Title: Identification and characterization of pleiotropic high-persistence mutations in the beta subunit of the bacterial RNA polymerase

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Abstract:

Individual bacteria can escape killing by bactericidal antibiotics by becoming dormant. Such cells, also known as persisters, naturally occur in bacterial populations at a low frequency. Here we present the finding that antibiotic-resistance mutations in the *rpoB* gene, encoding the beta subunit of RNA polymerase, increase the frequency of persisters by orders of magnitude. Furthermore, we show that: i) the persistent state depends on the (p)ppGpp transcriptional program and not on (p)ppGpp itself; ii) the high persistence (*hip*) is associated with increased populational heterogeneity in transcription; iii) indole overproduction, caused by transcriptional changes in the *hip* mutants, explains 50-80% of the *hip* phenotype. We report that the analogous *rpoB* mutations occur frequently in clinical isolates of *Acinetobacter baumannii*, *Mycobacterium tuberculosis* and *Staphylococcus aureus*, and we demonstrate that one of those *rpoB* mutations causes high persistence in MRSA. We also show that the RpoB-associated *hip* phenotype can be reversed by inhibiting protein synthesis.

Importance: Persistence is an inevitable consequence of antibiotic usage. Although persistence is not a genetically heritable trait, here we demonstrate for the first time that antibiotic resistance, which is heritable, can promote persistence formation. Our finding that resistance to one antibiotic, rifampicin, can boost persistence to other antibiotics, such as ciprofloxacin and ampicillin, may help explain why certain chronic infections are particularly recalcitrant to antibiotic therapies. Our results also emphasize the need to assess the effects of combination antibiotic therapies on persistence.

Keywords: Persistence, RNA polymerase, RpoB, stringent response, *E. coli*, MRSA, MTB, antibiotic resistance, ppGpp, rifampicin, fluoroquinolones, ciprofloxacin

Introduction

Persisters make up a small subpopulation of metabolically slowed cells that are recalcitrant to many types of stress, including antibiotics. Persisters can be induced via changes in the environment or arise spontaneously. Environmental challenges such as starvation (1) and exposure to chemicals/antibiotics (2) can increase the persister frequency manifold; such an increase can be mediated by peptides and metabolites (3,4). For example, indole, a by-product of tryptophan metabolism, can contribute to a rapid accumulation of persister cells in early stationary cultures (5,6), likely by reversibly inhibiting cell growth and division (7). Persisters can also arise spontaneously due to a heterogeneity of physiological states among individual cells in bacterial populations (8,9). The extent of the heterogeneity can be increased by mutations that unbalance toxin-antitoxin activity in the cell, the insight stemming from the work of Moyed *et al.* showing that overexpression of HipA toxin in certain *hipA* mutants increases persistence by 10^3 to 10^4 -fold (10,11). With several dozen identified toxin-antitoxin systems, others such as *relE/relB* and *mazE/mazF* have been also shown to contribute to the formation of the persister cells (12,13). The toxin-induced dormant state, in which bacteria are recalcitrant to bactericidal antibiotics, is achieved by a reversible growth inhibition (13,14).

Whether induced via macroscopic environmental cues or spontaneously generated, the persistence phenotype most of the time is triggered through stress-response regulatory circuit. Several stress-response pathways were demonstrated to be involved in the induction of the persister state, including SOS, oxidative stress, and stringent response (2,5,15,16). Stringent response is normally triggered by starvation (17). In the absence of a key nutrient(s), enzymes RelA and SpoT are recruited to synthesize the alarmone (p)ppGpp (18,19), which in turn interacts with RNA polymerase to globally adjust transcription within the cell (20). Bacteria utilizes stringent response to reprogram their metabolism when transitioning from rich to poor nutritional sources (21,22). Many toxin-antitoxins act by “hijacking” the stringent response pathway, forcing cells to experience starvation in the presence of nutrients and consequently triggering the persister state (23,24). In addition to starvation and toxin-antitoxin action, stringent response can be constitutively activated by mutations in the RNA polymerase (25,26). Although stringent RNA polymerase mutations have been extensively studied (27), their role in persister formation has been overlooked, presumably because of their relatively slow-growth phenotype (25). Here we disentangle the growth phenotype from the persister phenotype and demonstrate that *rpoB* stringent mutations represent a common evolutionary path toward high persistence in different bacterial species. We also show that mutations in the RpoB switch region (28,29), which could be readily selected for at low concentrations of the quinolone ciprofloxacin, mimic ppGpp transcriptional response and, as a result, confer high persistence phenotype.

Results

High survival frequency is caused by rpoB mutations

We have selected *E. coli* MG1655 mutants with improved survival frequency by incrementally increasing concentration of ciprofloxacin. Among mutants that were resistant to 0.25 mg/L of ciprofloxacin, but not 0.5 mg/L, we identified two independent clones with dramatically elevated survival at 4 mg/L. Whole-genome sequencing revealed that each of the mutants contained only two mutations: a *gyrB* mutation (S464Y) and an *rpoB* mutation, one of the mutants carried a substitution in 1279 residue of RpoB (E→A) and another in 1304 (M→R). To determine the optimal concentration of ciprofloxacin for testing strains' persistence, at 10x MIC or higher, we measured MIC and MBC of the parent and the mutants. The GyrB

S464Y substitution caused an increase in MIC but not in survival frequency (Table 1, Fig. 1A). By contrast, the RpoB E1279A and RpoB M1304R substitutions resulted in an 1.5-2-fold increase in MIC and MBC (Table 1) while also increasing the survival frequency at 10x MIC by more than 100 times (Fig. 1A).

To determine if the high survival frequency phenotype was caused by RpoB M1304R substitution alone or it required a combination with GyrB S464Y, we transduced the *rpoB* mutant allele into a clean MG1655 background and tested the survival frequency of the resulting strain at 10x respective ciprofloxacin MIC. Without the *gyrB* mutation, the allele encoding RpoB M1304R increased the survival frequency by a factor of 1,000 (Fig. 1B). The wild type *rpoB* expressed from a plasmid fully reversed the phenotype (Fig. 1C). The survival phenotype was not limited to ciprofloxacin. The strain carrying RpoB M1304R substitution yielded 20-25 times as many survivors as its parent strain when treated with ampicillin at 100 mg/L (Fig. 1D). (The RpoB E1279A mutant had a pronounced growth defect and was excluded from further analysis.)

RpoB M1304R substitution mimics the (p)ppGpp response

Using RNA-seq we identified 379 genes that were differentially expressed (FDR < 0.01) between a strain carrying RpoB M1304R substitution and its parent (Sup. File 1). These genes represented 116 regulons, which were compiled from RegulonDB and EcoCyc (30,31). Of the 116, 12 regulons were represented by at least 10 differentially expressed genes and were significantly enriched (hypergeometric test, adjusted p-value < 0.05) (Fig. 2, panel A). Two regulons stood out from the list of significantly enriched sets. First, the set least likely to be overrepresented by chance was the ppGpp regulon (96 genes out of 167 genes in the regulon were differentially expressed between the two strains, FDR < 0.01). Second, the set with the largest per gene variation in transcript abundances was the DksA-ppGpp regulon. These findings raised the possibility that the effect of RpoB M1304R mimics the effect of (p)ppGpp on transcription and adaptation.

One of the salient features of the ppGpp-dependent response is an adaptive lag during the amino acid downshift (32,33). We compared the lags of the RpoB M1304R strain and its parent MG1655. Upon the downshift, the parent strain exhibited a 20-min delay before resuming growth whereas the mutant started recovering in 5-10 minutes (Fig. 2B). This shortened lag could be due to elevated transcription of amino acid biosynthetic genes in the *rpoB* mutant prior to amino acid downshift. To test this possibility, we examined the activity of *ilvL*::GFP fusion in a flow cytometry experiment. We found that the isoleucine promoter was constitutively up-regulated in the *rpoB* mutant but not in its isogenic parent (Sup. Fig. 1), strongly suggesting that the C-terminal RpoB mutation “behaves” like a typical stringent mutation, which is usually found between 526-533 aa residues of RpoB.

However, since the stringent-like phenotype in the M1304R strain was observed in ppGpp+ cells, it was also possible that the mutant has a higher basal level of ppGpp. We tested this possibility by directly measuring ppGpp levels in cell extracts. The alarmone abundance was indistinguishable between the parent and the *rpoB* mutant in presence of amino acids (Fig. 3A). After 1h amino acid downshift, ppGpp levels increased 10 times over the basal level in both strains (Fig. 3B). Thus, the RpoB M1304R substitution either makes RNA polymerase more sensitive to ppGpp or mimics the response in a ppGpp-independent manner.

We tested the ppGpp dependence of RpoB M1304R by transducing the mutation into the *relA*⁻ and *relA*⁻ *spoT* (ppGpp⁰) backgrounds. While the removal of *relA* alone slightly reduced the frequency of survivors

compared to the RpoB M1304R *relA*⁺ parent, the RpoB M1304R persistence phenotype without ppGpp was similar to that of the wild type (Fig. 2C). Thus, the *rpoB* persistence mutation, while being dependent on ppGpp for its full effect, makes the basal persistence independent of the alarmone. Such independence, or ppGpp mimicking, can be manifested by phenotypic rescuing of the amino acid auxotrophy of ppGpp⁰ mutants (19, 35). However, we found that the RpoB M1304R ppGpp⁰ mutant still required amino acids for growth (data not shown).

Bone fide rpoB stringent mutations cause high-persistence (hip) phenotype

To determine if stringent *rpoB* mutations (27), which are known to rescue the ppGpp⁰ auxotrophy, can also rescue the persistence phenotype, we selected rifampicin resistant, *rpoB* stringent mutants in a ppGpp⁰ strain (“Materials and Methods”) and characterized persistence of one of them, RpoB L533P. While ppGpp⁰ yielded no persisters between OD₆₀₀ 0.3 -1.6, RpoB L533P ppGpp⁰ had as many persisters throughout the growth curve as wild type MG1655 in the early stationary phase (Fig. 4A and B).

Interpretation of the persistence data from strains carrying RpoB M1304R and RpoB L533P substitutions is confounded by a relatively slower growth of both mutants (Table 2). To evaluate the effect of growth rate on persistence, we measured the frequency of persisters in MG1655 at OD₆₀₀ of 0.5 slowed by chloramphenicol to a 22, 27, 30, 35- and 40-min doubling time. Predictably, there was an inverse relationship between growth rate and persister frequency. Yet, when MG1655 was slowed down to the RpoB L533P level, the stringent mutant still yielded over 600 times as many persisters (Sup. Fig. 2). The higher persistence observed in slow-growing cultures could also be a consequence of the ppGpp effect, which controls the growth rate (36), and not of the slow growth itself. To test this, the growth of the ppGpp⁰ parent was halved by chloramphenicol (Sup. Fig. 3A) and the survival frequency was measured at different points along the growth curve. The slowing down had no measurable effect on persistence (Fig. 4A), implying that ppGpp is required for the effect of growth rate on persistence. This straightforward conclusion, however, may not be possible if chloramphenicol kills a substantial fraction of cells and the persistence is measured only over the surviving sub-population. We tested whether this is the case by plating MG1655, RpoB1304 and RpoB533 (both in MG1655 background) as well as their ppGpp⁰ derivatives on plates containing 0, 0.5, 1, 2, 4 and 25 mg/L of chloramphenicol, as was done in (37). We found that chloramphenicol had no effect on CFU’s at concentrations between 0 and 4 mg/L (Sup. Fig. 3B and C) and hence the aforementioned conclusion stands.

We next asked what effect would slowing down high persister mutants by sub-inhibitory concentrations of chloramphenicol would have on the frequency of persisters? We expected to see an even higher levels of persistence in RpoB L533P and RpoB L533P(ppGpp⁰) mutants in presence of the translation inhibitor. Surprisingly, the opposite was the case. Persistence in the RpoB L533P mutant had decreased by almost two logs (93-97% depending on the time point). The drop in the persistence was even greater when it came to the RpoB L533P ppGpp⁰ mutant: no observable persistence in the first 90 minutes and over two logs decrease in persistence over the remaining time points (Fig. 4C).

Indole contributes to the RpoB-mediated persistence

To determine if there are any commonalities between the molecular phenotypes of strains carrying RpoB L533P and RpoB M1304R mutations, we compared their transcriptional profiles in wild type and ppGpp⁰ backgrounds. Among 697 significantly differentially expressed genes, one operon, *tnaCBA*, stood out as the most upregulated (Sup. File 2). We confirmed activation of the *tnaC* promoter in both of the

rpoB mutants by flow cytometry (Fig. 5A). Of note, the distribution of the fluorescent signal in the mutants was quantitatively and qualitatively different from that in the parent: not only it was shifted to the right, but it also had two modes, with the second mode representing about 3-5% of all fluorescent counts with about 10-times higher fluorescence than the corresponding mutant average. A *tnaA* knockout in RpoB L533P and RpoB M1304R mutants reduced the frequency of persisters by 50% and 80%, respectively (Fig. 5B). Concentration of indole in the RpoB L533P and RpoB M1304R cultures was 15 μ M and 50 μ M, respectively, compared to undetectable levels in the parent. However, when we added up to 50 μ M indole to a wild-type culture we did not observe any increase in persister formation. When we added indole to a final concentration of 500 μ M (a stationary culture equivalent), persistence increased 7-10 times. Given the distribution of the activity of *tnaC* promoter in a population of the *rpoB* mutant cells, it is plausible that only 3-5% of the population produce indole in quantities sufficient to trigger the dormant state, which in turn will happen only in a fraction of that sub-population.

RpoB high-persistence mutations are found among clinical isolates

We used sequences stored in PATRIC database (38) to determine if the *rpoB* high-persistence mutations occur in clinical isolates. Since in our selection mutations in *rpoB* followed a *gyrB* mutation, we first analyzed the co-occurrence of *gyrB* mutations known to contribute to quinolone resistance (39,40) and *rpoB* mutations occurring at or in the vicinity of 1279 and 1304 residues (41). Sequences were processed and the statistical significance of co-occurrences was analyzed as described in (42). Although we did not find E1279A and M1304R among RpoB sequences of *E. coli* clinical isolates, W1275G and T1286P substitutions did significantly co-occur with D426N and S464Y substitutions in GyrB (Chi-squared test, adjusted p-value = 0.002). We introduced the mutation resulting in W1275G substitution into the *E. coli* chromosome. RpoB W1275G mutant yielded nearly as many persisters as the M1304R strains (Sup. Fig. 4). (We were unable to construct a strain with RpoB1286P substitution.)

Although rifampicin is not normally used against *E. coli* infections, *rpoB* sequences from 22 clinical isolates carried known Rif^R mutations (43). Three out of the 22 (13.6%) had substitutions in Ser531 residue, which is a known stringent mutation (35) and exhibited high persistence (similar to L533 substitution) when transferred into MG1655 (data not shown). Coincidentally, all three mutations were found in the isolates that also carried known *gyrA* (40) and/or *gyrB* (44) quinolone resistance mutations.

Next, we investigated if stringent mutants could outcompete other Rif^R mutants in presence of bactericidal antibiotics. We selected 104 Rif^R mutants in MG1655 ppGpp⁰ background, so that the stringency could be easily confirmed by plating on amino acid-less M9 plates. Out of 104 rifampicin resistant mutants, only 3 were stringent. After pooled colonies were treated with ciprofloxacin, the fraction of stringent mutants increased to 23%, compared to the 3% observed after the rifampicin selection, suggesting that stringent mutations can confer competitive survival advantage.

We also determined the frequency of stringent mutations among the Rif^R isolates of pathogens that are routinely treated by rifampicin, *A. baumannii*, *M. tuberculosis*, and *S. aureus*. The prevalence of the mutations that are homologous to *E. coli* Rif^R stringent was even higher than what we had observed in *E. coli*: 96.2%, 23.3%, and 50.9%, respectively. To determine if such mutations can confer high persistence, we investigated the effect of the RpoB S586L substitution in MRSA (an equivalent of S531L substitution in *E. coli*). Stringent mutants were selected as described in “Materials and Methods”. The persister frequency of the RpoB S586L mutant was more than 10,000 times higher than that of the parent in the

early exponential phase, and even in the late stationary phase the mutant produced 8 times as many persisters (Fig. 6A, B).

Discussion

Bacteria adapt to antibiotic-containing environments by acquiring resistance mutations. Here, we demonstrated that some of these mutations, including those that are highly prevalent in clinical isolates, can confer an additional benefit of increased persistence to bactericidal antibiotics. These high-persistence mutations resided in two regions of the beta subunit of the RNA polymerase: 1275-1304 and 531-533 and 526 *E. coli* equivalent in MRSA. Mutations in the first region can be readily selected at low concentrations of ciprofloxacin and those in the second are commonly occurring rifampicin-resistance mutations. Thus *hip* mutations can be fixed in a bacterial population not only through cyclical exposure to bactericidal antibiotics (45,46,47), but also as a result of pleiotropy of certain antibiotic resistance mutations.

The RpoB M1304R substitution resulted in two key phenotypes: reduced susceptibility to ciprofloxacin by 1.5-2-fold and increased persistence by up to a factor of 1,000. The two effects depend on different mechanisms, however. Among top 50 significantly over-expressed genes as a consequence of RpoB M1304R substitution, the function of only one of them, *mdtK*, which encodes a multi-antimicrobial extrusion transporter, could be directly linked to drug resistance (48) (Sup. File 3). Pietsch *et al.* found that similar *rpoB* mutations increased fluoroquinolone MIC by upregulating *mdtK* (41). However, while an *mdtK* knockout in RpoB M1304R strain resulted in the full reversal of the resistance phenotype (Table 1), it had no effect on persistence (Sup. Fig. 5), suggesting that the two phenotypes can be segregated.

MG1655 strain carrying RpoB L533P substitution, which confers rifampicin resistance, had no measurable effect on ciprofloxacin MIC. And yet it resulted in a striking persister phenotype; the frequency of persisters was independent of the growth phase (Fig. 4A).

Another relevant phenotype exhibited by the mutants is a slower growth. Decreasing the growth rate resulted in an increased number of persisters. However, the persister frequency of the *rpoB* rifampicin resistant mutant was more than 600 times higher when persistence was measured using ciprofloxacin and more than 80 times higher when using ampicillin, compared to what would be expected from the reduced growth rate alone in both ppGpp+ and null cells (Fig. 4A, Sup. Fig. 2). These findings strongly argue against the notion that a decreased target abundance, which should be a consequence of slowed growth, is sufficient to explain increase in persistence or that it confounds the phenomenon altogether.

The *rpoB* mutations completely overrode the ppGpp requirement for persister formation. This strongly suggests that the persister state is the result of a transcriptional program and ppGpp effects persistence primarily, if not solely, as a modulator of transcription. The mutants also illuminated the importance of differences in transcriptional activity among individual cells as an attribute of the *hip* phenotype: a sub-population of mutant cells had the promoter of the *tnaA* gene upregulated at least 10 times, while most of the population showed only marginal shift in the promoter activity. We demonstrated that this *tnaA* activation resulted in accumulation of indole that accounted for 50-80% of the *hip* phenotype in the *rpoB* mutants. Although these results are qualitatively consistent with earlier observations of the effect of indole on persistence (5, 6), we also found that indole had no effect on persistence without ppGpp or its transcriptional mimics. The role of *tnaA* and indole in the persister state formation may tie together the metabolic state of individual cells with transition to dormancy. The low-affinity tryptophan

transporter TnaA is activated when tryptophan is used as a carbon source (49,50), which happens only when all other preferred carbon sources in rich media have been exhausted (51,52). Switching to tryptophan, or other “lesser” carbon resources, may signal imminent starvation which, in combination with other yet unknown factors, establishes the persister state. In the *rpoB* mutants, *tnaA* transcription is constitutively upregulated in a number of cells, resulting in the “out-of-order” tryptophan utilization, starvation signaling by means of indole, and dormancy. This explanation also applies to indole-free species, where the “quality” of carbon and nitrogen source facilitates state transition. For example, Halsey *et al.* have suggested that histidine catabolism may be involved in regulation of CcpA response in *MRSA* (53,54,55), a major transcriptional regulator involved in metabolic regulation under suboptimal growth conditions, virulence, antibiotic resistance and biofilm formation (56,57).

The primary effect of rifampicin resistance mutations is to provide protection against the drug. Over one hundred mutations in RNA polymerase have been shown to confer varying degrees of rifampicin resistance (58). However, 17 mutations, which map between 505-690 amino acid positions of RNA polymerase β -subunit, make up the majority of the clinically relevant variants (59). About half of these mutations appear to have no growth defect (25). Yet, growth-defective stringent mutants can be frequently found in pathogenic species (60,61), indicating that stringent mutations must be providing sufficient adaptive/survival advantage even before the mutants have a chance to accumulate compensatory mutations restoring their growth fitness (62). Our findings suggest that persistence may be one of such advantages.

Finally, rifampicin is almost always used in combinations with other bactericidal antibiotics against some of the more antibiotic-recalcitrant bacteria (63). From adaptation prospective, the most direct path to surviving an onslaught by several antibiotics may go through acquisition of a single *hip* mutation rather than multiple resistance mutations to different antibiotics. Hence, selecting for *rpoB*-dependent persisters may promote the establishment of chronic infections (64), rather than subverting them, in a long run. However, there may be a simple and elegant solution to revering the mutations’ effect. The drastic decrease in persistence which we observed in the MG1655 RpoB L533P and its ppGpp⁰ derivative treated with sub-inhibitory chloramphenicol concentrations suggests that transcriptional dysregulation induced by *rpoB* mutations may be counteracted at a translational level. Just as with any phenotypic switch, expression of genes contributing to induction of the persister state has to reach a certain threshold. Compromising the cell’s ability to reach that threshold may negate the phenotype.

Materials and Methods

Bacterial strains and culture conditions

Antibiotics, strains, and plasmids used in the study are listed in Supplementary Tables 1-3. *E. coli* strains were derived from K-12 MG1655 (65) by selection, P1 transduction or λ -red recombination (66,67). *E. coli* cultures were grown in LB or MOPS-glucose (33), *S. aureus* – in tryptic soy broth/agar (TSB/TSA) (68) at 37°C with aeration at 250 rpm.

Determining MIC and MBC

MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) estimates were obtained according to standard protocols (69). MIC was determined by inoculating $5 \times 10^5 (\pm 2 \times 10^5)$ cells into 3ml Mueller-Hinton containing a range of drug concentrations (1, 0.5, 0.25, 0.125, 0.062, 0.031, 0.015, 0.008, 0.004 mg/L) and checking turbidity the following day. After establishing initial MIC

range, the procedure was repeated until MIC was determined within 0.001 mg/L for the mutants in the MG1655 background, and within 0.02 mg/L for mutants in the MG1655 GyrB S464Y background. To measure MBC, the same cultures that were used for MIC measurements were washed and plated for survivors. Prior to addition of the antibiotic all cultures were plated by serial dilution to determine the starting CFU/ml count. The concentration corresponding to a 3-log drop in viability was recorded as the MBC for the corresponding strain. The MICs and MBCs for each strain were obtained from testing at least 3 independent biological samples. Both MIC and MBC measurement were also conducted in LB media (70), resulting in identical values across all mutants.

Persistence measurement

Persistence was measured following a protocol described in (71). Bacteria were maintained by repeated dilutions in an early exponential phase between an OD₆₀₀ 0.05-0.3 for at least 10 generations. Upon reaching an OD₆₀₀ of 0.3±0.03 after the 10th doubling, a 3ml sample was taken out every 30 min for the next 3 h and ciprofloxacin or ampicillin was added to a final concentration of 1 mg/L (or 4 mg/L in the case of *gyrB* mutants to assure killing at 10X MIC) and 100 mg/L, respectively. After 17h incubation, samples were plated for CFU. Persistence was determined as a number of survivors per ml normalized to the CFU/ml counts of the culture at the time of antibiotic application.

(p)ppGpp quantification using TLC

Overnight cultures were diluted 1:1,000 in 3.8ml of glucose-MOPS supplemented with 20 L-amino acids and grown to an OD₆₀₀ of 0.3. Cultures were then split into two 1.5ml tubes and spun down. Half of the sample was resuspended in fresh 3ml MOPS supplemented with amino acids, and another half was used to inoculate amino-acid-free MOPS to a starting OD₆₀₀ of 0.15 for all samples. From each sample CFU/ml were determined by serial dilution. All samples were then supplemented with 20μCi of ³²P orthophosphate. Following 1h incubation cells were lysed and 20 μl of lysate was spotted on a nitrocellulose TLC plate. Samples were mobilized by pH3.5 water-based phosphate buffer (72). Samples were visualized by Amersham Typhoon control software and analyzed using Fiji software (73).

Single gene expression assay and flow cytometry

Strains were transformed with a pUA66 plasmid carrying a *ilvI-p:gfp*, *hisL-p:gfp*, *tnaC-p:gfp* and *mdtK-p:gfp* promoter fusion (74). Overnight cultures of newly-obtained transformants were diluted 1:1,000 into pre-warmed glucose-MOPS supplemented with 20 L-amino acids, with each amino acid present at a final concentration of 0.04 mg/L, and maintained for at least 10 generations in an early exponential phase as described above. When an OD₆₀₀ of 0.3 was reached after the 10th doubling, cultures were diluted 100 times for flow cytometry. The GFP signal was measured at 14-66 μl/min flow rate. Data were analyzed using FlowJo. Fluorescence was normalized to both OD₆₀₀ and CFU/ml. The *tnaC-p:gfp* experiment was carried out in LB and GFP signal was measured in saline.

Whole Genome Sequencing

Isolates were grown overnight from a single colony in LB at standard conditions. DNA was extracted using a Promega Wizard Genomic DNA Purification Kit. Libraries were prepared using a TruSeq Nano library preparation kit. Sequencing was conducted using Illumina HiSeq2500. De-multiplexing was performed using FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/index.html). The reads were mapped to the reference genome (GCF_000005845.2_ASM584v2) using Bowtie 2 (78,79). The SAM files of mapped reads were converted to BAM format and sorted using SAMTOOLS (69). Mutation were

identified using Breseq (80) and confirmed using standard Sanger sequencing, using primers listed in Supplementary Table 4.

RNA-seq experiment and analysis

Overnight cultures were diluted 1:1,000 into 50ml LB and maintained in exponential phase as described above. After at least 10 generations in exponential phase and upon reaching an OD₆₀₀ of 0.3, 10ml samples were transferred into 15ml conical tubes containing 1.25 ml of the “stop” solution (ethanol v/v 95%, and phenol v/v 5%). Cells were then spun down and decanted. Pellets were flash frozen in liquid nitrogen and kept at -80°C until all samples were collected. Pellets were thawed on ice and resuspended in 200µl of TE buffer containing 20,000 mg/L of lysozyme and incubated at 37°C for 10 min. Total RNA was purified following a standard RNAeasy mini prep kit protocol (Qiagen, Hilden, Germany).

Before constructing the sequencing library rRNA was removed. The library was made using TruSeq Stranded mRNA library prep kit. Sequencing was done using Illumina HiSeq2500. De-multiplexing was performed using Illumina’s bcl2fastq software 2.20. The reads were mapped to the reference genome (GCF_000005845.2_ASM584v2) using HISAT2 (75). The final per feature read counts were obtained using Rsubread (76). Analysis of differential expression was done using DESeq2-based (77).

Indole assay

Indole concentration was measured by adding 400 µL of Kovack’s reagent to a 3ml culture of exponential cells at an OD₆₀₀ of 0.3 ± 0.05. Cells were incubated with the reagent for 30 min at room temperature in the dark. 200 µL from the surface alcohol layer was moved into a flat-bottom, 96-well plate and absorbance was measured at 535 nm using a plate reader. A standard curve was constructed using Kovack’s reagent colorimetric assay with following concentrations of indole: 10, 25, 50, 100, 200, 400, 500 µM in LB.

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Table 1 MIC/MBC

<i>Parental genotype</i>	<i>mg/L ciprofloxacin</i>	
	<i>MIC</i>	<i>MBC</i>
<i>MG1655</i>	0.015	0.033
<i>MG1655 RpoB 1304</i>	0.025	0.055
<i>MG1655 RpoB 533</i>	0.009	0.033
<i>Mg1655 Δmdtk</i>	0.015	0.033
<i>MG1655 RpoB 1304 Δmdtk</i>	0.014	0.033
<i>MG1655 gyrB S464Y</i>	0.16	0.2
<i>MG1655 gyrB S464Y RpoB 1304</i>	0.35	0.4
<i>MG1655 gyrB S464Y RpoB 1279</i>	0.35	0.4
<i>MG1655 gyrB S464Y RpoB 1275</i>	0.25	0.3

Ciprofloxacin MIC's and MBC's against strains with various RpoB substitutions: MIC and MBC were tested in two different backgrounds, in MG1655 GyrB S464Y background and in the MG1655. MBC and MIC were determined with approximately 5×10^5 cell inoculum in 3 ml of media.

587 **Table 2: Doubling times**

	Doubling time
Strains	Minutes
<i>MG1655</i>	20±1.2
<i>MG1655 RpoB L533P</i>	27.2±2.3
<i>MG1655 RpoB M1304R</i>	25.2±1.4

588 Growth rates of strains with RpoB substitutions in MG1655 background: Doubling time was determined
589 by CFU/ml.

Figure 1A

Figure 1B

Figure 1C

Figure 1D

Figure 1: Ciprofloxacin-selected *rpoB* mutations confer high persistence phenotype: (A) Survival curves in presence of 4mg/L ciprofloxacin of a parent strain carrying the GyrB S464Y substitution (●) and two RpoB mutants in the same genetic background: RpoB E1279A (●) and RpoB M1304R (●). (B) Genetic complementation: RpoB E1279A (●) and RpoB M1304R (●) and GyrB S464Y (●) with a pDJJ11-*rpoB*. (C) Genetic complementation: RpoB E1279A (●) and RpoB M1304R (●) and GyrB S464Y (●) with a pDJJ11-*rpoB*. (D) Comparison of persistence to ampicillin (18h, 100 mg/L) between MG1655 (●) and RpoB M1304R (●) along the growth curve.

Figure 2A

Figure 2B

Figure 2C

Figure 2: **The *rpoB* M1304R substitution mimics (p)ppGpp response:** (A) Significantly enriched regulons in RpoB M1304R mutant characterized by the fold change and fraction of the regulon effected by the mutation. (B) An adaptation lag of MG1655 parent (●) and MG1655 RpoB M1304R (●) measured in OD₆₀₀ and CFU/ml. (C) Ciprofloxacin persistence of RpoBwt (●) and RpoB M1304R (●) in MG1655, Δ relA and Δ relA Δ spoT (ppGpp⁰) backgrounds.

Figure 3A

Figure 3B

Figure 3: **ppGpp mimicry is not a result of ppGpp accumulation:** Prior to the experiment all strains were grown in the presence on amino acids, at the start of the experiment cells were washed and placed in the media containing ^{32}P with (+AA) or lacking (-AA) amino acids. **(A)** Radiolabeled ^{32}P nucleotide TLC plate comparing MG1655 RpoB M1304R +/- amino acids, to MG1655 RpoB M1304R ppGpp⁰ + amino acids, to MG1655 +/- amino acids. A faint, ^{32}P trace in the middle three lanes is the background noise (34). A small accumulation of ppGpp can be observed in the fourth lane as a result of cultures' entry into early stationary state. **(B)** Fiji analyzed TLC plate and normalized to corresponding CFU/ml microbial counts: MG1655 RpoB M1304R (●) - AA, MG1655 RpoB M1304R (●) +AA, MG1655 RpoB M1304R ppGpp⁰ (●), MG1655 +AA (●), MG1655 -AA (●).

Figure 4A

Figure 4B

Figure 4C

Figure 4: ***rpoB* stringent mutations confer high persistence phenotype that can't be explained by a slower growth:** (A) Persister frequency comparison between the MG1655 RpoB L533P (●), MG1655 RpoB L533P ppGpp⁰ (●), MG1655 (●), MG1655 ppGpp⁰ (●) as well as MG1655 ppGpp⁰ (●) slowed with 0.63 mg/L chloramphenicol. The persistence phenotype of stringent mutant is consistently maintained at 1:10,000 -50,000 and is independent of ppGpp. (B) Comparison of persistence to ciprofloxacin (18h, 1mg/L) between MG1655 (●) and MG1655 RpoB L533P (●) along the growth curve. Persistence exhibited by stringent mutant is independent of the growth state. (C) Comparison of persister formation between six different strains throughout the exponential and stationary states, in the presence and absence of chloramphenicol (Chl). MG1655 RpoB L533P (●), MG1655 RpoB L533P (ppGpp⁰) (●), MG1655 (●), MG1655 RpoB L533P +Chl (●), MG1655 RpoB L533P (ppGpp⁰)+Chl (●), MG1655 (ppGpp⁰) (●).

Figure 5B

Figure 5C

Figure 5: The effects of indole on persistence: (A) Activation of *tnaC(p)* in MG1655 RpoB M1304R (●) and MG1655 RpoB L533P (●) compared to MG1655 (●). The bottom left panel compares the activity of the *tnaC* promoter between exponential and overnight MG1655 cells (●). (B) Effect of *tnaA* knockout on ciprofloxacin persistence in MG1655 RpoB M1304R (●) and MG1655 RpoB L533P (●) was measured by averaging percent survival of *tnaA* across 7 time points (from t0 at OD₆₀₀ of 0.3 all the way to stationary state). At each time point fraction of survivors was determined for *rpoB* mutant and its *tnaA* null counterpart. The error bars represent standard deviation of survivor fraction across all seven time points (C) Ciprofloxacin persistence of MG1655 RpoB M1304R (●), MG1655 RpoB L533P (●), MG1655 (●) and MG1655 + 500μM (●).

Figure 6A

Figure 6B

Figure 6: **An *rpoB* stringent mutation confers high persistence in *Staphylococcus aureus*:** (A) Comparison of ampicillin persistence (18h, 100 mg/L) between MRSA WCUH29 (●) and WCUH29 RpoB S586L (●). (B) Photographs of plates with survivors during exponential phase (*left*) and early stationary phase (*right*), the left side of each plate is the parent, and the right is the *rpoB* stringent mutant. Dilution ranges are shown above the horizontal arrows on each plate.

Supplementary figure 1. Flow cytometry of *ilvL(p)::GFP* reporter: cells grown in MOPS medium supplemented with all 0.2% glucose and all 20 amino acids. Samples for flow cytometry were taken after culture had reached OD_{600} of 0.3 and diluted down using the same pre-warmed media to 0.03 ± 0.01 . Comparison is between MG1655 wild type (●) and RpoB M1304R (●) in the same backgrounds.

Supplementary figure 2. Stringent mutant persistence is not a consequence of slowed growth: Comparison of persistence between MG1655 RpoB L533P (●) and MG1655 (●) slowed to 30 min doubling time using chloramphenicol. The left bar represents persister frequency when strains were treated by ciprofloxacin, and the right bar shows persister frequency following ampicillin treatment. All treatments were performed on exponentially growing cultures at OD₆₀₀ of 0.5.

Figure S3 A

Figure S3 B

Figure S3 C

Supplementary figure 3. Effects of sub-inhibitory concentrations of chloramphenicol on growth of *E. coli*: (A) MG1655 was grown in presence of 0.4, 0.6, 0.75, 0.8 and 1 μ g/mL of chloramphenicol and the doubling time at each concentration was determined using CFU/ml. (B) Percentage of visible CFU counts plated on LB plates containing sub inhibitory concentrations of chloramphenicol (0, 0.5, 1, 2, 4, 25 mg/L) for the six strains used in the study. All strains tested were in MG1655 background. Error bars represent standard deviation from three biological replicates (C) A photograph depicting MG1655, RpoB1304 and RpoB533 both in MG1655 background plated on LB plates containing 0 and 0.5 mg/L of chloramphenicol.

Supplementary figure 4. The *rpoB* mutations co-occurring with gyrase mutations from clinical isolates confer increased persistence. Ciprofloxacin (4µg/mL) 24h kill curves comparing the parent strain with a GyrB S464Y substitution (●) to the mutants in the same background carrying E1279A (●), M1304R (●) and V1275G (●) RpoB substitutions.

Supplementary figure 5. Deletion of *mdtK* has no effect on persistence. Comparison of persistence between MG1655 RpoB M1304R / MG1655 RpoB M1304R Δ *mdtK* (●) and MG1655 / MG1655 Δ *mdtK* (●) along the growth curve.

Supplementary table 1: Antibiotics

Antibiotic	Cat #	Manufacturer	Concentration of stock	Stock age	Final dilution
Ampicillin	BP176025	Fisher BioReagents	100mg/ml (water)	≤ 1 months (-20C) or 4 freeze cycles	100mg/L
Kanamycin	100218-998	VWR Lifescience	50mg/ml (water)	≤ 3 months (-20C)	50mg/L
Chloramphenicol	TCC2255	TCI	25 mg/ml (70% ethanol)	≤ 2months (-20C)	0.63mg/L 25mg/L
Rifampicin	R3501	Sigma-Aldrich	50mg/ml (methanol)	≤ 2months (-20C)	100mg/L
Ciprofloxacin	NC9553331	Lkt Laboratories	20, 10, 1, 0.1, 0.01mg/ml (water)	≤ 1 months (-20C) or 4 freeze cycles	1mg/L or 4mg/L

Supplementary table 2: Strains

Name	Relevant amino acid substitution	Genotype	Source
MG1655	-	F ⁻ , lambda ⁻ , rph-1	Plunkett, G. III
OKR5	RpoB L533P	MG1655, <i>rpoB</i> 1598 T>C	This study
OKR13	RpoB M1304R	MG1655, <i>rpoB</i> 3911 T>G, Δ <i>AceB</i>	This study
MG1655, pDJJ11		MG1655, pDJJ11	This study
OKR5, pDJJ11	RpoB L533P	MG1655, <i>rpoB</i> 1598 T>C, pDJJ11	This study
OKR13, pDJJ11	RpoB M1304R	MG1655, <i>rpoB</i> 3911 T>G, Δ <i>AceB</i> , pDJJ11	This study
OKR1	GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A	This study
OKR1, pUA66-M	GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, pUA66 (<i>mdtK</i> -p: <i>GFP</i> , <i>kanR</i>)	This study
OKR1, pUA66-I	GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, pUA66 (<i>ilvL</i> -p: <i>GFP</i> , <i>kanR</i>)	This study
OKR1, pUA66-H	GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, pUA66 (<i>hisL</i> -p: <i>GFP</i> , <i>kanR</i>)	This study
OKR2, pUA66-M	RpoB M1304R, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G, pUA66 (<i>mdtK</i> : <i>GFP</i> , <i>kanR</i>)	This study
OKR2, pUA66-I	RpoB M1304R, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G, pUA66 (<i>ilvL</i> : <i>GFP</i> , <i>kanR</i>)	This study
OKR2, pUA66-H	RpoB M1304R, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G, pUA66 (<i>hisL</i> : <i>GFP</i> , <i>kanR</i>)	This study
OKR2	RpoB M1304R, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G	This study
OKR3	RpoB E1279A, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3836 A>C	This study
OKR4	RpoB V1275G, GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3824 T>G: <i>kanR</i>	This study
MG1655(p)	-	Δ <i>dgoR</i> , Δ <i>relA</i> , Δ <i>spoT</i>	This study
OKR5(p)	RpoB L533P	MG1655, Δ <i>dgoR</i> , Δ <i>relA</i> , Δ <i>spoT</i> Δ <i>aceB</i> : <i>kanR</i> , <i>rpoB</i> 1598 T>C	This study
OKR13(p)	RpoB M1304R	MG1655, Δ <i>dgoR</i> , Δ <i>relA</i> , Δ <i>spoT</i> Δ <i>aceB</i> : <i>kanR</i> , <i>rpoB</i> 3911 T>G	This study
OKR1(p)	GyrB S464Y	MG1655, <i>gyrB</i> 1391 C>A, Δ <i>relA</i> , Δ <i>spoT</i>	This study

OKR15(p)	GyrB S464Y, RpoB L533P	MG1655, <i>gyrB</i> 1391 C>A, <i>ΔrelA</i> , <i>ΔspoT</i> , <i>ΔAceB:kanR</i> , <i>rpoB</i> 1598 T>C	This study
OKR113(p)	GyrB S464Y, RpoB M1304R	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G, <i>ΔrelA</i> , <i>ΔspoT</i>	This study
OKR1135(p)	GyrB S464Y, RpoB M1304R, RpoB L533P	MG1655, <i>gyrB</i> 1391 C>A, <i>rpoB</i> 3911 T>G, <i>ΔrelA</i> , <i>ΔspoT</i> , <i>rpoB</i> 1598 T>C	This study
OKR6	GyrA S83L	MG1655, <i>gyrA</i> 248 C>T	This study
OKR65	RpoB L533P, GyrA S83L	MG1655, <i>rpoB</i> 1598 T>C, <i>gyrA</i> 248 C>T	This study
OKR613	RpoB M1304R, GyrA S83L	MG1655, <i>rpoB</i> 3911 T>G, <i>gyrA</i> 248 C>T, <i>ΔAceB:kanR</i>	This study
WCUH29	-	HA-MRSA	(82)
WCUH29-5	RpoBS486L	<i>rpoB</i> 1457 C>T	This study

Supplementary table 3: Plasmids

Name	Relevant components	Source
pDJJ11	Wt <i>rpoB</i>	(43)
pKD46	λ -red recombination	(67)
pCP20	FLP recombinase	(67)
pUA66	<i>mdtK-p:GFP/ ilvL-p:GFP/ hisL-p:GFP, kanR</i>	(74)

Supplementary table 4: Primers

Primer name	Sequence	Description
ΔSpoT F	TGC TGA AGG TCG TCG TTA ATC ACA AAG CGG GTC GCC CTT GGT GTA GGC TGG AGC TGC TTC	SpoT knockout-F amplified with FRT from pKD3
ΔSpoT R	GTG TTG GGT TCA TAA AAC ATT AAT TTC GGT TTC GGG TGA CAT GGG AAT TAG CCA TGG TCC	SpoT knockout-R amplified with FRT from pKD3
SpoT i F	CGC ACC GTT TAG GTA TCC AC	SpoT confirmation internal F
SpoT i R	GCT CAT TGC GTT ACC AAG TCC	SpoT confirmation internal R
SpoT e F	CAG GAA CAG CAA GAG CAG GA	SpoT confirmation external F
SpoT e R	CCA TGC AGA CGG TCA GAT CA	SpoT confirmation external R
RelA F	TGT AGA TAC GAG CAA ATT TCG GC	relA confirmation F
RelA R	GGC AGG TCT GGT CCC TAA AG	relA confirmation R
RpoB end F	GACGGTGCGAAAGAAGCAGA	C-terminal confirmation
RpoB end R	GCAGTGACCTGTTTGAGCGA	C-terminal confirmation / C- terminal seq
RifR F	GTCTGAGCGCACTGGTAGAA	Rif resistance F
RifR R	CTG AAC AAG CTG GAT TCG CC	Rif resistance R
RifR seq	GTC TCA GTT TAT GGA CCA GAA C	Rif resistance seq
1275 1F	CCT GAG TAC CTT CAG CGA TG	RpoB 1275 mut 1F
1275 1R	GCT TCC AGC GCC CAC CCT TCC ATC TCC	RpoB 1275 mut 1R
1275 2F	CGG GGA GAT GGA AGG GTG GGC GCT GGA	RpoB 1275 mut 2F
KanR F	GGAGTTAGCACTTAGAAGAAGCTCGTCAAGAAG	KanR flip F
Link 1R	TTGATCCCCCTTACTCGTCTTCCAGTTCGATG	Link 1
KanR R	GACGAGTAAGGGGATCAAGATCTGATCAAG	KanR flip R
Link 2F	GTTCTTCTAAGTGCTAACTCCGACGGGAG	Link 2
Uni 2R	TGGTTTGAACGTACGGTAGTTGA	RpoC homology arm
1224 1F	TGACCTGAGTACCTTCAGC	RpoB 1224 mut 1F
1224 1R	ACA TGT AAC CAA CGG TTA CTG GAC GCT	RpoB 1224 mut 1R
1224 2F	TCG AGC GTC CAG TAA CCG TTG GTT ACA	RpoB 1224 mut 2F
Uni rpoB R	CAT CTT GGT ACG ACC GTT C	RpoB mut 2R
S RpoB F	AAT TCA TGG ACC AAG CAA ACC	S aureus RpoB Rif F
S RpoB R	CCA TAA CTG TAT TGT TAC CAC GG	S aureus RpoB Rif R
GyrA F	GCCATACCTACGGCGATACC	GyrA F
GyrA R	AGCGACCTTGCGAGAGAAAAT	GyrA R

Supplementary File 1: DE genes between RpoB M1304R and its parent; gene names are organized by row

aceB aceE aceF add adeQ agaV agaW alaV aldA aphA araG arcA argI argT argX arnB arnE
ascB ascF atpA bcsE bcsF bioH bluF bola
btuC cadA carB cbl cfa chbA chbF cheA cheB cheR cheW cheY cheZ chpB citB cobB codB
crp csgD csgE csgF csgG cspA cspD cspE
cspG csrA csrB cydX dadA dadX deoA deoC dhaK dhaL dicF dksA dmsA dnaA dnaC dnaN dsdX
dtpD dusB eaeH ecpA ecpR efeB envY eutS
exuT fabA fabH fadB fadJ fadL fadR fimA fimB fkpA flgA flgB flgC flgD flgE flgF flgH
flgI flgJ flgK flgL flgM flgN flhA flhB
fliC fliF fliG fliH fliI fliJ fliN fliO fliP fliR fliS fliT fliZ flu flxA frdB frdC
frlA fruA ftsA ftsK ftsQ ftsZ fucA fucR
galE galP galT garD glgC glgP glnV glpB glpT gltI gluQ glvG glyA grcA grxB gspM hcr
higA hipA hisJ hisM hisP hisQ hisR hmp
hokB hsrA htrE hypF ihfA ihfB ileX ilvA ilvB ilvD ilvE ilvG ilvH ilvI ilvL ilvM ilvN
ilvX infC inte intG iraD iraP isrC ivbL
kdpA kdpB kdpC kduI kgtP lacZ leuA leuB leuC leuD leuL leuO leuT leuV leuW lgoT livJ
lpd lrhA lrp malY manX mdtI mdtK meta
metR mglC mhpR motA motB mutT nagB ndh nemA nfrA nmpC nuoA nuoB nuoC oppC oppD paaK
pabB patD pcnB pgaC php potF preA psaa
psd psuG psuT purU putA putP pyrG rayT rbsB rclR relB rfbB rfbC rnk rpe rplK rplM
rplN rplU rpoE rpoS rpoZ rpsA rpsJ rpsL
rpsM rpsO rpsP rseA rspB sdhC sdhD serT sgcC sibA smrA sodB spy srlM sseA tap tar
tdcD tdcG tesB tfaX thrL thrS tnaC treA
treB tsr tsx uacT ubiC ucpA udp ugpB uhpA uhpC uhpT ulaA uspf uxaA uxaB uxaC uxuB ves
xdhA xdhC xylG yagE yagG yaiO ybaK
ybcM ybdD ybdL ybfA ycdU ycgR ychH yciG ydaM ydbC ydbJ ydeP ydeQ ydeR ydeS ydfI ydhR
ydhT ydiM yeaC yeaH yecR yecT yedE yedF
yedL yegS yehW yejA yfbK yfcQ yfdQ yfeA yfgI ygcQ yghG ygjI yhaI yhaL yhaM yhcD yhcN
yhft yhjB yhjG yhjH yiaA yiaK yieK yieL
yifL yigI yihA yihQ yihY yjbQ yjcZ yjdP yjhI yjhP yjhX yjhY yjiV yjji yjjP ykfA ykgF
ymcE ymgD ymgG ynfE ynjE ypeC ypfG yphF
yphH yqiI ytfF zapC

Supplementary File 2: DE genes in both RpoB L533P and RpoB M1304R mutants relative to wt

gene	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	
tnaA	1438.896086	-9.56927463	0.860925182	-11.11510598	1.06E-28	4.17E-26	
tnaC	54.38604539	-8.971567108	1.307688108	-6.860632175	6.86E-12	3.03E-10	
mglB	2532.655229	-8.62236831	0.771998392	-11.16889414	5.79E-29	2.51E-26	
malK	155.4142003	-7.796254311	1.413203895	-5.516722915	3.45E-08	7.43E-07	
mglA	1057.523043	-7.137987296	0.762225222	-9.364669511	7.63E-21	1.14E-18	
mglC	649.2445041	-7.01005947	0.788480967	-8.890588053	6.08E-19	6.93E-17	
yhjX	1569.593897	-6.720682588	0.789787075	-8.509486672	1.75E-17	1.72E-15	
srlE	463.8479112	-6.399726472	0.878745898	-7.282795276	3.27E-13	1.84E-11	
malE	514.0415802	-6.326353308	1.24867211	-5.066464812	4.05E-07	6.94E-06	
srlA	288.3722768	-6.139140814	0.895356805	-6.856641709	7.05E-12	3.08E-10	
gatD	2444.698747	-6.128063718	1.277468419	-4.797037349	1.61E-06	2.32E-05	
glpT	839.1864039	-5.95459034	1.437347419	-4.14276344	3.43E-05	0.000330259	
srlB	218.8075361	-5.916027232	0.916851958	-6.452543596	1.10E-10	3.87E-09	
treB	2556.889153	-5.863627325	0.611357439	-9.591160505	8.71E-22	1.45E-19	
nanA	2239.525745	-5.861473296	0.465424229	-12.59382932	2.28E-36	1.41E-33	
aldA	3666.37519	-5.809441725	0.697161758	-8.332989666	7.88E-17	7.42E-15	
nanT	717.5454377	-5.712882974	0.406038281	-14.06981372	5.82E-45	6.30E-42	
gatB	1309.083922	-5.655362427	0.90205379	-6.269429259	3.62E-10	1.18E-08	
gatC	6500.825367	-5.60288313	0.929522425	-6.027700872	1.66E-09	4.83E-08	
lamB	322.2749316	-5.593307205	1.351900291	-4.13736667	3.51E-05	0.000337371	
eutP	6.260855273	-5.575773396	1.654485248	-3.370095565	0.000751421	0.004380088	
gatA	3475.602656	-5.483720106	0.814325817	-6.734061467	1.65E-11	6.74E-10	
lldP	1973.227987	-5.432146845	0.392578001	-13.83711474	1.52E-43	1.32E-40	
nanE	539.2429653	-5.331113723	0.419280134	-12.71492087	4.89E-37	3.53E-34	
treC	1863.260851	-5.237957384	0.63194372	-8.288645358	1.15E-16	1.01E-14	
tnaB	120.2000863	-5.135548684	0.745780585	-6.88613888	5.73E-12	2.56E-10	
yjiY	5749.162208	-5.119715052	1.156220346	-4.427975229	9.51E-06	0.000111949	
rbsB	8225.011104	-5.054449758	0.74808261	-6.756539577	1.41E-11	5.94E-10	
srlD	919.9889568	-5.000249898	0.879851519	-5.683061052	1.32E-08	3.18E-07	
acs	366.6121404	-4.917003613	0.499807318	-9.837798366	7.74E-23	1.40E-20	
galS	252.0120375	-4.90555137	0.960401925	-5.107810849	3.26E-07	5.75E-06	
fadB	307.5086933	-4.88774047	0.465542762	-10.49901507	8.73E-26	2.36E-23	
yagE	345.4394186	-4.850295388	0.47088281	-10.30042993	7.01E-25	1.69E-22	
gatZ	13116.3677	-4.803866508	0.709034039	-6.775226918	1.24E-11	5.27E-10	
lldR	660.30086	-4.774056017	0.458175346	-10.4197139	2.02E-25	5.14E-23	
gntP	335.8681713	-4.74313234	0.524852895	-9.037069977	1.61E-19	2.05E-17	
hcaR	354.8611608	-4.74053733	0.55304049	-8.571772616	1.02E-17	1.03E-15	
nanK	538.2251096	-4.700604765	0.424265317	-11.07939908	1.58E-28	5.70E-26	
fadI	210.8816146	-4.679030423	0.593791736	-7.879918391	3.28E-15	2.49E-13	
rbsC	3270.950065	-4.579264302	0.827146946	-5.536216176	3.09E-08	6.80E-07	
yhch	413.2578738	-4.565210384	0.50540258	-9.032819711	1.67E-19	2.07E-17	
yjhI	22.46294027	-4.517043208	0.968059898	-4.666078224	3.07E-06	4.07E-05	
gatY	10047.24059	-4.482845686	0.594732897	-7.537578144	4.79E-14	3.01E-12	
dctA	2740.535786	-4.460386729	0.633952422	-7.035838294	1.98E-12	9.53E-11	
malF	223.24109	-4.41890216	0.955683346	-4.623814129	3.77E-06	4.87E-05	
nupG	1768.555666	-4.401983125	0.574010947	-7.668813891	1.74E-14	1.14E-12	
aphA	680.9028211	-4.398392532	0.488039658	-9.012367049	2.02E-19	2.36E-17	
lldD	1181.422759	-4.394852027	0.588809777	-7.463958991	8.40E-14	5.12E-12	
psuK	21.84391041	-4.291180337	1.050616172	-4.084441543	4.42E-05	0.00040677	
glpF	670.7014856	-4.233301742	1.259062669	-3.36226452	0.00077306	0.004494126	
rbsA	5498.413947	-4.194809962	0.853619348	-4.914145832	8.92E-07	1.37E-05	
aspA	5419.901656	-4.155761545	0.598569013	-6.94282773	3.84E-12	1.75E-10	
udp	9376.205588	-4.136561925	0.470221134	-8.797056587	1.40E-18	1.52E-16	
srlM	104.9006267	-4.134471486	0.809756524	-5.105820535	3.29E-07	5.78E-06	
yqeF	1381.836986	-4.117353588	0.648328854	-6.350717792	2.14E-10	7.31E-09	
yjch	34.37637131	-4.099154445	0.712600334	-5.752389175	8.80E-09	2.22E-07	
cdd	2160.91558	-4.092263583	0.585952964	-6.983945527	2.87E-12	1.35E-10	

cstA	1626.37314	-4.090662723	0.64451345	-6.346900473	2.20E-10	7.41E-09
malG	143.4984172	-4.076079496	0.917752192	-4.441372664	8.94E-06	0.000106064
gntT	1349.84675	-4.003312675	0.689502715	-5.806086893	6.39E-09	1.66E-07
sdhC	2166.196843	-3.982648844	0.474396839	-8.395184188	4.65E-17	4.48E-15
sdhD	1108.151402	-3.979901339	0.479048888	-8.307923128	9.74E-17	8.79E-15
yihN	163.7141096	-3.966983532	0.716581639	-5.535982667	3.09E-08	6.80E-07
yagF	656.6642169	-3.932699037	0.394893749	-9.958878921	2.31E-23	4.54E-21
malT	11515.14098	-3.929041896	0.60600935	-6.483467448	8.96E-11	3.26E-09
rbsD	4509.198305	-3.895893272	0.764164869	-5.098236559	3.43E-07	5.96E-06
sdhA	6623.144307	-3.892247325	0.504362151	-7.717167753	1.19E-14	8.18E-13
uidA	69.39525943	-3.866025237	0.492685314	-7.846844894	4.27E-15	3.19E-13
glpK	2388.838854	-3.865270362	0.814409164	-4.746103721	2.07E-06	2.94E-05
gltA	4193.974993	-3.800451221	0.408643897	-9.300154126	1.40E-20	2.02E-18
yhaO	1153.594545	-3.800222938	0.748827694	-5.07489636	3.88E-07	6.66E-06
ychH	403.1232319	-3.794594383	0.569502206	-6.663002082	2.68E-11	1.06E-09
lacZ	294.3923172	-3.793245115	0.383706061	-9.885809736	4.80E-23	9.03E-21
mtfA	652.3688455	-3.774912087	0.648488432	-5.821093947	5.85E-09	1.54E-07
sdhB	4264.855166	-3.766574488	0.519018682	-7.257107733	3.95E-13	2.17E-11
dmlR	212.9054229	-3.743131521	0.560442714	-6.678883365	2.41E-11	9.75E-10
yjiX	146.7582964	-3.729224971	0.882886661	-4.223900003	2.40E-05	0.000242405
fadJ	372.8002468	-3.722497583	0.567121712	-6.563842477	5.24E-11	1.97E-09
cspD	1066.229927	-3.629144548	0.410294296	-8.845223006	9.13E-19	1.01E-16
uxuA	1206.864072	-3.615855618	0.383588705	-9.426387098	4.24E-21	6.57E-19
dadA	5176.604513	-3.613982825	0.507747239	-7.117680904	1.10E-12	5.53E-11
fadH	185.3791254	-3.58196318	0.618846491	-5.788128772	7.12E-09	1.82E-07
paaB	5.964380193	-3.580377744	1.288160801	-2.779449384	0.005445114	0.020925278
nmpC	13478.288	-3.548846593	0.607409716	-5.84259109	5.14E-09	1.38E-07
deoA	4070.334177	-3.539619569	0.349042669	-10.14093659	3.64E-24	7.87E-22
glpQ	822.2733742	-3.515972056	0.809613605	-4.342777884	1.41E-05	0.000157221
yedF	498.7860617	-3.5103535	0.455436285	-7.707671993	1.28E-14	8.67E-13
yedE	2263.601147	-3.490782573	0.475500257	-7.341284308	2.12E-13	1.22E-11
rbsK	2906.033182	-3.483548979	0.521991301	-6.673576691	2.50E-11	9.92E-10
manX	5737.773991	-3.434589881	0.363977438	-9.436271381	3.86E-21	6.20E-19
dadX	3173.097724	-3.406324671	0.500026199	-6.812292395	9.61E-12	4.16E-10
frlA	62.36149332	-3.385119518	0.48986663	-6.91028805	4.84E-12	2.18E-10
gcvT	2178.218553	-3.377121616	0.758656797	-4.451448438	8.53E-06	0.000101485
chiP	173.5195685	-3.366030916	0.779317605	-4.31920297	1.57E-05	0.000173012
cmtB	5.268865012	-3.365718543	1.186799213	-2.835962904	0.004568775	0.01837267
uxuB	986.3834126	-3.35003147	0.179694999	-18.64287533	1.44E-77	3.12E-74
malX	291.6649018	-3.346242258	0.584077297	-5.729108591	1.01E-08	2.53E-07
uxaC	580.1095125	-3.345278673	0.314231821	-10.64589406	1.82E-26	5.64E-24
mtlA	3194.200203	-3.341023821	0.413166316	-8.086389651	6.15E-16	5.12E-14
lgoR	95.17158732	-3.328844243	0.803351762	-4.143694455	3.42E-05	0.000329653
fadE	363.3075933	-3.313602172	0.42623263	-7.774163547	7.59E-15	5.48E-13
yhaM	1676.454684	-3.298801906	0.458360481	-7.196959697	6.16E-13	3.21E-11
ygeV	285.1081476	-3.288102739	0.499475063	-6.583116918	4.61E-11	1.75E-09
agp	359.8300136	-3.281404475	0.464932914	-7.057802057	1.69E-12	8.33E-11
deoC	2976.968738	-3.269164425	0.352174094	-9.282807785	1.65E-20	2.31E-18
gcvH	1264.444162	-3.252513613	0.843572955	-3.855639979	0.000115427	0.000925769
exuT	272.1293765	-3.21686713	0.421832782	-7.625929681	2.42E-14	1.57E-12
melR	179.4966587	-3.197477636	0.680640236	-4.69774995	2.63E-06	3.61E-05
preT	125.1738711	-3.136790903	0.524602021	-5.979372515	2.24E-09	6.38E-08
preA	155.7791284	-3.133884814	0.424848835	-7.376470305	1.63E-13	9.51E-12
rihA	884.317668	-3.132975526	0.572897146	-5.468652701	4.53E-08	9.58E-07
manY	5241.891821	-3.12051968	0.311740978	-10.00997591	1.38E-23	2.84E-21
sucA	12744.37117	-3.107793106	0.516591358	-6.01596031	1.79E-09	5.16E-08
tdcA	43.68498647	-3.092174579	0.92306996	-3.349881064	0.000808463	0.004668602
ygiS	373.2445485	-3.089778285	0.494389876	-6.249679525	4.11E-10	1.33E-08
dhaL	1738.782477	-3.078958701	0.395295133	-7.789012423	6.75E-15	4.96E-13
yoaG	16.93148547	-3.06334761	1.009248937	-3.035274548	0.002403168	0.011037244

yihM	377.436833	-3.022320023	0.824702125	-3.664741402	0.000247589	0.001746427
kbaZ	73.90536277	-3.021587592	0.573540848	-5.268304083	1.38E-07	2.58E-06
dhaM	4003.227945	-2.980121185	0.412049468	-7.232435461	4.74E-13	2.57E-11
rpiB	62.94335208	-2.978290702	0.563850951	-5.282053165	1.28E-07	2.42E-06
manZ	5820.662451	-2.971250253	0.32787126	-9.06224674	1.28E-19	1.68E-17
actP	171.9739395	-2.96487539	0.48939783	-6.058211153	1.38E-09	4.03E-08
dhaK	3043.008212	-2.961171562	0.443531868	-6.67634454	2.45E-11	9.82E-10
fucA	25.35267035	-2.949889757	0.53803547	-5.482704987	4.19E-08	8.89E-07
uxaA	521.6051144	-2.943926218	0.305027925	-9.651333474	4.85E-22	8.41E-20
agaV	39.23719302	-2.931308762	0.528208912	-5.549525377	2.86E-08	6.41E-07
putA	7492.180048	-2.870169365	0.492774405	-5.824509831	5.73E-09	1.52E-07
yhaL	149.6309985	-2.844251577	0.268775091	-10.58227369	3.60E-26	1.04E-23
ycaM	129.8641789	-2.831649571	0.581932246	-4.865943745	1.14E-06	1.70E-05
feaR	134.6991336	-2.829887496	0.617640102	-4.581774219	4.61E-06	5.83E-05
sucC	8687.573187	-2.805401944	0.693315084	-4.046359305	5.20E-05	0.00047332
gcvP	3464.189024	-2.800367328	0.827707958	-3.383279454	0.000716257	0.004207986
yiaL	6.821210117	-2.794098568	1.148010712	-2.433861059	0.014938728	0.046693708
ivbL	294.496993	-2.78617035	0.529328214	-5.263596912	1.41E-07	2.64E-06
aceA	4379.431714	-2.784869226	0.473174123	-5.885506177	3.97E-09	1.09E-07
rbsR	751.6403711	-2.745130488	0.491118887	-5.589543715	2.28E-08	5.24E-07
uspF	187.221893	-2.739313092	0.337236554	-8.12282376	4.55E-16	3.87E-14
ygjH	36.20959289	-2.731519737	0.5494154	-4.971683973	6.64E-07	1.06E-05
malM	259.5186889	-2.711694894	0.824972251	-3.287013459	0.00101256	0.005537118
sucD	6521.938932	-2.703707966	0.706056033	-3.829310764	0.000128503	0.001013743
araC	583.7667426	-2.696141357	0.552971339	-4.875734357	1.08E-06	1.63E-05
yiaK	28.25158621	-2.68807739	0.546134324	-4.922007776	8.57E-07	1.32E-05
cytR	1890.472721	-2.680078197	0.457050315	-5.863858114	4.52E-09	1.23E-07
ebgC	21.84241846	-2.677520477	0.585161481	-4.575695023	4.75E-06	5.98E-05
ucpA	1560.707949	-2.672326709	0.333029332	-8.024298328	1.02E-15	8.04E-14
ycaC	66.11595569	-2.62268407	0.530918088	-4.939903405	7.82E-07	1.23E-05
yehU	572.0368534	-2.612154802	0.639581933	-4.084159774	4.42E-05	0.00040677
sibA	9.491983511	-2.601759578	0.812894825	-3.200610335	0.001371369	0.006987526
psuG	38.64226326	-2.598718186	0.482279362	-5.388408441	7.11E-08	1.45E-06
nupC	7647.77075	-2.59429761	0.48300818	-5.37112562	7.82E-08	1.58E-06
ugpB	178.466422	-2.593544535	0.34952382	-7.420222563	1.17E-13	7.03E-12
sdaC	54803.87441	-2.568683305	0.453856059	-5.659687146	1.52E-08	3.62E-07
kduI	185.9863362	-2.566691278	0.317557493	-8.082603413	6.34E-16	5.18E-14
yjiA	1026.397589	-2.552310017	0.579278576	-4.406014865	1.05E-05	0.000122255
acrS	44.63024655	-2.544562914	0.636902217	-3.995217549	6.46E-05	0.000566749
murQ	390.4610868	-2.541247094	0.403107376	-6.304144369	2.90E-10	9.51E-09
agaW	22.2248056	-2.540422036	0.586836089	-4.329014664	1.50E-05	0.00016633
serU	60.84689118	-2.526681353	0.628629797	-4.019347103	5.84E-05	0.000522222
yebK	978.7250458	-2.520269508	0.510566757	-4.936219354	7.97E-07	1.25E-05
csiE	368.4029216	-2.512895792	0.609736298	-4.121282926	3.77E-05	0.000358634
sdaB	28708.78616	-2.508468971	0.430669093	-5.824585538	5.73E-09	1.52E-07
fucI	241.7979986	-2.497247206	0.271751404	-9.189454664	3.95E-20	5.34E-18
mlc	1087.732119	-2.479508437	0.448825615	-5.524436109	3.31E-08	7.23E-07
fxsA	1392.262554	-2.463670876	0.405872098	-6.07006712	1.28E-09	3.79E-08
phoH	232.227717	-2.45445734	0.596692509	-4.113437494	3.90E-05	0.000369424
yjhP	108.3312359	-2.451535284	0.373760239	-6.559112042	5.41E-11	2.02E-09
maeB	2870.415687	-2.439250971	0.32649613	-7.47099506	7.96E-14	4.92E-12
yehT	445.4126735	-2.412548904	0.540406269	-4.464324422	8.03E-06	9.61E-05
sucB	10637.64097	-2.398491106	0.618100055	-3.880425324	0.000104274	0.000856946
agaA	43.79078091	-2.396120973	0.507767078	-4.718937243	2.37E-06	3.31E-05
yjhX	61.8753101	-2.376453887	0.457897229	-5.189928517	2.10E-07	3.83E-06
yhdU	27.99054511	-2.376002466	0.752559608	-3.157228265	0.001592766	0.007883737
astC	35.16416994	-2.365778856	0.606301804	-3.901982216	9.54E-05	0.000791595
tsx	14256.60168	-2.354642748	0.557054203	-4.226954462	2.37E-05	0.000240651
paaK	152.4998524	-2.349803544	0.333308322	-7.049939613	1.79E-12	8.71E-11
malP	449.4120075	-2.345260699	0.767514492	-3.055656568	0.002245683	0.010458123

fumA	3891.240072	-2.330552217	0.334269037	-6.972085227	3.12E-12	1.45E-10
kduD	196.9139015	-2.325192201	0.283169028	-8.211322477	2.19E-16	1.89E-14
astD	44.13461489	-2.321444661	0.471380343	-4.924780371	8.45E-07	1.31E-05
ebgA	222.2510644	-2.320418137	0.547994735	-4.234380349	2.29E-05	0.000234799
frlB	189.5511087	-2.311484883	0.459915114	-5.02589459	5.01E-07	8.44E-06
rmuC	1029.174888	-2.308080971	0.501082979	-4.606185141	4.10E-06	5.24E-05
fucP	47.29754031	-2.293833259	0.694270468	-3.303947616	0.000953336	0.005300257
yqeC	23.59498837	-2.273386416	0.802411732	-2.833191895	0.004608571	0.018481224
mtlD	2207.175001	-2.259707775	0.313824863	-7.200537764	6.00E-13	3.17E-11
yjhY	112.6054817	-2.256796301	0.480133815	-4.700348594	2.60E-06	3.59E-05
yjhB	119.8180387	-2.256575634	0.34683446	-6.506203662	7.71E-11	2.83E-09
bsmA	129.3157957	-2.254303071	0.684695377	-3.292417545	0.0009933	0.00545245
ptsG	42537.9304	-2.23945458	0.360806337	-6.206805008	5.41E-10	1.72E-08
ygjI	33.73023022	-2.23262529	0.527190154	-4.234952559	2.29E-05	0.000234799
gatR	424.4419159	-2.223123112	0.789989998	-2.814115519	0.004891165	0.01925785
paaJ	123.1753591	-2.221685463	0.440466744	-5.043934632	4.56E-07	7.75E-06
cdaR	151.9514822	-2.220988304	0.419975742	-5.28837283	1.23E-07	2.36E-06
lacY	70.63432463	-2.216703427	0.431109241	-5.141860155	2.72E-07	4.89E-06
glcD	38.70780978	-2.211220907	0.517366881	-4.273990058	1.92E-05	0.000205836
dsdX	45.7451947	-2.207117919	0.456971579	-4.829880062	1.37E-06	1.99E-05
pepE	203.1640969	-2.190531717	0.427056601	-5.12937094	2.91E-07	5.16E-06
ybdD	89.40823142	-2.180543607	0.572657351	-3.807763235	0.000140229	0.001090366
aldB	42.60071917	-2.174806192	0.616194034	-3.529417798	0.000416475	0.002704278
ycjN	22.2404234	-2.165488764	0.574800656	-3.767373506	0.000164974	0.001244778
leuL	27.815645	-2.157246218	0.570467148	-3.781543297	0.000155859	0.001184256
ybaE	185.41265	-2.153112649	0.524992282	-4.101227244	4.11E-05	0.000386932
xdhC	30.37661846	-2.146758788	0.562786004	-3.81452057	0.000136448	0.001064783
galP	1422.751989	-2.144195208	0.177885581	-12.05378874	1.85E-33	1.00E-30
ydjL	44.66967246	-2.136740023	0.559071707	-3.82194269	0.000132404	0.001037103
glcC	210.3259038	-2.130509699	0.443933651	-4.799162426	1.59E-06	2.30E-05
ydcI	1155.649011	-2.119723955	0.37990845	-5.57956517	2.41E-08	5.53E-07
mhpR	161.801572	-2.11177794	0.330458328	-6.390451573	1.65E-10	5.78E-09
allS	17.31586922	-2.107399495	0.643436871	-3.275223396	0.001055784	0.005709635
glk	1355.120902	-2.101759537	0.291648506	-7.206481421	5.74E-13	3.07E-11
argT	596.2911081	-2.084923799	0.290945076	-7.166039136	7.72E-13	3.98E-11
ypfM	73.30941827	-2.080725963	0.446154108	-4.663693391	3.11E-06	4.10E-05
dppA	1649.081409	-2.079539139	0.204975487	-10.14530648	3.48E-24	7.87E-22
ugpA	42.11289856	-2.078856354	0.623563078	-3.333834903	0.000856575	0.004857329
yeiQ	596.3836774	-2.072901207	0.560945299	-3.695371386	0.000219566	0.001574402
fucO	154.9851137	-2.072578504	0.488525413	-4.242519325	2.21E-05	0.000229558
yjhQ	88.01117587	-2.066992588	0.385673487	-5.359436562	8.35E-08	1.66E-06
yeiL	17.60915321	-2.056947543	0.638215262	-3.222968274	0.001268696	0.006541336
ycdZ	3090.353011	-2.056417231	0.554311579	-3.709857973	0.000207376	0.001496906
fucK	142.0175856	-2.040687732	0.293137752	-6.961531632	3.37E-12	1.55E-10
murP	345.0667762	-2.038824039	0.443629251	-4.595783606	4.31E-06	5.48E-05
lsrA	36.08143272	-2.038486906	0.623466343	-3.269602167	0.001076988	0.005787142
lacA	50.92814064	-2.030157545	0.496218184	-4.091259871	4.29E-05	0.000400464
ycjM	51.73189158	-2.029795905	0.551853692	-3.678141391	0.00023494	0.001670811
malQ	608.8281355	-2.020210069	0.643323473	-3.140271035	0.001687916	0.008213892
yedK	53.87793167	-2.003931851	0.551895668	-3.630997611	0.000282328	0.001950178
treA	299.5223597	-1.979477181	0.302730904	-6.538735067	6.20E-11	2.30E-09
idnD	51.16481688	-1.974311573	0.47786561	-4.131520521	3.60E-05	0.000345303
ykgF	144.9420038	-1.952963405	0.372040866	-5.249324956	1.53E-07	2.84E-06
nuoA	5547.30518	-1.925424798	0.323978551	-5.943062566	2.80E-09	7.92E-08
galK	1613.350076	-1.923256109	0.439528175	-4.375728832	1.21E-05	0.000137217
yjiT	579.9051562	-1.920538132	0.34302906	-5.5987622	2.16E-08	5.03E-07
yjfN	93.65510281	-1.895513529	0.714948759	-2.651257875	0.008019259	0.028515115
yobD	300.9583602	-1.894836306	0.334829007	-5.659116339	1.52E-08	3.62E-07
lsrF	51.03879537	-1.88364354	0.475622529	-3.960374927	7.48E-05	0.000643052
abgR	149.1534434	-1.881625258	0.478465922	-3.932621263	8.40E-05	0.000709377

alsB	113.7635704	-1.878698817	0.369510525	-5.084290409	3.69E-07	6.37E-06
ugpE	41.92956861	-1.876512477	0.499233507	-3.75878712	0.000170739	0.001275801
ykgE	55.20182854	-1.868592853	0.462157759	-4.04319265	5.27E-05	0.000477753
xdhB	36.57705114	-1.857786555	0.542302954	-3.425735636	0.000613137	0.003708793
lsrB	36.58736878	-1.855832994	0.595999273	-3.113817548	0.001846837	0.008838286
eutT	14.74565029	-1.850402168	0.687970463	-2.689653505	0.007152624	0.025988268
mdh	12425.88636	-1.834540769	0.259768219	-7.06222177	1.64E-12	8.16E-11
gpr	352.1788888	-1.827455003	0.461032806	-3.963828557	7.38E-05	0.000635075
fruB	9812.536473	-1.818567905	0.747225278	-2.433761221	0.014942849	0.046693708
ymfD	172.7428794	-1.813502901	0.268861504	-6.745119228	1.53E-11	6.37E-10
araB	42.94780975	-1.810042283	0.501418335	-3.609844628	0.00030638	0.002092956
yihV	29.92852939	-1.797514378	0.639827564	-2.809373147	0.004963808	0.019473053
yjdP	55.65171614	-1.793269827	0.356615843	-5.028575884	4.94E-07	8.36E-06
csgG	178.4965213	-1.792223709	0.608793635	-2.943893637	0.003241114	0.01389828
sra	425.3262037	-1.788887911	0.413871145	-4.322330594	1.54E-05	0.000171013
yagG	78.14476709	-1.779205907	0.359811029	-4.944834265	7.62E-07	1.21E-05
fucR	333.7805687	-1.776047834	0.27987041	-6.345965019	2.21E-10	7.41E-09
ybhQ	303.059966	-1.769539673	0.417386653	-4.239569375	2.24E-05	0.000231485
yegK	18.55922207	-1.755480467	0.662660224	-2.64914115	0.008069662	0.02861985
nuoB	9305.531986	-1.753270424	0.241041395	-7.273731664	3.50E-13	1.94E-11
csiD	62.67678966	-1.75232574	0.548331394	-3.195742136	0.001394717	0.007089811
yqfA	964.6706785	-1.742690174	0.37778344	-4.612934258	3.97E-06	5.10E-05
yffS	821.0974253	-1.733665977	0.236553165	-7.328864007	2.32E-13	1.32E-11
alsR	607.3603306	-1.722205217	0.368237813	-4.676883141	2.91E-06	3.92E-05
gntK	232.300195	-1.717034361	0.502569496	-3.416511298	0.00063429	0.003793643
mhpB	18.13822596	-1.713134162	0.628826108	-2.724336889	0.006443075	0.023974571
mepS	8949.710415	-1.71083441	0.34608994	-4.943323145	7.68E-07	1.21E-05
yaiZ	139.6909864	-1.710490497	0.602911386	-2.837051245	0.00455323	0.018344224
yghO	72.94031782	-1.708340056	0.431693591	-3.9572977	7.58E-05	0.000648815
garD	126.6867546	-1.705327964	0.364799018	-4.674705474	2.94E-06	3.92E-05
rtcA	285.2794974	-1.698414037	0.383964126	-4.423366461	9.72E-06	0.000114055
idnK	30.07623312	-1.695642081	0.502011485	-3.377695794	0.000730959	0.004266554
astA	23.88127743	-1.685404578	0.593352501	-2.84047775	0.004504602	0.018199094
glgS	83.06108924	-1.662558537	0.512104345	-3.246523007	0.00116824	0.006192959
fruA	14380.77341	-1.66229442	0.656627814	-2.531562607	0.011355554	0.037657661
ysgA	230.4317032	-1.656587268	0.310255902	-5.339422259	9.32E-08	1.83E-06
clpA	10946.63833	-1.646872304	0.351442267	-4.686039383	2.79E-06	3.78E-05
rsd	413.1617829	-1.643338292	0.248330938	-6.617533467	3.65E-11	1.41E-09
uxaB	150.3910179	-1.641845793	0.27814227	-5.902899231	3.57E-09	9.92E-08
paaA	18.74126312	-1.641367577	0.599170936	-2.739397853	0.006155184	0.023120643
lhgO	61.82952265	-1.628055876	0.514891199	-3.161941553	0.00156721	0.007792867
frlC	96.44482932	-1.585287189	0.445548649	-3.558056326	0.000373609	0.002466618
uhpA	809.1585076	-1.580173509	0.322432957	-4.900781614	9.55E-07	1.46E-05
wrbA	250.0026242	-1.578596761	0.363389298	-4.344092603	1.40E-05	0.000156917
ybeM	140.8785874	-1.577403887	0.382404865	-4.12495769	3.71E-05	0.000353733
astB	58.58765447	-1.566166618	0.466070404	-3.360364884	0.000778396	0.004519079
rhaS	50.21776377	-1.563622013	0.457135504	-3.420478173	0.000625112	0.003749803
asnT	28.24873582	-1.562131137	0.596641032	-2.618209364	0.008839255	0.030730117
mgsA	1511.7579	-1.556451386	0.17267764	-9.013624387	1.99E-19	2.36E-17
pka	1064.745153	-1.555183331	0.433952037	-3.583767783	0.000338673	0.00227763
yegL	20.86039235	-1.547228724	0.573006208	-2.700195396	0.006929876	0.025413458
ydeN	85.97386653	-1.539843303	0.38905607	-3.957895592	7.56E-05	0.000648475
nuoC	17281.02762	-1.537186001	0.193523356	-7.943154921	1.97E-15	1.52E-13
eutD	20.20516548	-1.533541115	0.548474296	-2.79601273	0.005173736	0.020114409
ilvC	1468.292818	-1.519230912	0.394076183	-3.855170591	0.000115649	0.000925833
ybgS	149.0926639	-1.519036731	0.442848588	-3.430149201	0.000603249	0.003659206
ycjQ	32.09314325	-1.507531951	0.479870247	-3.141540782	0.001680614	0.008196778
alaE	136.0538747	-1.506563697	0.540686084	-2.786392586	0.005329828	0.020628673
sthA	3590.560832	-1.499275077	0.31907603	-4.698801965	2.62E-06	3.60E-05
flhD	1142.353551	-1.499192539	0.489338749	-3.063711062	0.002186099	0.010202582

hchA	781.1528481	-1.492878201	0.502555519	-2.97057369	0.002972441	0.01289944
narV	27.25476859	-1.485606483	0.515395944	-2.882456683	0.003945874	0.016322426
yhdW	29.57918084	-1.474464834	0.49314321	-2.989932344	0.002790392	0.01227698
yfeW	237.4833243	-1.47331724	0.479418947	-3.073131024	0.002118255	0.009918012
ydiP	104.1961507	-1.472362845	0.428119748	-3.43913789	0.00058357	0.003564797
nac	47.82779992	-1.469561296	0.439202843	-3.345974009	0.000819941	0.004716021
gabP	61.25748407	-1.4577043	0.442695023	-3.29279577	0.000991965	0.005452031
flhC	1505.909865	-1.445322741	0.496877569	-2.908810601	0.003628066	0.015196473
aceK	867.7834128	-1.445059714	0.451792371	-3.198504017	0.001381426	0.007030501
lsrR	151.6578992	-1.44319355	0.374290244	-3.855813962	0.000115345	0.000925769
yidQ	421.1343101	-1.436170077	0.269060263	-5.337726438	9.41E-08	1.84E-06
uspA	3857.454905	-1.432332178	0.380629138	-3.763064974	0.000167844	0.001262032
iraP	116.5155394	-1.429152777	0.540744393	-2.642935915	0.008219059	0.028963991
frlD	137.8636042	-1.426992157	0.416222931	-3.428432337	0.000607078	0.003677279
ymfE	129.6515005	-1.425986002	0.565946415	-2.519648439	0.01174721	0.038748793
acnB	24985.20878	-1.425274283	0.324161416	-4.396804225	1.10E-05	0.000126204
ytfQ	192.5056872	-1.419805985	0.427740993	-3.319312406	0.000902394	0.005075674
malY	459.1510566	-1.41251367	0.353291586	-3.998152594	6.38E-05	0.00056264
gabD	169.7639687	-1.410364585	0.504077711	-2.797911024	0.005143428	0.020050573
mtlR	1151.150648	-1.409099788	0.226941607	-6.209085278	5.33E-10	1.71E-08
yahD	26.46596791	-1.408127369	0.525320766	-2.680509621	0.007351015	0.026575331
nagB	1134.08127	-1.407919216	0.434554808	-3.239911724	0.001195667	0.006315164
ybfA	421.5107997	-1.400903598	0.339520826	-4.126119792	3.69E-05	0.000352728
nuoF	9784.575103	-1.400205756	0.211154511	-6.631190358	3.33E-11	1.30E-09
nuoE	4790.244814	-1.397547315	0.216288179	-6.461505772	1.04E-10	3.74E-09
xdhA	113.6909933	-1.392059573	0.35397043	-3.932700176	8.40E-05	0.000709377
ulaA	38.61473284	-1.390316199	0.420705373	-3.304726513	0.000950691	0.005292922
gntU	624.4040516	-1.387280968	0.469983934	-2.951762533	0.003159658	0.013589354
allA	40.417385	-1.38622726	0.443453912	-3.125978196	0.001772147	0.008566036
yhdY	25.34188413	-1.384756992	0.493880676	-2.803829062	0.005049967	0.019775233
dgoK	128.8780035	-1.373915349	0.263246664	-5.219117797	1.80E-07	3.30E-06
dppB	210.7437127	-1.372422623	0.361192675	-3.799696723	0.000144873	0.001118442
glpC	63.08075515	-1.363646636	0.431139241	-3.162891487	0.001562105	0.007782035
rclR	68.94792997	-1.362007693	0.347656242	-3.917685144	8.94E-05	0.000747502
hscC	109.4552058	-1.361979342	0.411118459	-3.312863509	0.00092346	0.005187428
yahO	160.0245109	-1.361290691	0.531252973	-2.562415194	0.010394697	0.035061864
ygjR	382.8032153	-1.35979011	0.323696838	-4.200813695	2.66E-05	0.000266019
metE	869.6920066	-1.354772539	0.4686205	-2.890980099	0.003840424	0.015940771
ilvL	208.6861527	-1.349085367	0.359379648	-3.753928124	0.000174085	0.001295466
araG	102.6702726	-1.342663901	0.384586483	-3.491188488	0.000480877	0.003058264
maa	1136.876386	-1.339703251	0.39216339	-3.416186431	0.000635048	0.003793643
ydjI	47.97648552	-1.337245659	0.428062347	-3.123950677	0.001784404	0.008615666
fabB	20737.90244	-1.333687852	0.239754906	-5.562713497	2.66E-08	5.99E-07
ydeE	211.0209253	-1.315117232	0.492208178	-2.671871967	0.007542942	0.027110552
ycaN	117.066491	-1.311124251	0.328199797	-3.994896594	6.47E-05	0.000566749
betI	1258.735184	-1.310091993	0.323300316	-4.052244699	5.07E-05	0.000463514
eutM	25.11903785	-1.308885147	0.530231437	-2.468516682	0.013567433	0.043350803
betB	2593.611402	-1.308513788	0.333972327	-3.918030578	8.93E-05	0.000747502
mdtQ	29.83638259	-1.305629669	0.543509008	-2.402222687	0.016295785	0.049807371
frdD	273.3582042	-1.304121506	0.214764559	-6.072331067	1.26E-09	3.77E-08
yehA	33.86020523	-1.302113969	0.458465462	-2.840157169	0.004509131	0.018200417
ilvI	353.3854166	-1.287020861	0.378427527	-3.400970516	0.000671471	0.003983753
mhpC	30.51169239	-1.28505886	0.494618881	-2.59807886	0.009374696	0.032198104
rmf	635.8507666	-1.281515994	0.438834026	-2.920274906	0.003497227	0.014705332
nagE	4151.456369	-1.262354208	0.316804498	-3.984647366	6.76E-05	0.000589963
fadA	316.1437475	-1.259455086	0.268494403	-4.690805741	2.72E-06	3.71E-05
gabT	192.56203	-1.258239343	0.509567107	-2.469231877	0.013540345	0.043350803
pykA	6350.495186	-1.255038127	0.320874049	-3.911310785	9.18E-05	0.000766033
yfeC	170.7431519	-1.250349688	0.418042688	-2.990961749	0.002781003	0.012252823
yciE	51.1621601	-1.248359675	0.425226621	-2.93575146	0.003327408	0.014198034

yheV	159.1147264	-1.245003257	0.331806432	-3.752197476	0.000175291	0.001302207
ydcJ	84.20919105	-1.24464548	0.330977815	-3.760510295	0.000169567	0.00127058
frdA	1251.394779	-1.244462769	0.282319059	-4.408001268	1.04E-05	0.000121465
idnO	53.73070187	-1.242341833	0.419431966	-2.961962686	0.003056848	0.013225984
qorA	345.6974162	-1.234563702	0.313539505	-3.937506058	8.23E-05	0.000699184
msrA	561.9180855	-1.234460911	0.305289573	-4.043573775	5.26E-05	0.000477753
narZ	154.5388823	-1.230469895	0.329222783	-3.737499216	0.00018586	0.001371309
ydjY	49.57731081	-1.227732542	0.39518716	-3.106711617	0.001891809	0.009013666
mals	179.8970601	-1.226857811	0.429902154	-2.853807083	0.004319876	0.017551014
ynfK	224.847659	-1.225304907	0.342141307	-3.581283177	0.000341911	0.002292284
ilvH	116.7029136	-1.224464169	0.40441519	-3.027740302	0.002463897	0.01120918
metA	303.0527984	-1.203919243	0.232615908	-5.175567103	2.27E-07	4.12E-06
ytfI	37.95598055	-1.201601209	0.409838523	-2.93188937	0.003369067	0.014300325
ascF	131.5727842	-1.198619012	0.397644756	-3.014296039	0.002575763	0.011524412
psuT	79.45551328	-1.197593213	0.321924048	-3.720111067	0.000199135	0.001451944
adhE	23445.01338	-1.197120108	0.362071191	-3.306311402	0.00094533	0.00527606
dppC	177.0856609	-1.196531024	0.428058411	-2.795251755	0.005185931	0.020143739
yhdX	42.70946053	-1.190763321	0.392222903	-3.035935211	0.002397909	0.01102478
pspE	527.9606241	-1.190209494	0.254493608	-4.676775596	2.91E-06	3.92E-05
ygdH	1995.224593	-1.188290493	0.275366886	-4.315299168	1.59E-05	0.000175204
nuoG	16284.70297	-1.187860298	0.278858271	-4.259727685	2.05E-05	0.000217268
glgC	1000.531335	-1.186688608	0.433635775	-2.736602181	0.006207731	0.023277649
dppD	244.6710679	-1.180421845	0.452834352	-2.606740941	0.009140849	0.031494842
hyaF	28.38066235	-1.175992737	0.470920611	-2.497220785	0.0125171	0.040746073
serA	1553.69557	-1.169999887	0.484337247	-2.41567192	0.015706206	0.0483122
yaiE	850.7095083	-1.167738112	0.231100517	-5.052944614	4.35E-07	7.42E-06
yihQ	48.55254923	-1.167428723	0.454434606	-2.568969674	0.010200138	0.034513124
atoC	122.1397951	-1.164381521	0.387810118	-3.002452659	0.002678136	0.011908633
fumC	633.7763786	-1.163430747	0.275264744	-4.226588305	2.37E-05	0.000240651
frdC	240.1237592	-1.16271335	0.284539362	-4.08630054	4.38E-05	0.00040585
yjbQ	225.9975215	-1.161064368	0.232543249	-4.99289647	5.95E-07	9.72E-06
yjeI	1136.107692	-1.1603564	0.328875218	-3.528257338	0.000418305	0.002712096
galM	2690.338951	-1.159998345	0.37425389	-3.099495763	0.001938504	0.009215871
rihC	741.3637718	-1.157101801	0.27621172	-4.189184303	2.80E-05	0.000276827
ygjK	80.04322467	-1.150031652	0.369324869	-3.113875476	0.001846474	0.008838286
glgB	2025.753905	-1.148659443	0.417501027	-2.751273334	0.005936409	0.0224573
nuoH	4508.871645	-1.143035554	0.346179702	-3.301856078	0.000960473	0.005326262
yegT	83.10916651	-1.142541691	0.345098988	-3.310765119	0.000930413	0.005219712
rhaR	57.55081998	-1.138963727	0.395933192	-2.87665634	0.00401913	0.016562183
glgX	1067.907264	-1.138876471	0.408965917	-2.784771115	0.005356552	0.020695117
dgoR	253.6348836	-1.136707776	0.267336648	-4.251971387	2.12E-05	0.000223836
clpB	9110.626976	-1.136498092	0.405587256	-2.802105037	0.005077034	0.019845338
frdB	460.6793314	-1.132587674	0.257305433	-4.401724683	1.07E-05	0.000123703
yjhC	336.1710451	-1.130501038	0.270026754	-4.186626036	2.83E-05	0.000279327
fbaB	475.2297179	-1.120720048	0.383369636	-2.923340667	0.003462974	0.014603837
rcdA	160.2619939	-1.118197739	0.46049355	-2.428259289	0.015171492	0.047271751
cpdB	1119.883929	-1.116769209	0.248437951	-4.495163503	6.95E-06	8.46E-05
ytfT	45.15122705	-1.115603597	0.461378768	-2.417977753	0.015607031	0.048167933
yceH	854.7609503	-1.114236461	0.217218724	-5.129559918	2.90E-07	5.16E-06
yicH	1112.268572	-1.109183329	0.352875406	-3.143271844	0.001670706	0.008177283
ampH	972.550118	-1.108727217	0.417919998	-2.652965212	0.007978809	0.028417947
ydbC	135.5237434	-1.107308029	0.338227214	-3.273858473	0.001060897	0.00572911
yidE	614.3207378	-1.10478908	0.25929389	-4.260760172	2.04E-05	0.000216798
atoS	100.927612	-1.104174349	0.358364662	-3.081147404	0.002062045	0.009696763
hdhA	784.3802536	-1.101013003	0.345299301	-3.188575826	0.001429755	0.007223865
rimJ	754.5005706	-1.094405797	0.161404264	-6.780525944	1.20E-11	5.13E-10
srlR	600.2316414	-1.08850175	0.321153322	-3.389352295	0.000700579	0.004128176
galT	1240.30572	-1.088320589	0.176508445	-6.165827307	7.01E-10	2.17E-08
gltI	1388.994488	-1.078038956	0.221917175	-4.857843733	1.19E-06	1.76E-05
tas	1661.507899	-1.076177601	0.342511401	-3.142019791	0.001677867	0.008192606

pptA	64.2663662	-1.075722486	0.380666485	-2.825892291	0.004714912	0.018785908
chaC	201.4620092	-1.072703506	0.405756568	-2.643711997	0.00820024	0.028943121
lsrK	155.810723	-1.072539958	0.258201089	-4.153894013	3.27E-05	0.0003167
ykgG	92.24923882	-1.070044003	0.291693457	-3.668385346	0.000244087	0.001724537
nuoI	2036.529193	-1.064407075	0.381986555	-2.786504031	0.005327996	0.020628673
yciK	614.9581705	-1.062205716	0.298612979	-3.557131771	0.000374926	0.002471545
dosC	164.6687297	-1.060345822	0.358695238	-2.956119034	0.003115368	0.013412187
leuA	360.6003737	-1.060205902	0.409032664	-2.591983467	0.009542436	0.032696431
araA	96.00397873	-1.059952782	0.43501921	-2.436565462	0.014827485	0.046467322
ybiH	225.3069592	-1.054919534	0.227674746	-4.633449921	3.60E-06	4.68E-05
betA	1777.937585	-1.054662964	0.31020228	-3.399920091	0.000674055	0.003993617
cspE	43802.15751	-1.054662759	0.225090025	-4.685515311	2.79E-06	3.78E-05
alaC	462.6938168	-1.052113433	0.389195428	-2.703303684	0.006865399	0.025241123
yjhG	324.5799983	-1.049264165	0.246931714	-4.249207803	2.15E-05	0.000224969
nuoJ	2400.11327	-1.047741768	0.379255349	-2.762628851	0.005733793	0.021879344
pheA	2318.636381	-1.04575482	0.387790446	-2.696700834	0.007003015	0.025638259
yciI	409.6745765	-1.042479778	0.351201009	-2.968327973	0.002994247	0.012968082
ygfT	68.40931045	-1.041866257	0.3481903	-2.992232284	0.002769455	0.012214366
yhjB	114.7230804	-1.034082847	0.275123009	-3.758620016	0.000170853	0.001275801
ygcB	117.2900407	-1.026597896	0.33536474	-3.061138436	0.002204971	0.010279581
yeaG	349.2887441	-1.024322314	0.324789584	-3.153802845	0.001611579	0.007967751
yceM	686.4144325	-1.023984719	0.207401626	-4.937206806	7.92E-07	1.24E-05
nuoK	656.407429	-1.016335212	0.388188635	-2.618147779	0.008840851	0.030730117
mnaT	201.9918115	-1.014743093	0.407958067	-2.48737107	0.012869109	0.041687443
sgcC	57.8376858	-1.014193774	0.373788631	-2.713281489	0.006662049	0.024660969
crp	6607.393511	-1.004958074	0.201897333	-4.977569836	6.44E-07	1.04E-05
rof	536.6853714	-1.003774462	0.228958276	-4.384093378	1.16E-05	0.000133095
yeaH	78.16449385	-1.001979818	0.389174437	-2.574629067	0.010034764	0.034113471
yhfT	76.01795139	-1.001239525	0.331223626	-3.022850567	0.002504059	0.01133237
yghD	135.8600441	1.000111583	0.288517666	3.466379021	0.000527519	0.003287317
rplE	121064.0201	1.001541326	0.269177311	3.720749427	0.000198632	0.001451944
rplD	97860.68816	1.001977292	0.224107043	4.470976353	7.79E-06	9.37E-05
potB	2386.403782	1.002326781	0.340714602	2.941836876	0.003262717	0.01396327
rimP	6382.520326	1.002482298	0.247423249	4.051689972	5.08E-05	0.000463636
pqiA	1332.854557	1.00561132	0.295129472	3.40735649	0.000655954	0.003902385
rsxC	3175.824027	1.006095936	0.260257526	3.865770767	0.000110739	0.000896468
waaF	4080.631907	1.007291418	0.240222837	4.193154283	2.75E-05	0.000273272
ylaB	748.6047726	1.008447112	0.284999415	3.538418183	0.000402532	0.002621603
proY	2675.564784	1.0092331	0.266190759	3.791390451	0.000149806	0.001146309
ybaO	303.3226968	1.009747944	0.301498667	3.349095885	0.000810757	0.004673331
frmB	1681.839295	1.011159788	0.328664657	3.076569896	0.002093972	0.009814927
waaC	1895.88487	1.011266245	0.194059166	5.211123308	1.88E-07	3.43E-06
pphB	61.82988518	1.011561508	0.355995354	2.841501996	0.004490157	0.018174645
rplR	56815.64565	1.012096971	0.27777133	3.643633679	0.000268816	0.001871771
ecnA	927.1796599	1.014775564	0.30930675	3.280806399	0.001035108	0.005624908
mnmA	6483.933649	1.016053076	0.230733353	4.403581287	1.06E-05	0.000123304
infA	11098.54525	1.017311061	0.188720513	5.390569614	7.02E-08	1.44E-06
mutM	875.7915725	1.019749454	0.239663521	4.25492144	2.09E-05	0.000221445
yadE	467.1168698	1.021926565	0.179792645	5.683917532	1.32E-08	3.18E-07
rplF	101754.702	1.022728275	0.256021018	3.994704351	6.48E-05	0.000566749
pheS	11465.03199	1.024580397	0.132189479	7.750846766	9.13E-15	6.48E-13
yfiR	271.5625793	1.026011928	0.350615151	2.926319427	0.003429986	0.014507097
aroK	8809.664576	1.026120472	0.244510401	4.196633216	2.71E-05	0.000269729
menE	1782.78345	1.026477872	0.192156343	5.341889082	9.20E-08	1.81E-06
ecnB	487.3431156	1.026717939	0.376139086	2.729623105	0.006340677	0.023694109
yjaA	81.68253032	1.028824052	0.333316966	3.086623715	0.002024437	0.009530257
mltF	686.4264016	1.029147574	0.295672742	3.480698182	0.000500109	0.003152796
prmC	837.4886984	1.029824253	0.226894211	4.538785941	5.66E-06	6.98E-05
yhdJ	82.14100963	1.031522651	0.341780898	3.018081636	0.002543804	0.011416802
rpsN	80894.85961	1.032046887	0.244160194	4.226925246	2.37E-05	0.000240651

phoU	1471.982651	1.032482291	0.395499039	2.610581033	0.009038855	0.031267798
rplW	66042.55746	1.034035159	0.195571446	5.287250172	1.24E-07	2.37E-06
mrda	4906.925753	1.035305608	0.246696053	4.196684935	2.71E-05	0.000269729
yfeA	1543.005608	1.039640207	0.169344645	6.139197427	8.29E-10	2.53E-08
artQ	1431.656319	1.041078461	0.27134909	3.836675708	0.000124711	0.000989237
yfiP	337.9958823	1.045124208	0.345907027	3.021402068	0.00251607	0.011361569
murI	2067.087726	1.04532844	0.393703698	2.655114607	0.007928147	0.028260744
rnt	1214.80278	1.047450928	0.26170725	4.002376418	6.27E-05	0.000555408
folM	488.9575878	1.050305786	0.308708346	3.402259122	0.000668312	0.003970454
perR	147.0644609	1.050840533	0.341223941	3.079621349	0.002072639	0.009736009
nrdA	11729.92971	1.052306169	0.181345842	5.802758731	6.52E-09	1.68E-07
frmR	700.5082611	1.053860721	0.261498849	4.030077856	5.58E-05	0.000501016
rfbB	6850.552763	1.057591404	0.245889157	4.301090046	1.70E-05	0.000184949
lysQ	423.0442205	1.057731488	0.313096452	3.378292798	0.000729374	0.004263047
rpsO	44278.39311	1.058352039	0.259108767	4.084585983	4.42E-05	0.00040677
nlpI	15457.31928	1.058763166	0.231561779	4.572270815	4.82E-06	6.06E-05
cmoB	1680.622535	1.059440467	0.35499111	2.984414079	0.00284122	0.012454781
nikC	37.1640325	1.060086778	0.409676147	2.587621434	0.009664113	0.032930977
valZ	3574.108554	1.060547713	0.192259201	5.516239054	3.46E-08	7.43E-07
acrA	6939.331829	1.061336463	0.277284418	3.827609472	0.000129394	0.001018918
rsxB	1073.120274	1.0616328	0.240188704	4.419994711	9.87E-06	0.000115536
ymfA	137.4656109	1.061978724	0.330990388	3.208488112	0.001334348	0.00684723
msbA	7948.999571	1.062190159	0.368925501	2.879145402	0.003987544	0.016463351
lpxK	2381.057741	1.062860564	0.348147605	3.052902126	0.002266398	0.010531944
rpsJ	78947.30479	1.066599223	0.192352115	5.545035076	2.94E-08	6.53E-07
ruvC	3770.472592	1.067155298	0.353362085	3.020005102	0.002527704	0.011379924
yebC	8496.736617	1.068420893	0.375535792	2.845057425	0.004440342	0.018006667
brnQ	3016.727382	1.068437385	0.23244946	4.596428771	4.30E-06	5.47E-05
rpsH	67781.52184	1.068750613	0.264791577	4.03619565	5.43E-05	0.000490169
nirC	175.0201979	1.072670716	0.446281938	2.403571877	0.016235775	0.049694093
rnhB	2028.070871	1.078435394	0.201194129	5.360173277	8.31E-08	1.66E-06
yqaE	122.7585939	1.084546511	0.434161041	2.498028168	0.012488627	0.040698453
apt	8611.879815	1.090238488	0.384580433	2.834877682	0.004584323	0.018401024
menA	1215.577866	1.092655838	0.364869596	2.994647538	0.002747621	0.012130426
argD	831.0861423	1.093365279	0.218619182	5.001232141	5.70E-07	9.38E-06
ygdQ	830.9307225	1.093413433	0.38706125	2.824910612	0.004729381	0.018808951
focA	1079.429197	1.093742301	0.202571121	5.399300244	6.69E-08	1.38E-06
cspF	191.0786251	1.093750862	0.409399747	2.671596335	0.00754914	0.027110552
bax	5301.207175	1.09581832	0.213410737	5.134785313	2.82E-07	5.06E-06
ssb	3579.81571	1.096487417	0.387292555	2.831160588	0.004637943	0.018530379
mgtA	4457.696476	1.098390937	0.447146894	2.456443177	0.014031999	0.04448945
nikB	49.2852437	1.098771032	0.440022286	2.497080416	0.012522056	0.040746073
metG	12882.51692	1.100122953	0.199168578	5.523576889	3.32E-08	7.23E-07
artM	1703.094356	1.100943328	0.26940835	4.086522657	4.38E-05	0.00040585
ypdA	646.6873708	1.101540471	0.234378337	4.699839089	2.60E-06	3.59E-05
rplC	180374.6204	1.106731294	0.182509844	6.063953964	1.33E-09	3.91E-08
dnaG	10865.91336	1.116642124	0.305002931	3.661086541	0.000251148	0.001765782
pyrE	244.3680501	1.118052565	0.341071134	3.278062708	0.001045222	0.005665651
yiiX	478.2389161	1.118269885	0.199132763	5.615700141	1.96E-08	4.61E-07
yohK	64.116563	1.120970161	0.427328895	2.623202349	0.008710752	0.030399893
rlmH	2784.935233	1.121362279	0.217022477	5.167032892	2.38E-07	4.29E-06
lysW	2810.337794	1.123149313	0.225517158	4.98032753	6.35E-07	1.03E-05
yeaY	1799.42702	1.123618872	0.454457689	2.472438907	0.013419465	0.043083545
emrB	1602.64287	1.124515652	0.189433198	5.936212156	2.92E-09	8.20E-08
csrC	8454.519942	1.124886133	0.411185488	2.735714577	0.006224499	0.023320333
pstA	1016.010983	1.125415625	0.468309264	2.403146192	0.016254688	0.049716845
lpd	63135.5516	1.12951992	0.207398583	5.446131328	5.15E-08	1.08E-06
fdnG	301.7645196	1.132132925	0.425650551	2.659770843	0.007819383	0.027965111
typA	52481.68683	1.133807364	0.308478475	3.675482917	0.0002374	0.001680954
lpxH	1629.258297	1.13658601	0.257690672	4.410660275	1.03E-05	0.000120306

lysP	4268.45081	1.139592672	0.410134992	2.778579478	0.005459715	0.020944223
yncD	2263.394476	1.147822749	0.343752932	3.339092238	0.000840527	0.004815238
valT	6256.907213	1.157781982	0.179328294	6.456214785	1.07E-10	3.84E-09
psrD	851.2041254	1.162379197	0.466926857	2.489424585	0.012795006	0.041509492
agrB	54.63513802	1.162731937	0.42703098	2.722828066	0.006472573	0.02404178
mdfA	1301.434355	1.164073308	0.222339483	5.235567218	1.64E-07	3.03E-06
stpA	3946.816165	1.164392417	0.441176388	2.639289972	0.008307988	0.029201552
ldtC	220.5153199	1.165263796	0.328890211	3.54301757	0.000395576	0.002598023
pyrH	6409.742965	1.170199194	0.348599013	3.35686319	0.000788321	0.004564463
rnd	1995.151957	1.17198936	0.315228465	3.717904598	0.000200882	0.001462219
ompX	68431.4222	1.177979578	0.283007473	4.162362094	3.15E-05	0.00030863
lysT	7296.251155	1.183043721	0.191250965	6.185818314	6.18E-10	1.95E-08
yjgX	479.3992602	1.185686628	0.373413683	3.175262941	0.001497008	0.007512794
ydcX	123.7907621	1.190616414	0.383576866	3.103983898	0.001909337	0.009087186
yfcJ	597.5036101	1.191271971	0.392006601	3.038907936	0.002374374	0.010939802
mcbR	155.3424332	1.191721975	0.450803165	2.643552811	0.008204097	0.028943121
emrA	1689.619638	1.196398054	0.221981244	5.389635781	7.06E-08	1.44E-06
menD	1227.382123	1.196668414	0.383181939	3.122977078	0.001790317	0.008634591
gmk	4626.281882	1.200029071	0.255279161	4.70085011	2.59E-06	3.59E-05
argO	309.9120775	1.201350977	0.239146206	5.023500049	5.07E-07	8.52E-06
ygjP	217.9555073	1.208950061	0.349781117	3.456304537	0.000547636	0.003398012
idi	223.7747803	1.209179456	0.247059862	4.894277219	9.87E-07	1.50E-05
pstB	1570.37987	1.209592305	0.412353278	2.93338836	0.003352842	0.014272093
ybjL	1837.02367	1.210639338	0.3253963	3.720507383	0.000198823	0.001451944
nirD	102.0595409	1.211328349	0.491979612	2.46215152	0.013810631	0.043883963
argS	10506.82182	1.211586424	0.400648677	3.024061961	0.002494054	0.011298897
yidD	3976.863869	1.217436487	0.353389502	3.445027314	0.000571002	0.003512796
mgrR	84.02035162	1.21892709	0.298490272	4.083640921	4.43E-05	0.000406816
gsk	3000.465755	1.219515445	0.278610585	4.377132488	1.20E-05	0.000136695
wzxB	3089.265774	1.221331168	0.217468326	5.616133592	1.95E-08	4.61E-07
rsxD	1639.693634	1.226759208	0.332745329	3.686781155	0.000227109	0.001623114
obgE	6620.620984	1.230645217	0.326442822	3.769864532	0.000163336	0.001234571
tsaB	2337.479372	1.239981435	0.467645835	2.651539565	0.008012572	0.028514751
pppA	669.1367636	1.242150445	0.423523062	2.93289919	0.003358129	0.014272873
ycaO	7856.965279	1.243099943	0.470694054	2.640993511	0.00826633	0.029106891
der	7845.669185	1.244358204	0.45938997	2.708718705	0.006754358	0.024938725
yegH	929.6792045	1.246875026	0.223781097	5.571851435	2.52E-08	5.72E-07
queE	919.00619	1.249284722	0.329414813	3.792436379	0.000149176	0.001143582
xseA	2934.50518	1.252604168	0.396659649	3.157881505	0.001589201	0.007875093
nikA	131.1601742	1.268962868	0.368862494	3.440205737	0.000581272	0.003555776
cydB	10765.47396	1.269190014	0.417100706	3.042886275	0.002343209	0.010830776
metY	579.9337667	1.275395909	0.3835943	3.324856258	0.000884641	0.004982291
cydX	1492.488462	1.295101986	0.430554638	3.007985218	0.002629859	0.011718025
yhdT	191.8103738	1.303934727	0.438336743	2.974732894	0.002932438	0.012764208
aaeB	270.3285359	1.304597183	0.214748441	6.075001869	1.24E-09	3.73E-08
yfiB	540.7468827	1.304672883	0.307414996	4.244011845	2.20E-05	0.000228805
artP	1660.479215	1.306900744	0.27949127	4.675998437	2.93E-06	3.92E-05
yehQ	291.2133346	1.309428705	0.235972794	5.54906641	2.87E-08	6.41E-07
uraA	1502.703162	1.310289498	0.433558286	3.022176118	0.002509645	0.011345795
nhaA	4075.686895	1.317860284	0.518397107	2.542182944	0.01101625	0.03678595
yfiN	503.7649104	1.329769787	0.361720312	3.676237536	0.000236699	0.001680564
thrC	3625.962482	1.333336377	0.399243018	3.339661104	0.000838807	0.004811751
epmA	1104.429716	1.334353762	0.495345794	2.693782361	0.007064628	0.025798401
ansP	840.2668157	1.335423645	0.312731762	4.270188729	1.95E-05	0.000208344
aaeA	147.1582546	1.340748708	0.292649131	4.581420423	4.62E-06	5.83E-05
panF	1434.715889	1.356328526	0.396176971	3.423542062	0.000618107	0.003728441
mdtI	76.95846909	1.357689148	0.349726934	3.882140651	0.000103541	0.00085254
ygiQ	4139.685172	1.361676748	0.442531876	3.07701393	0.002090855	0.009810936
ybgE	1865.127856	1.364997964	0.376443118	3.626040428	0.0002878	0.001981658
cspB	275.7056492	1.366304296	0.556867958	2.453551647	0.014145323	0.044651098

thrB	2227.935631	1.367297504	0.410157087	3.333594731	0.000857315	0.004857329
metK	13905.80076	1.385982153	0.373097374	3.714800072	0.000203364	0.001470403
yebG	762.8101419	1.399699049	0.477146448	2.933478926	0.003351864	0.014272093
xanP	547.8632175	1.401353097	0.302043699	4.639570701	3.49E-06	4.55E-05
ackA	45887.86569	1.403160868	0.363836163	3.856573395	0.000114988	0.000925671
purR	3418.806789	1.406957844	0.438913271	3.205548653	0.001348053	0.0069012
cydA	16343.55246	1.414707855	0.424234131	3.334733705	0.000853811	0.004857329
pyrG	22594.91896	1.418319046	0.423166858	3.351677996	0.000803234	0.004644601
yqhH	96.2521764	1.423880911	0.437139268	3.257270658	0.001124891	0.00600728
yihG	554.340943	1.436251894	0.421385637	3.408402582	0.000653444	0.003892801
nirB	962.6655869	1.448094631	0.455808709	3.17697886	0.001488179	0.007477149
yfcC	131.2083526	1.453128696	0.388221265	3.743042507	0.000181805	0.001348287
pfo	5658.538577	1.463542382	0.339357546	4.312685542	1.61E-05	0.000176615
rapA	13705.37699	1.482040173	0.540479005	2.74208648	0.006105027	0.022972085
yeeE	183.0088845	1.483514511	0.432184565	3.432594845	0.000597835	0.003636548
rluA	2821.64588	1.486097143	0.509990836	2.913968328	0.003568661	0.014962121
lipA	10961.29501	1.51749251	0.26127046	5.808128896	6.32E-09	1.65E-07
fabI	23016.43407	1.518755182	0.423581281	3.585510624	0.000336419	0.00226952
thrA	7193.343094	1.519743579	0.53672869	2.831493096	0.004633123	0.018528215
deaD	24409.06387	1.527444913	0.268603831	5.686608807	1.30E-08	3.15E-07
kdpB	753.5692102	1.538048218	0.406545828	3.783209937	0.000154819	0.001178418
dauA	1305.367811	1.549752626	0.180191264	8.600598017	7.93E-18	8.18E-16
yhbE	5665.529894	1.557171304	0.431987562	3.604666991	0.000312553	0.00212841
ldrB	15.70349748	1.561940306	0.650284871	2.401932406	0.016308722	0.049811758
argC	146.265434	1.566447854	0.271699646	5.765365818	8.15E-09	2.08E-07
fis	16006.50371	1.579774952	0.526737508	2.999169281	0.002707168	0.012025381
bcsQ	164.5503146	1.580140625	0.545131605	2.898640638	0.003747842	0.015622621
yecJ	662.545089	1.598233364	0.459707092	3.476634126	0.00050775	0.003177841
insK	141.7084158	1.611026253	0.487714035	3.303218968	0.000955817	0.005307236
ydjM	193.247669	1.621118769	0.438321959	3.69846579	0.000216907	0.001557914
ldhA	951.6824841	1.621485444	0.323172244	5.017403179	5.24E-07	8.76E-06
ycfJ	389.4801406	1.638918508	0.308528984	5.312040663	1.08E-07	2.11E-06
yafU	16.16224975	1.645041901	0.648836923	2.535370358	0.01123285	0.037422671
dusB	19936.08087	1.665205931	0.416523542	3.997867501	6.39E-05	0.00056264
sslE	10792.74056	1.666077577	0.515111699	3.234400577	0.001218984	0.006387096
yghG	352.2471556	1.70133024	0.50984698	3.336942862	0.000847054	0.004839827
mscS	4690.527814	1.7015418	0.522991745	3.253477357	0.001140018	0.006065625
yedJ	477.3074948	1.788930656	0.314160712	5.694316915	1.24E-08	3.05E-07
dtpD	246.4516906	1.792054977	0.321376352	5.576188069	2.46E-08	5.60E-07
yrbN	641.8336121	1.809423029	0.258469163	7.000537338	2.55E-12	1.21E-10
mdtJ	83.82558407	1.810134841	0.468135272	3.866691848	0.000110322	0.000894763
guaA	24695.43802	1.81249395	0.521062645	3.478456899	0.00050431	0.00317005
suhB	8411.50675	1.813030513	0.442131803	4.100656186	4.12E-05	0.000387047
ydjN	1858.138019	1.829246997	0.425224745	4.30183572	1.69E-05	0.000184792
fimD	151.6946656	1.838520313	0.402467236	4.568124179	4.92E-06	6.16E-05
yghF	466.8737746	1.859290113	0.515426438	3.607285108	0.000309418	0.002110374
ydjO	23.83287242	1.874390987	0.763449424	2.455160654	0.014082164	0.044568236
asr	29.09412215	1.887673264	0.760638039	2.481697164	0.013075835	0.042293832
cpxP	1023.96659	1.907317638	0.681163282	2.800088744	0.005108856	0.019951718
trpE	138.2769999	1.923493848	0.635543307	3.026534661	0.002473745	0.011237895
yicS	81.73737095	1.935462621	0.520667908	3.717268901	0.000201388	0.001463442
ydiY	1025.550176	1.979832628	0.406757336	4.867355675	1.13E-06	1.69E-05
kdpA	680.8763869	1.991027677	0.402036091	4.952360546	7.33E-07	1.17E-05
tsgA	7977.655763	2.07921591	0.607570665	3.42217956	0.000621213	0.003736767
insJ	149.4802317	2.11173634	0.565721293	3.732821028	0.000189347	0.001389936
yjhV	107.6741383	2.115220381	0.752562519	2.810690577	0.00494353	0.019428702
rhIE	2818.023116	2.152019823	0.364437147	5.905050685	3.53E-09	9.85E-08
alx	535.8713763	2.191521164	0.391769354	5.593906573	2.22E-08	5.14E-07
aceF	101268.9331	2.237566182	0.579120969	3.863728481	0.000111669	0.000902313
flgL	3875.813218	2.30450396	0.913773282	2.521964699	0.011670142	0.038553306

ydgI	1333.182185	2.314549187	0.488330193	4.739721652	2.14E-06	3.03E-05
cspA	51377.99838	2.346176295	0.618571321	3.792895365	0.000148901	0.001143582
yoeI	734.5182621	2.393324585	0.768099427	3.11590466	0.001833816	0.008805161
plaP	17829.08961	2.458352764	0.774844879	3.172703119	0.001510269	0.00756182
flgK	4427.692905	2.465072588	0.923680648	2.668749847	0.007613413	0.027296102
aaaE	73.53053612	2.499886892	0.943741166	2.648911567	0.008075146	0.02861985
fecE	1120.28166	2.63451277	0.825864387	3.190006509	0.001422696	0.007198243
guaB	13287.02785	2.646137438	0.695417176	3.805107971	0.000141742	0.001100154
pmrR	161.5569566	2.655594742	0.450084	5.900220273	3.63E-09	1.00E-07
aceE	184386.0761	2.718356506	0.544955517	4.988217239	6.09E-07	9.92E-06
yneE	279.1184858	2.730338517	0.456052293	5.98689791	2.14E-09	6.13E-08
yohJ	32.78530041	2.809090058	0.616079852	4.559620069	5.12E-06	6.38E-05
cspG	304.7967907	2.845207836	0.606237283	4.693224777	2.69E-06	3.67E-05
gcd	4327.988665	2.852851281	0.328074119	8.695752322	3.45E-18	3.64E-16
beeE	14.23286873	2.954833336	1.218518569	2.42493911	0.015310955	0.047566756
serT	13.49247504	3.023422432	0.89051911	3.395123583	0.000685976	0.004053156
grcA	1869.627093	3.036929823	0.620569665	4.893777432	9.89E-07	1.50E-05
nepI	692.4751397	3.058329736	0.577296836	5.297672781	1.17E-07	2.26E-06
fecD	943.6770959	3.22068065	1.185656722	2.716368565	0.00660024	0.024494977
proP	6061.398581	3.25624678	0.671238334	4.851103717	1.23E-06	1.81E-05
yedR	136.4782821	3.340033828	0.732281918	4.561131098	5.09E-06	6.35E-05
fecB	2735.804006	3.342353119	1.378404794	2.42479795	0.015316909	0.047566756
yjcB	638.0155856	3.40779516	0.537085208	6.34498048	2.22E-10	7.41E-09
ymcE	31.83696811	3.41785751	0.866394753	3.944919449	7.98E-05	0.000679234
fimC	65.4954424	3.457656383	0.535771186	6.453606455	1.09E-10	3.87E-09
fecC	1588.11088	3.460480147	1.276680398	2.710529708	0.006717583	0.024845305
ydeA	493.0769605	3.486940264	0.488799226	7.133686134	9.77E-13	4.98E-11
yhcN	1296.163014	3.495843213	0.518884437	6.737228878	1.61E-11	6.66E-10
fimA	1218.735111	3.507423269	0.464062847	7.558078155	4.09E-14	2.61E-12
fimI	109.5335366	3.640846576	0.472855944	7.699695056	1.36E-14	9.09E-13
ndh	9278.156547	3.661057123	0.440317578	8.314583165	9.21E-17	8.48E-15
fecA	8955.337006	3.80960404	1.447196032	2.632403596	0.008478308	0.029684359
bhsA	287.8727832	3.998161579	0.656121152	6.093633114	1.10E-09	3.34E-08
aceB	298.6557785	4.042547498	0.502386077	8.046694936	8.51E-16	6.82E-14
pdhR	6818.854132	4.255359596	0.669671912	6.354394621	2.09E-10	7.19E-09
yeeS	121.9185127	4.475813228	0.417329181	10.7248988	7.78E-27	2.59E-24
mokA	5.932076387	4.565889516	1.450314287	3.148206948	0.001642753	0.008066627
azuC	71.10058627	4.613715055	0.881050875	5.236604591	1.64E-07	3.03E-06
yeeR	789.9224362	6.366073981	0.413523922	15.39469338	1.78E-53	2.56E-50
isrC	63.24717118	7.297383236	0.641119606	11.38224938	5.13E-30	2.47E-27
flu	8241.055429	8.102402397	0.3159781	25.64229102	5.15E-145	2.23E-141

Supplementary File 3 (only top 50 genes are shown): Genes, their functions, and probabilities of rejecting the null hypothesis of non-differential expression between RpoB M1304R and wt

order	rowname	idx	pval	sorted name
1	bolA	1	6.11E-10	DNA-binding transcriptional dual regulator BolA
2	rpoS	3	1.75E-09	RNA polymerase, sigma S (sigma 38) factor
3	ilvX	4	2.10E-09	uncharacterized protein IlvX
4	ilvM	5	2.29E-09	acetolactate synthase II subunit IlvM
5	leuA	6	2.48E-09	2-isopropylmalate synthase
6	argT	7	2.61E-09	lysine/arginine/ornithine ABC transporter periplasmic binding protein
7	leuB	8	3.31E-09	3-isopropylmalate dehydrogenase
8	leuC	9	3.56E-09	3-isopropylmalate dehydratase subunit LeuC
9	ilvN	10	3.84E-09	acetohydroxy acid synthase I subunit IlvN
10	ilvB	11	3.88E-09	acetohydroxy acid synthase I subunit IlvB
11	glgP	12	4.26E-09	glycogen phosphorylase
12	ilvI	13	4.27E-09	acetolactate synthase/acetohydroxybutanoate synthase, catalytic subunit
13	leuD	14	4.36E-09	3-isopropylmalate dehydratase subunit LeuD
14	ivbL	15	4.45E-09	ilvBN operon leader peptide
15	ilvE	16	5.44E-09	branched-chain-amino-acid aminotransferase
16	cfa	17	5.44E-09	cyclopropane fatty acyl phospholipid synthase
17	ilvH	18	5.49E-09	acetolactate synthase/acetohydroxybutanoate synthase, regulatory subunit
18	ilvL	19	6.34E-09	ilvXGMEDA operon leader peptide
19	ilvG	20	7.29E-09	acetolactate synthase II subunit IlvG, N-terminal fragment (pseudogene)
20	ilvD	21	7.89E-09	dihydroxy-acid dehydratase
21	hisP	22	7.93E-09	lysine/arginine/ornithine ABC transporter/histidine ABC transporter, ATP binding subunit
22	cspA	23	7.96E-09	cold shock protein CspA
23	dusB	24	8.05E-09	tRNA-dihydrouridine synthase B
24	rpoE	25	8.58E-09	RNA polymerase sigma E factor
25	mdtK	26	9.29E-09	multidrug efflux pump MdtK
26	leuO	27	9.51E-09	DNA-binding transcriptional dual regulator LeuO
27	rplK	28	1.02E-08	50S ribosomal subunit protein L11
28	lrp	29	1.06E-08	DNA-binding transcriptional dual regulator Lrp
29	ilvA	30	1.35E-08	threonine deaminase
30	dksA	31	1.37E-08	RNA polymerase-binding transcription factor DksA
31	thrL	32	1.38E-08	thr operon leader peptide
32	rplN	34	2.03E-08	50S ribosomal subunit protein L14
33	rpsA	35	2.22E-08	30S ribosomal subunit protein S1
34	glgC	36	2.47E-08	glucose-1-phosphate adenyltransferase
35	iraP	37	2.58E-08	anti-adaptor protein for sigma(S) stabilization
36	cheB	38	2.68E-08	protein-glutamate methylesterase/protein glutamine deamidase
37	hisQ	39	2.92E-08	lysine/arginine/ornithine ABC transporter/histidine ABC transporter, membrane subunit HisQ
38	csgG	41	5.52E-08	curli secretion channel
39	motA	42	6.39E-08	motility protein A
40	fadL	43	6.52E-08	long-chain fatty acid outer membrane channel/bacteriophage T2 receptor
41	rplU	44	8.18E-08	50S ribosomal subunit protein L21
42	rplM	45	9.32E-08	50S ribosomal subunit protein L13
43	ftsK	46	1.11E-07	cell division DNA translocase FtsK
44	infC	47	1.31E-07	translation initiation factor IF-3
45	gluQ	48	1.42E-07	glutamyl-Q tRNA(Asp) synthetase
46	ftsZ	49	1.62E-07	cell division protein FtsZ
47	hmp	50	1.83E-07	nitric oxide dioxygenase
48	fimB	51	2.32E-07	regulator for fimA