	-0.385640804	0.104469996	-0.573526169	7.16814E-05	-0.573526169	7.16814E-05
891	W903_RS04390	W903_0904	817832	818020	NA	glycerophosphoryl diester phosphodiesterase family protein	0.808596764	0.165421465	2.598467587	2.17267E-12	2.598467587	2.17267E-12
892	W903_RS04395	W903_0905	818055	818339	NA	hypothetical protein	0.085936628	0.860408926	2.516327272	1.88898E-17	2.516327272	1.88898E-17
893	W903_RS04400	W903_0906	818384	818599	NA	helix-turn-helix family protein	0.440382766	0.574080165	1.539731819	0.003091065	1.539731819	0.003091065
894	W903_RS04405	W903_0907	818602	819360	NA	hypothetical protein	0.258670512	0.648586851	2.47084304	1.80481E-11	2.47084304	1.80481E-11
895	W903_RS04410	W903_0908	819445	820008	thiT	thiamine transporter ThiT	0.182907042	0.519354825	2.105923512	2.65045E-32	2.105923512	2.65045E-32
896	W903_RS04415	W903_0909	820249	821208	NA	ribonucleotide reductase, small chain family protein	-0.143734595	0.406936176	0.236586595	0.033451815	0.236586595	0.033451815
897	W903_RS04420	W903_0910	821411	823570	NA	ribonucleoside-diphosphate reductase, alpha subunit	0.101452533	0.549536178	0.623617703	6.27125E-08	0.623617703	6.27125E-08
898	W903_RS04425	W903_0911	823648	823872	nrdH	glutaredoxin-like protein nrdH	-0.389103678	0.058233186	1.185255559	6.77703E-16	1.185255559	6.77703E-16
899	W903_RS04430	W903_0912	824254	824517	ptsH	phosphocarrier protein HPr	-0.736971121	3.33987E-07	-0.731073704	1.12893E-12	-0.731073704	1.12893E-12
900	W903_RS04435	W903_0913	824522	826255	ptsP	phosphoenolpyruvate-protein phosphotransferase	-0.311034953	0.040469854	-0.955647936	4.51502E-28	-0.955647936	4.51502E-28
901	W903_RS04440	W903_0914	826405	827832	gapN	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	0.743243547	1.84679E-06	-0.701534439	5.92303E-15	-0.701534439	5.92303E-15
902	W903_RS04445	W903_0915	827972	829225	NA	polysaccharide deacetylase family protein	0.339478092	0.060262783	-0.480837761	0.000327832	-0.480837761	0.000327832
903	W903_RS04450	W903_0916	829256	830338	NA	DEAD/DEAH box helicase family protein	-0.103857016	0.559276733	-0.632135298	5.86111E-10	-0.632135298	5.86111E-10
904	W903_RS04455	W903_0917	830483	831112	udk	uridine kinase	-1.636782399	8.5766E-26	0.148009732	0.137643547	0.148009732	0.137643547
905	W903_RS04460	W903_0918	831200	831697	NA	GAF domain protein	-0.299762495	0.079081585	0.179501265	0.141328327	0.179501265	0.141328327
906	W903_RS04465	W903_0919	831697	833361	dnaX	DNA polymerase III, subunit gamma and tau	-0.417022037	0.007096258	0.149145634	0.110455436	0.149145634	0.110455436
907	W903_RS04470	W903_0920	833450	833644	NA	hypothetical protein	1.655190916	7.02613E-05	0.987798056	0.013552105	0.987798056	0.013552105
908	W903_RS04475	W903_0921	833625	834560	NA	biotin--[acetyl-CoA-carboxylase] ligase	0.176816451	0.377928802	0.129187624	0.296728612	0.129187624	0.296728612
909	W903_RS04480	W903_0922	834745	835941	metK	methionine adenosyltransferase	0.07262008	0.687671982	-1.009813404	1.45567E-29	-1.009813404	1.45567E-29
910	W903_RS04490	W903_0923	836462	838453	NA	coagulase family protein	-1.27773695	1.15101E-09	-1.69534454	1.13382E-21	-1.69534454	1.13382E-21
911	W903_RS04495	W903_0924	838520	839065	NA	hypothetical protein	-1.296128561	7.22377E-07	-1.572137612	1.09427E-09	-1.572137612	1.09427E-09
912	W903_RS04500	W903_0925	839461	840027	NA	thiamine-transporter family protein	-0.187253712	0.747730994	2.54022457	9.09392E-15	2.54022457	9.09392E-15
913	W903_RS04505	W903_0926	840024	840578	NA	putative HMP/thiamine permease protein ykoE	0.214380894	0.731761702	1.47222816	4.83686E-08	1.47222816	4.83686E-08
914	W903_RS04510	W903_0927	840582	841868	NA	heme ABC exporter, ATP-binding protein CcmA	0.551387343	0.191586598	2.152761673	3.36552E-18	2.152761673	3.36552E-18
915	W903_RS04515	W903_0928	841856	842524	NA	putative membrane protein	0.216671925	0.76807246	1.915527421	2.76566E-09	1.915527421	2.76566E-09
916	W903_RS04520	W903_0929	842608	843288	tenA	thiaminase II	0.660164437	0.165913277	1.281699335	3.67004E-06	1.281699335	3.67004E-06
917	W903_RS04525	W903_0930	843290	844087	thiD	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	0.865869684	0.013905768	1.562102293	8.88578E-13	1.562102293	8.88578E-13
918	W903_RS04530	W903_0931	844089	844859	thiM	hydroxyethylthiazole kinase	0.649564754	0.054921009	1.355437684	9.60419E-11	1.355437684	9.60419E-11
919	W903_RS04535	W903_0932	844873	845544	thiE	thiamine-phosphate pyrophosphorylase	0.111559806	0.827375315	1.702970419	1.49322E-12	1.702970419	1.49322E-12
920	W903_RS04540	W903_0933	845671	846930	NA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.126808875	0.502942487	0.048554572	0.726361185	0.048554572	0.726361185
921	W903_RS04545	W903_0934	847032	847586	NA	acetyltransferase family protein	-0.006844134	0.973222982	1.089903919	2.2781E-21	1.089903919	2.2781E-21
922	W903_RS04550	W903_0935	847579	848862	NA	CBS domain protein	0.1979352	0.252500145	0.422247474	1.36959E-05	0.422247474	1.36959E-05
923	W903_RS04555	W903_0936	848885	849745	map	methionine aminopeptidase, type I	0.700862764	1.463E-05	0.163100331	0.129617586	0.163100331	0.129617586
924	W903_RS04560	W903_0937	849747	850667	NA	virulence factor BrkB family protein	0.635292113	4.78083E-05	0.335821379	0.001432285	0.335821379	0.001432285
925	W903_RS04565	W903_0938	850684	851139	NA	gtrA-like family protein	-0.969942647	0.005076862	0.412538158	0.204414793	0.412538158	0.204414793
926	W903_RS04570	W903_0939	851321	851830	queT	queuosine transporter QueT	-0.820233541	4.1732E-08	-1.555717816	3.48248E-33	-1.555717816	3.48248E-33
927	W903_RS04575	W903_0940	851982	853928	ligA	DNA ligase, NAD-dependent	0.499522963	0.001105734	0.094260677	0.341223627	0.094260677	0.341223627
928	W903_RS04580	W903_0941	853940	854959	NA	lipid kinase, YegS/Rv2252/BmrU family protein	0.538295361	0.000460978	0.039197986	0.733689214	0.039197986	0.733689214
929	W903_RS04585	W903_0942	854963	857263	pulA	pullulanase, type I	0.180721998	0.275766915	-0.199103221	0.03565578	-0.199103221	0.03565578
930	W903_RS04590	W903_0943	857469	859337	glgB	1,4-alpha-glucan branching enzyme	1.147536936	7.20686E-10	0.689094887	3.16448E-12	0.689094887	3.16448E-12
931	W903_RS04595	W903_0944	859379	860518	glgC	glucose-1-phosphate adenylyltransferase	1.738736481	7.30603E-21	0.480783946	5.57154E-05	0.480783946	5.57154E-05
932	W903_RS04600	W903_0945	860508	861641	glgD	glucose-1-phosphate adenylyltransferase, GlgD subunit	1.625405378	1.32511E-17	0.581260459	4.38414E-05	0.581260459	4.38414E-05
933	W903_RS04605	W903_0946	861638	863068	glgA	glycogen/starch synthase, ADP-glucose type family protein	1.254972527	8.69757E-15	0.425758519	0.002453192	0.425758519	0.002453192
934	W903_RS04610	W903_0947	863400	863600	NA	ATP synthase subunit C family protein	0.113499867	0.565005127	-0.648632548	5.17678E-08	-0.648632548	5.17678E-08
935	W903_RS04615	W903_0948	863632	864348	atpB	ATP synthase F0, A subunit	0.096971111	0.566833212	-0.704060931	1.66235E-12	-0.704060931	1.66235E-12
936	W903_RS04620	W903_0949	864366	864863	atpF	ATP synthase F0, B subunit	0.594541876	6.49823E-05	-0.516535419	5.11704E-06	-0.516535419	5.11704E-06
937	W903_RS04625	W903_0950	864863	865399	atpH	ATP synthase F1, delta subunit	0.706212105	2.61462E-06	-0.879868289	1.12479E-17	-0.879868289	1.12479E-17
938	W903_RS04630	W903_0951	865415	866920	atpA	ATP synthase F1, alpha subunit	0.849687546	6.5073E-09	-0.62307236	1.37651E-10	-0.62307236	1.37651E-10
939	W903_RS04635	W903_0952	866936	867817	atpG	ATP synthase F1, gamma subunit	0.692146799	3.55732E-06	-0.693101048	2.01354E-11	-0.693101048	2.01354E-11
940	W903_RS04640	W903_0953	867891	869297	atpD	ATP synthase F1, beta subunit	0.783040975	3.23016E-08	-0.738559477	3.22541E-15	-0.738559477	3.22541E-15
941	W903_RS04645	W903_0954	869310	869723	atpC	ATP synthase F1, epsilon subunit	1.329937158	1.08436E-16	-0.395196372	0.001681175	-0.395196372	0.001681175
942	W903_RS04650	W903_0955	869788	870018	NA	hypothetical protein	0.734576826	0.001272911	-1.03416977	1.80514E-07	-1.03416977	1.80514E-07
943	W903_RS04655	W903_0956	870081	871352	NA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.749580013	8.9586E-07	0.4368301	1.70934E-05	0.4368301	1.70934E-05
944	W903_RS04660	W903_0957	871354	871545	NA	DNA-directed RNA polymerase subunit beta family protein	0.825946141	0.001376657	0.193972897	0.363249424	0.193972897	0.363249424
945	W903_RS04665	W903_0958	871620	872477	NA	DNA/RNA non-specific endonuclease family protein	-0.188041779	0.28022116	-0.193781955	0.087342605	-0.193781955	0.087342605
946	W903_RS04670	W903_0959	872768	873808	pheS	phenylalanine--tRNA ligase, alpha subunit	0.227233409	0.167861172	-1.570721215	8.34367E-27	-1.570721215	8.34367E-27
947	W903_RS04675	W903_0960	873891	874412	NA	acetyltransferase family protein	0.125444731	0.490201152	-1.789312478	5.1102E-45	-1.789312478	5.1102E-45
948	W903_RS04680	W903_0961	874466	876871	pheT	phenylalanine--tRNA ligase, beta subunit	0.240197075	0.137041773	-1.85193665	2.7745E-44	-1.85193665	2.7745E-44
949	W903_RS04685	W903_0962	876939	877841	NA	neutral zinc metallopeptidase family protein	0.317367129	0.110401251	2.05864763	1.84115E-93	2.05864763	1.84115E-93
950	W903_RS04690	W903_0963	878019	881252	rexB	ATP-dependent nuclease subunit B	0.391482996	0.017653818	0.502130919	2.10902E-07	0.502130919	2.10902E-07
951	W903_RS04695	W903_0964	881242	884865	addA	helicase-exonuclease AddAB, AddA subunit	0.211443288	0.208680463	0.017994262	0.8647731	0.017994262	0.8647731
952	W903_RS04700	W903_0965	884878	885795	NA	corA-like Mg2+ transporter family protein	-0.189294265	0.334106354	-0.451918576	5.52356E-05	-0.451918576	5.52356E-05
953	W903_RS04705	W903_0966	885827	887203	trmE	tRNA modification GTPase TrmE	-0.195553936	0.290890617	0.000537306	0.997018054	0.000537306	0.997018054
954	W903_RS04710	W903_0967	887508	887858	NA	hypothetical protein	-1.490340285	2.55238E-11	-4.128840511	8.0402E-199	-4.128840511	8.0402E-199
955	W903_RS04715	W903_0968	888203	890113	NA	ABC transporter family protein	-0.15239356	0.38790006	-0.591778495	6.46995E-08	-0.591778495	6.46995E-08
956	W903_RS04720	W903_0969	890262	891230	NA	thiamine pyrophosphate enzyme, C-terminal TPP binding domain protein	0.248347419	0.192577816	1.396252508	5.47321E-47	1.396252508	5.47321E-47
957	W903_RS04725	W903_0970	891305	892303	NA	transketolase, pyrimidine binding domain protein	0.465439034	0.006084625	1.431849224	7.46068E-39	1.431849224	7.46068E-39
958	W903_RS04730	W903_0971	892430	893818	NA	e3 binding domain protein	0.445085532	0.005100077	1.266415484	1.8157E-40	1.266415484	1.8157E-40
959	W903_RS04735	W903_0972	893878	895635	lpdA	dihydrolipoyl dehydrogenase	0.668969552	5.5686E-06	1.029621219	1.62365E-21	1.029621219	1.62365E-21
960	W903_RS04740	W903_0973	895733	896722	NA	lipoyltransferase and lipoate-ligase family protein	0.168595424	0.426882086	-0.090503022	0.497184259	-0.090503022	0.497184259
961	W903_RS04745	W903_0974	896830	897615	NA	cobB/CobQ-like glutamine amidotransferase domain protein	0.2068702	0.232196112	-0.177741973	0.081294498	-0.177741973	0.081294498
962	W903_RS04750	W903_0975	897615	898958	NA	mur ligase middle domain protein	0.327748104	0.043817578	0.265326678	0.004760232	0.265326678	0.004760232
963	W903_RS04755	W903_0976	899098	899949	NA	disA bacterial checkpoint controller nucleotide-binding family protein	-0.137479698	0.514758507	0.589146484	3.73204E-09	0.589146484	3.73204E-09
964	W903_RS04760	W903_0977	899952	900911	NA	hypothetical protein	-0.387866288	0.012850878	-0.18708536	0.045923079	-0.18708536	0.045923079
965	W903_RS04765	W903_0978	900965	902317	glmM	phosphoglucosamine mutase	-0.453411839	0.001988807	-0.246906462	0.0053025	-0.246906462	0.0053025

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966	W903_RS04770	W903_0979	902440	902811	NA	hypothetical protein	0.015317681	0.944361683	0.373736065	0.008723108	0.373736065	0.008723108
967	W903_RS04775	W903_0980	902836	903216	NA	pyrimidine dimer DNA glycosylase family protein	0.530030905	0.120099062	0.772471959	0.003091065	0.772471959	0.003091065
968	W903_RS04780	W903_0981	903310	904440	NA	radical SAM superfamily protein	-0.245245007	0.149383746	1.148482687	1.79779E-32	1.148482687	1.79779E-32
969	W903_RS04785	W903_0982	904444	905181	NA	acyl-ACP thioesterase family protein	-0.64196342	4.81156E-05	0.829806056	2.30494E-15	0.829806056	2.30494E-15
970	W903_RS04790	W903_0983	905182	905952	NA	hydrolase, haloacid dehalogenase-like family	-0.385232253	0.044189912	0.722493515	1.27746E-10	0.722493515	1.27746E-10
971	W903_RS04795	W903_0984	905927	906598	NA	hypothetical protein	-0.708924041	0.000189977	0.598523583	8.89813E-07	0.598523583	8.89813E-07
972	W903_RS04800	W903_0985	906987	911111	NA	HNH endonuclease family protein	-0.679028455	2.2204E-06	0.27234835	0.005217265	0.27234835	0.005217265
973	W903_RS04805	W903_0986	911113	911982	cas1	CRISPR-associated endonuclease Cas1	-0.665322705	0.000251548	0.285077782	0.015513928	0.285077782	0.015513928
974	W903_RS04810	W903_0987	911979	912320	cas2	CRISPR-associated endoribonuclease Cas2	-1.335496895	1.38538E-08	-0.04188144	0.829234282	-0.04188144	0.829234282
975	W903_RS04815	W903_0988	912307	912972	NA	CRISPR-associated family protein	-0.927890899	5.35334E-09	0.48828333	1.80761E-05	0.48828333	1.80761E-05
976	NA	W903_0989	913084	913464	NA	hypothetical protein	-1.127185294	1.45102E-07	0.63823914	1.24958E-07	0.63823914	1.24958E-07
977	NA	W903_0990	913480	913593	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.360436845	0.426630721	0.757413363	0.000246443	0.757413363	0.000246443
978	NA	W903_0991	914013	914150	NA	hypothetical protein	-0.715979221	NA	1.341763201	0.007392586	1.341763201	0.007392586
979	NA	W903_0992	914244	914381	NA	putative membrane protein	-0.299057454	0.701826668	1.446888733	0.000214025	1.446888733	0.000214025
980	W903_RS04825	W903_0993	914522	914938	awd	nucleoside diphosphate kinase	0.743428884	2.02559E-05	-0.097028393	0.358860404	-0.097028393	0.358860404
981	W903_RS04830	W903_0994	915074	916906	lepA	GTP-binding protein LepA	-0.326564932	0.042811516	0.016074657	0.879954279	0.016074657	0.879954279
982	NA	W903_0995	916957	917100	NA	hypothetical protein	-0.394517434	NA	4.191601493	0.127064085	4.191601493	0.127064085
983	W903_RS04835	W903_0996	917152	919785	NA	histidine triad domain protein	-0.827218848	8.1812E-06	-1.36470238	1.12179E-24	-1.36470238	1.12179E-24
984	W903_RS04840	W903_0997	919891	920544	NA	HD domain protein	-0.290680628	0.159911711	0.757717577	3.091E-14	0.757717577	3.091E-14
985	W903_RS04845	W903_0998	920553	921017	NA	acetyltransferase family protein	-0.349486284	0.077791473	0.45472412	1.18142E-05	0.45472412	1.18142E-05
986	W903_RS04850	W903_0999	921017	921451	msrB	peptide methionine sulfoxide reductase MsrB	0.374668368	0.117276802	0.590541669	0.000151643	0.590541669	0.000151643
987	W903_RS04855	W903_1000	921603	924395	NA	HAD ATPase, P-type, IC family protein	0.234978826	0.183944453	1.130264495	1.24617E-33	1.130264495	1.24617E-33
988	W903_RS04860	W903_1001	924395	925498	NA	hypothetical protein	0.019183562	0.929646957	1.069954729	1.55446E-22	1.069954729	1.55446E-22
989	W903_RS04865	W903_1002	925617	926186	NA	bacterial transferase hexapeptide family protein	-0.087880786	NA	3.842935328	2.308E-09	3.842935328	2.308E-09
990	W903_RS04870	W903_1003	926872	927483	NA	hypothetical protein	-0.525775316	0.002136569	0.614254055	9.43318E-07	0.614254055	9.43318E-07
991	W903_RS04875	W903_1004	927520	928302	NA	putative membrane protein	0.72198109	7.37723E-07	-0.99318671	5.1281E-27	-0.99318671	5.1281E-27
992	W903_RS04880	W903_1005	928314	929012	NA	ABC transporter family protein	-0.035082814	0.842938478	-1.610800849	2.09409E-63	-1.610800849	2.09409E-63
993	W903_RS04885	W903_1006	929013	929381	NA	bacterial regulatory s, gntR family protein	-0.211226338	0.192257021	-1.394950694	1.37574E-41	-1.394950694	1.37574E-41
994	W903_RS04890	W903_1007	929526	932630	dnaE	DNA polymerase III, alpha subunit	-0.036996004	0.842938478	-0.002845509	0.978444394	-0.002845509	0.978444394
995	W903_RS04895	W903_1008	932711	933733	pfkA	6-phosphofructokinase	0.394831271	0.009634177	-1.144514647	2.07751E-30	-1.144514647	2.07751E-30
996	W903_RS04900	W903_1009	933782	935284	pyk	pyruvate kinase	0.131263983	0.423805945	-1.353117956	1.9412E-44	-1.353117956	1.9412E-44
997	W903_RS04905	W903_1010	935455	936012	NA	signal peptidase I	-0.876288753	7.48811E-07	-0.020089791	0.879954279	-0.020089791	0.879954279
998	NA	W903_1011	936030	936161	NA	hypothetical protein	-1.499887449	0.011610497	-0.018514995	0.971479693	-0.018514995	0.971479693
999	W903_RS04910	W903_1012	936270	938084	glmS	glutamine-fructose-6-phosphate transaminase	-2.117060745	2.33753E-19	-1.257799978	1.04005E-15	-1.257799978	1.04005E-15
1000	W903_RS04915	W903_1013	938247	938576	NA	phnA family protein	-0.922398391	7.53337E-05	-0.200771601	0.525067759	-0.200771601	0.525067759
1001	W903_RS04920	W903_1014	938711	939352	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	-1.040921967	2.14802E-09	-0.446121438	2.48943E-05	-0.446121438	2.48943E-05
1002	W903_RS04925	W903_1015	939362	939991	NA	ABC transporter family protein	-0.912858801	5.27257E-07	-0.561417008	5.65561E-08	-0.561417008	5.65561E-08
1003	W903_RS04930	W903_1016	940053	940838	NA	polar amino acid ABC uptake transporter substrate binding protein	-1.206954827	1.15038E-12	-0.802246588	6.77636E-12	-0.802246588	6.77636E-12
1004	W903_RS04935	W903_1017	940923	941156	rpsT	ribosomal protein S20	-1.105516521	1.95216E-09	-0.580864885	0.005341415	-0.580864885	0.005341415
1005	W903_RS04940	W903_1018	941225	942145	coaA	pantothenate kinase	-0.60535395	0.000884833	-0.413705912	0.003076482	-0.413705912	0.003076482
1006	W903_RS04945	W903_1019	942251	942841	NA	mycolic acid cyclopropane synthetase family protein	-0.885244065	4.80153E-06	-0.105947149	0.521261113	-0.105947149	0.521261113
1007	W903_RS04950	W903_1020	943167	943556	cdd	cytidine deaminase	-0.037159333	0.858438886	-0.757667579	1.94808E-07	-0.757667579	1.94808E-07
1008	W903_RS04955	W903_1021	943621	944670	NA	basic membrane family protein	-0.01553147	0.935760556	-1.4448642	1.60762E-24	-1.4448642	1.60762E-24
1009	W903_RS04960	W903_1022	944815	946350	NA	heme ABC exporter, ATP-binding protein CcmA	0.19054838	0.299971351	-1.361568311	1.30159E-36	-1.361568311	1.30159E-36
1010	W903_RS04965	W903_1023	946343	947404	NA	branched-chain amino acid transport system / permease component family protein	0.122605214	0.529108033	-1.383217537	2.34324E-33	-1.383217537	2.34324E-33
1011	W903_RS04970	W903_1024	947406	948362	NA	branched-chain amino acid transport system / permease component family protein	0.286336675	0.131385468	-1.38822	1.03265E-21	-1.38822	1.03265E-21
1012	W903_RS04975	W903_1025	948568	949938	NA	putative NADH oxidase	0.359578089	0.031813237	-0.800446947	5.11772E-12	-0.800446947	5.11772E-12
1013	W903_RS04980	W903_1026	950059	951048	NA	L-lactate dehydrogenase	0.459327378	0.001743195	-0.275358255	0.001939386	-0.275358255	0.001939386
1014	W903_RS04985	W903_1027	951287	953746	gyrA	DNA gyrase, A subunit	0.056016647	0.74558947	0.202381064	0.029736522	0.202381064	0.029736522
1015	W903_RS04990	W903_1028	953753	954496	NA	sortase family protein	-0.437252663	0.004077726	0.025149018	0.830532698	0.025149018	0.830532698
1016	W903_RS04995	W903_1029	954512	954925	NA	hypothetical protein	-0.572663473	0.000533008	-0.265478625	0.010396499	-0.265478625	0.010396499
1017	W903_RS05000	W903_1030	955031	955993	NA	hypothetical protein	-0.213803056	0.242243803	-0.800979699	3.01264E-20	-0.800979699	3.01264E-20
1018	W903_RS05005	W903_1031	956056	957183	NA	sodium/hydrogen exchanger family protein	0.107254602	0.603411444	1.130283088	2.40344E-14	1.130283088	2.40344E-14
1019	W903_RS05010	W903_1032	957574	958164	NA	helix-turn-helix family protein	-0.743654325	7.96905E-05	-1.421425854	2.0911E-17	-1.421425854	2.0911E-17
1020	W903_RS05015	W903_1033	958413	958904	NA	hypothetical protein	0.149684612	NA	1.032758133	0.213587937	1.032758133	0.213587937
1021	W903_RS05020	W903_1034	959221	959643	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.449507019	NA	0.313947655	0.673406985	0.313947655	0.673406985
1022	W903_RS05025	W903_1035	959636	960694	NA	replication initiation factor family protein	0.02558737	0.950325218	1.919446089	2.4225E-21	1.919446089	2.4225E-21
1023	W903_RS05035	W903_1036	960918	961136	NA	hypothetical protein	0.600027814	0.204883473	0.243000764	0.507515057	0.243000764	0.507515057
1024	W903_RS05040	W903_1037	961129	962310	NA	phage integrase family protein	0.308672824	0.346377236	-0.032925265	0.885454913	-0.032925265	0.885454913
1025	NA	W903_1038	962437	962550	NA	putative membrane protein	-0.277468129	0.125079485	-0.571072423	6.41649E-08	-0.571072423	6.41649E-08
1026	W903_RS05045	W903_1039	962786	964348	guaA	GMP synthase domain protein	0.465461831	0.001566678	-0.588688537	2.38376E-09	-0.588688537	2.38376E-09
1027	W903_RS05050	W903_1040	964561	965259	NA	bacterial regulatory s, gntR family protein	0.175666594	0.334549017	-0.458367517	2.42966E-05	-0.458367517	2.42966E-05
1028	W903_RS05055	W903_1041	965373	966707	trmFO	m(5)U-54 methyltransferase	0.044728945	0.798496828	-0.048921778	0.622519677	-0.048921778	0.622519677
1029	W903_RS05060	W903_1042	966794	967537	NA	acetyltransferase family protein	-0.13057707	0.566833212	0.139623828	0.266694644	0.139623828	0.266694644
1030	W903_RS05065	W903_1043	967670	968518	NA	NLPA lipofamily protein	-0.23197186	0.295683724	0.238692558	0.041743461	0.238692558	0.041743461
1031	W903_RS05070	W903_1044	968550	969038	NA	hypothetical protein	0.88477219	2.55269E-06	0.598801215	1.6234E-10	0.598801215	1.6234E-10
1032	W903_RS05075	W903_1045	969204	970166	NA	peptidase S41 family protein	0.698236375	0.013978764	1.721640789	7.17993E-25	1.721640789	7.17993E-25
1033	W903_RS05080	W903_1046	970192	970944	NA	ABC transporter family protein	0.21510272	0.330951294	0.236678106	0.074331436	0.236678106	0.074331436
1034	W903_RS05085	W903_1047	970946	972901	NA	ftsX-like permease family protein	-0.160311424	0.437073844	0.245144496	0.030623076	0.245144496	0.030623076
1035	W903_RS05090	W903_1048	973011	973670	NA	response regulator	0.203244592	0.330951294	0.528501549	4.65191E-05	0.528501549	4.65191E-05
1036	W903_RS05095	W903_1049	973703	974614	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	0.109266094	0.56709391	0.079332922	0.487119712	0.079332922	0.487119712
1037	W903_RS05100	W903_1050	974652	975722	NA	phage integrase family protein	0.05348529	0.800421156	0.673451243	1.19823E-05	0.673451243	1.19823E-05
1038	W903_RS05105	W903_1051	976181	977842	NA	bacterial extracellular solute-binding s, 5 Middle family protein	-0.131777185	0.576503921	-1.213494805	2.48408E-08	-1.213494805	2.48408E-08
1039	W903_RS05110	W903_1052	977875	978648	NA	hypothetical protein	0.244176225	0.355685142	-0.439413437	0.027758752	-0.439413437	0.027758752
1040	W903_RS05115	W903_1053	978645	979325	NA	putative dNA-binding protein	-0.16283813	0.549536178	-0.444370331	0.064405998	-0.444370331	0.064405998
1041	W903_RS05120	W903_1054	979392	980957	ffh	signal recognition particle protein	-0.087806129	0.62592635	-0.547678564	8.4829E-09	-0.547678564	8.4829E-09
1042	W903_RS05125	W903_1055	980975	981307	NA	sigma-70, region 4 family protein	-0.497038222	0.004636477	0.151544867	0.241301424	0.151544867	0.241301424
1043	W903_RS05130	W903_1056	981396	982709	NA	his Kinase A domain protein	0.133534307	0.495003156	-0.236881108	0.025859052	-0.236881108	0.025859052
1044	W903_RS05135	W903_1057	982693	983373	NA	response regulator	0.046018626	0.834002409	-0.182602882	0.134991815	-0.182602882	0.134991815
1045	W903_RS05140	W903_1058	983535	986084	NA	peptidase M1 family protein	0.394244282	0.014605413	-0.005649973	0.960968817	-0.005649973	0.960968817
1046	W903_RS05145	W903_1059	986230	986883	NA	phosphate transport system regulatory protein PhoU	-0.035622952	0.851542185	-1.097246084	2.19634E-23	-1.097246084	2.19634E-23
1047	W903_RS05150	W903_1060	986917	987675	NA	phosphate ABC transporter, ATP-binding protein	0.05462653	0.778085155	-0.787718413	1.121E-13	-0.787718413	1.121E-13
1048	W903_RS05155	W903_1061	987687	988490	NA	phosphate ABC transporter, ATP-binding protein	0.257207452	0.145574329	-0.516320058	3.85918E-07	-0.516320058	3.85918E-07
1049	W903_RS05160	W903_1062	988502	989389	NA	phosphate ABC transporter, permease protein PstA	0.522045471	0.000639817	-0.251763097	0.041256441	-0.251763097	0.041256441
1050	W903_RS05165	W903_1063	989379	990296	NA	phosphate ABC transporter, permease protein PstC	0.608769445	0.000154533	-0.237010445	0.046369028	-0.237010445	0.046369028
1051	W903_RS05170	W903_1064	990342	991202	pstS	phosphate binding family protein	0.281682283	0.092175742	-0.743157971	2.48408E-08	-0.743157971	2.48408E-08
1052	W903_RS05175	W903_1065	991387	992697	NA	ftsJ-like methyltransferase family protein	0.163588202	0.390412221	-0.047537206	0.709747935	-0.047537206	0.709747935
1053	W903_RS05180	W903_1066	992765	993529	NA	inositol monophosphatase family protein	-0.083323932	0.669580883	0.268329235	0.021806423	0.268329235	0.021806423
1054	W903_RS05185	W903_1067	993519	993800	NA	hypothetical protein	0.016802247	0.938553751	0.135859	0.403553308	0.135859	0.403553308
1055	W903_RS05190	W903_1068	993793	994206	spxA	regulatory protein spx	-0.554021654	0.000452079	0.020634245	0.853816698	0.020634245	0.853816698
1056	W903_RS05195	W903_1069	994249	995181	ribF	riboflavin biosynthesis protein RibF	0.491763362	0.003331312	1.130789841	7.76635E-30	1.130789841	7.76635E-30
1057	W903_RS05200	W903_1070	995194	996078	truB	tRNA pseudouridine(55) synthase	-0.033011312	0.861869569	0.628038424	1.1865E-07	0.628038424	1.1865E-07
1058	W903_RS05205	W903_1071	996170	996601	NA	acetyltransferase family protein	-0.290254613	0.17335524	0.320186287	0.012890278	0.320186287	0.012890278
1059	W903_RS05210	W903_1072	996614	997885	NA	hypothetical protein	-0.425374872	0.006895447	0.244982897	0.022675249	0.244982897	0.022675249
1060	W903_RS05215	W903_1073	997919	998509	NA	type I restriction modification DNA specificity domain protein	-0.373322776	0.032840104	0.547784026	2.6099E-08	0.547784026	2.6099E-08
1061	W903_RS05220	W903_1074	998616	999494	NA	CAAX protease self-immunity family protein	-0.835354967	7.66601E-07	1.422368186	2.53374E-21	1.422368186	2.53374E-21
1062	W903_RS05225	W903_1075	999600	1002230	NA	ftsX-like permease family protein	0.038770624	0.851821574	3.624720564	3.09334E-87	3.624720564	3.09334E-87
1063	W903_RS05230	W903_1076	1002242	1002943	NA	ABC transporter family protein	-0.024755527	0.92288861	2.895117123	5.35815E-54	2.895117123	5.35815E-54
1064	W903_RS05235	W903_1077	1003080	1005200	topA	DNA topoisomerase I	0.118578784	0.521627441	0.698862247	2.98749E-14	0.698862247	2.98749E-14
1065	W903_RS05240	W903_1078	1005295	1006137	dprA	DNA protecting protein DprA	-0.050319992	0.927127413	0.741231601	0.024319473	0.741231601	0.024319473
1066	W903_RS05245	W903_1079	1006276	1007304	NA	hypothetical protein	-0.512384535	0.001986404	0.116491089	0.294963144	0.116491089	0.294963144
1067	W903_RS05250	W903_1080	1007366	1008127	NA	ABC transporter family protein	-0.354709529	0.051345143	0.472744412	1.26168E-06	0.472744412	1.26168E-06
1068	W903_RS05255	W903_1081	1008124	1009098	NA	fecCD transport family protein	-0.293154303	0.095916955	0.513511973	3.10491E-08	0.513511973	3.10491E-08
1069	W903_RS05260	W903_1082	1009095	1010057	NA	fecCD transport family protein	0.103943913	0.566833212	0.760960972	1.86107E-10	0.760960972	1.86107E-10
1070	W903_RS05265	W903_1083	1010297	1010845	NA	bacterial transferase hexapeptide family protein	-0.34746529	0.057826884	-0.349344681	0.002709689	-0.349344681	0.002709689
1071	W903_RS05270	W903_1084	1010866	1011627	NA	ribonuclease HII family protein	-0.077299993	0.730573433	-0.109696718	0.4214648	-0.109696718	0.4214648
1072	W903_RS05275	W903_1085	1011614	1012465	yIqF	ribosome biogenesis GTP-binding protein YlqF	0.074936839	0.690197928	-0.088890143	0.527329565	-0.088890143	0.527329565
1073	W903_RS05290	W903_1089	1014521	1014742	NA	helix-turn-helix family protein	0.329823509	0.216420552	-0.483948614	0.003697406	-0.483948614	0.003697406
1074	W903_RS05295	W903_1090	1014848	1015444	NA	bacterial regulatory s, luxR family protein	-1.259681053	3.45274E-14	-1.811246594	5.63076E-42	-1.811246594	5.63076E-42
1075	W903_RS05300	W903_1091	1015425	1016999	NA	putative membrane protein	-1.373358235	5.70773E-16	-1.307870428	1.49247E-33	-1.307870428	1.49247E-33
1076	W903_RS05305	W903_1092	1017176	1019194	NA	ftsX-like permease family protein	-0.94614881	9.0664E-05	1.126136888	8.0194E-18	1.126136888	8.0194E-18
1077	W903_RS05310	W903_1093	1019206	1019940	NA	ABC transporter family protein	-0.996542015	0.013431719	0.81326389	0.000994203	0.81326389	0.000994203
1078	W903_RS05315	W903_1094	1020496	1020672	NA	hypothetical protein	-1.123540428	2.95302E-13	0.713385014	1.35147E-13	0.713385014	1.35147E-13
1079	W903_RS05320	W903_1095	1020760	1020942	NA	hypothetical protein	-0.539872638	0.126627854	-0.037295534	0.889974398	-0.037295534	0.889974398
1080	W903_RS05325	W903_1096	1021026	1021208	NA	hypothetical protein	-1.183168427	0.000480529	-0.417738301	0.038603155	-0.417738301	0.038603155
1081	W903_RS05330	W903_1097	1022147	1024270	NA	ABC transporter family protein	-0.536941065	0.017858701	1.455318183	3.5163E-15	1.455318183	3.5163E-15
1082	W903_RS05335	W903_1098	1024283	1027234	lanM	type 2 lantibiotic biosynthesis LanM family protein	0.019228186	0.927127413	2.520135474	9.7698E-160	2.520135474	9.7698E-160
1083	W903_RS05340	W903_1099	1027412	1027894	NA	lantibiotic streptin immunity family protein	-0.608195888	0.083786987	2.430676904	8.30669E-47	2.430676904	8.30669E-47
1084	W903_RS05345	W903_1100	1027966	1028607	NA	relaxase/mobilization nuclease domain protein	0.003681667	0.994427047	2.123147543	1.17366E-28	2.123147543	1.17366E-28
1085	W903_RS05350	W903_1101	1028975	1029547	NA	L,D-transpeptidase catalytic domain protein	-0.84974796	1.67301E-07	0.183810998	0.267299509	0.183810998	0.267299509
1086	W903_RS05355	W903_1102	1029748	1031232	NA	carbon starvation CstA family protein	2.707598809	4.95695E-55	-0.04341803	0.764577305	-0.04341803	0.764577305
1087	W903_RS05360	W903_1103	1031388	1032122	NA	response regulator	0.172190109	0.47748382	1.590185046	4.18683E-39	1.590185046	4.18683E-39
1088	W903_RS05365	W903_1104	1032134	1033873	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-0.14259219	0.496067777	1.331373512	1.01551E-37	1.331373512	1.01551E-37
1089	NA	W903_1105	1034411	1034533	NA	putative lipoprotein	0.075430553	0.798433935	1.10012684	9.21107E-15	1.10012684	9.21107E-15
1090	NA	W903_1106	1034760	1034882	NA	hypothetical protein	-1.006396532	0.005759166	0.612537894	0.019444779	0.612537894	0.019444779
1091	W903_RS05375	W903_1107	1034895	1035092	NA	N-acetylmuramoyl-L-alanine amidase domain protein	0.397312623	0.246905013	1.170772539	2.66387E-08	1.170772539	2.66387E-08
1092	W903_RS05380	W903_1108	1035609	1036025	NA	hypothetical protein	-0.467800692	0.083234472	0.250996769	0.176041325	0.250996769	0.176041325
1093	W903_RS05385	W903_1109	1036196	1036441	NA	hypothetical protein	-0.428866621	0.366086675	0.1286682	0.689485296	0.1286682	0.689485296
1094	W903_RS05390	W903_1110	1036495	1037145	NA	glycerophosphoryl diester phosphodiesterase family protein	0.508004462	0.12356904	0.731959295	0.002698068	0.731959295	0.002698068
1095	W903_RS05395	W903_1111	1037158	1037934	NA	hypothetical protein	0.633337996	0.000587297	0.578185948	1.44392E-05	0.578185948	1.44392E-05
1096	W903_RS05400	W903_1112	1038229	1038579	NA	hypothetical protein	0.339247553	0.125003968	0.153445255	0.315205531	0.153445255	0.315205531
1097	W903_RS05405	W903_1113	1038734	1039039	NA	hypothetical protein	0.071064649	0.733854288	-0.220246804	0.087125947	-0.220246804	0.087125947
1098	W903_RS05410	W903_1114	1039041	1039694	NA	hypothetical protein	0.305822406	0.096549476	0.000423475	0.997018054	0.000423475	0.997018054
1099	W903_RS05425	W903_1117	1040973	1041278	NA	hypothetical protein	0.675373737	0.000221839	0.216358045	0.132408127	0.216358045	0.132408127
1100	W903_RS05435	W903_1118	1041470	1041970	NA	glycerophosphoryl diester phosphodiesterase family protein	0.272508901	0.214111123	-0.163938988	0.321132808	-0.163938988	0.321132808
1101	W903_RS05440	W903_1119	1041983	1043419	NA	LXG domain of WXG superfamily protein	1.222771331	1.72555E-16	0.508549227	7.27455E-06	0.508549227	7.27455E-06
1102	W903_RS05445	W903_1120	1043400	1043801	NA	glycerophosphoryl diester phosphodiesterase family protein	1.065459578	9.24753E-07	0.472664432	0.01549857	0.472664432	0.01549857
1103	W903_RS05450	W903_1121	1043807	1044187	NA	type VII secretion effector, TIGR04197 family protein	1.29441355	2.1653E-10	0.697657825	2.39622E-05	0.697657825	2.39622E-05

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1104	W903_RS05455	W903_1122	1044201	1048610	essC	type VII secretion protein EssC	1.650125219	1.62442E-25	0.916936862	3.72887E-15	0.916936862	3.72887E-15
1105	W903_RS05460	W903_1123	1048617	1049894	essB	type VII secretion protein EssB	1.551773359	5.69163E-14	1.077341693	2.27303E-12	1.077341693	2.27303E-12
1106	W903_RS05465	W903_1124	1049894	1050106	NA	yukD family protein	1.707846687	2.92519E-08	1.42227992	1.55977E-12	1.42227992	1.55977E-12
1107	W903_RS05470	W903_1125	1050120	1050548	essA	type VII secretion protein EssA	0.758825789	0.003754263	0.576742385	0.000662629	0.576742385	0.000662629
1108	W903_RS05475	W903_1126	1050602	1053613	esaA	type VII secretion protein EsaA	1.513785472	3.57802E-10	1.055397543	3.70801E-19	1.055397543	3.70801E-19
1109	NA	W903_1127	1053764	1053985	NA	virulence factor esxA	0.958831873	0.001370887	2.300780357	1.29522E-46	2.300780357	1.29522E-46
1110	W903_RS05485	W903_1128	1054152	1054442	NA	virulence factor esxA	0.33311804	0.171350406	-0.862474361	5.3001E-10	-0.862474361	5.3001E-10
1111	W903_RS05490	W903_1129	1054559	1055341	NA	lipase family protein	1.627813081	0.367966213	-0.272089017	0.079675359	-0.272089017	0.079675359
1112	W903_RS05495	W903_1130	1055338	1055661	NA	hypothetical protein	1.349117117	0.508587412	-0.567816165	0.000110681	-0.567816165	0.000110681
1113	W903_RS05500	W903_1131	1055787	1058969	carB	carbamoyl-phosphate synthase, large subunit	2.423695939	0.302225232	-0.49571727	0.000509529	-0.49571727	0.000509529
1114	W903_RS05505	W903_1132	1059000	1060076	NA	carbamoyl-phosphate synthase, small subunit	3.241283673	0.18396017	-0.658533218	6.9593E-06	-0.658533218	6.9593E-06
1115	W903_RS05510	W903_1133	1060087	1061013	pyrB	aspartate carbamoyltransferase	3.330470062	0.185033565	-0.81648181	1.08118E-09	-0.81648181	1.08118E-09
1116	W903_RS05515	W903_1134	1061182	1062474	pyrC	dihydroorotase, multifunctional complex type domain protein	2.926347114	0.171028626	-0.531821574	3.51623E-07	-0.531821574	3.51623E-07
1117	W903_RS05520	W903_1135	1062486	1063115	pyrE	orotate phosphoribosyltransferase	2.968996739	0.170250592	-0.897893956	1.40427E-21	-0.897893956	1.40427E-21
1118	W903_RS05525	W903_1136	1063128	1063829	pyrF	orotidine 5'-phosphate decarboxylase	3.273827889	0.140850224	-0.933074958	9.43323E-15	-0.933074958	9.43323E-15
1119	W903_RS05530	W903_1137	1064042	1065274	NA	hypothetical protein	0.650334646	2.41743E-05	1.157503483	7.29086E-34	1.157503483	7.29086E-34
1120	W903_RS05535	W903_1138	1065314	1066851	NA	heme ABC exporter, ATP-binding protein CcmA	0.594362592	0.00021008	1.008559552	5.31242E-26	1.008559552	5.31242E-26
1121	W903_RS05540	W903_1139	1066986	1067324	NA	ATP cone domain protein	-0.219607479	0.301270944	0.690430484	3.07363E-10	0.690430484	3.07363E-10
1122	W903_RS05545	W903_1140	1067494	1068570	asd	aspartate-semialdehyde dehydrogenase	0.150487429	0.423756017	-0.647972123	2.96697E-09	-0.647972123	2.96697E-09
1123	W903_RS05550	W903_1141	1068779	1069867	NA	LPXTG cell wall anchor domain protein	1.145750511	2.32386E-14	-0.903220082	1.61028E-16	-0.903220082	1.61028E-16
1124	W903_RS05555	W903_1142	1070557	1072152	cls	cardiolipin synthase	0.127070903	0.495327691	0.05865886	0.568288627	0.05865886	0.568288627
1125	W903_RS05560	W903_1143	1072271	1073941	NA	formate--tetrahydrofolate ligase family protein	0.844441711	1.463E-05	-0.284625866	0.009051042	-0.284625866	0.009051042
1126	W903_RS05565	W903_1144	1074030	1075049	NA	lipoyltransferase and lipoate-ligase family protein	0.430575315	0.018037897	1.147878918	5.25972E-34	1.147878918	5.25972E-34
1127	W903_RS05570	W903_1145	1075076	1075954	NA	hypothetical protein	0.696186533	0.000522225	1.400309026	4.12082E-36	1.400309026	4.12082E-36
1128	W903_RS05575	W903_1146	1075923	1076741	NA	macro domain protein	0.374497796	0.070238826	1.044396607	1.45015E-24	1.044396607	1.45015E-24
1129	W903_RS05580	W903_1147	1076734	1077066	NA	glycine cleavage H-family protein	-0.166035262	0.484301603	0.674557387	0.000128659	0.674557387	0.000128659
1130	W903_RS05585	W903_1148	1077095	1078081	NA	luciferase oxidoreductase, group 1 family protein	-0.149717797	0.430969743	1.031021223	1.2815E-27	1.031021223	1.2815E-27
1131	W903_RS05590	W903_1149	1078078	1079277	NA	flavin oxidoreductase / NADH oxidase family protein	0.309929852	0.070856166	1.391738507	1.15079E-30	1.391738507	1.15079E-30
1132	W903_RS05595	W903_1150	1079270	1080106	NA	biotin/lipoate A/B ligase family protein	0.125281788	0.549536178	1.148741662	4.91333E-20	1.148741662	4.91333E-20
1133	W903_RS05600	W903_1151	1080260	1080946	coaB	phosphopantothenate--cysteine ligase	0.270932893	0.252500145	0.198772191	0.203463071	0.198772191	0.203463071
1134	W903_RS05605	W903_1152	1080939	1081481	coaC	phosphopantothenoylcysteine decarboxylase	0.918076042	6.49053E-06	0.379602767	0.012429057	0.379602767	0.012429057
1135	W903_RS05610	W903_1153	1081527	1082099	panT	pantothenic acid transporter PanT	-0.139438521	0.547728992	0.268508956	0.064799571	0.268508956	0.064799571
1136	W903_RS05615	W903_1154	1082209	1083927	NA	phosphoglucomutase/phosphomannomutase, C-terminal domain protein	0.239411047	0.133952618	-0.258334275	0.020187344	-0.258334275	0.020187344
1137	W903_RS05625	W903_1155	1084201	1085934	NA	ABC transporter family protein	-0.213973402	0.259242344	0.496848661	2.57132E-05	0.496848661	2.57132E-05
1138	W903_RS05630	W903_1156	1085935	1087656	NA	ABC transporter family protein	0.185023834	0.355552361	0.503704357	1.62826E-06	0.503704357	1.62826E-06
1139	W903_RS05635	W903_1157	1087668	1088270	NA	lysozyme-like family protein	0.241550808	0.144486237	0.424820018	5.12463E-05	0.424820018	5.12463E-05
1140	W903_RS05640	W903_1158	1088272	1089246	NA	37-kD nucleoid-associated bacterial family protein	0.170454638	0.330951294	0.133263844	0.263576189	0.133263844	0.263576189
1141	W903_RS05645	W903_1159	1089254	1090510	NA	serine hydroxymethyltransferase family protein	0.559992261	0.000142889	0.27810538	0.004686857	0.27810538	0.004686857
1142	W903_RS05650	W903_1160	1090602	1091198	NA	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/YrdC/YwlC family	0.625360642	7.96905E-05	0.564086128	7.9152E-08	0.564086128	7.9152E-08
1143	W903_RS05655	W903_1161	1091191	1092021	prmC	protein-(glutamine-N5) methyltransferase, release factor-specific	0.398330508	0.013077952	0.458487662	3.91675E-05	0.458487662	3.91675E-05
1144	W903_RS05660	W903_1162	1092021	1093100	prfA	peptide chain release factor 1	0.287284446	0.103410495	0.357905848	0.001202895	0.357905848	0.001202895
1145	W903_RS05665	W903_1163	1093135	1093704	NA	thymidine kinase family protein	-0.004491633	0.98220294	0.690716371	3.28328E-10	0.690716371	3.28328E-10
1146	W903_RS05670	W903_1164	1093842	1094024	NA	tautomerase enzyme family protein	0.616317107	0.17915471	-1.217106807	0.000235652	-1.217106807	0.000235652
1147	W903_RS05675	W903_1165	1094200	1095111	NA	apbE family protein	-0.111380911	0.648243664	-1.322793257	1.31129E-48	-1.322793257	1.31129E-48
1148	W903_RS05680	W903_1166	1095129	1095731	NA	NADPH-dependent FMN reductase family protein	0.582951876	0.00609631	-1.195898511	7.74918E-34	-1.195898511	7.74918E-34
1149	W903_RS05685	W903_1167	1095755	1096990	NA	NADPH-dependent FMN reductase family protein	0.487477817	0.011787837	-0.911037261	7.04866E-20	-0.911037261	7.04866E-20
1150	W903_RS05690	W903_1168	1097089	1097877	NA	formate/nitrite transporter family protein	-0.497316611	0.002888992	-0.69288253	3.87193E-12	-0.69288253	3.87193E-12
1151	W903_RS05695	W903_1169	1097976	1099250	pbuX	xanthine permease family protein	-0.525898388	0.503169838	-1.167897525	8.68515E-18	-1.167897525	8.68515E-18
1152	W903_RS05700	W903_1170	1099250	1099831	xpt	xanthine phosphoribosyltransferase	-0.91877624	0.126321509	-1.351270535	1.19076E-17	-1.351270535	1.19076E-17
1153	W903_RS05705	W903_1171	1100086	1101069	guaC	guanosine monophosphate reductase	0.258014347	0.801246181	-1.38532491	5.82959E-30	-1.38532491	5.82959E-30
1154	W903_RS05710	W903_1172	1101272	1102612	NA	major Facilitator Superfamily protein	-1.605247484	6.36731E-17	0.035851383	0.828867428	0.035851383	0.828867428
1155	W903_RS05715	W903_1173	1102904	1103575	NA	hypothetical protein	-0.564104835	0.012778518	2.529667467	2.4636E-126	2.529667467	2.4636E-126
1156	W903_RS05720	W903_1174	1103647	1105088	NA	potassium uptake protein	-0.236874465	0.165421465	0.36216689	0.001689706	0.36216689	0.001689706
1157	W903_RS05725	W903_1175	1105782	1106543	NA	short chain dehydrogenase family protein	-0.330988688	0.119042498	1.328049876	3.6958E-19	1.328049876	3.6958E-19
1158	W903_RS05730	W903_1176	1106605	1107597	pta	phosphate acetyltransferase	-0.428051591	0.009686322	0.687897419	1.39181E-14	0.687897419	1.39181E-14
1159	W903_RS05735	W903_1177	1107623	1108507	NA	pseudouridine synthase, RluA family protein	0.427402882	0.011872739	1.398731405	2.27186E-35	1.398731405	2.27186E-35
1160	W903_RS05740	W903_1178	1108504	1109340	NA	ATP-NAD kinase family protein	0.174910545	0.337197526	1.141608995	1.97082E-17	1.141608995	1.97082E-17
1161	W903_RS05745	W903_1179	1109315	1109986	NA	RelA / SpoT s family protein	-0.075755542	0.701826668	1.301743108	6.63042E-29	1.301743108	6.63042E-29
1162	W903_RS05750	W903_1180	1111096	1110668	NA	CYTH domain protein	-0.652537108	0.001794779	-0.888093863	1.41542E-15	-0.888093863	1.41542E-15
1163	W903_RS05755	W903_1181	1110845	1111819	prs2	ribose-phosphate pyrophosphokinase 2	0.429331647	0.004709769	0.055689572	0.605838703	0.055689572	0.605838703
1164	W903_RS05760	W903_1182	1111823	1112938	NA	aminotransferase class-V family protein	0.337548613	0.045426067	0.270928538	0.003671115	0.270928538	0.003671115
1165	W903_RS05765	W903_1183	1112940	1113287	NA	amino acid metabolism family protein	0.144460416	0.421324797	-0.034561809	0.77640213	-0.034561809	0.77640213
1166	W903_RS05770	W903_1184	1113442	1114080	NA	coA binding domain protein	-0.54220383	0.00473903	0.780417862	3.90463E-14	0.780417862	3.90463E-14
1167	W903_RS05775	W903_1185	1114093	1114773	NA	DNA repair RadC family protein	-0.1454613	0.705759832	0.959755583	2.9645E-07	0.959755583	2.9645E-07
1168	W903_RS05780	W903_1186	1114869	1116002	NA	hypothetical protein	-0.402381061	0.012299144	-0.12658035	0.246865747	-0.12658035	0.246865747
1169	W903_RS05785	W903_1187	1116093	1117532	NA	glycosyl hydrolase 1 family protein	0.361735279	0.067561666	1.456424106	1.84123E-43	1.456424106	1.84123E-43
1170	W903_RS05790	W903_1188	1117692	1118306	NA	GDSL-like Lipase/Acylhydrolase family protein	-0.252185205	0.322923737	1.23876817	1.38931E-22	1.23876817	1.38931E-22
1171	W903_RS05795	W903_1189	1118407	1119228	NA	HAD hydrolase, IIB family protein	-0.15706692	0.446374739	0.628907367	9.63239E-09	0.628907367	9.63239E-09
1172	W903_RS05800	W903_1190	1119853	1120782	NA	cupin domain protein	-0.430235599	0.064894799	1.208060492	4.62239E-19	1.208060492	4.62239E-19
1173	W903_RS05805	W903_1191	1120839	1121237	NA	voltage gated chloride channel family protein	0.440239374	0.009762869	-0.21031068	0.049176934	-0.21031068	0.049176934
1174	W903_RS05810	W903_1192	1122480	1123553	NA	bacterial extracellular solute-binding family protein	0.296117743	0.087957605	-0.125902827	0.271291798	-0.125902827	0.271291798
1175	W903_RS05815	W903_1193	1123546	1124322	NA	binding--dependent transport system inner membrane component family protein	-0.043865788	0.83442661	-0.167537451	0.212139333	-0.167537451	0.212139333
1176	W903_RS05820	W903_1194	1124319	1125113	NA	binding--dependent transport system inner membrane component family protein	0.355579134	0.042927774	-0.026565417	0.840175823	-0.026565417	0.840175823
1177	W903_RS05825	W903_1195	1125097	1126251	NA	polyamine ABC transporter, ATP-binding family protein	0.246198791	0.144808373	-0.304811282	0.00100782	-0.304811282	0.00100782
1178	W903_RS05830	W903_1196	1126300	1127202	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	-0.043559086	0.820911404	-0.618220932	5.14632E-09	-0.618220932	5.14632E-09
1179	W903_RS05835	W903_1197	1127346	1127834	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	0.942179839	3.08386E-07	0.789384685	1.1223E-05	0.789384685	1.1223E-05
1180	W903_RS05840	W903_1198	1127831	1128193	folB	dihydroneopterin aldolase	0.468780425	0.003312238	0.514965258	3.60574E-07	0.514965258	3.60574E-07
1181	W903_RS05845	W903_1199	1128195	1128998	folP	dihydropteroate synthase	0.612429765	7.72947E-05	0.580318447	5.71887E-08	0.580318447	5.71887E-08
1182	W903_RS05850	W903_1200	1129002	1129565	folE	GTP cyclohydrolase I	0.666816908	2.3133E-05	0.320061633	0.012172152	0.320061633	0.012172152
1183	W903_RS05855	W903_1201	1129584	1130846	folC	bifunctional FolC family protein	0.618889598	4.64408E-05	0.369783781	0.000122622	0.369783781	0.000122622
1184	W903_RS05860	W903_1202	1130848	1131735	NA	eamA-like transporter family protein	0.799495799	1.80896E-06	0.522289464	5.53317E-06	0.522289464	5.53317E-06
1185	W903_RS05865	W903_1203	1131722	1132588	thrB	homoserine kinase	1.052446577	7.13862E-11	0.617470643	3.26812E-07	0.617470643	3.26812E-07
1186	W903_RS05870	W903_1204	1132590	1133873	NA	homoserine dehydrogenase family protein	0.616431214	0.000575006	0.211564123	0.029145032	0.211564123	0.029145032
1187	W903_RS05875	W903_1205	1134050	1134937	NA	polysaccharide deacetylase family protein	0.950537346	2.44262E-09	-0.463548235	0.000127039	-0.463548235	0.000127039
1188	W903_RS05880	W903_1206	1134960	1136507	NA	transporter, betaine/carnitine/choline transporter family protein	0.972959617	1.55178E-10	1.287231249	3.49508E-40	1.287231249	3.49508E-40
1189	W903_RS05885	W903_1207	1136650	1138026	ssdh	NAD-dependent aldehyde dehydrogenase	0.344435673	0.062591184	1.65375241	2.4803E-46	1.65375241	2.4803E-46
1190	W903_RS05890	W903_1208	1138100	1139107	NA	conserved hypothetical 698 family protein	0.701790639	5.03372E-06	0.001963468	0.98621151	0.001963468	0.98621151
1191	W903_RS05895	W903_1209	1139215	1139901	NA	hypothetical protein	-0.160451877	0.576355478	0.287730718	0.016836589	0.287730718	0.016836589
1192	W903_RS05900	W903_1210	1140380	1141660	NA	putative streptokinase-like protein	0.90550979	1.17861E-08	1.217714795	2.26244E-15	1.217714795	2.26244E-15
1193	W903_RS05910	W903_1211	1142154	1142687	NA	hypothetical protein	0.086327497	0.78773361	2.3099964	2.31596E-50	2.3099964	2.31596E-50
1194	W903_RS05915	W903_1212	1142763	1143257	NA	putative thiol peroxidase	-0.812735287	0.000370662	1.831980755	1.34119E-66	1.831980755	1.34119E-66
1195	W903_RS05920	W903_1213	1143330	1143989	NA	DNA alkylation repair enzyme family protein	-0.693155265	7.02613E-05	0.637553272	2.12756E-09	0.637553272	2.12756E-09
1196	W903_RS05925	W903_1214	1143989	1144753	NA	HAD hydrolase, IIB family protein	-0.47220092	0.003389623	1.112707791	4.42738E-24	1.112707791	4.42738E-24
1197	W903_RS05930	W903_1215	1144758	1145399	NA	deoR-like helix-turn-helix domain protein	-0.661303643	2.27955E-05	1.113454187	6.35989E-32	1.113454187	6.35989E-32
1198	W903_RS05935	W903_1216	1145563	1146114	NA	asp23 family protein	-0.659066947	2.54872E-05	1.99526403	2.27956E-69	1.99526403	2.27956E-69
1199	W903_RS05940	W903_1217	1146136	1146333	NA	csbD-like family protein	-0.397407744	0.032607546	2.125890036	5.145E-58	2.125890036	5.145E-58
1200	W903_RS05945	W903_1218	1146380	1146922	NA	asp23 family protein	-0.516934381	0.001989825	2.025334204	1.93516E-92	2.025334204	1.93516E-92
1201	W903_RS05950	W903_1219	1146978	1147172	NA	hypothetical protein	-0.345507573	0.069792582	2.03096036	3.72483E-92	2.03096036	3.72483E-92
1202	W903_RS05955	W903_1220	1147182	1147763	NA	hypothetical protein	-0.26571018	0.15126138	1.968075446	2.38217E-61	1.968075446	2.38217E-61
1203	W903_RS05960	W903_1221	1147778	1148026	NA	transglycosylase associated family protein	0.105280137	0.606893258	2.129049005	4.55176E-75	2.129049005	4.55176E-75
1204	W903_RS05965	W903_1222	1148438	1150717	pcrA	ATP-dependent DNA helicase PcrA	0.13338851	0.503712789	-0.486116286	2.20027E-06	-0.486116286	2.20027E-06
1205	W903_RS05970	W903_1223	1150823	1151209	NA	hypothetical protein	0.314464252	0.855132285	-1.359597336	3.41174E-22	-1.359597336	3.41174E-22
1206	W903_RS05975	W903_1224	1151342	1152667	NA	uracil-xanthine permease family protein	0.263974689	0.892719202	-2.425016088	8.49354E-91	-2.425016088	8.49354E-91
1207	W903_RS05980	W903_1225	1153264	1154610	agcS	amino acid carrier family protein	-0.377288236	0.033407674	-1.340368812	2.56998E-36	-1.340368812	2.56998E-36
1208	W903_RS05985	W903_1226	1154674	1155909	NA	cation diffusion facilitator transporter family protein	-0.166794557	0.377928802	-0.265264007	0.034954341	-0.265264007	0.034954341
1209	W903_RS05990	W903_1227	1156068	1156460	NA	lrgA family protein	-0.045159707	0.849655992	0.292383519	0.016014306	0.292383519	0.016014306
1210	W903_RS05995	W903_1228	1156441	1157136	NA	lrgB-like family protein	-0.308798074	0.093988955	-0.242360806	0.056328032	-0.242360806	0.056328032
1211	W903_RS06000	W903_1229	1157205	1157828	NA	hypothetical protein	0.419703502	0.010676812	0.034734518	0.786620424	0.034734518	0.786620424
1212	W903_RS06005	W903_1230	1158097	1158168	rRNA	NA	0.436011686	0.57647511	0.141413279	0.744297935	0.141413279	0.744297935
1213	W903_RS06010	W903_1231	1158241	1159443	NA	S1 RNA binding domain protein	-0.637177534	5.25301E-06	-1.7814513	7.62959E-53	-1.7814513	7.62959E-53
1214	W903_RS06015	W903_1232	1159566	1159640	rRNA	NA	-0.038063934	NA	2.749820137	0.005102876	2.749820137	0.005102876
1215	W903_RS06020	W903_1233	1159646	1159726	rRNA	NA	0.285116626	NA	0.298445605	0.816430743	0.298445605	0.816430743
1216	W903_RS06025	W903_1234	1159787	1160017	NA	hypothetical protein	-0.960295824	0.000992352	1.767058055	1.30186E-14	1.767058055	1.30186E-14
1217	W903_RS06030	W903_1235	1160101	1161123	ilvE	branched-chain amino acid aminotransferase	-0.103235648	0.612207657	-1.020942623	1.23107E-24	-1.020942623	1.23107E-24
1218	W903_RS06035	W903_1236	1161237	1163696	parC	DNA topoisomerase IV, A subunit	0.041222279	0.817491868	0.172917936	0.074709372	0.172917936	0.074709372
1219	W903_RS06040	W903_1237	1163830	1165779	parE	DNA topoisomerase IV, B subunit	0.176187341	0.306496536	0.125394577	0.358647227	0.125394577	0.358647227
1220	W903_RS06045	W903_1238	1165908	1166531	plsY	acyl-phosphate glycerol 3-phosphate acyltransferase	-0.780577206	8.00499E-07	-0.308781143	0.039225265	-0.308781143	0.039225265
1221	W903_RS06050	W903_1239	1166597	1167250	ung	uracil-DNA glycosylase	0.68094111	0.000233553	1.215807235	2.14412E-21	1.215807235	2.14412E-21
1222	W903_RS06055	W903_1240	1167349	1167834	NA	hypothetical protein	-0.062071294	0.76251576	0.676496582	3.53153E-11	0.676496582	3.53153E-11
1223	W903_RS06060	W903_1241	1167948	1169189	NA	GDSL-like Lipase/Acylhydrolase family protein	-0.412813556	0.010498911	-2.423410121	3.35475E-67	-2.423410121	3.35475E-67
1224	W903_RS06065	W903_1242	1169200	1169829	NA	sugar O-acyltransferase, sialic acid O-acetyltransferase NeuD family protein	-0.339664177	0.045859063	-1.818653716	2.71737E-38	-1.818653716	2.71737E-38
1225	W903_RS06070	W903_1243	1169826	1170980	neuC	UDP-N-acetyl-D-glucosamine 2-epimerase, UDP-hydrolysing	0.131262536	0.483957846	-1.519232702	6.42632E-28	-1.519232702	6.42632E-28
1226	W903_RS06075	W903_1244	1171057	1172082	neuB	N-acetylneuraminate synthase	0.222264648	0.219518125	-1.200500069	4.43591E-16	-1.200500069	4.43591E-16
1227	W903_RS06080	W903_1245	1172082	1173482	NA	polysaccharide biosynthesis family protein	-0.242510614	0.200727304	-0.940259488	8.6663E-15	-0.940259488	8.6663E-15
1228	W903_RS06085	W903_1246	1173479	1174435	NA	glycosyltransferase 52 family protein	-0.012583334	0.94796136	-0.807641134	1.90287E-13	-0.807641134	1.90287E-13
1229	W903_RS06090	W903_1247	1174432	1175397	NA	glycosyl transferase 2 family protein	-0.408612253	0.019814003	-0.882085157	6.30826E-15	-0.882085157	6.30826E-15
1230	W903_RS06095	W903_1248	1175390	1176373	NA	glycosyl transferase 2 family protein	-0.045032633	0.816605926	-0.710346408	7.83276E-12	-0.710346408	7.83276E-12
1231	W903_RS06100	W903_1249	1176377	1177264	NA	glycosyl transferase 2 family protein	-0.883121765	2.20188E-07	-1.203866886	5.59528E-32	-1.203866886	5.59528E-32
1232	W903_RS06105	W903_1250	1177290	1178015	NA	tcdA/TcdB catalytic glycosyltransferase domain protein	-0.514335692	0.001518599	-0.752536872	3.65107E-12	-0.752536872	3.65107E-12
1233	W903_RS06110	W903_1251	1178054	1179148	NA	putative membrane protein	-1.03021102	1.52546E-08	-0.868209449	4.21881E-09	-0.868209449	4.21881E-09
1234	W903_RS06115	W903_1252	1179135	1179626	NA	glycosyltransferase family 28 C-terminal domain protein	-0.545837285	0.002556422	-0.783399408	9.32472E-10	-0.783399408	9.32472E-10
1235	W903_RS06120	W903_1253	1179626	1180075	NA	oligosaccharide biosynthesis Alg14 like family protein	-0.988405645	6.80475E-08	-0.966728685	1.99526E-15	-0.966728685	1.99526E-15
1236	W903_RS06125	W903_1254	1180099	1181448	NA	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase family protein	-0.736463214	3.41419E-06	-0.619695835	4.59342E-11	-0.619695835	4.59342E-11
1237	W903_RS06130	W903_1255	1181500	1182198	cpsD	tyrosine-protein kinase CpsD	-0.799099788	2.33193E-07	-0.501045827	7.70307E-08	-0.501045827	7.70307E-08
1238	W903_RS06135	W903_1256	1182209	1182901	NA	chain length determinant family protein	-0.983432878	7.80592E-12	-0.832232818	1.01166E-18	-0.832232818	1.01166E-18
1239	W903_RS06140	W903_1257	1182910	1183641	cpsB	tyrosine-protein phosphatase CpsB	-0.881125201	1.04858E-07	-0.383651223	0.010569112	-0.383651223	0.010569112
1240	W903_RS06145	W903_1258	1183647	1184990	NA	cell envelope-related function transcriptional attenuator common domain protein	-0.688567059	2.82859E-06	0.233807532	0.013589572	0.233807532	0.013589572
1241	W903_RS06150	W903_1259	1185293	1186216	NA	bacterial regulatory helix-turn-helix , lysR family protein	-0.817446687	1.35979E-06	-0.235388983	0.041620173	-0.235388983	0.041620173

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1242	W903_RS06155	W903_1260	1186241	1187008	NA	CRISPR-associated family protein	-0.014869539	0.935760556	-0.121538364	0.281119065	-0.121538364	0.281119065
1243	W903_RS06160	W903_1261	1187017	1187727	deoD	purine nucleoside phosphorylase	0.44233566	0.006967	0.099957538	0.388409219	0.099957538	0.388409219
1244	W903_RS06165	W903_1262	1187711	1188883	NA	voltage gated chloride channel family protein	1.1157725	1.48836E-14	0.959724014	2.94891E-25	0.959724014	2.94891E-25
1245	W903_RS06170	W903_1263	1188969	1189778	NA	purine nucleoside phosphorylase I, inosine and guanosine-specific	1.319582178	2.12645E-20	0.709501786	4.3196E-12	0.709501786	4.3196E-12
1246	W903_RS06175	W903_1264	1189817	1190224	arsC	arsenate reductase	0.78640106	3.69583E-07	0.496833407	4.61343E-06	0.496833407	4.61343E-06
1247	W903_RS06180	W903_1265	1190275	1191486	NA	phosphopentomutase	1.046136699	6.41305E-13	0.774658234	5.28046E-18	0.774658234	5.28046E-18
1248	W903_RS06185	W903_1266	1191543	1192214	rpiA	ribose 5-phosphate isomerase A	0.730565372	1.25088E-06	1.028777953	9.37056E-21	1.028777953	9.37056E-21
1249	W903_RS06190	W903_1267	1192452	1193144	NA	peptidase M54 family protein	-0.030601951	0.874114533	0.142224479	0.132778843	0.142224479	0.132778843
1250	W903_RS06195	W903_1268	1193252	1194040	NA	esterase family protein	0.237961195	0.14722531	0.361615016	0.001786465	0.361615016	0.001786465
1251	W903_RS06200	W903_1269	1194097	1195758	NA	metallo-beta-lactamase superfamily protein	0.129167674	0.446374739	0.361893839	0.006250497	0.361893839	0.006250497
1252	W903_RS06205	W903_1270	1196054	1196812	NA	ABC transporter family protein	-0.163198849	0.483314144	0.266884185	0.042722465	0.266884185	0.042722465
1253	W903_RS06210	W903_1271	1196815	1197678	NA	branched-chain amino acid transport system / permease component family protein	-0.054433612	0.823792061	0.435841824	0.000293885	0.435841824	0.000293885
1254	W903_RS06215	W903_1272	1197691	1198695	NA	hypothetical protein	-0.282510574	0.170805376	-0.133662015	0.246936264	-0.133662015	0.246936264
1255	W903_RS06220	W903_1273	1199054	1200709	NA	fibronectin-binding A family protein	1.062881388	1.80086E-09	-0.182390586	0.179148679	-0.182390586	0.179148679
1256	W903_RS06225	W903_1274	1200763	1201482	budA	alpha-acetolactate decarboxylase	0.627754496	0.001080054	0.873599719	4.92057E-22	0.873599719	4.92057E-22
1257	W903_RS06230	W903_1275	1201496	1203178	alsS	acetolactate synthase, catabolic	0.191794177	0.36122005	1.065991421	1.24994E-36	1.065991421	1.24994E-36
1258	W903_RS06235	W903_1276	1203288	1204514	NA	TPR repeat family protein	0.829610696	5.93578E-09	-0.243697025	0.008243248	-0.243697025	0.008243248
1259	W903_RS06240	W903_1277	1204504	1205694	NA	hypothetical protein	0.775212866	6.4908E-08	-0.237509944	0.008945849	-0.237509944	0.008945849
1260	W903_RS06245	W903_1278	1205786	1206247	NA	NUDIX domain protein	1.059250345	1.2197E-08	0.451716124	0.001516639	0.451716124	0.001516639
1261	W903_RS06250	W903_1279	1206237	1206719	mutX	mutator mutT protein	0.914259811	1.67172E-06	0.317639926	0.026068244	0.317639926	0.026068244
1262	W903_RS06260	W903_1282	1210208	1211254	rfbB	dTDP-glucose 4,6-dehydratase	0.707387072	8.20836E-07	-0.219618241	0.03300524	-0.219618241	0.03300524
1263	W903_RS06265	W903_1283	1211461	1212054	NA	putative dTDP-4-dehydrorhamnose 3,5-epimerase	0.665520691	1.13108E-05	-0.468147519	1.81042E-06	-0.468147519	1.81042E-06
1264	W903_RS06270	W903_1284	1212054	1212923	rfbA	glucose-1-phosphate thymidylyltransferase	0.73068025	5.55494E-07	-0.414202125	0.000636484	-0.414202125	0.000636484
1265	W903_RS06275	W903_1285	1212982	1214085	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.687975377	2.68445E-05	0.015148529	0.900332109	0.015148529	0.900332109
1266	W903_RS06280	W903_1286	1214094	1214882	NA	hypothetical protein	0.304078638	0.068552366	-0.42634577	3.45276E-05	-0.42634577	3.45276E-05
1267	W903_RS06285	W903_1287	1214872	1215555	NA	hypothetical protein	-0.176894511	0.367966213	-0.464266995	0.000117539	-0.464266995	0.000117539
1268	W903_RS06290	W903_1288	1215659	1216339	NA	hypothetical protein	-0.305717431	0.082114182	0.146274415	0.404141085	0.146274415	0.404141085
1269	W903_RS06295	W903_1289	1216457	1216975	apt	adenine phosphoribosyltransferase	-0.884541823	8.18391E-07	-0.214420962	0.046764803	-0.214420962	0.046764803
1270	W903_RS06300	W903_1290	1217098	1219662	NA	kxYKxGKxW signal peptide domain protein	0.468013821	0.007850889	-1.302257542	1.61566E-46	-1.302257542	1.61566E-46
1271	W903_RS06305	W903_1291	1219814	1222012	recJ	single-stranded-DNA-specific exonuclease RecJ	0.008608861	0.958972063	0.004391513	0.973133722	0.004391513	0.973133722
1272	W903_RS06310	W903_1292	1222009	1222770	NA	short chain dehydrogenase family protein	-0.00569148	0.977276951	0.108544845	0.361422285	0.108544845	0.361422285
1273	W903_RS06315	W903_1293	1222772	1223701	rnz	ribonuclease Z	0.272906195	0.090008853	0.253915637	0.007874373	0.253915637	0.007874373
1274	W903_RS06320	W903_1294	1223743	1224390	NA	putative tRNA delta(2)-isopentenylpyrophosphate transferase	0.026938684	0.885855408	-0.137910466	0.240816638	-0.137910466	0.240816638
1275	W903_RS06325	W903_1295	1224383	1225621	hflX	GTP-binding protein HflX	-0.105243094	0.549948356	-0.03857239	0.720005868	-0.03857239	0.720005868
1276	W903_RS06330	W903_1296	1225712	1226602	miaA	tRNA dimethylallyltransferase	-0.884788133	1.72768E-07	-0.80305294	1.28616E-10	-0.80305294	1.28616E-10
1277	W903_RS06335	W903_1297	1226713	1226889	NA	hypothetical protein	0.497129996	0.040946436	-0.288325125	0.038074983	-0.288325125	0.038074983
1278	W903_RS06340	W903_1298	1226931	1227848	NA	C4-dicarboxylate transporter/malic acid transport family protein	-0.083699749	0.666552071	0.914056899	4.82761E-12	0.914056899	4.82761E-12
1279	W903_RS06345	W903_1299	1227983	1231741	NA	pullulanase, extracellular	0.000298067	0.999136702	1.466147175	1.22525E-09	1.466147175	1.22525E-09
1280	W903_RS06355	W903_1302	1232658	1233242	NA	hypothetical protein	1.104859171	1.28257E-11	0.533576269	3.3551E-07	0.533576269	3.3551E-07
1281	W903_RS06360	W903_1303	1233339	1234745	pepV	dipeptidase PepV	1.147838782	1.82309E-16	0.25474762	0.010374128	0.25474762	0.010374128
1282	W903_RS06365	W903_1304	1234792	1235394	NA	putative NAD(P)H nitroreductase	0.448813982	0.00423563	-0.129828803	0.216159401	-0.129828803	0.216159401
1283	W903_RS06375	W903_1307	1237387	1239168	uvrC	excinuclease ABC subunit C	0.249237072	0.143974617	0.681578818	2.1055E-12	0.681578818	2.1055E-12
1284	W903_RS06380	W903_1308	1239327	1240094	NA	hypothetical protein	-0.445374222	0.016377276	-0.631055952	7.31889E-08	-0.631055952	7.31889E-08
1285	W903_RS06385	W903_1309	1240153	1241493	NA	MATE efflux family protein	0.332351958	0.05092725	0.911357584	8.22077E-21	0.911357584	8.22077E-21
1286	W903_RS06390	W903_1310	1241593	1242003	NA	3-demethylubiquinone-9 3-methyltransferase family protein	-0.066813326	0.733554053	0.696658616	3.23855E-11	0.696658616	3.23855E-11
1287	W903_RS06395	W903_1311	1242013	1242510	NA	hypothetical protein	-0.552976785	0.00040011	0.861183525	1.63237E-19	0.861183525	1.63237E-19
1288	W903_RS06400	W903_1312	1242732	1243328	NA	host cell surface-exposed lipofamily protein	-0.623776182	0.001751002	-0.481820623	0.001560769	-0.481820623	0.001560769
1289	NA	W903_1313	1243517	1243807	NA	transposase family protein	-0.098115519	0.828736007	1.389982092	8.67796E-11	1.389982092	8.67796E-11
1290	W903_RS06410	W903_1314	1243987	1244622	NA	integrase core domain protein	-0.221859151	0.545409579	1.370941158	1.34053E-13	1.370941158	1.34053E-13
1291	W903_RS06415	W903_1315	1244830	1245999	NA	hypothetical protein	-0.794913031	0.000222738	0.615909109	4.1605E-05	0.615909109	4.1605E-05
1292	W903_RS06420	W903_1316	1246134	1246499	rplL	ribosomal protein L7/L12	-0.814184588	8.7789E-08	-2.697783052	7.9602E-114	-2.697783052	7.9602E-114
1293	W903_RS06425	W903_1317	1246563	1247063	NA	ribosomal L10 family protein	-1.262489267	4.70311E-19	-2.905014541	1.1519E-197	-2.905014541	1.1519E-197
1294	W903_RS06430	W903_1318	1247496	1249604	NA	putative ATP-dependent Clp protease ATP-binding subunit	-0.08991759	0.733854288	4.868058095	1.01264E-17	4.868058095	1.01264E-17
1295	W903_RS06435	W903_1319	1249697	1250641	mmuM	homocysteine S-methyltransferase	0.939282781	0.000160331	0.365299822	0.10411911	0.365299822	0.10411911
1296	W903_RS06440	W903_1320	1250646	1252022	NA	amino acid permease family protein	1.340926526	2.30524E-09	0.668714182	0.000124543	0.668714182	0.000124543
1297	W903_RS06445	W903_1321	1252152	1252802	NA	hypothetical protein	1.068569436	0.021849764	0.694678934	0.013097361	0.694678934	0.013097361
1298	NA	W903_1322	1252960	1253283	NA	hypothetical protein	0.674374824	0.251726351	0.488780419	0.088632077	0.488780419	0.088632077
1299	W903_RS06455	W903_1323	1253555	1254103	NA	bacterial regulatory s, tetR family protein	0.444943371	0.129641826	1.098087639	9.384E-13	1.098087639	9.384E-13
1300	W903_RS06460	W903_1324	1254165	1254761	ysxC	ribosome biogenesis GTP-binding protein YsxC	0.317737574	0.098023272	0.736055939	1.44175E-10	0.736055939	1.44175E-10
1301	W903_RS06465	W903_1325	1254772	1255998	clpX	ATP-dependent Clp protease, ATP-binding subunit ClpX	0.404603763	0.012061269	0.913589361	2.48631E-16	0.913589361	2.48631E-16
1302	NA	W903_1326	1256028	1256198	NA	putative membrane protein	0.300086558	0.141342389	1.127863919	7.88471E-21	1.127863919	7.88471E-21
1303	W903_RS06475	W903_1327	1256216	1256710	dhfR	dihydrofolate reductase	0.078244302	0.701826668	1.045913486	8.46275E-13	1.045913486	8.46275E-13
1304	W903_RS06480	W903_1328	1256790	1257629	NA	thymidylate synthase family protein	0.244788563	0.156956193	1.047811315	5.00144E-21	1.047811315	5.00144E-21
1305	W903_RS06485	W903_1329	1257783	1258955	NA	hydroxymethylglutaryl-CoA synthase	0.012839345	0.942141234	-0.216461793	0.058167976	-0.216461793	0.058167976
1306	W903_RS06490	W903_1330	1258957	1260240	NA	hydroxymethylglutaryl-CoA reductase, degradative	-0.135720091	0.43289178	-0.17416308	0.166981255	-0.17416308	0.166981255
1307	W903_RS06495	W903_1331	1260332	1260781	NA	hypothetical protein	1.326113554	4.94156E-14	-1.007639004	1.3367E-14	-1.007639004	1.3367E-14
1308	W903_RS06500	W903_1332	1260774	1261430	NA	channel , hemolysin III family protein	2.35489015	4.47616E-31	-0.251797588	0.100943123	-0.251797588	0.100943123
1309	W903_RS06505	W903_1333	1261517	1262431	NA	lipid kinase, YegS/Rv2252/BmrU family protein	1.923535338	4.52609E-26	-0.073782144	0.626202626	-0.073782144	0.626202626
1310	W903_RS06510	W903_1334	1262532	1263586	NA	glutathione S-transferase, C-terminal domain protein	-1.007463458	9.79895E-07	1.436449017	8.12215E-29	1.436449017	8.12215E-29
1311	W903_RS06515	W903_1335	1263432	1263650	NA	hypothetical protein	0.695097777	0.075787491	0.631027735	0.043044182	0.631027735	0.043044182
1312	W903_RS06520	W903_1336	1263718	1264713	fni	isopentenyl-diphosphate delta-isomerase, type 2	0.243106555	0.133078652	0.325805303	0.007811223	0.325805303	0.007811223
1313	W903_RS06525	W903_1337	1264710	1265702	NA	phosphomevalonate kinase	0.1108823	0.560572697	0.34613809	0.003465317	0.34613809	0.003465317
1314	W903_RS06530	W903_1338	1265695	1266639	mvaD	diphosphomevalonate decarboxylase	0.228058283	0.192634382	0.457307743	2.16126E-05	0.457307743	2.16126E-05
1315	W903_RS06535	W903_1339	1266621	1267499	mvk	mevalonate kinase	-0.121620569	0.525444689	0.68663371	1.92994E-06	0.68663371	1.92994E-06
1316	W903_RS06540	W903_1340	1267615	1268844	NA	his Kinase A domain protein	-0.274286715	0.102080595	0.39782384	2.32854E-05	0.39782384	2.32854E-05
1317	W903_RS06545	W903_1341	1268844	1269530	NA	putative transcriptional activator CadC	0.220094913	0.243397527	0.599164467	1.48202E-09	0.599164467	1.48202E-09
1318	W903_RS06550	W903_1342	1269532	1270158	NA	RelA / SpoT s family protein	-0.007615803	0.966792967	0.458017716	3.59172E-06	0.458017716	3.59172E-06
1319	W903_RS06555	W903_1343	1270307	1270513	NA	hypothetical protein	0.070046984	0.881155871	1.005955167	1.19022E-05	1.005955167	1.19022E-05
1320	W903_RS06560	W903_1344	1271165	1273573	NA	LPXTG cell wall anchor domain protein	0.148861692	0.355685142	0.295323837	0.00202924	0.295323837	0.00202924
1321	W903_RS06565	W903_1345	1274332	1274772	NA	marR family protein	-0.939103981	2.25955E-07	1.534992088	1.95984E-43	1.534992088	1.95984E-43
1322	W903_RS06570	W903_1346	1275048	1277120	NA	calcineurin-like phosphoesterase family protein	-0.579925293	0.001251359	-1.077817143	2.31256E-08	-1.077817143	2.31256E-08
1323	W903_RS06575	W903_1347	1277157	1277567	NA	polypeptide deformylase family protein	0.532350286	0.007514823	0.586773874	2.91923E-05	0.586773874	2.91923E-05
1324	W903_RS06580	W903_1348	1277637	1278986	NA	glutamate/Leucine/Phenylalanine/Valine dehydrogenase family protein	0.664612425	0.00041814	0.159291638	0.132778843	0.159291638	0.132778843
1325	W903_RS06585	W903_1349	1279154	1279663	NA	hypothetical protein	0.745122779	6.92818E-06	0.395586347	0.000154703	0.395586347	0.000154703
1326	W903_RS06590	W903_1350	1279704	1281473	NA	ABC transporter family protein	0.208181092	0.270803414	0.524254028	6.38585E-07	0.524254028	6.38585E-07
1327	W903_RS06595	W903_1351	1281478	1283217	NA	ABC transporter family protein	0.304015198	0.092519667	0.481762227	2.79395E-06	0.481762227	2.79395E-06
1328	W903_RS06605	W903_1354	1283754	1285622	NA	ABC transporter family protein	0.396521493	0.027448288	0.203131307	0.043937525	0.203131307	0.043937525
1329	W903_RS06610	W903_1355	1285633	1286826	NA	poly A polymerase head domain protein	0.14455382	0.423756017	-0.031591939	0.805210061	-0.031591939	0.805210061
1330	W903_RS06615	W903_1356	1287026	1287874	NA	degV family protein	0.252083238	0.11442041	-0.096705524	0.354936197	-0.096705524	0.354936197
1331	W903_RS06620	W903_1357	1287874	1288254	NA	hypothetical protein	-0.464013483	0.003622254	-0.594975114	5.34182E-10	-0.594975114	5.34182E-10
1332	W903_RS06625	W903_1358	1288326	1288859	NA	hypothetical protein	0.415950972	0.03611521	0.351100069	0.008290542	0.351100069	0.008290542
1333	W903_RS06630	W903_1359	1288910	1289404	NA	hypothetical protein	-0.171826751	0.364890673	0.26303013	0.029727196	0.26303013	0.029727196
1334	W903_RS06635	W903_1360	1289593	1291557	fruA	PTS system, fructose subfamily, IIA component domain protein	0.722412793	4.56038E-07	-0.058154159	0.575881752	-0.058154159	0.575881752
1335	W903_RS06640	W903_1361	1291554	1292465	pfkB	1-phosphofructokinase	-0.105356133	0.561356379	-0.637423848	3.61998E-12	-0.637423848	3.61998E-12
1336	W903_RS06645	W903_1362	1292462	1293205	NA	deoR C terminal sensor domain protein	-0.30880776	0.045859063	-0.822034936	1.0368E-14	-0.822034936	1.0368E-14
1337	W903_RS06650	W903_1363	1293336	1294571	NA	femAB family protein	-0.166889229	0.330951294	0.985739964	0.078839324	0.985739964	0.078839324
1338	W903_RS06655	W903_1364	1294715	1296349	NA	gram-positive signal peptide, YSIRK family domain protein	-0.465186349	0.002147831	0.514410915	0.282483334	0.514410915	0.282483334
1339	W903_RS06660	W903_1365	1296561	1297484	NA	2-dehydropantoate 2-reductase family protein	-0.047266514	0.828736007	-1.862496808	9.32617E-75	-1.862496808	9.32617E-75
1340	W903_RS06665	W903_1366	1297497	1298567	NA	phosphotransferase system, EIIC family protein	0.335635238	0.087948687	-1.348876987	4.62285E-39	-1.348876987	4.62285E-39
1341	W903_RS06670	W903_1367	1298704	1299696	NA	pyridine nucleotide-disulfide oxidoreductase family protein	-0.351319009	0.098516323	-0.572307069	2.0121E-05	-0.572307069	2.0121E-05
1342	W903_RS06675	W903_1368	1299677	1300429	trmD	tRNA (guanine(37)-N(1))-methyltransferase	-0.199812013	0.368429976	-0.462777011	0.000105813	-0.462777011	0.000105813
1343	W903_RS06680	W903_1369	1300419	1300937	rimM	16S ribosome processing protein RimM	-0.840052156	0.00040299	-0.500432977	0.003776266	-0.500432977	0.003776266
1344	W903_RS06685	W903_1370	1301000	1301071	rRNA	NA	-1.361794617	NA	1.749024832	0.394304118	1.749024832	0.394304118
1345	W903_RS06690	W903_1371	1301080	1301151	rRNA	NA	-1.693603038	NA	1.414811274	0.464350799	1.414811274	0.464350799
1346	W903_RS06695	W903_1372	1301259	1302770	NA	M trans-acting positive regulator (MGA) PRD domain protein	-0.509845934	0.001559194	0.614415611	2.44493E-11	0.614415611	2.44493E-11
1347	W903_RS06700	W903_1373	1302902	1303144	NA	KH domain protein	-1.795302431	3.83034E-16	-3.028437101	2.57868E-15	-3.028437101	2.57868E-15
1348	W903_RS06705	W903_1374	1303154	1303426	rpsP	ribosomal protein S16	-2.02658652	2.13764E-26	-3.291055952	8.00682E-13	-3.291055952	8.00682E-13
1349	W903_RS06710	W903_1375	1303555	1304802	NA	ftsX-like permease family protein	0.246565079	0.154337021	-2.538618827	2.3512E-154	-2.538618827	2.3512E-154
1350	W903_RS06715	W903_1376	1304817	1305527	NA	ABC transporter family protein	0.59265889	0.000489113	-2.132492155	1.11724E-89	-2.132492155	1.11724E-89
1351	W903_RS06720	W903_1377	1305530	1306774	NA	efflux transporter, RND family, MFP subunit	0.173158621	0.370894861	-2.403392787	5.5274E-111	-2.403392787	5.5274E-111
1352	W903_RS06725	W903_1378	1306976	1308574	NA	carbamoyl-phosphate synthase L chain, ATP binding domain protein	-0.120773013	0.655104421	-0.220658026	0.059189362	-0.220658026	0.059189362
1353	W903_RS06730	W903_1379	1308630	1309700	NA	carbamoyl-phosphate synthase, small subunit	0.180794479	0.535808713	-0.378271061	7.24933E-05	-0.378271061	7.24933E-05
1354	W903_RS06735	W903_1380	1309749	1310270	pyrR	bifunctional protein pyrR	0.079428098	0.795809871	-0.511303123	6.40686E-08	-0.511303123	6.40686E-08
1355	W903_RS06740	W903_1381	1310446	1311336	NA	pseudouridine synthase, RluA family protein	0.054909352	0.78773361	-0.254498121	0.016235582	-0.254498121	0.016235582
1356	W903_RS06745	W903_1382	1311320	1311784	lspA	signal peptidase II	-0.628270137	0.001863435	-0.153410799	0.293289048	-0.153410799	0.293289048
1357	W903_RS06750	W903_1383	1311793	1312698	NA	bacterial regulatory helix-turn-helix , lysR family protein	-0.405665497	0.016838871	0.002313954	0.986368808	0.002313954	0.986368808
1358	W903_RS06755	W903_1384	1312914	1313207	rpmA	ribosomal protein L27	-0.577157549	0.000252231	-0.880677398	2.2785E-07	-0.880677398	2.2785E-07
1359	W903_RS06760	W903_1385	1313229	1313567	NA	hypothetical protein	-1.235234514	3.01443E-16	-1.081589142	5.37872E-25	-1.081589142	5.37872E-25
1360	W903_RS06765	W903_1386	1313574	1313888	rplU	ribosomal protein L21	-0.75634837	4.73097E-05	-0.496488432	0.000374705	-0.496488432	0.000374705
1361	W903_RS06770	W903_1387	1314078	1315256	NA	bacterial capsule synthesis PGA_cap family protein	-0.17030046	0.368868788	0.117404307	0.464958121	0.117404307	0.464958121
1362	W903_RS06775	W903_1388	1315358	1316572	thiI	tRNA sulfurtransferase ThiI	0.150625232	0.423657793	-0.210993406	0.033853887	-0.210993406	0.033853887
1363	W903_RS06780	W903_1389	1316574	1317719	NA	aminotransferase class-V family protein	-0.232708256	0.014357076	0.899203501	0.014357076	0.899203501	0.899203501
1364	W903_RS06785	W903_1390	1317966	1318418	NA	hypothetical protein	-0.129900141	0.560572697	0.939992577	1.30111E-13	0.939992577	1.30111E-13
1365	W903_RS06790	W903_1391	1318461	1319810	gor	glutathione-disulfide reductase	0.628021329	0.00014327	1.074522511	1.27263E-28	1.074522511	1.27263E-28
1366	W903_RS06795	W903_1392	1319985	1320320	NA	hypothetical protein	-0.749726588	1.36475E-05	-0.261003704	0.013223196	-0.261003704	0.013223196
1367	W903_RS06800	W903_1393	1320404	1321570	aroC	chorismate synthase	0.010186278	0.955813252	0.386138695	0.000668051	0.386138695	0.000668051
1368	W903_RS06805	W903_1394	1321571	1322638	aroB	3-dehydroquinate synthase	0.38752971	0.030488964	0.935249611	1.51222E-12	0.935249611	1.51222E-12
1369	W903_RS06810	W903_1395	1322732	1323409	aroD	3-dehydroquinate dehydratase	-0.900433087	3.80062E-10	-0.328489882	0.000392025	-0.328489882	0.000392025
1370	W903_RS06815	W903_1396	1323409	1324566	NA	methyltransferase domain protein	-0.623238881	3.5705E-05	0.293997236	0.001558514	0.293997236	0.001558514
1371	W903_RS06820	W903_1397	1324701	1326845	NA	sulfatase family protein	-0.074388727	0.682977733	-0.567651659	3.98817E-08	-0.567651659	3.98817E-08
1372	W903_RS06825	W903_1398	1327086	1327445	rplT	ribosomal protein L20	-0.504123731	0.018433975	-1.306325271	6.86701E-11	-1.306325271	6.86701E-11
1373	W903_RS06830	W903_1399	1327503	1327703	rpmI	ribosomal protein L35	-1.112150779	4.02772E-10	-1.475473442	5.87667E-20	-1.475473442	5.87667E-20
1374	W903_RS06835	W903_1400	1327743	1328273	infC	translation initiation factor IF-3	-1.179292007	2.72453E-11	-0.910003297	1.92455E-10	-0.910003297	1.92455E-10
1375	W903_RS06840	W903_1401	1328434	1329117	cmk	cytidylate kinase	-0.124901878	0.525444689	-0.015115236	0.89958526	-0.015115236	0.89958526
1376	W903_RS06845	W903_1402	1329128	1329652	NA	hypothetical protein	-0.177075791	0.310469581	-0.216295672	0.025995864	-0.216295672	0.025995864
1377	W903_RS06850	W903_1403	1329698	1329895	NA	4Fe-4S binding domain protein	0.263452627	0.251844765	0.329730178	0.007661664	0.329730178	0.007661664
1378	W903_RS06855	W903_1404	1329882	1330373	NA	putative pore forming protein	0.253736828	0.165035668	-0.029858032	0.810879367	-0.029858032	0.810879367
1379	W903_RS06860	W903_1405	1330402	1331622	pepT	peptidase T	0.13423112	0.435156558	-0.034771615	0.754408822	-0.034771615	0.754408822

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1380	W903_RS06865	W903_1406	1331758	1333392	NA	polysaccharide biosynthesis family protein	0.813544453	1.44649E-07	0.788578082	4.5371E-16	0.788578082	4.5371E-16
1381	W903_RS06870	W903_1407	1333516	1334970	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase	0.181912597	0.274844361	0.133255122	0.189790019	0.133255122	0.189790019
1382	W903_RS06875	W903_1408	1335125	1335919	NA	ABC transporter family protein	-0.682991415	0.000491514	-0.715610064	1.75685E-08	-0.715610064	1.75685E-08
1383	W903_RS06880	W903_1409	1335943	1336875	NA	periplasmic binding family protein	-0.568058596	0.000852337	-1.256590812	2.68174E-33	-1.256590812	2.68174E-33
1384	W903_RS06885	W903_1410	1336891	1337916	NA	fecCD transport family protein	0.16522813	0.479431807	-0.372344989	0.004450061	-0.372344989	0.004450061
1385	W903_RS06890	W903_1411	1337913	1338914	NA	fecCD transport family protein	0.279664695	0.251844765	-0.124473906	0.373490113	-0.124473906	0.373490113
1386	W903_RS06895	W903_1412	1338943	1339596	NA	hypothetical protein	-0.422681444	0.060494851	-0.509160218	0.000937089	-0.509160218	0.000937089
1387	W903_RS06900	W903_1413	1339656	1340591	NA	putative manganese-dependent inorganic pyrophosphatase	-0.739396518	6.07421E-07	-1.076197571	4.97235E-34	-1.076197571	4.97235E-34
1388	W903_RS06905	W903_1414	1340708	1341496	pflA	pyruvate formate-lyase 1-activating enzyme	-0.620320638	0.000214091	0.462063876	2.46811E-05	0.462063876	2.46811E-05
1389	W903_RS06910	W903_1415	1341564	1342898	NA	transporter associated domain protein	-0.271095964	0.082629392	0.116846777	0.283039273	0.116846777	0.283039273
1390	W903_RS06915	W903_1416	1343078	1343644	NA	hypothetical protein	0.548003677	0.0007287	-0.474915844	2.2489E-06	-0.474915844	2.2489E-06
1391	W903_RS06920	W903_1417	1343637	1344572	NA	radical SAM superfamily protein	0.047599699	0.80486759	-0.533530966	6.88665E-07	-0.533530966	6.88665E-07
1392	W903_RS06925	W903_1418	1344665	1345306	NA	PAP2 superfamily protein	-0.525482118	0.007276705	1.294917334	1.47522E-15	1.294917334	1.47522E-15
1393	W903_RS06930	W903_1419	1345287	1345871	NA	hypothetical protein	-0.656667285	0.002088991	1.475005754	4.42607E-14	1.475005754	4.42607E-14
1394	W903_RS06935	W903_1420	1346172	1347098	NA	LPXTG cell wall anchor domain protein	-1.352033317	2.32386E-14	-2.300720382	4.02072E-68	-2.300720382	4.02072E-68
1395	W903_RS06940	W903_1421	1347095	1347979	NA	sortase C	-1.216812399	5.73715E-09	-1.87965627	1.47273E-36	-1.87965627	1.47273E-36
1396	W903_RS06945	W903_1422	1347979	1348857	NA	sortase C	-0.714891231	0.001320461	-1.379970314	1.11852E-20	-1.379970314	1.11852E-20
1397	W903_RS06950	W903_1423	1348969	1351017	NA	fimbrial isopeptide formation D2 domain protein	-1.053240393	3.45372E-11	-4.047861594	1.0303E-294	-4.047861594	1.0303E-294
1398	W903_RS06955	W903_1424	1351136	1353826	NA	cell wall surface anchor family protein	-1.036081682	5.89644E-08	-3.343663823	5.3409E-229	-3.343663823	5.3409E-229
1399	W903_RS06960	W903_1425	1354110	1355639	NA	M trans-acting positive regulator (MGA) PRD domain protein	-0.169330666	0.523824366	0.085609469	0.507515057	0.085609469	0.507515057
1400	W903_RS06965	W903_1426	1355691	1356830	NA	glycosyl transferases group 1 family protein	0.055971101	0.774979832	-0.833792203	1.08805E-16	-0.833792203	1.08805E-16
1401	W903_RS06970	W903_1427	1356820	1357668	NA	glycosyl transferase 2 family protein	0.027227047	0.89099822	-0.86426016	1.57976E-18	-0.86426016	1.57976E-18
1402	W903_RS06975	W903_1428	1357665	1359089	NA	polysaccharide biosynthesis family protein	0.165919388	0.38790006	-0.616896109	4.88057E-12	-0.616896109	4.88057E-12
1403	W903_RS06980	W903_1429	1359089	1360453	NA	hypothetical protein	0.207135171	0.295806045	-0.620151506	1.29533E-10	-0.620151506	1.29533E-10
1404	W903_RS06985	W903_1430	1360455	1361402	NA	glycosyl transferase 2 family protein	0.153283832	0.453150756	-0.581467677	3.69181E-10	-0.581467677	3.69181E-10
1405	W903_RS06990	W903_1431	1361411	1362346	NA	glycosyl transferase 2 family protein	0.165398188	0.377432566	-0.668287461	1.41021E-12	-0.668287461	1.41021E-12
1406	W903_RS06995	W903_1432	1362348	1363403	NA	NAD dependent epimerase/dehydratase family protein	0.142935692	0.433694308	-0.648220384	2.03741E-11	-0.648220384	2.03741E-11
1407	W903_RS07000	W903_1433	1363406	1364125	NA	hypothetical protein	0.25763547	0.16938444	-0.608830928	3.90547E-09	-0.608830928	3.90547E-09
1408	W903_RS07005	W903_1434	1364128	1364952	NA	licD family protein	0.575884936	0.001471444	-0.301392283	0.00212951	-0.301392283	0.00212951
1409	W903_RS07010	W903_1435	1364977	1366710	NA	putative lipoprotein	-0.163561998	0.352424613	-0.787202197	6.70563E-18	-0.787202197	6.70563E-18
1410	W903_RS07015	W903_1436	1366703	1367056	NA	hypothetical protein	0.307613914	0.117859086	-0.194404759	0.109006868	-0.194404759	0.109006868
1411	W903_RS07020	W903_1437	1367053	1367781	NA	glycosyl transferase 2 family protein	0.164044873	0.344004389	-0.256037243	0.00765911	-0.256037243	0.00765911
1412	W903_RS07025	W903_1438	1367786	1368727	NA	glycosyl transferase 2 family protein	-0.158310096	0.362515556	-0.304738451	0.003474711	-0.304738451	0.003474711
1413	W903_RS07030	W903_1439	1368717	1369871	NA	glycosyl transferases group 1 family protein	0.07504716	0.688067609	0.316188499	0.001211492	0.316188499	0.001211492
1414	W903_RS07035	W903_1440	1369988	1370842	rfbD	dTDP-4-dehydrorhamnose reductase	-0.30001968	0.13085724	-0.840559022	1.9238E-10	-0.840559022	1.9238E-10
1415	W903_RS07040	W903_1441	1370932	1371273	NA	hypothetical protein	-0.75874698	9.58718E-06	-0.865067277	1.269E-11	-0.865067277	1.269E-11
1416	W903_RS07045	W903_1442	1371381	1372490	rpoD	RNA polymerase sigma factor RpoD	-0.603242192	0.000101683	-0.497314123	6.17148E-07	-0.497314123	6.17148E-07
1417	W903_RS07050	W903_1443	1372498	1374279	dnaG	DNA primase	-0.667026278	6.09867E-06	0.09289736	0.418282977	0.09289736	0.418282977
1418	W903_RS07055	W903_1444	1374496	1374873	mscL	large conductance mechanosensitive channel protein	0.070286937	0.755212804	0.830611224	2.59101E-09	0.830611224	2.59101E-09
1419	W903_RS07060	W903_1445	1374970	1375146	rpsU	ribosomal protein S21	-0.586440349	0.007276705	-0.71255138	6.105E-05	-0.71255138	6.105E-05
1420	W903_RS07065	W903_1446	1375250	1375753	NA	flagellin N-methylase family protein	-0.567222514	0.012308375	0.641506157	1.20901E-05	0.641506157	1.20901E-05
1421	W903_RS07070	W903_1447	1375836	1376642	NA	bacterial extracellular solute-binding s, 3 family protein	-0.899991089	0.000388739	-0.319556368	0.103344382	-0.319556368	0.103344382
1422	W903_RS07075	W903_1448	1376967	1377950	NA	ammonium Transporter family protein	0.546032732	0.376532116	1.24510401	0.000500841	1.24510401	0.000500841
1423	W903_RS07080	W903_1449	1378090	1379217	NA	pyridine nucleotide-disulfide oxidoreductase family protein	-0.091790479	0.809360802	2.014188166	1.55815E-19	2.014188166	1.55815E-19
1424	W903_RS07085	W903_1450	1379254	1380240	NA	rhodanese-like domain protein	-0.637637511	0.002162424	1.576122893	6.65344E-36	1.576122893	6.65344E-36
1425	W903_RS07090	W903_1451	1380403	1380708	NA	hypothetical protein	-0.343363949	0.324889793	1.307486312	1.19958E-08	1.307486312	1.19958E-08
1426	W903_RS07095	W903_1452	1380863	1382236	NA	major Facilitator Superfamily protein	0.667043282	0.000406817	0.860000603	2.5766E-13	0.860000603	2.5766E-13
1427	W903_RS07100	W903_1453	1382652	1384916	glgP	glycogen/starch/alpha-glucan phosphorylases family protein	-0.892630195	7.19092E-08	0.363904966	0.133732721	0.363904966	0.133732721
1428	W903_RS07105	W903_1454	1384928	1386424	malQ	4-alpha-glucanotransferase	-0.994139175	2.08136E-08	0.758370367	0.169343986	0.758370367	0.169343986
1429	W903_RS07110	W903_1455	1386552	1387574	NA	helix-turn-helix family protein	-0.328887615	0.129985556	-0.316702514	0.014763377	-0.316702514	0.014763377
1430	W903_RS07115	W903_1456	1387830	1389077	NA	bacterial extracellular solute-binding family protein	-0.530068348	0.005626831	0.196852718	0.362680838	0.196852718	0.362680838
1431	W903_RS07120	W903_1457	1389205	1390545	NA	binding--dependent transport system inner membrane component family protein	0.056390702	0.814729644	0.384965212	0.121209805	0.384965212	0.121209805
1432	W903_RS07125	W903_1458	1390545	1391381	NA	binding--dependent transport system inner membrane component family protein	-0.267572112	0.280531005	0.35275358	0.069177011	0.35275358	0.069177011
1433	W903_RS07130	W903_1459	1391612	1393084	NA	H+ symporter family protein	0.310924923	0.066830443	0.428299116	0.000876209	0.428299116	0.000876209
1434	W903_RS07135	W903_1460	1393129	1393593	NA	NUDIX domain protein	-0.001577055	0.996232944	-0.078329941	0.666663035	-0.078329941	0.666663035
1435	W903_RS07140	W903_1461	1393677	1393865	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.236372335	4.39404E-11	-1.619847244	4.67218E-31	-1.619847244	4.67218E-31
1436	W903_RS07145	W903_1462	1393876	1395201	gtfB	accessory Sec system glycosyltransferase GtfB	-0.275524004	0.086116923	-0.839623653	2.2121E-20	-0.839623653	2.2121E-20
1437	W903_RS07150	W903_1463	1395194	1396702	gtfA	accessory Sec system glycosylation protein GtfA	0.285804382	0.106218391	-0.348221773	0.001024914	-0.348221773	0.001024914
1438	W903_RS07155	W903_1464	1396716	1399103	secA2	accessory Sec system translocase SecA2	0.399508451	0.014818108	-0.09485244	0.353952072	-0.09485244	0.353952072
1439	W903_RS07160	W903_1465	1399090	1400082	asp3	accessory Sec system protein Asp3	0.059443503	0.774979832	-0.227492004	0.05646919	-0.227492004	0.05646919
1440	W903_RS07165	W903_1466	1400079	1401638	asp2	accessory Sec system protein Asp2	0.06353573	0.734621538	-0.206363889	0.034195137	-0.206363889	0.034195137
1441	W903_RS07170	W903_1467	1401645	1403189	asp1	accessory Sec system protein Asp1	-0.109295595	0.570060513	-0.255690188	0.024498859	-0.255690188	0.024498859
1442	W903_RS07175	W903_1468	1403189	1404418	secY2	accessory Sec system translocase SecY2	-0.174418535	0.309794012	-0.117185776	0.234354938	-0.117185776	0.234354938
1443	W903_RS07180	W903_1469	1404551	1405738	NA	hypothetical protein	-0.208556877	0.240876774	-0.354757897	0.000137031	-0.354757897	0.000137031
1444	W903_RS07185	W903_1470	1405799	1406674	NA	glycosyl transferase 2 family protein	-0.349429768	0.043830037	-0.525180147	2.51002E-07	-0.525180147	2.51002E-07
1445	W903_RS07190	W903_1471	1406667	1407851	NA	glycosyl transferase 8 family protein	0.096903616	0.592240846	-0.190995527	0.091141142	-0.190995527	0.091141142
1446	W903_RS07195	W903_1472	1407841	1409082	NA	glycosyl transferase 8 family protein	0.258581752	0.161486188	0.057363028	0.712424109	0.057363028	0.712424109
1447	W903_RS07200	W903_1473	1409079	1410284	NA	glycosyl transferase 8 family protein	0.180525119	0.3320891	-0.083164752	0.476467653	-0.083164752	0.476467653
1448	W903_RS07205	W903_1474	1410293	1411300	nss	nucleotide sugar synthetase-like protein	0.274226516	0.142331643	-0.07250433	0.533125342	-0.07250433	0.533125342
1449	NA	W903_1475	1411631	1414939	NA	serine-rich repeat adhesion glycoprotein	0.250469665	0.215888709	-1.677266764	8.33241E-57	-1.677266764	8.33241E-57
1450	W903_RS07220	W903_1476	1415322	1416818	NA	M trans-acting positive regulator (MGA) PRD domain protein	-0.055183362	0.821237299	2.652482198	1.3927E-153	2.652482198	1.3927E-153
1451	W903_RS07225	W903_1477	1416915	1418906	uvrB	excinuclease ABC subunit B	0.245150765	0.165387542	0.708644946	7.35714E-13	0.708644946	7.35714E-13
1452	W903_RS07230	W903_1478	1418967	1419887	NA	CAAX protease self-immunity family protein	-0.034021036	0.856711352	0.045475803	0.66458976	0.045475803	0.66458976
1453	W903_RS07235	W903_1479	1420070	1422253	NA	lysine-arginine-ornithine-binding periplasmic family protein	-0.663510233	0.000490758	0.524757547	0.000550351	0.524757547	0.000550351
1454	W903_RS07240	W903_1480	1422253	1422993	NA	ABC transporter family protein	-0.83204429	4.99687E-08	0.288293587	0.024498859	0.288293587	0.024498859
1455	W903_RS07245	W903_1481	1423187	1423492	NA	hypothetical protein	-0.483434725	0.280296301	0.703947631	0.001601873	0.703947631	0.001601873
1456	NA	W903_1482	1423584	1423742	NA	putative uDP-N-acetylglucosamine 1-carboxyvinyltransferase	2.811408311	3.94437E-06	0.473682686	0.370308421	0.473682686	0.370308421
1457	W903_RS07255	W903_1483	1423768	1425081	cgtA	obg family GTPase CgtA	0.36800494	0.033233312	-1.065583313	2.45937E-20	-1.065583313	2.45937E-20
1458	W903_RS07260	W903_1484	1425142	1425270	NA	hypothetical protein	-0.156817441	0.784408717	0.574823015	0.111949519	0.574823015	0.111949519
1459	W903_RS07265	W903_1485	1425448	1426689	NA	thermophilic metalloprotease family protein	0.785933113	5.31769E-06	-0.472619266	1.19763E-06	-0.472619266	1.19763E-06
1460	W903_RS07270	W903_1486	1426723	1427301	NA	LPXTG cell wall anchor domain protein	0.191940988	0.344444325	1.016469948	2.83655E-20	1.016469948	2.83655E-20
1461	W903_RS07275	W903_1487	1427411	1429450	NA	LPXTG cell wall anchor domain protein	0.455599444	0.027363481	1.804565716	5.08301E-57	1.804565716	5.08301E-57
1462	W903_RS07280	W903_1488	1429535	1430257	NA	pseudouridine synthase family protein	0.467247953	0.051755221	-1.059213913	2.61028E-08	-1.059213913	2.61028E-08
1463	W903_RS07285	W903_1489	1430448	1431290	NA	aldo/keto reductase family protein	0.474792386	0.048619216	2.560398632	4.21293E-63	2.560398632	4.21293E-63
1464	W903_RS07290	W903_1490	1431557	1432231	NA	putative NAD(P)H nitroreductase yfkO	1.495668273	1.574E-19	0.471867818	7.08162E-05	0.471867818	7.08162E-05
1465	W903_RS07295	W903_1491	1432319	1432711	gloA	lactoylglutathione lyase	0.833028769	0.000110647	1.46441753	4.75203E-29	1.46441753	4.75203E-29
1466	W903_RS07300	W903_1492	1432840	1433766	NA	glycosyl transferase 2 family protein	0.473002653	0.017858701	0.538883962	3.94801E-05	0.538883962	3.94801E-05
1467	W903_RS07305	W903_1493	1433895	1435283	NA	amino acid permease family protein	0.342043802	0.082656145	-0.230622253	0.030623076	-0.230622253	0.030623076
1468	W903_RS07310	W903_1494	1435367	1435834	smpB	ssrA-binding protein	-0.220399263	0.274477724	0.027190957	0.827468074	0.027190957	0.827468074
1469	W903_RS07315	W903_1495	1435837	1438242	rnr	ribonuclease R	-0.04725524	0.798496828	0.482253274	9.54619E-06	0.482253274	9.54619E-06
1470	W903_RS07320	W903_1496	1438355	1438591	secG	preprotein translocase, SecG subunit	-0.524075059	0.019069696	0.476757164	0.011312258	0.476757164	0.011312258
1471	W903_RS07325	W903_1497	1438781	1439950	NA	multidrug resistance family protein	-0.083711247	0.664595983	0.824200861	4.20431E-13	0.824200861	4.20431E-13
1472	W903_RS07330	W903_1498	1440146	1441792	NA	putative membrane protein	-0.038686485	0.877849387	-0.868243765	1.66499E-08	-0.868243765	1.66499E-08
1473	W903_RS07335	W903_1499	1441782	1442483	NA	ABC transporter family protein	-0.090113124	0.746248871	-0.956284495	1.8187E-06	-0.956284495	1.8187E-06
1474	W903_RS07340	W903_1500	1442608	1443195	coaE	dephospho-CoA kinase	0.158385809	0.541626703	0.803492997	2.38004E-08	0.803492997	2.38004E-08
1475	W903_RS07345	W903_1501	1443192	1444013	mutM	formamidopyrimidine-DNA glycosylase	-0.05941393	0.78773361	0.939175689	8.33189E-14	0.939175689	8.33189E-14
1476	W903_RS07350	W903_1502	1444162	1445010	NA	transcriptional activator, Rgg/GadR/MutR family, C-terminal domain protein	-0.091537116	0.78773361	1.428642202	1.09966E-17	1.428642202	1.09966E-17
1477	W903_RS07355	W903_1503	1445227	1446819	NA	transglutaminase-like superfamily protein	0.093555423	0.66650765	-1.093687562	2.79629E-13	-1.093687562	2.79629E-13
1478	NA	W903_1504	1446855	1447031	NA	hypothetical protein	1.467525725	NA	-1.507976142	0.103344382	-1.507976142	0.103344382
1479	NA	W903_1505	1447082	1447207	NA	hypothetical protein	1.027862569	NA	0.805700789	0.263576189	0.805700789	0.263576189
1480	NA	W903_1506	1447779	1447916	NA	glycerophosphoryl diester phosphodiesterase family protein	0.263367413	0.434399494	0.443797651	0.03654145	0.443797651	0.03654145
1481	W903_RS07375	W903_1507	1448788	1449177	NA	putative membrane protein	-0.258878541	0.349244784	0.509953603	0.002792875	0.509953603	0.002792875
1482	W903_RS07380	W903_1508	1449414	1450313	era	GTP-binding protein Era	-0.282537673	0.07935691	-0.578392565	1.57085E-09	-0.578392565	1.57085E-09
1483	W903_RS07385	W903_1509	1450355	1450753	dgkA	undecaprenol kinase	-0.454990229	0.004447202	0.716638094	2.33648E-11	-0.716638094	2.33648E-11
1484	W903_RS07390	W903_1510	1450734	1452119	NA	putative rRNA maturation factor YbeY	-0.343683226	0.050167456	-0.449711681	9.44617E-05	-0.449711681	9.44617E-05
1485	W903_RS07395	W903_1511	1451625	1452431	NA	leucine carboxyl methyltransferase family protein	-0.552979326	0.022827022	-0.698970464	4.24311E-07	-0.698970464	4.24311E-07
1486	W903_RS07400	W903_1512	1452754	1453230	NA	NUDIX domain protein	-1.360624944	2.25122E-10	0.23380444	0.099323405	0.23380444	0.099323405
1487	W903_RS07405	W903_1513	1453422	1454225	NA	hypothetical protein	0.085820399	0.717288774	0.013154843	0.931286353	0.013154843	0.931286353
1488	W903_RS07410	W903_1514	1454317	1455303	NA	istB-like ATP binding family protein	-0.235142725	0.229316616	-0.565083057	2.54757E-09	-0.565083057	2.54757E-09
1489	W903_RS07415	W903_1515	1455425	1457197	NA	myosin-cross-reactive antigen family protein	0.882197798	6.53542E-08	1.6193005	7.4048E-52	1.6193005	7.4048E-52
1490	W903_RS07420	W903_1516	1457354	1457569	NA	hypothetical protein	1.078089016	0.001357887	0.148479234	0.600759461	0.148479234	0.600759461
1491	W903_RS07425	W903_1517	1457566	1458075	msrA	peptide-methionine (S)-S-oxide reductase	0.050705182	0.789718528	-0.112786392	0.331073284	-0.112786392	0.331073284
1492	W903_RS07430	W903_1518	1458213	1459067	NA	S1 domain protein	-0.086291112	0.628327964	-0.638733817	2.63292E-06	-0.638733817	2.63292E-06
1493	W903_RS07435	W903_1519	1459185	1459742	frr	ribosome recycling factor	-0.508874171	0.000533842	-0.778378763	2.20851E-14	-0.778378763	2.20851E-14
1494	W903_RS07440	W903_1520	1459758	1460486	pyrH	UMP kinase	-0.744016864	2.34669E-06	-0.374957225	0.000106603	-0.374957225	0.000106603
1495	W903_RS07445	W903_1521	1460607	1461287	NA	ABC transporter family protein	-0.22013671	0.506939331	0.596402235	0.000132804	0.596402235	0.000132804
1496	W903_RS07450	W903_1522	1461274	1462062	NA	ABC transporter family protein	0.194873912	0.570214659	0.861179295	5.48434E-08	0.861179295	5.48434E-08
1497	W903_RS07455	W903_1523	1462050	1462856	NA	binding--dependent transport system inner membrane component family protein	0.125365886	0.808409811	0.295288423	0.173092651	0.295288423	0.173092651
1498	W903_RS07460	W903_1524	1462856	1463800	NA	binding--dependent transport system inner membrane component family protein	0.73160318	0.157715534	0.034952251	0.894008319	0.034952251	0.894008319
1499	W903_RS07465	W903_1525	1463787	1465403	nikA	nickel ABC transporter, nickel/metallophore periplasmic binding protein	-0.624090235	0.054953125	-0.698927734	7.05339E-05	-0.698927734	7.05339E-05
1500	W903_RS07470	W903_1526	1465792	1466481	rplA	ribosomal protein L1	-0.939526627	1.88838E-07	-1.705022444	1.69726E-86	-1.705022444	1.69726E-86
1501	W903_RS07475	W903_1527	1466585	1467010	rplK	ribosomal protein L11	-1.150454003	3.19285E-09	-2.068415977	1.2916E-130	-2.068415977	1.2916E-130
1502	W903_RS07480	W903_1528	1467217	1468599	norB	quinolone resistance protein norB	-0.600772361	0.00034075	-0.858032102	9.87016E-13	-0.858032102	9.87016E-13
1503	W903_RS07485	W903_1529	1468607	1469806	NA	amidohydrolase family protein	-0.247225636	0.169884599	-0.637683533	9.4038E-06	-0.637683533	9.4038E-06
1504	W903_RS07490	W903_1530	1470101	1470985	NA	bacterial regulatory helix-turn-helix , lysR family protein	-0.594126369	0.000589242	2.263310676	6.06078E-36	2.263310676	6.06078E-36
1505	NA	W903_1531	1471142	1471399	NA	hypothetical protein	-0.792659685	NA	2.05137614	0.173092651	2.05137614	0.173092651
1506	W903_RS07500	W903_1532	1471428	1473143	pabB	aminodeoxychorismate synthase, component I	-0.19522404	0.272689622	-0.043137956	0.705204536	-0.043137956	0.705204536
1507	W903_RS07505	W903_1533	1473225	1475666	NA	ftsK/SpoIIIE family protein	0.264529194	0.099359894	-0.814209374	2.17307E-14	-0.814209374	2.17307E-14
1508	W903_RS07510	W903_1534	1475841	1476644	NA	cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD family protein	-0.791990317	6.03427E-06	-1.410193394	7.38353E-34	-1.410193394	7.38353E-34
1509	W903_RS07515	W903_1535	1476696	1477529	NA	fecCD transport family protein	-0.760484963	5.03682E-05	-2.183815241	6.92982E-35	-2.183815241	6.92982E-35
1510	W903_RS07520	W903_1536	1477531	1478247	NA	ABC transporter family protein	-0.767487394	3.14237E-05	-2.225432082	8.62241E-52	-2.225432082	8.62241E-52
1511	W903_RS07525	W903_1537	1478418	1479344	fimA	manganese ABC transporter substrate-binding lipoprotein	-1.466350234	1.1629E-19	-2.960544957	1.9021E-146	-2.960544957	1.9021E-146
1512	W903_RS07530	W903_1538	1479511	1480158	scaR	metalloregulator ScaR	-0.686806594	8.68469E-05	-0.060465832	0.588788665	-0.060465832	0.588788665
1513	W903_RS07535	W903_1539	1480198	1480887	mtnN	MTA/SAH nucleosidase	0.579582402	0.000350848	-0.232405192	0.020187344	-0.232405192	0.020187344
1514	W903_RS07540	W903_1540	1480897	1481166	NA	putative foldase protein PrsA	0.543767068	0.008170216	-0.452048725	0.000833946	-0.452048725	0.000833946
1515	W903_RS07545	W903_1541	1481166	1481720	NA	NUDIX domain protein	0.5546231	0.000383195	-0.513320325	9.4038E-06	-0.513320325	9.4038E-06
1516	W903_RS07550	W903_1542	1481741	1483120	glmU	UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase	0.231117109	0.17915471	-0.652526335	6.42432E-11	-0.652526335	6.42432E-11
1517	W903_RS07555	W903_1543	1483364	1483777	NA	3-demethylubiquinone-9 3-methyltransferase family protein	0.324274203	0.370786992	0.926448307	1.47288E-06	0.926448307	1.47288E-06

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1518	NA	W903_1544	1483790	1483975	NA	putative lactoylglutathione lyase	-0.257601515	0.589651879	0.771380501	0.006479785	0.771380501	0.006479785
1519	W903_RS07565	W903_1545	1484256	1485212	NA	oxidoreductase , NAD-binding Rossmann fold family protein	-0.091371574	0.627955026	-0.085951182	0.57055785	-0.085951182	0.57055785
1520	W903_RS07570	W903_1546	1485209	1485661	NA	ASCH domain protein	-0.313987162	0.095763598	-0.118442761	0.433635575	-0.118442761	0.433635575
1521	W903_RS07575	W903_1547	1485658	1485903	NA	hypothetical protein	0.306151477	0.150272362	0.276635989	0.09618279	0.276635989	0.09618279
1522	W903_RS07580	W903_1548	1485900	1486598	NA	short chain dehydrogenase family protein	0.356176686	0.065019973	0.206541357	0.150324397	0.206541357	0.150324397
1523	W903_RS07585	W903_1549	1486591	1486827	NA	hypothetical protein	0.522635234	0.070688377	0.25261522	0.329723128	0.25261522	0.329723128
1524	W903_RS07590	W903_1550	1486917	1487093	NA	putative ybaK/prolyl-tRNA synthetase associated domain-containing protein	-0.283133381	0.244713212	-0.401437743	0.008198443	-0.401437743	0.008198443
1525	W903_RS07595	W903_1551	1487329	1487862	NA	acetyltransferase family protein	-0.273918839	0.388160613	-0.267214213	0.280364998	-0.267214213	0.280364998
1526	W903_RS07600	W903_1552	1488107	1489519	NA	glycosyl transferase 2 family protein	-0.424766212	0.006621952	-1.251536564	7.30628E-30	-1.251536564	7.30628E-30
1527	W903_RS07605	W903_1553	1489659	1491818	NA	hypothetical protein	-0.373340414	0.038740238	-1.214808822	2.70511E-33	-1.214808822	2.70511E-33
1528	W903_RS07610	W903_1554	1491825	1493102	NA	cotH family protein	-0.578803539	0.001041071	-1.13155417	1.49653E-30	-1.13155417	1.49653E-30
1529	W903_RS07615	W903_1555	1493263	1493940	NA	hypothetical protein	-0.890701892	1.03979E-07	-0.967957117	4.03151E-18	-0.967957117	4.03151E-18
1530	W903_RS07620	W903_1556	1493991	1494602	NA	VTC domain protein	-1.362235318	5.1369E-16	-0.004024393	0.978444394	-0.004024393	0.978444394
1531	W903_RS07625	W903_1557	1495052	1496389	NA	branched-chain amino acid transport system II carrier protein	-0.081376119	0.795848747	0.508468125	0.001960237	0.508468125	0.001960237
1532	W903_RS07630	W903_1558	1496585	1498582	metG	methionine--tRNA ligase	-0.036185183	0.842711997	-1.169243024	2.9256E-32	-1.169243024	2.9256E-32
1533	W903_RS07635	W903_1559	1498725	1499600	tehB	tellurite resistance protein TehB	0.328262077	0.071814014	0.201065019	0.121134866	0.201065019	0.121134866
1534	W903_RS07640	W903_1560	1499758	1500453	NA	hypothetical protein	-1.136612121	7.02613E-05	0.272377572	0.173092651	0.272377572	0.173092651
1535	W903_RS07645	W903_1561	1500789	1502006	NA	phosphotransferase system, EIIC family protein	0.487245433	0.007128116	0.803954377	2.35636E-18	0.803954377	2.35636E-18
1536	W903_RS07650	W903_1562	1501990	1502832	NA	hypothetical protein	1.117049844	5.29956E-10	1.373468754	2.70456E-44	1.373468754	2.70456E-44
1537	W903_RS07655	W903_1563	1502909	1503736	NA	exodeoxyribonuclease III family protein	0.530013472	0.002541416	0.80738119	1.69708E-13	0.80738119	1.69708E-13
1538	W903_RS07660	W903_1564	1503778	1504134	NA	putative arsenate reductase	0.091725905	0.78773361	0.157464472	0.449901665	0.157464472	0.449901665
1539	W903_RS07665	W903_1565	1504136	1504612	NA	methylated-DNA-[]-cysteine S-methyltransferase family protein	0.174550969	0.392991647	0.602078433	4.11763E-07	0.602078433	4.11763E-07
1540	W903_RS07670	W903_1566	1504668	1505849	NA	ACT domain protein	0.136885903	0.572454169	-1.760161113	2.7229E-83	-1.760161113	2.7229E-83
1541	W903_RS07675	W903_1567	1505912	1506460	NA	acetyltransferase, GNAT family	-0.145461667	0.598058959	-2.153080516	3.6168E-120	-2.153080516	3.6168E-120
1542	W903_RS07680	W903_1568	1506528	1507619	serC	phosphoserine transaminase	0.25304901	0.332406371	-2.091791196	2.0695E-121	-2.091791196	2.0695E-121
1543	W903_RS07685	W903_1569	1507752	1508387	NA	cutC-like protein	-0.61335632	0.000486794	0.514196394	0.000145166	0.514196394	0.000145166
1544	W903_RS07690	W903_1570	1508656	1509519	NA	tetrapyrrole (Corrin/Porphyrin) Methylases family protein	-0.605646639	5.88535E-05	-0.211210528	0.04397493	-0.211210528	0.04397493
1545	W903_RS07695	W903_1571	1509525	1509851	NA	hypothetical protein	-1.484304593	4.55491E-26	-0.891051679	1.45923E-10	-0.891051679	1.45923E-10
1546	W903_RS07700	W903_1572	1509882	1510745	NA	DNA polymerase III, delta subunit	-0.726367572	5.28589E-07	-0.571926811	1.47859E-08	-0.571926811	1.47859E-08
1547	W903_RS07705	W903_1573	1510765	1511400	tmk	thymidylate kinase	-0.669798815	5.38044E-06	0.03298252	0.805210061	0.03298252	0.805210061
1548	W903_RS07710	W903_1574	1511489	1512148	NA	CBS domain protein	0.596624575	0.324446752	0.109632238	0.789706167	0.109632238	0.789706167
1549	W903_RS07715	W903_1575	1512167	1512877	NA	ABC transporter family protein	0.161571638	0.78773361	0.380384798	0.28297559	0.380384798	0.28297559
1550	W903_RS07720	W903_1576	1512877	1513641	NA	ABC transporter family protein	0.521193052	0.409695168	1.092051177	0.009164051	1.092051177	0.009164051
1551	W903_RS07725	W903_1577	1513642	1514595	NA	branched-chain amino acid transport system / permease component family protein	0.86243753	0.157715534	0.542924273	0.18028891	0.542924273	0.18028891
1552	W903_RS07730	W903_1578	1514598	1515467	NA	branched-chain amino acid transport system / permease component family protein	0.539545641	0.482215313	0.865318311	0.05529493	0.865318311	0.05529493
1553	W903_RS07735	W903_1579	1515575	1516741	NA	receptor ligand binding region family protein	-0.183996811	0.642192846	-0.627935632	0.038074983	-0.627935632	0.038074983
1554	W903_RS07740	W903_1580	1516897	1517142	NA	hypothetical protein	-1.956962722	1.10492E-11	-0.524028485	0.098484959	-0.524028485	0.098484959
1555	W903_RS07745	W903_1581	1517242	1517832	clpP	ATP-dependent Clp protease proteolytic subunit	-0.0669727	0.734062253	-0.124502682	0.219762312	-0.124502682	0.219762312
1556	W903_RS07750	W903_1582	1517957	1518586	upp	uracil phosphoribosyltransferase	-0.912166887	2.68394E-09	-1.986976127	8.43205E-92	-1.986976127	8.43205E-92
1557	W903_RS07755	W903_1583	1518696	1519865	NA	putative beta-cystathionase	0.102053809	0.665634427	0.151514323	0.194418772	0.151514323	0.194418772
1558	W903_RS07760	W903_1584	1520000	1520548	NA	putative tRNA (cytidine/uridine-2'-O-)-methyltransferase	-1.229731999	9.39152E-12	-0.426349547	0.000974329	-0.426349547	0.000974329
1559	W903_RS07765	W903_1585	1520721	1522073	NA	amino acid permease family protein	-0.768436618	3.31367E-06	-0.382048348	0.000575682	-0.382048348	0.000575682
1560	W903_RS07770	W903_1586	1522279	1523628	NA	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	0.704267163	2.20021E-06	1.153178235	1.66335E-23	1.153178235	1.66335E-23
1561	W903_RS07775	W903_1587	1523645	1525072	NA	cation transport family protein	0.733631642	1.56293E-06	0.651419608	1.35758E-10	0.651419608	1.35758E-10
1562	W903_RS07780	W903_1588	1525096	1525347	NA	putative membrane protein insertion efficiency factor	0.605144524	0.251844765	-0.029066168	0.943692261	-0.029066168	0.943692261
1563	W903_RS07785	W903_1589	1525347	1526069	NA	pseudouridine synthase family protein	-0.050769837	0.795622196	-0.318217676	0.007747297	-0.318217676	0.007747297
1564	W903_RS07790	W903_1590	1526059	1526643	scpB	segregation and condensation protein B	-0.063099885	0.734062253	0.046632446	0.73319654	0.046632446	0.73319654
1565	W903_RS07795	W903_1591	1526640	1527347	NA	scpA/B family protein	-0.116139405	0.549948356	-0.061508903	0.629127772	-0.061508903	0.629127772
1566	NA	W903_1592	1527347	1527793	NA	phage integrase family protein	0.090546769	0.658733956	0.155491743	0.162873965	0.155491743	0.162873965
1567	W903_RS07805	W903_1593	1528077	1528550	NA	CBS domain protein	0.257240403	0.137687003	0.045358237	0.715229253	0.045358237	0.715229253
1568	W903_RS07810	W903_1594	1528547	1529068	NA	phosphodiesterase, MJ0936 family protein	0.241043548	0.179534464	0.027066746	0.866466723	0.027066746	0.866466723
1569	W903_RS07815	W903_1595	1529050	1530024	rdgB	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	0.258626909	0.123738284	0.077402623	0.533125342	0.077402623	0.533125342
1570	W903_RS07820	W903_1596	1530021	1530815	murI	glutamate racemase	0.258146556	0.129946656	-0.334924173	0.002236428	0.334924173	0.002236428
1571	W903_RS07825	W903_1597	1530990	1531229	NA	hypothetical protein	-0.557995488	0.000751358	-0.029653654	0.832864156	-0.029653654	0.832864156
1572	W903_RS07830	W903_1598	1531387	1531929	NA	putative membrane protein	-0.970406436	0.010713828	-0.747686854	0.009454176	-0.747686854	0.009454176
1573	W903_RS07835	W903_1599	1531991	1532512	nadR	transcription repressor NadR	0.06162763	0.816605926	-0.251570638	0.075482189	-0.251570638	0.075482189
1574	W903_RS07840	W903_1600	1532580	1533269	NA	inhibitor of apoptosis-promoting Bax1 family protein	0.236403242	0.157666073	0.121572636	0.427621248	0.121572636	0.427621248
1575	W903_RS07845	W903_1601	1533292	1533795	NA	hypothetical protein	0.515120032	0.001094055	0.195563364	0.041109007	0.195563364	0.041109007
1576	W903_RS07850	W903_1602	1533833	1534576	NA	RNA 2'-O ribose methyltransferase substrate binding family protein	0.426162783	0.006387938	0.314831947	0.0067343	0.314831947	0.0067343
1577	W903_RS07855	W903_1603	1534608	1534886	NA	acylphosphatase family protein	-0.054900269	0.823792061	-0.732072257	7.10507E-07	-0.732072257	7.10507E-07
1578	W903_RS07860	W903_1604	1534971	1535903	NA	membrane insertase, YidC/Oxa1 family domain protein	-0.014905601	0.933659036	-0.782257429	8.14824E-15	-0.782257429	8.14824E-15
1579	W903_RS07865	W903_1605	1536103	1536768	NA	amino ABC transporter, permease , 3-TM region, His/Glu/Gln/Arg/opine family domain protein	0.597966817	0.001470233	1.272259854	1.38725E-17	1.272259854	1.38725E-17
1580	W903_RS07870	W903_1606	1536792	1537649	NA	putative ABC transporter extracellular-binding protein yckB	0.213241502	0.306567098	2.168994875	1.58908E-71	2.168994875	1.58908E-71
1581	W903_RS07875	W903_1607	1537810	1539270	NA	amidase family protein	0.122852683	0.535771604	-0.32355636	0.039786013	-0.32355636	0.039786013
1582	W903_RS07880	W903_1608	1539373	1539855	greA	transcription elongation factor GreA domain protein	-1.180109613	1.27264E-11	-1.641226254	1.22595E-65	-1.641226254	1.22595E-65
1583	W903_RS07885	W903_1609	1539928	1541730	NA	yceG-like family protein	-0.610170692	2.30894E-05	-0.890979987	3.63526E-25	-0.890979987	3.63526E-25
1584	W903_RS07890	W903_1610	1541817	1542320	NA	acetyltransferase family protein	-0.129094875	0.506982826	-0.801390861	5.02282E-15	-0.801390861	5.02282E-15
1585	W903_RS07895	W903_1611	1542406	1543737	murC	UDP-N-acetylmuramate--alanine ligase	-0.263224996	0.099516955	-0.854411244	1.03001E-19	-0.854411244	1.03001E-19
1586	W903_RS07900	W903_1612	1543747	1544364	NA	hypothetical protein	-0.431132746	0.010493967	0.06683623	0.549881366	0.06683623	0.549881366
1587	W903_RS07905	W903_1613	1544529	1547627	NA	helicase domain protein	0.072336702	0.719967852	0.852476158	1.40209E-20	0.852476158	1.40209E-20
1588	W903_RS07910	W903_1614	1547782	1549092	engA	ribosome-associated GTPase EngA	0.510475203	0.000987298	-0.023774962	0.818696636	-0.023774962	0.818696636
1589	W903_RS07915	W903_1615	1549140	1550042	NA	istB-like ATP binding family protein	0.263313194	0.126321509	0.207123226	0.033305523	0.207123226	0.033305523
1590	W903_RS07920	W903_1616	1550039	1551214	NA	replication initiation and membrane attachment family protein	-0.049349668	0.798455981	0.107160882	0.411968516	0.107160882	0.411968516
1591	W903_RS07925	W903_1617	1551214	1551693	nrdR	transcriptional regulator NrdR	-0.307328483	0.127010881	0.249041499	0.046610215	0.249041499	0.046610215
1592	W903_RS07930	W903_1618	1551842	1553347	NA	HAMP domain protein	0.114572055	0.534615849	0.644651706	2.20999E-05	0.644651706	2.20999E-05
1593	W903_RS07935	W903_1619	1553337	1554026	NA	putative transcriptional activator CadC	0.226400528	0.223189077	-0.764050538	1.08171E-16	-0.764050538	1.08171E-16
1594	W903_RS07940	W903_1620	1554262	1554795	NA	hypothetical protein	-0.048833789	0.789718528	-1.066079948	1.844E-22	-1.066079948	1.844E-22
1595	W903_RS07945	W903_1621	1554900	1555790	NA	peptidase M48 family protein	0.090845442	0.61223294	-0.707341629	5.01091E-13	-0.707341629	5.01091E-13
1596	W903_RS07950	W903_1622	1555811	1556365	NA	lemA family protein	-0.093621661	0.64576643	-1.417755589	1.34829E-47	-1.417755589	1.34829E-47
1597	W903_RS07955	W903_1623	1556493	1557206	gidB	16S rRNA (guanine(527)-N(7))-methyltransferase GidB	0.624041052	0.000275248	-0.055951301	0.667464794	-0.055951301	0.667464794
1598	W903_RS07960	W903_1624	1557221	1558600	NA	cation transport family protein	0.874782077	1.22964E-09	-0.079019465	0.430105865	-0.079019465	0.430105865
1599	W903_RS07965	W903_1625	1558613	1559284	NA	oxidoreductase , NAD-binding Rossmann fold family protein	1.082631017	9.48589E-12	-0.197069029	0.102643961	-0.197069029	0.102643961
1600	W903_RS07970	W903_1626	1559319	1560149	NA	cobalt transport family protein	-0.458889039	0.038510502	-0.631935365	1.00107E-08	-0.631935365	1.00107E-08
1601	W903_RS07975	W903_1627	1560142	1561818	NA	heme ABC exporter, ATP-binding protein CcmA	-0.322211683	0.122332628	-0.463487593	2.23876E-06	-0.463487593	2.23876E-06
1602	W903_RS07980	W903_1628	1561835	1562383	NA	ECF-type riboflavin transporter, S component family protein	-0.792672219	1.4832E-05	-0.376253676	0.000437181	-0.376253676	0.000437181
1603	W903_RS07985	W903_1629	1562552	1563760	NA	dicarboxylate symporter family protein	-0.150639234	0.38120064	0.102741555	0.373490113	0.102741555	0.373490113
1604	W903_RS07990	W903_1630	1563936	1565303	NA	branched-chain amino acid transport system II carrier protein	0.080368509	0.664768671	-1.563948653	3.50548E-13	-1.563948653	3.50548E-13
1605	W903_RS07995	W903_1631	1565417	1566472	NA	zinc-binding dehydrogenase family protein	-0.428968291	0.00897114	-0.064962311	0.686314149	-0.064962311	0.686314149
1606	W903_RS08000	W903_1632	1566521	1567213	NA	binding--dependent transport system inner membrane component family protein	0.408360774	0.029988359	-0.803080121	3.4262E-09	-0.803080121	3.4262E-09
1607	W903_RS08005	W903_1633	1567210	1568280	NA	ABC transporter family protein	-0.071717021	0.717464977	-1.016524617	4.76227E-25	-1.016524617	4.76227E-25
1608	W903_RS08010	W903_1634	1568273	1569649	NA	peptidase M20/M25/M40 family protein	-0.506646448	0.001518599	-0.9503528	6.27566E-16	-0.9503528	6.27566E-16
1609	W903_RS08015	W903_1635	1569783	1570607	NA	NLPA lipofamily protein	-1.034842418	4.51584E-11	-2.153908117	1.16915E-92	-2.153908117	1.16915E-92
1610	W903_RS08020	W903_1636	1570748	1571581	NA	bacterial extracellular solute-binding s, 3 family protein	-0.72647848	2.38556E-06	-1.336312988	8.47636E-32	-1.336312988	8.47636E-32
1611	W903_RS08025	W903_1637	1571683	1572372	NA	glutamine amidotransferase class-I family protein	-1.090098113	5.84055E-11	-0.857684313	7.80248E-09	-0.857684313	7.80248E-09
1612	W903_RS08030	W903_1638	1572527	1573243	NA	hypothetical protein	-0.867354705	3.31822E-07	-0.619199588	2.50785E-08	-0.619199588	2.50785E-08
1613	W903_RS08035	W903_1639	1573361	1574347	NA	putative dihydroxyacetone kinase DhaK1b subunit	0.107649368	0.631284966	0.514950067	1.64178E-05	0.514950067	1.64178E-05
1614	W903_RS08040	W903_1640	1574357	1574893	dhaS	HTH-type dhaKLM operon transcriptional activator dhaS	-0.793908664	0.030430284	0.08177946	0.803556471	0.08177946	0.803556471
1615	W903_RS08045	W903_1641	1575067	1576056	dhaK	dihydroxyacetone kinase, DhaK subunit	-0.191786197	0.366086675	-0.684561723	2.41817E-10	-0.684561723	2.41817E-10
1616	W903_RS08050	W903_1642	1576094	1576672	dhaL	dihydroxyacetone kinase, L subunit	0.922864853	8.46431E-08	1.921138118	2.70581E-39	1.921138118	2.70581E-39
1617	W903_RS08055	W903_1643	1576672	1577046	dhaM	PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit dhaM	0.450765041	0.022280295	1.447891591	3.71227E-28	1.447891591	3.71227E-28
1618	W903_RS08060	W903_1644	1577056	1577769	NA	MIP channel s family protein	0.999401842	1.06098E-06	2.039148341	2.71301E-56	2.039148341	2.71301E-56
1619	W903_RS08065	W903_1645	1578034	1578438	NA	cupin domain protein	0.140410552	0.47998015	0.267030548	0.015128732	0.267030548	0.015128732
1620	W903_RS08070	W903_1646	1578577	1579290	NA	merR regulatory family protein	-0.532194715	0.011222826	-0.614706025	4.79752E-05	-0.614706025	4.79752E-05
1621	W903_RS08075	W903_1647	1579383	1580492	NA	HIGH Nucleotidyl Transferase family protein	-0.337337221	0.073842666	-0.516089681	0.001026254	-0.516089681	0.001026254
1622	W903_RS08080	W903_1648	1580489	1580740	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.428426783	0.08993515	-0.295502395	0.182676067	-0.295502395	0.182676067
1623	W903_RS08085	W903_1649	1580763	1581497	NA	ubiE/COQ5 methyltransferase family protein	-0.354768778	0.075629973	-0.664402708	0.001543421	-0.664402708	0.001543421
1624	W903_RS08090	W903_1650	1581563	1581919	NA	oligomerization domain protein	0.331844509	0.107167871	-0.216554995	0.112075635	-0.216554995	0.112075635
1625	W903_RS08095	W903_1651	1581921	1582442	NA	isochorismatase family protein	-0.684973593	6.78746E-05	-0.82010594	6.16998E-17	-0.82010594	6.16998E-17
1626	W903_RS08100	W903_1652	1582505	1583092	NA	HD domain protein	0.086308202	0.705155762	-0.305310928	0.006665851	-0.305310928	0.006665851
1627	W903_RS08105	W903_1653	1583089	1583721	nadD	nicotinate (nicotinamide) nucleotide adenylyltransferase	-0.148864183	0.441516503	-0.423804966	7.61299E-05	-0.423804966	7.61299E-05
1628	W903_RS08110	W903_1654	1583851	1584168	NA	CRS1 / YhbY domain protein	-0.385048162	0.044216917	-0.484178516	0.000864787	-0.484178516	0.000864787
1629	W903_RS08115	W903_1655	1584261	1585379	yqeH	ribosome biogenesis GTPase YqeH	-0.119190405	0.561356379	-0.037710223	0.7803261	-0.037710223	0.7803261
1630	W903_RS08120	W903_1656	1585379	1585906	NA	HAD hydrolase, family IIIA domain protein	-0.519334558	0.01804916	0.49790082	0.005810612	0.49790082	0.005810612
1631	W903_RS08125	W903_1657	1586023	1586937	NA	eamA-like transporter family protein	0.431252506	0.020169789	-0.385728215	0.008164277	-0.385728215	0.008164277
1632	W903_RS08130	W903_1658	1587067	1588509	gatB	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit	-0.058949871	0.74077786	-0.879460594	1.61089E-17	-0.879460594	1.61089E-17
1633	W903_RS08135	W903_1659	1588509	1589975	gatA	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, A subunit	-0.043992114	0.802690043	-0.91415112	2.8338E-25	-0.91415112	2.8338E-25
1634	W903_RS08140	W903_1660	1589975	1590277	gatC	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, C subunit	0.236940127	0.149701198	-0.445749137	0.000169103	-0.445749137	0.000169103
1635	W903_RS08145	W903_1661	1590415	1593060	ppdK	pyruvate, phosphate dikinase	0.450989315	0.018088852	1.05559725	1.12079E-18	1.05559725	1.12079E-18
1636	W903_RS08150	W903_1662	1593073	1593903	NA	putative phosphotransferase yqfL	-0.233232928	0.354583094	0.377117989	0.007874373	0.377117989	0.007874373
1637	W903_RS08155	W903_1663	1593914	1594411	NA	CBS domain protein	0.043404535	0.863740633	0.512029911	0.001702434	0.512029911	0.001702434
1638	W903_RS08160	W903_1664	1594732	1595697	NA	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	-0.361047051	0.086603111	2.114170025	2.5675E-61	2.114170025	2.5675E-61
1639	W903_RS08165	W903_1665	1595744	1596292	NA	isochorismatase family protein	0.533994689	0.002467358	-1.349400379	1.09941E-30	-1.349400379	1.09941E-30
1640	W903_RS08170	W903_1666	1596359	1597144	codY	GTP-sensing transcriptional pleiotropic repressor CodY	-0.338329503	0.026138651	-2.048935546	1.6998E-103	-2.048935546	1.6998E-103
1641	W903_RS08175	W903_1667	1597270	1598481	NA	aminotransferase class-V family protein	0.606537621	0.000187386	-1.083511983	5.36243E-22	-1.083511983	5.36243E-22
1642	W903_RS08180	W903_1668	1598748	1599200	NA	universal stress family protein	-0.553441596	0.002150964	0.823880827	2.7804E-12	0.823880827	2.7804E-12
1643	W903_RS08185	W903_1669	1599256	1600638	NA	cof-like hydrolase family protein	-0.407676918	0.031816433	-0.173232458	0.121735888	-0.173232458	0.121735888
1644	W903_RS08190	W903_1670	1600707	1601669	NA	asparaginase family protein	0.746829686	3.70455E-05	-0.194018089	0.220452171	-0.194018089	0.220452171
1645	W903_RS08195	W903_1671	1601704	1602582	aroE	shikimate 5-dehydrogenase	-0.172686779	0.437073844	-1.274970377	1.01929E-24	-1.274970377	1.01929E-24
1646	W903_RS08200	W903_1672	1602680	1603594	NA	aldo/keto reductase family protein	0.316576187	0.106581382	-0.99604639	9.41742E-14	-0.99604639	9.41742E-14
1647	W903_RS08205	W903_1673	1603885	1605900	recG	ATP-dependent DNA helicase RecG	0.291482664	0.083297881	0.340344434	0.001101518	0.340344434	0.001101518
1648	W903_RS08210	W903_1674	1605980	1607518	NA	mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein	0.422520404	0.007484845	-0.527263253	2.79047E-09	-0.527263253	2.79047E-09
1649	W903_RS08215	W903_1675	1607611	1608711	alr	alanine racemase	0.277316952	0.181018251	-0.010833093	0.941876554	-0.010833093	0.941876554
1650	W903_RS08220	W903_1676	1608708	1609067	acpS	holo-[acyl-carrier-protein] synthase	0.752043287	0.000156836	0.159927324	0.224934497	0.159927324	0.224934497
1651	W903_RS08225	W903_1677	1609092	1610099	NA	3-deoxy-7-phosphoheptulonate synthase	0.177028982	0.409695168	-0.0375122	0.809786215	-0.0375122	0.809786215
1652	W903_RS08230	W903_1678	1610225	1612753	secA	preprotein translocase, SecA subunit	-0.225012032	0.146022994	-0.936604963	1.24855E-21	-0.936604963	1.24855E-21
1653	W903_RS08235	W903_1679	1612862	1613809	manA	mannose-6-phosphate isomerase, class I	-0.321063012	0.107454755	-0.888280888	5.88431E-20	-0.888280888	5.88431E-20
1654	W903_RS08240	W903_1680	1613927	1614808	NA	ROK family protein	-0.180403659	0.402234902	-0.617218321	0.000454839	-0.617218321	0.000454839
1655	W903_RS08245	W903_1681	1614876	1616795	NA	PTS system, sucrose-specific IIBC component	0.033567387	0.851542185	-1.799433745	2.25867E-44	-1.799433745	2.25867E-44

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1656	W903_RS08250	W903_1682	1616980	1618419	NA	sucrose-6-phosphate hydrolase family protein	0.456048091	0.003498671	-0.169914789	0.145407556	-0.169914789	0.145407556
1657	W903_RS08255	W903_1683	1618421	1619383	NA	helix-turn-helix family protein	0.245743107	0.165272261	-0.353347171	0.001702434	-0.353347171	0.001702434
1658	W903_RS08260	W903_1684	1619470	1619904	nusB	transcription antitermination factor NusB	-0.94956815	1.80137E-09	-1.736868894	8.48765E-66	-1.736868894	8.48765E-66
1659	W903_RS08265	W903_1685	1619897	1620286	NA	hypothetical protein	-1.067868252	7.61316E-14	-1.844933477	2.96241E-66	-1.844933477	2.96241E-66
1660	W903_RS08270	W903_1686	1620375	1620935	efp	translation elongation factor P	-1.205057963	2.95699E-17	-1.886278289	2.54715E-87	-1.886278289	2.54715E-87
1661	NA	W903_1687	1620966	1621082	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.040417287	0.914541872	1.471104076	1.92833E-14	1.471104076	1.92833E-14
1662	NA	W903_1688	1621664	1621804	NA	hypothetical protein	0.237857486	0.299845493	1.568080412	3.60909E-41	1.568080412	3.60909E-41
1663	W903_RS10500	W903_1689	1622455	1622820	NA	hypothetical protein	-1.392591364	5.76347E-07	0.309394394	0.199593713	0.309394394	0.199593713
1664	NA	W903_1690	1622833	1623003	NA	glycerophosphoryl diester phosphodiesterase family protein	0.07228399	0.834002409	0.786482153	0.000104928	0.786482153	0.000104928
1665	W903_RS08280	W903_1691	1623016	1623456	NA	hypothetical protein	-1.188841321	0.000252682	0.32902453	0.332527466	0.32902453	0.332527466
1666	W903_RS10510	W903_1692	1623593	1623715	NA	hypothetical protein	-0.335707993	0.180011398	0.47922254	0.001399302	0.47922254	0.001399302
1667	W903_RS08285	W903_1693	1624058	1624510	NA	cytidine and deoxycytidylate deaminase zinc-binding region family protein	0.228866585	0.277470661	0.382919959	0.000470333	0.382919959	0.000470333
1668	W903_RS08290	W903_1694	1624522	1625589	pepP	aminopeptidase P	0.125454143	0.500410795	0.090120412	0.372042982	0.090120412	0.372042982
1669	W903_RS08295	W903_1695	1625689	1626405	NA	hypothetical protein	0.187754774	0.494912393	2.356565611	1.0553E-101	2.356565611	1.0553E-101
1670	W903_RS08300	W903_1696	1626407	1627906	NA	H+ antiporter-2 family protein	0.841831808	2.0698E-06	2.952354868	1.8631E-212	2.952354868	1.8631E-212
1671	NA	W903_1697	1627994	1628110	NA	hypothetical protein	-0.064920286	0.864846675	3.342082774	4.139E-102	3.342082774	4.139E-102
1672	W903_RS08305	W903_1698	1628242	1631070	uvrA	excinuclease ABC subunit A	1.118089741	5.78596E-14	0.495367346	2.08816E-07	0.495367346	2.08816E-07
1673	W903_RS08310	W903_1699	1631202	1631873	NA	hypothetical protein	-0.018058289	0.934706308	-0.902314724	2.11074E-16	-0.902314724	2.11074E-16
1674	W903_RS08315	W903_1700	1631898	1632842	NA	corA-like Mg2+ transporter family protein	-0.090695241	0.702717756	-0.637683611	8.56274E-08	-0.637683611	8.56274E-08
1675	W903_RS08320	W903_1701	1633012	1633251	rpsR	ribosomal protein S18	-1.034511286	2.00645E-10	-3.355785491	1.213E-160	-3.355785491	1.213E-160
1676	W903_RS08325	W903_1702	1633296	1633787	NA	single-stranded DNA-binding family protein	-1.299281718	2.91549E-15	-3.274456858	1.9738E-229	-3.274456858	1.9738E-229
1677	W903_RS08330	W903_1703	1633799	1634086	rpsF	ribosomal protein S6	-1.6598835	1.45243E-24	-3.395225719	1.1708E-193	-3.395225719	1.1708E-193
1678	W903_RS08335	W903_1704	1635149	1636303	mutY	A/G-specific adenine glycosylase	0.496727159	0.003153271	0.901639141	6.42436E-16	0.901639141	6.42436E-16
1679	W903_RS08340	W903_1705	1636480	1637073	NA	helix-turn-helix family protein	0.024261442	0.922793656	0.418416837	0.007236236	0.418416837	0.007236236
1680	W903_RS08345	W903_1706	1637119	1637433	trxA	thioredoxin	-0.305588838	0.085081391	-0.521124961	1.40947E-05	-0.521124961	1.40947E-05
1681	W903_RS08350	W903_1707	1637514	1638014	NA	PAP2 superfamily protein	0.062787814	0.746248871	-0.375542218	0.001038634	-0.375542218	0.001038634
1682	W903_RS08355	W903_1708	1638018	1640357	NA	mutS2 family protein	0.298806033	0.055319871	-0.396183666	2.17646E-05	-0.396183666	2.17646E-05
1683	W903_RS08360	W903_1709	1640442	1640984	NA	colicin V production family protein	-0.437535937	0.056189077	0.397960952	0.011548615	0.397960952	0.011548615
1684	W903_RS08365	W903_1710	1640987	1641298	NA	putative cell division protein ZapA	-0.914400992	1.12186E-06	0.619325284	6.31891E-07	0.619325284	6.31891E-07
1685	W903_RS08370	W903_1711	1641424	1642302	rnhC	ribonuclease HIII	-0.226740455	0.183867077	-0.165891009	0.132142401	-0.165891009	0.132142401
1686	W903_RS08375	W903_1712	1642318	1642911	NA	signal peptidase I	-0.043703803	0.82365983	-0.672032012	2.10054E-08	-0.672032012	2.10054E-08
1687	W903_RS08380	W903_1713	1643040	1645460	NA	viral (Super1) RNA helicase family protein	0.148092762	0.529715837	-0.093886011	0.353519471	-0.093886011	0.353519471
1688	W903_RS08385	W903_1714	1645574	1646056	NA	putative membrane protein	-0.032209201	0.876832988	-0.984721966	2.38776E-11	-0.984721966	2.38776E-11
1689	W903_RS08390	W903_1715	1646127	1647221	NA	impB/mucB/samB family protein	-0.187801941	0.346377236	0.642274233	5.54563E-09	0.642274233	5.54563E-09
1690	W903_RS08395	W903_1716	1647406	1649718	pflB	formate acetyltransferase	0.066757232	0.734621538	-0.368353614	0.000119118	-0.368353614	0.000119118
1691	W903_RS08400	W903_1717	1649819	1650193	NA	FMN-binding protein	1.087214858	0.000598806	0.336647545	0.083914006	0.336647545	0.083914006
1692	W903_RS08405	W903_1718	1650228	1651157	NA	beta-lactamase family protein	-0.190636157	0.316474166	0.234324978	0.144823595	0.234324978	0.144823595
1693	W903_RS08410	W903_1719	1651154	1651909	cppA	C3-degrading proteinase	-0.39353164	0.034343288	0.525403061	1.26896E-05	0.525403061	1.26896E-05
1694	W903_RS08415	W903_1720	1652034	1652930	NA	sulfite exporter TauE/SafE family protein	-0.320964442	0.071230182	-0.370978854	0.002913308	-0.370978854	0.002913308
1695	W903_RS08420	W903_1721	1653008	1653835	gla	glycerol facilitator-aquaporin gla	-0.398753891	0.021467784	-1.830409754	9.10951E-89	-1.830409754	9.10951E-89
1696	W903_RS08425	W903_1722	1654025	1654477	NA	universal stress family protein	1.193577739	8.99585E-08	-0.951818699	1.82646E-22	-0.951818699	1.82646E-22
1697	W903_RS08430	W903_1723	1654495	1655697	NA	sugar (and other) transporter family protein	-0.109093243	0.549536178	-2.038037572	7.56677E-85	-2.038037572	7.56677E-85
1698	W903_RS08435	W903_1724	1655853	1656512	NA	crp-like helix-turn-helix domain protein	-0.03980127	0.842711997	-0.130250416	0.457950226	-0.130250416	0.457950226
1699	W903_RS08440	W903_1725	1656536	1658821	pepX	xaa-Pro dipeptidyl-peptidase	0.175694371	0.302225232	-0.450326404	1.26448E-05	-0.450326404	1.26448E-05
1700	W903_RS08445	W903_1726	1658825	1659184	NA	hypothetical protein	-0.862482773	6.7014E-07	-1.18346694	5.00761E-21	-1.18346694	5.00761E-21
1701	W903_RS08450	W903_1727	1659230	1660210	NA	geranylgeranyl pyrophosphate synthase	0.217067731	0.205169742	1.181924403	3.03728E-24	1.181924403	3.03728E-24
1702	W903_RS08455	W903_1728	1660295	1662043	cydC	thiol reductant ABC exporter, CydC subunit	0.54093964	0.000536344	1.206275226	2.40652E-22	1.206275226	2.40652E-22
1703	W903_RS08460	W903_1729	1662036	1663754	cydD	thiol reductant ABC exporter, CydD subunit	0.585920948	0.000127171	1.519369362	2.86191E-33	1.519369362	2.86191E-33
1704	W903_RS08465	W903_1730	1663754	1664773	cydB	cytochrome d ubiquinol oxidase, subunit II	0.858998949	1.34288E-08	1.37367034	5.48649E-51	1.37367034	5.48649E-51
1705	W903_RS08470	W903_1731	1664774	1666201	NA	bacterial Cytochrome Ubiquinol Oxidase family protein	0.988831525	1.15305E-10	1.564354553	1.07232E-59	1.564354553	1.07232E-59
1706	W903_RS08475	W903_1732	1666304	1667512	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.362894971	0.025739642	1.352235775	2.38934E-51	1.352235775	2.38934E-51
1707	W903_RS08480	W903_1733	1667525	1668424	NA	ubiA prenyltransferase family protein	-0.037258108	0.842711997	1.874323182	3.99509E-80	1.874323182	3.99509E-80
1708	W903_RS08485	W903_1734	1668833	1669279	NA	hypothetical protein	0.90535041	0.82220868	5.81671E-08	0.82220868	5.81671E-08	5.81671E-08
1709	NA	W903_1735	1669893	1670039	NA	hypothetical protein	-0.364668948	0.448100444	0.92593623	0.002211472	0.92593623	0.002211472
1710	W903_RS08490	W903_1736	1670162	1670461	NA	DNA-binding protein, YbaB/EbfC family	-1.47634131	1.18012E-17	-1.360159116	1.53222E-17	-1.360159116	1.53222E-17
1711	W903_RS08495	W903_1737	1670622	1671812	NA	methyltransferase domain protein	0.443418836	0.002888992	0.118795852	0.315767408	0.118795852	0.315767408
1712	W903_RS08505	W903_1740	1672732	1673319	NA	exonuclease family protein	-0.998160611	3.74698E-07	0.718071314	4.81515E-09	0.718071314	4.81515E-09
1713	W903_RS08510	W903_1741	1673363	1673899	NA	hypothetical protein	-1.573353892	4.34334E-20	0.159403395	0.292032486	0.159403395	0.292032486
1714	W903_RS08520	W903_1744	1675250	1675906	NA	hypothetical protein	-0.000446989	0.998547303	0.428117957	0.003002164	0.428117957	0.003002164
1715	W903_RS08525	W903_1745	1676191	1676460	rpsN2	alternate 30S ribosomal protein S14	-1.198762283	1.1711E-15	-3.643587372	1.1196E-181	-3.643587372	1.1196E-181
1716	W903_RS08530	W903_1746	1676822	1677847	NA	aminotransferase class-V family protein	-0.694328079	4.19675E-05	-1.126790433	7.53933E-23	-1.126790433	7.53933E-23
1717	W903_RS08535	W903_1747	1677968	1678978	NA	tRNA threonylcarbamoyl adenosine modification protein YgjD	0.064882628	0.740170779	1.214430442	2.05027E-27	1.214430442	2.05027E-27
1718	W903_RS08540	W903_1748	1679058	1679465	rimI	ribosomal-protein-alanine acetyltransferase	-0.069942951	0.736690134	0.986263408	2.19824E-21	0.986263408	2.19824E-21
1719	W903_RS08545	W903_1749	1679467	1680156	yeaZ	tRNA threonylcarbamoyl adenosine modification protein YeaZ	-0.381913915	0.032203904	0.851507035	2.18763E-17	0.851507035	2.18763E-17
1720	W903_RS08550	W903_1750	1680338	1680568	NA	hypothetical protein	-0.511963432	0.010713828	-0.832381072	1.25276E-07	-0.832381072	1.25276E-07
1721	W903_RS08555	W903_1751	1680622	1682301	NA	putative permease	0.65980316	3.5941E-06	0.032772837	0.76682987	0.032772837	0.76682987
1722	W903_RS08560	W903_1752	1682469	1682966	NA	CHAP domain protein	-1.593140471	1.53209E-12	0.904958633	5.69726E-07	0.904958633	5.69726E-07
1723	W903_RS08565	W903_1753	1683126	1684472	glnA	glutamine synthetase, type I	-0.866579555	7.00312E-05	-0.605384517	0.000174009	-0.605384517	0.000174009
1724	W903_RS08570	W903_1754	1684506	1684877	NA	merR regulatory family protein	-1.197445062	7.23226E-09	-0.405995975	0.006700449	-0.405995975	0.006700449
1725	W903_RS08575	W903_1755	1684957	1685496	NA	hypothetical protein	-0.092701862	0.727209397	0.48606698	0.005205645	0.48606698	0.005205645
1726	W903_RS08580	W903_1756	1685759	1686955	NA	phosphoglycerate kinase family protein	0.711529679	7.31218E-07	-0.80401642	2.35508E-18	-0.80401642	2.35508E-18
1727	W903_RS08585	W903_1757	1687090	1687959	NA	5'-nucleotidase, lipoprotein e(P4) family	0.099655843	0.665634427	-0.682747364	1.91425E-05	-0.682747364	1.91425E-05
1728	W903_RS08590	W903_1758	1688168	1689178	gap	glyceraldehyde-3-phosphate dehydrogenase, type I	-0.020352785	0.903260831	-1.242269849	6.55406E-36	-1.242269849	6.55406E-36
1729	W903_RS08595	W903_1759	1689382	1691460	fusA	translation elongation factor G	0.113783152	0.497060166	-1.285292764	1.07899E-42	-1.285292764	1.07899E-42
1730	W903_RS08600	W903_1760	1691615	1692085	rpsG	ribosomal protein S7	-0.222014367	0.206759631	-1.759692822	1.42595E-81	-1.759692822	1.42595E-81
1731	W903_RS08605	W903_1761	1692107	1692520	rpsL	ribosomal protein S12	-0.333073829	0.051573608	-1.221159054	4.06291E-21	-1.221159054	4.06291E-21
1732	W903_RS08610	W903_1762	1692739	1693551	purR	pur operon repressor PurR	-0.348252729	0.023937559	-0.530814664	2.64349E-08	-0.530814664	2.64349E-08
1733	W903_RS08615	W903_1763	1693648	1694589	NA	OB-fold nucleic acid binding domain protein	0.275783425	0.089070255	-0.298941746	0.002763438	-0.298941746	0.002763438
1734	W903_RS08620	W903_1764	1694579	1695853	NA	rmuC family protein	0.408528379	0.011872739	-0.150510537	0.15555551	-0.150510537	0.15555551
1735	W903_RS08625	W903_1765	1695855	1696487	NA	thiamine pyrophosphokinase	0.534666245	0.001743195	0.049444164	0.713960404	0.049444164	0.713960404
1736	W903_RS08630	W903_1766	1696480	1697142	rpe	ribulose-phosphate 3-epimerase	0.3641407	0.024183283	0.425369246	1.26617E-05	0.425369246	1.26617E-05
1737	W903_RS08635	W903_1767	1697149	1698021	rsgA	ribosome small subunit-dependent GTPase A	0.238753238	0.162932846	0.330878401	0.004568194	0.330878401	0.004568194
1738	W903_RS08640	W903_1768	1698177	1699028	NA	methyltransferase domain protein	-0.222019862	0.257219764	-0.55435461	5.46574E-07	-0.55435461	5.46574E-07
1739	W903_RS08645	W903_1769	1699032	1699904	ksgA	dimethyladenosine transferase	0.093919973	0.650703911	-0.509390284	5.7351E-06	-0.509390284	5.7351E-06
1740	W903_RS08650	W903_1770	1700079	1700315	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.090320123	0.667345462	-0.31845199	0.011544977	-0.31845199	0.011544977
1741	W903_RS08655	W903_1771	1700429	1701046	rnmV	ribonuclease M5	0.055496821	0.786454518	-0.730406626	4.29952E-10	-0.730406626	4.29952E-10
1742	W903_RS08660	W903_1772	1701033	1701815	NA	hydrolase, TatD family protein	0.198948458	0.333429233	-0.408561603	0.000851918	-0.408561603	0.000851918
1743	NA	W903_1773	1701792	1701905	NA	putative membrane protein	0.495574403	NA	2.121063891	0.008681719	2.121063891	0.008681719
1744	W903_RS08665	W903_1774	1701997	1702278	NA	hypothetical protein	0.168159736	0.402234902	0.221253774	0.224953026	0.221253774	0.224953026
1745	W903_RS08670	W903_1775	1702288	1702680	NA	hypothetical protein	0.211331829	0.331350991	0.257760664	0.22132204	0.257760664	0.22132204
1746	W903_RS08675	W903_1776	1702671	1703963	NA	lipase family protein	0.212189602	0.216011431	-0.024812421	0.843220044	-0.024812421	0.843220044
1747	W903_RS08680	W903_1777	1703963	1704355	NA	hypothetical protein	0.231225716	0.256969376	-0.372487989	0.040120052	-0.372487989	0.040120052
1748	W903_RS08685	W903_1778	1704530	1705792	dltD	D-alanyl-lipoteichoic acid biosynthesis protein DltD	-0.349038277	0.039098661	-0.874085647	3.64258E-24	-0.874085647	3.64258E-24
1749	W903_RS08690	W903_1779	1705785	1706024	dltC	D-alanine--poly(phosphoribitol) ligase, subunit 2	0.315071846	0.093926896	-0.443784032	8.79723E-06	-0.443784032	8.79723E-06
1750	W903_RS08695	W903_1780	1706039	1707304	dltB	D-alanyl-lipoteichoic acid biosynthesis protein DltB	0.064092766	0.733854288	-0.616460379	1.12703E-11	-0.616460379	1.12703E-11
1751	W903_RS08700	W903_1781	1707301	1708836	dltA	D-alanine--poly(phosphoribitol) ligase, subunit 1	0.438996846	0.004405075	-0.511722047	1.98838E-07	-0.511722047	1.98838E-07
1752	W903_RS08710	W903_1782	1708982	1710169	NA	his Kinase A domain protein	-0.564701267	0.00012166	-0.137704404	0.185762219	-0.137704404	0.185762219
1753	W903_RS08715	W903_1783	1710169	1710843	NA	response regulator	-0.716877253	1.89622E-06	-0.188339115	0.071196555	-0.188339115	0.071196555
1754	W903_RS08720	W903_1784	1711199	1711333	rpmH	ribosomal protein L34	-1.048192663	4.77255E-09	-1.103709876	8.74607E-08	-1.103709876	8.74607E-08
1755	W903_RS08725	W903_1785	1711517	1712872	NA	nucleoside recognition family protein	-0.621208281	0.001094055	-0.794895514	7.55025E-13	-0.794895514	7.55025E-13
1756	W903_RS08730	W903_1786	1713118	1714845	busAB	betaine ABC transporter permease and substrate binding protein	-2.058855367	1.48427E-33	1.911953586	2.49282E-83	1.911953586	2.49282E-83
1757	W903_RS08735	W903_1787	1714864	1716087	NA	glycine betaine/L-proline transport ATP binding subunit	-1.929986391	2.9184E-29	1.92039778	1.16596E-59	1.92039778	1.16596E-59
1758	NA	W903_1788	1716230	1716349	NA	glycerophosphoryl diester phosphodiesterase family protein	1.98598427	NA	2.756212616	0.105253183	2.756212616	0.105253183
1759	W903_RS08740	W903_1789	1716464	1718842	xpkA	xylulose-5-phosphate phosphoketolase	0.147474762	0.680975887	0.529123992	0.007816336	0.529123992	0.007816336
1760	W903_RS08745	W903_1790	1718932	1720023	NA	beta-lactamase superfamily domain protein	-1.09382911	5.35526E-10	-2.375228529	4.21293E-63	-2.375228529	4.21293E-63
1761	W903_RS08750	W903_1791	1720340	1722019	NA	PRD domain protein	-0.482457448	0.001988807	-1.085452177	4.95837E-24	-1.085452177	4.95837E-24
1762	W903_RS08755	W903_1792	1722085	1722846	NA	xylose isomerase-like TIM barrel family protein	0.212206103	NA	1.229455587	0.038691516	1.229455587	0.038691516
1763	W903_RS08760	W903_1793	1722865	1724382	NA	badF/BadG/BcrA/BcrD ATPase family protein	1.084277082	0.050329076	2.268588304	3.04639E-15	2.268588304	3.04639E-15
1764	W903_RS08765	W903_1794	1724448	1725437	NA	amidohydrolase family protein	0.68603113	0.318469963	2.06112027	7.47916E-10	2.06112027	7.47916E-10
1765	W903_RS08770	W903_1795	1725459	1726910	NA	PTS system sugar-specific permease component family protein	0.392539291	0.454068409	2.508017002	1.92798E-20	2.508017002	1.92798E-20
1766	W903_RS08775	W903_1796	1727008	1727964	gyaR	glyoxylate reductase	0.507157153	0.058233186	0.853653279	0.000244916	0.853653279	0.000244916
1767	W903_RS08780	W903_1797	1727983	1729002	NA	hypothetical protein	0.445910152	0.240876774	0.906517818	0.005029472	0.906517818	0.005029472
1768	W903_RS08785	W903_1798	1729237	1730220	NA	bacterial regulatory s, lacI family protein	-1.332663088	5.40762E-12	-1.411459797	4.5387E-29	-1.411459797	4.5387E-29
1769	W903_RS08790	W903_1799	1730384	1731031	fsa	fructose-6-phosphate aldolase	0.079215501	NA	2.867450652	4.55025E-08	2.867450652	4.55025E-08
1770	W903_RS08795	W903_1800	1731042	1731746	NA	class II Aldolase and Adducin N-terminal domain protein	0.17353828	0.785262915	2.724692757	3.41371E-25	2.724692757	3.41371E-25
1771	W903_RS08800	W903_1801	1731760	1732623	NA	xylose isomerase-like TIM barrel family protein	-0.325083744	0.669954532	2.367096818	2.1709E-17	2.367096818	2.1709E-17
1772	W903_RS08805	W903_1802	1732627	1733292	NA	orotidine 5'-phosphate decarboxylase / HUMPS family protein	-0.002367485	0.997456768	1.216345263	0.00699783	1.216345263	0.00699783
1773	W903_RS08810	W903_1803	1733405	1733890	ulaC	ascorbate-specific phosphotransferase enzyme IIA component	-0.746012369	0.352448028	0.819750413	0.218024453	0.819750413	0.218024453
1774	W903_RS08815	W903_1804	1733957	1734235	ulaB	ascorbate-specific phosphotransferase enzyme IIB component	-0.782974168	0.153759352	-0.03142964	0.962400513	-0.03142964	0.962400513
1775	W903_RS08820	W903_1805	1734263	1735702	NA	PTS system sugar-specific permease component family protein	-0.438392056	0.014074658	-3.318957402	6.9561E-118	-3.318957402	6.9561E-118
1776	W903_RS08825	W903_1806	1735870	1736487	NA	putative membrane protein	-0.505489708	0.0048532	0.386930235	0.000893779	0.386930235	0.000893779
1777	W903_RS10750	W903_1807	1736726	1737119	NA	putative membrane protein	-0.247772735	0.628562232	1.747248407	7.24724E-07	1.795337772	7.24724E-07
1778	W903_RS08835	W903_1808	1737142	1738434	purA	adenylosuccinate synthase	0.163200606	0.484301603	-0.245639965	0.0711446	-0.245639965	0.0711446
1779	W903_RS08840	W903_1809	1738805	1739827	NA	phosphotransferase system, EIIC family protein	-0.281960589	0.113933064	0.462592459	0.009282981	0.462592459	0.009282981
1780	W903_RS08845	W903_1810	1740189	1740863	NA	sensory box protein	-0.54214029	0.035084742	0.105664927	0.551873035	0.105664927	0.551873035
1781	W903_RS08850	W903_1811	1741033	1743285	gshAB	glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	1.122717602	7.39753E-14	0.273696217	0.009830684	0.273696217	0.009830684
1782	W903_RS08855	W903_1812	1743409	1744227	NA	5-bromo-4-chloroindolyl phosphate hydrolysis family protein	0.421357043	0.011321873	-0.955673459	6.51055E-19	-0.955673459	6.51055E-19
1783	W903_RS08860	W903_1813	1744224	1745480	NA	toxic anion resistance family protein	0.773978854	2.43314E-07	-0.470943043	4.86716E-05	-0.470943043	4.86716E-05
1784	W903_RS08865	W903_1814	1745620	1746495	NA	hsp33 family protein	-0.124672424	0.484301603	0.193614549	0.059396249	0.193614549	0.059396249
1785	W903_RS08870	W903_1815	1746479	1747456	NA	TIM-barrel , nifR3 family protein	0.168011556	0.340236682	-0.266988295	0.009454176	-0.266988295	0.009454176
1786	W903_RS08875	W903_1816	1747577	1748218	NA	deoxyguanosine kinase	-0.380226553	0.017385085	-1.339422784	2.72085E-18	-1.339422784	2.72085E-18
1787	W903_RS08880	W903_1817	1748232	1748723	NA	acetyltransferase family protein	0.157864591	0.446374739	-1.032154292	1.91541E-16	-1.032154292	1.91541E-16
1788	W903_RS08885	W903_1818	1748943	1751390	NA	istB-like ATP binding family protein	0.366568706	0.020156518	0.17101991	0.165234204	0.17101991	0.165234204
1789	W903_RS08890	W903_1819	1751387	1751851	ctsR	transcriptional regulator CtsR	-0.257854134	0.202251087	0.53352448	0.000296096	0.53352448	0.000296096
1790	W903_RS08895	W903_1820	1752024	1752485	NA	small multi-drug export family protein	0.564673968	0.000748712	0.975150827	7.52584E-11	0.975150827	7.52584E-11
1791	W903_RS08900	W903_1821	1752645	1753685	tsf	translation elongation factor Ts	-1.002817767	1.1873E-12	-2.479614173	3.4915E-150	-2.479614173	3.4915E-150
1792	W903_RS08905	W903_1822	1753779	1754549	rpsB	ribosomal protein S2	-1.197429297	5.25843E-13	-0.718622256	4.32787E-09	-0.718622256	4.32787E-09
1793	W903_RS08910	W903_1823	1754826	1755386	ahpC	peroxiredoxin	0.106791668	0.566833212	0.44407329	0.001406202	0.44407329	0.001406202

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1794	W903_RS08915	W903_1824	1755404	1756936	ahpF	alkyl hydroperoxide reductase subunit F	0.377287838	0.020388883	0.824500377	4.71265E-12	0.824500377	4.71265E-12
1795	W903_RS08920	W903_1825	1757070	1757140	tRNA	NA	3.58862055	NA	0.640064274	0.889840444	0.640064274	0.889840444
1796	W903_RS08925	W903_1826	1757212	1759281	NA	sodium/hydrogen exchanger family protein	0.024350129	0.904494477	0.389707137	3.19069E-05	0.389707137	3.19069E-05
1797	W903_RS08930	W903_1827	1759283	1759519	NA	hypothetical protein	-0.564285431	0.010372194	0.069172668	0.705439019	0.069172668	0.705439019
1798	W903_RS08935	W903_1828	1759686	1760639	NA	LD-carboxypeptidase family protein	1.57847549	1.59909E-24	0.04239461	0.754725798	0.04239461	0.754725798
1799	W903_RS08940	W903_1829	1760689	1762584	NA	peptidase M13 family protein	0.100668347	0.560572697	-0.536717053	2.53782E-09	-0.536717053	2.53782E-09
1800	W903_RS08945	W903_1830	1762732	1763715	NA	oxidoreductase , NAD-binding Rossmann fold family protein	1.241598171	2.10787E-13	0.580533905	6.37142E-07	0.580533905	6.37142E-07
1801	W903_RS08950	W903_1831	1763761	1764912	NA	major Facilitator Superfamily protein	0.123107091	0.532862789	1.016154446	8.79972E-14	1.016154446	8.79972E-14
1802	W903_RS08955	W903_1832	1765036	1765680	NA	cyclic nucleotide-binding domain protein	0.199651016	0.41083729	0.705935946	1.13949E-05	0.705935946	1.13949E-05
1803	W903_RS08960	W903_1833	1765746	1766360	def	peptide deformylase	-0.212124699	0.295652635	-0.053418469	0.644760747	-0.053418469	0.644760747
1804	W903_RS08965	W903_1834	1766432	1767433	NA	periplasmic binding s and sugar binding domain of LacI family protein	-0.612630321	0.000520967	-0.117741847	0.30573053	-0.117741847	0.30573053
1805	W903_RS08970	W903_1835	1767513	1769417	NA	heparinase II/III-like family protein	0.441419016	0.300281871	1.817279985	4.1687E-15	1.817279985	4.1687E-15
1806	W903_RS08975	W903_1836	1769497	1770312	NA	PTS system mannose/fructose/sorbose IID component family protein	0.652121671	0.335504362	2.192251117	2.78161E-07	2.192251117	2.78161E-07
1807	W903_RS08980	W903_1837	1770299	1771165	NA	PTS system sorbose-specific iic component family protein	1.324229028	NA	1.818960378	9.91968E-05	1.818960378	9.91968E-05
1808	W903_RS08985	W903_1838	1771201	1771695	NA	PTS system sorbose subIIB component family protein	0.248075814	NA	1.923720464	0.000140452	1.923720464	0.000140452
1809	W903_RS08990	W903_1839	1771750	1772946	NA	unsaturated glucuronyl hydrolase	0.477534755	0.509464899	1.851647171	2.31732E-08	1.851647171	2.31732E-08
1810	W903_RS08995	W903_1840	1772949	1773383	NA	PTS system fructose IIA component family protein	-0.696269897	NA	0.717170993	0.236949627	0.717170993	0.236949627
1811	W903_RS09000	W903_1841	1773661	1774473	NA	short chain dehydrogenase family protein	2.302661039	0.000740448	2.482918186	1.05919E-05	2.482918186	1.05919E-05
1812	W903_RS09005	W903_1842	1774490	1775131	NA	ribose/galactose isomerase	1.329868427	NA	2.948395948	2.13528E-06	2.948395948	2.13528E-06
1813	W903_RS09010	W903_1843	1775157	1776164	NA	pfkB carbohydrate kinase family protein	0.654423958	NA	3.366898733	4.51641E-07	3.366898733	4.51641E-07
1814	W903_RS09015	W903_1844	1776176	1776814	NA	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase family protein	1.023085894	NA	3.938262657	7.94108E-05	3.938262657	7.94108E-05
1815	W903_RS09020	W903_1845	1776861	1777475	NA	nitroreductase family protein	-0.75536597	1.83832E-06	0.023198656	0.915869759	0.023198656	0.915869759
1816	W903_RS09025	W903_1846	1777608	1778033	NA	marR family protein	-0.256830541	0.240481793	-1.096387009	2.09373E-11	-1.096387009	2.09373E-11
1817	W903_RS09030	W903_1847	1778160	1782566	polC	DNA polymerase III, alpha subunit, Gram-positive type	0.242466109	0.137418058	-0.426271925	0.003271423	-0.426271925	0.003271423
1818	W903_RS09035	W903_1848	1782689	1783273	NA	mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein	0.392750886	0.115557171	1.642789124	4.53427E-30	1.642789124	4.53427E-30
1819	W903_RS09040	W903_1849	1783398	1785236	proS	proline--tRNA ligase	0.312636586	0.05092725	-0.449592564	8.15087E-07	-0.449592564	8.15087E-07
1820	W903_RS09045	W903_1850	1785343	1786602	rseP	RIP metalloprotease RseP	0.797060122	1.43422E-07	0.000669335	0.995648905	0.000669335	0.995648905
1821	W903_RS09050	W903_1851	1786633	1787427	NA	cytidylyltransferase family protein	1.182985936	7.03393E-14	0.411449217	7.44742E-05	0.411449217	7.44742E-05
1822	W903_RS09055	W903_1852	1787442	1788194	uppS	di-trans,poly-cis-decaprenylcistransferase	0.976481453	2.74553E-10	0.943393411	7.19223E-16	0.943393411	7.19223E-16
1823	W903_RS09060	W903_1853	1788361	1788702	yajC	preprotein translocase, YajC subunit	-0.629888857	3.35718E-05	-1.490840994	1.06913E-29	-1.490840994	1.06913E-29
1824	W903_RS09065	W903_1854	1788779	1789123	NA	thioredoxin family protein	-1.239386845	6.37043E-11	-1.183437968	1.62706E-15	-1.183437968	1.62706E-15
1825	W903_RS09070	W903_1855	1789314	1790477	NA	malic enzyme, NAD binding domain protein	0.476020366	0.304435229	1.328945391	3.10285E-06	1.328945391	3.10285E-06
1826	W903_RS09075	W903_1856	1790502	1791839	NA	citrate carrier , CCS family protein	0.228924556	0.64054486	1.814860165	2.93254E-13	1.814860165	2.93254E-13
1827	W903_RS09080	W903_1857	1791993	1793519	NA	putative sensor kinase dpiB	-0.061941792	0.749755627	1.232187728	6.6466E-31	1.232187728	6.6466E-31
1828	W903_RS09085	W903_1858	1793521	1794201	NA	response regulator	-0.100931597	0.735007232	1.046856428	1.77402E-11	1.046856428	1.77402E-11
1829	W903_RS09090	W903_1859	1794222	1795217	NA	UDP-glucose 4-epimerase GalE	0.396767748	0.014621274	0.18680356	0.061233605	0.18680356	0.061233605
1830	W903_RS09095	W903_1860	1795305	1796912	dexB	glucan 1,6-alpha-glucosidase	0.18329191	0.32052743	0.545615542	0.017465327	0.545615542	0.017465327
1831	W903_RS09100	W903_1861	1797041	1798174	NA	ABC transporter family protein	-0.62686271	1.67942E-05	-0.674809314	3.41538E-12	-0.674809314	3.41538E-12
1832	W903_RS09105	W903_1862	1798275	1799126	NA	bacterial regulatory , Fis family protein	-0.28797207	0.156525661	-0.651147949	1.71571E-07	-0.651147949	1.71571E-07
1833	W903_RS09110	W903_1863	1799221	1800117	NA	aldose 1-epimerase family protein	0.469780747	0.549536178	2.340875741	9.20468E-05	2.340875741	9.20468E-05
1834	W903_RS09115	W903_1864	1800171	1801148	lacD	tagatose 1,6-diphosphate aldolase	0.902731941	0.047311061	1.933487849	3.55339E-05	1.933487849	3.55339E-05
1835	W903_RS09120	W903_1865	1801150	1802082	lacC	tagatose-6-phosphate kinase	0.750568329	0.014781856	1.915687076	2.56544E-10	1.915687076	2.56544E-10
1836	W903_RS09125	W903_1866	1802093	1802608	lacB	galactose-6-phosphate isomerase, LacB subunit	0.51252228	0.123170371	1.416979224	1.57061E-10	1.416979224	1.57061E-10
1837	W903_RS09130	W903_1867	1802629	1803054	lacA	galactose-6-phosphate isomerase, LacA subunit	1.240007871	7.16966E-05	1.678658436	5.86751E-24	1.678658436	5.86751E-24
1838	W903_RS09135	W903_1868	1803301	1805751	NA	BNR repeat-like domain protein	-0.713197212	0.000147486	-0.688516247	1.10426E-06	-0.688516247	1.10426E-06
1839	W903_RS09140	W903_1869	1805990	1807438	NA	PTS system sugar-specific permease component family protein	0.496412278	0.246836258	2.003000477	1.30212E-12	2.003000477	1.30212E-12
1840	W903_RS09145	W903_1870	1807478	1807783	NA	PTS system, Lactose/Cellobiose specific IIB subunit	0.295555851	0.420365776	1.260872598	3.352E-06	1.260872598	3.352E-06
1841	W903_RS09150	W903_1871	1807785	1808249	NA	phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein	-0.161037089	0.678957096	1.445820488	3.84701E-05	1.445820488	3.84701E-05
1842	W903_RS09155	W903_1872	1808467	1809243	NA	deoR C terminal sensor domain protein	-0.357080092	0.05821367	-0.261324798	0.054015945	-0.261324798	0.054015945
1843	W903_RS09160	W903_1873	1809525	1812107	NA	histidine triad domain protein	0.19746083	0.483314144	0.117504302	0.566340884	0.117504302	0.566340884
1844	W903_RS09165	W903_1874	1812134	1813057	lmb	lipoprotein	-0.057915715	0.920058563	0.438448838	0.311105051	0.438448838	0.311105051
1845	W903_RS09170	W903_1875	1813312	1813795	dtd	D-tyrosyl-tRNA(Tyr) deacylase	-0.071786932	0.725515949	-0.892879636	2.02294E-12	-0.892879636	2.02294E-12
1846	W903_RS09175	W903_1876	1813765	1815981	relA	bifunctional (p)ppGpp synthase/hydrolase RelA	0.262164354	0.110401251	-0.603326177	9.53769E-11	-0.603326177	9.53769E-11
1847	W903_RS09180	W903_1877	1816241	1818643	yfkN	trifunctional nucleotide phosphoesterase protein YfkN	-0.036379424	0.901111124	0.178128927	0.342788828	0.178128927	0.342788828
1848	W903_RS09185	W903_1878	1818800	1819255	NA	nrdI protein	0.07942557	0.705759832	-0.885508111	6.45738E-15	-0.885508111	6.45738E-15
1849	W903_RS09190	W903_1879	1819266	1820303	NA	M42 glutamyl aminopeptidase family protein	0.226076305	0.184861237	-0.520346327	1.0302E-07	-0.520346327	1.0302E-07
1850	W903_RS09195	W903_1880	1820303	1820800	NA	AAA domain protein	-0.101602583	0.574080165	-0.438194915	2.35986E-05	-0.438194915	2.35986E-05
1851	NA	W903_1881	1820857	1820976	NA	putative membrane protein	1.148016801	NA	1.091254364	0.184629227	1.091254364	0.184629227
1852	W903_RS09205	W903_1882	1821022	1822059	NA	bacterial extracellular solute-binding family protein	-0.397462601	0.057187032	0.183833937	0.21848066	0.183833937	0.21848066
1853	W903_RS09210	W903_1883	1822071	1822844	NA	response regulator	-0.509813018	0.0389296	0.163497498	0.301672743	0.163497498	0.301672743
1854	W903_RS09215	W903_1884	1822848	1824497	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-0.596704615	0.00628389	0.322604854	0.019176813	0.322604854	0.019176813
1855	W903_RS09220	W903_1885	1824635	1825462	NA	PTS system mannose/fructose/sorbose IID component family protein	0.510558896	0.400428001	1.300089904	1.07978E-05	1.300089904	1.07978E-05
1856	W903_RS09225	W903_1886	1825459	1826268	NA	PTS system sorbose-specific iic component family protein	0.629927415	0.280296301	1.811951471	1.40328E-09	1.811951471	1.40328E-09
1857	W903_RS09230	W903_1887	1826284	1826775	NA	putative phosphotransferase enzyme IIB component	-0.548171823	0.433931975	0.128224475	0.785179748	0.128224475	0.785179748
1858	W903_RS09235	W903_1888	1826793	1827218	NA	PTS system fructose IIA component family protein	-1.562085984	0.000841296	-0.785707558	0.010778327	-0.785707558	0.010778327
1859	W903_RS09240	W903_1889	1827465	1828517	NA	putative membrane protein	-0.154223101	0.647719608	-0.747991428	3.63882E-05	-0.747991428	3.63882E-05
1860	W903_R|10555	W903_1890	1828551	1828733	NA	hypothetical protein	-0.153776473	NA	-0.434852691	0.555258975	-0.434852691	0.555258975
1861	W903_RS09245	W903_1891	1828728	1829891	NA	ABC-2 transporter family protein	-0.005632795	0.976894053	-1.179049078	2.97635E-26	-1.179049078	2.97635E-26
1862	W903_RS09250	W903_1892	1829897	1830745	NA	ABC transporter family protein	-0.214400407	0.304901614	-1.280684144	3.24504E-33	-1.280684144	3.24504E-33
1863	W903_RS09255	W903_1893	1830868	1831249	rgfC	sensor histidine kinase domain protein	-0.822729403	0.000525381	-1.193728301	3.68487E-12	-1.193728301	3.68487E-12
1864	W903_RS09260	W903_1894	1831236	1831988	NA	response regulator	-0.494915443	0.082441176	-0.455985941	0.014763377	-0.455985941	0.014763377
1865	W903_RS09265	W903_1895	1832265	1833080	NA	endonuclease/Exonuclease/phosphatase family protein	-0.28473305	0.626463743	1.960720837	1.94667E-10	1.960720837	1.94667E-10
1866	W903_RS09270	W903_1896	1833134	1835317	ptbA	PTS system, glucose subfamily, IIA component domain protein	-0.406382789	0.069411897	2.013888255	2.8476E-27	2.013888255	2.8476E-27
1867	W903_RS09275	W903_1897	1835475	1837130	NA	his Kinase A domain protein	-0.015379779	0.935760556	0.344681345	0.001740056	0.344681345	0.001740056
1868	W903_RS09280	W903_1898	1837123	1837800	NA	putative transcriptional activator CadC	0.237654184	0.32718836	0.517649365	5.2319E-05	0.517649365	5.2319E-05
1869	W903_RS09285	W903_1899	1837800	1838456	NA	phosphate transport system regulatory protein PhoU	0.699317112	0.094489493	0.906351817	0.000657655	0.906351817	0.000657655
1870	W903_RS09290	W903_1900	1838453	1839202	NA	phosphate ABC transporter, ATP-binding protein	0.537006539	0.210346037	0.403704864	0.151963522	0.403704864	0.151963522
1871	W903_RS09295	W903_1901	1839195	1840073	NA	phosphate ABC transporter, permease protein PstA	0.74599229	0.216011431	0.976929731	0.004053678	0.976929731	0.004053678
1872	W903_RS09300	W903_1902	1840075	1840920	NA	phosphate ABC transporter, permease protein PstC	1.253744795	0.084095498	1.425081536	0.001379337	1.425081536	0.001379337
1873	W903_RS09305	W903_1903	1840935	1841816	NA	PBP superfamily domain protein	0.739032471	0.106581382	0.914729006	0.001765546	0.914729006	0.001765546
1874	W903_RS09315	W903_1906	1842502	1843242	NA	RNA methyltransferase, RsmE family protein	0.707876654	7.57372E-06	-0.766757664	2.28973E-08	-0.766757664	2.28973E-08
1875	W903_RS09320	W903_1907	1843242	1844195	prmA	ribosomal protein L11 methyltransferase	1.223357141	5.86408E-15	-0.443152557	0.000430606	-0.443152557	0.000430606
1876	W903_RS09325	W903_1908	1844212	1845855	NA	viral (Super1) RNA helicase family protein	0.553717304	0.000299026	-1.201745836	3.84366E-32	-1.201745836	3.84366E-32
1877	W903_RS09330	W903_1909	1845865	1846335	NA	hypothetical protein	0.269460236	0.3563629	-1.3483521	1.24473E-13	-1.3483521	1.24473E-13
1878	W903_RS09335	W903_1910	1846409	1846936	NA	hypothetical protein	-0.294050149	0.256969376	0.928556159	4.70087E-11	0.928556159	4.70087E-11
1879	W903_RS09340	W903_1911	1846939	1847127	NA	helix-turn-helix family protein	-0.672259617	0.016993817	1.038912052	2.00925E-12	1.038912052	2.00925E-12
1880	W903_RS09345	W903_1912	1847746	1848227	NA	putative acetyltransferase	1.314847223	7.04296E-15	1.099584727	3.83179E-20	1.099584727	3.83179E-20
1881	W903_RS09350	W903_1913	1848215	1849483	NA	sigma-54 interaction domain protein	0.989237669	7.53022E-12	0.751420034	1.75825E-13	0.751420034	1.75825E-13
1882	W903_RS09355	W903_1914	1849765	1849837	tRNA	NA	2.088336601	NA	3.822955837	0.000256494	3.822955837	0.000256494
1883	W903_RS09360	W903_1915	1850026	1850331	NA	hypothetical protein	-0.151312278	0.734062253	0.942616132	5.38624E-05	0.942616132	5.38624E-05
1884	W903_RS09365	W903_1916	1850315	1850716	NA	hypothetical protein	-0.516214972	0.035040964	0.881225027	7.82426E-06	0.881225027	7.82426E-06
1885	W903_RS09370	W903_1917	1850704	1851912	NA	lipase family protein	-0.031660205	0.875177314	0.626278092	2.58628E-10	0.626278092	2.58628E-10
1886	W903_RS09375	W903_1918	1851914	1852246	NA	hypothetical protein	0.044058184	0.858438886	0.77764404	7.0316E-08	0.77764404	7.0316E-08
1887	W903_RS09380	W903_1919	1852518	1852847	NA	hypothetical protein	-0.504225634	0.51480251	1.509272727	0.001470484	1.509272727	0.001470484
1888	NA	W903_1920	1853743	1853889	NA	hypothetical protein	-0.620765488	0.450275205	1.841980042	0.000155583	1.841980042	0.000155583
1889	NA	W903_1921	1854327	1854455	NA	hypothetical protein	1.203542895	4.49436E-06	2.448434855	6.13206E-49	2.448434855	6.13206E-49
1890	NA	W903_1922	1855114	1855233	NA	hypothetical protein	-0.712296421	NA	0.700099716	0.17448358	0.700099716	0.17448358
1891	W903_RS09395	W903_1923	1855334	1855717	NA	hypothetical protein	0.023852356	0.950641272	-0.17114939	0.462725173	-0.17114939	0.462725173
1892	NA	W903_1926	1856750	1856869	NA	putative membrane protein	-0.244198542	NA	-0.105872245	0.864322941	-0.105872245	0.864322941
1893	W903_RS09410	W903_1927	1857020	1857214	NA	addiction module antitoxin, RelB/DinJ family protein	-0.393734696	NA	0.524329755	0.35048364	0.524329755	0.35048364
1894	W903_RS09415	W903_1928	1857350	1857640	NA	hypothetical protein	-1.398064442	0.000992727	-0.134544776	0.642537481	-0.134544776	0.642537481
1895	W903_RS09420	W903_1929	1857925	1858323	NA	hypothetical protein	-0.970082763	4.35696E-06	-0.506379027	0.000373093	-0.506379027	0.000373093
1896	W903_RS09425	W903_1930	1858477	1859199	NA	ABC-2 transporter family protein	-1.184638829	1.0928E-09	-0.710245067	2.21015E-05	-0.710245067	2.21015E-05
1897	W903_RS09430	W903_1931	1859203	1859820	NA	ABC transporter family protein	-1.014064255	1.52055E-08	-0.336124397	0.001878773	-0.336124397	0.001878773
1898	W903_RS09435	W903_1932	1860499	1861353	NA	streptomycin adenylyltransferase family protein	-1.034655223	1.33437E-08	-0.762530094	5.41636E-08	-0.762530094	5.41636E-08
1899	NA	W903_1933	1861645	1861764	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.009828217	NA	0.34591432	0.729077664	0.34591432	0.729077664
1900	W903_RS09440	W903_1934	1861725	1862321	NA	phosphoribulokinase / Uridine kinase family protein	-0.557805575	0.000243819	0.308295339	0.00776568	0.308295339	0.00776568
1901	W903_RS09445	W903_1935	1862356	1862913	NA	histidine phosphatase super family protein	-0.420653465	0.062042403	0.899922377	1.04926E-09	0.899922377	1.04926E-09
1902	W903_RS09450	W903_1936	1862950	1863285	NA	transcriptional regulator PadR-like family protein	0.119445267	0.625465629	1.341083336	8.02463E-17	1.341083336	8.02463E-17
1903	W903_RS09455	W903_1937	1863807	1864295	NA	acetyltransferase family protein	-0.858129344	0.012457606	-0.189166947	0.39066178	-0.189166947	0.39066178
1904	W903_RS09460	W903_1938	1864464	1865225	NA	ABC-2 transporter family protein	-0.450201652	0.177720765	0.107965483	0.561814829	0.107965483	0.561814829
1905	W903_RS09465	W903_1939	1865222	1866124	NA	ABC transporter family protein	-0.699404253	0.010307756	-0.168872503	0.309379118	-0.168872503	0.309379118
1906	W903_RS09470	W903_1940	1866121	1866327	NA	phospholipase D family protein	-1.115061898	0.038932854	-0.629626077	0.045148438	-0.629626077	0.045148438
1907	W903_RS09475	W903_1941	1866329	1867405	NA	helix-turn-helix family protein	-0.780810233	0.000234013	-0.030046012	0.83454704	-0.030046012	0.83454704
1908	NA	W903_1942	1867492	1867638	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.697992011	NA	3.349244553	0.008678291	3.349244553	0.008678291
1909	W903_RS09480	W903_1943	1867654	1868268	NA	PAP2 superfamily protein	-0.346415506	0.049102307	-1.584123579	3.8947E-40	-1.584123579	3.8947E-40
1910	W903_RS09485	W903_1944	1868482	1868799	NA	mazG nucleotide pyrophosphohydrolase domain protein	0.124152702	0.62856232	-1.219418321	2.79824E-12	-1.219418321	2.79824E-12
1911	W903_RS09490	W903_1945	1868796	1869356	NA	putative lysine decarboxylase family protein	0.835505709	2.95629E-05	-0.463381338	0.001718665	-0.463381338	0.001718665
1912	W903_RS09495	W903_1946	1869661	1870524	NA	CAAX protease self-immunity family protein	-0.036621259	0.857640534	-1.136283781	1.28132E-13	-1.136283781	1.28132E-13
1913	W903_RS09500	W903_1947	1870681	1870983	NA	rhodanese-like domain protein	-0.193996927	0.525444689	1.878396785	6.82964E-47	1.878396785	6.82964E-47
1914	W903_RS09505	W903_1948	1871156	1871923	NA	protein B	-0.974021122	1.12582E-05	1.101056964	4.27015E-19	1.101056964	4.27015E-19
1915	W903_RS09510	W903_1949	1872709	1874111	NA	major Facilitator Superfamily protein	0.423861457	0.015340361	1.83444E-20	1.11491106E7	1.83444E-20	1.11491106E7
1916	W903_RS09515	W903_1950	1874348	1874974	NA	transcriptional regulator	-0.179786002	0.362457208	-0.518378403	0.000665604	-0.518378403	0.000665604
1917	W903_RS09520	W903_1951	1875046	1875585	NA	AAA domain protein	0.363316973	0.062591184	-0.334824656	0.006456007	-0.334824656	0.006456007
1918	W903_RS09525	W903_1952	1875786	1876871	NA	iron-containing alcohol dehydrogenase family protein	0.715805961	2.82007E-05	0.060876785	0.605746199	0.060876785	0.605746199
1919	W903_RS09530	W903_1953	1877035	1877742	NA	hypothetical protein	-0.661999869	0.001504386	-1.387274331	8.69805E-32	-1.387274331	8.69805E-32
1920	W903_RS09535	W903_1954	1878089	1879933	NA	homocysteine S-methyltransferase family protein	0.131807857	0.699641117	0.743946525	5.64354E-05	0.743946525	5.64354E-05
1921	W903_RS09540	W903_1955	1879978	1882215	metE	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	0.199538816	0.551312517	0.745474307	1.65438E-05	0.745474307	1.65438E-05
1922	W903_RS09545	W903_1956	1882585	1882908	NA	branched-chain amino acid transport family protein	-0.05401302	NA	-0.144547049	0.835875842	-0.144547049	0.835875842
1923	W903_RS09550	W903_1957	1882898	1883590	NA	azlC family protein	-0.204929624	0.449631468	0.119520289	0.558128426	0.119520289	0.558128426
1924	W903_RS09555	W903_1958	1883913	1888406	NA	gram-positive signal peptide, YSIRK family domain protein	0.650212267	0.009224565	0.562242566	0.004433204	0.562242566	0.004433204
1925	W903_RS09560	W903_1959	1888434	1888628	NA	LPXTG cell wall anchor domain protein	0.252585086	NA	0.777355776	0.301442646	0.777355776	0.301442646
1926	W903_RS09565	W903_1960	1888861	1889547	NA	response regulator	-0.43601328	0.028260269	-0.354888585	0.004331399	-0.354888585	0.004331399
1927	W903_RS09570	W903_1961	1889544	1890932	NA	his Kinase A domain protein	-0.103554469	0.60183357	-0.35162728	0.0080325	-0.35162728	0.0080325
1928	W903_RS09575	W903_1962	1891025	1891633	NA	putative exported protein	-0.457731914	0.04595567	-0.40433864	0.009660559	-0.40433864	0.009660559
1929	W903_RS09580	W903_1963	1891723	1894224	leuS	leucine--tRNA ligase	0.660723434	3.76096E-06	-0.81807287	1.0077E-20	-0.81807287	1.0077E-20
1930	W903_RS09585	W903_1964	1894601	1895848	NA	sugar (and other) transporter family protein	3.039378551	0.091840069	-0.143967231	0.205053582	-0.143967231	0.205053582
1931	W903_RS09590	W903_1965	1895891	1896733	NA	patatin-like phospholipase family protein	-0.198623618	0.297989939	-0.494759867	1.8647E-05	-0.494759867	1.8647E-05

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1932	W903_RS09595	W903_1966	1896874	1897413	nusG	transcription termination/antitermination factor NusG	-1.208839109	3.22774E-15	-1.378717901	1.16165E-34	-1.378717901	1.16165E-34
1933	W903_RS09600	W903_1967	1897619	1899004	NA	LPXTG cell wall anchor domain protein	-1.304320289	5.1369E-16	-3.255514858	6.1038E-110	-3.255514858	6.1038E-110
1934	W903_RS09605	W903_1968	1899317	1899490	secE	preprotein translocase, SecE subunit	-0.047633004	0.858438886	-0.839671211	0.000109533	-0.839671211	0.000109533
1935	W903_RS09610	W903_1969	1899765	1902047	NA	penicillin-binding , 1A family protein	0.639938287	3.70455E-05	-0.483043991	3.0871E-07	-0.483043991	3.0871E-07
1936	W903_RS09615	W903_1970	1902091	1902975	NA	pseudouridine synthase, RluA family protein	0.287662222	0.137561528	0.161506342	0.204744079	0.161506342	0.204744079
1937	W903_RS09625	W903_1973	1904809	1906020	NA	phosphopentomutase	1.177924877	2.68857E-14	0.949149301	4.02823E-24	0.949149301	4.02823E-24
1938	W903_RS09630	W903_1974	1906087	1906758	deoC	deoxyribose-phosphate aldolase	1.221102238	5.4948E-16	0.98623458	1.37353E-24	0.98623458	1.37353E-24
1939	W903_RS09635	W903_1975	1906788	1907990	NA	na+ dependent nucleoside transporter family protein	1.111800215	1.41332E-14	1.183843475	1.24836E-39	1.183843475	1.24836E-39
1940	W903_RS09640	W903_1976	1908011	1908790	udp	uridine phosphorylase	2.002679947	1.05838E-31	1.132675401	2.38995E-26	1.132675401	2.38995E-26
1941	W903_RS09645	W903_1977	1908949	1909686	NA	bacterial regulatory s, gntR family protein	-4.228036374	4.50401E-69	-3.541994742	4.8467E-135	-3.541994742	4.8467E-135
1942	W903_RS09655	W903_1978	1910096	1911718	groL	chaperonin GroL	0.536491172	0.000233887	-0.307006683	0.022800768	-0.307006683	0.022800768
1943	W903_RS09660	W903_1979	1911814	1912098	groS	10 kDa chaperonin	0.550375039	0.002144701	-1.079673131	6.46002E-19	-1.079673131	6.46002E-19
1944	W903_RS09665	W903_1980	1912273	1913076	NA	ABC transporter family protein	0.158973584	0.483314144	-2.377166985	4.72852E-42	-2.377166985	4.72852E-42
1945	NA	W903_1981	1913081	1913977	NA	branched-chain amino acid transport system / permease component family protein	0.248850788	0.306567098	-2.419194222	3.14119E-43	-2.419194222	3.14119E-43
1946	NA	W903_1982	1913993	1914955	NA	ABC transporter substrate binding family protein	0.591105321	0.007850889	-3.367332011	5.55691E-63	-3.367332011	5.55691E-63
1947	W903_RS09680	W903_1983	1915420	1916217	NA	HAD hydrolase, IIB family protein	-0.870796137	1.13824E-06	-0.250340302	0.038978604	-0.250340302	0.038978604
1948	W903_RS09685	W903_1984	1916403	1917263	NA	glyoxalase/Bleomycin resistance /Dioxygenase superfamily protein	-0.531549124	0.384231534	1.741676535	1.63268E-13	1.741676535	1.63268E-13
1949	W903_RS09690	W903_1985	1917306	1918037	NA	hypothetical protein	-0.741757511	8.09099E-05	-0.130991514	0.310910114	-0.130991514	0.310910114
1950	W903_RS09695	W903_1986	1918394	1919011	nrdG	anaerobic ribonucleoside-triphosphate reductase activating protein	0.171862561	0.546474694	1.310569932	1.21114E-28	1.310569932	1.21114E-28
1951	W903_RS09700	W903_1987	1919084	1919575	NA	acetyltransferase family protein	-0.228400935	0.265487886	1.158714352	3.15483E-25	1.158714352	3.15483E-25
1952	W903_RS09705	W903_1988	1919584	1920516	NA	oxidoreductase , NAD-binding Rossmann fold family protein	-0.177418865	0.338526977	0.820723238	7.02761E-16	0.820723238	7.02761E-16
1953	NA	W903_1989	1920529	1920672	NA	putative 30S ribosomal protein S10	0.3653722	0.060886057	0.946500358	6.44316E-21	0.946500358	6.44316E-21
1954	W903_RS09715	W903_1990	1920747	1922945	nrdD	anaerobic ribonucleoside-triphosphate reductase	-0.704233078	6.81189E-05	0.030387336	0.795751374	0.030387336	0.795751374
1955	W903_RS09720	W903_1991	1923044	1924585	NA	putative membrane protein	-0.859302431	1.31967E-09	-0.134888823	0.204453777	-0.134888823	0.204453777
1956	NA	W903_1992	1924631	1924753	NA	hypothetical protein	0.572714056	0.318469963	0.279113848	0.609439204	0.279113848	0.609439204
1957	W903_RS09730	W903_1993	1924836	1925153	NA	hypothetical protein	-0.823923718	3.90391E-08	-0.087414761	0.471982532	-0.087414761	0.471982532
1958	W903_RS09735	W903_1994	1925179	1925589	NA	hypothetical protein	-0.57802275	0.000308364	0.164554204	0.118151879	0.164554204	0.118151879
1959	W903_RS09740	W903_1995	1925598	1925864	NA	hypothetical protein	0.11731725	0.586984816	0.457282136	0.000157186	0.457282136	0.000157186
1960	W903_RS09745	W903_1996	1926066	1926464	NA	transcriptional regulator, Spx/MgsR family protein	0.213323993	0.219716273	0.19519702	0.050133133	0.19519702	0.050133133
1961	W903_RS09750	W903_1997	1926680	1927819	recA	protein RecA	0.547046052	0.000260862	-0.196535925	0.126115349	-0.196535925	0.126115349
1962	W903_RS09755	W903_1998	1927893	1929152	NA	competence/damage-inducible CinA C-terminal domain protein	0.914318589	1.4888E-09	0.078709915	0.457950226	0.078709915	0.457950226
1963	W903_RS09760	W903_1999	1929241	1929792	NA	methyladenine glycosylase family protein	0.325411333	0.082241734	0.842961329	2.15325E-15	0.842961329	2.15325E-15
1964	W903_RS09765	W903_2000	1929815	1930405	ruvA	holliday junction DNA helicase RuvA	0.080339562	0.661340936	0.604183743	3.25462E-09	0.604183743	3.25462E-09
1965	W903_RS09770	W903_2001	1930407	1931639	NA	major Facilitator Superfamily protein	0.458496306	0.003515823	0.696207937	2.9024E-13	0.696207937	2.9024E-13
1966	W903_RS09775	W903_2002	1931671	1933644	mutL	DNA mismatch repair MutL family protein	0.216989954	0.201350226	0.368064369	0.001124196	0.368064369	0.001124196
1967	W903_RS09780	W903_2003	1933869	1934072	NA	'Cold-shock' DNA-binding domain protein	-1.793581594	0.177260421	-3.621337945	2.7883E-11	-3.621337945	2.7883E-11
1968	W903_RS09785	W903_2004	1934129	1936705	mutS	DNA mismatch repair protein MutS	-0.890461185	7.91414E-09	-1.226116704	2.86833E-27	-1.226116704	2.86833E-27
1969	W903_RS09790	W903_2005	1936762	1937199	NA	arginine repressor	-0.883231549	4.15632E-07	-1.305090775	1.17455E-32	-1.305090775	1.17455E-32
1970	W903_RS09795	W903_2006	1937421	1939112	argS	arginine--tRNA ligase	0.226532149	0.155594447	-0.802961751	1.11911E-13	-0.802961751	1.11911E-13
1971	W903_RS09800	W903_2007	1939200	1939508	uviB	bacteriocin	-0.054275787	0.85392705	-0.944285539	3.46814E-06	-0.944285539	3.46814E-06
1972	W903_RS09805	W903_2008	1939535	1940407	NA	hypothetical protein	-0.146271005	0.484301603	-0.609877644	5.39408E-08	-0.609877644	5.39408E-08
1973	W903_RS09810	W903_2009	1940515	1941459	NA	hypothetical protein	-0.273178268	0.114842415	-1.210585143	2.6124E-41	-1.210585143	2.6124E-41
1974	W903_RS09815	W903_2010	1941449	1943200	aspS	aspartate--tRNA ligase	-0.136035966	0.42574285	-1.591497581	3.57409E-67	-1.591497581	3.57409E-67
1975	W903_RS09820	W903_2011	1943293	1944573	hisS	histidine--tRNA ligase	-0.116490384	0.536398445	-1.130289601	5.44202E-31	-1.130289601	5.44202E-31
1976	W903_RS09825	W903_2012	1944793	1944975	rpmF	ribosomal protein L32	-1.033203143	6.73104E-09	-1.500454515	0.000864787	-1.500454515	0.000864787
1977	W903_RS09830	W903_2013	1944991	1945140	rpmG	ribosomal protein L33	0.336589039	0.102080595	-1.006318353	4.92906E-19	-1.006318353	4.92906E-19
1978	W903_RS09835	W903_2014	1945433	1946047	NA	cadmium resistance transporter family protein	-0.885202701	9.23129E-06	-0.773935076	0.000207777	-0.773935076	0.000207777
1979	W903_RS09840	W903_2015	1946059	1946397	NA	bacterial regulatory , arsR family protein	-1.205222859	1.45377E-11	-0.977230095	1.11715E-07	-0.977230095	1.11715E-07
1980	W903_RS09845	W903_2016	1946441	1947856	NA	hypothetical protein	-0.96818615	1.33437E-08	-0.681502384	6.10496E-05	-0.681502384	6.10496E-05
1981	W903_RS09850	W903_2017	1948178	1948627	NA	sigma-70, region 4 family protein	1.421948427	0.068653209	1.499204768	2.78646E-06	1.499204768	2.78646E-06
1982	W903_RS09855	W903_2018	1948830	1949150	NA	hypothetical protein	1.767873677	NA	1.687066843	0.005623457	1.687066843	0.005623457
1983	W903_RS09860	W903_2019	1949150	1950250	NA	ftsK/SpoIIIE family protein	1.799928498	0.000589242	1.08667606	3.03157E-05	1.08667606	3.03157E-05
1984	W903_RS09865	W903_2020	1950247	1950852	NA	hypothetical protein	0.015053813	0.98246628	1.249592291	0.000313745	1.249592291	0.000313745
1985	W903_RS09870	W903_2021	1951051	1951656	NA	plasmid replication family protein	0.155731761	0.844341147	0.516311159	0.237846132	0.516311159	0.237846132
1986	W903_RS09875	W903_2022	1951649	1951897	NA	merR HTH regulatory family protein	-2.551407256	NA	-0.687838552	0.611805082	-0.687838552	0.611805082
1987	W903_RS09880	W903_2023	1951986	1953251	NA	phage integrase family protein	0.211125078	0.280824017	0.981926879	6.67953E-21	0.981926879	6.67953E-21
1988	W903_RS09885	W903_2024	1953609	1954280	NA	peptidase propeptide and YPEB domain protein	-0.121451704	0.842711997	-2.066406596	6.3639E-11	-2.066406596	6.3639E-11
1989	W903_RS09890	W903_2025	1954365	1955036	NA	response regulator	-0.442736694	0.04309935	0.014100853	0.929147843	0.014100853	0.929147843
1990	W903_RS09895	W903_2026	1955020	1956384	NA	HAMP domain protein	0.091850704	0.644585685	0.138360195	0.207857147	0.138360195	0.207857147
1991	W903_RS09900	W903_2027	1956496	1958049	NA	citrate transporter family protein	0.874943039	0.19150187	1.623589449	0.000126246	1.623589449	0.000126246
1992	W903_RS09905	W903_2028	1958143	1959069	NA	carbamate kinase	0.73399848	0.344511372	1.717749938	9.73771E-05	1.717749938	9.73771E-05
1993	W903_RS09910	W903_2029	1959081	1960079	NA	ornithine carbamoyltransferase	0.717719715	0.299030732	1.325929875	0.000455035	1.325929875	0.000455035
1994	W903_RS09915	W903_2030	1960172	1961467	NA	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-0.465776924	0.17915471	0.655771265	0.000638759	0.655771265	0.000638759
1995	W903_RS09920	W903_2031	1961464	1962297	NA	response regulator	-0.421696458	0.405459082	1.010405506	1.66551E-05	1.010405506	1.66551E-05
1996	W903_RS09925	W903_2032	1962519	1963241	NA	ABC transporter family protein	0.600320552	0.001577285	1.054586337	7.94189E-21	1.054586337	7.94189E-21
1997	W903_RS09930	W903_2033	1963244	1964758	NA	substrate binding domain of ABC-type glycine betaine transport system family protein	0.782197739	2.55269E-06	0.663345581	1.75685E-08	0.663345581	1.75685E-08
1998	W903_RS09935	W903_2034	1964836	1967376	NA	hypothetical protein	0.302759879	0.083297881	0.015460451	0.880187916	0.015460451	0.880187916
1999	W903_RS09940	W903_2035	1967360	1968109	NA	alpha/beta hydrolase fold family protein	-0.15406601	0.374246483	0.602864026	4.74302E-07	0.602864026	4.74302E-07
2000	W903_RS09945	W903_2036	1968237	1968593	NA	hypothetical protein	0.008419905	0.992189052	2.255895415	2.06169E-11	2.255895415	2.06169E-11
2001	W903_RS09950	W903_2037	1968660	1970978	NA	yhgE/Pip N-terminal domain protein	0.381958588	0.087187835	2.049196976	2.45153E-57	2.049196976	2.45153E-57
2002	W903_RS09955	W903_2038	1971117	1971656	NA	bacterial regulatory s, tetR family protein	-1.002874769	0.000217519	0.670045713	0.0002586	0.670045713	0.0002586
2003	W903_RS09960	W903_2039	1971742	1972038	NA	hypothetical protein	0.003533634	0.995623902	1.503969485	5.93146E-06	1.503969485	5.93146E-06
2004	W903_RS09965	W903_2040	1972282	1972893	rpsD	ribosomal protein S4	-0.662014912	0.000240839	-2.226532275	3.7419E-135	-2.226532275	3.7419E-135
2005	W903_RS09970	W903_2041	1973223	1973510	NA	hypothetical protein	1.046032862	9.94861E-08	1.305065241	1.37829E-10	1.305065241	1.37829E-10
2006	W903_RS09975	W903_2042	1973522	1974877	dnaB	replicative DNA helicase	0.201517916	0.232940747	0.341477472	9.14611E-05	0.341477472	9.14611E-05
2007	W903_RS09980	W903_2043	1974920	1975372	rplI	ribosomal protein L9	0.453591747	0.003977185	0.218659435	0.066115276	0.218659435	0.066115276
2008	W903_RS09985	W903_2044	1975378	1977360	NA	DHHA1 domain protein	-0.711684182	1.01233E-06	0.415037193	7.70726E-06	0.415037193	7.70726E-06
2009	W903_RS09990	W903_2045	1977427	1979328	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	0.387583186	0.014404326	-1.293714109	1.94062E-32	-1.293714109	1.94062E-32
2010	W903_RS09995	W903_2046	1979498	1980109	NA	marC integral membrane family protein	1.140820888	4.35962E-09	0.536817731	0.007468917	0.536817731	0.007468917
2011	W903_RS10000	W903_2047	1980146	1981267	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	0.618945146	0.000799965	-0.138695512	0.491687749	-0.138695512	0.491687749
2012	W903_RS10005	W903_2048	1981513	1982181	sdaAB	L-serine dehydratase, iron-sulfur-dependent, beta subunit	0.028913711	0.876832988	0.05426951	0.723359137	0.05426951	0.723359137
2013	W903_RS10010	W903_2049	1982196	1983068	sdaAA	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	0.421648709	0.008233986	0.018567459	0.912279779	0.018567459	0.912279779
2014	W903_RS10015	W903_2050	1983203	1983880	NA	transglycosylase SLT domain protein	-2.340634132	3.99635E-32	0.493749481	1.3357E-07	0.493749481	1.3357E-07
2015	W903_RS10020	W903_2051	1984013	1984552	NA	lysM domain protein	-2.354301098	4.55491E-26	1.56229905	2.15718E-47	1.56229905	2.15718E-47
2016	W903_RS10025	W903_2052	1984768	1985562	ecfT	energy-coupling factor transporter transmembrane protein EcfT	0.430804839	0.006108359	-0.128899421	0.445223688	-0.128899421	0.445223688
2017	W903_RS10030	W903_2053	1985555	1986397	NA	ABC transporter family protein	0.487784996	0.00234211	-0.233920954	0.197309173	-0.233920954	0.197309173
2018	W903_RS10035	W903_2054	1986373	1987212	NA	ABC transporter family protein	-0.227313389	0.210500581	-0.319410436	0.001702434	-0.319410436	0.001702434
2019	W903_RS10040	W903_2055	1987212	1987751	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	-0.39260945	0.011457307	-0.502635092	1.21981E-07	-0.502635092	1.21981E-07
2020	W903_RS10045	W903_2056	1987877	1989160	NA	peptidase M16 inactive domain protein	-0.271943731	0.155541445	-0.598801922	1.59311E-06	-0.598801922	1.59311E-06
2021	W903_RS10050	W903_2057	1989162	1990406	NA	peptidase M16 inactive domain protein	-0.930224427	4.54475E-08	-0.712188833	1.22854E-09	-0.712188833	1.22854E-09
2022	W903_RS10055	W903_2058	1990645	1990998	NA	S4 domain protein	-1.124722471	9.23878E-12	0.196026433	0.132791205	0.196026433	0.132791205
2023	W903_RS10060	W903_2059	1991001	1992110	recF	DNA replication and repair RecF family protein	-1.141044264	2.04946E-13	-0.578584449	7.92181E-08	-0.578584449	7.92181E-08
2024	W903_RS10065	W903_2060	1992122	1992988	NA	sugar transport family protein	-0.612517746	0.00012166	0.84356435	2.61559E-13	0.84356435	2.61559E-13
2025	W903_RS10070	W903_2061	1993044	1993706	NA	helix-turn-helix family protein	-1.326476902	4.07285E-16	0.757373459	1.3733E-06	0.757373459	1.3733E-06
2026	W903_RS10075	W903_2062	1993781	1995262	guaB	inosine-5'-monophosphate dehydrogenase	-0.030935472	0.869731936	-0.266077175	0.007712364	-0.266077175	0.007712364
2027	W903_RS10080	W903_2063	1995419	1995904	NA	arginine regulator	0.399258056	0.045135298	-0.202432702	0.131126092	-0.202432702	0.131126092
2028	W903_RS10085	W903_2064	1995914	1996594	NA	cyclic nucleotide-binding domain protein	-1.22856987	9.01453E-12	-1.535580212	7.724E-41	-1.535580212	7.724E-41
2029	W903_RS10090	W903_2065	1996802	1997506	NA	B3/4 domain protein	-0.677817743	0.013077952	0.514797222	0.014637218	0.514797222	0.014637218
2030	W903_RS10095	W903_2066	1997773	1999005	arcA	arginine deiminase	-0.863548983	3.08386E-07	0.210407438	0.07780587	0.210407438	0.07780587
2031	NA	W903_2067	1999101	1999442	NA	acetyltransferase family protein	0.040903096	0.872590989	3.198095092	4.4486E-202	3.198095092	4.4486E-202
2032	W903_RS10105	W903_2068	1999458	2000471	NA	ornithine carbamoyltransferase	0.428846235	0.087948687	4.015566188	8.5186E-250	4.015566188	8.5186E-250
2033	W903_RS10110	W903_2069	2000534	2001961	arcD	arginine-ornithine antiporter	0.15560012	0.549536178	4.683935603	2.0375E-297	4.683935603	2.0375E-297
2034	W903_RS10115	W903_2070	2001982	2002938	NA	carbamate kinase	-0.238916228	0.446374739	4.706848033	0	4.706848033	0
2035	W903_RS10120	W903_2071	2003048	2004073	trpS	tryptophan--tRNA ligase	-0.918860711	4.12945E-10	-0.120299826	0.277888046	-0.120299826	0.277888046
2036	W903_RS10125	W903_2072	2004181	2004873	NA	hypothetical protein	-1.386788767	2.35475E-12	-0.064309076	0.632450797	-0.064309076	0.632450797
2037	W903_RS10130	W903_2073	2005117	2005989	NA	hypothetical protein	-0.93610709	1.44791E-06	-1.20897515	1.34149E-26	-1.20897515	1.34149E-26
2038	W903_RS10135	W903_2074	2006055	2007674	NA	ABC transporter family protein	0.010577469	0.9495054	-0.701971158	1.73807E-13	-0.701971158	1.73807E-13
2039	W903_RS10140	W903_2075	2007797	2010376	NA	bacterial membrane YfhO family protein	-0.141927832	0.484301603	0.174797879	0.232430401	0.174797879	0.232430401
2040	W903_RS10145	W903_2076	2010444	2010517	NA	NA	NA	NA	NA	NA	NA	NA
2041	W903_RS10150	W903_2077	2010547	2010618	rRNA	NA	-1.319861842	NA	2.619633458	0.546966741	2.619633458	0.546966741
2042	W903_RS10155	W903_2078	2010810	2010883	tRNA	NA	5.983581516	NA	-3.965965277	0.334290595	-3.965965277	0.334290595
2043	W903_RS10160	W903_2079	2010955	2011434	rlmH	rRNA large subunit m3Psi methyltransferase RlmH	-0.224996669	0.272179322	1.1328715	1.29697E-13	1.1328715	1.29697E-13
2044	W903_RS10165	W903_2080	2011635	2012864	NA	trypsin family protein	-0.471948839	0.001425449	-1.905234906	5.73704E-52	-1.905234906	5.73704E-52
2045	W903_RS10170	W903_2081	2012962	2013735	NA	parB/RepB/Spo0J family partition domain protein	-0.065278084	0.750272478	-0.326422211	0.015128732	-0.326422211	0.015128732