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

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.

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, inhospitable 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

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 *mrpR*, 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

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-counters selectable 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.

To establish proof-of-concept for this approach we knocked down the first open reading frame (*cy/X*) in the *cy/* operon that encodes genes responsible for synthesis of the pigmented cytotoxin β -hemolysin/cytolysin (50). p3015b encoding anti-*cy/X* 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-*cy/X* 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.

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

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 *mrpR* gene.

MrpR controls GBS biofilm formation

We observed phenotypic differences in growth of the *mrpR* 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.

MrpR activity does not affect vaginal colonization

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

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.

232

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

240

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

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

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

254

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

260

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

267

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

270

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

275

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

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—

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.

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

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

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

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)

medium (Fisher Scientific cat. # DF0370-17-3), supplemented with 5 µg/ml erythromycin, 150 µg/ml spectinomycin, or rifampin 10 µg/ml as needed for selection. *Escherichia coli* was grown at 37°C (or 28°C with extrachromosomal pMBSacB present) with shaking in Luria-Bertani (LB) medium (Fisher Scientific cat. # DF9446-07-5) supplemented with 300 µg/ml erythromycin and 150 µg/ml spectinomycin as needed for selection. *Brevibacillus choshinensis* for expression of recombinant MrvR was grown at 28°C in TM or 2SY media supplemented with neomycin 50 µg/mL according to the recommendations of Takara Bio.

Tn-seq on GBS grown in human amniotic fluid

Discarded, anonymous amniotic fluid from amniocentesis was obtained from the NYU-Langone Medical Center Department of Obstetrics and Gynecology. Samples were stored frozen at -20°C, then thawed on ice. Before use in outgrowth experiments, the amniotic fluid was passed through a 0.2 µm sterile filter.

A previously described saturated transposon mutant library in an A909 background (41) was thawed from frozen stock. The library was washed twice in sterile PBS to remove glycerol cryoprotectant, then resuspended in 3 mL PBS and seeded into 100 mL of TS broth with erythromycin selection. After overnight outgrowth, 20 mL of the library was seeded into fresh TS broth with erythromycin and allowed to grow to mid-log phase (OD₆₀₀=1). 120 mL of this culture was then pelleted and washed twice with PBS, then resuspended in 1 mL of PBS.

50 μ L 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 Mmel 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

minimum was at a log₂ fold-change value of -3.22. The five candidate genes evaluated had log₂ 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 minipreped 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

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 OD₆₀₀ of 0.8. These suspensions were

then plated as serial dilutions to confirm that the starting CFU concentrations were approximately equal.

500 μ L from each of the 11 normalized GBS suspensions were then combined to make a starting mixed culture. A sample of this mixed culture was used for plasmid DNA purification using the Thermo MagJET plasmid DNA Kit (cat. # K2791) according to manufacturer instructions.

Amniotic fluid or TS broth containing erythromycin for continued plasmid selection was pre-warmed to 37°C and seeded 1:50 with the mixed culture, then allowed to grow stationary overnight. 24 hours after seeding, plasmid DNA was extracted from the amniotic fluid and TS samples.

At both the starting and 24-hour timepoints, prior to purification, DNA from dead bacteria was removed using ethidium monoazide using techniques described by Soejima et al. (100). Ethidium monoazide—which binds to extracellular DNA or DNA within dead bacteria, but not to DNA within live cells—was added to a final concentration of 10 μ g/mL, after which the cultures were allowed to incubate at 4°C for five minutes. They were then placed under a high intensity white light source, which destroys DNA bound to ethidium monoazide. The treated samples were then spun down, washed once in PBS, then used for plasmid purification.

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: $\ln((NE^{\text{target}}_{T24}/NE^{\text{target}}_{T0})/(NE^{\text{sham}}_{T24}/NE^{\text{sham}}_{T0}))$ 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

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 *mrpR* 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 = $\ln((\text{CFU}^{\text{expt}}_{\text{T24}}/\text{CFU}^{\text{expt}}_{\text{T0}})/(\text{CFU}^{\text{WT}}_{\text{T24}}/\text{CFU}^{\text{WT}}_{\text{T0}}))$; here, expt represents the

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 *mrpR* knockout GBS were grown to late logarithmic phase in TS broth. The two cultures were then normalized to an OD₆₀₀ 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. OD₆₀₀ 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. OD₆₀₀ absorbance readings of the planktonic phase bacteria were recorded.

601

602 The plate that grew overnight was then used to stain the residual biofilms. 500 μ L of 1% crystal
603 violet was carefully added to each well, being cautious not to disturb the biofilm. After 10
604 minutes of gentle shaking at room temperature, the stain was removed and each well was
605 washed three times in 1 mL of sterile PBS. After the final wash, the stained biofilm was allowed
606 to dry, then solubilized with 1 mL of a 20% acetone/80% ethanol solution. Absorbance at 550
607 nm was measured. Biofilm indices were calculated as OD₅₅₀/OD₆₀₀. The experiment was
608 performed three times with three technical replicates for each condition.

609

610 *Murine vaginal colonization model*

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

613

614 6- to 8-week old mice were injected subcutaneously with 0.5 mg β -estradiol on two successive
615 days to synchronize estrus. On the third day, stationary phase GBS was pelleted and
616 resuspended in a 1:1 mixture of PBS and a sterile 10% gelatin solution to enhance viscosity. The
617 mixtures were diluted and plated for CFU enumeration. Mice were vaginally colonized with 50
618 μ L, corresponding to 10^7 CFU.

619

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

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 *mrpR* 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.

645

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

648

649 *Generation of luciferase reporter GBS*

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

656

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

662

663 *Adult mouse sepsis model with in vivo imaging*

664 Six- to eight-week old female BALB/c mice were injected intraperitoneally under general
665 anesthesia with 10⁸ CFU of PBS-washed, stationary phase WT 10/84 or *mrpR* knockout 10/84
666 bearing the pFfluc-Erm plasmid and 500 µg of D-luciferin in 500 µL PBS. Immediately after the

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 *mrpR* 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 OD₆₀₀ 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.

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,

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

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.

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754

755 Data availability

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

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 (mrpR)
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

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 log₂ 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, *mrpR*.

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

to wild type in a human erythrocyte hemolysis assay (**A**). Targeting protospacers against the five candidate conditionally essential genes from amniotic fluid Tn-seq. For each gene, the number indicates the targeted nucleotide; the protospacer sequence is shown in parentheses (**B**). A qPCR-based multiplex CRISPRi screen using knockdowns of all five candidate genes revealed decreased fitness in amniotic fluid compared to tryptic soy (TS) broth (**C**); black columns show the competition index of strains bearing individual targeting protospacer plasmids, while red columns show pooled results from both targeting plasmids for each gene. Statistical significance of each knockdown phenotype was determined relative to growth of the knockdowns in TS broth. Growth curves of the $\Delta mrvR$ and wild type (WT) 10/84 in broth (**D**). Colony forming unit enumeration-based competition assays between $\Delta mrvR$ and $\Delta mrvR$ +pBSU101::*mrvR* in TS broth (TSB) and amniotic fluid (AF); **E**). Biofilm assay results comparing WT 10/84, $\Delta mrvR$, and $\Delta mrvR$ +pBSU101::*mrvR*. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.005$, **** $p < 0.001$; t test. Error bars show SEM surrounding mean.

Figure 3. MrvR does not affect establishment or maintenance of vaginal colonization. Adult nonpregnant C57/BLJ mice were vaginally colonized with wild type (WT) 10/84 or $\Delta mrvR$. Neither the colonization density at the initial swab 48 hours after inoculation (**A**) nor duration of colonization (**B**) showed significant differences (CFU: colony forming units, NS: not significant).

Figure 4. MrvR has a significant effect on the outcome of chorioamnionitis. Pregnant BALB/c mice were vaginally colonized with wild type (WT) or knockout (KO) 10/84 on pregnancy day 13.

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 $\Delta mrvR$, 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 $\Delta mrvR$ 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

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

838

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 log₂ 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 *ΔmrvR* with wild type 10/84 genome-wide gene expression

Output from DESeq analysis of RNA-seq read alignments. Log₂ 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 *ΔmrvR*

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

Figure 2

Figure 3

Figure 4

Figure 5

Figure 6

Supplemental Figure 1

E.

F.

Supplemental Figure 2

A.

WT 10/84

$\Delta mrvR$

B.

Supplemental Figure 3

Supplemental Figure 4

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	-

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 thil
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 -

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	dnal
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	tkl
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	-

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	-0.660648445	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

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	-0.527373741	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 -

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	bgIF
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	-

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	-0.367773083	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	0.532638663	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	-0.327373747	0.554895886	155947	157821 +	1875 -
799	SAK_RS03985	SAK_0799	-0.318648488	0.561984187	735195	737390 +	2196 cyll
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	-0.31009844	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	1484748 -	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 -

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	hybB
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	cykK
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	-0.141141427	0.668875802	795642	799181	+	3540	smc
1436	SAK_RS07225	SAK_1436	-0.138844243	0.650587689	1417758	1418342	-	585	-
1567	SAK_RS07905	SAK_1567	-0.138672776	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	-

218	SAK_RS01080	SAK_0218	0.014173891	0.801399041	181691	182401 +
1269	SAK_RS06365	SAK_1269	0.016561348	0.798575081	1239085	1240296 -
362	SAK_RS01795	SAK_0362	0.0166615119	0.790842059	310141	310953 +
1205	SAK_RS06030	SAK_1205	0.017902944	0.808557912	1181759	1183042 -
1431	SAK_RS07200	SAK_1431	0.023907149	0.754165972	1413179	1413967 -
1211	SAK_RS06065	SAK_1211	0.024530554	0.813648074	1186680	1188056 -
710	SAK_RS03550	SAK_0710	0.031296895	0.806112633	643666	644307 +
1598	#N/A	SAK_1598	0.031491128	0.809601261	1592635	1593801 +
482	SAK_RS02405	SAK_0482	0.034581454	0.820363131	425814	426629 +
660	SAK_RS03300	SAK_0660	0.034987949	0.815439636	590323	591543 +
324	SAK_RS01600	SAK_0324	0.038668395	0.787363092	270039	270389 +
1014	SAK_RS05075	SAK_1014	0.04172686	0.815439636	977761	978498 +
1207	#N/A	SAK_1207	0.043482882	0.813648074	1184129	1184866 -
1912	SAK_RS09630	SAK_1912	0.045764087	0.808018227	1915327	1916379 -
1653	SAK_RS08330	SAK_1653	0.045784301	0.823482079	1644268	1645338 -
457	SAK_RS02275	SAK_0457	0.050593189	0.824716875	401507	402511 -
1358	SAK_RS06835	SAK_1358	0.058038438	0.824716875	1340542	1341771 -
1321	SAK_RS06635	SAK_1321	0.05864016	0.813710336	1302923	1303948 -
244	SAK_RS01200	SAK_0244	0.058645393	0.831771161	208114	208740 +
1283	SAK_RS06435	SAK_1283	0.059978048	0.813759978	1255047	1255529 -
1727	SAK_RS08685	SAK_1727	0.06058739	0.837397003	1715067	1717406 -
1559	SAK_RS07860	SAK_1559	0.063681056	0.768846129	1556415	1556684 -
209	SAK_RS01035	SAK_0209	0.065684913	0.813710336	172789	173835 +
2069	SAK_RS10410	SAK_2069	0.067996187	0.842249492	2062058	2063572 +
1933	SAK_RS09735	SAK_1933	0.069105753	0.837987743	1934944	1935414 -
1656	SAK_RS08345	SAK_1656	0.071651311	0.835884371	1647806	1648639 -
1601	SAK_RS08075	SAK_1601	0.072715782	0.824716875	1595016	1595645 -
1652	SAK_RS08325	SAK_1652	0.072844969	0.836057263	1643579	1644271 -
546	SAK_RS02715	SAK_0546	0.073168196	0.791821529	486768	487460 +
2122	SAK_RS10690	SAK_2122	0.075768657	0.837987743	2113016	2113426 +
877	SAK_RS04385	SAK_0877	0.077470491	0.843925747	822747	823649 +
1301	SAK_RS06525	SAK_1301	0.080402841	0.844224164	1275768	1276685 -
950	SAK_RS04750	SAK_0950	0.080665286	0.813648074	904400	905029 +
511	SAK_RS02540	SAK_0511	0.081493685	0.837987743	453701	454016 -
1777	SAK_RS08945	SAK_1777	0.084486755	0.824716875	1770522	1770791 +
1274	SAK_RS06390	SAK_1274	0.089467652	0.852242343	1244864	1245625 -
1191	SAK_RS05960	SAK_1191	0.101062103	0.844026277	1169022	1169951 +
1713	SAK_RS08615	SAK_1713	0.105131823	0.86485475	1701106	1701558 -
531	SAK_RS02640	SAK_0531	0.107578594	0.866941123	472910	473740 -
687	SAK_RS03435	SAK_0687	0.108798334	0.868220847	622158	623093 -
1875	SAK_RS09440	SAK_1875	0.111782044	0.857851698	1874658	1874999 -
194	SAK_RS00960	SAK_0194	0.117512411	0.871012075	154261	155811 -
990	SAK_RS04955	SAK_0990	0.117855872	0.744868906	945541	945732 +
822	SAK_RS04115	SAK_0822	0.121695069	0.880862072	764592	766142 +
1427	SAK_RS07180	SAK_1427	0.128199326	0.844224164	1409362	1410387 +
1491	SAK_RS07500	SAK_1491	0.128771989	0.868220847	1481120	1482325 -
9	SAK_RS00040	SAK_0009	0.130201961	0.877799791	10032	10304 +
261	SAK_RS01285	SAK_0261	0.130243916	0.878494612	226518	227873 +
1923	SAK_RS09685	SAK_1923	0.13094789	0.865709617	1927213	1927869 -
2008	SAK_RS10100	SAK_2008	0.131508246	0.884241512	2002262	2003473 -
2075	SAK_RS10440	SAK_2075	0.133054552	0.813648074	2070494	2070790 -
1169	SAK_RS05850	SAK_1169	0.136237429	0.844026277	1146247	1147035 +
1938	SAK_RS09760	SAK_1938	0.139422529	0.884166911	1937468	1938736 +
497	#N/A	SAK_0497	0.144050382	0.893244474	437701	441403 +
1013	SAK_RS05070	SAK_1013	0.145103661	0.882439255	976627	977757 +
2115	SAK_RS10655	SAK_2115	0.146474027	0.893244474	2106106	2106972 -
1258	SAK_RS06310	SAK_1258	0.14859937	0.874294761	1228909	1230297 -
2079	SAK_RS10455	SAK_2079	0.148740463	0.875889185	2072866	2073252 -
1256	SAK_RS06300	SAK_1256	0.149557676	0.865801714	1227954	1228436 -
1796	SAK_RS09040	SAK_1796	0.15176649	0.871012075	1788898	1790172 -
878	SAK_RS04390	SAK_0878	0.151790988	0.870973876	823685	824326 -
1183	SAK_RS05920	SAK_1183	0.152700909	0.871167183	1160993	1162108 +
86	SAK_RS00425	SAK_0086	0.153231056	0.725612393	68961	71603 +
1294	SAK_RS06490	SAK_1294	0.154663053	0.893244474	1268651	1270849 -
262	SAK_RS01290	SAK_0262	0.154730201	0.871919603	227876	228733 +
237	SAK_RS01165	SAK_0237	0.159764971	0.890748321	203775	204230 +
1074	SAK_RS05370	SAK_1074	0.162748148	0.888249397	1045289	1046950 +
1813	SAK_RS09130	SAK_1813	0.172426136	0.882439255	1803206	1804393 -
1642	SAK_RS08275	SAK_1642	0.177320394	0.879569896	1632870	1633424 -
81	SAK_RS00400	SAK_0081	0.177333208	0.899028989	63833	64741 +
2051	SAK_RS10315	SAK_2051	0.180120041	0.890748321	2044224	2044838 +
935	SAK_RS04675	SAK_0935	0.180940165	0.87602693	888356	889072 +
205	SAK_RS01015	SAK_0205	0.181888614	0.871167183	167571	168806 -
1978	SAK_RS09955	SAK_1978	0.188528322	0.917868692	1965725	1966339 -
962	SAK_RS04815	SAK_0962	0.190743806	0.910846078	916794	917474 +
1858	SAK_RS09355	SAK_1858	0.191286009	0.888249397	1853911	1854864 +
552	SAK_RS02745	SAK_0552	0.199219037	0.932749146	495079	496071 +
193	SAK_RS00955	SAK_0193	0.200715698	0.910846078	153511	154251 -
1419	SAK_RS07140	SAK_1419	0.203369236	0.922003891	1401599	1402123 -
1930	SAK_RS09720	SAK_1930	0.205032118	0.899028989	1932657	1933610 -
1474	SAK_RS07410	SAK_1474	0.205971008	0.922888442	1458587	1459615 -
5	#N/A	SAK_0005	0.206834276	0.922888442	4113	4229 +
1773	SAK_RS08925	SAK_1773	0.209114726	0.940662421	1767064	1767651 -
1137	SAK_RS05685	SAK_1137	0.210888485	0.930371688	1112336	1113037 -
1633	SAK_RS08230	SAK_1633	0.213318173	0.899028989	1621589	1624687 -
1465	SAK_RS07365	SAK_1465	0.214212726	0.935910013	1447293	1447796 -
1275	SAK_RS06395	SAK_1275	0.216122026	0.930371688	1245625	1246488 -
216	SAK_RS01070	SAK_0216	0.216358469	0.922985095	180308	181159 +
1819	SAK_RS09160	SAK_1819	0.221060494	0.860634817	1810687	1813065 -
1279	SAK_RS06415	SAK_1279	0.226845972	0.938026098	1250306	1251988 -
1482	SAK_RS07455	SAK_1482	0.227688247	0.899977066	1468757	1471144 -
1775	SAK_RS08935	SAK_1775	0.229998032	0.946168569	1768366	1769538 +
1411	SAK_RS07100	SAK_1411	0.230417915	0.956185751	1394041	1395108 -

711	adcC
1212	deoB
813	-
1284	hom
789	pflA
1377	-
642	serB
1167	livK
816	-
1221	-
351	-
738	-
738	-
1053	-
1071	-
1005	-
1230	-
1026	-
627	-
483	mutX
2340	-
270	-
1047	oppD
1515	-
471	-
834	-
630	upp
693	metI
693	-
411	-
903	-
918	-
630	udk
316	-
270	rpsN
762	-
930	-
453	-
831	-
936	-
342	yajC
1551	-
192	-
1551	-
1026	fluB
1206	-
273	-
1356	ulaA
657	phoU
1212	deoB
297	-
789	-
1269	-
3703	scpA
1131	-
867	-
1389	cpsE
387	-
483	-
1275	-
642	-
1116	-
2643	-
2199	recJ
858	-
456	-
1662	-
1188	dlrS
555	-
909	-
615	cadD
717	-
1236	-
615	-
681	-
954	-
993	asnA
741	-
525	-
954	prmA
1029	-
117	-
588	-
702	pyrF
3099	-
504	-
864	-
852	ipk
2379	xpkA
1683	budB
2388	secA
1173	-
1068	aroB

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	rbxC
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	rbxK
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

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

1026	ItaE
999	argF
609	-
744	-
1134	glgD
540	-
1206	-
1353	-
546	-
726	-
756	-
1431	glgA
1587	-
303	-
465	-
957	-
819	-
116	rrfG
420	-
1350	-
116	rrfA
876	hslO
237	-
345	-
837	-
756	-
1230	-
116	rrfB
657	-
2319	-
930	-
558	lepB
729	-
804	-
1443	gatB
2016	recG
954	cylF
600	recU
630	neuD
189	rpmB
540	-
651	-
357	rplR
396	-
237	-
387	-
732	-
1356	-
771	proC
1485	cstA
1782	uvrC
2037	-
681	-
116	rrfF
1284	-
339	-
2073	-
357	-
489	-
1242	neuA
405	-
930	cylA
600	-
684	-
1896	pepO
975	prs
948	mraW
1635	-
1482	guaB
2070	-
714	-
828	-
927	-
2121	topA
2130	pnp
1023	pfoR
1188	-
306	-
1740	-
1035	-
2448	clpC
507	-
1998	metG
849	-
116	rrfC
813	-
465	lspA
1416	-
723	-
1746	-
717	araD
429	-
444	-

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 -

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 rhuD
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 -

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	0.362607473	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 gltA
250	SAK_RS01230	SAK_0250	2.578352142	0.198989025	213417	213872 +	456 -
1649	SAK_RS08310	SAK_1649	2.581309298	0.145369724	1639611	1640819 -	1209 yggJ
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

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	rhsB
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	psrA
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	rhsD
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	rhsA
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	-

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	3.234775503	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	0.198898025	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

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 -

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	-

128	#N/A	SAK_0128	NA	NA
129	#N/A	SAK_0129	NA	NA
131	#N/A	SAK_0131	NA	NA
132	#N/A	SAK_0132	NA	NA
133	#N/A	SAK_0133	NA	NA
134	#N/A	SAK_0134	NA	NA
135	#N/A	SAK_0135	NA	NA
136	#N/A	SAK_0136	NA	NA
138	#N/A	SAK_0138	NA	NA
145	SAK_RS00715	SAK_0145	NA	NA
146	SAK_RS00720	SAK_0146	NA	NA
147	SAK_RS00725	SAK_0147	NA	NA
148	SAK_RS00730	SAK_0148	NA	NA
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156	SAK_RS00770	SAK_0156	NA	NA
157	SAK_RS00775	SAK_0157	NA	NA
159	#N/A	SAK_0159	NA	NA
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165	SAK_RS00815	SAK_0165	NA	NA
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181	SAK_RS00895	SAK_0181	NA	NA
182	SAK_RS00900	SAK_0182	NA	NA
185	SAK_RS00920	SAK_0185	NA	NA
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200	SAK_RS00990	SAK_0200	NA	NA
201	SAK_RS00995	SAK_0201	NA	NA
202	SAK_RS01000	SAK_0202	NA	NA
203	SAK_RS01005	SAK_0203	NA	NA
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213	#N/A	SAK_0213	NA	NA
215	#N/A	SAK_0215	NA	NA
221	SAK_RS01095	SAK_0221	NA	NA
223	SAK_RS01105	SAK_0223	NA	NA
231	SAK_RS01140	SAK_0231	NA	NA
235	SAK_RS01160	SAK_0235	NA	NA
265	SAK_RS01305	SAK_0265	NA	NA
267	SAK_RS01315	SAK_0267	NA	NA
268	SAK_RS01320	SAK_0268	NA	NA
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277	SAK_RS01360	SAK_0277	NA	NA
279	SAK_RS01370	SAK_0279	NA	NA
280	SAK_RS01375	SAK_0280	NA	NA
281	SAK_RS01380	SAK_0281	NA	NA
289	SAK_RS01425	SAK_0289	NA	NA
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304	#N/A	SAK_0304	NA	NA
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306	#N/A	SAK_0306	NA	NA
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334	SAK_RS01655	SAK_0334	NA	NA
336	SAK_RS01665	SAK_0336	NA	NA
340	SAK_RS01685	SAK_0340	NA	NA
342	SAK_RS01695	SAK_0342	NA	NA
343	SAK_RS01700	SAK_0343	NA	NA
350	SAK_RS01735	SAK_0350	NA	NA
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361	SAK_RS01790	SAK_0361	NA	NA
363	SAK_RS01800	SAK_0363	NA	NA
364	SAK_RS01805	SAK_0364	NA	NA
366	SAK_RS01815	SAK_0366	NA	NA
367	SAK_RS01820	SAK_0367	NA	NA
368	SAK_RS01825	SAK_0368	NA	NA
373	SAK_RS01850	SAK_0373	NA	NA
383	SAK_RS01900	SAK_0383	NA	NA
384	SAK_RS01905	SAK_0384	NA	NA
386	SAK_RS01915	SAK_0386	NA	NA
388	SAK_RS01925	SAK_0388	NA	NA
392	SAK_RS01945	SAK_0392	NA	NA
394	SAK_RS01955	SAK_0394	NA	NA
398	SAK_RS01975	SAK_0398	NA	NA
399	SAK_RS01980	SAK_0399	NA	NA
409	#N/A	SAK_0409	NA	NA
410	#N/A	SAK_0410	NA	NA
411	#N/A	SAK_0411	NA	NA
413	#N/A	SAK_0413	NA	NA

96357	96428 +	72 -
96442	96531 +	90 -
96618	96690 +	73 -
96702	96782 +	81 -
96789	96859 +	71 -
96874	96946 +	73 -
96953	97024 +	72 -
97035	97118 +	84 -
98033	98203 +	171 -
103266	104300 +	1035 hrcA
104342	104875 +	534 grpE
105056	106885 +	1830 dnaK
107174	108289 +	1116 dnaJ
110460	111218 +	759 -
114766	115341 +	576 rpoE
115614	117218 +	1605 pyrG
118300	118385 +	86 -
118448	118894 +	447 dut
120556	121053 +	498 -
124303	125739 +	1437 gltX
138113	138994 +	882 fba
140555	140920 +	366 -
140953	142584 +	1632 -
145294	145512 -	219 -
159583	160743 +	1161 -
160908	161678 +	771 sufC
161715	162977 +	1263 sufD
162979	164211 +	1233 sufS
164198	164641 +	444 -
164741	166159 +	1419 sufB
175172	176678 +	1507 rrsD
176768	176840 +	73 -
176997	179899 +	2903 rrlD
180095	180168 +	74 -
185024	186283 -	1260 tyrS
189215	192790 +	3576 rpoB
200125	200517 +	393 -
203332	203538 +	207 -
231115	231384 +	270 rpsO
233896	234648 +	753 -
234657	235241 +	585 cysE
235430	236773 +	1344 cysS
239823	239942 +	120 -
240359	240805 +	447 rplM
240826	241218 +	393 rpsL
242569	243120 -	552 -
243285	243578 +	294 -
243719	244000 +	282 -
249463	249750 -	288 -
253046	253144 +	99 -
259761	261267 +	1507 rrsE
261357	261429 +	73 -
261584	264486 +	2903 rrlE
264680	264752 +	73 -
264758	264828 +	71 -
264865	264941 +	77 -
264949	265020 +	72 -
265034	265123 +	90 -
265210	265282 +	73 -
265294	265374 +	81 -
265381	265451 +	71 -
265466	265538 +	73 -
265545	265616 +	72 -
265627	265710 +	84 -
269757	270029 +	273 -
278593	279309 -	717 -
280277	280588 -	312 -
283887	284801 +	915 glyQ
285446	287485 +	2040 glyS
287497	287754 +	258 -
295252	297237 +	1986 tkt
304962	305288 +	327 -
305397	307550 +	2154 pbpX
307552	308562 +	1011 mraY
308660	310003 +	1344 -
311048	311851 +	804 -
311851	312594 +	744 -
313009	313923 +	915 trxB
314081	315541 +	1461 -
315538	316359 +	822 nadE
321398	321730 +	333 -
331680	332309 +	630 gmk
332332	332646 +	315 rpoZ
335157	336092 +	936 fmt
337442	338179 +	738 stp1
341999	342640 +	642 -
344066	344440 +	375 -
347445	347768 +	324 -
347785	348105 +	321 -
358663	360169 +	1507 rrsF
360259	360331 +	73 -
360486	363388 +	2903 rrlF
363584	363657 +	74 -

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 ezhA
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 -

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

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 -

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 -

Supplemental Data 2

	new_locus_tag	old_locus_tag	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 II, beta subunit	-0.088189456	0.62961196	-0.856579541	6.52875613	-0.856579541	6.52975613
3	W903_RS00015	W903_0003	2812	3705	NA	diacylglycerol kinase catalytic domain protein	0.0056217457	8.13016707	0.391108878	0.005227467	0.391108878	0.005227467
4	W903_RS00020	W903_0004	3715	3912	NA	hypothetical protein	-1.31569835	9.20913812	-0.259427933	0.100153884	-0.259427933	0.100153884
5	NA	W903_0005	4037	4177	NA	helix-turn-helix family protein	-0.125996563	0.566833212	0.275656155	0.098843389	0.275656155	0.098843389
6	W903_RS00030	W903_0006	4535	5650	NA	S05 ribosome-binding GTPase family protein	-0.547306916	0.001019086	-1.170317955	7.36474632	-1.170317955	7.36474632
7	W903_RS00037	W903_0007	5734	6309	gph	peptidyl-RNA hydrolase	-0.648196454	0.000656025	-1.397500868	1.65455621	-1.397500868	1.65455621
8	W903_RS00040	W903_0008	6306	9803	hfl	transcription-repair coupling factor	8.1218067E-05	-1.812549654	-1.812549654	2.81494654	-1.812549654	2.81494654
9	W903_RS00045	W903_0009	10094	10366	NA	S4 domain protein	-0.931606411	1.20706E-06	-1.075244929	1.19573614	-1.075244929	1.19573614
10	W903_RS00050	W903_0010	10353	10724	NA	septum formation initiator family protein	-0.812343739	8.9586E-07	-0.762572504	1.67237E-08	-0.762572504	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	his	tRNA(Ile)-tyrosine synthetase	-0.5595875518	5.64499E-06	0.112876081	0.276457054	0.112876081	0.276457054
14	W903_RS00070	W903_0014	13970	14728	NA	hypoxanthine phosphoribosyltransferase	0.50380912	-0.264722774	0.50380912	5.74846E-25	-0.264722774	5.74846E-25
15	W903_RS00075	W903_0015	13969	15698	HflB	ATP-dependent metalloprotease HflB family protein	0.566663928	0.001008051	-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	-0.053706497	0.960968817	0.960968817	-0.053706497	0.960968817
18	W903_RS00090	W903_0018	18292	21192	rRNA	NA	2.788051858	0.238216465	-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	1.048062688	NA	0.86167603	1.048062688	0.86167603	1.048062688
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	0.158210387	0.856110387	0.158210387	0.856110387
26	W903_RS00130	W903_0026	21896	21980	rRNA	NA	-0.517943311	NA	-0.085994339	0.945693439	-0.085994339	0.945693439
27	W903_RS00135	W903_0027	21992	22065	rRNA	NA	-0.259052178	NA	2.130341804	0.436877967	2.130341804	0.436877967
28	W903_RS00140	W903_0028	22073	22146	rRNA	NA	2.707266024	NA	1.317858829	0.055468389	1.317858829	0.055468389
29	W903_RS00145	W903_0029	22298	23834	rRNA	NA	0.403759877	0.377928802	-0.329608987	0.025957193	-0.329608987	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	0.789209799	-0.238216465	-4.469244884	0.025130499	-4.469244884	0.025130499
32	W903_RS00160	W903_0032	27101	27214	rRNA	NA	0.618388837	0.260142929	0.089765495	0.037412149	0.089765495	0.037412149
33	W903_RS00165	W903_0033	27217	27289	rRNA	NA	-0.205930653	NA	1.833398181	0.400871853	1.833398181	0.400871853
34	W903_RS00170	W903_0034	27292	27364	rRNA	NA	-1.228152108	NA	0.596972864	0.765232568	0.596972864	0.765232568
35	W903_RS00175	W903_0035	27367	27439	rRNA	NA	-0.792984594	NA	0.817416983	0.496498369	0.817416983	0.496498369
36	W903_RS00180	W903_0036	27449	27530	rRNA	NA	1.170348617	NA	0.935454221	0.737862841	-1.943554221	0.737862841
37	W903_RS00185	W903_0037	27541	27613	rRNA	NA	0.156810351	NA	1.704132164	0.570912164	1.704132164	0.570912164
38	W903_RS00190	W903_0038	27647	27718	rRNA	NA	-1.095308005	NA	0.639745024	0.384515154	0.639745024	0.384515154
39	W903_RS00195	W903_0039	27727	27811	rRNA	NA	0.300571073	NA	0.807643153	0.300571073	0.807643153	0.300571073
40	W903_RS00200	W903_0040	27823	27896	rRNA	NA	-0.08838173	NA	-0.364985829	0.946331025	-0.364985829	0.946331025
41	W903_RS00205	W903_0041	27904	27977	rRNA	NA	-0.257947718	NA	0.019395492	0.402091417	0.019395492	0.402091417
42	W903_RS00210	W903_0042	27983	28066	rRNA	NA	-0.053834414	NA	0.627721987	0.979450843	0.627721987	0.979450843
43	W903_RS00215	W903_0043	28086	28159	rRNA	NA	0.805293183	0.435886345	1.856524344	0.051326539	1.856524344	0.051326539
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	rRNA	NA	-1.98032567	NA	0.50158491	0.453048129	0.50158491	0.453048129
47	W903_RS00235	W903_0047	28443	28513	rRNA	NA	-3.751779086	NA	2.731406411	0.275636328	2.731406411	0.275636328
48	W903_RS00240	W903_0048	28548	28621	rRNA	NA	-1.70053101	NA	0.909607097	0.94123837	0.909607097	0.94123837
49	W903_RS00245	W903_0049	28548	28712	rRNA	NA	-1.413670643	NA	-0.040787376	0.986162366	-0.040787376	0.986162366
50	W903_RS00250	W903_0050	28958	30295	NA	CHAP domain protein	-1.27039514	3.50543E-17	-0.946475236	1.14662E-26	-0.946475236	1.14662E-26
51	W903_RS00255	W903_0051	30419	31387	prs	ribose-phosphate dihydrokinase family protein	-0.106069267	0.536398445	-0.015310527	0.8830912	-0.015310527	0.8830912
52	W903_RS00260	W903_0052	31495	36720	NA	aminotransferase class-V family protein	0.022672516	0.909836741	-0.237594713	0.015101179	-0.237594713	0.015101179
53	W903_RS00265	W903_0053	32660	34211	recD	DNA repair protein RecD	-0.368482884	0.058233186	-0.234067788	0.010470242	-0.234067788	0.010470242
54	W903_RS00270	W903_0054	34264	34362	NA	CAK protease self-immunity family protein	0.136827932	1.22792E-14	-2.191444446	0.625719807	-2.191444446	0.625719807
55	W903_RS00275	W903_0055	34440	34542	plxX	fatty acid/phospholipid synthetase protein PlxX	-0.107411442	0.554005697	-0.433921214	8.80476E-05	-0.433921214	8.80476E-05
56	W903_RS00280	W903_0056	35443	35682	NA	phosphatopentaine attachment site family protein	0.942089407	1.15664E-09	-0.064272295	0.550545629	-0.064272295	0.550545629
57	W903_RS00285	W903_0057	35806	36510	purC	phosphoribosylaminimidazolecarboxamide synthase	-0.141940036	0.446374739	-2.389249605	1.03297E-26	-2.389249605	1.03297E-26
58	NA	W903_0058	36527	36640	NA	phosphoribosylformylglycinamide synthase domain protein	-0.21814021	NA	-0.392522068	2.00702E-06	-0.392522068	2.00702E-06
59	W903_RS00290	W903_0059	36633	40358	NA	phosphoribosylformylglycinamide synthase	1.167106317	2.44698E-06	-2.858703217	1.9143E-31	-2.858703217	1.9143E-31
60	W903_RS00295	W903_0060	40398	40720	NA	glycylphosphoryl diester phosphodiesterase family protein	0.886525574	0.021623864	-2.810261941	0.5055451E-05	-2.810261941	0.5055451E-05
61	W903_RS00300	W903_0061	40880	42334	purF	amidophosphoribosyltransferase	1.654871277	9.53326E-14	-2.795438952	2.8787E-13	-2.795438952	2.8787E-13
62	W903_RS00305	W903_0062	42362	43384	purM	phosphoribosylformylglycinamide cyclo-ligase	1.660658336	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	-1.063149939	8.15491E-79	-1.063149939	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	purI	phosphoribosylaminimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.368327932	1.22792E-14	-2.191444446	0.625719807	-2.191444446	0.625719807
66	W903_RS00325	W903_0066	46536	47534	NA	peptidase M23 family protein	1.561402587	0.031402678	1.592106764	0.29665E-12	1.592106764	0.29665E-12
67	W903_RS00330	W903_0067	47681	48991	NA	lysM domain protein	-0.187298588	2.6916E-13	0.17465421	0.052700956	0.17465421	0.052700956
68	W903_RS00335	W903_0068	49238	49936	NA	putative N-acetylmannosamine-6-phosphate 2-epimerase	-1.08421958	0.735549557	0.904653999	0.000484969	0.904653999	0.000484969
69	W903_RS00340	W903_0069	49983	51299	NA	bacterial extracellular solute-binding family protein	0.050958373	0.932692932	0.489373303	1.02642E-07	0.489373303	1.02642E-07
70	W903_RS00345	W903_0070	51387	52274	NA	hinge-dependent transport system inner membrane component family protein	0.32456847	0.674964304	2.73974743	7.78981E-14	2.73974743	7.78981E-14
71	W903_RS00350	W903_0071	52284	52834	NA	hinge-dependent transport system inner membrane component family protein	0.385465145	0.120259953	0.385465145	9.38151E-12	0.385465145	9.38151E-12
72	W903_RS00355	W903_00										

138	W903_R500680	W903_0139	97971	98043	NA	NA	NA	NA	NA	NA
139	W903_R500685	W903_0140	98050	98121	rRNA	NA	NA	NA	NA	NA
140	W903_R500690	W903_0141	98132	98215	rRNA	NA	NA	NA	NA	NA
141	W903_R500745	W903_0142	98597	99062	NA	NA	NA	NA	NA	NA
142	W903_R500700	W903_0143	99132	99335	NA	NA	NA	NA	NA	NA
143	W903_R500705	W903_0144	99552	99926	NA	NA	NA	NA	NA	NA
144	W903_R500710	W903_0145	100062	100262	NA	NA	NA	NA	NA	NA
145	W903_R500715	W903_0146	100152	101648	NA	NA	NA	NA	NA	NA
146	W903_R500725	W903_0147	102222	102241	NA	NA	NA	NA	NA	NA
147	W903_R500725	W903_0148	102441	102920	NA	NA	NA	NA	NA	NA
148	W903_R500730	W903_0149	103042	103734	NA	NA	NA	NA	NA	NA
149	W903_R500735	W903_0150	103731	104483	NA	NA	NA	NA	NA	NA
150	W903_R500740	W903_0151	104480	105055	NA	NA	NA	NA	NA	NA
151	W903_R500745	W903_0152	105198	106232	hcrA	NA	NA	NA	NA	NA
152	W903_R500750	W903_0153	106807	106807	NA	NA	NA	NA	NA	NA
153	W903_R500755	W903_0154	106968	108817	NA	NA	NA	NA	NA	NA
154	W903_R500760	W903_0155	108933	109283	NA	NA	NA	NA	NA	NA
155	W903_R500765	W903_0156	109536	110675	dnaJ	NA	NA	NA	NA	NA
156	W903_R500770	W903_0157	110793	112040	NA	NA	NA	NA	NA	NA
157	W903_R500775	W903_0158	112111	112287	trnA	NA	NA	NA	NA	NA
158	W903_R500780	W903_0159	112850	113608	NA	NA	NA	NA	NA	NA
159	W903_R500785	W903_0160	113618	114082	NA	NA	NA	NA	NA	NA
160	W903_R500790	W903_0161	114079	114648	NA	NA	NA	NA	NA	NA
161	W903_R500795	W903_0162	114685	115527	NA	NA	NA	NA	NA	NA
162	W903_R500800	W903_0163	115684	116967	tig	NA	NA	NA	NA	NA
163	W903_R500805	W903_0164	117156	117740	NA	NA	NA	NA	NA	NA
164	W903_R500810	W903_0165	118013	119517	pyrG	NA	NA	NA	NA	NA
165	W903_R500815	W903_0166	119726	120562	NA	NA	NA	NA	NA	NA
166	W903_R500820	W903_0167	120699	120784	rRNA	NA	NA	NA	NA	NA
167	W903_R500825	W903_0168	120847	121293	udtP	phosphatase family protein	NA	NA	NA	NA
168	W903_R500830	W903_0169	122455	122819	radA	DNA repair protein RadA	NA	NA	NA	NA
169	W903_R500835	W903_0170	123452	124524	NA	carbonic anhydrase family protein	NA	NA	NA	NA
170	W903_R500840	W903_0171	123606	124925	NA	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	NA	NA	NA	NA
171	W903_R500845	W903_0172	125134	126588	glx	glutamate--trNA ligase	NA	NA	NA	NA
172	W903_R500850	W903_0173	126628	127594	NA	sugar-binding protein	NA	NA	NA	NA
173	W903_R500855	W903_0174	127649	128590	NA	branched chain amino acid transport system / permease component family protein	NA	NA	NA	NA
174	W903_R500860	W903_0175	128592	130070	NA	heme ABC exporter, ATP-binding protein CcmA	NA	NA	NA	NA
175	W903_R500865	W903_0176	130086	130484	rbx	ribosome	NA	NA	NA	NA
176	W903_R500870	W903_0177	130459	131370	rbx	ribonuclease	NA	NA	NA	NA
177	W903_R500875	W903_0178	131363	132349	NA	helix-turn-helix family protein	NA	NA	NA	NA
178	W903_R500880	W903_0179	132531	133619	NA	ftsX-like permease family protein	NA	NA	NA	NA
179	W903_R500885	W903_0180	133619	134305	NA	ABC transporter family protein	NA	NA	NA	NA
180	W903_R500890	W903_0181	134336	135007	NA	putative transcriptional activator CsdC	NA	NA	NA	NA
181	W903_R500895	W903_0182	135070	136070	NA	HAMP domain protein	NA	NA	NA	NA
182	W903_R500900	W903_0183	136212	137414	argG	argininosuccinate synthase	NA	NA	NA	NA
183	W903_R500905	W903_0184	137433	138821	argH	argininosuccinate lyase	NA	NA	NA	NA
184	W903_R500910	W903_0185	138962	139843	fba	fructose-1,6-bisphosphate aldolase, class II	NA	NA	NA	NA
185	W903_R500915	W903_0186	139928	140845	NA	L-2-hydroxyisocaproate dehydrogenase	NA	NA	NA	NA
186	W903_R500920	W903_0187	141084	141272	gmpB	ribosomal protein L28	NA	NA	NA	NA
187	W903_R500925	W903_0188	141404	141769	naP	asps3 family protein	NA	NA	NA	NA
188	W903_R500930	W903_0189	141769	143433	NA	DAK2 domain fusion YioV family protein	NA	NA	NA	NA
189	W903_R500935	W903_0190	143581	144465	NA	SPFH domain / Band 7 family protein	NA	NA	NA	NA
190	W903_R500940	W903_0191	144557	144673	NA	hypothetical protein	NA	NA	NA	NA
191	W903_R500945	W903_0192	145040	145270	NA	hypothetical protein	NA	NA	NA	NA
192	W903_R500950	W903_0193	145612	146352	NA	ABC transporter family protein	NA	NA	NA	NA
193	W903_R500955	W903_0194	146362	147912	NA	amino ABC transporter, permease, 3-TM region, His/Glu/Ala/Gln/opine family domain protein	NA	NA	NA	NA
194	W903_R500960	W903_0195	148048	149931	NA	hypothetical protein	NA	NA	NA	NA
195	W903_R500965	W903_0196	149977	150816	NA	bactracin resistance Bact family protein	NA	NA	NA	NA
196	W903_R500970	W903_0197	150936	151691	NA	negative regulator of genetic competence family protein	NA	NA	NA	NA
197	W903_R500975	W903_0198	151693	152853	NA	glycosyl transferase 4 family protein	NA	NA	NA	NA
198	W903_R500980	W903_0199	152853	153788	suD	Fe ²⁺ assembly ATPase SufC	NA	NA	NA	NA
199	W903_R500985	W903_0200	153825	155087	suD	Fe ²⁺ assembly protein SufD	NA	NA	NA	NA
200	W903_R500990	W903_0201	155089	156321	sufS	cysteine desulfurase, SufS family protein	NA	NA	NA	NA
201	W903_R500995	W903_0202	156308	156751	NA	SUF system FeS assembly protein, NifU family	NA	NA	NA	NA
202	W903_R501000	W903_0203	156851	158269	sufB	Fe ²⁺ assembly protein SufB	NA	NA	NA	NA
203	W903_R501005	W903_0204	158241	159528	NA	D-alanyl-D-alanine carboxypeptidase family protein	NA	NA	NA	NA
204	W903_R501010	W903_0205	159581	160688	NA	D-alanyl-D-alanine carboxypeptidase family protein	NA	NA	NA	NA
205	W903_R501015	W903_0206	161158	162813	NA	bacterial extracellular solute-binding S, Middle family protein	NA	NA	NA	NA
206	W903_R501020	W903_0207	162932	163846	NA	binding--dependent transport system inner membrane component family protein	NA	NA	NA	NA
207	W903_R501025	W903_0208	163856	164887	NA	N-terminal TM domain of oligopeptide transporter permease C family protein	NA	NA	NA	NA
208	W903_R501030	W903_0209	164900	165949	NA	oligopeptide/dipeptide ABC transporter, ATP-binding, C-terminal domain protein	NA	NA	NA	NA
209	W903_R501035	W903_0210	165946	166946	NA	ABC transporter family protein	NA	NA	NA	NA
210	W903_R501040	W903_0211	167284	168820	rRNA	NA	NA	NA	NA	NA
211	W903_R501045	W903_0212	168880	168952	rRNA	NA	NA	NA	NA	NA
212	W903_R501050	W903_0213	169109	172009	rRNA	NA	NA	NA	NA	NA
213	W903_R501055	W903_0214	172087	172200	rRNA	NA	NA	NA	NA	NA
214	W903_R501060	W903_0215	172205	172778	rRNA	NA	NA	NA	NA	NA
215	W903_R501065	W903_0216	173396	173956	NA	4-(cytidine 5'-diphosphor)-2-C-methyl-D-erythritol kinase	NA	NA	NA	NA
216	W903_R501070	W903_0217	173355	173798	adrR	transcriptional repressor AdrR	NA	NA	NA	NA
217	W903_R501075	W903_0218	173801	174511	NA	ABC transporter family protein	NA	NA	NA	NA
218	W903_R501080	W903_0219	174501	175313	NA	fecCD transport family protein	NA	NA	NA	NA
219	W903_R501085	W903_0220	175523	176554	NA	RNA non-specific endonuclease family protein	NA	NA	NA	NA
220	W903_R501090	W903_0221	177134	178393	lys	tyrosine--RNA ligase	NA	NA	NA	NA
221	W903_R501095	W903_0222	178504	180801	NA	penicillin-binding transpeptidase domain protein	NA	NA	NA	NA
222	W903_R501100	W903_0223	181325	184900	rpob	DNA-directed RNA polymerase, beta subunit	NA	NA	NA	NA
223	W903_R501105	W903_0224	185044	188667	rpoc	DNA-directed RNA polymerase, beta' subunit	NA	NA	NA	NA
224	NA	W903_0225	188624	188758	NA	glycerophosphoryl diester phosphodiesterase family protein	NA	NA	NA	NA
225	W903_R501110	W903_0226	188781	189146	NA	hypothetical protein	NA	NA	NA	NA
226	W903_R501115	W903_0227	189118	190839	NA	ATPase associated with various cellular activities family protein	NA	NA	NA	NA
227	W903_R501120	W903_0228	190354	191226	NA	type II secretion system (T2S), F family protein	NA	NA	NA	NA
228	W903_R501125	W903_0229	191223	191552	NA	prelpin-type N-terminal cleavage/methylation domain protein	NA	NA	NA	NA
229	W903_R501130	W903_0230	191602	191940	NA	putative competence protein Gld	NA	NA	NA	NA
230	W903_R501135	W903_0231	191966	192211	NA	type II secretory pathway pseudopilin family protein	NA	NA	NA	NA
231	NA	W903_0232	192294	192626	NA	putative com operon protein 6	NA	NA	NA	NA
232	W903_R501145	W903_0233	192975	193648	NA	putative com operon protein 7	NA	NA	NA	NA
233	W903_R501150	W903_0234	193900	194064	NA	N-6 DNA methylase family protein	NA	NA	NA	NA
234	W903_R501155	W903_0235	194096	195289	ackA	acetate kinase	NA	NA	NA	NA
235	NA	W903_0236	195478	195609	NA	helix-turn-helix family protein	NA	NA	NA	NA
236	W903_R5012030	W903_0237	195603	195854	NA	putative membrane protein	NA	NA	NA	NA
237	W903_R501165	W903_0238	195923	196888	NA	CAAX protease self-immunity family protein	NA	NA	NA	NA
238	W903_R501170	W903_0239	197379	197379	ppc	pyruvate-5-carboxylase reductase	NA	NA	NA	NA
239	W903_R501175	W903_0240	197449	198516	pepA	glutamyl aminopeptidase	NA	NA	NA	NA
240	W903_R501180	W903_0241	198696	198935	NA	putative membrane protein	NA	NA	NA	NA
241	W903_R501185	W903_0242	199096	199380	NA	hypothetical protein	NA	NA	NA	NA
242	W903_R501190	W903_0243	199377	199700	NA	thioredoxin family protein	NA	NA	NA	NA
243	W903_R501195	W903_0244	199733	200359	NA	putative tRNA binding domain protein	NA	NA	NA	NA
244	W903_R501200	W903_0245	200599	201129	NA	methyltransferase domain protein	NA	NA	NA	NA
245	W903_R501205	W903_0246	201210	201605	NA	single-stranded DNA-binding family protein	NA	NA	NA	NA
246	W903_R501210	W903_0247	201729	202373	NA	HAD hydrolase, IA, variant 1 family protein	NA	NA	NA	NA
247	W903_R501215	W903_0248	202400	204145	NA	histidine kinase, DNA gyrase B-, and HSP90-like ATPase family protein	NA	NA	NA	NA
248	W903_R501220	W903_0249	204126	204866	NA	response regulator	NA	NA	NA	NA
249	W903_R501225	W903_0250	205049	205914	NA	rigA family protein	NA	NA	NA	NA
250	W903_R501230	W903_0251	205493	206221	lrgB	antiholin-like protein LrgB	NA	NA	NA	NA
251	W903_R501235	W903_0252	206464							

276	W03_0301350	W03_0277	231635	231757	NA	helix-turn-helix family protein	0.883158209	0.006679815	1.06330298	7.02663635	1.06330298	7.02663635
277	W03_0301355	W03_0278	231979	232425	gPiM	ribosomal protein L13	-0.418273259	0.006084625	-0.27558357	0.038024879	-0.27558357	0.038024879
278	W03_0301360	W03_0279	232446	232847	g7400	30S ribosomal protein S9	0.374677400	0.024139031	0.065241177	0.009574104	-0.365241177	0.009574104
279	W03_0301365	W03_0280	233396	233586	NA	virulence factor esxA	-0.771416427	2.55634E-07	-0.238058517	0.102017803	-0.238058517	0.102017803
280	W03_0301370	W03_0281	233760	234095	NA	hypothetical protein	-0.940520496	2.5138E-08	-1.320281434	3.00473E-34	-1.320281434	3.00473E-34
281	NA	W03_0282	234095	235309	NA	hypothetical protein	0.126663777	0.47998015	-0.641089265	1.25534E-12	-0.641089265	1.25534E-12
282	W03_0301385	W03_0283	235294	235680	NA	hypothetical protein	-0.524607154	0.005148331	-1.204766872	2.07247E-24	-1.204766872	2.07247E-24
283	W03_0301390	W03_0284	235724	235995	NA	hypothetical protein	0.115658851	0.536398445	-0.698150881	1.90349E-07	-0.698150881	1.90349E-07
284	NA	W03_0285	236704	236882	NA	hypothetical protein	0.330738976	-0.211333933	0.121333933	0.73139654	-0.211333933	0.73139654
285	W03_0301405	W03_0286	236826	237686	NA	transcriptional activator, Rgg/GaDr/MuR family, C-terminal domain protein	-0.358972245	0.087957605	-0.253637376	0.060963871	-0.253637376	0.060963871
286	W03_0301410	W03_0287	237758	238939	NA	major Facilitator Superfamily protein	-0.039755594	0.892105609	0.470319227	0.004651838	0.470319227	0.004651838
287	W03_0301415	W03_0288	239001	239651	NA	binding-dependent transport system inner membrane component family protein	0.982975101	6.68086E-09	0.449436032	0.000140452	0.449436032	0.000140452
288	W03_0301420	W03_0289	239652	240578	gPuCC	glycine betaine/carnitine/choline-binding protein	0.987667686	2.20645E-09	0.21459113	0.024737316	0.21459113	0.024737316
289	W03_0301425	W03_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	W03_0301430	W03_0291	242126	242816	NA	glycine betaine/L-proline transport ATP binding subunit	0.156033095	0.78773321	-0.108930869	1.568770419	-0.108930869	1.568770419
291	W03_0301435	W03_0292	242789	244325	rRNA	NA	2.4052954	0.3806502152	-0.42388054	0.026897209	-0.42388054	0.026897209
292	W03_0301440	W03_0293	244385	244457	rRNA	NA	-0.844621431	NA	0.387279407	0.765272841	0.387279407	0.765272841
293	W03_0301445	W03_0294	244614	247515	rRNA	NA	0.238326902	0.217098082	-0.028684939	0.034422254	-0.028684939	0.034422254
294	W03_0301450	W03_0295	247593	247706	rRNA	NA	-0.1449859	0.0426321	0.500192879	0.377625001	0.500192879	0.377625001
295	W03_0301455	W03_0296	247709	247781	rRNA	NA	-2.96875926	NA	0.024916062	0.699719099	0.024916062	0.699719099
296	W03_0301460	W03_0297	247877	247857	rRNA	NA	-2.615095903	0.070700075	0.007070075	0.980059476	0.007070075	0.980059476
297	W03_0301465	W03_0298	247894	247970	rRNA	NA	-0.531150352	0.501170254	1.378076463	0.121735888	1.378076463	0.121735888
298	W03_0301470	W03_0299	247978	248049	rRNA	NA	-0.019240045	NA	0.297353191	0.899203501	0.297353191	0.899203501
299	W03_0301475	W03_0300	248063	248152	rRNA	NA	-1.563337395	0.038467454	0.188459699	0.838094249	0.188459699	0.838094249
300	W03_0301480	W03_0301	248163	248236	NA	NA	NA	NA	NA	NA	NA	NA
301	W03_0301485	W03_0302	248229	248311	rRNA	NA	-0.549913977	0.456861165	-0.456861165	0.605105891	-0.456861165	0.605105891
302	W03_0301490	W03_0303	248323	248403	rRNA	NA	0.162396429	0.839238676	0.245726274	0.774863441	0.245726274	0.774863441
303	W03_0301495	W03_0304	248410	248480	rRNA	NA	-0.408814678	0.604754542	-0.883741427	0.173947427	-0.883741427	0.173947427
304	W03_0301500	W03_0306	248495	248567	rRNA	NA	-0.277184968	NA	0.226621826	0.780618505	0.226621826	0.780618505
305	W03_0301505	W03_0307	248574	248645	rRNA	NA	0.054661514	NA	-0.364985259	0.946331025	-0.364985259	0.946331025
306	W03_0301510	W03_0308	248656	248739	NA	NA	NA	NA	NA	NA	NA	NA
307	W03_0301515	W03_0309	248944	249004	NA	acetyltransferase domain protein	0.228113903	0.330951294	0.653300775	0.000141032	0.653300775	0.000141032
308	W03_0301520	W03_0310	248955	250215	NA	acetyltransferase family protein	-0.157778352	0.528875534	0.993699646	2.98824E-11	0.993699646	2.98824E-11
309	W03_0301525	W03_0311	250205	250912	NA	acetyltransferase domain protein	-0.404864239	0.039475339	0.321094882	0.004215923	0.321094882	0.004215923
310	W03_0301530	W03_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	W03_0301535	W03_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	W03_0314	252737	252895	NA	glycerophosphoryl diester phosphodiesterase family protein	0.76736975	0.138665132	0.979857005	0.000213975	0.979857005	0.000213975
313	W03_0301540	W03_0315	253058	253058	NA	putative lipoprotein	0.109225553	1.251626089	0.196374009	1.48721E-09	0.196374009	1.48721E-09
314	W03_0301545	W03_0316	253193	253801	NA	bacterial regulatory s, tetR family protein	-0.247820553	0.046417074	0.161011305	0.383763582	0.161011305	0.383763582
315	W03_0301550	W03_0317	253825	254922	NA	ABC-2 type transporter family protein	-0.120005994	0.647719608	0.631329999	8.22248E-05	0.631329999	8.22248E-05
316	W03_0301555	W03_0318	254925	255641	NA	ABC transporter family protein	-0.317604623	0.30968107	0.50555317	0.003187135	0.50555317	0.003187135
317	W03_0301560	W03_0319	255904	256587	NA	hypothetical protein	-0.432736318	0.100497184	1.702090024	1.64181E-36	1.702090024	1.64181E-36
318	W03_0301565	W03_0320	256607	256918	NA	transcriptional regulator PadR-like family protein	-0.710068697	0.00913626	-0.955335364	1.54408E-07	-0.955335364	1.54408E-07
319	W03_0301570	W03_0321	257817	258177	NA	hypothetical protein	0.25758E-04	0.37153E-08	-0.509233728	2.07548E-59	-0.509233728	2.07548E-59
320	W03_0301575	W03_0322	258005	259243	naG	N-acetylglucosamine-6-phosphate deacetylase	0.399373858	0.004114629	0.646032219	1.89313E-11	0.646032219	1.89313E-11
321	W03_0301580	W03_0323	259362	259904	NA	isoprenylcysteine carboxyl methyltransferase family protein	-1.996014176	1.26356E-46	-2.978437285	3.1349E-138	-2.978437285	3.1349E-138
322	W03_0301585	W03_0324	260217	261131	gLyQ	glycine-tRNA ligase, alpha subunit	0.359440226	0.020363643	-1.849539232	4.70434E-37	-1.849539232	4.70434E-37
323	W03_0301590	W03_0325	261131	261772	NA	NAD(P)-dependent FMN reductase family protein	0.193593043	0.243397527	-0.207903011	6.0079E-46	-0.207903011	6.0079E-46
324	W03_0301595	W03_0326	261776	263815	gLyS	glycine-tRNA ligase, beta subunit	0.458355481	0.160471057	-1.963470755	2.6409E-38	-1.963470755	2.6409E-38
325	W03_0301600	W03_0327	263827	264084	NA	hypothetical protein	1.2923427	0.598477E-14	-1.371007189	6.24028E-23	-1.371007189	6.24028E-23
326	W03_0301605	W03_0328	264173	264436	NA	hypothetical protein	1.13930424	4.21228E-07	-0.910634714	5.58598E-06	-0.910634714	5.58598E-06
327	W03_0301610	W03_0329	264551	266059	gLPK	glycerol kinase	3.29177E-10	0.042944223	0.001948223	0.801929886	0.001948223	0.801929886
328	W03_0301615	W03_0330	266072	267901	NA	FAD dependent oxidoreductase family protein	0.0117210885	0.59895E-07	0.632104089	0.000176952	0.632104089	0.000176952
329	W03_0301620	W03_0331	267913	268611	NA	MIP channel s family protein	1.348498922	1.29539E-05	0.934406481	2.17623E-05	0.934406481	2.17623E-05
330	W03_0301625	W03_0332	268699	270566	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.407714604	0.407714604	0.000970794	1.0309E-17	0.000970794	1.0309E-17
331	W03_0301630	W03_0333	270027	271457	NA	mega helix-turn-helix domain protein	0.242961527	0.279637146	0.5772429	0.000154982	0.5772429	0.000154982
332	W03_0301635	W03_0334	271582	273567	tkT	transketolase	0.469851069	0.001199773	-0.730457877	8.27676E-09	-0.730457877	8.27676E-09
333	W03_0301640	W03_0335	273779	274084	NA	enterocin A Immunity family protein	0.094574186	0.699641117	-1.001254106	6.3047E-17	-1.001254106	6.3047E-17
334	W03_0301645	W03_0336	274104	274838	NA	ABC transporter family protein	0.348810801	0.046727717	-1.005571055	5.535E-14	-1.005571055	5.535E-14
335	W03_0301650	W03_0337	274842	274644	NA	putative membrane protein	0.448291208	0.003976592	-0.740291607	2.52419E-09	-0.740291607	2.52419E-09
336	W03_0301655	W03_0338	275019	276019	NA	PTS system, glucose-6-phosphate	0.72474563	2.884438811	1.8631E-15	3.884138811	1.8631E-15	3.884138811
337	W03_0301660	W03_0339	278330	278983	proB	glutamate-5-kinase	0.167614067	1.39166E-05	0.558010481	1.86929E-05	0.558010481	1.86929E-05
338	W03_0301665	W03_0340	278993	280246	proP	glutamate-5-semialdehyde dehydrogenase	0.526459783	0.000479238	0.45174082	2.32431E-05	0.45174082	2.32431E-05
339	W03_0301670	W03_0341	280380	281276	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase	-0.037872496	0.832460017	0.746066445	5.37115E-15	0.746066445	5.37115E-15
340	W03_0301675	W03_0342	281291	281617	rTSL	cell division protein FtsL	-0.283763348	0.181232223	-0.129388626	0.404141085	-0.129388626	0.404141085
341	W03_0301680	W03_0343	281792	283879	NA	penicillin binding transpeptidase domain protein	0.038435741	0.833343489	-0.395324063	0.000135626	-0.395324063	0.000135626
342	W03_0301685	W03_0344	283881	284851	mraY	peptidoglycan N-acetylmuramyl-pentapeptide-transferase	0.880002932	0.430214837	0.192458199	8.33598E-05	0.192458199	8.33598E-05
343	W03_0301690	W03_0345	284989	286332	NA	helicase domain protein	0.047110785	0.798035044	-1.084909764	8.76801E-34	-1.084909764	8.76801E-34
344	W03_0301695	W03_0346	286470	287282	NA	bacterial extracellular solute-binding s, 3 family protein	0.01401825	0.047109325	-1.338337849	2.96155E-25	-1.338337849	2.96155E-25
345	W03_0301700	W03_0347	287377	288180	NA	amino ABC transporter, permease, 3-TM region, His						

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	0.8005959492	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 ic component family protein	0.9079354986	2.19436E-08	-0.794075633	1.17576E-26	-1.335043514	1.7576E-26
417	W903_RS02060	W903_0419	359109	360119	manX	PTS system mannose-specific EIIB component	0.52257258	0.117396937	-1.83776494	2.0303E-05	-1.83776494	2.0303E-05
418	W903_RS02065	W903_0420	360422	361234	NA	HAO hydrolase, IIB family protein	-0.68585182	7.44243E-05	-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	0.00505877	-0.187319893	0.00505877
420	W903_RS02075	W903_0422	361997	362608	NA	hypothetical protein	-0.429862919	0.004487954	-0.205091956	0.032057896	-0.205091956	0.032057896
421	W903_RS02080	W903_0423	362711	364312	NA	permease family protein	0.323194554	0.140752348	-0.794075633	5.89751E-15	-0.794075633	5.89751E-15
422	W903_RS02085	W903_0424	364381	364724	NA	tRNA threonylcarbamoyl adenosine modification protein YjeE	0.011313474	0.364634807	-0.364634807	0.002558756	-0.364634807	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	0.14304325	0.427430056	0.134937268	0.143554214	0.134937268	0.143554214
425	W903_RS02100	W903_0427	366618	366914	NA	hypothetical protein	-0.635554006	0.004850929	-0.151549388	0.367209097	-0.151549388	0.367209097
426	W903_RS02105	W903_0428	366911	367330	NA	HT domain protein	0.502117402	0.002135669	1.569375276	1.83152E-29	1.569375276	1.83152E-29
427	W903_RS02110	W903_0429	367666	368169	NA	hypothetical protein	-0.1167807085	1.74349E-27	-3.629377703	0	-3.629377703	0
428	W903_RS02115	W903_0430	368279	369222	NA	ABC transporter family protein	0.154148	0.165017486	-1.94020553	4.98014E-31	-1.94020553	4.98014E-31
429	W903_RS02120	W903_0431	369206	370240	NA	bacterial ABC transporter EcsB family protein	-0.01914786	0.914074262	-0.106400558	5.1572E-08	-0.106400558	5.1572E-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	tmhB	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	0.09206873	NA	0.473960349	0.776325669	0.473960349	0.776325669
433	NA	W903_0435	372176	372439	NA	hypothetical protein	-0.17386303	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	0.753514117	0.062174513	0.753514117	0.062174513
435	NA	W903_0437	373292	373468	NA	glycerophosphoryl diester phosphodiesterase family protein	0.295420677	NA	0.161664968	0.169864073	0.161664968	0.169864073
436	NA	W903_0438	373575	373739	NA	hypothetical protein	-0.183138384	NA	1.191920984	0.040036379	1.191920984	0.040036379
437	W903_RS02150	W903_0439	373741	374775	NA	replication initiator A family protein	-0.443583534	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	0.133984764	0.774419109	0.005312801	0.774419109	0.005312801
439	NA	W903_0441	375455	375595	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.378845664	NA	0.500213408	0.8002132408	0.500213408	0.8002132408
440	W903_RS02160	W903_0442	375789	375792	NA	helic-tum-helic family protein	0.106565087	0.050639429	0.246498892	0.470020239	0.246498892	0.470020239
441	W903_RS02165	W903_0443	376172	376471	NA	hypothetical protein	-0.362287433	0.0468176574	0.898926256	0.042442646	0.898926256	0.042442646
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	-0.124135161	0.525446689	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	-0.086177769	0.504130818	-0.086177769	0.504130818
445	W903_RS02185	W903_0448	382891	384794	NA	putative membrane protein	0.04148452	0.050038787	-2.618273984	0.10919E-06	-2.618273984	0.10919E-06
446	W903_RS02190	W903_0448	382956	383577	NA	hypothetical protein	-0.7551924	1.37849E-05	0.733669591	0.07616E-13	0.733669591	0.07616E-13
447	W903_RS02195	W903_0449	383628	384380	NA	putative membrane protein	-0.556628858	0.143974617	-0.216800211	0.450284242	-0.216800211	0.450284242
448	W903_RS02200	W903_0450	384417	384713	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.29423176	0.083125569	-0.631028613	0.201124848	-0.631028613	0.201124848
449	W903_RS02205	W903_0451	384706	385164	NA	hypothetical protein	-0.711554523	0.577115431	0.07805731	0.577115431	0.07805731	0.577115431
450	W903_RS02210	W903_0452	385226	385858	NA	hypothetical protein	-1.02897839	0.03641127	-1.126034514	0.005168433	-1.126034514	0.005168433
451	W903_RS02215	W903_0453	385566	387926	NA	AAA-like domain protein	0.4514854	0.124472984	-0.209648519	0.250265109	-0.209648519	0.250265109
452	W903_RS02220	W903_0454	387919	388512	NA	hypothetical protein	0.316301403	0.046040359	0.176518068	0.532192284	0.176518068	0.532192284
453	W903_RS02225	W903_0455	388536	388662	NA	glycerophosphoryl diester phosphodiesterase family protein	0.593030205	0.427465018	0.565863559	0.0535035	0.565863559	0.0535035
454	W903_RS02230	W903_0456	388897	391587	NA	peptidase M23 family protein	0.475338649	0.162768884	0.443946164	0.005852891	0.443946164	0.005852891
455	W903_RS02235	W903_0457	391608	392213	NA	putative prGL	0.238421203	0.714084999	-0.7569336	0.08722286	-0.7569336	0.08722286
456	W903_RS02240	W903_0458	392233	392505	NA	hypothetical protein	0.044184452	0.56607518	-0.271425984	0.655883749	-0.271425984	0.655883749
457	W903_RS02245	W903_0459	392535	393200	NA	hypothetical protein	0.093284633	0.052394653	-0.702844855	0.03392519	-0.702844855	0.03392519
458	W903_RS02250	W903_0460	393312	393803	NA	hypothetical protein	0.275313281	0.50440675	0.403023707	0.11442897	0.403023707	0.11442897
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	0.122684016	0.079081585	0.121000325	0.8014881	0.121000325	0.8014881
461	W903_RS02265	W903_0463	396257	399496	NA	hypothetical protein	0.1044061335	0.536882E-05	0.33192262	0.11737803	0.33192262	0.11737803
462	W903_RS02270	W903_0464	399478	400274	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.11434124	0.531709821	-2.618273984	0.10919E-06	-2.618273984	0.10919E-06
463	W903_RS02275	W903_0465	400190	400750	NA	glycerophosphoryl diester phosphodiesterase family protein	0.173173387	0.58313645	1.500314548	0.06384E-06	1.500314548	0.06384E-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	0.005190671	0.910297555	0.005190671
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	402978	403283	NA	hypothetical protein	-0.149682661	0.160474542	0.364706579	0.036828065	0.364706579	0.036828065
468	W903_RS02295	W903_0470	403214	405957	NA	hypothetical protein	0.11434124	0.046832077	-0.666950606	0.062141498	-0.666950606	0.062141498
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	406161	406762	nusA	transcription termination factor NusA	-0.152571017	0.381549257	-0.565599676	0.010522808	-0.565599676	0.010522808
471	W903_RS02310	W903_0473	406784	407800	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	401078	infB	translation initiation factor Inf-2	0.60759179	7.43109E-05	-0.299446878	0.090099592	-0.299446878	0.090099592
474	W903_RS02325	W903_0476	410637	410637	NA	hypothetical protein	0.37142424	0.059014648	0.234682134	0.255681035	0.234682134	0.255681035
475	W903_RS02330	W903_0477	410721	411725	NA	alpha/beta hydrolase fold family protein	0.08428631	0.733854288	0.902148242	1.56582E-18	0.902148242	1.56582E-18
476	W903_RS02335	W903_0478	411888	412304	NA	copper transport repressor, CopY/CytY family	0.239011143	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	0.769509554	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	0.083314144	0.139180713	1.12324E-11	0.139180713	1.12324E-11
479	W903_RS02350	W903_0481	414908	415522	NA	hypothetical protein	0.555106435	0.00003937	0.624647911	0.17873E-37	0.624647911	0.17873E-37
480	W903_RS02355	W903_0482	415537	416349	NA	HAO hydrolase, IIB family protein	0.163490945	0.446669424	-0.462849452	5.36623E-07	-0.462849452	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	0.407970269	-0.591106209	1.59006E-07	-0.591106209	1.59006E

552	W903_S020710	W903_0556	482318	galK	galactokinase	1.007620157	0.006936004	1.643528593	3.30874E-10	1.643528593	3.30874E-10
553	W903_S020715	W903_0557	483500	galT	galactose-1-phosphate uridylyltransferase	0.812628166	0.039699193	1.432144731	6.76386E-14	1.432144731	6.76386E-14
554	W903_S020720	W903_0558	484896	galE	UDP-glucose 4-epimerase GalE	0.855810721	0.048027578	1.697373124	2.62894E-14	1.697373124	2.62894E-14
555	W903_S020725	W903_0559	486107	galP	aldose 1-epimerase family protein	0.380614682	0.41083729	1.117675245	1.63971E-07	1.117675245	1.63971E-07
556	W903_S020730	W903_0560	487299	NA	hypothetical protein	-1.172838854	1.95216E-09	-1.267690046	5.96498E-17	-1.267690046	5.96498E-17
557	W903_S020735	W903_0561	487662	NA	hypothetical protein	-1.251948042	1.64751E-14	-1.267276462	5.98618E-24	-1.267276462	5.98618E-24
558	W903_S020740	W903_0562	488241	NA	acetyltransferase family protein	1.093299541	0.38303E-13	-0.526424401	1.154848E-05	-0.526424401	1.154848E-05
559	W903_S020745	W903_0563	488808	NA	acetyltransferase family protein	1.017395107	3.09976E-10	-0.474316949	0.000185505	-0.474316949	0.000185505
560	W903_S020750	W903_0564	490055	NA	AAA domain protein	0.135441173	1.1975E-08	-1.135877194	2.55734E-16	-1.135877194	2.55734E-16
561	W903_S020755	W903_0565	490055	valS	valine-tRNA ligase	1.15701368	1.17372E-16	-1.389050413	4.69668E-33	-1.389050413	4.69668E-33
562	W903_S020760	W903_0566	492787	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.02021347	5.65525E-08	0.101081539	0.946381898	0.101081539	0.946381898
563	W903_S020765	W903_0567	493775	NA	putative membrane protein	-0.646640294	0.018608585	0.395395181	0.024304504	0.395395181	0.024304504
564	NA	W903_0568	494667	NA	hypothetical protein	-0.702374701	0.327552535	0.453368625	0.006871657	0.453368625	0.006871657
565	NA	W903_0569	494842	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.976238392	0.037178662	0.471924617	0.157366473	0.471924617	0.157366473
566	W903_S020770	W903_0570	495076	NA	oxidoreductase, NAD-binding Rossmann fold family protein	-0.585950833	0.321323356	0.925144889	2.93254E-13	0.925144889	2.93254E-13
567	W903_S020775	W903_0571	496227	NA	cork-like Mg2+ transporter family protein	-0.170474002	0.445557003	0.717537609	2.42256E-50	0.717537609	2.42256E-50
568	W903_S020780	W903_0572	497290	NA	hypothetical protein	0.350557058	0.12356904	0.94547938	1.7359E-11	0.94547938	1.7359E-11
569	W903_S020785	W903_0573	498470	aspA	aspartate-ammonia ligase	0.371984985	0.05130082	-0.253945946	0.011524372	-0.253945946	0.011524372
570	W903_S020790	W903_0574	499507	NA	hypothetical protein	0.890009272	0.226214476	0.049102666	0.262214476	0.049102666	0.262214476
571	W903_S020795	W903_0575	500508	NA	RNA methyltransferase, RsmD family	-0.095788887	0.590511184	-0.048868668	0.643701007	-0.048868668	0.643701007
572	W903_S020800	W903_0576	500638	NA	putative membrane protein	-0.717602116	3.38407E-05	-0.352838632	0.002157577	-0.352838632	0.002157577
573	W903_S020805	W903_0577	500925	cooD	paranthethine-phosphate adenylyltransferase	-0.186956056	0.274774767	-0.084159407	0.42755962	-0.084159407	0.42755962
574	W903_S020810	W903_0578	501400	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_S020815	W903_0579	502671	NA	5'-nucleotidase, C-terminal domain protein	0.266121231	0.136213354	0.798077074	2.82181E-15	0.798077074	2.82181E-15
576	W903_S020820	W903_0580	503952	NA	hypothetical protein	0.60165733	0.003153271	0.139541258	0.182291217	0.139541258	0.182291217
577	W903_S020825	W903_0581	504581	rhmA	23S rRNA methyltransferase	0.603101724	0.16183E-05	-0.233012815	0.595931285	-0.233012815	0.595931285
578	W903_S020830	W903_0582	505587	NA	varZ like family protein	0.5062012	0.890224022	0.462721694	0.78402113	0.462721694	0.78402113
579	W903_S020835	W903_0583	506387	NA	ABC transporter family protein	0.326504597	0.130891152	-0.115440514	0.35232653	-0.115440514	0.35232653
580	W903_S020840	W903_0584	508122	NA	ABC transporter family protein	0.208409961	0.43371711	-0.374629159	0.000425799	-0.374629159	0.000425799
581	W903_S020845	W903_0585	509899	NA	glutamine amidotransferase of anthranilate synthase/aminodeoxychorismate synthase family protein	0.014650905	0.961982117	-0.091121581	0.647122672	-0.091121581	0.647122672
582	W903_S020850	W903_0586	510622	NA	biotin transporter BioY	0.583950698	0.126093445	-0.930597554	0.003772281	-0.930597554	0.003772281
583	W903_S020855	W903_0587	511162	tsuB	biotin synthase	0.463224242	0.463224242	0.053530922	0.053530922	0.053530922	0.053530922
584	W903_S020860	W903_0588	512794	NA	hypothetical protein	0.794435808	0.027719201	0.650230961	0.037889125	0.650230961	0.037889125
585	W903_S020865	W903_0589	512784	NA	acetyl-CoA C-acetyltransferase family protein	1.253269125	7.27072E-07	0.372784065	0.065808305	0.372784065	0.065808305
586	W903_S020870	W903_0590	513892	NA	AMP-binding enzyme family protein	0.58515121	0.069270068	0.654527002	0.000499994	0.654527002	0.000499994
587	W903_S020875	W903_0591	515234	rnh	adenosine III	0.27836378	0.164668168	1.035464129	7.39198E-13	1.035464129	7.39198E-13
588	W903_S020880	W903_0592	515867	NA	type IV leader peptidase family protein	-0.830393599	NA	1.255963196	1.11531931	1.255963196	1.11531931
589	W903_S020885	W903_0593	516417	NA	hypothetical protein	0.586509531	0.805164568	0.25454581	1.29416E-06	0.25454581	1.29416E-06
590	W903_S020890	W903_0594	516623	NA	ROK family protein	0.271833835	0.088864179	-0.268765431	0.005211136	-0.268765431	0.005211136
591	W903_S020895	W903_0595	517603	NA	rhodanese-like domain protein	0.6826342	0.000332729	-0.116891469	0.326112248	-0.116891469	0.326112248
592	W903_S020900	W903_0596	518215	tyaP	GTP-binding protein TyaP/BipA	0.239096819	0.139982028	-0.905361446	2.73212E-17	-0.905361446	2.73212E-17
593	W903_S020905	W903_0597	520101	NA	hypothetical protein	-0.361487829	0.108402596	-0.651641469	0.20961E-06	-0.651641469	0.20961E-06
594	W903_S020910	W903_0598	520476	murD	UDP-N-acetylmuramoylalanine-D-glutamate ligase	0.193201041	0.257210764	-0.443021813	1.17257E-06	-0.443021813	1.17257E-06
595	W903_S020915	W903_0599	521534	NA	glycosyltransferase family 28 C-terminal domain protein	0.165415993	0.238559631	0.402926179	0.00111776	0.402926179	0.00111776
596	W903_S020920	W903_0600	522014	ftsZ	cell division FtsZ family protein	-0.165581722	0.035551042	-0.530961386	1.28323E-06	-0.530961386	1.28323E-06
597	W903_S020925	W903_0601	524325	ftsA	cell division protein FtsA	0.188148684	0.252500145	-0.540146346	2.96226E-07	-0.540146346	2.96226E-07
598	W903_S020930	W903_0602	525720	ftsZ	cell division protein FtsZ	0.545311575	0.000130106	-0.487042783	1.3357E-07	-0.487042783	1.3357E-07
599	W903_S020935	W903_0603	527009	NA	alanine racemase, N-terminal domain protein	0.269350435	0.089752589	-0.54128445	7.20896E-05	-0.54128445	7.20896E-05
600	W903_S020940	W903_0604	527697	NA	hypothetical protein	0.439670869	0.050540146	-0.438389057	0.94036E-05	-0.438389057	0.94036E-05
601	W903_S020950	W903_0605	529344	NA	54 domain protein	0.023685241	0.892365241	-0.267090748	0.00320721	-0.267090748	0.00320721
602	W903_S020955	W903_0606	529354	NA	divIVA domain protein	-0.391331683	0.009367493	-0.890284641	2.19947E-20	-0.890284641	2.19947E-20
603	W903_S020960	W903_0607	530409	NA	isoleucine-tRNA ligase	0.48474049	0.000853006	-1.672939204	1.6328E-47	-1.672939204	1.6328E-47
604	W903_S020965	W903_0608	533318	NA	hypothetical protein	-0.526899286	0.00956987	-0.652128622	2.7838E-11	-0.652128622	2.7838E-11
605	W903_S020970	W903_0609	533884	NA	NUDIX domain protein	-0.907680946	1.1776E-08	-1.264927942	5.58068E-28	-1.264927942	5.58068E-28
606	W903_S020975	W903_0610	535856	NA	18S-like ATP binding family protein	0.080925215	0.278009215	0.127805905	0.4165E-19	0.127805905	0.4165E-19
607	W903_S020980	W903_0611	536884	NA	hypothetical protein	0.837519279	0.004795017	1.135739379	0.00303638	1.135739379	0.00303638
608	W903_S020985	W903_0612	537255	NA	amino ABC transporter, permease, 3-TM region, His/Glu/Arg/Gln/opine family domain protein	0.255519279	0.206759631	0.327589497	0.0242945	0.327589497	0.0242945
609	W903_S020990	W903_0613	537940	NA	ABC transporter family protein	0.338674	0.26326899	-0.164672704	0.249518326	-0.164672704	0.249518326
610	W903_S020995	W903_0614	538960	NA	phosphoglucosylase/phosphomannosylase, C-terminal domain protein	-0.163036657	0.418459993	-0.920938312	4.21822E-10	-0.920938312	4.21822E-10
611	W903_S020300	W903_0615	540793	NA	tetrahydrofolate dehydrogenase/cylichydrolase, catalytic domain protein	-0.184742419	0.293839945	-0.977078665	3.11773E-19	-0.977078665	3.11773E-19
612	W903_S020305	W903_0616	541647	NA	hypothetical protein	0.096804322	0.524874523	0.248674523	1.29416E-06	0.248674523	1.29416E-06
613	W903_S020310	W903_0617	542606	NA	exodeoxyribonuclease VII, large subunit	0.126846395	0.495327691	-0.101235359	0.34313155	-0.101235359	0.34313155
614	W903_S020315	W903_0618	543924	NA	exodeoxyribonuclease VII, small subunit	0.293348488	0.331233356	-0.210451783	0.300594877	-0.210451783	0.300594877
615	W903_S020320	W903_0619	544139	NA	polyphenyl synthetase family protein	-0.051879243	0.780671567	0.028969135	0.814047835	0.028969135	0.814047835
616	W903_S020325	W903_0620	545004	NA	hemolysin TlyA family protein	0.078487792	0.757598832	-0.109273596	0.309264296	-0.109273596	0.309264296
617	W903_S020330	W903_0621	545818	NA	arginine repressor, DNA binding domain protein	-0.360026667	0.037886566	-0.526744663	0.309264296	-0.526744663	0.309264296
618	W903_S020335	W903_0622	547961	NA	DNA repair protein RecK	0.278351679	0.278351679	0.420264179	2.56312E-05	0.420264179	2.56312E-05
619	W903_S020340	W903_0623	548074	NA	degV family protein	-0.115380378	0.549536178	-0.182410587	0.089494663	-0.182410587	0.089494663
620	W903_S020345	W903_0624	548978	NA	GDSL-like Lipase/Acylhydrolase family protein	-0.194363146	0.300532643	-0.38929555	0.001044907	-0.38929555	0.001044907
621	W903_S020350	W903_0625	549717	NA	hypothetical protein	-0.155903409	0.549536178	-0.18277579	0.186866153	-0.18277579	0.186866153
622	W903_S020355	W903_0626	550697	hup	DNA-binding protein HU	-0.821413266	1.21209E-08	-0.875741976	1.8222E-21	-0.875741976	1.8222E-21
623	W903_S020360	W903_0627	550785	NA	phage integrase family protein	0.368354876	-0.364389376	0.364389376	0.003615179	0.364389376	0.003615179
624	W903_S02036										

690 W903_R503385	W903_0694	605600	606724 ueqE	epoxyquiescent reductase	-0.6523716947	0.026176266	1.656159125	8.43291E-62	1.656159125	8.43291E-62
691 W903_R503390	W903_0695	606911	607891 prfB	peptide chain release factor 2	0.23808682	0.126321509	-0.549030919	8.8808E-10	-0.549030919	8.8808E-10
692 W903_R503395	W903_0696	607010	608602 tseE	cell division ATP-binding protein FtsE	0.248088289	0.126747878	-0.379972928	6.3735E-05	-0.379972928	6.3735E-05
693 W903_R503400	W903_0697	608595	609515 NA	ftsX-like permease family protein	0.0200773371	0.0200773371	0.628579047	3.87196E-09	-0.628579047	3.87196E-09
694 W903_R503405	W903_0698	609588	610278 NA	alpha/beta hydrolase family protein	0.314815798	0.080799139	1.032606006	2.16697E-29	1.032606006	2.16697E-29
695 W903_R503410	W903_0699	610275	610910 NA	hypothetical protein	0.34623521	0.065377276	0.823642438	1.71515E-16	0.823642438	1.71515E-16
696 W903_R503415	W903_0700	611141	611905 NA	acetoin reductase family protein	0.170346665	0.047588989	0.48908263	1.71555E-06	0.48908263	1.71555E-06
697 W903_R503420	W903_0701	612055	614520 NA	exonuclease, DNA polymerase III, epsilon subunit family domain protein	0.080224691	0.661507684	-0.15870886	0.128890507	-0.15870886	0.128890507
698 W903_R503425	W903_0702	615796 NA	degT/DnaE	5'-5' aminotransferase family protein	0.043081412	0.056198347	0.101386348	0.30801055	-0.101386348	0.30801055
699 W903_R503430	W903_0703	615820	617166 xns	asparagine--thRNA ligase	0.078298208	0.654620604	-0.803643522	1.00693E-18	-0.803643522	1.00693E-18
700 W903_R503435	W903_0704	617206	617763 NA	hypothetical protein	0.01165345	0.027393254	-0.728900043	1.72935E-06	-0.728900043	1.72935E-06
701 W903_R503440	W903_0705	617760	618743 NA	inosine-uridine preferring nucleoside hydrolase family protein	-0.537363165	0.000250615	-0.743460108	6.35351E-12	-0.743460108	6.35351E-12
702 W903_R503445	W903_0706	618988	619401 NA	osmC-like family protein	0.017413227	0.000185571	-0.423172244	0.002341797	-0.423172244	0.002341797
703 W903_R503450	W903_0707	619555	620445 NA	P-loop ATPase family protein	0.578920129	0.000877752	-0.499784653	1.85188E-05	-0.499784653	1.85188E-05
704 W903_R503455	W903_0708	621416 NA	622042	hypothetical protein	0.584308412	0.25252E-07	0.550561512	0.54705E-08	0.550561512	0.54705E-08
705 W903_R503460	W903_0709	621413	622324 NA	sporulation Regulator WNA C-terminal domain protein	0.30870459	0.057293238	0.003865388	0.97334254	0.003865388	0.97334254
706 W903_R503465	W903_0710	622339	623736 pepD	dipeptidase	0.323045155	0.0426321	-0.068121845	0.50209611	-0.068121845	0.50209611
707 W903_R503470	W903_0711	623878	625398 NA	yodA lipocalin-like domain protein	-0.782828123	1.199237E-05	-1.801895815	2.17638E-17	-1.801895815	2.17638E-17
708 W903_R503475	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_R503480	W903_0713	625879	626814 NA	DHH1 domain protein	0.26899004	0.287022861	0.495590809	1.36574E-05	0.495590809	1.36574E-05
710 W903_R503485	W903_0714	627080	628102 add	adenosine deaminase	-0.075218343	0.806170452	-1.559596434	7.52714E-30	-1.559596434	7.52714E-30
711 W903_R503490	W903_0715	628161	628604 NA	flavodoxin	-0.956739803	9.10932E-07	-0.437960314	2.40012E-25	-0.437960314	2.40012E-25
712 W903_R503495	W903_0716	628681	628956 NA	chorismate mutase	-0.863879864	7.49766E-06	0.098116545	0.62029631	0.098116545	0.62029631
713 W903_R503500	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_R503505	W903_0718	630279	631076 rpsL	ribosomal protein L19	-1.18388736	3.17084E-16	-0.766216129	1.05248E-10	-0.766216129	1.05248E-10
715 W903_R503510	W903_0719	631187	631258 rRNA	NA	1.747111785	0.512434274	0.205820569	0.812442474	0.205820569	0.812442474
716 W903_R503520	W903_0721	632093	632497 NA	transposase family protein	0.913783469	1.00413E-06	1.138713583	1.26318E-17	1.138713583	1.26318E-17
717 W903_R503525	W903_0722	632659	632859 NA	putative integrase	-1.116348073	3.45948E-09	1.2965346	2.4353E-24	1.2965346	2.4353E-24
718 W903_R503530	W903_0723	632884	633141 tpsHts1	IS5th1, transposase (Orf2), IS3 family	-1.261396398	7.41255E-10	1.592862038	1.82199E-17	1.592862038	1.82199E-17
719 W903_R503510	W903_0724	633649	63810 NA	TMD domain protein	-0.676858352	0.29098286	3.011610275	2.55488E-41	3.011610275	2.55488E-41
720 W903_R503535	W903_0725	634553	635830 NA	ftsX-like permease family protein	-1.295958172	7.32005E-14	0.37658312	0.001878773	0.37658312	0.001878773
721 W903_R503540	W903_0726	634696 NA	635840	ABC transporter family protein	0.543789213	0.0113448	0.0113448	0.000809043	0.0113448	0.000809043
722 W903_R503545	W903_0727	634964	637872 NA	ftsX-like permease family protein	0.1219314833	0.149383746	0.636741836	3.02247E-08	0.636741836	3.02247E-08
723 W903_R503550	W903_0728	637969	638622 NA	putative transcriptional activator CadC	-0.86417661	0.000118972	-0.348450892	0.0270274	-0.348450892	0.0270274
724 W903_R503555	W903_0729	638619	639398 NA	HAMP domain protein	-1.174777275	0.50705E-10	-0.75435972	1.37799E-07	-0.75435972	1.37799E-07
725 W903_R503560	W903_0730	639990	640601 NA	integrase core domain protein	-0.408680777	0.075582676	0.351721995	0.018010755	0.351721995	0.018010755
726 W903_R503565	W903_0731	640815	641015 NA	csbD-like family protein	0.11134485	0.758765308	0.59730218	0.008090943	0.59730218	0.008090943
727 W903_R503570	W903_0732	641245 NA	641245	hypothetical protein	-0.052258651	0.1738511499	0.338515499	0.07740652	0.338515499	0.07740652
728 W903_R503570	W903_0733	641670	642875 NA	cell cycle family protein	-0.521779406	0.000700963	0.267438828	0.006754369	0.267438828	0.006754369
729 W903_R503575	W903_0734	642994	643554 NA	HAD hydrolase, IA, variant 1 family protein	-0.718716083	2.42897E-06	1.403788222	5.20103E-40	1.403788222	5.20103E-40
730 W903_R503580	W903_0735	643555	645507 gyrB	DNA gyrase, B subunit	-0.680929219	0.116374595	0.059878105	0.58635249	0.059878105	0.58635249
731 W903_R503585	W903_0736	645601	647325 NA	separation ring formation regulator, EzrA family protein	-0.632784439	1.36352E-05	-0.814740774	1.02031E-16	-0.814740774	1.02031E-16
732 W903_R503590	W903_0737	647419	648060 serB	phosphoserine phosphatase SerB	-0.023050505	0.003202219	-0.441504587	0.000505527	-0.441504587	0.000505527
733 W903_R503595	W903_0738	648081	648506 NA	NUX domain protein	0.1737070731	0.412450587	0.179518516	0.383844701	0.179518516	0.383844701
734 W903_R503600	W903_0739	648749	649034 NA	hypothetical protein	-0.084880001	0.005759832	-0.267419265	0.04397493	-0.267419265	0.04397493
735 W903_R503605	W903_0740	649232	650539 eno	phosphopyruvate hydratase	-0.077209541	0.681248828	-1.252777837	4.2941E-48	-1.252777837	4.2941E-48
736 W903_R503610	W903_0741	650647	651711 NA	DNA/RNA non-specific endonuclease family protein	-0.194989691	0.337668674	1.716504665	3.60922E-56	1.716504665	3.60922E-56
737 W903_R503615	W903_0742	651940	653223 araA	3-phosphoshikimate 1-carboxyvinyltransferase	0.438207322	0.00830005	0.539938503	3.70185E-09	0.539938503	3.70185E-09
738 W903_R503620	W903_0743	653216	653728 NA	shikimate kinase family protein	0.215698126	0.0511985143	0.198518513	0.060212356	0.198518513	0.060212356
739 W903_R503625	W903_0744	655158 NA	655158	cell envelope-related function transcriptional attenuator common domain protein	0.0290468317	0.877355147	0.179860772	0.093460728	0.179860772	0.093460728
740 W903_R503630	W903_0745	655259	656620 NA	23S rRNA (uracil-S-) methyltransferase RumA	-0.725564929	1.92147E-05	-1.141193926	8.89396E-28	-1.141193926	8.89396E-28
741 NA	W903_0746	657718	657894 NA	hypothetical protein	-0.65310255	0.015353759	1.847643387	2.6128E-56	1.847643387	2.6128E-56
742 NA	W903_0747	659098	659292 NA	putative succinyl-diaminopimelate desuccinylase	-0.149025228	NA	1.997429693	0.010902711	1.997429693	0.010902711
743 W903_R503645	W903_0748	659278	659508 NA	hypothetical protein	0.621818999	NA	2.519475396	0.036458903	2.519475396	0.036458903
744 W903_R503650	W903_0749	660720	660938 NA	beta-lactamase family protein	-0.346382713	0.083411153	0.498082971	0.02371E-07	0.498082971	0.02371E-07
745 W903_R503655	W903_0750	660920	661912 NA	ABC transporter family protein	-0.357032355	0.065391433	0.657520336	2.53782E-09	0.657520336	2.53782E-09
746 W903_R503665	W903_0751	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_R503675	W903_0755	664451	665299 NA	glycerophosphoryl diester phosphodiesterase family protein	-0.398512326	0.05157722	-1.011052642	2.62201E-17	-1.011052642	2.62201E-17
749 W903_R503680	W903_0756	665296	666018 NA	short chain dehydrogenase family protein	0.09689397	0.171464977	-0.307942051	1.56032E-19	-0.307942051	1.56032E-19
750 W903_R503685	W903_0757	666116	666316 NA	phosphotransferase attachment site family protein	-0.632845652	1.623128458	0.632845652	0.08956E-57	0.632845652	0.08956E-57
751 W903_R503690	W903_0758	666333	666776 NA	fabA-like family protein	0.529081378	0.010546432	-0.638473044	4.4074E-12	-0.638473044	4.4074E-12
752 W903_R503695	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_R503700	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_R503705	W903_0761	668563	670566 NA	putative cysE	-0.09348488	0.673128496	-0.754945133	1.51003E-19	-0.754945133	1.51003E-19
755 W903_R503710	W903_0762	670563	671516 NA	aminomethyltransferase folate-binding domain protein	-0.22006598	0.12329139	-0.82516651	1.8824E-21	-0.82516651	1.8824E-21
756 W903_R503715	W903_0763	671522	673708 NA	beta-ketolactyl synthase, C-terminal domain protein	0.144365038	0.398258687	-0.424951816	1.40947E-05	-0.424951816	1.40947E-05
757 W903_R503720	W903_0764	673713	674924 NA	UDP-glucuronosyl and UDP-glucosyl transferase family protein	-0.578400574	0.000120828	-0.622065394	1.84752E-09	-0.622065394	1.84752E-09
758 W903_R503725	W903_0765	674893	675867 NA	hypothetical protein	-0.17587674	0.457745E-06	-0.786115754	1.63938E-15	-0.786115754	1.63938E-15
759 W903_R503730	W903_0766	675611	676264 NA	ftsX-like permease family protein	0.027057889	0.534175267	1.265330929	8.00323E-11	1.265330929	8.00323E-11
760 W903_R503735	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_R503740	W903_0768	676328 NA	676328	ABC transporter family protein	0.091231071	0.022265017	0.089184372	0.45464E-07	0.089184372	0.45464E-07

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	1.215776195	1.625786-05	1.215776195	1.625786-05
830	W903_RS04085	W903_0841	748954	749692 NA	glycosyl hydrolases 25 family protein	-0.107888142	0.475286-11	0.545129564	5.22116E-05	0.545129564	5.22116E-05
831	W903_RS04090	W903_0842	750599	750583 NA	ECF-type riboflavin transporter, 5 component family protein	-0.237451516	0.278190502	0.577325002	5.17211E-05	0.577325002	5.17211E-05
832	W903_RS04095	W903_0843	750567	750596 NA	putative lipoprotein	-0.540334155	0.003170788	-0.17625167	0.324269643	-0.17625167	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	1.806064537	0.106335863	1.806064537	0.106335863
836	W903_RS04115	W903_0847	757448	757840 NA	translation elongation factor Tu	0.137348865	0.237744576	-1.079868749	2.48687E-37	-1.079868749	2.48687E-37
837	W903_RS04120	W903_0848	758921	759679 tpsA	triose-phosphate isomerase	0.12687131	0.437073844	-1.594378153	3.35735E-37	-1.594378153	3.35735E-37
838	W903_RS04125	W903_0849	759856	760548 NA	phosphoglycerate mutase 1 family protein	0.1722519346	0.344073825	-1.717253266	6.46049E-68	-1.717253266	6.46049E-68
839	W903_RS04130	W903_0850	760681	760689 NA	phage integrase family protein	-0.765640307	NA	1.5448946	0.057256852	1.5448946	0.057256852
840	W903_RS04135	W903_0851	760984	761376 NA	phage integrase family protein	-0.209390653	NA	1.163522903	0.150585639	1.163522903	0.150585639
841	NA	W903_0852	761549	762157 NA	glycerophosphoryl diester phosphodiesterase family protein	0.859679747	NA	2.359897755	0.002963539	2.359897755	0.002963539
842	NA	W903_0853	762571 NA	762571 NA	glycerophosphoryl diester phosphodiesterase family protein	-0.802842702	NA	1.948350858	0.010470242	1.948350858	0.010470242
843	W903_RS04145	W903_0854	763171	764094 NA	hypothetical protein	-0.794467367	0.680388E-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	767405 NA	penicillin binding transpeptidase domain protein	-0.022248401	0.893990343	0.018895362	0.88545913	0.018895362	0.88545913
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 dtd	D-alanine-D-alanine ligase	-0.385742313	0.015980682	-0.320986301	0.000623687	-0.320986301	0.000623687
848	W903_RS04170	W903_0859	768651	770328 murF	UDP-N-acetylmuramoyl-trisphosphate-D-alanyl-D-alanine ligase family protein	0.855503E-05	0.291818003	0.002996617	0.291818003	0.002996617	0.291818003
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	0.117555698	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	5.95905E-08	0.484481731	5.95905E-08
852	W903_RS04195	W903_0865	776075	776455 NA	hypothetical protein	-0.468004993	0.013735518	0.013579824	0.931269254	0.013579824	0.931269254
853	W903_RS04200	W903_0866	776649	777383 NA	ABC transporter family protein	-0.697465825	0.73358E-28	0.801239569	4.7841E-155	0.801239569	4.7841E-155
854	W903_RS04205	W903_0867	777076	778358 NA	binding-dependent transport system inner membrane component family protein	-0.147777807	0.488081032	3.051460719	6.4904E-122	3.051460719	6.4904E-122
855	W903_RS04210	W903_0868	778374	778884 NA	NLPA lipopolymer protein	-0.67326089	0.005954694	0.225538309	4.98769E-59	0.225538309	4.98769E-59
856	W903_RS04215	W903_0869	779119	780705 NA	helicase domain protein	-0.35626763	0.03638661	-2.221657152	3.01433E-36	-2.221657152	3.01433E-36
857	W903_RS04220	W903_0870	780890	781156 NA	Gi-YIG catalytic domain protein	0.014979291	0.040491728	0.86230103	0.040491728	0.86230103	0.040491728
858	W903_RS04225	W903_0871	781149	781913 NA	methyltransferase domain protein	0.164390927	0.385206427	-0.612567971	0.301981E-07	-0.612567971	0.301981E-07
859	W903_RS04230	W903_0872	782786	782786 pncC	1-acyl-S-adenosyl-5-phosphate acyltransferase	-0.343692444	0.277651666	-0.227085308	0.055145191	-0.227085308	0.055145191
860	W903_RS04235	W903_0873	782887	783540 NA	competence ComEA helix-hairpin-helix repeat region domain protein	-0.151434401	NA	0.767795749	0.30472E-09	0.767795749	0.30472E-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	786958 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	0.467362662	0.348960601	1.303932212	3.9727E-17	1.303932212	3.9727E-17
864	W903_RS04255	W903_0877	787810	788702 NA	alpha/beta hydrolase fold family protein	0.957805213	1.35023E-38	2.10511535	3.84806E-87	2.10511535	3.84806E-87
865	W903_RS04260	W903_0878	789065	790431 NA	methyltransferase domain protein	-0.211345049	0.446374709	0.021867182	7.00216E-07	0.021867182	7.00216E-07
866	W903_RS04265	W903_0879	789659	790906 hsdA	DNA polymerase III, delta subunit	-0.807326836	1.8301E-07	1.02563183	5.41004E-25	1.02563183	5.41004E-25
867	W903_RS04270	W903_0880	790776	791384 soaA	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 antiterminal protein	-0.023905541	0.915404482	2.116245743	1.61949E-70	2.116245743	1.61949E-70
869	W903_RS04280	W903_0882	792567	794435 NA	PTS system, beta-glucoside-specific IIAB component family protein	0.676901086	0.005273908	1.43235082	2.34928E-22	1.43235082	2.34928E-22
870	W903_RS04285	W903_0883	794452	795879 NA	cellulase family protein	0.613255951	0.002033212	0.595525857	5.56628E-05	0.595525857	5.56628E-05
871	W903_RS04290	W903_0884	795947	797041 NA	sugar diacid recognition family protein	-0.127778037	0.074554757	2.410863135	2.78345E-12	2.410863135	2.78345E-12
872	W903_RS04295	W903_0885	798208	798350 NA	glycerate kinase family protein	0.673475349	0.346377292	0.915259299	0.000128038	0.915259299	0.000128038
873	W903_RS04300	W903_0886	798375	799631 NA	citrate transporter family protein	0.497265329	0.950785469	0.900721E-05	0.950785469	0.900721E-05	0.950785469
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_RS04310	W903_0888	800851	801288 NA	mark family protein	0.143499842	0.400439867	-0.391312728	6.34074E-05	-0.391312728	6.34074E-05
876	W903_RS04315	W903_0889	801375	802403 pncB	rRNA ribosyltransferase-isomerase	0.690205171	0.32039E-05	-0.459139461	0.85121E-05	-0.459139461	0.85121E-05
877	W903_RS04320	W903_0890	802556	803236 NA	vit family protein	-0.424702931	0.068611693	-1.235226273	0.00219478	-1.235226273	0.00219478
878	W903_RS04325	W903_0891	803387	804088 nagB	glutathione S-phosphate deaminase	-0.797368198	1.02679E-06	0.120494924	0.58148367	0.120494924	0.58148367
879	W903_RS04330	W903_0892	804160	805116 NA	glutathione 5-transferase, C-terminal domain protein	-0.171033052	0.549536178	0.559716885	0.00460747	0.559716885	0.00460747
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	0.463046761	0.040928568	0.288907958	0.006393623	0.288907958	0.006393623
882	W903_RS04345	W903_0895	807207	808154 NA	competence ComE helix-hairpin-helix repeat region domain protein	-0.256296909	0.664489887	-0.564489887	0.33389E-11	-0.564489887	0.33389E-11
883	W903_RS04350	W903_0896	808170	809075 NA	oligoendopeptidase F	0.679209021	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	810689	811576 NA	methyltransferase domain protein	-0.85099831	2.01201E-18	-0.16019632	5.91598E-25	-0.16019632	5.91598E-25
886	W903_RS04365	W903_0899	811637	812566 NA	PP1C-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 2 family protein	0.319605157	0.056414009	-1.537315698	3.6479E-36	-1.537315698	3.6479E-36
888	W903_RS04375	W903_0901	813309	815927 naB	alanine-ribonucleoside transferase	0.608483541	1.80157E-05	1.453071853	1.1199E-40	1.453071853	1.1199E-40
889	W903_RS04380	W903_0902	816009	816725 NA	hypothetical protein	0.543141317	0.001712706	-0.64635599	0.56691E-06	-0.64635599	0.56691E-06
890	W903_RS04385	W903_0903	816813	817631 NA	glycosyl transferase 8 family protein	-0.385640804	0.104469996	-0.573526169	7.16814E-45	-0.573526169	7.16814E-45
891	W903_RS04390	W903_0904	817832	818200 NA	glycerophosphoryl diester phosphodiesterase family protein	0.809596764	0.165421465	2.598467587	2.12767E-12	2.598467587	2.12767E-12
892	W903_RS04395	W903_0905	818055	818339 NA	hypothetical protein	0.085936628	0.864048926	1.576327272	1.88898E-17	1.576327272	1.88898E-17
893	W903_RS04400	W903_0906	818384	818599 NA	helix-turn-helix family protein	0.440388766	0.547800165	1.597318189	0.00391065	1.597318189	0.00391065
894	W903_RS04405	W903_0907	818602	819360 NA	hypothetical protein	0.258670512	0.648589657	1.07884924	1.8048E-11	1.07884924	1.8048E-11
895	W903_RS04410	W903_0908	819445	820008 thtT	thiamine transporter ThT	0.182907042	0.519354825	2.010592512	2.65045E-32	2.010592512	2.65045E-32
896	W903_RS04415	W903_0909	820249	821208 NA	ribonucleotide reductase, small chain family protein	-0.174334595	0.406936176	0.236586955	0.033451815	0.236586955	0.033451815
897	W903_RS04420	W903_0910	821411	823570 NA	glutaredione-1-phosphate reductase, alpha subunit	-0.110452533	0.549536178	0.62361703	6.27125E-08	0.62361703	6.27125E-08

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	0.530039005	0.120099062	0.772471959	0.003909105	0.772471959	0.003909105
968	W903_RS04780	W903_0981	903030	904440	NA	radical SAM superfamily protein	0.245204507	0.149380746	0.148482687	1.79779632	1.79779632	0.01513928
969	W903_RS04785	W903_0982	903181	905181	NA	acyl-ACP thioesterase family protein	0.64195342	0.48115565	0.623980656	2.304045-15	2.304045-15	2.304045-15
970	W903_RS04790	W903_0983	905182	905952	NA	hydrolase, haloacid dehalogenase-like family	0.385232553	0.004189912	0.722493515	1.277466-10	1.277466-10	1.277466-10
971	W903_RS04795	W903_0984	905927	906598	NA	hypothetical protein	0.708924041	0.000189977	0.598523583	8.898136-07	0.598523583	8.898136-07
972	W903_RS04800	W903_0985	905987	911111	NA	HNH endonuclease family protein	0.328512855	2.22046-06	0.27234835	0.005217265	0.27234835	0.005217265
973	W903_RS04805	W903_0986	911633	911982	cas1	CRISPR-associated endonuclease Cas1	0.665322705	0.000251548	0.285077782	0.015513928	0.285077782	0.015513928
974	W903_RS04810	W903_0987	912320	cas2	CRISPR-associated endonuclease Cas2	0.913534509	0.136536908	0.04188144	0.039234092	0.04188144	0.039234092	
975	W903_RS04815	W903_0988	912307	912972	NA	CRISPR-associated family protein	0.927890899	5.53334e-09	0.48828333	1.80761e-05	0.48828333	1.80761e-05
976	NA	W903_0989	913084	913464	NA	hypothetical protein	0.112781594	1.45102e-07	0.68323914	1.24958E-07	0.68323914	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	0.1715979221	NA	1.341763201	0.007392586	1.341763201	0.007392586
979	NA	W903_0992	914244	914381	NA	putative membrane protein	0.2799057454	0.701826668	1.446888733	0.000214025	1.446888733	0.000214025
980	W903_RS04825	W903_0993	914938	swd	nucleoside diphosphate kinase	0.7192428837	0.007242893	0.007242893	0.358804004	0.007242893	0.358804004	
981	W903_RS04830	W903_0994	915074	916906	lepA	GTP-binding protein LepA	0.326564938	0.004281516	0.016074657	0.879542979	0.016074657	0.879542979
982	NA	W903_0995	916957	917100	NA	hypothetical protein	0.394517434	NA	1.491601493	0.127064085	1.491601493	0.127064085
983	W903_RS04835	W903_0996	917152	919785	NA	histidine triad domain protein	0.827218848	8.1812E-06	1.36470238	1.22179E-24	1.36470238	1.22179E-24
984	W903_RS04840	W903_0997	919891	920544	NA	HD domain protein	0.290860628	0.159911711	0.757171577	3.091E-14	0.757171577	3.091E-14
985	W903_RS04845	W903_0998	920553	921017	NA	acetyltransferase family protein	0.349486284	0.07791473	0.45472412	1.18142E-05	0.45472412	1.18142E-05
986	W903_RS04850	W903_0999	921017	921451	msrB	peptide methionine sulfide reductase MsrB	0.314668368	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	0.18394453	1.130264495	1.24617E-37	1.130264495	1.24617E-37
988	W903_RS04860	W903_1001	924395	925498	NA	hypothetical protein	0.019183562	0.929646957	1.069954729	1.55466E-22	1.069954729	1.55466E-22
989	W903_RS04865	W903_1002	925617	926186	NA	bacterial transferase hexapeptide family protein	0.087880786	NA	3.842935328	2.38E-09	3.842935328	2.38E-09
990	W903_RS04870	W903_1003	926872	927483	NA	hypothetical protein	0.525775316	0.002136569	0.614255055	9.4338E-07	0.614255055	9.4338E-07
991	W903_RS04875	W903_1004	928320	928302	NA	putative membrane protein	0.21398109	0.72172E-27	0.99318671	5.1281E-27	0.99318671	5.1281E-27
992	W903_RS04880	W903_1005	928314	929012	NA	ABC transporter family protein	0.035052814	0.842938478	1.610800849	2.04009E-63	1.610800849	2.04009E-63
993	W903_RS04885	W903_1006	929013	929811	NA	bacterial regulator y, gntR family protein	0.211263388	0.192257021	1.394905694	1.37574E-41	1.394905694	1.37574E-41
994	W903_RS04890	W903_1007	929526	932630	dnaE	DNA polymerase III, alpha subunit	0.036996004	0.842938478	1.610800849	0.978444394	1.610800849	0.978444394
995	W903_RS04895	W903_1008	932711	933733	pfkA	6-phosphofructokinase	0.394831271	0.009634177	1.144514647	2.0775E-10	1.144514647	2.0775E-10
996	W903_RS04900	W903_1009	933782	935284	pyk	pyruvate kinase	0.131263983	0.042380594	1.353117956	1.9412E-44	1.353117956	1.9412E-44
997	W903_RS04905	W903_1010	935455	936012	sigP	signal peptide	0.476288753	0.702089179	0.020384639	0.879954279	0.020384639	0.879954279
998	NA	W903_1011	936300	936161	NA	hypothetical protein	0.1499887449	0.011610497	0.081514995	0.971479693	0.081514995	0.971479693
999	W903_RS04910	W903_1012	936270	938084	glnS	glutamine-fructose-6-phosphate transaminase	0.2117067045	2.33753E-19	1.257799978	1.40005E-15	1.257799978	1.40005E-15
1000	W903_RS04915	W903_1013	938247	938576	NA	pHnA family protein	0.922438391	7.53337E-05	0.200771601	0.52506759	0.200771601	0.52506759
1001	W903_RS04920	W903_1014	938711	939352	NA	amino ABC transporter, permease, 3-TM region, His/Glu/Arg/Gln/opine family domain protein	0.140921967	2.14802E-07	0.466121438	2.48943E-05	0.466121438	2.48943E-05
1002	W903_RS04925	W903_1015	939362	939991	NA	ABC transporter family protein	0.912858803	5.27275E-07	0.546417008	0.65561E-08	0.546417008	0.65561E-08
1003	W903_RS04930	W903_1016	940428	941593	NA	polar amino acid ABC uptake transporter substrate binding protein	0.103349387	1.45039E-02	0.802146588	6.3831E-07	0.802146588	6.3831E-07
1004	W903_RS04935	W903_1017	940923	941156	pyk	ribosomal protein S20	0.1105516521	1.95216E-09	0.580864885	0.005341415	0.580864885	0.005341415
1005	W903_RS04940	W903_1018	941225	942145	coaA	paranthionate kinase	0.60535395	0.000884833	0.413705912	0.003076482	0.413705912	0.003076482
1006	W903_RS04945	W903_1019	942251	942841	NA	mycolic acid cyclopentane synthetase family protein	0.885244065	0.40153E-06	0.909714149	0.521261113	0.909714149	0.521261113
1007	W903_RS04950	W903_1020	943167	943556	cds	cytidine deaminase	0.037159333	0.858488886	0.757667579	1.94808E-07	0.757667579	1.94808E-07
1008	W903_RS04955	W903_1021	943621	944670	NA	basic membrane family protein	0.01553147	0.935706556	1.44448662	1.60762E-24	1.44448662	1.60762E-24
1009	W903_RS04960	W903_1022	944815	946350	NA	heme ABC exporter, ATP-binding protein CcmA	0.029971351	1.361568311	0.3525488	1.3015E-31	1.361568311	1.3015E-31
1010	W903_RS04965	W903_1023	946343	947404	NA	branched-chain amino acid transport system / permease component family protein	0.122605214	0.029010833	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	949398	NA	putative NADH oxidase	0.395978089	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	gylA	DNA gyrase, A subunit	0.054016647	0.74558947	0.202318164	0.29736522	0.202318164	0.29736522
1015	W903_RS04990	W903_1028	953733	954496	NA	sorvase family protein	0.437252663	0.004077762	0.025149018	0.803532698	0.025149018	0.803532698
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	0.174754602	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	7.69095E-05	1.412245854	2.0911E-17	1.412245854	2.0911E-17
1020	W903_RS05015	W903_1033	958904	960124	NA	hypothetical protein	0.149846613	NA	0.323758139	0.032158133	0.323758139	0.032158133
1021	W903_RS05020	W903_1034	959221	959643	NA	glycerophosphoryl diester phosphodiesterase family protein	0.449507019	NA	0.313974655	0.673406985	0.313974655	0.673406985
1022	W903_RS05025	W903_1035	959636	960694	NA	replication initiation factor family protein	0.02558737	0.950325218	1.919460809	2.4225E-21	1.919460809	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	0.366872824	0.346377236	0.032925265	0.88545913	0.032925265	0.88545913
1025	NA	W903_1038	962437	962550	NA	putative membrane protein	0.277468129	0.125079495	0.571072423	6.41649E-08	0.571072423	6.41649E-08
1026	W903_RS05045	W903_1039	962786	964448	gusA	GMP synthase family protein	0.465461831	0.05166678	0.588068537	2.38317E-09	0.588068537	2.38317E-09
1027	W903_RS05050	W903_1040	964561	965259	NA	bacterial regulator y, gntR family protein	0.175665994	0.334549017	0.548367517	2.42966E-05	0.548367517	2.42966E-05
1028	W903_RS05055	W903_1041	965373	966707	trmFO	m(S)-5,4 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	0.566883212	1.139623828	0.266694644	1.139623828	0.266694644
1030	W903_RS05065	W903_1043	967670	968518	NA	NLP4 lipofamily protein	0.23197186	0.29568372	0.38692555	0.04174361	0.38692555	0.04174361
1031	W903_RS05070	W903_1044	968550	969038	NA	hypothetical protein	0.680027219	2.55269E-06	0.598802115	1.62346E-15	0.598802115	1.62346E-15
1032	W903_RS05075	W903_1045	969024	970166	NA	peptidase S41 family protein	0.698236575	0.013978751	1.721640789	7.17939E-25	1.721640789	7.17939E-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	0.031141424	0.430773844	0.24514496	0.030623076	0.2	

1104	W903_K505455	W903_1122	1044201	1048610	essC	type VII secretion protein EssC	1.650125219	1.62442E-25	0.916938682	3.72887E-15	0.916938682	3.72887E-15
1105	W903_K505460	W903_1123	1048617	1049894	essB	type VII secretion protein EssB	1.551773359	5.6193E-14	1.077341693	2.27308E-12	1.077341693	2.27308E-12
1106	W903_K505465	W903_1124	1049894	1051006	NA	ykdJ family protein	1.079466878	1.42251E-08	1.422517992	1.55977E-12	1.422517992	1.55977E-12
1107	W903_K505470	W903_1125	1050120	1050548	esaA	type VII secretion protein EssA	0.903754263	0.5758835789	0.5758835789	0.000662829	0.5758835789	0.000662829
1108	W903_K505475	W903_1126	1050602	1053613	esaA	type VII secretion protein EssA	1.513785472	3.57802E-10	1.055397543	3.78081E-19	1.055397543	3.78081E-19
1109	NA	W903_1127	1053764	1053985	NA	virulence factor essA	0.958831873	0.001370887	2.300780357	1.29522E-26	2.300780357	1.29522E-26
1110	W903_K505485	W903_1128	1054152	1054442	NA	virulence factor essA	0.171350406	0.862474361	0.862474361	5.3001E-10	0.862474361	5.3001E-10
1111	W903_K505490	W903_1129	1045559	1055341	NA	lipase family protein	1.627813081	0.367966213	0.272089017	0.079675359	0.272089017	0.079675359
1112	W903_K505495	W903_1130	1055614	1056614	NA	hypothetical protein	0.134911711	0.508587412	0.508587412	0.000110881	0.508587412	0.000110881
1113	W903_K505500	W903_1131	1055787	1058969	carB	carbamoyl-phosphate synthase, large subunit	2.423695939	0.302225232	0.495717277	0.000509529	0.495717277	0.000509529
1114	W903_K505505	W903_1132	1059000	1060076	NA	carbamoyl-phosphate synthase, small subunit	3.241283673	0.18396017	0.658533218	6.9593E-36	0.658533218	6.9593E-36
1115	W903_K505510	W903_1133	1060087	1061013	pyrB	aspartate carbamoyltransferase	3.330470062	0.185033565	0.81648181	0.08118E-09	0.81648181	0.08118E-09
1116	W903_K505515	W903_1134	1061182	1062474	pyrC	dihydroorotate, multi-functional complex type domain protein	3.263647114	0.171028626	0.531821574	3.51623E-37	0.531821574	3.51623E-37
1117	W903_K505520	W903_1135	1062486	1063115	pyrE	orotate phosphoribosyltransferase	2.968996739	0.170250592	0.897893956	1.40427E-21	0.897893956	1.40427E-21
1118	W903_K505525	W903_1136	1063829	1063829	pyrF	orotidine 5'-phosphate decarboxylase	0.135099290	0.333047889	0.743074558	9.43321E-15	0.743074558	9.43321E-15
1119	W903_K505530	W903_1137	1064042	1065274	NA	hypothetical protein	0.650334646	2.41743E-05	1.157030483	7.29086E-34	1.157030483	7.29086E-34
1120	W903_K505535	W903_1138	1065314	1068685	NA	heme ABC exporter, ATP-binding protein CcmA	0.594362592	0.000210008	1.008559552	5.31424E-26	1.008559552	5.31424E-26
1121	W903_K505540	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_K505545	W903_1140	1067494	1068570	asd	aspartate-semialdehyde dehydrogenase	0.150487429	0.642756017	0.647972123	2.96697E-09	0.647972123	2.96697E-09
1123	W903_K505550	W903_1141	1068779	1069867	NA	LPXTG cell wall anchor domain protein	1.145750511	2.32388E-14	0.903220087	1.61028E-16	0.903220087	1.61028E-16
1124	W903_K505555	W903_1142	1070557	1072152	ds	cardiolipin synthase	0.127070903	0.495127691	0.95865886	0.568288627	0.95865886	0.568288627
1125	W903_K505560	W903_1143	1072721	1073941	NA	formate-tetrahydrofolate ligase family protein	0.844441711	1.463E-05	0.284625866	0.009051042	0.284625866	0.009051042
1126	W903_K505565	W903_1144	1074030	1075049	NA	lipoyltransferase and lipoyate-ligase family protein	0.430575315	0.018037897	1.147878918	5.25972E-24	1.147878918	5.25972E-24
1127	W903_K505570	W903_1145	1075076	1075954	NA	hypothetical protein	0.696186533	0.00522225	1.400390926	4.12082E-36	1.400390926	4.12082E-36
1128	W903_K505575	W903_1146	1075923	1076741	NA	macro domain protein	0.374497796	0.070238826	1.043396607	1.45015E-24	1.043396607	1.45015E-24
1129	W903_K505580	W903_1147	1076734	1077066	NA	glycine cleavage H-family protein	0.166035282	0.484031603	0.745737587	0.000128659	0.745737587	0.000128659
1130	W903_K505585	W903_1148	1077095	1078081	NA	luciferase oxidoreductase, group 1 family protein	0.149717797	0.430969743	1.031021223	1.2815E-17	1.031021223	1.2815E-17
1131	W903_K505590	W903_1149	1078078	1079277	NA	flavin oxidoreductase / NADH oxidase family protein	0.309925862	0.070856166	1.391738507	1.15079E-30	1.391738507	1.15079E-30
1132	W903_K505595	W903_1150	1079270	1080106	NA	biotin/lipoate A/B ligase family protein	0.125281878	0.549536178	1.148741662	4.91333E-20	1.148741662	4.91333E-20
1133	W903_K505600	W903_1151	1080260	1080466	coaB	phosphopantothenate-cysteine ligase	0.270932893	0.252500145	1.018772191	0.203463071	1.018772191	0.203463071
1134	W903_K505605	W903_1152	1080399	1081481	coaC	phosphopantothenate-cysteine decarboxylase	0.918076042	6.49035E-36	0.739602767	0.012429507	0.739602767	0.012429507
1135	W903_K505610	W903_1153	1082290	1082990	panT	panthoic acid transporter PanT	0.135099290	0.477808424	0.658509556	0.049799571	0.658509556	0.049799571
1136	W903_K505615	W903_1154	1082929	1083922	NA	phosphoglucomutase/phosphomannomutase, C-terminal domain protein	0.231041047	0.133952618	0.332334275	0.002187344	0.332334275	0.002187344
1137	W903_K505625	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_K505630	W903_1156	1085935	1087554	NA	ABC transporter family protein	0.185023834	0.355552361	0.503704357	1.62826E-06	0.503704357	1.62826E-06
1139	W903_K505635	W903_1157	1087668	1088270	NA	lysosome-like family protein	0.214550808	0.264242509	0.424820018	5.12463E-05	0.424820018	5.12463E-05
1140	W903_K505640	W903_1158	1088272	1089246	NA	37-KD nucleoid-associated bacterial family protein	0.170454638	0.330951294	1.133263844	0.263576189	1.133263844	0.263576189
1141	W903_K505645	W903_1159	1089120	1090510	NA	serine hydroxymethyltransferase family protein	0.135099290	0.333047889	0.743074558	9.43321E-15	0.743074558	9.43321E-15
1142	W903_K505650	W903_1160	1090602	1091198	NA	tRNA threonylcarbamoyl adenosine modification protein, Saa/Yco/YrdC/Ywc family	0.625360642	7.69050E-05	0.564086128	7.9152E-08	0.564086128	7.9152E-08
1143	W903_K505655	W903_1161	1091191	1092021	prnC	protein-(glutamine-N5) methyltransferase, release factor-specific	0.398330508	0.013077952	0.548487662	3.91675E-05	0.548487662	3.91675E-05
1144	W903_K505660	W903_1162	1092021	1093100	prfA	peptide chain release factor 1	0.287284446	0.103410495	0.357905848	0.001202895	0.357905848	0.001202895
1145	W903_K505665	W903_1163	1093135	1093704	NA	thymidine kinase family protein	0.098220294	0.690716371	1.328328E-10	0.690716371	1.328328E-10	0.690716371
1146	W903_K505670	W903_1164	1093842	1094024	NA	tautomerase enzyme family protein	0.616317017	0.77915471	1.217106807	0.000235652	1.217106807	0.000235652
1147	W903_K505675	W903_1165	1094200	1095111	NA	ap6C family protein	0.131380911	0.232173891	0.327783157	1.3129E-48	0.327783157	1.3129E-48
1148	W903_K505680	W903_1166	1095129	1095731	NA	NADPH-dependent FMN reductase family protein	0.502951876	0.0069531	1.195898511	7.74918E-34	1.195898511	7.74918E-34
1149	W903_K505685	W903_1167	1095755	1096990	NA	NADPH-dependent FMN reductase family protein	0.487477817	0.01187837	0.911037261	7.04866E-20	0.911037261	7.04866E-20
1150	W903_K505690	W903_1168	1097089	1097877	NA	formate/nitrite transporter family protein	0.471931611	0.00288992	0.69288253	3.87193E-12	0.69288253	3.87193E-12
1151	W903_K505695	W903_1169	1097976	1099250	puoC	xanthine permease family protein	0.525898388	0.503169838	1.167897525	8.68515E-18	1.167897525	8.68515E-18
1152	W903_K505700	W903_1170	1099831	1100981	apf	xanthine phosphoribosyltransferase family protein	0.155700759	0.351217035	0.731974515	1.19076E-17	0.731974515	1.19076E-17
1153	W903_K505705	W903_1171	1100086	1101069	gucC	guanosine monophosphate reductase	0.58014347	0.001246181	1.38532491	5.82959E-30	1.38532491	5.82959E-30
1154	W903_K505710	W903_1172	1101272	1102612	NA	major Facilitator Superfamily protein	1.605247484	6.36731E-17	0.035851383	0.82867428	0.035851383	0.82867428
1155	W903_K505715	W903_1173	1102904	1103575	NA	hypothetical protein	0.564104835	0.012778518	2.52967467	2.4636E-126	2.52967467	2.4636E-126
1156	W903_K505720	W903_1174	1103647	1105647	NA	potassium uptake protein	0.238674465	0.165421465	0.36216689	0.001687906	0.36216689	0.001687906
1157	W903_K505725	W903_1175	1105782	1106543	NA	short chain dehydrogenase family protein	0.333886868	0.119042498	1.280489676	3.6958E-19	1.280489676	3.6958E-19
1158	W903_K505730	W903_1176	1107597	1108725	NA	phosphate acetyltransferase	0.242805674	0.008678744	0.12878817	0.39191E-14	0.12878817	0.39191E-14
1159	W903_K505735	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_K505740	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_K505745	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_K505750	W903_1180	1110096	1110668	NA	CyH domain protein	0.652537108	0.001794779	0.888093863	1.14542E-15	0.888093863	1.14542E-15
1163	W903_K505755	W903_1181	1110845	1111819	prn2	ribose-phosphate pyrophosphokinase 2	0.429331647	0.04070769	0.955689572	0.605838703	0.955689572	0.605838703
1164	W903_K505760	W903_1182	1112918	1113823	NA	aminotransferase-V family protein	0.375458613	0.054528697	0.170923815	0.00671E-15	0.170923815	0.00671E-15
1165	W903_K505765	W903_1183	1112940	1113287	NA	amino acid metabolism family protein	0.144640316	0.212374927	0.034561809	0.776402317	0.034561809	0.776402317
1166	W903_K505770	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_K505775	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_K505780	W903_1186	1114869	1116002	NA	hypothetical protein	0.32481061	0.01229944	0.12658035	0.246865747	0.12658035	0.246865747
1169	W903_K505785	W903_1187	1116093	1117532	NA	glycolyl hydrolase 1 family protein	0.36175279	0.067561666	1.456424106	1.84123E-43	1.456424106	1.84123E-43
1170	W903_K505790	W903_1188	1									

1242	W903_W030155	W903_1260	1186241	1187008	CRISPR-associated family protein	-0.014869539	0.935760556	-0.121538364	0.281119065	-0.121538364	0.281119065
1243	W903_W030160	W903_1261	1187017	1187727	deO	0.44233566	0.006967	0.099957538	0.388409219	0.099957538	0.388409219
1244	W903_W030165	W903_1262	1187711	1188863	NA	1.1177295	0.599715778	1.4808365	2.948016125	0.599715778	2.948016125
1245	W903_W030170	W903_1263	1188869	1189778	NA	1.216456E-20	0.705920786	4.3196E-12	0.705920786	4.3196E-12	0.705920786
1246	W903_W030175	W903_1264	1189817	1190224	arsC	0.78640106	3.695838E-07	0.496833407	0.641334E-06	0.496833407	0.641334E-06
1247	W903_W030180	W903_1265	1190275	1191486	NA	0.184136699	6.41305E-13	0.774658234	5.28046E-18	0.774658234	5.28046E-18
1248	W903_W030185	W903_1266	1191453	1192214	gpiA	0.730565372	1.250886E-06	0.1028777953	9.37056E-21	0.1028777953	9.37056E-21
1249	W903_W030190	W903_1267	1192452	1193144	NA	0.030601951	0.874114533	0.142224479	0.132778843	0.142224479	0.132778843
1250	W903_W030195	W903_1268	1193152	1194040	NA	0.14722531	0.3161159165	0.001765465	0.001765465	0.3161159165	0.001765465
1251	W903_W030200	W903_1269	1194097	1195758	NA	0.129167674	0.446374739	0.361893839	0.006250497	0.361893839	0.006250497
1252	W903_W030205	W903_1270	1196054	1196518	NA	-0.163198849	0.483314144	0.266848185	0.042722465	0.266848185	0.042722465
1253	W903_W030210	W903_1271	1196815	1197678	NA	-0.054433612	0.823792061	0.435841824	0.000293885	0.435841824	0.000293885
1254	W903_W030215	W903_1272	1197691	1198695	NA	-0.2210574	0.170805376	-0.133662015	0.246936264	-0.133662015	0.246936264
1255	W903_W030220	W903_1273	1199054	1200709	NA	1.062881388	1.80086E-09	-0.182390586	0.179148679	-0.182390586	0.179148679
1256	W903_W030225	W903_1274	1200763	1201482	budA	0.572754498	0.003803024	0.373599719	0.420257E-20	0.373599719	0.420257E-20
1257	W903_W030230	W903_1275	1201490	1203178	alsC	0.511794177	0.36122005	0.1065991421	1.24949E-36	0.1065991421	1.24949E-36
1258	W903_W030235	W903_1276	1203288	1204514	NA	0.829610696	5.93578E-09	-0.243697025	0.008243248	-0.243697025	0.008243248
1259	W903_W030240	W903_1277	1204504	1205694	NA	0.125712866	6.4908E-08	-0.237509944	0.008945849	-0.237509944	0.008945849
1260	W903_W030245	W903_1278	1205678	1206247	NA	0.105920345	0.451716124	0.001165139	0.451716124	0.001165139	0.451716124
1261	W903_W030250	W903_1279	1206237	1206719	mutK	0.914259811	1.67172E-06	0.317399926	0.026068244	0.317399926	0.026068244
1262	W903_W030255	W903_1280	1210208	1211254	rfbA	0.707387072	0.20836E-07	-0.219618241	0.0300524	-0.219618241	0.0300524
1263	W903_W030265	W903_1283	1211461	1212054	NA	0.665520691	1.13108E-05	-0.468147519	0.181042E-06	-0.468147519	0.181042E-06
1264	W903_W030270	W903_1284	1212054	1212923	rfaA	0.73680825	5.55494E-07	-0.414202125	0.000636484	-0.414202125	0.000636484
1265	W903_W030275	W903_1285	1212982	1214085	NA	0.687975377	2.68445E-05	0.015148529	0.900332109	0.015148529	0.900332109
1266	W903_W030280	W903_1286	1214094	1214882	NA	0.003078638	0.068552366	-0.42634577	3.45276E-05	-0.42634577	3.45276E-05
1267	W903_W030285	W903_1287	1214872	1215555	NA	-0.17689511	-0.464266995	-0.464266995	0.000175339	-0.464266995	0.000175339
1268	W903_W030290	W903_1288	1215559	1216339	NA	0.082114182	0.1465217431	0.00174415	0.404141085	0.1465217431	0.404141085
1269	W903_W030295	W903_1289	1216457	1216975	apt	-0.885451823	0.18391E-07	-0.214420962	0.046748003	-0.214420962	0.046748003
1270	W903_W030300	W903_1290	1217098	1219662	NA	0.468013821	0.007850889	-1.302257542	1.61566E-46	-1.302257542	1.61566E-46
1271	W903_W030305	W903_1291	1219614	1220121	recJ	0.958972063	0.004395113	0.004395113	0.973137272	0.004395113	0.973137272
1272	W903_W030310	W903_1292	1222709	1222770	NA	0.00569148	0.977276951	0.108544845	0.36142285	0.108544845	0.36142285
1273	W903_W030315	W903_1293	1223701	1223701	NA	0.272006195	0.290002638	0.159216387	0.007814373	0.159216387	0.007814373
1274	W903_W030320	W903_1294	1224300	1224390	NA	0.026939684	0.888554058	-0.137910466	0.240816638	-0.137910466	0.240816638
1275	W903_W030325	W903_1295	1224383	1225621	hflX	-0.105243094	0.549948356	-0.03857239	0.720005868	-0.03857239	0.720005868
1276	W903_W030330	W903_1296	1225712	1226602	miaA	-0.88476133	1.72768E-07	-0.8035294	1.28616E-10	-0.8035294	1.28616E-10
1277	W903_W030335	W903_1297	1226713	1226889	NA	0.497129996	0.404946436	-0.288325125	0.038074983	-0.288325125	0.038074983
1278	W903_W030340	W903_1298	1226931	1227484	NA	0.083697949	0.1666552071	0.01456889	4.82761E-12	0.1666552071	4.82761E-12
1279	W903_W030345	W903_1299	1227083	1227100	ecfA	0.300280558	0.009912475	0.46617475	1.25257E-29	0.46617475	1.25257E-29
1280	W903_W030355	W903_1302	1232658	1233242	NA	1.104859171	1.28257E-11	0.533576269	3.3551E-07	0.533576269	3.3551E-07
1281	W903_W030360	W903_1303	1233339	1234745	pepV	1.282309E-16	0.25474762	0.0010374128	0.25474762	0.0010374128	0.25474762
1282	W903_W030365	W903_1304	1234792	1235394	NA	0.484813982	0.0423563	-0.129828803	0.216159401	-0.129828803	0.216159401
1283	W903_W030375	W903_1307	1237387	1239168	uwrC	0.249237072	0.143974617	0.681578818	2.1055E-12	0.681578818	2.1055E-12
1284	W903_W030380	W903_1308	1239327	1240094	NA	0.445374222	0.016377276	0.015305952	7.31889E-08	0.015305952	7.31889E-08
1285	W903_W030385	W903_1309	1240153	1241493	NA	0.333351958	0.00202745	0.511375784	8.22077E-21	0.511375784	8.22077E-21
1286	W903_W030390	W903_1310	1241593	1242003	NA	-0.066813326	0.733554053	0.096658616	3.23855E-11	0.096658616	3.23855E-11
1287	W903_W030395	W903_1311	1242013	1242510	NA	-0.552976785	0.00400011	0.861183525	1.63237E-19	0.861183525	1.63237E-19
1288	W903_W030400	W903_1312	1242732	1243328	NA	-0.623776182	0.001751002	-0.481820623	0.001560769	-0.481820623	0.001560769
1289	W903_1311	1243517	1243807	1243807	transposase	-0.098115519	0.828736607	0.138992092	8.67796E-11	0.138992092	8.67796E-11
1290	W903_W030410	W903_1314	1243987	1244622	NA	-0.121895115	1.730914515	0.137094158	1.34053E-13	0.137094158	1.34053E-13
1291	W903_W030415	W903_1315	1244830	1245999	NA	-0.794913031	0.000222738	0.155910919	4.1605E-06	0.155910919	4.1605E-06
1292	W903_W030420	W903_1316	1246134	1246499	rplL	-0.81484588	8.7789E-08	-2.697783052	7.9602E-114	-2.697783052	7.9602E-114
1293	W903_W030425	W903_1317	1246563	1247063	NA	-1.262493267	4.70311E-19	-2.905014541	1.1591E-197	-2.905014541	1.1591E-197
1294	W903_W030430	W903_1318	1247496	1249604	NA	-0.08991759	0.733854288	0.868058905	0.12646E-17	0.868058905	0.12646E-17
1295	W903_W030435	W903_1319	1249607	1250641	mmuM	0.939282781	0.00106331	0.365299822	0.10411911	0.365299822	0.10411911
1296	W903_W030440	W903_1320	1250646	1252022	NA	0.140925518	0.340925518	0.568714342	0.000124549	0.568714342	0.000124549
1297	W903_W030445	W903_1321	1252152	1252802	NA	1.068509436	0.021849764	0.064678934	0.103097361	0.064678934	0.103097361
1298	W903_1322	1252960	1253283	1253283	NA	0.647374824	0.251726351	0.488780419	0.088632077	0.488780419	0.088632077
1299	W903_W030455	W903_1323	1253555	1254103	NA	0.444943371	0.129641826	0.109807639	9.384E-13	0.109807639	9.384E-13
1300	W903_W030460	W903_1324	1254165	1254761	ysxC	0.317737574	0.098023272	0.736055939	1.44175E-10	0.736055939	1.44175E-10
1301	W903_W030465	W903_1325	1254772	1255998	ecpX	0.404603763	0.012061269	0.915389361	2.48631E-16	0.915389361	2.48631E-16
1302	W903_1326	1256012	1256100	1256100	NA	0.300280558	0.141342389	0.134924561	7.88471E-19	0.134924561	7.88471E-19
1303	W903_W030475	W903_1327	1256216	1256710	dhrR	0.078244302	0.107186668	0.104591346	8.4627E-15	0.104591346	8.4627E-15
1304	W903_W030480	W903_1328	1256790	1257629	NA	0.244788563	0.156956193	0.104781135	5.00144E-21	0.104781135	5.00144E-21
1305	W903_W030485	W903_1329	1257783	1258955	NA	0.942141234	-0.216461793	0.058167976	0.058167976	-0.216461793	0.058167976
1306	W903_W030490	W903_1330	1258957	1260240	NA	-0.135720091	0.43289178	-0.17416308	0.166981255	-0.17416308	0.166981255
1307	W903_W030495	W903_1331	1260732	1260781	NA	0.136113554	4.94156E-14	-1.007639004	1.3367E-14	-1.007639004	1.3367E-14
1308	W903_W030500	W903_1332	1260774	1261430	NA	0.75489025	4.47161E-05	0.251797588	0.100943123	0.251797588	0.100943123
1309	W903_W030505	W903_1333	1261517	1262431	NA	1.923353338	4.52609E-26	-0.073782144	0.626202626	-0.073782144	0.626202626
1310	W903_W030510	W903_1334	1262532	1263386	NA	-1.007463458	9.79895E-07	0.143649017	8.1221E-29	0.143649017	8.1221E-29
1311	W903_W030515	W903_1335	1263432	1263650	NA	0.695097777	0.07578491	0.631027735	0.043044812	0.631027735	0.043044812
1312	W903_W030520	W903_1336	1263718	1264713	frtI	0.234106555	0.133078652	0.235805303	0.007811223	0.235805303	0.007811223
1313	W903_W030525	W903_1337	1265702	1266700							

1380	W903_RS06865	W903_1406	1331758	1333392	NA	polyaccharide biosynthesis family protein	0.81354453	1.446496-07	0.788578082	4.5371E-16	0.788578082	4.5371E-16
1381	W903_RS06870	W903_1407	1335516	1334970	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	0.181912597	0.274844661	0.133255122	0.189790909	0.133255122	0.189790909
1382	W903_RS06875	W903_1408	1335519	1335919	NA	ABC transporter family protein	0.682991415	0.040094154	-0.715610064	1.76868E-08	-0.715610064	1.76868E-08
1383	W903_RS06880	W903_1409	1335943	1336875	NA	periplasmic binding family protein	0.568085936	0.00852337	-1.256590812	2.58174E-33	-1.256590812	2.58174E-33
1384	W903_RS06885	W903_1410	1336891	1337916	NA	fecCD transport family protein	0.16522813	0.479431807	-0.372344989	0.004045061	-0.372344989	0.004045061
1385	W903_RS06890	W903_1411	1337913	1338914	NA	fecD transport family protein	0.279664695	0.251844765	-0.124473906	0.073490131	-0.124473906	0.073490131
1386	W903_RS06895	W903_1412	1338943	1339596	NA	hypothetical protein	0.427268144	0.060494851	-0.509160218	0.000937089	-0.509160218	0.000937089
1387	W903_RS06900	W903_1413	1339566	1340591	NA	putative manganese-dependent inorganic pyrophosphatase	-0.739396518	0.67421E-07	-0.107619571	4.97235E-34	-0.107619571	4.97235E-34
1388	W903_RS06905	W903_1414	1340708	1341496	pflA	pyruvate formate-lyase 1-activating enzyme	0.000214991	0.646369876	-0.000214991	2.46811E-05	-0.000214991	2.46811E-05
1389	W903_RS06910	W903_1415	1415564	1342898	NA	transporter associated domain protein	-0.27105964	0.006262932	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	0.08406759	-0.533530966	6.86656E-07	-0.533530966	6.86656E-07
1392	W903_RS06925	W903_1418	1344665	1345306	NA	PAF2 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	1347248	1347098	NA	LPXTG cell wall anchor domain protein	1.352035317	0.230387E-04	0.300730382	4.02077E-68	0.300730382	4.02077E-68
1395	W903_RS06940	W903_1421	1348059	1347979	NA	sortase C	-1.216812399	5.73715E-09	-0.187965227	1.47272E-36	-0.187965227	1.47272E-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	1351071	NA	fimbrial isopeptide formation D2 domain protein	1.053240393	3.45372E-11	-0.047861594	1.0303E-294	-0.047861594	1.0303E-294
1398	W903_RS06955	W903_1424	1351136	1353826	NA	cell wall surface anchor family protein	-1.036801682	5.89644E-08	-0.343663823	5.3409E-229	-0.343663823	5.3409E-229
1399	W903_RS06960	W903_1425	1354110	1355639	NA	M trans-acting positive regulator (MGA) PRD domain protein	-0.109330666	0.523824366	0.086509469	0.507515057	0.086509469	0.507515057
1400	W903_RS06965	W903_1426	1355691	1356830	NA	glycosyl transferases group 1 family protein	0.055971101	0.747497983	-0.833792203	1.08805E-16	-0.833792203	1.08805E-16
1401	W903_RS06970	W903_1427	1356820	1357668	NA	glycosyl transferase 2 family protein	0.0272727407	0.80909822	-0.86426016	1.57976E-16	-0.86426016	1.57976E-16
1402	W903_RS06975	W903_1428	1357665	1359089	NA	polyaccharide 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	0.152383832	0.453150756	-0.581467767	3.69181E-10	-0.581467767	3.69181E-10
1405	W903_RS06990	W903_1431	1361411	1362345	NA	glycosyl transferase 2 family protein	0.165398188	0.377432566	-0.668287461	1.41012E-12	-0.668287461	1.41012E-12
1406	W903_RS06995	W903_1432	1362348	1363403	NA	NAD dependent epimerase/dehydratase family protein	0.442935602	0.483949438	-0.642020384	0.548220384	-0.642020384	0.548220384
1407	W903_RS07000	W903_1433	1363406	1364125	NA	hypothetical protein	0.25763547	0.1693844	-0.60830928	3.90547E-09	-0.60830928	3.90547E-09
1408	W903_RS07005	W903_1434	1364128	1364952	NA	licI 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	-0.877202197	6.70563E-18	-0.877202197	6.70563E-18
1410	W903_RS07015	W903_1436	1366703	1367056	NA	hypothetical protein	0.307613914	0.117859086	-0.19404759	0.109096688	-0.19404759	0.109096688
1411	W903_RS07020	W903_1437	1367056	1367781	NA	glycosyl transferase 2 family protein	0.004151729	0.394404937	-0.256037243	0.00765911	-0.256037243	0.00765911
1412	W903_RS07025	W903_1438	1367781	1368772	NA	glycosyl transferase 2 family protein	0.135810096	0.362515556	-0.304738451	0.00347741	-0.304738451	0.00347741
1413	W903_RS07030	W903_1439	1368717	1369871	NA	glycosyl transferases group 1 family protein	0.07504716	0.688067609	0.316188499	0.00211492	0.316188499	0.00211492
1414	W903_RS07035	W903_1440	1369988	1370842	rfbD	dTDP-4-dehydrohamose reductase	-0.30001968	0.130857241	-0.840559022	1.9238E-10	-0.840559022	1.9238E-10
1415	W903_RS07040	W903_1441	1370932	1371273	NA	hypothetical protein	-0.75874698	5.98718E-06	-0.865067277	1.269E-11	-0.865067277	1.269E-11
1416	W903_RS07045	W903_1442	1371281	1372490	spoB	RNA polymerase sigma factor RpoB	-0.603241292	0.00101683	-0.497314123	6.17148E-07	-0.497314123	6.17148E-07
1417	W903_RS07050	W903_1443	1372498	1374279	anaA	DNA primase	0.606705217	0.002837639	-0.73810936	0.41829977	-0.73810936	0.41829977
1418	W903_RS07055	W903_1444	1374496	1374873	mscL	large conductance mechanosensitive channel protein	0.070786937	0.755212804	0.830611224	2.59010E-09	0.830611224	2.59010E-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	1375230	1375753	NA	flagellin N-methylase family protein	0.567222514	0.12038375	0.641506157	1.20901E-05	0.641506157	1.20901E-05
1421	W903_RS07070	W903_1447	1375856	1376642	NA	bacterial extracellular solute-binding s, 3 family protein	-0.899991089	0.00038739	-0.319565368	0.00344382	-0.319565368	0.00344382
1422	W903_RS07075	W903_1448	1376667	1377950	NA	ammonium Transporter family protein	0.546027232	0.765216121	1.545460041	0.000500841	1.545460041	0.000500841
1423	W903_RS07080	W903_1449	1377950	1379217	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.091790479	0.892936802	2.014188166	1.55815E-19	2.014188166	1.55815E-19
1424	W903_RS07085	W903_1450	1379254	1380240	NA	rhodanese-like domain protein	-0.637637511	0.002562424	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	0.860000063	2.5766E-13	0.860000063	2.5766E-13
1427	W903_RS07100	W903_1453	1382652	1384916	glpG	glycerol/starch/alpha-glucan phosphorylase family protein	-0.82620195	1.713092E-08	-0.39340956	0.133737271	-0.39340956	0.133737271
1428	W903_RS07105	W903_1454	1384916	1386248	mglQ	4-alpha-glucan phosphorylase	0.291319175	0.004213915	-0.758140367	0.169343986	-0.758140367	0.169343986
1429	W903_RS07110	W903_1455	1386552	1387574	NA	helix-turn-helix family protein	-0.328876515	0.129985556	-0.316705124	0.014763377	-0.316705124	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	0.384956212	0.121209805	0.384956212	0.121209805
1432	W903_RS07125	W903_1458	1390545	1391381	NA	binding-dependent transport system inner membrane component family protein	-0.267577212	0.280531005	0.352753358	0.06917701	0.352753358	0.06917701
1433	W903_RS07130	W903_1459	1391612	1393084	NA	H+ symporter family protein	0.310924923	0.086830443	0.428299116	0.000876209	0.428299116	0.000876209
1434	W903_RS07135	W903_1460	1393593	1395129	NA	NUXD domain protein	0.004517055	0.291461878	-0.073630826	0.666653025	-0.073630826	0.666653025
1435	W903_RS07140	W903_1461	1393677	1393865	NA	glycerophosphoryl diester phosphodiesterase family protein	-1.236372335	4.39404E-11	-1.161987424	4.67218E-31	-1.161987424	4.67218E-31
1436	W903_RS07145	W903_1462	1393876	1395201	gfbB	accessory Sec system glycosyltransferase GfB	-0.275524004	0.086116923	-0.839623653	2.2121E-20	-0.839623653	2.2121E-20
1437	W903_RS07150	W903_1463	1395194	1396702	gfaA	accessory Sec system glycosylation protein GfA	0.285804382	0.10621839	-0.348221773	0.001024914	-0.348221773	0.001024914
1438	W903_RS07155	W903_1464	1396716	1399103	secA2	accessory Sec system translocase SecA2	0.395908451	0.014818108	-0.09485244	0.353952072	-0.09485244	0.353952072
1439	W903_RS07160	W903_1465	1399990	1400082	aspA	accessory Sec system protein AspA	0.059444503	0.074979632	-0.227492004	0.05646199	-0.227492004	0.05646199
1440	W903_RS07165	W903_1466	1400138	1400799	aspB	accessory Sec system protein Asp2	0.063531573	0.296325389	-0.002636889	0.034195137	-0.002636889	0.034195137
1441	W903_RS07170	W903_1467	1401645	1403189	aspC	accessory Sec system protein Asp3	-0.102955959	0.570065133	-0.255660188	0.024498859	-0.255660188	0.024498859
1442	W903_RS07175	W903_1468	1403189	1404418	secY2	accessory Sec system translocase SecY2	-0.174418535	0.309794012	-0.117185776	0.234554988	-0.117185776	0.234554988
1443	W903_RS07180	W903_1469	1404551	1405738	NA	hypothetical protein	-0.20856877	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	0.096093616	0.592240846	-0.19095527	0.09114142	-0.19095527	0.09114142
1446	W903_RS07195	W903_1472	1407841	1409882	NA	glycosyl transferase 8 family protein	0.255881753	0.154861878	-0.073630826	0.712424109	-0.073	

1518 NA	W903_1544	1483790	1483975 NA	putative lactoylglutathione lyase	-0.257601515	0.589651879	0.771380501	0.006479785	0.771380501	0.006479785
1519 W903_R507565	W903_1545	1484256	1485212 NA	oxidoreductase, NAD-binding Rossmann fold family protein	-0.091371574	0.627955026	-0.08951182	0.57055785	-0.08951182	0.57055785
1520 W903_R507570	W903_1546	1484209	1485561 NA	ASCH domain protein	0.135987162	0.095763598	-0.11844761	0.43835575	-0.11844761	0.43835575
1521 W903_R507575	W903_1547	1485588	1485903 NA	hypothetical protein	0.150272362	0.27663989	0.09618279	0.27663989	0.09618279	0.27663989
1522 W903_R507580	W903_1548	1485900	1486598 NA	short chain dehydrogenase family protein	0.356176686	0.065019973	0.206541357	0.150324397	0.206541357	0.150324397
1523 W903_R507585	W903_1549	1486591	1486827 NA	hypothetical protein	0.252635234	0.070688377	0.25261522	0.329723128	0.25261522	0.329723128
1524 W903_R507590	W903_1550	1486917	1487093 NA	putative ybaK/prolyl-RNA synthetase associated domain-containing protein	-0.281313381	0.244713212	-0.40143743	0.008198443	-0.40143743	0.008198443
1525 W903_R507595	W903_1551	1487329	1487862 NA	acetyltransferase family protein	-0.273918839	0.388150613	-0.267214213	0.28036498	-0.267214213	0.28036498
1526 W903_R507600	W903_1552	1488107	1489519 NA	glycosyl transferase 2 family protein	0.006612362	0.87732361	-0.251536514	0.7306208	-0.251536514	0.7306208
1527 W903_R507605	W903_1553	1489659	1491818 NA	hypothetical protein	-0.373404414	0.038740238	-0.214808822	0.2705113	-0.214808822	0.2705113
1528 W903_R507610	W903_1554	1491825	1493102 NA	cystyl family protein	-0.578803539	0.001041071	-0.13155417	1.4965363	-0.13155417	1.4965363
1529 W903_R507615	W903_1555	1493263	1493460 NA	hypothetical protein	-0.890701892	1.039796	-0.967957117	0.4351518	-0.967957117	0.4351518
1530 W903_R507620	W903_1556	1493991	1494602 NA	VTG domain protein	-1.362235318	1.53696	-0.004024393	0.978444394	-0.004024393	0.978444394
1531 W903_R507625	W903_1557	1495052	1496389 NA	branched-chain amino acid transport system II carrier protein	-0.081376119	0.795848747	0.50848125	0.001960237	0.50848125	0.001960237
1532 W903_R507630	W903_1558	1496526	1497897 NA	methionine - RNA ligase	0.058751983	0.940421953	-0.169243024	0.20565	-0.169243024	0.20565
1533 W903_R507635	W903_1559	1498725	1499600 tdbH	tellurite resistance protein TdbH	0.328262077	0.371814014	0.010650919	0.121134866	0.010650919	0.121134866
1534 W903_R507640	W903_1560	1499758	1500453 NA	hypothetical protein	-1.1361121	0.726136	-0.527237572	0.173092651	-0.527237572	0.173092651
1535 W903_R507645	W903_1561	1500789	1502006 NA	phosphotransferase system, EIIc family protein	0.487245433	0.007128116	0.803954377	2.3563618	0.803954377	2.3563618
1536 W903_R507650	W903_1562	1501990	1502832 NA	hypothetical protein	0.117049844	5.299566	-0.1	2.7045664	-0.1	2.7045664
1537 W903_R507655	W903_1563	1502909	1503736 NA	exodeoxynucleotidase III family protein	0.530013472	0.02514416	0.80738119	1.6970813	0.80738119	1.6970813
1538 W903_R507660	W903_1564	1503778	1504134 NA	putative arsenate reductase	0.091725905	0.78773361	0.157464472	0.44901665	0.157464472	0.44901665
1539 W903_R507665	W903_1565	1504136	1504612 NA	methylated-DNA-(L)-cysteine S-methyltransferase family protein	0.174550969	0.392991647	0.602078433	0.4176367	0.602078433	0.4176367
1540 W903_R507670	W903_1566	1504668	1505482 NA	ACT domain protein	0.136885903	0.57245169	-1.76016113	0.72298	-1.76016113	0.72298
1541 W903_R507675	W903_1567	1505912	1506460 NA	acetyltransferase, GNAT family	-0.145461667	0.598058959	-2.153800516	0.31688	-2.153800516	0.31688
1542 W903_R507680	W903_1568	1506528	1507619 serC	phosphoserine transaminase	0.25304001	0.332406371	-2.091791196	2.06956	-2.091791196	2.06956
1543 W903_R507685	W903_1569	1507525	1508387 NA	cutC-like protein	-0.13335632	0.000476574	0.514186394	0.00041556	0.514186394	0.00041556
1544 W903_R507690	W903_1570	1508556	1509519 NA	tetrapyrrole (Cortic/Porphyrin) Methylases family protein	0.656546639	5.88535E-05	-0.211210528	0.04397489	-0.211210528	0.04397489
1545 W903_R507695	W903_1571	1509525	1509851 NA	hypothetical protein	-1.48404593	0.00549126	-0.891051679	1.495236	-0.891051679	1.495236
1546 W903_R507700	W903_1572	1509882	1510745 NA	DNA polymerase III, delta subunit	-0.723667572	0.528589E-07	-0.571926811	1.47859E-08	-0.571926811	1.47859E-08
1547 W903_R507705	W903_1573	1510765	1511400 tmk	thymidylate kinase	-0.669798815	0.38044E-06	0.0329852	0.805210661	0.0329852	0.805210661
1548 W903_R507710	W903_1574	1511489	1512148 NA	CBS domain protein	0.59626475	0.324446752	0.109632278	0.78970617	0.109632278	0.78970617
1549 W903_R507715	W903_1575	1512167	1512877 NA	ABC transporter family protein	0.161571538	0.87773361	0.803028798	0.82827559	0.803028798	0.82827559
1550 W903_R507720	W903_1576	1512877	1513641 NA	ABC transporter family protein	0.521193052	0.409695168	1.092051177	0.009164051	1.092051177	0.009164051
1551 W903_R507725	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_R507730	W903_1578	1514598	1515467 NA	branched-chain amino acid transport system / permease component family protein	0.95345641	0.482215313	0.86531831	0.05529493	0.86531831	0.05529493
1553 W903_R507735	W903_1579	1515575	1516741 NA	receptor ligand binding: intron family protein	-0.139998611	0.642192846	-0.627935632	0.38074893	-0.627935632	0.38074893
1554 W903_R507740	W903_1580	1516897	1517142 NA	phage integrase family protein	-1.956967272	1.110492E-11	-0.524028485	0.99844959	-0.524028485	0.99844959
1555 W903_R507745	W903_1581	1517832	1518211 NA	ATP-dependent Clp protease proteolytic subunit	0.091265977	0.744026206	0.124025202	0.19216212	0.124025202	0.19216212
1556 W903_R507750	W903_1582	1517957	1518856 up	acid phosphoribosyltransferase	-0.912166887	2.68394E-09	-1.986976127	8.43205E-92	-1.986976127	8.43205E-92
1557 W903_R507755	W903_1583	1518696	1519865 NA	putative beta-cystathione	0.00523809	0.665634427	0.151514323	0.194418772	0.151514323	0.194418772
1558 W903_R507760	W903_1584	1520000	1520548 NA	putative tRNA (cytidine/uridine-2'-O)-methyltransferase	-1.229731999	0.39152E-12	-0.426349547	0.000974329	-0.426349547	0.000974329
1559 W903_R507765	W903_1585	1520721	1522073 NA	amino acid permease family protein	-0.768436618	0.33167E-06	-0.382048348	0.000575682	-0.382048348	0.000575682
1560 W903_R507770	W903_1586	1522279	1523628 NA	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	0.704267163	2.20021E-16	1.15317823	0.66356E-23	1.15317823	0.66356E-23
1561 W903_R507775	W903_1587	1523465	1525072 NA	cation transporter family protein	0.732633167	0.52628E-06	0.651439061	0.0551E-08	0.651439061	0.0551E-08
1562 W903_R507780	W903_1588	1525096	1525347 NA	putative membrane protein insertion efficiency factor	0.605144524	0.2158447E5	-0.02906618	0.943692621	-0.02906618	0.943692621
1563 W903_R507785	W903_1589	1525347	1526069 NA	pseudouridine synthase family protein	-0.050769837	0.795622196	-0.318217676	0.007747297	-0.318217676	0.007747297
1564 W903_R507790	W903_1590	1526059	1526643 scpB	segregation and condensation protein B	-0.063099885	0.734062253	0.046632446	0.73319654	0.046632446	0.73319654
1565 W903_R507795	W903_1591	1526640	1527347 NA	scpB/A family protein	-0.116139405	0.549948365	-0.061580903	0.629127772	-0.061580903	0.629127772
1566 NA	W903_1592	1527247	1527793 NA	phage integrase family protein	0.085431760	0.1554897163	0.476866564	0.1542873965	0.476866564	0.1542873965
1567 W903_R507805	W903_1593	1528077	1528550 NA	CBS domain protein	0.257240403	0.137687003	0.055358237	0.715229253	0.055358237	0.715229253
1568 W903_R507810	W903_1594	1528547	1529068 NA	phosphodiesterase, Mf0936 family protein	0.241043548	0.179534464	0.027066746	0.866466723	0.027066746	0.866466723
1569 W903_R507815	W903_1595	1529050	1530024 rdgB	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	0.265269099	0.12378284	0.077402623	0.533125342	0.077402623	0.533125342
1570 W903_R507820	W903_1596	1530021	1530815 murI	glutamate racemase	0.558165556	0.129946656	0.334247173	0.002236428	0.334247173	0.002236428
1571 W903_R507825	W903_1597	1530993	1531229 NA	hypothetical protein	-0.257995488	0.000731538	-0.029633654	0.832864156	-0.029633654	0.832864156
1572 W903_R507830	W903_1598	1531929	1532636 NA	membrane insertase, YidC/Oxa1 family domain protein	0.007516536	0.123631906	0.147086436	0.00945176	0.147086436	0.00945176
1573 W903_R507835	W903_1599	1532191	1532512 nadR	transcriptional repressor NadR	0.06162763	0.811660526	-0.251570638	0.075482189	-0.251570638	0.075482189
1574 W903_R507840	W903_1600	1532580	1532639 NA	inhibitor of apoptosis-promoting Bax1 family protein	0.262403242	0.157666073	0.121572636	0.427621248	0.121572636	0.427621248
1575 W903_R507845	W903_1601	1533292	1533795 NA	hypothetical protein	0.515120032	0.001094055	0.195563364	0.041109007	0.195563364	0.041109007
1576 W903_R507850	W903_1602	1533833	1534576 NA	RNA 2'-O ribose methyltransferase substrate binding family protein	0.066162783	0.006387938	0.314831947	0.0067343	0.314831947	0.0067343
1577 W903_R507855	W903_1603	1534608	1534886 NA	acylphosphatase family protein	-0.054900269	0.823792061	-0.732072257	1.70507E-07	-0.732072257	1.70507E-07
1578 W903_R507860	W903_1604	1534971	1535903 NA	membrane insertase, YidC/Oxa1 family domain protein	0.014950601	0.236529036	0.782475429	0.81482E-15	0.782475429	0.81482E-15
1579 W903_R507865	W903_1605	1536103	1536768 NA	amino ABC transporter, permease, 3-TM region, His/Glu/Arg/Arg/opine family amino acid transport protein	0.597666817	0.001472033	0.732725854	1.38725E-17	0.732725854	1.38725E-17
1580 W903_R507870	W903_1606	1536792	1537649 NA	putative ABC transporter extracellular-binding protein ycbK	0.213241502	0.306567098	0.2168994875	1.58908E-71	0.2168994875	1.58908E-71
1581 W903_R507875	W903_1607	1537810	1539270 NA	amidase family protein	0.152825683	0.535771604	0.32355636	0.039786013	0.32355636	0.039786013
1582 W903_R507880	W903_1608	1539373	1539855 greA	transcription elongation factor GreA domain protein	-1.180019613	1.27264E-11	-1.641226254	1.22595E-65	-1.641226254	1.22595E-65
1583 W903_R507885	W903_1609	1539928	1541730 NA	ycgE-like family protein	-0.610170692	0.23809E-05	-0.800979887	0.63526E-25	-0.800979887	0.63526E-25
1584 W903_R507890	W903_1610	1541817	1542320 NA	acetyltransferase family protein	0.5259E-15	0.5259E-15	-0.801390861	0.0228E-15	-0.801390861	0.0228E-15
1585 W903_R507895	W903_1611	1542406	1543737 murC	UDP-N-acetylmuramate-alanine ligase	-0.263224996	0.095916955	-0.854411244	1.03001E-19	-0.854411244	1.03001E-19
1586 W903_R507900	W903_1612	1543747	1543634 NA	hypothetical protein	0.413127246	0.010493967	0.06683623	0.549881366	0.06683623	0.549881366
1587 W903_R50905	W903_1613	1544529	1547627 NA	helicase domain protein	0.072367082	0.719967872	0.825476158	1.40290E-20	0.825476158	1.40290E-20
1588 W903_R50910	W903_1614	1547782	1549092 engA	ribosome-associated GTPase EngA	0.510475203	0.000987298	-0.023774962	0.818696636	-0.023774962	

1656	W903_S08250	W903_1682	1616980	1618419	NA	sucrose 6-phosphate hydrolase family protein	0.456048091	0.003498671	-0.169914789	0.145407556	0.145407556
1657	W903_S08255	W903_1683	1618421	1619383	NA	helix-turn-helix family protein	0.245743107	0.165272261	-0.353347171	0.001702434	0.001702434
1658	W903_S08260	W903_1684	1619040	1619004	nusB	transcription antitermination factor NusB	-0.349859815	1.8013176-09	-1.376868894	8.487656-66	-1.376868894
1659	W903_S08265	W903_1685	1620286	1620286	NA	hypothetical protein	0.150788252	7.13116E-14	-1.84493477	2.96241E-66	-1.84493477
1660	W903_S08270	W903_1686	1620375	1620395	efp	translation elongation factor P	-1.205057963	2.56509E-17	-1.886278289	2.54751E-87	-1.886278289
1661	NA	W903_1687	1620966	1621082	NA	glycerophosphoryl diester phosphodiesterase family protein	-0.040417287	0.91541872	1.471104076	1.92833E-14	1.471104076
1662	NA	W903_1688	1621664	1621804	NA	hypothetical protein	0.237857486	0.299845493	1.568080412	3.60909E-41	1.568080412
1663	W903_S10500	W903_1689	1622455	1622820	NA	hypothetical protein	-1.392591364	5.76347E-07	0.303934934	0.199593713	0.303934934
1664	NA	W903_1690	1622833	1623003	NA	glycerophosphoryl diester phosphodiesterase family protein	0.034002407	0.253234068	0.786482131	0.003104978	0.786482131
1665	W903_S08280	W903_1691	1623016	1623456	NA	hypothetical protein	-1.188841321	0.000252682	0.23902453	0.332527466	0.23902453
1666	W903_S10510	W903_1692	1623593	1623715	NA	hypothetical protein	-0.335707993	0.180011398	0.47922254	0.003199302	0.47922254
1667	W903_S08285	W903_1693	1624058	1624510	NA	cytidine and deoxycytidylate deaminase zinc-binding region family protein	0.228668585	0.277470661	0.382919559	0.000470333	0.382919559
1668	W903_S08290	W903_1694	1624522	1625589	pepP	aminopeptidase P	0.125454143	0.500410795	0.090120412	0.372042982	0.090120412
1669	W903_S08295	W903_1695	1625589	1626405	NA	hypothetical protein	0.187574774	0.484912393	2.356566511	1.0535E-101	2.356566511
1670	W903_S08300	W903_1700	1626407	1627906	NA	Hv antiporter-2 family protein	0.2634607	2.6989E-288	2.525234068	1.8631E-212	2.525234068
1671	NA	W903_1697	1627994	1628110	NA	hypothetical protein	0.064902086	0.864846575	3.342082774	4.139E-102	3.342082774
1672	W903_S08305	W903_1698	1628242	1631070	uorA	exonuclease ABC subunit A	1.118089741	5.78596E-14	0.495367346	2.0881E-07	0.495367346
1673	W903_S08310	W903_1699	1631202	1631873	NA	hypothetical protein	-0.018058289	0.934706308	-0.902314724	2.11074E-16	-0.902314724
1674	W903_S08315	W903_1700	1631898	1632842	NA	cork-like Mg ²⁺ transporter family protein	-0.090695241	0.702717756	-0.637683611	8.56274E-08	-0.637683611
1675	W903_S08320	W903_1701	1633012	1633251	rsbR	ribosomal protein S18	-1.034511286	2.06456E-10	-3.355785491	1.213E-160	-3.355785491
1676	W903_S08325	W903_1702	1633296	1633787	NA	single-stranded DNA-binding family protein	-1.292921718	2.915406E-15	-3.274456858	1.9738E-229	-3.274456858
1677	W903_S08330	W903_1703	1633799	1634086	rsbP	ribosomal protein S6	-1.6598835	1.45243E-24	-3.395252719	1.1708E-193	-3.395252719
1678	W903_S08335	W903_1704	1635149	1636303	mutY	A/G-specific adenine glycosylase	0.496277159	0.003153271	0.90139141	6.42436E-16	0.90139141
1679	W903_S08340	W903_1705	1636480	1637073	NA	helix-turn-helix family protein	0.024621442	0.922793656	0.418416837	0.00726236	0.418416837
1680	W903_S08345	W903_1706	1637119	1637433	tnaA	threonine	-0.05388838	0.080581031	-0.521124961	1.40947E-05	-0.521124961
1681	W903_S08350	W903_1707	1637514	1638014	NA	PAD2 superfamily protein	0.062787814	0.297154071	-0.37542218	0.001388634	-0.37542218
1682	W903_S08355	W903_1708	1638018	1640357	tnaB	mutS family protein	0.055119871	0.055119871	0.396183603	2.17646E-05	0.396183603
1683	W903_S08360	W903_1709	1640042	1640984	NA	colicin V production family protein	-0.437553597	0.056180077	0.397956052	0.01548651	0.397956052
1684	W903_S08365	W903_1710	1640987	1641298	NA	putative cell division protein ZapA	0.014400992	1.21886E-06	0.619325284	6.31891E-07	0.619325284
1685	W903_S08370	W903_1711	1641424	1642302	rnhC	ribonuclease Hill	-0.226740455	0.183867077	-0.165891009	0.132142401	-0.165891009
1686	W903_S08375	W903_1712	1642518	1642914	NA	signal peptidase I	-0.043703803	0.82635988	-0.672032012	2.10054E-08	-0.672032012
1687	W903_S08380	W903_1713	1645460	1646056	NA	beta-lactamase family protein	0.148091761	0.023886611	0.023886611	0.033519473	0.023886611
1688	W903_S08385	W903_1714	1645574	1646056	NA	putative membrane protein	0.031202901	0.876832988	0.94271966	2.38776E-11	0.94271966
1689	W903_S08390	W903_1715	1646127	1647221	NA	impB/mucB/samB family protein	-0.187801941	0.346377236	0.642274233	5.54563E-09	0.642274233
1690	W903_S08395	W903_1716	1647406	1649718	pflB	formate acetyltransferase	0.066156732	0.734621538	-0.36835614	0.00011918	-0.36835614
1691	W903_S08400	W903_1717	1649819	1650193	NA	FMN-binding protein	1.087214858	0.00598806	0.336647545	0.083914006	0.336647545
1692	W903_S08405	W903_1718	1650228	1651157	NA	beta-lactamase family protein	-0.190636157	0.131647416	0.234124978	0.144823595	0.234124978
1693	W903_S08410	W903_1719	1651154	1651909	copA	C3-degrading proteolysin	0.004343164	0.024934232	0.25400961	1.2689E-05	0.25400961
1694	W903_S08415	W903_1720	1652034	1652930	NA	sulfite exporter TauE/SafE family protein	-0.320964442	0.071230182	-0.37078854	0.002913308	-0.37078854
1695	W903_S08420	W903_1721	1653008	1653835	gla	glycerol facilitator-aquaporin gla	-0.398753891	0.021467784	-1.830409754	9.10951E-18	-1.830409754
1696	W903_S08425	W903_1722	1654405	1654477	NA	universal stress family protein	1.193577739	8.99585E-08	-0.951818699	1.82646E-22	-0.951818699
1697	W903_S08430	W903_1723	1654529	1655697	NA	sugar (and other) transporter family protein	-0.100993243	0.549536178	-0.208037572	7.56677E-85	-0.208037572
1698	W903_S08435	W903_1724	1655853	1656512	NA	crp-like helix-turn-helix domain protein	0.025980127	0.842711997	-0.138205416	0.457950226	-0.138205416
1699	W903_S08440	W903_1725	1656536	1658821	pepA	ser-Pro dipeptidyl-peptidase	-0.175694371	0.20225232	0.450263404	1.56448E-05	0.450263404
1700	W903_S08445	W903_1726	1658825	1659184	NA	hypothetical protein	-0.862487273	0.7014E-07	-1.18346694	5.00761E-21	-1.18346694
1701	W903_S08450	W903_1727	1659230	1660210	NA	geranyl/geranyl pyrophosphate synthase	0.217067731	0.205169742	1.81924403	3.03728E-24	1.81924403
1702	W903_S08455	W903_1728	1660295	1660343	cydC	thiol reductant ABC exporter, CydC subunit	0.54093964	0.000536344	1.206275226	2.40652E-22	1.206275226
1703	W903_S08460	W903_1729	1662036	1663754	cydD	thiol reductant ABC exporter, CydD subunit	0.585920498	0.000127171	1.519393662	2.86191E-33	1.519393662
1704	W903_S08465	W903_1730	1664773	1664773	cydE	cytochrome d ubiquinol oxidase subunit II	0.058990929	1.34788E-08	0.1378747034	5.48406E-01	0.1378747034
1705	W903_S08470	W903_1731	1664774	1666201	NA	bacterial Cytochrome Ubiquinol Oxidase family protein	0.588831525	1.15305E-10	1.564354553	1.07323E-59	1.564354553
1706	W903_S08475	W903_1732	1666304	1667512	NA	pyridine nucleotide-disulfide oxidoreductase family protein	0.362894971	0.025739642	1.352235775	2.38934E-51	1.352235775
1707	W903_S08480	W903_1733	1667525	1668424	NA	ubik prenyltransferase family protein	-0.037258108	0.842711997	-1.874323182	3.99509E-80	-1.874323182
1708	NA	W903_1735	1668833	1669279	NA	hypothetical protein	0.905350411	0.00118909	0.822208884	5.81671E-08	0.822208884
1709	W903_S08485	W903_1736	1669893	1670309	NA	hypothetical protein	-0.364668948	0.448100044	0.92593623	0.002711472	0.92593623
1710	W903_S08490	W903_1737	1670162	1670461	NA	DNA-binding protein class V family protein	0.14934131	0.18011E-17	-1.360119116	1.53322E-17	-1.360119116
1711	W903_S08495	W903_1737	1670622	1671812	NA	methyltransferase domain protein	0.443418836	0.002889992	0.118795852	0.315767408	0.118795852
1712	W903_S08500	W903_1740	1672732	1673319	NA	exonuclease family protein	-0.998160611	3.74698E-07	0.718071314	4.81515E-09	0.718071314
1713	W903_S08510	W903_1741	1673363	1673899	NA	hypothetical protein	-1.573353892	4.34334E-20	0.159403395	0.292032486	0.159403395
1714	W903_S08520	W903_1744	1675250	1675906	NA	hypothetical protein	-0.000446989	0.998547303	0.482117957	0.003002164	0.482117957
1715	W903_S08525	W903_1745	1676191	1676460	rsn2A	alterate S30 ribosomal protein S14	-1.19867283	1.7171E-15	-3.643587372	1.1196E-181	-3.643587372
1716	W903_S08530	W903_1746	1678482	1678784	NA	aminotransferase class V family protein	0.014382007	4.1967E-05	0.212790423	7.5393E-23	0.212790423
1717	W903_S08535	W903_1747	1679687	1678978	NA	tRNA (threonylcarbamoyl adenine modification) protein YgiD	0.064882628	0.704017079	1.214430442	2.05027E-27	1.214430442
1718	W903_S08540	W903_1748	1679058	1679465	rnlA	ribosomal-protein-alanine acetyltransferase	-0.069942951	0.736690134	0.986263408	2.19824E-21	0.986263408
1719	W903_S08545	W903_1749	1679467	1679651	yeaZ	tRNA (threonylcarbamoyl adenine modification) protein YeaZ	-0.381913915	0.032203904	0.851570305	1.28763E-17	0.851570305
1720	W903_S08550	W903_1750	1680338	1680568	NA	hypothetical protein	-0.511963432	0.010713828	-0.832381072	1.25276E-07	-0.832381072
1721	W903_S08555	W903_1751	1680622	1682001	NA	putative permease	0.65980361	3.5941E-06	0.032772837	0.76682987	0.032772837
1722	W903_S08560	W903_1752	1682469	1682966	NA	CHAP domain protein	0.158244071	1.53209E-12	0.904538434	5.69726E-07	0.904538434
1723	W903_S08565	W903_1753	1683126	1684472	glnA	glutamine synthetase, type I	-0.866579555	7.00312E-05	-0.605384517	0.000174009	-0.605384517
1724	W903_S08570	W903_1754	1684506	1684877	rplA	merR regulatory family protein	-1.197445062	7.23226E-09	-0.405995975	0.006700409	-0.405995975
1725	W903_S08575	W903_1755	1684959	1684954	NA	hypothetical protein	-0.092161862	0.772029397	0.480606698	0.00520545	0.480606698
1726	W903_S08580	W903_1756	1685759	1686955	NA	phosphoglycerate kinase family protein	0.171529679	7.31218E-07	0.80401642	2.35508E-18	0.80401642
1727	W903_S08585	W903_1757	1687590	1687959	NA	S'-nucleoside diphosphate kinase (P1) family protein	0.099555841	0.068247364	0.682147264	0.024215E-07	0.682147264
1728	W903_S08590	W903_1758	1688168	1689178	phd	glyceraldehyde-3-phosphate dehydrogenase, type I	0.020352785	0.903260831	-1.242269849	6.55406E-36	-1.242269849
1729	W903_S08595	W903_1759	1689382	1691460</							

1794 W903_R508915	W903_1824	1755404	1756936	ahpF	alkyl hydroperoxide reductase subunit F	0.377287838	0.020388883	0.824500377	4.712655E-12	0.824500377	4.712655E-12
1795 W903_R508920	W903_1825	1757070	1757140	rRNA	NA	3.58862055	NA	0.640064274	0.889840444	0.640064274	0.889840444
1796 W903_R508925	W903_1826	1757212	1759281	NA	sodium/hydrogen exchanger family protein	0.014350129	0.094944477	0.388970137	3.180696E-07	0.388970137	3.180696E-07
1797 W903_R508930	W903_1827	1757383	1759519	NA	hyposulfite protein	0.010372194	0.069172668	0.069172668	0.705439019	0.069172668	0.705439019
1798 W903_R508935	W903_1828	1759686	1760639	NA	LD-carboxypeptidase family protein	1.57847549	1.599006E-24	0.04239461	0.754725798	0.04239461	0.754725798
1799 W903_R508940	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_R508945	W903_1830	1767372	1767315	NA	major dehydratase, NAD-binding Rossmann fold family protein	1.241598171	2.10787E-13	0.080533905	6.37412E-07	0.080533905	6.37412E-07
1801 W903_R508950	W903_1831	1767361	1764912	NA	protein Facilitator Superfamily protein	0.123107091	0.532862789	0.106154446	8.79972E-14	0.106154446	8.79972E-14
1802 W903_R508955	W903_1832	1765036	1765680	NA	cyclic nucleotide binding domain protein	0.10832729	0.10832729	0.10832729	1.33949E-05	0.10832729	1.33949E-05
1803 W903_R508960	W903_1833	1767546	1766360	def	peptide deformylase	0.212124699	0.295652635	-0.053418469	0.644760707	-0.053418469	0.644760707
1804 W903_R508965	W903_1834	1766432	1767433	NA	periplasmic binding and sugar binding domain of LacI family protein	-0.612630321	0.000520967	-0.117741847	0.30573053	-0.117741847	0.30573053
1805 W903_R508970	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_R508975	W903_1836	1769497	1770312	NA	PTS system mannose/fructose/sorbitose IID component family protein	0.6252121671	0.335504362	1.192251117	2.78161E-07	1.192251117	2.78161E-07
1807 W903_R508980	W903_1837	1770299	1771165	NA	PTS system sorbose-specific IIC component family protein	1.324224028	NA	1.818960378	9.91938E-07	1.818960378	9.91938E-07
1808 W903_R508985	W903_1838	1771015	1772095	NA	PTS system sorbose/sorbitol component family protein	0.120380894	0.120380894	0.120380894	0.000140452	0.120380894	0.000140452
1809 W903_R508990	W903_1839	1771750	1772946	NA	unstructured glucuronid hydrolase	0.077534755	0.509464899	1.851647171	2.31732E-08	1.851647171	2.31732E-08
1810 W903_R508995	W903_1840	1772949	1773383	NA	PTS system fructose IIA component family protein	-0.692698987	0.017170993	0.236946627	0.71710993	0.236946627	0.71710993
1811 W903_R509000	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_R509005	W903_1842	1774490	1775131	NA	ribose/galactose isomerase	1.329868427	NA	2.948395948	2.13528E-06	2.948395948	2.13528E-06
1813 W903_R509010	W903_1843	1775547	1776164	NA	pflB carbohydrate kinase family protein	0.654423958	NA	3.366898733	4.51641E-07	3.366898733	4.51641E-07
1814 W903_R509015	W903_1844	1776176	1776814	NA	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase family protein	1.021308594	NA	3.938262567	7.94108E-05	3.938262567	7.94108E-05
1815 W903_R509020	W903_1845	1776861	1777475	NA	nitroreductase family protein	-0.75356597	1.88332E-06	0.023198656	0.915869759	0.023198656	0.915869759
1816 W903_R509025	W903_1846	1777608	1778033	NA	mark family protein	-0.256830541	0.240481793	-1.096387009	2.09373E-11	-1.096387009	2.09373E-11
1817 W903_R509030	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_R509035	W903_1848	1782689	1783273	NA	mannosyl-glucosyl-endo-N-acetylglucosaminidase family protein	0.392750886	0.115557171	1.642789124	4.53427E-10	1.642789124	4.53427E-10
1819 W903_R509040	W903_1849	1783938	1785236	proS	proline-tRNA ligase	0.132636586	0.05097275	-0.449576586	0.15087E-07	-0.449576586	0.15087E-07
1820 W903_R509045	W903_1850	1786402	1786602	naP	RIP metalloproteinase RseP	0.170502122	1.42432E-07	0.000669315	0.995648095	0.000669315	0.995648095
1821 W903_R509050	W903_1851	1786343	1787427	NA	cytidyltransferase family protein	1.182985936	7.70339E-14	0.41149217	7.44742E-05	0.41149217	7.44742E-05
1822 W903_R509055	W903_1852	1787442	1788194	uups	di-trans,poly-cis-decaprenyltransferase	0.976841453	2.74553E-10	0.943393411	1.79232E-16	0.943393411	1.79232E-16
1823 W903_R509060	W903_1853	1788361	1788361	naC	preprotein translocase, YajC subunit	-0.628888857	3.35718E-05	-0.149040994	1.06913E-29	-1.49040994	1.06913E-29
1824 W903_R509065	W903_1854	1787779	1789123	NA	thioredoxin family protein	-1.239388445	6.37043E-11	-1.183437968	1.62706E-15	-1.183437968	1.62706E-15
1825 W903_R509070	W903_1855	1790214	1790477	NA	malic enzyme, NAD-binding domain protein	0.512525228	0.32052743	0.545615542	3.10285E-05	0.545615542	3.10285E-05
1826 W903_R509075	W903_1856	1790502	1791839	NA	citrate carrier, CCS family protein	0.128292456	0.64054488	-0.18460165	2.93245E-13	-0.18460165	2.93245E-13
1827 W903_R509080	W903_1857	1791993	1793519	NA	putative sensor kinase dPB	-0.061941792	0.749756627	1.232187728	6.6466E-31	1.232187728	6.6466E-31
1828 W903_R509085	W903_1858	1793521	1794201	NA	response regulator	-0.100731597	0.735007232	1.046856428	1.77402E-11	1.046856428	1.77402E-11
1829 W903_R509090	W903_1859	1795222	1795217	NA	UDP-glucose 4-epimerase GalE	0.396767748	0.014621274	0.18680356	0.06123605	0.18680356	0.06123605
1830 W903_R509095	W903_1860	1794305	1796912	doxG	glucose 1,6-alpha-glucosidase	0.18329191	0.32052743	0.545615542	0.07146537	0.545615542	0.07146537
1831 W903_R509100	W903_1861	1797041	1798174	NA	ABC transporter family protein	0.152468621	1.67942E-05	0.167489214	0.17405E-12	0.167489214	0.17405E-12
1832 W903_R509105	W903_1862	1798275	1799126	NA	bacterial regulatory, Fis family protein	-0.28797207	0.156525661	-0.651147949	1.7517E-10	-0.651147949	1.7517E-10
1833 W903_R509110	W903_1863	1799221	1800117	NA	aldose 1-epimerase family protein	-0.694870747	0.549536178	2.340875741	9.20468E-05	2.340875741	9.20468E-05
1834 W903_R509115	W903_1864	1800171	1801148	lacC	tagatase 1,6-diphosphate aldolase	0.902731941	0.047311061	1.933487849	3.5339E-05	1.933487849	3.5339E-05
1835 W903_R509120	W903_1865	1801150	1802082	lacC	tagatase-6-phosphate kinase	0.750568329	0.014781856	1.915687076	2.65644E-10	1.915687076	2.65644E-10
1836 W903_R509125	W903_1866	1802093	1802608	lacB	galactose-6-phosphate isomerase, LacB subunit	0.512525228	0.123107091	0.141697924	1.57061E-10	0.141697924	1.57061E-10
1837 W903_R509130	W903_1867	1803014	1803924	lacA	galactose-6-phosphate isomerase, LacA subunit	1.240007871	7.16966E-05	1.478458494	5.8675E-24	1.478458494	5.8675E-24
1838 W903_R509135	W903_1868	1803831	1805751	NA	RN repeat-like domain protein	0.173197122	0.000147486	-0.688516247	1.10426E-06	-0.688516247	1.10426E-06
1839 W903_R509140	W903_1869	1805990	1807438	NA	PTS system sugar-specific permease component family protein	0.496412278	0.246836258	2.003004477	1.30212E-12	2.003004477	1.30212E-12
1840 W903_R509145	W903_1870	1807478	1807783	NA	PTS system, Lactose/Cellobiose specific IIB subunit	0.295555851	0.240365776	1.260872598	3.352E-06	1.260872598	3.352E-06
1841 W903_R509150	W903_1871	1807785	1808249	NA	phosphoenolpyruvate-dependent sugar phosphotransferase system, Elia 2 family protein	-0.161037089	0.678957096	1.445820048	3.84701E-15	1.445820048	3.84701E-15
1842 W903_R509155	W903_1872	1808259	1809005	NA	dead C terminus/Exonuclease family protein	0.07424557	0.205438289	0.261234798	0.564015945	0.261234798	0.564015945
1843 W903_R509160	W903_1873	1809525	1812107	NA	histidine triad domain protein	0.19746083	0.843314144	0.117504302	0.566340884	0.117504302	0.566340884
1844 W903_R509165	W903_1874	1812134	1813057	imb	liprotein	-0.057915715	0.920058563	0.43844838	0.31105051	0.43844838	0.31105051
1845 W903_R509170	W903_1875	1813312	1813755	NA	D-tyrosyl-tRNA(Tyr) deacylase	-0.071786932	0.725515949	-0.892879636	2.02294E-12	-0.892879636	2.02294E-12
1846 W903_R509175	W903_1876	1813765	1815981	relA	bifunctional (p)ppGpp synthase/hydrolase RelA	0.262164354	0.110402151	-0.603326127	9.53769E-11	-0.603326127	9.53769E-11
1847 W903_R509180	W903_1877	1816241	1818643	YfhN	trifunctional nucleotide phosphotransferase protein YfhN	0.036379424	0.010111214	0.178128927	0.342788828	0.178128927	0.342788828
1848 W903_R509185	W903_1878	1819255	1820525	NA	ndf protein	0.07342457	0.188525811	-0.885508111	6.45738E-11	-0.885508111	6.45738E-11
1849 W903_R509190	W903_1879	1819266	1820303	NA	MA2 glutamyl aminopeptidase family protein	0.226076305	0.194862137	-0.520346327	1.0302E-07	-0.520346327	1.0302E-07
1850 W903_R509195	W903_1880	1820303	1820800	NA	AAA domain protein	-0.101602583	0.574080165	-0.438194915	2.53986E-05	-0.438194915	2.53986E-05
1851 NA	W903_1881	1820857	1820976	NA	putative membrane protein	1.148016801	NA	1.091254364	0.184629227	1.091254364	0.184629227
1852 W903_R509205	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_R509210	W903_1883	1822071	1822844	NA	response regulator	-0.509813018	0.0389296	0.163497498	0.301672743	0.163497498	0.301672743
1854 W903_R509215	W903_1884	1822848	1824907	NA	histidine kinase, GYA gyrase B-, and HSP90-like ATPase family protein	0.056704615	0.026528389	0.143468591	0.031776813	0.143468591	0.031776813
1855 W903_R509220	W903_1885	1824635	1825462	NA	PTS system mannose/fructose/sorbitose IID component family protein	0.510558896	0.400428001	1.300089904	1.07978E-05	1.300089904	1.07978E-05
1856 W903_R509225	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_R509230	W903_1887	1826284	1826775	NA	putative phosphotransferase enzyme IIB component	-0.54711823	0.433931975	0.128224475	0.78517948	0.128224475	0.78517948
1858 W903_R509235	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_R509240	W903_1889	1827465	1828517	NA	putative membrane protein	0.122453101	0.164771968	-0.747991428	3.63882E-05	-0.747991428	3.63882E-05
1860 W903_R509245	W903_1890	1828551	1828713	NA	hyposulfite protein	0.07375647	0.026438591	0.43484591	0.555758975	0.43484591	0.555758975
1861 W903_R509245	W903_1891	1828728	1828991	NA	ABC-2 transporter family protein	-0.005632795	0.976894053	-1.179040978	2.97635E-26	-1.179040978	2.97635E-26
1862 W903_R509250											

1932	W903_R509595	W903_1966	1896874	1897413	musG	transcription termination/antitermination factor NusG	-1.208839109	3.22774E-15	-1.378717901	1.16165E-34	-1.378717901	1.16165E-34
1933	W903_R509600	W903_1967	1897619	1899004	NA	LPTXG cell wall anchor domain protein	-1.304320289	5.1369E-16	-3.255514858	6.1038E-110	-3.255514858	6.1038E-110
1934	W903_R509605	W903_1968	1899317	1899490	secE	preprotein translocase, SecE subunit	-0.047633004	0.858438886	-0.839671211	0.000109533	-0.839671211	0.000109533
1935	W903_R509610	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_R509615	W903_1970	1902091	1902975	NA	pseudouridine synthase, RluA family protein	0.287662222	0.137561528	0.161506342	0.204744079	0.161506342	0.204744079
1937	W903_R509625	W903_1973	1904809	1906020	NA	phosphopentomutase	1.177924877	2.68857E-14	0.949149301	4.02823E-24	0.949149301	4.02823E-24
1938	W903_R509630	W903_1974	1906087	1906758	deoC	deoxyribose-phosphate aldolase	1.221102238	5.4948E-16	0.98623458	1.3735E-34	0.98623458	1.3735E-34
1939	W903_R509635	W903_1975	1906788	1907990	NA	na+ dependent nucleoside transporter family protein	1.11800215	1.41333E-14	1.183848475	1.24836E-39	1.183848475	1.24836E-39
1940	W903_R509640	W903_1976	1908011	1908790	udg	uridine phosphorylase	2.0024612947	1.05838E-11	1.137675401	2.3895E-26	1.137675401	2.3895E-26
1941	W903_R509645	W903_1977	1908049	1909686	NA	bacterial regulatory s, gntR family protein	-0.4228036374	4.50401E-69	-3.541994742	4.8467E-135	-3.541994742	4.8467E-135
1942	W903_R509655	W903_1978	1910096	1911718	grol	chaperonin GroL	0.536491172	0.000233887	-0.307006683	0.022800768	-0.307006683	0.022800768
1943	W903_R509660	W903_1979	1911814	1912098	groS	10 kDa chaperonin	0.550375039	0.002144701	-1.079673131	6.46002E-19	-1.079673131	6.46002E-19
1944	W903_R509665	W903_1980	1912273	1913076	NA	ABC transporter family protein	0.158973584	0.483314144	-2.377166985	4.7285E-42	-2.377166985	4.7285E-42
1945	NA	W903_1981	1913081	1913977	NA	branched-chain amino acid transport system / permease component family protein	0.248850788	0.306567098	-2.415194222	3.14119E-48	-2.415194222	3.14119E-48
1946	NA	W903_1982	1913983	1914895	NA	ABC transporter substrate binding family protein	0.991023129	0.007850889	-3.267333011	5.55691E-63	-3.267333011	5.55691E-63
1947	W903_R509680	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_R509685	W903_1984	1916403	1917263	NA	glyoxalase/Bleomycin resistance /Dioxygenase superfamily protein	-0.531549124	0.384231534	1.741617635	1.63268E-13	1.741617635	1.63268E-13
1949	W903_R509690	W903_1985	1917306	1918037	NA	hypothetical protein	-0.174175711	8.09099E-05	-0.130991514	0.310910114	-0.130991514	0.310910114
1950	W903_R509695	W903_1986	1918394	1919011	nrpG	anabolic ribonucleoside-triphosphate reductase activating protein	0.171862561	0.546474694	1.310569932	1.21114E-28	1.310569932	1.21114E-28
1951	W903_R509700	W903_1987	1919084	1919575	NA	acetyltransferase family protein	-0.224800935	0.265487886	1.158714352	3.15483E-25	1.158714352	3.15483E-25
1952	W903_R509705	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	0.06086057	0.946500358	6.44316E-21	0.946500358	6.44316E-21
1954	W903_R509715	W903_1990	1920747	1922945	nrpD	anabolic ribonucleoside-triphosphate reductase	0.681189E-05	0.030387336	0.795751374	0.030387336	0.795751374	0.030387336
1955	W903_R509720	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	0.318469963	0.279113848	0.609439204	0.279113848	0.609439204	0.279113848
1957	W903_R509730	W903_1993	1924836	1925153	NA	hypothetical protein	-0.823923718	0.30391E-08	-0.087414761	0.071089532	-0.087414761	0.071089532
1958	W903_R509735	W903_1994	1925179	1925589	NA	hypothetical protein	0.003038364	0.661340936	0.164554204	0.118151879	0.164554204	0.118151879
1959	W903_R509740	W903_1995	1925598	1925864	NA	hypothetical protein	-0.171731725	0.586984816	0.457282136	0.000157186	0.457282136	0.000157186
1960	W903_R509745	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_R509750	W903_1997	1926680	1927819	recA	protein RecA	0.05746052	0.000260862	-0.196535925	0.126151549	-0.196535925	0.126151549
1962	W903_R509755	W903_1998	1927893	1929152	NA	competence/damage-inducible Cna C-terminal domain protein	0.914318589	1.4888E-09	0.078709915	0.457950226	0.078709915	0.457950226
1963	W903_R509760	W903_1999	1930362	1931293	NA	methyladenine glycosylase family protein	0.325411333	0.000383129	0.164554204	0.118151879	0.164554204	0.118151879
1964	W903_R509765	W903_2000	1929815	1930405	nuvA	holliday junction DNA helicase RuvA	0.080339562	0.661340936	0.604183743	3.25462E-09	0.604183743	3.25462E-09
1965	W903_R509770	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_R509775	W903_2002	1931671	1931634	mutL	DNA mismatch repair MutL family protein	0.216892524	0.201350226	0.368064369	0.00121496	0.368064369	0.00121496
1967	W903_R509780	W903_2003	1933869	1934072	NA	'Cold-shock' DNA-binding domain protein	-1.793581594	0.177260421	-3.621337945	2.7838E-11	-3.621337945	2.7838E-11
1968	W903_R509785	W903_2004	1934129	1934705	mutS	DNA mismatch repair protein MutS	-0.890461185	7.91414E-09	-1.226116704	2.86833E-27	-1.226116704	2.86833E-27
1969	W903_R509790	W903_2005	1936162	1937199	NA	arginine repressor	0.254131547	0.134317E-08	-1.305900775	1.74705E-13	-1.305900775	1.74705E-13
1970	W903_R509795	W903_2006	1937421	1939112	argB	arginine-tRNA ligase	0.226532149	0.155594447	-0.802961751	1.11911E-13	-0.802961751	1.11911E-13
1971	W903_R509800	W903_2007	1939200	1939508	walG	bacteriocin	-0.054275787	0.85392705	-0.944285539	3.46814E-06	-0.944285539	3.46814E-06
1972	W903_R509805	W903_2008	1939535	1940407	NA	hypothetical protein	-0.146271005	0.484301603	-0.609877644	5.39408E-08	-0.609877644	5.39408E-08
1973	W903_R509810	W903_2009	1940515	1941459	NA	hypothetical protein	-0.273178268	0.114842415	-1.210585143	2.6124E-41	-1.210585143	2.6124E-41
1974	W903_R509815	W903_2010	1941449	1942000	aspS	aspartate-tRNA ligase	-0.136055966	0.24574285	-1.591497581	3.57409E-07	-1.591497581	3.57409E-07
1975	W903_R509820	W903_2011	1943293	1943773	hisE	histidine-tRNA ligase	0.116403984	0.563698445	-1.130789601	5.44022E-31	-1.130789601	5.44022E-31
1976	W903_R509825	W903_2012	1944793	1944975	rpmF	ribosomal protein L32	-1.032031413	6.73104E-09	-1.50045515	0.00086487	-1.50045515	0.00086487
1977	W903_R509830	W903_2013	1944991	1945140	rpmG	ribosomal protein L33	0.336589039	0.102080595	-1.006318353	4.92906E-19	-1.006318353	4.92906E-19
1978	W903_R509835	W903_2014	1945433	1946007	NA	cadmium resistance transporter family protein	-0.885202701	9.23129E-06	-0.773935076	0.00020777	-0.773935076	0.00020777
1979	W903_R509840	W903_2015	1946059	1946397	NA	bacterial regulatory, arsk family protein	-1.205222859	1.45377E-11	-0.977230095	1.11715E-07	-0.977230095	1.11715E-07
1980	W903_R509845	W903_2016	1947856	1948178	NA	hypothetical protein	0.181861515	1.34317E-08	-0.681502384	6.10496E-05	-0.681502384	6.10496E-05
1981	W903_R509850	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_R509855	W903_2018	1948830	1949150	NA	hypothetical protein	1.767873677	NA	1.687066843	0.005623457	1.687066843	0.005623457
1983	W903_R509860	W903_2019	1949150	1950250	NA	ftsX/SpolIIE family protein	1.799928498	0.000589242	1.08667606	3.03157E-05	1.08667606	3.03157E-05
1984	W903_R509865	W903_2020	1950247	1950582	NA	hypothetical protein	0.015053813	0.98246628	1.249592921	0.000313745	1.249592921	0.000313745
1985	W903_R509870	W903_2021	1951051	1951656	NA	plasmid replication family protein	0.1515571761	0.844341147	0.516311159	0.237846132	0.516311159	0.237846132
1986	W903_R509875	W903_2022	1951649	1951897	NA	merR-like regulatory family protein	0.082397881	0.001546951	0.589738552	0.618058292	0.589738552	0.618058292
1987	W903_R509880	W903_2023	1951986	1953251	NA	phage integrase family protein	0.211125078	0.208024017	0.981926879	6.7953E-21	0.981926879	6.7953E-21
1988	W903_R509885	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_R509890	W903_2025	1954365	1955036	NA	response regulator	-0.442736694	0.04309935	0.014100853	0.929147843	0.014100853	0.929147843
1990	W903_R509895	W903_2026	1955020	1955634	HAMP	HAMP domain protein	0.091850704	0.644585685	0.138360195	0.207851747	0.138360195	0.207851747
1991	W903_R509900	W903_2027	1956496	1958409	NA	citrate transporter family protein	0.874943039	0.19151087	1.623589449	0.000126246	1.623589449	0.000126246
1992	W903_R509905	W903_2028	1958143	1959069	NA	carbamate kinase	0.731399848	0.344511372	0.68938652	9.73717E-15	0.68938652	9.73717E-15
1993	W903_R509910	W903_2029	1959081	1960079	NA	ornithine carbamoyltransferase	0.717719715	0.299030732	1.252929875	0.000455035	1.252929875	0.000455035
1994	W903_R509915	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_R509920	W903_2031	1961464	1962297	NA	response regulator	-0.421696458	0.405490802	1.010405506	1.66551E-15	1.010405506	1.66551E-15
1996	W903_R509925	W903_2032	1962519	1963241	NA	ABC transporter family protein	0.600232052	0.001572285	1.054586337	7.94189E-21	1.054586337	7.94189E-21
1997	W903_R509930	W903_2033	1963244	1964758	NA	substrate binding domain of ABC-type glycine betaine transport system family protein	-0.271877739	2.52626E-06	0.663345581	1.75685E-08	0.663345581	1.75685E-08
1998	W903_R509935	W903_2034	1964536	1967376	NA	hypothetical protein	-0.27579879	0.082397881	0.01546951	0.880187916		