

Metformin alters the gut microbiome of individuals with treatment-naïve type 2 diabetes, contributing to the therapeutic effects of the drug

Hao Wu^{1,12}, Eduardo Esteve^{2–4,12}, Valentina Tremaroli¹, Muhammad Tanweer Khan¹, Robert Caesar¹, Louise Mannerås-Holm¹, Marcus Ståhlman¹, Lisa M Olsson¹, Matteo Serino⁵, Mercè Planas-Fèlix⁶, Gemma Xifra^{2–4}, Josep M Mercader⁶, David Torrents^{6,7}, Rémy Burcelin^{8,9}, Wifredo Ricart^{2–4}, Rosie Perkins¹, José Manuel Fernández-Real^{2–4} & Fredrik Bäckhed^{1,10,11}

Metformin is widely used in the treatment of type 2 diabetes (T2D), but its mechanism of action is poorly defined. Recent evidence implicates the gut microbiota as a site of metformin action. In a double-blind study, we randomized individuals with treatment-naïve T2D to placebo or metformin for 4 months and showed that metformin had strong effects on the gut microbiome. These results were verified in a subset of the placebo group that switched to metformin 6 months after the start of the trial. Transfer of fecal samples (obtained before and 4 months after treatment) from metformin-treated donors to germ-free mice showed that glucose tolerance was improved in mice that received metformin-altered microbiota. By directly investigating metformin–microbiota interactions in a gut simulator, we showed that metformin affected pathways with common biological functions in species from two different phyla, and many of the metformin-regulated genes in these species encoded metalloproteins or metal transporters. Our findings provide support for the notion that altered gut microbiota mediates some of metformin's antidiabetic effects.

Metformin is the most prescribed pharmacotherapy for the treatment of individuals with type 2 diabetes (T2D) because of its relative safety, low cost, and beneficial effects on blood glucose and cardiovascular mortality^{1,2}. However, its mechanism of action remains unclear. Although metformin is generally considered to mediate its antihyperglycemic effects by suppressing hepatic glucose output through the activation of AMP-activated protein kinase (AMPK)-dependent^{3–5} and AMPK-independent pathways^{6–8} in the liver, accumulating evidence indicates that it might also act through pathways in the gut^{9,10}. For example, its glucose-lowering effect is more pronounced when given orally than when administered intravenously¹¹. In addition, a study comparing metformin formulations with reduced and normal plasma exposure provided evidence to indicate that the lower bowel is a major site of action for metformin¹². Furthermore, recent studies in both rodents^{13–15} and humans^{16–18} suggest that gut microbial changes might contribute to the antidiabetic effect of metformin. So far, however, it is not known how metformin affects the gut microbiota of individuals with treatment-naïve T2D, nor how metformin interacts with gut bacteria.

Here we performed a randomized, placebo-controlled, double-blind study in individuals with newly diagnosed T2D on a calorie-restricted diet, and we combined metagenomics and targeted metabolomics to investigate the effect of metformin on the composition and function of the gut microbiota. We also transferred human fecal samples to germ-free mice to study the effects of metformin-altered microbiota on host glucose metabolism, and we used an *in vitro* gut simulator to investigate metformin–microbiota interactions directly.

RESULTS

Metformin alters the gut microbiota composition

To investigate how metformin affects the composition of the gut microbiota, we randomized treatment-naïve individuals with recently diagnosed T2D to receive either placebo ($n = 18$) or 1,700 mg/d of metformin ($n = 22$) for 4 months in a double-blind study. Clinical characteristics of these individuals before and after treatment are presented in **Table 1**. Both groups were recommended to consume a calorie-restricted diet for the 4-month study period (**Supplementary Table 1**); calorie intake was reduced by a median of 342 kcal/d, and

¹Department of Molecular and Clinical Medicine, Wallenberg Laboratory, Institute of Medicine, University of Gothenburg, Gothenburg, Sweden. ²Department of Diabetes, Endocrinology and Nutrition, Institut d'Investigació Biomèdica de Girona, Hospital Josep Trueta, Girona, Spain. ³Departament de Medicina, Facultat de Medicina, University of Girona, Girona, Spain. ⁴Centro de Investigación Biomédica en Red de Fisiopatología de la Obesidad y Nutrición (CIBEROBN), Instituto de Salud Carlos III, Madrid, Spain. ⁵IRSD, Université de Toulouse, INSERM, INRA, ENVT, UPS, Toulouse, France. ⁶Barcelona Supercomputing Center (BSC), Joint BSC–CRG–IRB Research Program in Computational Biology, Barcelona, Spain. ⁷Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain. ⁸Institut National de la Santé et de la Recherche Médicale (INSERM), Toulouse, France. ⁹Université Paul Sabatier (UPS), Unité Mixte de Recherche 1048, Institut de Maladies Métaboliques et Cardiovasculaires, Toulouse, France. ¹⁰Sahlgrenska University Hospital, Gothenburg, Sweden. ¹¹Novo Nordisk Foundation Center for Basic Metabolic Research, Section for Metabolic Receptology and Enteroendocrinology, Faculty of Health Sciences, University of Copenhagen, Copenhagen, Denmark. ¹²These authors contributed equally to this work. Correspondence should be addressed to J.M.F.-R. (jmfreal@idibgi.org) or F.B. (fredrik.backhed@wlab.gu.se).

Received 27 June 2016; accepted 19 April 2017; published online 22 May 2017; doi:10.1038/nm.4345

Table 1 Clinical characteristics for the 40 individuals with T2D enrolled in this study

	Placebo group (n = 18)			Metformin group (n = 22)		
	P0	P2	P4	M0	M2	M4
Age (years)	54.9 ± 1.9	—	—	52.6 ± 2.0	—	—
Sex (male/female)	9/9	—	—	8/14	—	—
Weight (kg)	85.4 ± 5.6	82.2 ± 5.6 ⁺	81.5 ± 5.4 [#]	96.5 ± 4.1	92.9 ± 4.0	91.4 ± 3.9
Waist circumference (cm)	106.1 ± 4.4	101.7 ± 4.3 [*]	101.9 ± 3.6	111.5 ± 2.7	108.3 ± 2.9 [*]	108.7 ± 2.9
HOMA	8.0 ± 1.5	8.9 ± 1.6	8.1 ± 1.8	8.3 ± 1.2	6.2 ± 0.9	6.0 ± 0.8 [*]
Total cholesterol (mg/dl)	205.8 ± 8.8	197.8 ± 7.7	190.7 ± 6.9 [*]	206.0 ± 7.4	196.6 ± 7.2	198.8 ± 7.5
HDL-C (mg/dl)	46.9 ± 3.4	45.0 ± 3.0	46.8 ± 3.1	48.4 ± 2.7	55.2 ± 6.1	51.1 ± 3.0 [*]
LDL-C (mg/dl)	126.8 ± 6.6	124.8 ± 5.7	118.1 ± 6.2 [*]	129.4 ± 6.4	117.4 ± 6.2 [*]	121.5 ± 6.8
Triglycerides (mg/dl)	151.9 ± 18.7	155.9 ± 15.2	129.3 ± 12.5	129.0 ± 17.8	139.6 ± 11.6	135.9 ± 12.7
ALT (U/liter)	33.2 ± 7.2	24.3 ± 2.9	22.3 ± 2.1	35.5 ± 3.5	28.0 ± 1.8 ⁺	32.8 ± 3.2
GGT (U/liter)	38.4 ± 5.4	28.2 ± 2.1 ⁺	26.3 ± 2.0 ⁺	44.0 ± 6.0	31.3 ± 3.2 ⁺	34.1 ± 3.9 [*]
CRP (mg/dl)	0.4 ± 0.1	0.6 ± 0.1	0.5 ± 0.1	0.4 ± 0.1	0.4 ± 0.1	0.4 ± 0.1
Statin treatment (n)	3	—	—	4	—	—
Antihypertensive treatment (n)	2	—	—	3	—	—

ALT, alanine transaminase; CRP, C-reactive protein; GGT, γ -glutamyl transferase; HDL-C, high-density lipoprotein cholesterol; HOMA, homeostatic model assessment; LDL-C, low-density lipoprotein cholesterol. ^{*} $P < 0.05$; ⁺ $P < 0.01$; [#] $P < 0.001$ versus P0 or M0. Wilcoxon signed-rank test; data are shown as means $\pm$ s.e.m.

no significant differences were seen between the groups ($P = 0.90$). A subset of the placebo group switched to receive metformin (850 or 1,700 mg/d; $n = 13$) 6 months after the start of the study; to validate our findings from the randomized study, we analyzed samples from this group after a further 6 months.

As expected given the reduced calorie intake, body-mass index (BMI) decreased significantly in both the placebo and metformin groups over the initial 4-month study period (**Fig. 1a**). However, significant decreases in % hemoglobin A1c (HbA1c) and fasting blood glucose were observed only in the group randomized to metformin treatment (**Fig. 1b,c**). BMI did not decrease further in the switched subgroup after 6 months on metformin (**Fig. 1a**), but %HbA1c and fasting blood glucose were significantly reduced by metformin in this subgroup (**Fig. 1b,c**).

To characterize the effects of metformin on the gut microbiome, we performed whole-genome shotgun sequencing of 131 fecal samples. On average, we obtained 38 million paired-end reads for each sample (ranging from 15 million to 116 million; **Supplementary Table 2**). The taxonomy and gene profiles were estimated by mapping the high-quality reads to nonredundant genome and gene catalogs implemented in the metagenomic data-utilization and analysis (MEDUSA) pipeline¹⁹, respectively. Only one bacterial strain was altered over the 4-month study period in the placebo group (**Fig. 1d**), despite the reduction in BMI. By contrast, metformin treatment for 2 and 4 months resulted in significant alterations in the relative abundance of 81 and 86 bacterial strains, respectively, most of which belonged to γ -proteobacteria (for example, *Escherichia coli*) and Firmicutes (**Fig. 1d** and **Supplementary Table 3**; false-discovery rate (FDR) < 0.05). At the genera level, we observed an increase of *Escherichia* and a decrease of *Intestinibacter* in the metformin-treated group (**Supplementary Table 3**). Notably, the microbial changes observed after 2 and 4 months of metformin treatment in our randomized study correlated with the microbial changes observed in the switched subgroup after 6 months on metformin (**Fig. 1e**). We also observed a metformin-induced increase in *Bifidobacterium* in this subgroup (**Supplementary Table 3**).

Earlier studies have shown an association between metformin and the abundance of *Akkermansia muciniphila*^{13–15,18} and between *A. muciniphila* and improved metabolic features in mice^{13,20,21} and humans²². In a targeted analysis of our metagenome data, we showed

increased abundance of *A. muciniphila* in individuals who received metformin for 4 months (**Supplementary Fig. 1**). However, we did not observe any significant correlations between %HbA1c and *A. muciniphila* abundance in our cohort ($P > 0.1$; **Supplementary Fig. 1**).

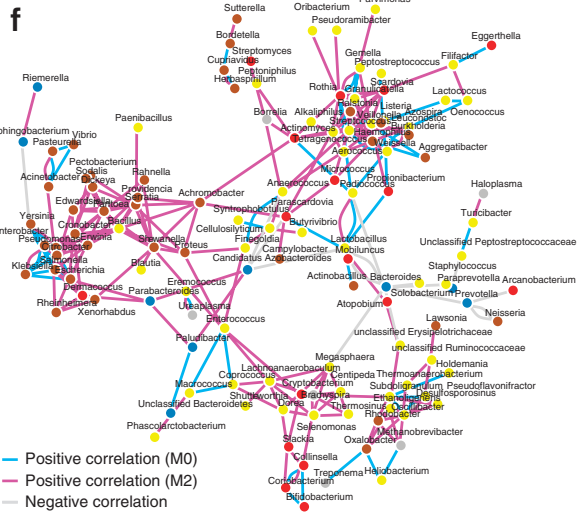
To investigate how different gut bacteria interact with each other, we performed a coabundance network analysis. We showed that 2 months of metformin treatment promoted an increased number of positive connections among microbial genera, especially those within Proteobacteria and Firmicutes (**Fig. 1f**). We also identified a few interphylum connections, such as between *Shewanella* (Proteobacteria) and *Blautia* (Firmicutes), a short-chain fatty acid (SCFA)-producing genus²³.

To test the effect of metformin on microbial growth, we mapped whole-genome shotgun reads to the genomes of common strains in the human gut to determine the ratio between DNA copy number near the replication origin and DNA copy number near the terminus (termed the peak-to-trough ratio, PTR) of bacterial genomes²⁴. After correction for FDR, we found that the PTR of only one bacterial species (*Bifidobacterium adolescentis*) was significantly increased by metformin (**Fig. 2a**). In agreement, the PTR of *B. adolescentis* was also increased in the switched subgroup after 6 months on metformin (**Fig. 2a**). Furthermore, in our cohort, we observed a negative correlation between the PTR of *B. adolescentis* and %HbA1c (Spearman coefficient $\rho = -0.28$, $P < 0.01$). Consistent with this observation, *in vitro* analysis showed that metformin directly promoted the growth of *B. adolescentis* in pure cultures (**Fig. 2b**). We also showed that metformin directly promoted the growth of *A. muciniphila*, but not of *E. coli*, in pure cultures (**Fig. 2c,d**).

Metformin-altered microbiota improves glucose tolerance

To investigate whether metformin-altered microbiota could contribute to the glucose-lowering effect of metformin, we transferred fecal samples from three metformin-treated participants (before and 4 months after metformin, here termed M0 and M4 microbiota) to germ-free mice. All three of the metformin recipients responded similarly to metformin in terms of reduced %HbA1c, as compared to baseline, after 2 and 4 months on metformin. The mice were fed a high-fat diet for 1 week before and during colonization for 18 d.

We did not observe any differences in body weight, body fat, or fasting insulin between mice that received M4 and M0 microbiota (**Fig. 3a,b** and **Supplementary Fig. 2a–c**). However, we found improvements



852 VOLUME 23 | NUMBER 7 | JULY 2017 NATURE MEDICINE

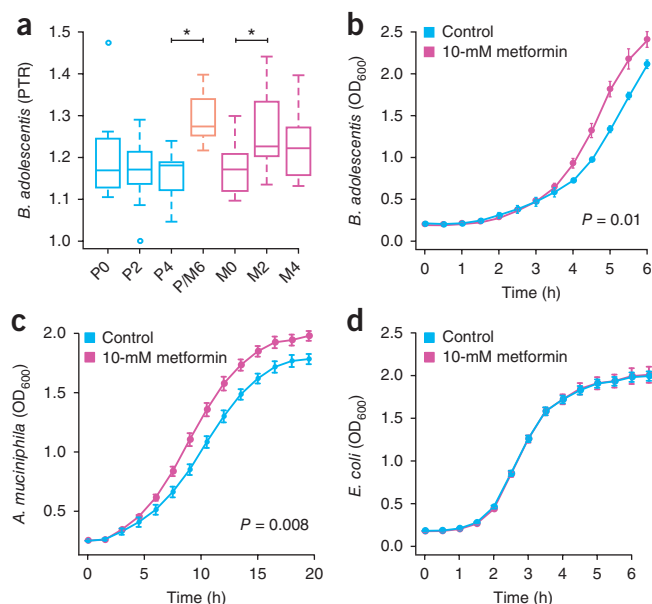


Figure 2 Metformin treatment promotes the growth of gut bacteria. (a) Boxplots (with median) showing *B. adolescentis* growth as estimated by peak-to-trough ratio (PTR) before treatment (P0 and M0) and after 2 and 4 months in individuals with T2D randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$) and 6 months after metformin in a subgroup that switched from placebo to metformin after the randomized study period (P/M6; $n = 13$). Wilcoxon signed-rank test; *FDR < 0.05 . (b–d) Growth of *B. adolescentis*, *A. muciniphila*, and *E. coli* as single cultures in the presence or absence of 10-mM metformin (with six technical replicates). P values were determined by two-way analysis of variance (ANOVA) with repeated measurements. Data are shown as means $\pm$ s.e.m.

in glucose tolerance in mice that received M4 microbiota, as compared to those that received M0 microbiota, from two of the three donors (Supplementary Fig. 2d–f) and when combining the results from all three transfer experiments (Fig. 3c).

Metformin promotes functional shifts in the gut microbiome

To further investigate functional changes in the gut microbiome after metformin treatment, we annotated genes to Kyoto encyclopedia of genes and genomes (KEGG) orthology (KO)²⁵. Only two KOs were significantly altered over the 4-month study period in the placebo group (FDR < 0.05). By contrast, 626 and 473 KOs were increased, whereas 130 and 69 KOs were decreased after 2 and 4 months of metformin, respectively (Supplementary Fig. 3 and Supplementary Table 4; FDR < 0.05), and most of the shifts were consistent between the two sampling times (Supplementary Fig. 3). Principal coordinate analysis (PCoA) of the relative abundance of all of the significantly altered KOs revealed similar gene functions in the placebo group at all time points and the metformin group at baseline (i.e., before treatment), but we observed significant shifts after metformin treatment for 2 months and 4 months (Fig. 4a). Pathway-enrichment analysis revealed that metformin treatment was linked mainly to the enrichment of genes for bacterial environmental responses (for example, bacterial secretion system, two component system, and ATP-binding cassette (ABC) transporters), drug resistance (bacterial chemotaxis and cationic antimicrobial peptide resistance), central carbohydrate metabolism (phosphotransferase system, pyruvate, butyrate, and propionate metabolism), amino acid metabolism, and lipopolysaccharide (LPS) biosynthesis (Fig. 4b and Supplementary Table 4; FDR < 0.05).

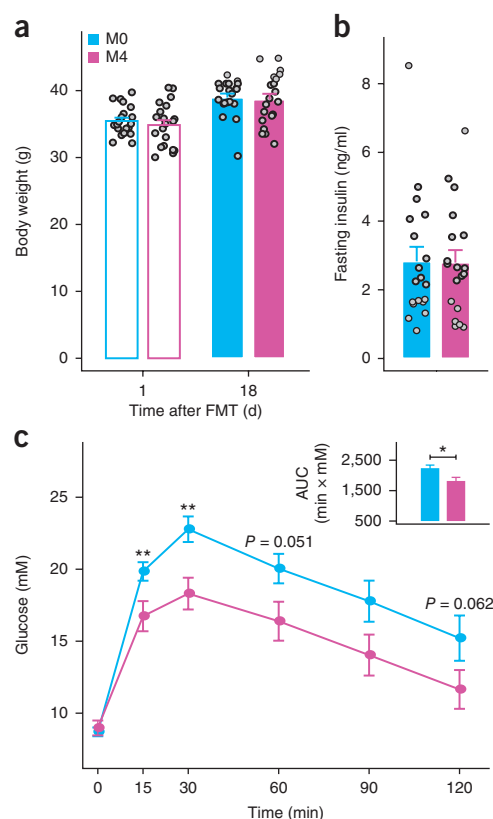


Figure 3 Metformin-altered microbiota improves glucose tolerance. (a) Body weight of mice 1 d and 18 d after colonization with fecal microbiota obtained from three individuals with T2D before (M0) and 4 months after metformin treatment (M4). (b) Fasting plasma insulin concentrations measured in the same mice used in (a) 18 d after colonization. (c) Plasma glucose concentrations measured in the same mice used in (a) during an intraperitoneal glucose-tolerance test 18 d after colonization. Data are shown as means $\pm$ s.e.m. and are the combined results of three independent transfer experiments (shown individually in Supplementary Fig. 2). M0: $n = 20$ mice; M4: $n = 21$. Wilcoxon rank-sum test; * $P < 0.05$; ** $P < 0.01$. FMT, fecal microbiota transplantation.

Although it is not clear how alterations in the gut microbiota promote beneficial effects in the host, a potential mechanism includes increased production of SCFAs, primarily acetate, propionate, and butyrate, and other organic acids^{26,27}. We therefore performed targeted metabolomics to investigate whether the observed enrichment in genes for SCFA metabolism in the gut microbiome following metformin treatment was paralleled by an increased production of SCFAs. We observed significantly larger increases in fecal propionate and butyrate concentrations in the metformin group, as compared to the placebo group, after 4 months of treatment in men; however, no differences were observed when results from men and women were combined (Fig. 4c). We also observed significantly larger increases in fecal concentrations of lactate and a trend toward a larger increase in fecal concentrations of succinate in the metformin group, as compared to the placebo group, after 4 months of treatment (Fig. 4d).

The gut microbiota is also known to be a major regulator of bile acid metabolism²⁸, which may contribute to its effects on host metabolism. Furthermore, a few studies have indicated a potential role of metformin in altering the bile acid profile^{29,30}, but this link is not well established. Here we investigated the effect of metformin treatment

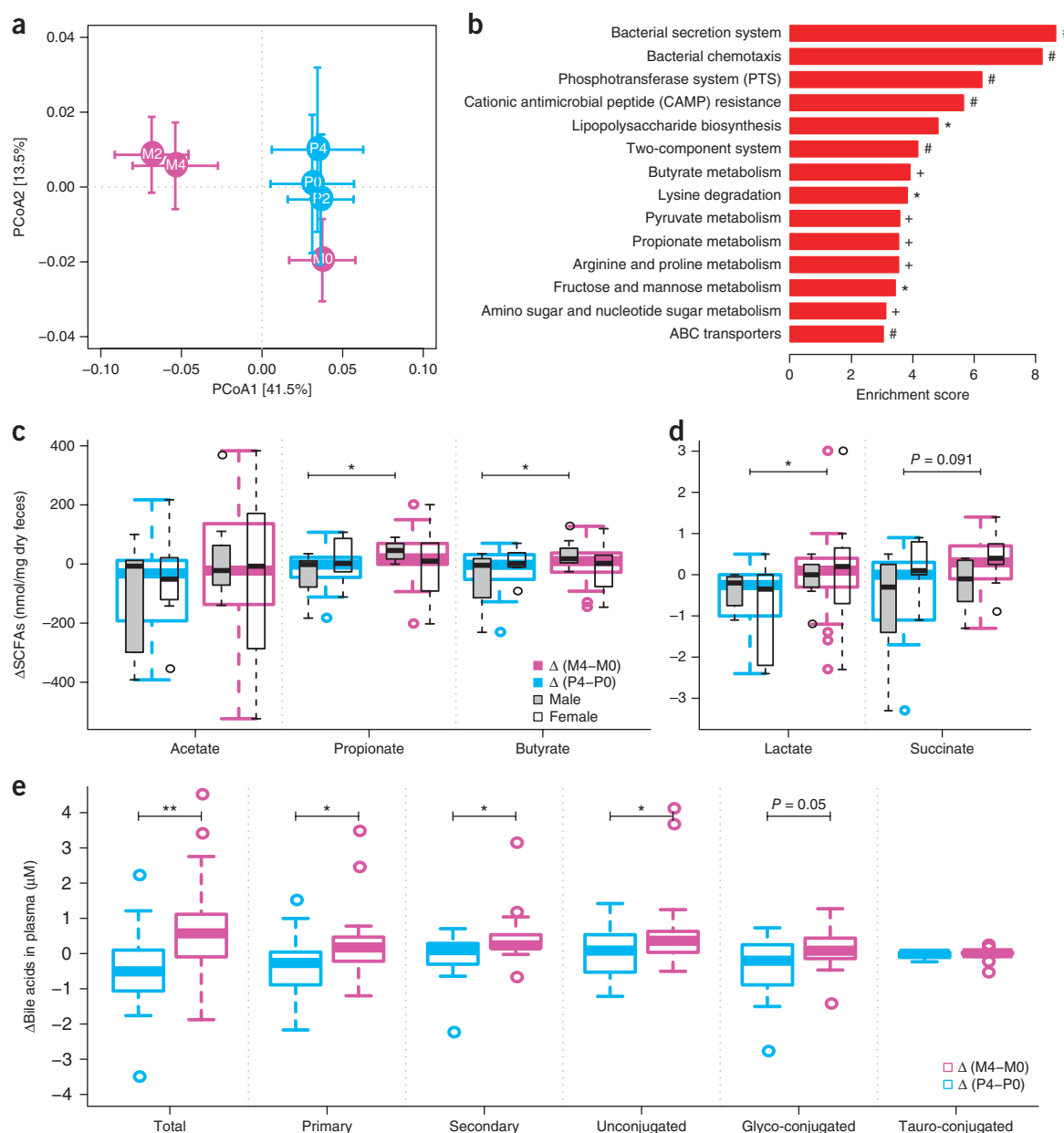


Figure 4 Metformin treatment promotes functional shifts in the gut microbiota. **(a)** Principal coordinate analysis (PCoA) of all KOs that are significantly altered from baseline (P0 and M0) after 2 and 4 months in individuals with T2D randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$). Adonis test based on 5,000 permutations; $P_{M0 \text{ vs. } M2} = 0.00040$; $P_{M0 \text{ vs. } M4} = 0.0062$. Data are shown as means $\pm$ s.e.m. **(b)** Pathway-enrichment analysis of all significantly altered KOs. Hypergeometric test; *FDR < 0.05; +FDR < 0.01; #FDR < 0.001. **(c–e)** Boxplots (with median) showing changes from baseline (P0 and M0) for fecal concentrations of SCFAs **(c)**, fecal concentrations of lactate and succinate **(d)**, and plasma concentrations of bile acids **(e)** after 4 months in individuals with T2D randomized to placebo (P4; $n = 18$) or metformin (M4; $n = 22$). Wilcoxon rank-sum test; * $P < 0.05$; ** $P < 0.01$.

for 4 months on fecal and plasma bile acid composition. No substantial changes in fecal bile acids were detected following metformin treatment (**Supplementary Fig. 4a**). However, we observed significantly larger increases in plasma bile acid concentrations (total, primary, secondary, and unconjugated) in the metformin group, as compared to the placebo group, after 4 months of treatment (**Fig. 4e**). By using a targeted metagenomic analysis, we showed an increased abundance of *bsh*, genes encoding bile salt hydrolases, after 2 months on metformin (**Supplementary Fig. 4b**). These enzymes are produced by the gut microbiota and catalyze the deconjugation of glycine- or taurine-conjugated bile acids, and thus increases in *bsh* could contribute to the

increased concentrations of unconjugated bile acids. Furthermore, we found a significant negative correlation between the concentrations of unconjugated bile acids and %HbA1c ($\rho = -0.27$, $P < 0.05$), which suggests a possible link between the modulation of bile acid composition and the therapeutic effect of metformin.

Direct effects of metformin on the gut microbiota

To directly investigate how metformin affects the gut microbiota, we cultured fecal samples (obtained before metformin treatment from two participants, donors 13 and 49) in two separate gut-simulator experiments, and exposed the samples to a constant flow of metformin

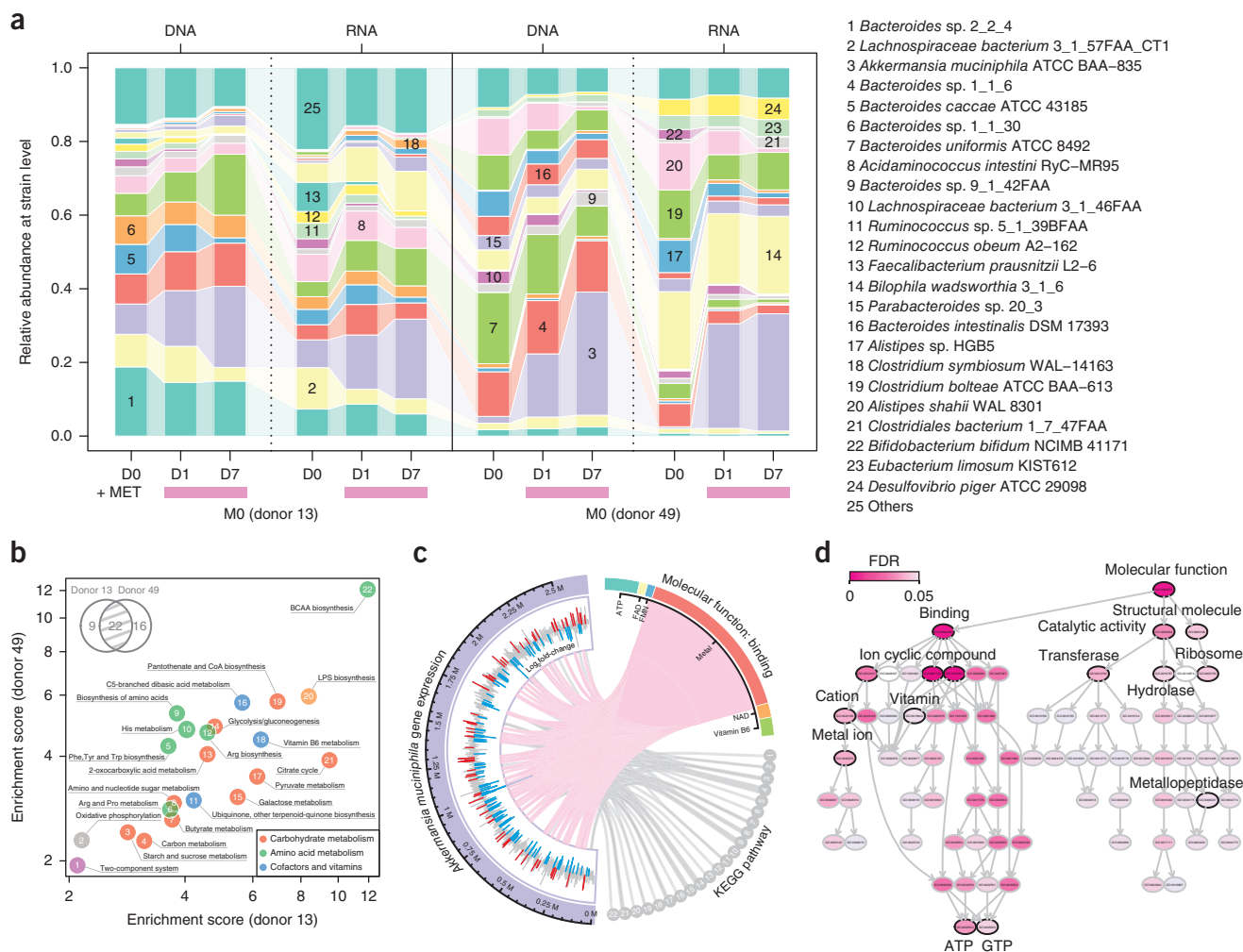


Figure 5 Direct metformin-microbiota interactions identified using an *in vitro* gut simulator. **(a)** Microbial compositional profiling of samples taken from the *in vitro* gut simulator before (D0) and after 1 d and 7 d (D1 and D7) of metformin exposure (+MET). Fecal material from two participants (donors 13 and 49) was used to inoculate the gut simulator in two independent experiments (i.e., the fecal material from the two samples was not pooled). The top ten bacterial strains detected in the samples at each time point are shown. **(b)** Metformin-enriched pathways identified by both metagenomic and metatranscriptomic analyses of samples taken from the *in vitro* gut simulator. Hypergeometric test; FDR < 0.05. Only the 22 pathways affected by metformin exposure in both experiments (inset) are shown. **(c)** Circos plot of KEGG pathway and molecular-function annotations for metformin-regulated genes in *A. muciniphila*. The circular bar plot on the left side indicates metformin-regulated genes along the genome. Red, significantly increased gene expression; blue, significantly decreased; gray, no statistical differences; Wald test; FDR < 0.1. The metformin-regulated genes involved in the 22 pathways shown in **(b)** (gray links) and coding for proteins with metal-binding abilities (pink links) are highlighted. **(d)** Gene ontology (GO) enrichment of all metformin-regulated genes in *A. muciniphila*; GO terms with direct hierarchical parent-child relationships are linked by arrows. Hypergeometric test; FDR < 0.05.

(10 mM) for 1 week. We then profiled the microbiomes by whole-genome shotgun sequencing at both the DNA and RNA level.

Compositional profiling revealed that metformin exposure significantly altered the DNA and RNA abundance of 24 bacterial strains when culturing the feces of donor 13 but of only 4 for the feces of donor 49 (Supplementary Table 5; FDR < 0.05). Donor-specific effects of metformin exposure included, for example, increased RNA abundance of *Bifidobacterium wadsworthia* (donor 13) and increased DNA abundance of *Lachnospiraceae* bacterium (donor 49) (Fig. 5a and Supplementary Table 5). *A. muciniphila* was the only taxon that increased in both DNA and RNA abundance in response to metformin in both samples, and it was also the taxon that increased the most in abundance (Fig. 5a and Supplementary Table 5).

Functional profiling of the combined metagenome and metatranscriptome showed that metformin exposure significantly altered the

abundance of 686 and 909 KOs in samples from donors 13 and 49, respectively (Supplementary Table 6; Wald test, FDR < 0.05). In total, 31 and 38 pathways were enriched after metformin exposure in samples from donors 13 and 49, respectively; of these, 22 enriched pathways were common to both samples (Fig. 5b and Supplementary Table 6; hypergeometric test, FDR < 0.05). Six pathways that were enriched in the metformin-treated samples in the *in vivo* metagenome analysis (see Fig. 4b)—including those for genes involved in LPS synthesis, butyrate and pyruvate metabolism, and two-component systems—were also shown to be enriched by metformin in both gut-simulator experiments (Fig. 5b). In addition, the *in vitro* analysis revealed enrichment of metabolic pathways linked to the metabolism of cofactors and vitamins (Fig. 5b). These results show that although metformin exerts donor-specific taxonomic effects, it induces overlapping microbial functional changes in samples from both donors.

Finally, we performed in-depth transcriptome analyses (using the *in vitro* cultured fecal sample from donor 13) to investigate direct interactions between metformin and individual bacterial species. We first examined the RNA reads that mapped to the gene catalog of *A. muciniphila* (the taxon with the overall highest abundance in this fecal sample; Fig. 5a). We found that nearly 10% (207/2138) of the protein-coding genes in *A. muciniphila* were significantly regulated by metformin; of these, 65% were downregulated by metformin (Supplementary Table 7; FDR < 0.1). Furthermore, 78 of the 207 metformin-regulated genes could be annotated to KOs, and of these, 41 genes mapped to the 22 metformin-enriched pathways common to cultured fecal samples from both donors (Fig. 5c and Supplementary Table 7). By manual annotation, we found that the protein products of 108/207 metformin-regulated genes required cofactors or coenzymes such as ATP, FAD, FMN, metal, NAD, and vitamin B6 (Fig. 5c and Supplementary Table 7); most of the remaining genes (63/99) have not been characterized (Supplementary Table 7). Of particular interest, 81 of the 108 metformin-regulated annotated genes encoded metalloprotein or metal transporters (Fig. 5c and Supplementary Table 7). Gene ontology (GO) analysis of metformin-regulated genes in *A. muciniphila* confirmed that their gene products were enriched in proteins that bind to metal ions in addition to several other cofactors and coenzymes, as well as transferase, hydrolase, ligase, and protein components of ribosomes (Fig. 5d). To address whether those observations were specific to *A. muciniphila*, we also analyzed *B. wadsworthia* (the second most abundant taxon in this cultured fecal sample after metformin treatment; Fig. 5a). According to protein-homology detection, only 14 metformin-regulated genes were orthologous between these two bacteria; however, most annotated metformin-regulated genes in *B. wadsworthia* also encoded metalloproteins (Supplementary Table 7).

DISCUSSION

In this study, we performed a randomized, placebo-controlled, double-blind study in individuals with newly diagnosed T2D on a calorie-restricted diet and showed that metformin, but not calorie restriction, had rapid effects on the composition and function of the gut microbiota in parallel with the reduction of %HbA1c and fasting blood glucose concentrations. Transfer of the microbiota to germ-free mice showed that the metformin-altered microbiota could improve glucose metabolism. Furthermore, transcriptome analyses of feces cultured with metformin *in vitro* in a gut simulator showed that metformin had direct effects on the microbiota and regulated the expression of genes encoding metalloproteins in the gut bacteria.

By using paired samples in our prospective human study, we reduced the effect of interindividual variations, a common issue in previous studies investigating the effect of metformin on the microbiota^{16,17,31}. A further strength of our cohort is that these individuals had been newly diagnosed with T2D and thus were not taking other medications for T2D, and only a small number in each group were taking statins or antihypertensive therapy. We also monitored the dietary intake of the participants before and 4 months after treatment and showed that calorie restriction did not affect the gut microbiome to any great extent in our study; it should be noted that the calorie reduction reported was mild relative to that in earlier studies showing profound changes in the gut microbiome in response to dietary intervention^{22,32}. The design of our study thus enabled us to minimize the effect of major confounding factors known to have an impact on the gut microbiome.

By performing whole-genome shotgun sequencing of fecal samples, we observed dramatic shifts in the composition of the gut microbiota after

2 and 4 months on metformin in individuals with newly diagnosed T2D. Notably, these changes were similar to those observed after 6 months on metformin in a placebo subgroup that switched to metformin 6 months after the study start. In particular, we observed significant changes in *Escherichia* and *Intestinibacter* abundance across all sampling points in the metformin-treated group, a finding that is in agreement with results reported in a cross-sectional study that compared metformin-treated and untreated groups of people with T2D¹⁷. Growth of *E. coli* in an *in vitro* analysis was not affected by metformin. Thus, the effects of metformin on the abundance of *Escherichia* spp. are likely indirect, and possibly, a result of modified bacteria–bacteria interactions or of other physiological and/or environmental changes within the gut upon metformin treatment. We showed that metformin promoted the growth of *B. adolescentis* both *in vivo* (after 2 months in the main study and after 6 months in the switched subgroup, as measured by PTR) and *in vitro* using pure cultures, and also that it increased the abundance of *Bifidobacterium* in the switched subgroup. Supplementation with *B. adolescentis* in a rodent model of the metabolic syndrome has previously been shown to increase insulin sensitivity³³. In our cohort, we also observed a negative correlation between the PTR of *B. adolescentis* and %HbA1c, which suggests that increased growth of this bacterial species could potentially contribute to the antidiabetic effect of metformin.

To observe direct metformin–microbiota interactions, we incubated fecal samples from treatment-naïve participants with metformin in a gut simulator. In this system, we did not observe any significant changes in *E. coli* or *B. adolescentis*. In fact, the only taxon that increased in response to metformin (at both DNA and RNA levels and in samples from two separate donors) was *A. muciniphila*. Metformin has previously been shown to increase the abundance of *A. muciniphila* in rodents on a high-fat diet^{13–15}, and this increased abundance has been linked to improved glucose metabolism^{13,20,21}. However, evidence for a link between metformin and *A. muciniphila* is less clear in humans^{16,17}. We did observe a significant increase in the abundance of *A. muciniphila* over time in the individuals who received metformin for 4 months, but only when we used a targeted analysis. Similarly, a recent study that screened mucin-degrading and butyrate-producing bacteria showed increased abundance of *A. muciniphila* in humans taking metformin¹⁸. In agreement with these observations, we showed that metformin increased the growth of *A. muciniphila* *in vitro* using pure cultures. However, it is likely that the growth of this taxon is affected in humans *in vivo* by factors that differ between individuals, such as fiber³⁴ and polyphenol availability^{35,36}, immune responses^{37,38}, and age^{39,40}. Furthermore, in our study, we did not observe any significant correlations between %HbA1c and *A. muciniphila* abundance, and therefore, cannot conclude that *A. muciniphila* is a major contributor to the beneficial effects of metformin in our human cohort.

By comparing results from the *in vivo* metagenomics analysis and the *in vitro* metagenomics and metatranscriptomics analyses, we noted that metformin promoted consistent shifts in microbial functions, including LPS biosynthesis and SCFA metabolism. Increased LPS biosynthesis might reflect the increased abundance of Gram-negative bacteria such as Proteobacteria, but it was not associated with increased systemic inflammation, because C-reactive protein was unaltered (Table 1). Similarly, enrichment of the LPS biosynthesis pathway without an increase in inflammation has been observed both in humans after bariatric surgery⁴¹ and in prebiotic-treated mice on a high-fat diet⁴². Increased SCFA metabolism in response to metformin has also been predicted in earlier metagenomics

analyses in humans^{17,18}, and in agreement, our targeted metabolomics analysis showed that metformin significantly increased butyrate and propionate in men.

In-depth transcriptome analysis of the effects of metformin on two distantly related bacterial species in the gut simulator showed that most of the metformin-regulated genes encoded metalloproteins or metal transporters. It is unlikely that the transcriptional responses of this subset of genes were due to a growth-induced increase in total transcripts because the majority of these genes were downregulated by metformin. Interestingly, some metals are known to contribute to T2D pathophysiology⁴³, and it has been known for many years that metformin binds to metals⁴⁴. Furthermore, a recent study showed that the effects of metformin on a mammalian liver cell line are dependent on the metal-binding properties of this drug⁴⁴. However, our study, to the best of our knowledge, is among the first to indicate a link between metformin and metal-binding proteins produced by the gut microbiota.

Fecal transfer to germ-free mice resulted in improved glucose tolerance in recipients of metformin-altered microbiota from two out of three donors, with overall substantial improvement of glucose metabolism, thus indicating that metformin-adapted microbiota could contribute to the beneficial effects of metformin on glucose homeostasis. It is not clear why the responses to the metformin-altered microbiota differed between the donors, given that all the donors showed improved glucose tolerance after both 2 and 4 months of metformin treatment. However, there are large interindividual differences in gut-microbiota composition in humans, and the lack of response of microbiota from one donor might be attributable to an incomplete transfer of key species, as has previously been described⁴⁵. Furthermore, the different diets of the recipient mice and the human donors (i.e., high fat as opposed to calorie restriction) would likely exacerbate differences in the gut-microbiota composition between the donors and recipients. The taxa that are successfully transferred to recipient mice will therefore be dependent not only on the composition of the donor gut microbiota, but also on how well the taxa respond to different macronutrients.

There is increasing evidence to indicate that SCFAs and bile acids have a role in the regulation of glucose homeostasis^{26,27,46,47}, and we recently reported that microbiota-produced succinate could improve glucose metabolism by activating intestinal gluconeogenesis in mice⁴⁸. Here we observed metformin-induced alterations in these microbially regulated metabolites, which suggests that they might be partly responsible for the stronger glucose-lowering effect that has been observed when metformin is administered orally as compared with intravenous injection¹¹. It should be noted that we cannot conclude that the major mechanism of action of metformin is through the microbiota. For example, a recent study in mice showed that the phosphorylation of acetyl-CoA carboxylases (ACC) 1 and 2 by AMPK is required to observe the insulin-sensitizing effects of metformin⁵, demonstrating the importance of AMPK/ACC signaling. However, it is possible that the gut microbiota might also act through ACCs, given that we previously showed that diet-induced obesity involved cross-talk between the microbiota, AMPK, and downstream ACC2 phosphorylation⁴⁹.

In summary, our work shows that metformin interacts with different gut bacteria, possibly through the regulation of metal homeostasis. However, additional studies combining untargeted metabolomics and metaproteomics are essential to identify further microbial metabolites or proteins and to determine how they interact with the host targets in improving host metabolism.

METHODS

Methods, including statements of data availability and any associated accession codes and references, are available in the [online version of the paper](#).

Note: Any Supplementary Information and Source Data files are available in the online version of the paper.

ACKNOWLEDGMENTS

We thank C. Arvidsson, S. Nordin-Larsson, C. Wennberg, and U. Enqvist for superb mouse husbandry. The administrative and technical help of J.M. Moreno Navarrete, E. Huertos, M. Sabater, and O. Rovira is also acknowledged. The strain *Akkermansia muciniphila* DSM22959 was kindly provided by W. de Vos (Wageningen University and Helsinki University). The strain *Bifidobacterium adolescentis* L2-32 was kindly provided by K. Scott (The Rowett Institute of Nutrition and Health, University of Aberdeen). Whole-genome shotgun sequencing was performed at the Genomics Core Facility at the Sahlgrenska Academy, University of Gothenburg. The computations for metagenomics analyses were performed on resources provided by the Swedish National Infrastructure for Computing (SNIC) through Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX). This study was supported by the Swedish Diabetes Foundation; Swedish Research Council; Swedish Heart Lung Foundation; Torsten Söderberg's Foundation; Göran Gustafsson's Foundation; Inga Britt and Arne Lundberg's Foundation; Swedish Foundation for Strategic Research; Knut and Alice Wallenberg Foundation; the Novo Nordisk Foundation; the regional agreement on medical training and clinical research (ALF) between Region Västra Götaland and Sahlgrenska University Hospital; the Ministerio de Economía y Competitividad (PI11-00214 and PI15/01934); and FEDER funds. CIBEROBN Fisiopatología de la Obesidad y Nutrición is an initiative from the Instituto de Salud Carlos III from Spain. M.P.-F. is funded by the Obra Social Fundación la Caixa fellowship under the Severo Ochoa 2013 program. J.M.M. was supported by the Sara Borrell Fellowship from the Instituto Carlos III, EFSO/Lilly Research Fellowship and Beatriz de Pinós Fellowship from the Agency for Management of University and Research Grants (AGAUR). E.B. is a recipient of ERC Consolidator Grant (European Research Council, Consolidator grant 615362—METABASE).

AUTHOR CONTRIBUTIONS

E.B., J.M.F.-R., V.T., and R.B. conceived and designed the study. E.E., M.P.-F., G.X., J.M.M., D.T., W.R., and J.M.F.-R. recruited cohort individuals and performed the clinical study. H.W., V.T., and E.B. conducted the bioinformatics study, analyzed all results unless otherwise indicated. H.W., V.T., R.P., and E.B. wrote the paper. M.T.K. performed the *in vitro* gut simulator and bacterial growth experiments. R.C. and L.M.-H. performed and analyzed the fecal microbiota transplantation experiments. M. Ståhlman performed the metabolomics experiments. M. Serino and V.T. extracted the bacterial DNA and discussed the results. L.M.O. and V.T. extracted the bacterial RNA and coordinated the metagenomics and metatranscriptomics sequencing. All authors commented on the manuscript.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

Reprints and permissions information is available online at <http://www.nature.com/reprints/index.html>. Publisher's note: Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

- Nathan, D.M. *et al.* Medical management of hyperglycemia in type 2 diabetes: a consensus algorithm for the initiation and adjustment of therapy: a consensus statement of the American Diabetes Association and the European Association for the Study of Diabetes. *Diabetes Care* **32**, 193–203 (2009).
- Pernicova, I. & Korbonits, M. Metformin—mode of action and clinical implications for diabetes and cancer. *Nat. Rev. Endocrinol.* **10**, 143–156 (2014).
- Zhou, G. *et al.* Role of AMP-activated protein kinase in mechanism of metformin action. *J. Clin. Invest.* **108**, 1167–1174 (2001).
- Shaw, R.J. *et al.* The kinase LKB1 mediates glucose homeostasis in liver and therapeutic effects of metformin. *Science* **310**, 1642–1646 (2005).
- Fullerton, M.D. *et al.* Single phosphorylation sites in Acc1 and Acc2 regulate lipid homeostasis and the insulin-sensitizing effects of metformin. *Nat. Med.* **19**, 1649–1654 (2013).
- Foretz, M. *et al.* Metformin inhibits hepatic gluconeogenesis in mice independently of the LKB1/AMPK pathway via a decrease in hepatic energy state. *J. Clin. Invest.* **120**, 2355–2369 (2010).
- Madiraju, A.K. *et al.* Metformin suppresses gluconeogenesis by inhibiting mitochondrial glycerophosphate dehydrogenase. *Nature* **510**, 542–546 (2014).
- Miller, R.A. *et al.* Biguanides suppress hepatic glucagon signalling by decreasing production of cyclic AMP. *Nature* **494**, 256–260 (2013).

9. McCreight, L.J., Bailey, C.J. & Pearson, E.R. Metformin and the gastrointestinal tract. *Diabetologia* **59**, 426–435 (2016).
10. Duca, F.A. *et al.* Metformin activates a duodenal Ampk-dependent pathway to lower hepatic glucose production in rats. *Nat. Med.* **21**, 506–511 (2015).
11. Stepsky, D., Friedman, M., Raz, I. & Hoffman, A. Pharmacokinetic-pharmacodynamic analysis of the glucose-lowering effect of metformin in diabetic rats reveals first-pass pharmacodynamic effect. *Drug Metab. Dispos.* **30**, 861–868 (2002).
12. Buse, J.B. *et al.* The primary glucose-lowering effect of metformin resides in the gut, not the circulation. Results from short-term pharmacokinetic and 12-week dose-ranging studies. *Diabetes Care* **39**, 198–205 (2016).
13. Shin, N.R. *et al.* An increase in the *Akkermansia* spp. population induced by metformin treatment improves glucose homeostasis in diet-induced obese mice. *Gut* **63**, 727–735 (2014).
14. Zhang, X. *et al.* Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. *Sci. Rep.* **5**, 14405 (2015).
15. Lee, H. & Ko, G. Effect of metformin on metabolic improvement and gut microbiota. *Appl. Environ. Microbiol.* **80**, 5935–5943 (2014).
16. Karlsson, F.H. *et al.* Gut metagenome in European women with normal, impaired and diabetic glucose control. *Nature* **498**, 99–103 (2013).
17. Forslund, K. *et al.* Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature* **528**, 262–266 (2015).
18. de la Cuesta-Zuluaga, J. *et al.* Metformin is associated with higher relative abundance of mucin-degrading *Akkermansia muciniphila* and several short-chain fatty acid-producing microbiota in the gut. *Diabetes Care* **40**, 54–62 (2017).
19. Karlsson, F.H., Nookaew, I. & Nielsen, J. Metagenomic data utilization and analysis (MEDUSA) and construction of a global gut microbial gene catalogue. *PLoS Comput. Biol.* **10**, e1003706 (2014).
20. Everard, A. *et al.* Cross-talk between *Akkermansia muciniphila* and intestinal epithelium controls diet-induced obesity. *Proc. Natl. Acad. Sci. USA* **110**, 9066–9071 (2013).
21. Plovier, H. *et al.* A purified membrane protein from *Akkermansia muciniphila* or the pasteurized bacterium improves metabolism in obese and diabetic mice. *Nat. Med.* **23**, 107–113 (2017).
22. Dao, M.C. *et al.* *Akkermansia muciniphila* and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. *Gut* **65**, 426–436 (2016).
23. Park, S.K., Kim, M.S., Roh, S.W. & Bae, J.W. *Blautia stercoris* sp. nov., isolated from human faeces. *Int. J. Syst. Evol. Microbiol.* **62**, 776–779 (2012).
24. Korem, T. *et al.* Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. *Science* **349**, 1101–1106 (2015).
25. Kanehisa, M. & Goto, S. KEGG: kyoto encyclopedia of genes and genomes. *Nucleic Acids Res.* **28**, 27–30 (2000).
26. Wong, J.M., de Souza, R., Kendall, C.W., Emam, A. & Jenkins, D.J. Colonic health: fermentation and short chain fatty acids. *J. Clin. Gastroenterol.* **40**, 235–243 (2006).
27. Koh, A., De Vadder, F., Kovatcheva-Datchary, P. & Bäckhed, F. From dietary fiber to host physiology: short-chain fatty acids as key bacterial metabolites. *Cell* **165**, 1332–1345 (2016).
28. Ridlon, J.M., Harris, S.C., Bhowmik, S., Kang, D.J. & Hylemon, P.B. Consequences of bile salt biotransformations by intestinal bacteria. *Gut Microbes* **7**, 22–39 (2016).
29. Caspary, W.F. *et al.* Alteration of bile acid metabolism and vitamin-B12-absorption in diabetics on biguanides. *Diabetologia* **13**, 187–193 (1977).
30. Scarpello, J.H., Hodgson, E. & Howlett, H.C. Effect of metformin on bile salt circulation and intestinal motility in type 2 diabetes mellitus. *Diabet. Med.* **15**, 651–656 (1998).
31. Zhernakova, A. *et al.* Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science* **352**, 565–569 (2016).
32. Cotillard, A. *et al.* Dietary intervention impact on gut microbial gene richness. *Nature* **500**, 585–588 (2013).
33. Chen, J., Wang, R., Li, X.F. & Wang, R.L. *Bifidobacterium adolescentis* supplementation ameliorates visceral fat accumulation and insulin sensitivity in an experimental model of the metabolic syndrome. *Br. J. Nutr.* **107**, 1429–1434 (2012).
34. Desai, M.S. *et al.* A dietary fiber-deprived gut microbiota degrades the colonic mucus barrier and enhances pathogen susceptibility. *Cell* **167**, 1339–1353.e21 (2016).
35. Roopchand, D.E. *et al.* Dietary polyphenols promote growth of the gut bacterium *Akkermansia muciniphila* and attenuate high-fat diet-induced metabolic syndrome. *Diabetes* **64**, 2847–2858 (2015).
36. Anhê, F.F. *et al.* A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation in association with increased *Akkermansia* spp. population in the gut microbiota of mice. *Gut* **64**, 872–883 (2015).
37. Greer, R.L. *et al.* *Akkermansia muciniphila* mediates negative effects of IFN γ on glucose metabolism. *Nat. Commun.* **7**, 13329 (2016).
38. Zhang, H., Sparks, J.B., Karyala, S.V., Settlage, R. & Luo, X.M. Host adaptive immunity alters gut microbiota. *ISME J.* **9**, 770–781 (2015).
39. Collado, M.C., Derrien, M., Isolauri, E., de Vos, W.M. & Salminen, S. Intestinal integrity and *Akkermansia muciniphila*, a mucin-degrading member of the intestinal microbiota present in infants, adults, and the elderly. *Appl. Environ. Microbiol.* **73**, 7767–7770 (2007).
40. Kong, F. *et al.* Gut microbiota signatures of longevity. *Curr. Biol.* **26**, R832–R833 (2016).
41. Tremaroli, V. *et al.* Roux-en-Y gastric bypass and vertical banded gastroplasty induce long-term changes on the human gut microbiome contributing to fat mass regulation. *Cell Metab.* **22**, 228–238 (2015).
42. Everard, A. *et al.* Microbiome of prebiotic-treated mice reveals novel targets involved in host response during obesity. *ISME J.* **8**, 2116–2130 (2014).
43. Fernández-Real, J.M. & Manco, M. Effects of iron overload on chronic metabolic diseases. *Lancet Diabetes Endocrinol.* **2**, 513–526 (2014).
44. Logie, L. *et al.* Cellular responses to the metal-binding properties of metformin. *Diabetes* **61**, 1423–1433 (2012).
45. Wahlström, A. *et al.* Induction of farnesoid X receptor signaling in germ-free mice colonized with a human microbiota. *J. Lipid Res.* **58**, 412–419 (2017).
46. Wahlström, A., Sayin, S.I., Marschall, H.U. & Bäckhed, F. Intestinal crosstalk between bile acids and microbiota and its impact on host metabolism. *Cell Metab.* **24**, 41–50 (2016).
47. Schaap, F.G., Trauner, M. & Jansen, P.L. Bile acid receptors as targets for drug development. *Nat. Rev. Gastroenterol. Hepatol.* **11**, 55–67 (2014).
48. De Vadder, F. *et al.* Microbiota-produced succinate improves glucose homeostasis via intestinal gluconeogenesis. *Cell Metab.* **24**, 151–157 (2016).
49. Bäckhed, F., Manchester, J.K., Semenkovich, C.F. & Gordon, J.I. Mechanisms underlying the resistance to diet-induced obesity in germ-free mice. *Proc. Natl. Acad. Sci. USA* **104**, 979–984 (2007).

ONLINE METHODS

Clinical study design. 40 individuals with T2D were recruited and randomized (using a computational random generator Aleator) to treatment with metformin ($n = 22$) or placebo ($n = 18$) for 4 months. Metformin (Acyfabrik, Madrid, Spain) was started at a dose of 425 mg/d and increased progressively during the first week to reach 1,700 mg/d (in three doses). We instructed both groups to maintain a reduction in daily caloric intake of 500 kcal during the entire treatment. We recommended a hypocaloric diet containing 25 kcal/kg or 20 kcal/kg and used a validated food-frequency questionnaire⁵⁰. The composition of the diet was 15% protein, 30% fat (<10% saturated fat), 55% carbohydrates, and 20–25 g dietary fiber (**Supplementary Table 1**). Lifestyle changes were also suggested, including regular physical activity (150 min/week). We collected both fecal and plasma samples at baseline and at 2 and 4 months after treatment. A subgroup of those on placebo switched to metformin treatment after 6 months of dietary intervention (850 or 1,700 mg/d, $n = 13$); we obtained fecal and plasma samples from these individuals after a further 6 months. People in this group were not randomly selected, but had agreed to be treated with metformin. Compliance and side effects were monitored at each visit.

Inclusion criteria were: (i) aged between 18 and 65 years; (ii) T2D diagnosis in the previous 6 months, as defined by the American Diabetes Association Criteria⁵¹; (iii) absence of systemic and metabolic disease other than T2D, and absence of infection within the previous month; (iv) absence of diet or medication that might interfere with glucose homeostasis, such as glucocorticoids or antibiotics in the previous 3 months; and (v) HbA1c lower than 9%.

Exclusion criteria were: (i) clinically significant major systemic disease, including malignancy; (ii) clinical evidence of hemoglobinopathies or anemia; (iii) history of drug or alcohol abuse, defined as >80 g/d in men and >40 g/d in women; (iv) acute major cardiovascular event in the previous 6 months; (v) acute illnesses or current evidence of acute or chronic inflammatory or infective disease; and (vi) mental illness rendering the participants unable to understand the nature, scope, and possible consequences of the study.

All individuals gave written informed consent. The experimental protocol was approved by the Ethics Committee and the Committee for Clinical Investigation of the Hospital Universitari Dr. Josep Trueta (Girona, Spain). We certify that all applicable institutional regulations concerning the ethical use of information and samples from human volunteers were followed during this research. Complete clinical trial registration is deposited in the EU clinical trials register (EudraCT number 2010-022394-34).

Extraction of fecal genomic DNA and whole-genome shotgun sequencing.

Fecal genomic DNA was extracted from 100 mg of frozen stools using the QIAamp DNA mini stool kit (Qiagen, Courtaboeuf, France) following repeated bead-beating (6,500 r.p.m., 3×30 s). The DNA was extracted from 131 fecal samples, obtained from the participants at three different time points during the study ($n = 118$; two fecal samples were not obtained) and from 13 participants additionally sampled 6 months after switch to metformin treatment. DNA fragments of approximately 300 bp were sequenced on an Illumina NextSeq 500 instrument (150 bp; paired-end) at Genomics Core Facility at the Sahlgrenska Academy, University of Gothenburg.

Metagenomics analyses. We obtained a total of 941 Gb of raw paired-end reads. The taxonomic and KO composition was obtained by using an updated version of the MEDUSA pipeline¹⁹, in which the raw reads were trimmed by FASTX (http://hannonlab.cshl.edu/fastx_toolkit/; with a quality threshold of 20 bp and minimum length of 35 bp), filtered to remove human reads (version hg19), and then mapped to bacterial gene and genome catalogs using Bowtie2 (ref. 52). An additional filter was applied during the mapping process containing reads with at least 95% identity to obtain high-quality reads. The mean mapping rates for the genome and gene catalogs were 36.6% and 64.6%, respectively (**Supplementary Table 2**). The obtained taxonomic composition and KO profile matrix were further analyzed by DESeq2 package⁵³. Pathway-enrichment analyses are based on KEGG annotation²⁵ and hypergeometric test using goseq⁵⁴. The beta diversity and PCoA analysis were calculated on the basis of the relative abundance of all significant KOs (further transformed by the square root to reduce the influence of dominant KOs, as suggested previously⁵⁵) using phyloseq (version 1.12.2)⁵⁶. Genus-to-genus

coabundance network analysis was based on Spearman correlation. Only genera present in at least 80% of samples were used for correlation analysis, and only connections with a rho value larger than 0.6 or smaller than -0.6 were used for network building and visualization, on the basis of igraph⁵⁷. For the estimation of PTRs, metagenomic reads were mapped to a local genome database containing ~200 common human bacterial strains, using the software PTRC²⁴. For the analysis of bile salt hydrolase (*bsh*) genes, a local gene database containing all available *bsh* genes was constructed by blasting⁵⁸ against NCBI reference genes⁵⁹, MEDUSA gene catalog¹⁹, and the integrated gene catalog for human microbiome (IGC)⁶⁰ using 16 randomly selected seed *bsh* genes (gi: 169212173, 47121626, 488267184, 489835719, 491501450, 491807128, 499725619, 503743756, 524844235, 558633790, 654788256, 753801014, 759977951, 814507153, 823277295 and 933135484). The local *bsh* gene database was then used for targeted reads screening on the basis of the MEDUSA pipeline¹⁹.

Targeted metabolomics analyses. Fecal SCFAs were measured using gas chromatography coupled to mass spectrometry detection (GC-MS), as described previously⁶¹. In brief, approximately 50–250 mg of feces were mixed with internal standards, added to glass vials and freeze-dried. All samples were then acidified with HCl, and SCFAs were extracted with two rounds of diethyl ether extraction. The organic supernatant was collected, the derivatization agent *N*-tert-butylidimethylsilyl-*N*-methyltrifluoroacetamide (Sigma-Aldrich, Stockholm, Sweden) was added, and samples were incubated overnight. SCFAs were quantified with a 7090A gas chromatograph coupled to a 5975C mass spectrometer (Agilent Technologies 5975C, Santa Clara, CA). SCFA standards were obtained from Sigma-Aldrich (Stockholm, Sweden).

Bile acids were analyzed using ultra-performance liquid chromatography coupled to tandem mass spectrometry (UPLC-MS/MS), as described before⁴¹. Briefly, bile acids from plasma were extracted using protein precipitation with ten volumes of methanol containing internal standards. After mixing and centrifugation, the samples were evaporated and reconstituted in 200 μ l of methanol:water (1:1) for analysis. For feces, about 50 mg of stool samples were placed in a 2-ml polypropylene tube together with six ceramic beads (3 mm; Retsch GmbH, Haan, Germany) and 500 μ l of internal standard containing methanol. Stools were homogenized and centrifuged, and the supernatant was diluted ten times in methanol:water (1:1) before analysis. Bile acids were separated using a Kinetex C18 column (2.1 $\times$ 100 mm with 1.7- μ m particles) (Phenomenex, Torrance, CA, USA) kept at 60 °C. The mobile phases consisted of water with 7.5-mM ammonium acetate and 0.019% formic acid (pH 4.5) as mobile phase A, and acetonitrile with 0.1% formic acid as phase B. A QTRAP 5500 instrument (Sciex, Toronto, Canada) was used for detection using multiple-reaction monitoring in negative mode. Bile acid standards were obtained from Sigma-Aldrich (Stockholm, Sweden), CDN Isotopes (Quebec, Canada), and Toronto Research Chemicals (Downsview, Ontario, Canada).

Animal procedures. Animal procedures were approved by the Gothenburg Animal Ethics Committee. For the fecal-microbiota transplant experiments, we used 10- to 12-week-old male Swiss Webster germ-free mice. Mice were kept in individually ventilated cages (ISOcage N System, Tecniplast, Buguggiate, Italy) with a maximum of five mice per cage. Water was given *ad libitum*. 500 mg of frozen stools obtained at baseline (M0) and 4 months after metformin treatment (M4) from three individuals were suspended in 5 ml of reduced PBS buffer containing 0.2 g/liter Na₂S and 0.5 g/liter cysteine as reducing agents. The three donors were chosen from the metformin arm of the randomized clinical study who showed a reduction in %HbA1c after 2 and 4 months of metformin treatment, and the individual stool samples were not pooled. The germ-free mice were randomized into two groups and colonized by oral gavage with 200 μ l of M0/M4 fecal slurry from each donor. The mice were fed an irradiated high-fat diet (40% kcal fat, TD09683, Harlan Teklad) for 1 week before and during the 18 d of colonization. Body composition was determined with an EchoMRI instrument (EchoMRI) 1 d after colonization and at the end of the experiment. Insulin was measured with a kit from Crystal Chem (Downers Grove, IL) according to the manufacturer's protocol, and an intraperitoneal glucose-tolerance test was performed at the end of the experiment, as previously described⁶². The investigators were not blinded to the group allocation. No mice were excluded from this study.

In vitro bacterial growth experiments. Precultures of *B. adolescentis* L2-32 and *E. coli* were inoculated anaerobically in a Coy chamber (5% hydrogen, 10% carbon dioxide, and 85% nitrogen) as single colonies in 7 ml of brain-heart infusion (BHI) medium containing (in g/liter) yeast extract (5), cellobiose (1), maltose (1), cysteine (0.5), and hemin (0.01). For *A. muciniphila*, modified BHI broth was used, into which cysteine (0.05%) and type II mucin (1%) were added. Before inoculation, the modified medium was filtered through a 0.22- μ m filter. After incubation for 14 h, each preculture was inoculated in freshly prepared BHI broth or modified BHI broth with or without metformin in a 24-well plate or 96-well microplate at a concentration (v/v) of 0.5% *E. coli* or 1% *B. adolescentis* in a volume of 2.5 ml and 2% *A. muciniphila* in a volume of 300 μ l. The effect of metformin on bacterial-growth kinetics was analyzed in a CLARIOstar microplate reader equipped with atmospheric control unit (BMG Labtech) by following the optical density (OD₆₀₀). The atmospheric oxygen concentration was reduced to 0.1% and was maintained with nitrogen as ground gas. The growth-curve data over 10 h for *E. coli* and *B. adolescentis* and 30 h for *A. muciniphila* were analyzed using MARS data-analysis software (BMG Labtech.).

In vitro gut simulator. A simulated human intestinal redox model (SHRIM) was used to explore the effect of metformin on a stabilized gut microbial community *in vitro*. SHRIM is a two-chamber fermenter with an anaerobic luminal chamber (250 ml) and an oxygen feeder (100 ml), which are separated by a Nafion Membrane N115 (DuPont, USA; diameter 2.5 cm) and continuously purged with nitrogen and oxygen, respectively. The luminal chamber was continuously stirred at 250 r.p.m. and kept at 37 °C. The oxygen feeder contained 100-mM potassium phosphate buffer. The luminal chamber was seeded with 250 ml of feed containing: (in g/liter) arabinogalactan (1.0), pectin (2.0), xylose (1.5), starch (3.0), glucose (0.4), yeast extract (3.0), peptone (1.0), mucin type II (4.0), and cysteine (0.5). To simulate digestion processes, the feed was acidified to around pH 2 with 6-M HCl, and neutralized with simulated pancreatic juice to a pH of around 6.9. The simulated pancreatic juice contained: (in g/liter) NaHCO₃ (12.5), Oxgall bile salts (6.0), and pancreatin (0.9). The feed and pancreatic juice mix (70:30), referred to as SHRIM feed, was kept anaerobic by continuously purging with nitrogen⁶³. The SHRIM feed was fed continuously to the luminal chamber at a rate giving a retention time of around 24 h, and pH was maintained between 6.9 and 6.6 with pH controller and dosing Pump (Black stone BL7912, Hanna Instruments, UK).

The SHRIM system was inoculated with an aliquot of the M0 fecal sample from each donor individually. A preculture was prepared anaerobically in a Coy chamber (5% hydrogen, 10% carbon dioxide, and 85% nitrogen) by adding 2% fecal material to 5 ml of BHI broth as described above. The preculture was incubated for 3 h at 37 °C, and 2% of the pre-culture was seeded into the luminal compartment of the SHRIM.

Analysis of metagenome and metatranscriptome of the microbial community in the *in vitro* gut simulator. After 1 week of stabilization, the microbial community was challenged with 10-mM metformin continuously, and samples (2 × 1 ml) were taken at baseline (time zero) and then daily for 1 week. After centrifugation at 16,000 r.p.m. for 2 min at 4 °C, the cellular pellet was suspended in 1 ml of Tris-EDTA buffer (10-mM Tris, 1-mM EDTA pH 7.5), and 500- μ l aliquots were used for DNA and RNA extractions. Total DNA was extracted by repeated bead-beating, as previously described⁶⁴. Total RNA was extracted according to the Macaloid isolation protocol using the Phase Lock Gel Heavy tubes (5 Prime GmbH) and the RNeasy mini kit with on-column DNaseI treatment (Qiagen) for purification, as previously described^{65,66}.

Whole-genome shotgun sequencing was performed both on isolated DNA and RNA from the gut simulator at baseline and after 1 d and 7 d of metformin treatment on Illumina NextSeq 500 instrument at Genomics Core Facility at the Sahlgrenska Academy, University of Gothenburg. An average of 21.6 million paired-end 150-bp DNA reads and 35.2 million paired-end 75-bp RNA reads from both donors were generated for metagenome and metatranscriptome analysis, respectively. Libraries for metagenome sequencing were prepared as mentioned above. Libraries for metatranscriptome sequencing were prepared from rRNA-depleted total RNA using the TruSeq Stranded Total RNA Library Preparation kit (Illumina). rRNA was depleted using the Ribo-Zero rRNA Removal Kit for Gram-positive and Gram-negative bacteria (Illumina).

Then the MEDUSA pipeline¹⁹ was used to obtain the taxonomical composition and functional KO profiles, as described for the metagenomics analysis. In addition, to analyze the gene expression profile of *A. muciniphila* and *B. wadsworthia*, a local gene database containing only genes from those two bacteria was downloaded from NCBI (accession number NC_010655.1 and NZ_ADGP00000000.2, respectively). The circos plot was produced using R package circlize⁶⁷. GO enrichment was performed using R package STRINGdb (version 1.10.0)⁶⁸.

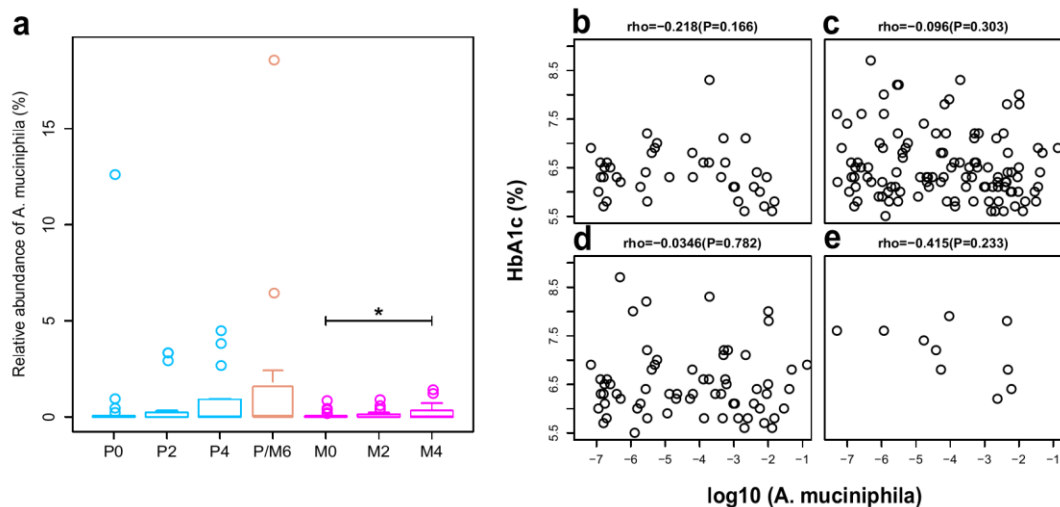
Statistical analysis. All statistical analyses were performed in the R environment⁶⁹. A power of 97% was obtained using pwr package⁷⁰ for this study, on the basis of 22 individuals, with paired design, 5% significance, and an estimated effect size of 0.87 for metformin in improving fasting blood glucose⁷¹. Because the primary aim of our randomized controlled study was to investigate the effect of metformin on the composition and function of the gut microbiota, we did not perform a power calculation for the placebo relative to metformin groups, because the effect size of metformin together with a calorie-restricted diet on the microbiota was previously unknown. For animal tests, sample size was chosen on the basis of our earlier experience and no statistical test was used to predetermine sample size.

Wald test with paired design implemented in DESeq2 (ref. 53) was used for differential abundance analyses for all count data (in the case of both metagenomics and metatranscriptomics). The Spearman's rank-order correlation was used to determine the strength and direction of the monotonic relationships between two variables unless strong collinearity was observed, in which case the Pearson product-moment correlation was calculated. Multivariate analysis with the Adonis test was performed on the basis of 5,000 permutations, using vegan⁷². Statistical testing for bacterial growth rates was examined by two-way ANOVA with repeated measures based on six technical replicates. Changes in SCFA concentrations between the metformin and placebo groups were compared by linear regression adjusted for BMI, gender, and fiber intake; the same procedure was used for bile acids, except the data were adjusted for total calorie intake instead of fiber intake. Otherwise, two-tailed Wilcoxon rank-sum tests or Wilcoxon signed-rank tests were used throughout the study, depending on whether the samples were paired. Raw *P* values were adjusted by the Benjamini-Hochberg method⁷³ with a false discovery rate of 5%, unless indicated otherwise.

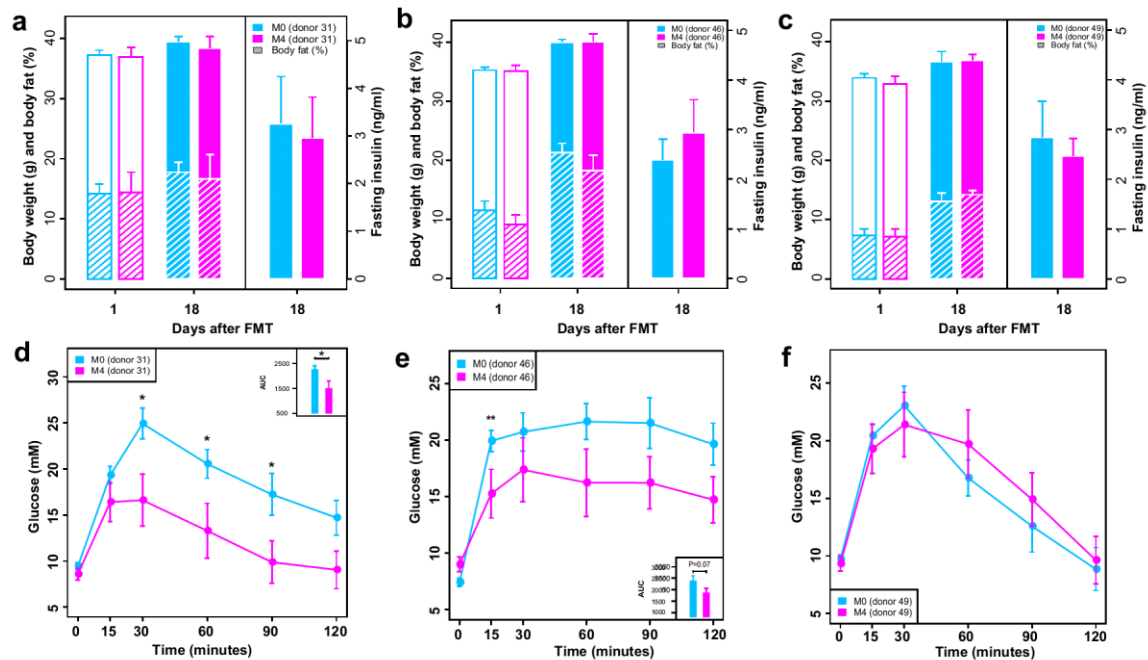
Data availability. Sequence data are available for download from the Sequence Read Archive with accession number [PRJNA361402](https://www.ncbi.nlm.nih.gov/sra/PRJNA361402).

50. Vioque, J. *et al.* Reproducibility and validity of a food frequency questionnaire among pregnant women in a Mediterranean area. *Nutr. J.* **12**, 26 (2013).
51. American Diabetes Association. Diagnosis and classification of diabetes mellitus. *Diabetes Care* **33** (Suppl. 1), S62–S69 (2010).
52. Langmead, B. & Salzberg, S.L. Fast gapped-read alignment with Bowtie 2. *Nat. Methods* **9**, 357–359 (2012).
53. Love, M.I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol.* **15**, 550 (2014).
54. Young, M.D., Wakefield, M.J., Smyth, G.K. & Oshlack, A. Gene ontology analysis for RNA-seq: accounting for selection bias. *Genome Biol.* **11**, R14 (2010).
55. Kindt, R. & Coe, R. *Tree diversity analysis. A manual and software for common statistical methods for ecological and biodiversity studies* (World Agroforestry Centre, Nairobi, Kenya, 2005).
56. McMurdie, P.J. & Holmes, S. phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS One* **8**, e61217 (2013).
57. Csárdi, G. & Nepusz, T. The igraph software package for complex network research. *InterJournal. Complex Syst.* **1695**, 1695 (2006).
58. Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. Basic local alignment search tool. *J. Mol. Biol.* **215**, 403–410 (1990).
59. Tatusova, T., Ciufu, S., Fedorov, B., O'Neill, K. & Tolstoy, I. RefSeq microbial genomes database: new representation and annotation strategy. *Nucleic Acids Res.* **42**, D553–D559 (2014).
60. Li, J. *et al.* An integrated catalog of reference genes in the human gut microbiome. *Nat. Biotechnol.* **32**, 834–841 (2014).
61. Wichmann, A. *et al.* Microbial modulation of energy availability in the colon regulates intestinal transit. *Cell Host Microbe* **14**, 582–590 (2013).
62. Lee, Y.S. *et al.* Insulin-like peptide 5 is a microbially regulated peptide that promotes hepatic glucose production. *Mol. Metab.* **5**, 263–270 (2016).
63. Van den Abbeele, P. *et al.* Microbial community development in a dynamic gut model is reproducible, colon region specific, and selective for *Bacteroidetes* and *Clostridium* cluster IX. *Appl. Environ. Microbiol.* **76**, 5237–5246 (2010).

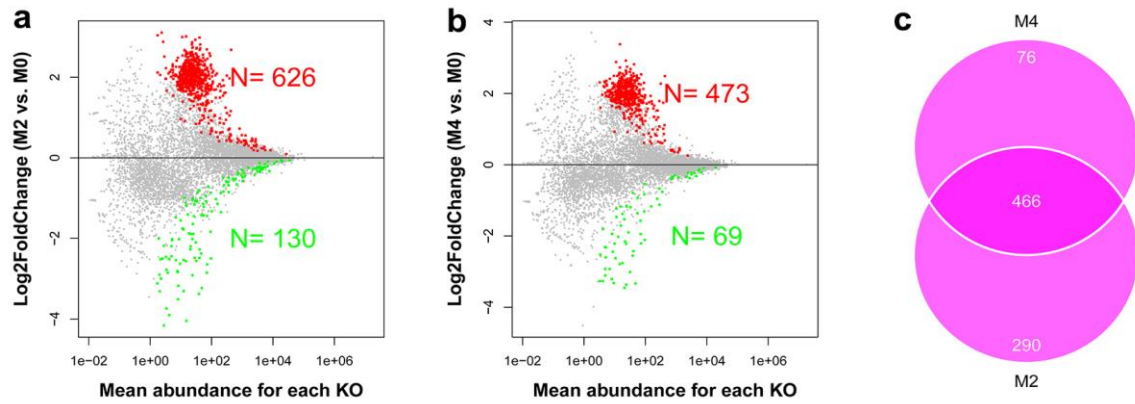
64. Salonen, A. *et al.* Comparative analysis of fecal DNA extraction methods with phylogenetic microarray: effective recovery of bacterial and archaeal DNA using mechanical cell lysis. *J. Microbiol. Methods* **81**, 127–134 (2010).
65. Murphy, N.R. & Hellwig, R.J. Improved nucleic acid organic extraction through use of a unique gel barrier material. *Biotechniques* **21**, 934–936, 938–939 (1996).
66. Zoetendal, E.G. *et al.* Isolation of RNA from bacterial samples of the human gastrointestinal tract. *Nat. Protoc.* **1**, 954–959 (2006).
67. Gu, Z., Gu, L., Eils, R., Schlesner, M. & Brors, B. circlize Implements and enhances circular visualization in R. *Bioinformatics* **30**, 2811–2812 (2014).
68. Franceschini, A. *et al.* STRING v9.1: protein-protein interaction networks, with increased coverage and integration. *Nucleic Acids Res.* **41**, D808–D815 (2013).
69. Team, R.C.R. A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. <http://www.R-project.org/> (2015).
70. Champely, S. pwr: Basic Functions for Power Analysis. R package version 1.1-3. <http://CRAN.R-project.org/package=pwr> (2015).
71. Leucht, S., Helfer, B., Gartlehner, G. & Davis, J.M. How effective are common medications: a perspective based on meta-analyses of major drugs. *BMC Med.* **13**, 253 (2015).
72. Oksanen, J. *et al.* vegan: Community Ecology Package. R package version 2.2-1 <http://CRAN.R-project.org/package=vegan> (2015).
73. Benjamini, Y. & Hochberg, Y. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J. R. Stat. Soc. B* **57**, 289–300 (1995).



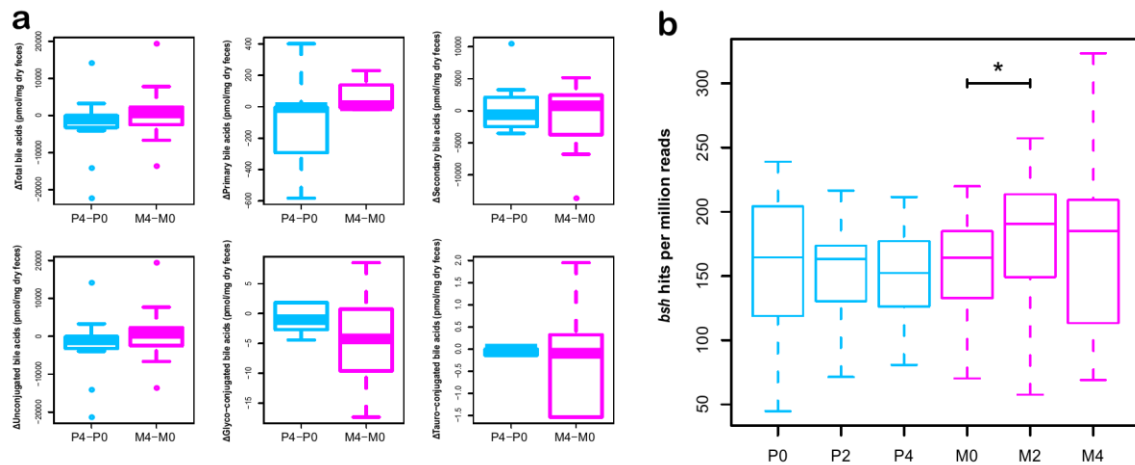
Supplementary Figure 1. Abundance of *A. muciniphila* is increased after metformin treatment but it does not correlate with HbA1c concentration. **(a)** Boxplots (with median) showing abundance of *A. muciniphila* in the gut microbiota of subjects with T2D before (P0 and M0) and after 2 and 4 months of treatment in the groups randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$) and 6 months after metformin in a subgroup that switched from placebo to metformin after the randomized study period (P/M6; $n = 13$). **(b-d)** Spearman correlations between relative abundance of *A. muciniphila* and HbA1c concentration. **(b)** Baseline and 4-month data from metformin recipients in whom HbA1c was reduced after 4 months of metformin. **(c)** Baseline, 2-month and 4-month data from all individuals in our study. **(d)** Baseline and 4-month data from individuals in whom HbA1c was reduced after 4 months of metformin or placebo. **(e)** Baseline and 4-month data from individuals in whom HbA1c was not reduced after 4 months of metformin or placebo.



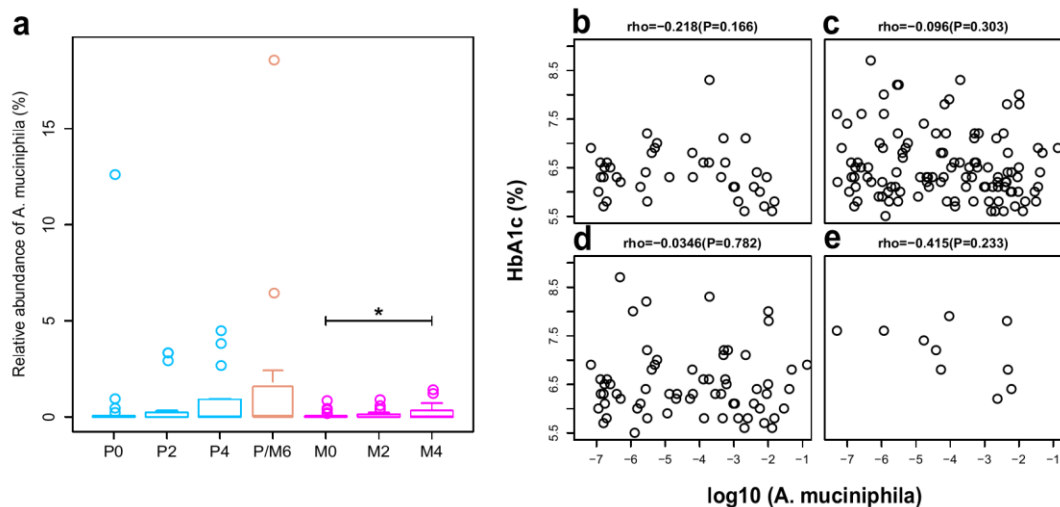
Supplementary Figure 2. Metformin-altered microbiota improves glucose tolerance. (**a-c**) Body weight and body fat of mice 1 and 18 days after colonization and fasting plasma insulin levels 18 days after colonization with fecal microbiota obtained from three individuals with T2D (donors 31, 46 and 49) before (M0) and 4 months after metformin treatment (M4). (**d-f**) Plasma glucose concentrations measured in the same mice used in (**a-c**) during an intraperitoneal glucose tolerance test 18 days after colonization. Data are shown as mean $\pm$ s.e.m. For **a** and **d**, $n = 7$ mice (M0) and $n = 6$ mice (M4). For **b** and **e**, $n = 8$ mice (M0) and $n = 9$ mice (M4). For **c** and **f**, $n = 5$ mice (M0) and $n = 6$ mice (M4). Wilcoxon rank-sum test; * $P < 0.05$; ** $P < 0.01$. FMT, fecal microbiota transplantation.



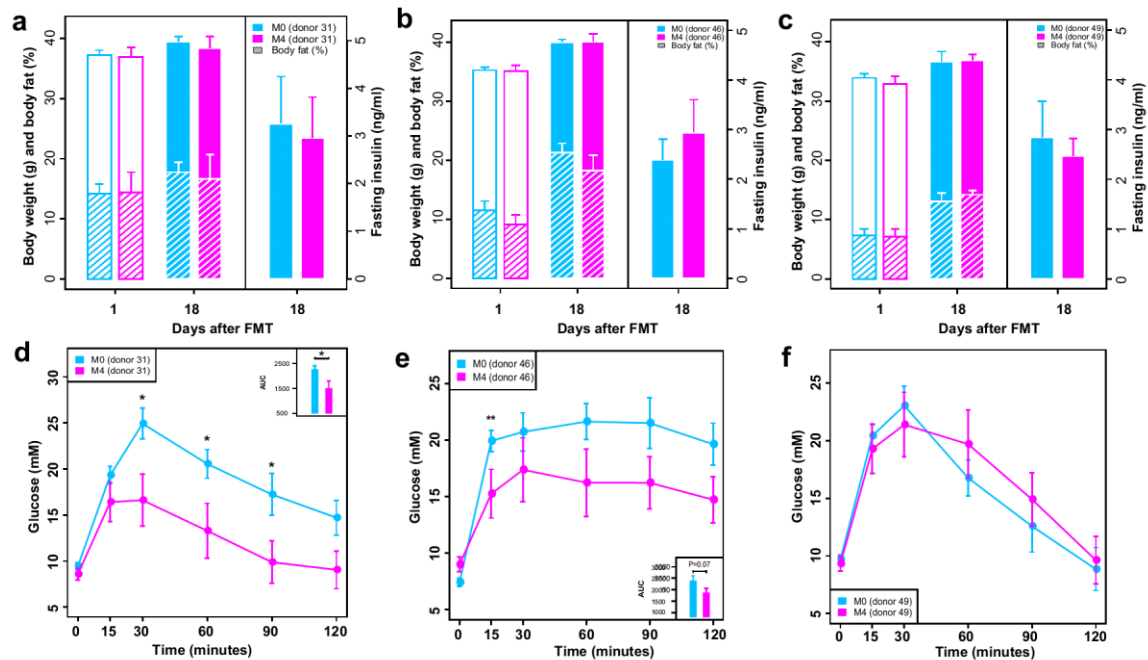
Supplementary Figure 3. KOs that are significantly altered (increased in red, depleted in green) in the gut microbiota of subjects with T2D after metformin treatment for (a) 2 months (M2) and (b) 4 months (M4) compared with baseline (M0) (Wald test; FDR<0.05). (c) Most metformin-regulated KOs overlapped between M2 and M4.



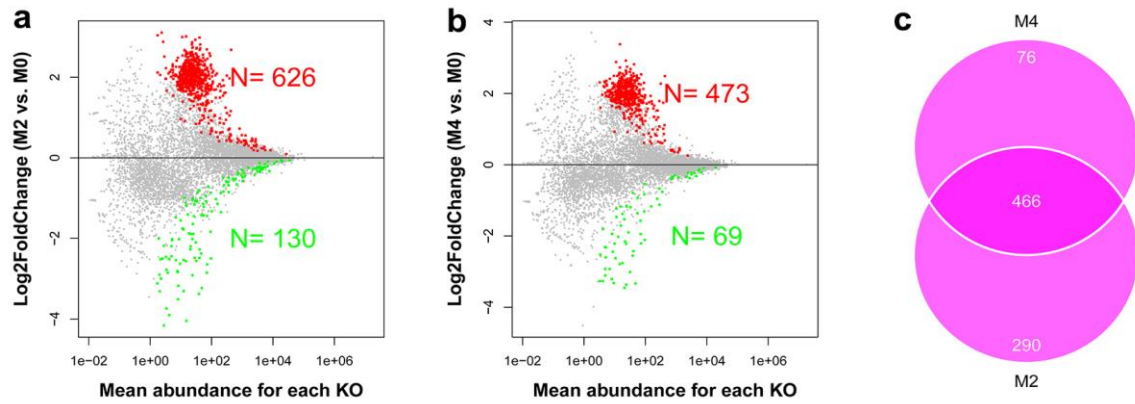
Supplementary Figure 4. Metformin treatment does not affect fecal bile acids but increases the fecal abundance of *bsh* genes. **(a)** Boxplots (with median) showing changes from baseline (P0 and M0) for fecal concentrations of bile acids after 4 months in subjects with T2D randomized to placebo (P4; $n = 18$) or metformin (M4; $n = 22$). Wilcoxon rank-sum test. **(b)** Boxplots (with median) showing abundance of *bsh* genes in gut microbiota of subjects with T2D before treatment (P0 and M0) and after 2 and 4 months in subjects with T2D randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$). Wilcoxon signed-rank test; $*P < 0.05$.



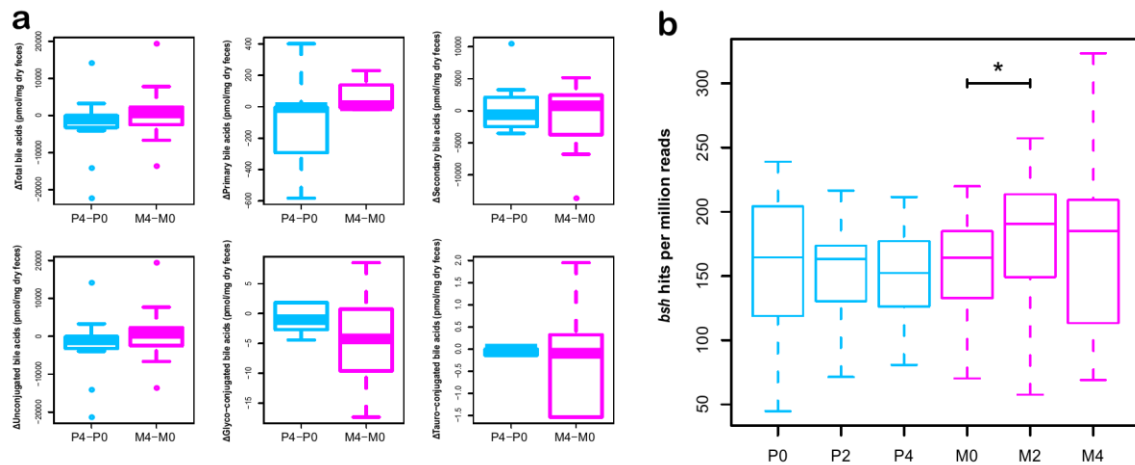
Supplementary Figure 1. Abundance of *A. muciniphila* is increased after metformin treatment but it does not correlate with HbA1c concentration. **(a)** Boxplots (with median) showing abundance of *A. muciniphila* in the gut microbiota of subjects with T2D before (P0 and M0) and after 2 and 4 months of treatment in the groups randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$) and 6 months after metformin in a subgroup that switched from placebo to metformin after the randomized study period (P/M6; $n = 13$). **(b-d)** Spearman correlations between relative abundance of *A. muciniphila* and HbA1c concentration. **(b)** Baseline and 4-month data from metformin recipients in whom HbA1c was reduced after 4 months of metformin. **(c)** Baseline, 2-month and 4-month data from all individuals in our study. **(d)** Baseline and 4-month data from individuals in whom HbA1c was reduced after 4 months of metformin or placebo. **(e)** Baseline and 4-month data from individuals in whom HbA1c was not reduced after 4 months of metformin or placebo.



Supplementary Figure 2. Metformin-altered microbiota improves glucose tolerance. (**a-c**) Body weight and body fat of mice 1 and 18 days after colonization and fasting plasma insulin levels 18 days after colonization with fecal microbiota obtained from three individuals with T2D (donors 31, 46 and 49) before (M0) and 4 months after metformin treatment (M4). (**d-f**) Plasma glucose concentrations measured in the same mice used in (**a-c**) during an intraperitoneal glucose tolerance test 18 days after colonization. Data are shown as mean $\pm$ s.e.m. For **a** and **d**, $n = 7$ mice (M0) and $n = 6$ mice (M4). For **b** and **e**, $n = 8$ mice (M0) and $n = 9$ mice (M4). For **c** and **f**, $n = 5$ mice (M0) and $n = 6$ mice (M4). Wilcoxon rank-sum test; $*P < 0.05$; $**P < 0.01$. FMT, fecal microbiota transplantation.



Supplementary Figure 3. KOs that are significantly altered (increased in red, depleted in green) in the gut microbiota of subjects with T2D after metformin treatment for (a) 2 months (M2) and (b) 4 months (M4) compared with baseline (M0) (Wald test; FDR<0.05). (c) Most metformin-regulated KOs overlapped between M2 and M4.



Supplementary Figure 4. Metformin treatment does not affect fecal bile acids but increases the fecal abundance of *bsh* genes. **(a)** Boxplots (with median) showing changes from baseline (P0 and M0) for fecal concentrations of bile acids after 4 months in subjects with T2D randomized to placebo (P4; $n = 18$) or metformin (M4; $n = 22$). Wilcoxon rank-sum test. **(b)** Boxplots (with median) showing abundance of *bsh* genes in gut microbiota of subjects with T2D before treatment (P0 and M0) and after 2 and 4 months in subjects with T2D randomized to placebo (P2 and P4; $n = 18$) or metformin (M2 and M4; $n = 22$). Wilcoxon signed-rank test; $*P < 0.05$.

Variable	Placebo group			
	Baseline (P0)	2 months (P2)	4 months (P4)	P value (P0 vs. P2)
Total energy (Kcal)	2616.2±183.8	-	2037.5±92	-
Carbohydrates (g)	261.3±22.5	-	204.1±11.5	-
monosaccharides (g)	26.2±3.1	-	20.5±1.9	-
disaccharides (g)	31.6±3.7	-	26.3±2.6	-
simple.carbohydrates (g)	105.6±10.6	-	79±5.8	-
complex.carbohydrates (g)	117.7±12.5	-	90.4±7.5	-
fiber (g)	23.9±2.6	-	19.3±1.1	-
soluble.fiber (g)	15.3±1.7	-	12.6±0.7	-
insoluble.fiber (g)	7.1±0.8	-	6.1±0.3	-
Protein (g)	114.6±8.4	-	95.2±3.9	-
alanine (g)	5.4±0.4	-	4.5±0.2	-
arginine (g)	6.1±0.5	-	5±0.2	-
aspartic.acid (g)	9.9±0.8	-	8.2±0.3	-
cysteine (g)	1.5±0.1	-	1.2±0	-
glutamine (g)	21.4±1.6	-	17.5±0.8	-
glycine (g)	4.7±0.4	-	3.8±0.1	-
histidine (g)	3.1±0.2	-	2.6±0.1	-
isoleucine (g)	5.4±0.4	-	4.4±0.2	-
leucine (g)	8.9±0.7	-	7.4±0.3	-
lysine (g)	8.1±0.6	-	6.8±0.3	-
proline (g)	7.5±0.6	-	6.2±0.3	-
phenylalanine (g)	5±0.4	-	4.2±0.2	-
methionine (g)	2.7±0.2	-	2.2±0.1	-
serine (g)	5.2±0.4	-	4.3±0.2	-
threonine (g)	4.5±0.4	-	3.7±0.1	-
tryptophan (g)	1.3±0.1	-	1.1±0	-
tyrosine (g)	4±0.3	-	3.4±0.2	-
valine (g)	6±0.4	-	5±0.2	-
total.lipids (g)	121.4±9.4	-	91.1±4.6	-
saturated.lipids (g)	34.2±2.7	-	24.7±1.5	-
FA.12.0 (g)	0.7±0.1	-	0.5±0.1	-
FA.14.0 (g)	2.6±0.3	-	1.8±0.2	-
FA.16.0 (g)	19.3±1.5	-	14.2±0.8	-
FA.18.0 (g)	7.5±0.6	-	5.3±0.3	-
FA.20.0 (g)	0.2±0	-	0.1±0	-
FA.22.0 (g)	0±0	-	0±0	-
FA.6.0 (g)	0.3±0	-	0.2±0	-
FA.8.0 (g)	0.2±0	-	0.2±0	-
FA10.0 (g)	0.6±0.1	-	0.4±0.1	-
trans.fatty.acids (g)	0.6±0.1	-	0.5±0	-
monounsaturated.lipids (g)	59.7±5.2	-	45.5±2.9	-
FA.14.1 (g)	0.3±0.1	-	0.1±0	-
FA.16.1 (g)	2.1±0.2	-	1.6±0.1	-
FA.18.1 (g)	56.2±5	-	42.9±2.8	-
FA.20.1 (g)	0.3±0	-	0.3±0	-
FA.22.1 (g)	0.1±0	-	0.1±0	-

polyunsaturated.lipids (g)	18.6±2	-	13.8±1.3	-
FA.18.2 (g)	16.4±2	-	11.9±1.3	-
FA.18.3 (g)	1.3±0.1	-	1±0	-
FA.18.4 (g)	0±0	-	0±0	-
FA.20.4 (g)	0.2±0	-	0.2±0	-
FA.20.5 (g)	0.2±0	-	0.2±0	-
FA.22.5 (g)	0±0	-	0±0	-
FA.22.6 (g)	0.3±0	-	0.4±0	-
omega.3 (g)	1.8±0.1	-	1.6±0.1	-
omega.6 (g)	16.6±2	-	12±1.3	-
cholesterol (mg)	395.6±34	-	305.9±14.9	-
water (gr)	1948.2±175.1	-	1610±92	-
ashes (gr)	30.5±2.3	-	26.2±1.2	-
alcohol (gr)	8.5±2.8	-	7.2±2.4	-
Vitamins	-	-	-	-
vitamin.A (µg)	2449.7±422.3	-	1773.9±314.6	-
vitamin.B1 (mg)	2.2±0.2	-	1.8±0.1	-
vitamin.B12 (µg)	12.2±2.5	-	9.1±1	-
vitamin.B2 (mg)	2.6±0.2	-	2.2±0.1	-
vitamin.B3 (mg)	27.3±1.9	-	22.9±0.9	-
vitamin.B6 (mg)	2.2±0.2	-	1.8±0.1	-
vitamin.C (mg)	174.6±22.8	-	136.2±11.9	-
vitamin.D (µg)	5.9±0.6	-	5.7±0.5	-
vitamin.E (mg)	17.8±1.7	-	13.8±0.9	-
vitamin.K (µg)	234.5±31	-	228.7±25.4	-
folic.acid (µg)	418.2±43.1	-	372±27.5	-
nicotinamide (mg)	26.7±1.9	-	22.2±0.9	-
pantothenic.acid (mg)	6.9±0.6	-	6±0.4	-
provitamin.A.carotenoids (µg)	1886.6±383.8	-	1293.6±221.8	-
retinoic.acid (µg)	557.4±128.1	-	474.5±110.9	-
Other micronutrients	-	-	-	-
iodide (µg)	146.1±16.9	-	130.3±11.1	-
iron (mg)	19±2	-	14.6±0.8	-
magnesium (mg)	388.9±32.7	-	320.8±17.6	-
manganese (mg)	4.2±0.5	-	3.6±0.3	-
molybdenum (µg)	62.2±9.2	-	53.5±4.9	-
phosphate (mg)	1862.4±135.1	-	1651±93.3	-
potassium (mg)	4201.7±402.2	-	3535.2±215.4	-
selenium (µg)	147.5±9.8	-	127.6±5.7	-
sodium (mg)	6296.6±470.6	-	5342.2±231.6	-
zinc (mg)	14.8±1.9	-	11.5±0.6	-
biotin (µg)	37.2±4	-	30.1±2.1	-
boron (mg)	8.3±1.2	-	6.6±1.1	-
cafein (mg)	94.3±20.9	-	90.9±29.7	-
calcium (mg)	1253.9±104.7	-	1100.9±76	-
chloride (mg)	1190.6±140	-	1013.5±93.5	-
chrome (µg)	19.8±3.2	-	19±3.1	-
copper (mg)	2.3±0.3	-	1.7±0.1	-

P value (P0 vs. P4)	Metformin group			
	Baseline (M0)	2 months (M2)	4 months (M4)	P value (M0 vs. M2)
0.009338	3035.8±405.4	-	2223.5±124.9	-
0.039536	303±36.5	-	215.1±16.3	-
0.012863	31±4.4	-	23.7±1.8	-
NS	39.6±7.5	-	28.1±2.6	-
0.005569	138.2±20.4	-	87.6±6.5	-
NS	118.5±12.6	-	94±9.6	-
NS	24±2.6	-	20.1±1.3	-
NS	14.5±1.4	-	12.9±0.9	-
NS	7.3±0.9	-	6.4±0.4	-
NS	128.4±19.9	-	101.7±4.9	-
NS	6.2±1	-	4.9±0.2	-
NS	6.8±1.1	-	5.4±0.2	-
NS	11±1.7	-	8.8±0.4	-
NS	1.6±0.2	-	1.3±0.1	-
NS	23.7±3.3	-	18.6±1	-
NS	5.4±1	-	4.2±0.2	-
NS	3.6±0.6	-	2.8±0.1	-
NS	6±0.9	-	4.8±0.2	-
NS	9.9±1.6	-	7.9±0.4	-
NS	9.2±1.6	-	7.4±0.3	-
NS	8.4±1.2	-	6.4±0.4	-
NS	5.6±0.8	-	4.4±0.2	-
NS	3±0.5	-	2.4±0.1	-
NS	5.7±0.8	-	4.5±0.2	-
NS	5±0.8	-	4±0.2	-
NS	1.4±0.2	-	1.1±0.1	-
NS	4.5±0.7	-	3.5±0.2	-
NS	6.7±1	-	5.3±0.3	-
0.003845	142±23.9	-	104.7±5.3	-
0.005569	43.2±9.7	-	27±1.8	-
NS	0.8±0.2	-	0.4±0.1	-
NS	3.3±0.8	-	1.9±0.2	-
0.004639	24.1±5	-	16±0.9	-
0.00209	10.2±2.6	-	5.8±0.4	-
NS	0.2±0	-	0.2±0	-
NS	0±0	-	0±0	-
NS	0.4±0.1	-	0.2±0	-
NS	0.3±0.1	-	0.2±0	-
NS	0.7±0.2	-	0.4±0.1	-
NS	0.7±0.1	-	0.7±0.1	-
0.023224	67.5±10.1	-	54.8±2.9	-
0.04373	0.3±0.1	-	0.2±0	-
0.020157	2.6±0.6	-	1.8±0.1	-
0.030518	62.9±9	-	51.9±2.8	-
0.009758	0.4±0	-	0.3±0	-
NS	0.1±0	-	0.1±0	-

0.017426	20.8±2.9	-	15.1±1.3	-
0.017426	18.3±2.7	-	12.9±1.3	-
0.012146	1.5±0.2	-	1.2±0.1	-
NS	0±0	-	0±0	-
NS	0.2±0	-	0.2±0	-
NS	0.2±0	-	0.2±0	-
NS	0±0	-	0.1±0	-
NS	0.3±0	-	0.4±0	-
NS	2±0.2	-	1.9±0.1	-
0.017426	18.5±2.7	-	13±1.3	-
0.020157	441.6±67.5	-	322.2±14.2	-
0.017426	2262.8±188.5	-	1885.2±140	-
0.0191	31±2.8	-	25.5±1.2	-
NS	11.1±3.5	-	6.5±2.5	-
-	-	-	-	-
NS	2026±268.4	-	1688±153.6	-
NS	2.5±0.4	-	1.9±0.1	-
NS	12.3±1.9	-	9.5±0.7	-
NS	2.9±0.4	-	2.2±0.1	-
NS	31.4±4.1	-	25.5±1.2	-
NS	2.4±0.3	-	2±0.1	-
0.044769	165.7±24.9	-	146.6±9.7	-
NS	5.9±0.8	-	6±0.4	-
0.009338	17.5±1.8	-	15±1	-
NS	217±19.6	-	252.1±18.2	-
NS	412.3±33.9	-	392.4±25.9	-
NS	30.5±4.1	-	24.7±1.1	-
NS	7.2±0.8	-	6±0.3	-
NS	1359.9±207.5	-	1223.9±111.1	-
NS	659.5±169.5	-	459.7±87.2	-
-	-	-	-	-
NS	138.6±17.5	-	121.1±12.2	-
0.023224	19.3±2.1	-	15.5±1	-
NS	408.5±42.8	-	338±20.4	-
NS	4.3±0.3	-	3.6±0.3	-
NS	52.9±4.6	-	59.3±6.5	-
NS	2087±283.4	-	1626.7±105.4	-
NS	4452.4±536.5	-	3716.4±202.3	-
NS	160.2±17.7	-	133.1±7.2	-
0.030518	6071±557.5	-	5164.5±318.1	-
NS	16.7±2.8	-	12.2±0.6	-
NS	34.5±3.1	-	28.6±1.6	-
NS	7.7±1.4	-	6.1±0.6	-
NS	231.1±46.8	-	187.5±32.1	-
NS	1342.3±167.3	-	1071.6±87.7	-
NS	1170.7±173.8	-	970.1±91.6	-
NS	15.8±1.9	-	17.5±1.3	-
0.027699	2.2±0.2	-	1.7±0.1	-

P value (M0 vs. M4)
0.011473
0.009274
NS
NS
0.005276
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
0.039073
0.030118
0.03345
NS
0.025139
0.014095
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
NS
0.014754

0.04616

0.032894

NS

NS

NS

0.007421

0.004697

0.008926

NS

0.036245

NS

0.025139

NS

NS

-

NS

0.039073

NS

0.03345

NS

NS

NS

NS

NS

NS

NS

NS

NS

NS

NS

-

NS

0.04616

NS

NS

NS

NS

NS

NS

NS

0.032894

0.042498

NS

NS

NS

NS

NS

0.007443

Sample	Treatment	Total_reads(PE)	Total_reads(R1+R2)	AfterQC	AfterFilterHuman
Mean		37849981.0	75699962.1	75667717.8	75553311.4
10V1	P0	22807656.0	45615312.0	45606924.0	45579376.0
10V3	P2	20831491.0	41662982.0	41654271.0	41624206.0
10V5	P4	21050286.0	42100572.0	42091160.0	42069763.0
11V1	M0	29511139.0	59022278.0	59000487.0	58953060.0
11V3	M2	30701692.0	61403384.0	61380394.0	61332547.0
11V5	M4	29119336.0	58238672.0	58217786.0	58179597.0
12V1	M0	29978579.0	59957158.0	59934298.0	59878735.0
12V3	M2	21210561.0	42421122.0	42412324.0	42332211.0
12V5	M4	30110035.0	60220070.0	60201555.0	60160049.0
13V1	M0	19696249.0	39392498.0	39383949.0	39340783.0
13V3	M2	22938452.0	45876904.0	45866824.0	45829097.0
13V5	M4	22968293.0	45936586.0	45927725.0	45896441.0
15V1	M0	23527308.0	47054616.0	47044014.0	47007417.0
15V3	M2	23482154.0	46964308.0	46955101.0	46927508.0
15V5	M4	21613975.0	43227950.0	43218807.0	43202141.0
16V1	M0	17855976.0	35711952.0	35704644.0	35693407.0
16V3	M2	19583143.0	39166286.0	39155223.0	39069613.0
16V5	M4	29153327.0	58306654.0	58285528.0	58244394.0
20V1	P0	30095964.0	60191928.0	60170987.0	60142372.0
20V3	P2	29258756.0	58517512.0	58497204.0	58465804.0
20V5	P4	82173526.0	164347052.0	164271714.0	164190508.0
20V6	P/M6	113569663.0	227139326.0	227001653.0	226874110.0
21V1	M0	30091668.0	60183336.0	60161785.0	60120584.0
21V3	M2	36427506.0	72855012.0	72829015.0	72774305.0
21V5	M4	23482039.0	46964078.0	46954269.0	46923341.0
22V1	M0	23047925.0	46095850.0	46085939.0	46053283.0
22V5	M4	22519364.0	45038728.0	45030755.0	45003417.0
23V1	M0	32287377.0	64574754.0	64559280.0	64496465.0
23V3	M2	21330199.0	42660398.0	42652538.0	42631683.0
23V5	M4	18345770.0	36691540.0	36683239.0	36655131.0
24V1	P0	20012760.0	40025520.0	40017051.0	39928726.0
24V3	P2	29337198.0	58674396.0	58652731.0	58469382.0
25V1	M0	32489590.0	64979180.0	64955854.0	64921533.0
25V3	M2	29481190.0	58962380.0	58939929.0	58892852.0
25V5	M4	21009453.0	42018906.0	42010503.0	41997558.0
26V1	P0	30235085.0	60470170.0	60448345.0	60409325.0
26V3	P2	33131492.0	66262984.0	66238294.0	66189979.0
26V5	P4	84602246.0	169204492.0	169114834.0	168980356.0
26V6	P/M6	116577761.0	233155522.0	233011798.0	232878889.0
27V1	P0	24295597.0	48591194.0	48579461.0	48531576.0
27V3	P2	22490813.0	44981626.0	44971433.0	44932577.0
27V5	P4	82082791.0	164165582.0	164086840.0	164046377.0
27V6	P/M6	113119687.0	226239374.0	226099114.0	225808790.0
29V1	M0	22398637.0	44797274.0	44788400.0	44761169.0
29V3	M2	22513325.0	45026650.0	45017994.0	44988575.0

29V5	M4	17640744.0	35281488.0	35274041.0	35254026.0
2V1	P0	32503278.0	65006556.0	64977726.0	64855659.0
2V3	P2	30722929.0	61445858.0	61420098.0	61340476.0
2V5	P4	37130262.0	74260524.0	74213974.0	74141563.0
2V6	P/M6	103423339.0	206846678.0	206717379.0	206563536.0
30V1	P0	15328591.0	30657182.0	30651143.0	30642257.0
30V3	P2	21149830.0	42299660.0	42290556.0	42136787.0
30V5	P4	28990239.0	57980478.0	57959270.0	57925674.0
30V6	P/M6	106046830.0	212093660.0	211958464.0	211713084.0
31V1	M0	33227759.0	66455518.0	66430701.0	66361001.0
31V3	M2	31933123.0	63866246.0	63838373.0	63718593.0
31V5	M4	32580200.0	65160400.0	65135343.0	65074353.0
32V1	M0	33779660.0	67559320.0	67533662.0	67434603.0
32V3	M2	23683993.0	47367986.0	47356596.0	47311324.0
32V5	M4	22671820.0	45343640.0	45333567.0	45284133.0
33V1	P0	20039574.0	40079148.0	40071293.0	40060492.0
33V3	P2	24044657.0	48089314.0	48079004.0	48015251.0
33V5	P4	79195488.0	158390976.0	158318874.0	158273414.0
33V6	P/M6	112996992.0	225993984.0	225849465.0	225626630.0
34V1	M0	23620668.0	47241336.0	47231561.0	47199129.0
34V3	M2	21233281.0	42466562.0	42457149.0	42418113.0
34V5	M4	22122455.0	44244910.0	44235884.0	44214872.0
35V1	P0	19075969.0	38151938.0	38143428.0	38103143.0
35V3	P2	21910179.0	43820358.0	43810253.0	43788171.0
35V5	P4	87639462.0	175278924.0	175189189.0	175102786.0
35V6	P/M6	112809910.0	225619820.0	225471140.0	225282550.0
37V1	P0	30331293.0	60662586.0	60639094.0	60539811.0
37V3	P2	31457964.0	62915928.0	62893168.0	62838214.0
37V5	P4	32020880.0	64041760.0	64018360.0	63972222.0
37V6	P/M6	106078560.0	212157120.0	212024737.0	211895749.0
38V1	P0	31981920.0	63963840.0	63940372.0	63816598.0
38V3	P2	31471373.0	62942746.0	62919931.0	62786338.0
38V5	P4	83938092.0	167876184.0	167782056.0	167263580.0
38V6	P/M6	114815175.0	229630350.0	229491046.0	229349395.0
3V1	P0	30255484.0	60510968.0	60484828.0	60370893.0
3V3	P2	31561788.0	63123576.0	63098276.0	63029093.0
3V5	P4	77708415.0	155416830.0	155314626.0	155025869.0
3V6	P/M6	111163653.0	222327306.0	222184578.0	221920974.0
42V1	M0	24394105.0	48788210.0	48776160.0	48710803.0
42V3	M2	24350282.0	48700564.0	48690695.0	43821049.0
42V5	M4	22592588.0	45185176.0	45174970.0	45129520.0
43V1	M0	23028246.0	46056492.0	46047544.0	46013726.0
43V3	M2	16574353.0	33148706.0	33141502.0	33119879.0
43V5	M4	22668695.0	45337390.0	45326847.0	45292505.0
44V1	P0	27263743.0	54527486.0	54507747.0	54354572.0
44V3	P2	29969095.0	59938190.0	59916050.0	59870046.0
44V5	P4	32155258.0	64310516.0	64286501.0	64238860.0
45V1	P0	30958364.0	61916728.0	61890143.0	61794454.0

45V3	P2	31641534.0	63283068.0	63259125.0	63205128.0
45V5	P4	20906666.0	41813332.0	41800388.0	41731083.0
46V1	M0	21853335.0	43706670.0	43696782.0	43615341.0
46V3	M2	22371554.0	44743108.0	44733481.0	44685581.0
46V5	M4	23855977.0	47711954.0	47700966.0	47625613.0
47V1	M0	20454787.0	40909574.0	40900357.0	40864899.0
47V3	M2	18251764.0	36503528.0	36495506.0	36422049.0
47V5	M4	19668278.0	39336556.0	39328681.0	39303230.0
49V1	M0	22460169.0	44920338.0	44909319.0	44877806.0
49V3	M2	22111581.0	44223162.0	44213262.0	44108132.0
49V5	M4	17820175.0	35640350.0	35633272.0	35624517.0
4V1	M0	26235510.0	52471020.0	52455332.0	52367158.0
4V3	M2	21868320.0	43736640.0	43727610.0	43686707.0
4V5	M4	21321390.0	42642780.0	42631442.0	42574480.0
50V1	M0	23427661.0	46855322.0	46845810.0	46604736.0
50V3	M2	21174345.0	42348690.0	42340110.0	42280184.0
50V5	M4	17423388.0	34846776.0	34839748.0	34819503.0
51V1	M0	23989874.0	47979748.0	47969873.0	47807542.0
51V3	M2	19813992.0	39627984.0	39620008.0	39604945.0
51V5	M4	18099089.0	36198178.0	36190887.0	36178631.0
52V1	M0	15528000.0	31056000.0	31048918.0	31034837.0
52V3	M2	19484681.0	38969362.0	38961494.0	38952279.0
52V5	M4	16565151.0	33130302.0	33120470.0	33073134.0
5V1	P0	22528136.0	45056272.0	45047260.0	45013005.0
5V3	P2	20506560.0	41013120.0	41002299.0	40918341.0
5V5	P4	82728165.0	165456330.0	165371298.0	165232981.0
5V6	P/M6	109101718.0	218203436.0	218070533.0	217953069.0
6V1	P0	29169057.0	58338114.0	58315504.0	58262967.0
6V3	P2	35123393.0	70246786.0	70220191.0	70159040.0
6V5	P4	58778124.0	117556248.0	117513199.0	117385690.0
6V6	P/M6	109044809.0	218089618.0	217954228.0	217831097.0
8V1	P0	31483857.0	62967714.0	62943963.0	62885930.0
8V3	P2	31269019.0	62538038.0	62514600.0	62446196.0
8V5	P4	20317009.0	40634018.0	40622976.0	40448303.0
9V1	P0	23572350.0	47144700.0	47134004.0	47077794.0
9V3	P2	22159900.0	44319800.0	44311568.0	44262342.0
9V5	P4	87602295.0	175204590.0	175120016.0	174956003.0
9V6	P/M6	108805986.0	217611972.0	217476416.0	217244809.0

Mapping to the genome catalogue

OriginalMappingReads	OriginalMappingRate	95%MappingReads	95%MappingRates
35103987.1	46.8	27675328.5	36.6
20509010.0	45.0	16787332.0	36.8
15335145.0	36.8	11734492.0	28.2
22362634.0	53.2	17531429.0	41.7
22519360.0	38.2	16841144.0	28.6
27820214.0	45.4	19485897.0	31.8
25453128.0	43.7	19080179.0	32.8
19897102.0	33.2	13185821.0	22.0
14484523.0	34.2	10097677.0	23.9
20495332.0	34.1	13959558.0	23.2
22561044.0	57.3	19084235.0	48.5
30978978.0	67.6	26890824.0	58.7
29497894.0	64.3	25468239.0	55.5
18923765.0	40.3	14306016.0	30.4
17997813.0	38.4	13679395.0	29.2
14150352.0	32.8	9691096.0	22.4
17239328.0	48.3	12917903.0	36.2
16857670.0	43.1	12918366.0	33.1
29549173.0	50.7	21590634.0	37.1
33289195.0	55.4	26244456.0	43.6
32625836.0	55.8	25603727.0	43.8
90178460.0	54.9	74335021.0	45.3
118594950.0	52.3	97405323.0	42.9
32263783.0	53.7	24298416.0	40.4
39570508.0	54.4	30395300.0	41.8
27603210.0	58.8	22013365.0	46.9
22894846.0	49.7	18477732.0	40.1
21101581.0	46.9	16830721.0	37.4
33838344.0	52.5	26766957.0	41.5
22833826.0	53.6	18389212.0	43.1
18834843.0	51.4	14485826.0	39.5
21775730.0	54.5	17789509.0	44.6
32538141.0	55.6	26133175.0	44.7
34462587.0	53.1	26144340.0	40.3
34985990.0	59.4	26728826.0	45.4
25472215.0	60.7	20329989.0	48.4
21835012.0	36.1	15675198.0	25.9
21101822.0	31.9	15312020.0	23.1
52229273.0	30.9	40401864.0	23.9
75158911.0	32.3	58084276.0	24.9
18400717.0	37.9	14739370.0	30.4
16991816.0	37.8	13621418.0	30.3
43339652.0	26.4	34216890.0	20.9
128530523.0	56.9	105722308.0	46.8
14804581.0	33.1	11518004.0	25.7
16974090.0	37.7	13494801.0	30.0

11434825.0	32.4	8525862.0	24.2
24950284.0	38.5	18951515.0	29.2
27204827.0	44.4	20021777.0	32.6
33475762.0	45.2	26363675.0	35.6
92073097.0	44.6	75321798.0	36.5
8458526.0	27.6	5758182.0	18.8
13333748.0	31.6	9653508.0	22.9
34631476.0	59.8	28043877.0	48.4
68307752.0	32.3	52825718.0	25.0
29616292.0	44.6	22685252.0	34.2
29521656.0	46.3	21398363.0	33.6
27863869.0	42.8	20259164.0	31.1
24497014.0	36.3	18928842.0	28.1
20349277.0	43.0	16704423.0	35.3
18681378.0	41.3	15434210.0	34.1
17262155.0	43.1	13267502.0	33.1
22334515.0	46.5	18145160.0	37.8
73126152.0	46.2	58728648.0	37.1
101296440.0	44.9	81405521.0	36.1
17258147.0	36.6	13658119.0	28.9
18589420.0	43.8	14718867.0	34.7
18725002.0	42.4	14034034.0	31.7
26505048.0	69.6	22450439.0	58.9
26825268.0	61.3	20856948.0	47.6
108067956.0	61.7	86980474.0	49.7
138526305.0	61.5	113847258.0	50.5
34929251.0	57.7	27116180.0	44.8
36111914.0	57.5	27740314.0	44.1
35733252.0	55.9	27483510.0	43.0
107981674.0	51.0	86748009.0	40.9
37098339.0	58.1	29463495.0	46.2
26326278.0	41.9	20100466.0	32.0
93910930.0	56.1	79206216.0	47.4
103191442.0	45.0	85179532.0	37.1
18927592.0	31.4	12644773.0	20.9
18162264.0	28.8	12126346.0	19.2
51510617.0	33.2	36779917.0	23.7
82790496.0	37.3	65802372.0	29.7
27966564.0	57.4	22581260.0	46.4
26730978.0	61.0	20839449.0	47.6
24036587.0	53.3	19226710.0	42.6
21546756.0	46.8	17836681.0	38.8
16897330.0	51.0	12908729.0	39.0
21497559.0	47.5	16638122.0	36.7
30128054.0	55.4	22306827.0	41.0
30792374.0	51.4	23314988.0	38.9
36327408.0	56.6	27032844.0	42.1
31630981.0	51.2	24038834.0	38.9

30929572.0	48.9	23270163.0	36.8
21920139.0	52.5	17403882.0	41.7
14701314.0	33.7	11408764.0	26.2
19687744.0	44.1	15215003.0	34.0
18811068.0	39.5	14623834.0	30.7
21804411.0	53.4	16537143.0	40.5
20080531.0	55.1	15587043.0	42.8
18612200.0	47.4	14273799.0	36.3
18661073.0	41.6	14414389.0	32.1
26718431.0	60.6	20825826.0	47.2
14831852.0	41.6	11170189.0	31.4
19207106.0	36.7	15763273.0	30.1
18073996.0	41.4	14243659.0	32.6
16447281.0	38.6	13169027.0	30.9
23583164.0	50.6	19021427.0	40.8
23156207.0	54.8	18460141.0	43.7
17485626.0	50.2	13563011.0	39.0
19424590.0	40.6	15483733.0	32.4
18425943.0	46.5	14253747.0	36.0
12888739.0	35.6	9535033.0	26.4
16084266.0	51.8	12377677.0	39.9
21077660.0	54.1	16454729.0	42.2
16428862.0	49.7	12588396.0	38.1
27629321.0	61.4	23790152.0	52.9
26219868.0	64.1	21860115.0	53.4
100503708.0	60.8	86613088.0	52.4
93190483.0	42.8	76871332.0	35.3
23492345.0	40.3	16547581.0	28.4
28464844.0	40.6	20083961.0	28.6
46924367.0	40.0	32989502.0	28.1
74131074.0	34.0	53331747.0	24.5
31154124.0	49.5	23775205.0	37.8
36215685.0	58.0	27558563.0	44.1
23322105.0	57.7	19280340.0	47.7
15746091.0	33.4	12603247.0	26.8
16023367.0	36.2	13465929.0	30.4
78974164.0	45.1	64852033.0	37.1
126986278.0	58.5	104820362.0	48.2

Mapping to the gene catalogue

OriginalMappingReads	OriginalMappingRates	95%MappingReads	95%MappingRates
58196413.7	77.1	49096307.2	64.6
34394913.0	75.5	29684647.0	65.1
30129194.0	72.4	24212936.0	58.2
31740410.0	75.4	26110063.0	62.1
44955475.0	76.3	36130936.0	61.3
46043126.0	75.1	36647108.0	59.8
44446227.0	76.4	35750606.0	61.4
43942414.0	73.4	33759947.0	56.4
31460203.0	74.3	25008427.0	59.1
44117492.0	73.3	34376376.0	57.1
31734358.0	80.7	27619624.0	70.2
37108771.0	81.0	32516981.0	71.0
37229184.0	81.1	32640556.0	71.1
35864122.0	76.3	30350923.0	64.6
36156218.0	77.0	30663793.0	65.3
31918456.0	73.9	25059145.0	58.0
28315609.0	79.3	23296565.0	65.3
30891995.0	79.1	25617923.0	65.6
45685365.0	78.4	37040064.0	63.6
46866690.0	77.9	38116018.0	63.4
45828706.0	78.4	37299924.0	63.8
131513204.0	80.1	112936188.0	68.8
178695829.0	78.8	155206693.0	68.4
47226399.0	78.6	38535836.0	64.1
57383543.0	78.9	46914281.0	64.5
37421393.0	79.8	32432471.0	69.1
36505775.0	79.3	31219387.0	67.8
35776608.0	79.5	30588802.0	68.0
51519394.0	79.9	44159129.0	68.5
34333423.0	80.5	29890707.0	70.1
28734598.0	78.4	23680612.0	64.6
30839064.0	77.2	25706261.0	64.4
44789854.0	76.6	36957091.0	63.2
51240663.0	78.9	42157647.0	64.9
46814414.0	79.5	38754447.0	65.8
32522489.0	77.4	26912439.0	64.1
44645898.0	73.9	35557745.0	58.9
47409579.0	71.6	37637316.0	56.9
120421955.0	71.3	101200998.0	59.9
170060489.0	73.0	144557224.0	62.1
37363863.0	77.0	32298110.0	66.6
33210636.0	73.9	28569481.0	63.6
119028831.0	72.6	100701865.0	61.4
172234184.0	76.3	150058167.0	66.5
34523171.0	77.1	29679343.0	66.3
35149798.0	78.1	30305372.0	67.4

25653659.0	72.8	20497673.0	58.1
49919950.0	77.0	40987766.0	63.2
47372099.0	77.2	38734205.0	63.1
56991065.0	76.9	48950766.0	66.0
163862557.0	79.3	142525695.0	69.0
22195804.0	72.4	17693365.0	57.7
30384294.0	72.1	24543193.0	58.2
46055891.0	79.5	38147953.0	65.9
147715303.0	69.8	125409350.0	59.2
51496367.0	77.6	42354012.0	63.8
44763596.0	70.3	36012042.0	56.5
48073856.0	73.9	39001402.0	59.9
51661773.0	76.6	42121134.0	62.5
37036258.0	78.3	32271231.0	68.2
34993434.0	77.3	30478693.0	67.3
31279778.0	78.1	25738004.0	64.2
37806490.0	78.7	32943918.0	68.6
124025138.0	78.4	106061335.0	67.0
172398118.0	76.4	148320725.0	65.7
36713948.0	77.8	32187691.0	68.2
32560402.0	76.8	28479933.0	67.1
34392479.0	77.8	28428497.0	64.3
30397448.0	79.8	25695522.0	67.4
35088414.0	80.1	29717921.0	67.9
139289987.0	79.5	120074488.0	68.6
178743219.0	79.3	154938468.0	68.8
48108064.0	79.5	40208343.0	66.4
49612953.0	79.0	40792711.0	64.9
50966289.0	79.7	42032959.0	65.7
168519697.0	79.5	146608370.0	69.2
49584361.0	77.7	40463654.0	63.4
47001040.0	74.9	37759964.0	60.1
130989407.0	78.3	113659940.0	68.0
176719287.0	77.1	152321382.0	66.4
44075176.0	73.0	34077536.0	56.4
46304787.0	73.5	35580874.0	56.5
115763950.0	74.7	96419691.0	62.2
166362953.0	75.0	140424883.0	63.3
38216510.0	78.5	32945661.0	67.6
33892233.0	77.3	29304978.0	66.9
35989354.0	79.7	31448215.0	69.7
34986331.0	76.0	30163777.0	65.6
25319021.0	76.4	20786300.0	62.8
33806926.0	74.6	27754367.0	61.3
41505239.0	76.4	33620987.0	61.9
45789130.0	76.5	37229982.0	62.2
49863641.0	77.6	40887933.0	63.6
48332260.0	78.2	39713719.0	64.3

49121059.0	77.7	40180015.0	63.6
32645103.0	78.2	28294231.0	67.8
31671345.0	72.6	26363005.0	60.4
33933543.0	75.9	28781615.0	64.4
35201077.0	73.9	29629049.0	62.2
31984887.0	78.3	26597486.0	65.1
28559340.0	78.4	23565395.0	64.7
30047116.0	76.4	24644720.0	62.7
32992782.0	73.5	26667151.0	59.4
34129931.0	77.4	28546668.0	64.7
27012975.0	75.8	21736648.0	61.0
41187029.0	78.7	36017390.0	68.8
34396835.0	78.7	29888434.0	68.4
33787909.0	79.4	29580065.0	69.5
36663351.0	78.7	30481593.0	65.4
33385881.0	79.0	27997541.0	66.2
27101229.0	77.8	22393878.0	64.3
35692076.0	74.7	29459237.0	61.6
30397123.0	76.8	25156950.0	63.5
26597009.0	73.5	21598057.0	59.7
24719412.0	79.7	20705797.0	66.7
31118896.0	79.9	26349285.0	67.6
25908723.0	78.3	21717048.0	65.7
36710396.0	81.6	32194936.0	71.5
32935714.0	80.5	27541450.0	67.3
133515292.0	80.8	116172635.0	70.3
173914272.0	79.8	151742570.0	69.6
43409777.0	74.5	35021007.0	60.1
52549131.0	74.9	41773637.0	59.5
87779942.0	74.8	70304921.0	59.9
167351529.0	76.8	144144048.0	66.2
50129666.0	79.7	41479959.0	66.0
50466648.0	80.8	42049384.0	67.3
32970520.0	81.5	29254048.0	72.3
36516134.0	77.6	31621649.0	67.2
34056725.0	76.9	29541428.0	66.7
136078920.0	77.8	117662882.0	67.3
172515474.0	79.4	150307395.0	69.2

Supplementary Table 3

Sheet1

Sheet2

List of microbial strains and genera in the fecal metagenomes that were significantly increased

Strain level.

Genus level.

Bacterial Strains

	baseMean
[Clostridium] sticklandii	25.368123497
Acinetobacter baumannii TDC-AB0715	NS
Acinetobacter haemolyticus ATCC 19194	NS
Actinomyces coleocanis DSM 15436	NS
Actinomyces sp. oral taxon 170 str. F0386	NS
Aeromonas caviae Ae398	NS
Agrobacterium tumefaciens F2	NS
Alkaliphilus metalliredigens QYMF	NS
Alkaliphilus oremlandii OhILAs	5.4850803591
Bacillus cereus SJ1	98.790533455
Bacillus coahuilensis m4-4	107.27894268
Bacteroides clarus YIT 12056	35865.94642
Bacteroides coprophilus DSM 18228 = JCM 13818	NS
Bifidobacterium adolescentis L2-32	66272.538675
Bifidobacterium bifidum NCIMB 41171	NS
Bifidobacterium dentium ATCC 27679	NS
Bifidobacterium pseudocatenulatum DSM 20438 = JCM 1200	NS
Brachyspira pilosicoli 95/1000	NS
Burkholderia mallei ATCC 23344	NS
Burkholderia vietnamiensis G4	NS
Campylobacter gracilis RM3268	NS
Campylobacter hominis ATCC BAA-381	NS
Capnocytophaga gingivalis ATCC 33624	26.275774808
Citrobacter koseri ATCC BAA-895	1233.2870998
Citrobacter rodentium ICC168	478.51035995
Citrobacter sp. 30_2	596.99174736
Citrobacter youngae ATCC 29220	217.15966352
Clostridium bartlettii DSM 16795	32312.980967
Clostridium beijerinckii NCIMB 8052	72.277438968
Clostridium botulinum A3 str. Loch Maree	10.501643932
Clostridium botulinum BKT015925	5.7067593841
Clostridium botulinum C str. Eklund	3.2859608866
Clostridium botulinum D str. 1873	6.3211114524
Clostridium botulinum E1 str. 'BoNT E Beluga'	80.484787916
Clostridium butyricum E4 str. BoNT E BL5262	55.710952806
Clostridium carboxidivorans P7	NS
Clostridium clariflavum DSM 19732	NS
Clostridium hiranonis DSM 13275	NS
Clostridium novyi NT	1.5405141177
Clostridium perfringens CPE str. F4969	3240.5753141
Clostridium perfringens E str. JGS1987	2618.7353661
Clostridium sp. 7_2_43FAA	438.93622156
Collinsella aerofaciens ATCC 25986	NS
Collinsella intestinalis DSM 13280	NS
Collinsella stercoris DSM 13279	NS
Coriobacterium glomerans PW2	NS
Corynebacterium jeikeium ATCC 43734	NS

<i>Corynebacterium lipophiloflavum</i> DSM 44291	13.36254783
<i>Corynebacterium pseudogenitalium</i> ATCC 33035	NS
<i>Corynebacterium resistens</i> DSM 45100	NS
<i>Corynebacterium striatum</i> ATCC 6940	20.895891166
<i>Cronobacter turicensis</i> z3032	56.42326257
<i>Deferribacter desulfuricans</i> SSM1	1.5463968924
<i>Dermacoccus</i> sp. Ellin185	118.41047517
<i>Desulfotalea psychrophila</i> L5v54	NS
<i>Desulfovibrio alaskensis</i> G20	NS
<i>Desulfurispirillum indicum</i> S5	NS
<i>Dickeya dadantii</i> 3937	6.5911096728
<i>Dickeya dadantii</i> Ech586	NS
<i>Dickeya dadantii</i> Ech703	4.856958311
<i>Dickeya zeae</i> Ech1591	4.7566112591
<i>Edwardsiella ictaluri</i> 93-146	NS
<i>Enterobacter aerogenes</i> KCTC 2190	73.331734457
<i>Enterobacter asburiae</i> LF7a	84.011827589
<i>Enterobacter cancerogenus</i> ATCC 35316	59.754403985
<i>Enterobacter cloacae</i> EcWSU1	314.13979587
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> ATCC 13047	548.4061756
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> NCTC 9394	1145.8651404
<i>Enterobacter lignolyticus</i> SCF1	57.582083648
<i>Enterobacter</i> sp. 638	18.793448315
<i>Enterococcus casseliflavus</i> EC10	171.46534747
<i>Erwinia amylovora</i> ATCC 49946	3.9303360806
<i>Erwinia billingiae</i> Eb661	6.4179834485
<i>Erwinia tasmaniensis</i> Et1/99	24.756362691
<i>Escherichia albertii</i> TW07627	5302.8978175
<i>Escherichia coli</i> TW10509	65967.216615
<i>Eubacterium limosum</i> KIST612	NS
<i>Faecalibacterium</i> cf. <i>prausnitzii</i> KLE1255	NS
<i>Fusobacterium necrophorum</i> D12	NS
<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i> ATCC 10953	NS
<i>Fusobacterium nucleatum</i> subsp. <i>vincentii</i> 4_1_13	NS
<i>Granulicatella elegans</i> ATCC 700633	NS
<i>Helicobacter mustelae</i> 12198	26.863344192
<i>Hippea maritima</i> DSM 10411	11.5491779
<i>Klebsiella oxytoca</i> KCTC 1686	349.7526908
<i>Klebsiella pneumoniae</i> 342	950.33440794
<i>Lactobacillus acidophilus</i> ATCC 4796	49.885876467
<i>Lactobacillus amylolyticus</i> DSM 11664	40.037234296
<i>Lactobacillus brevis</i> subsp. <i>gravesensis</i> ATCC 27305	92.708917769
<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> DSM 20072	2610.9418741
<i>Lactobacillus fermentum</i> CECT 5716	3814.5029083
<i>Lactobacillus gasseri</i> JV-V03	23806.058025
<i>Lactobacillus jensenii</i> 1153	255.47850845
<i>Lactobacillus johnsonii</i> NCC 533	471.46268741
<i>Lactobacillus ruminis</i> SPM0211	NS

<i>Lactobacillus sakei</i> subsp. <i>sakei</i> 23K	NS
<i>Lactobacillus ultunensis</i> DSM 16047	76.394042431
<i>Lactobacillus vaginalis</i> ATCC 49540	NS
<i>Lactococcus garvieae</i> Lg2	NS
<i>Listeria grayi</i> DSM 20601	NS
<i>Listeria seeligeri</i> FSL N1-067	NS
<i>Megasphaera elsdenii</i> DSM 20460	NS
<i>Neisseria bacilliformis</i> ATCC BAA-1200	NS
<i>Neisseria elongata</i> subsp. <i>glycolytica</i> ATCC 29315	14.860504745
<i>Neisseria mucosa</i> ATCC 25996	49.568533453
<i>Olsenella uli</i> DSM 7084	NS
<i>Pantoea ananatis</i> LMG 5342	5.1650267999
<i>Pantoea</i> sp. At-9b	6.7831477427
<i>Pectobacterium atrosepticum</i> SCRI1043	NS
<i>Pectobacterium wasabiae</i> WPP163	NS
<i>Peptoniphilus</i> sp. oral taxon 375 str. F0436	NS
<i>Peptostreptococcus stomatis</i> DSM 17678	NS
<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	NS
<i>Plautia stali</i> symbiont	3.1182338985
<i>Porphyromonas uenonis</i> 60-3	NS
<i>Prevotella oris</i> C735	NS
<i>Propionibacterium acnes</i> SK182B-JCVI	NS
<i>Providencia stuartii</i> ATCC 25827	NS
<i>Pseudoflavonifractor capillosus</i> ATCC 29799	14047.378148
<i>Pseudogulbenkiania</i> sp. NH8B	12.381919343
<i>Pseudomonas aeruginosa</i> NCGM2.S1	545.5768725
<i>Pseudomonas stutzeri</i> DSM 4166	NS
<i>Pseudomonas syringae</i> pv. <i>morsprunorum</i> str. M302280	NS
<i>Rahnella aquatilis</i> CIP 78.65 = ATCC 33071	NS
<i>Rahnella</i> sp. Y9602	NS
<i>Raphidiopsis brookii</i> D9	19.904112436
<i>Rheinheimera</i> sp. A13L	69.298857232
<i>Rothia mucilaginosa</i> DY-18	1619.8412634
<i>Ruminococcus flavefaciens</i> FD-1	961.52105393
<i>Ruminococcus</i> sp. 5_1_39BFAA	666322.2732
<i>Ruminococcus</i> sp. SR1/5	NS
<i>Salmonella bongori</i> NCTC 12419	51.387024124
<i>Salmonella enterica</i> subsp. <i>arizonae</i> serovar 62:z4,z23:- str. RSK2980	64.786747503
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Dublin str. SD3246	835.91859855
<i>Serratia odorifera</i> DSM 4582	10.823900334
<i>Serratia proteamaculans</i> 568	NS
<i>Serratia</i> sp. AS12	4.2878093816
<i>Shewanella frigidimarina</i> NCIMB 400	NS
<i>Shewanella putrefaciens</i> 200	NS
<i>Shewanella</i> sp. Ana-3	NS
<i>Slackia exigua</i> ATCC 700122	NS
<i>Slackia heliotrinireducens</i> DSM 20476	NS
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MRSA177	155.06773567

Staphylococcus epidermidis W23144	32.080926544
Streptococcus dysgalactiae subsp. dysgalactiae ATCC 27957	NS
Streptococcus infantarius subsp. infantarius CJ18	NS
Streptococcus parasanguinis ATCC 15912	NS
Streptococcus thermophilus JIM 8232	NS
Subdoligranulum variabile DSM 15176	14842.090085
Veillonella dispar ATCC 17748	NS
Veillonella sp. 6_1_27	NS
Veillonella sp. oral taxon 158 str. F0412	NS
Vibrio furnissii CIP 102972	NS
Weissella cibaria KACC 11862	10552.639551
Xanthomonas campestris pv. vesicatoria str. 85-10	NS
Xenorhabdus bovienii SS-2004	NS
Xenorhabdus nematophila ATCC 19061	NS
Yersinia enterocolitica subsp. enterocolitica 8081	118.13461594

log2FoldChange.M2	pvalue.M2	FDR.M2	baseMean	log2FoldChange.M4	pvalue.M4
-1.53115063011697	7.162019E-07	6.687535E-05	25.368123497	-1.6327481870587	1.541288E-07
NS	NS	NS	76.943210282	1.54794497881522	0.0023755472
NS	NS	NS	17.842827747	3.32047123406734	2.549009E-05
NS	NS	NS	11.954319002	1.4620581794965	0.0041022045
NS	NS	NS	NS	NS	NS
NS	NS	NS	9.0949744766	2.44043046925503	0.0023917877
NS	NS	NS	NS	NS	NS
NS	NS	NS	8.2796389372	-1.39673931211732	0.000650091
-1.2687666788918	0.0024771138	0.0292532355	5.4850803591	-1.40411317691713	0.0009734915
2.75027910688602	4.621676E-06	0.0002465994	98.790533455	2.17811742198975	0.0002929541
2.0316738721985	0.000529281	0.0091947191	107.27894268	2.07872900668748	0.0003888373
1.16836015869951	0.002515366	0.0292532355	NS	NS	NS
NS	NS	NS	NS	NS	NS
-1.74213865217226	0.000629459	0.0102218669	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
1.52195675748291	0.0031730981	0.0353776758	26.275774808	1.51078589627738	0.0034591001
2.32279586495706	3.963552E-05	0.0011843092	1233.2870998	2.55028408815592	6.385028E-06
2.66048887079818	3.904575E-07	4.166739E-05	478.51035995	2.67770485824872	3.246449E-07
2.65698045712334	6.960355E-06	0.0002888547	596.99174736	2.9523889111151	5.875753E-07
2.95511760476564	5.920866E-06	0.0002601698	217.15966352	2.85229824061369	1.245908E-05
-2.2303441912917	2.587622E-09	3.865907E-07	32312.980967	-2.64359469887623	1.676353E-12
-3.18096782161029	1.315819E-08	1.638194E-06	72.277438968	-3.9354562910674	4.504528E-12
-1.74931636481071	0.0001199619	0.002715502	10.501643932	-2.07560885685735	7.648945E-06
-2.75594069350799	0.0001604792	0.0032678569	5.7067593841	-3.81974491863052	1.133611E-06
-2.29984460713126	0.0017028045	0.0227141961	3.2859608866	-3.69531483428133	5.405108E-06
-2.8636633828974	5.00035E-05	0.0013834301	6.3211114524	-3.80963260431719	4.056054E-07
-3.35657499262067	2.552551E-09	3.865907E-07	80.484787916	-3.80222010388051	2.396843E-11
-3.35616692255002	1.623295E-09	3.865907E-07	55.710952806	-3.61794990456008	1.239278E-10
NS	NS	NS	9.5991377602	-2.32007418735443	0.0002362
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
-2.28491899391284	0.002525851	0.0292532355	1.5405141177	-2.3993683334445	0.0019882521
-3.47198195016414	2.059025E-09	3.865907E-07	3240.5753141	-2.15525023011069	0.0001815308
-2.68342800485769	2.572772E-06	0.0001601551	2618.7353661	-1.68912121178712	0.0029953812
-2.75571943837269	3.114024E-06	0.0001789366	438.93622156	-3.59549519879049	1.405186E-09
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS

	2.21364521211926	0.0002059248	0.0039442511	13.36254783	1.88772205443777	0.001655756
NS	NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS	NS
	2.33286783482424	0.0001439024	0.0030712885	20.895891166	1.93753156545736	0.0016674055
	2.45720172979501	0.0001041465	0.0025233097	56.42326257	2.9635269754945	2.687507E-06
	-2.31538513889524	0.0016385971	0.0222551282	NS	NS	NS
	2.50532764223169	8.716719E-05	0.0022453065	118.41047517	2.40839185292571	0.0001618298
NS	NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	8.9385418145	1.70036599759846	0.0022070299
NS	NS	NS	NS	10.30953283	2.11596880118276	0.0023258489
	1.80251935970298	0.0049441515	0.047280665	6.5911096728	2.26769235890902	0.000381339
NS	NS	NS	NS	9.1818600026	2.46793030210399	0.0025667954
	2.11454275519519	0.0037465354	0.0394177737	4.856958311	2.50194972621546	0.0005686771
	1.91045126680436	0.0043483715	0.0438950476	4.7566112591	1.97172692755379	0.0032864255
NS	NS	NS	NS	7.4977671972	2.08712092524427	0.001925814
	2.35453818652328	0.0001818296	0.0035743877	73.331734457	2.84262511449593	6.103187E-06
	2.32807204039954	0.0007668341	0.0114565018	84.011827589	2.79709553141196	5.18194E-05
	3.45560707670183	9.927936E-07	8.240187E-05	59.754403985	3.53021510638356	5.742808E-07
	2.12259286041941	0.0018352211	0.0240510555	314.13979587	2.16914820342499	0.0014591005
	2.40731872677861	9.426103E-06	0.0003520649	548.4061756	2.43274578819335	7.581408E-06
	4.0387697284759	2.423505E-09	3.865907E-07	1145.8651404	3.65996171396247	6.50951E-08
	2.05039052652199	0.0003512086	0.0063988503	57.582083648	2.44347426691734	1.964229E-05
	2.73204629046013	0.0001438504	0.0030712885	18.793448315	2.86918691399149	6.502562E-05
	2.18335422698436	0.0042333087	0.0438950476	NS	NS	NS
	2.2497061665972	0.0034421215	0.037264707	3.9303360806	2.87280434202158	0.0001631546
	2.6910496416334	0.0001065741	0.0025233097	6.4179834485	2.88847751664771	3.112606E-05
	2.59968866128033	4.264587E-05	0.0012252487	24.756362691	3.44990117529159	4.3774E-08
	2.64446848130426	2.295019E-06	0.0001558526	5302.8978175	2.55921627557927	4.801003E-06
	2.72106142402194	1.735623E-06	0.0001296511	65967.216615	2.56765835765681	6.409481E-06
NS	NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	152904.48956	-0.728616189190078	0.0021294354
NS	NS	NS	NS	3.8755885694	3.62793155073494	0.0015894598
NS	NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS	NS
	4.1305881086946	2.375436E-05	0.0007715003	26.863344192	4.5698217356102	2.698635E-06
	-1.41567560101292	0.005063525	0.047280665	NS	NS	NS
	2.7955822358973	5.25948E-06	0.0002601698	349.7526908	3.67278977729767	2.097281E-09
	3.02111568044143	8.740753E-06	0.0003436496	950.33440794	4.52214297062885	2.688129E-11
	1.91345719815606	0.0009568195	0.0137091849	49.885876467	1.69290513433655	0.0036043527
	1.77379280162261	0.0009910254	0.0137091849	NS	NS	NS
	1.29377182689269	0.0025454623	0.0292532355	NS	NS	NS
	1.86863369655508	0.002187244	0.0281701942	NS	NS	NS
	1.3488989345806	0.0035144682	0.0375043959	NS	NS	NS
	2.18935273364219	0.000219219	0.0040939147	NS	NS	NS
	2.21589422846047	0.004926976	0.047280665	NS	NS	NS
	1.86944883809999	0.0007824166	0.0114601022	NS	NS	NS
NS	NS	NS	NS	NS	NS	NS

NS	NS	NS	NS	NS	NS
1.7729852752782	0.0005891196	0.0097793852	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
2.56106070325197	0.0001080936	0.0025233097	NS	NS	NS
2.06388882725691	2.710203E-05	0.0008435507	49.568533453	1.93934053619175	8.063612E-05
NS	NS	NS	NS	NS	NS
2.8234753837725	1.095935E-05	0.0003721198	5.1650267999	2.70878852353633	2.634549E-05
1.76584870171083	0.0052365529	0.0482926548	6.7831477427	2.38211042433776	0.0001471931
NS	NS	NS	3.3803562707	2.30550986649541	0.0023608671
NS	NS	NS	5.8312197498	2.38124789980101	0.001689022
NS	NS	NS	360.2029533	0.421746652273874	0.0056555888
NS	NS	NS	131.16597563	-0.977184181390834	0.0028097967
NS	NS	NS	2.3472140182	3.02585226883282	0.0010150125
3.19273391653354	0.002517157	0.0292532355	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	8.6037232862	2.37429030951333	0.0004497353
-0.438854386721087	0.0022925601	0.0290261419	NS	NS	NS
-1.42738355647363	0.0045366601	0.0448704786	NS	NS	NS
1.76107341639418	0.0050519028	0.047280665	545.5768725	3.59479361709267	8.514394E-09
NS	NS	NS	6.6773045469	3.54625003346857	0.0005686373
NS	NS	NS	11.61903393	1.93438401431203	0.0030929547
NS	NS	NS	5.7889080902	2.13282294085403	0.0008907654
NS	NS	NS	5.5249849119	2.72485188235308	9.641566E-06
2.58846704121803	0.0006878118	0.0107040706	NS	NS	NS
2.16361008096994	0.0006665336	0.0105936294	69.298857232	2.28239829283324	0.000327919
1.19948088888579	0.0031349166	0.0353776758	NS	NS	NS
-0.974319460187461	0.0005634493	0.0095658319	NS	NS	NS
0.601222601085116	0.0032538081	0.0357440388	666322.2732	0.644897180868667	0.0015970322
NS	NS	NS	NS	NS	NS
2.26529061221862	7.897934E-05	0.002107056	51.387024124	2.38010721836913	3.329257E-05
2.52907744312106	1.080911E-05	0.0003721198	64.786747503	2.62665586269622	4.825864E-06
2.6152248595595	5.913154E-06	0.0002601698	835.91859855	2.78858846203728	1.358856E-06
2.32911673716467	0.0007510525	0.0114497192	10.823900334	2.21169193086938	0.0014165234
NS	NS	NS	3.4633900251	2.05561670090831	0.0050834217
1.97047784058293	0.0024023579	0.0292532355	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	13.19599182	3.43009765585714	1.970942E-05
NS	NS	NS	26.351266041	3.12116679223606	0.0002566806
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
2.32515757499796	0.0009744614	0.0137091849	NS	NS	NS

1.37478517059668	0.0045651357	0.0448704786	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	13282.137646	1.13467783166143	0.005042576
NS	NS	NS	NS	NS	NS
-0.55537018635721	0.0001618617	0.0032678569	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	16.767620708	3.24837234877127	0.0024013708
1.96481241322179	0.0043328945	0.0438950476	NS	NS	NS
NS	NS	NS	3.6212913885	2.78544280688267	8.822094E-05
NS	NS	NS	1.6535810805	2.22818364382664	0.0050019185
NS	NS	NS	13.203184905	2.35940738460366	0.0010598187
2.12003354108105	0.00037942	0.0067482561	118.13461594	2.40155542460314	5.520804E-05

FDR.M4	baseMean	log2FoldChange.P/M6	pvalue.P/M6	FDR.P/M6
1.046675E-05	NS	NS	NS	NS
0.0242408645	NS	NS	NS	NS
0.0005950343	NS	NS	NS	NS
0.0373700827	NS	NS	NS	NS
NS	630.19928657	1.05478696717928	0.002680305	0.0329081891
0.0242408645	NS	NS	NS	NS
NS	12.787817657	-1.02292197773248	0.0023414952	0.0298540641
0.0089929253	NS	NS	NS	NS
0.0129856812	NS	NS	NS	NS
0.0046561005	356.47187459	2.4676113587232	0.0003568338	0.0137966505
0.0058092294	585.80852556	2.2723503117749	0.0014734877	0.0218904946
NS	NS	NS	NS	NS
NS	252049.45392	-1.07469412462356	0.0020829114	0.0276194056
NS	1356246.7316	2.3085875561219	0.0010246208	0.0188701006
NS	189954.24252	3.30220190714555	3.3448634E-08	1.108822E-05
NS	3757.9204387	1.36301091890083	0.005202575	0.0496944925
NS	276790.60081	1.95720667808707	0.0002497915	0.0110407853
NS	3965.3900899	1.04283292379625	0.0014857802	0.0218904946
NS	11.091341737	-1.52533499339748	0.0005228903	0.0153260998
NS	41.36491558	-1.4659984995511	0.0054716409	0.0496944925
NS	54.645004187	-1.93718934154989	0.0007860775	0.0168119152
NS	396.57219583	-1.90118458113071	0.0041346238	0.0450941849
0.0322993471	114.98264576	1.89744609036072	0.0045741741	0.0489141522
0.0001915153	5573.9993545	3.09508707966754	0.0003745697	0.0137966505
2.020915E-05	2684.2513239	2.81136542780226	0.0005931734	0.0157309594
2.926125E-05	NS	NS	NS	NS
0.0003209286	NS	NS	NS	NS
1.252236E-09	NS	NS	NS	NS
1.682441E-09	187.41923152	-2.10015183743475	0.0011453803	0.0199838726
0.0002116208	NS	NS	NS	NS
5.292548E-05	NS	NS	NS	NS
0.000183528	9.3876591419	-2.54881275147342	0.0008706013	0.0177096942
2.330671E-05	NS	NS	NS	NS
5.020081E-09	208.32746123	-1.84934908783111	0.0049684621	0.0491655277
1.851482E-08	192.41991782	-2.10034464663409	0.0006480232	0.0165245924
0.0039209196	NS	NS	NS	NS
NS	199.01028154	0.876079677064421	0.0048733407	0.0489549229
NS	338.65186532	-0.996982304518662	0.0017178804	0.02419167
0.0221675271	NS	NS	NS	NS
0.0030818976	2514.0251873	-3.43759734100524	1.5904208E-07	3.51483E-05
0.0290590879	2106.1700602	-2.73446557451763	9.5698371E-06	0.0012689604
1.749457E-07	885.81840723	-2.8205683143957	1.9037514E-06	0.0003155468
NS	694185.21757	1.42267001278306	0.0002267155	0.0110407853
NS	1665.2554471	1.40631316483755	0.0001877648	0.0103740054
NS	3675.7682346	1.65529145336332	1.7460714E-05	0.0014470567
NS	125.3668717	1.44509564927714	6.847692E-05	0.0050444664
NS	60.174082368	1.5185146464035	0.0034923057	0.0406210296

0.0194107605	NS	NS	NS	NS
NS	33.100974427	1.78066919979187	0.001190574	0.0202397573
NS	144.44583091	1.66359183664429	0.0054319464	0.0496944925
0.0194107605	82.707248903	2.13251707267372	0.0047396007	0.0489549229
0.000106099	NS	NS	NS	NS
NS	NS	NS	NS	NS
0.002834337	652.40856114	2.43617105469815	0.0017514331	0.02419167
NS	63.939897895	2.47171823980319	0.0053423891	0.0496944925
0.0238934974	NS	NS	NS	NS
0.0242408645	NS	NS	NS	NS
0.0058092294	NS	NS	NS	NS
0.025565282	NS	NS	NS	NS
0.0080151275	NS	NS	NS	NS
0.0310754409	NS	NS	NS	NS
0.0217967126	NS	NS	NS	NS
0.0001915153	NS	NS	NS	NS
0.0010752526	NS	NS	NS	NS
2.926125E-05	NS	NS	NS	NS
0.0181658011	NS	NS	NS	NS
0.0002116208	NS	NS	NS	NS
4.862604E-06	NS	NS	NS	NS
0.0004749334	NS	NS	NS	NS
0.0012782669	NS	NS	NS	NS
NS	NS	NS	NS	NS
0.002834337	NS	NS	NS	NS
0.0006838579	NS	NS	NS	NS
3.633242E-06	NS	NS	NS	NS
0.0001716629	NS	NS	NS	NS
0.0001915153	318919.37726	2.4470923718907	0.0033458585	0.0396125751
NS	16622.335409	0.990998889131889	0.0009873547	0.0188701006
0.0233924744	NS	NS	NS	NS
0.0192416626	NS	NS	NS	NS
NS	84.229239598	-1.94431381247701	0.0035637506	0.0407373554
NS	250.65735715	-2.21757059914412	0.0005357682	0.0153260998
NS	133.66660883	-1.62928790432148	1.3540132E-05	0.0013002213
0.000106099	NS	NS	NS	NS
NS	NS	NS	NS	NS
2.238098E-07	NS	NS	NS	NS
5.020081E-09	NS	NS	NS	NS
0.0332401417	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	174.61457827	2.2053198920562	9.4589817E-05	0.0062713049
NS	2143.6509227	-2.12417335075787	0.0014470959	0.0218904946
NS	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	5990.4604517	0.714980028736685	0.0010181679	0.0188701006

NS	3741.7564849	2.377019356142	0.0003294447	0.0136513664
NS	NS	NS	NS	NS
NS	324.81088043	2.18928912374048	0.0026538124	0.0329081891
NS	71.904907381	-1.63755451235684	0.0006738847	0.0165476125
NS	9.7867118281	-1.5897230390573	0.0041489371	0.0450941849
NS	66.72457329	-2.05295853376816	0.0013197988	0.0208339666
NS	152172.76042	1.73204250880412	0.0018074896	0.0244564408
NS	10.030972884	2.84134659436974	0.0054036104	0.0496944925
NS	NS	NS	NS	NS
0.0015444918	NS	NS	NS	NS
NS	436.44102052	1.92112610622407	1.3727826E-05	0.0013002213
0.0005963661	NS	NS	NS	NS
0.0026817867	NS	NS	NS	NS
0.0242408645	NS	NS	NS	NS
0.0194107605	NS	NS	NS	NS
0.0491247073	NS	NS	NS	NS
0.0276173437	NS	NS	NS	NS
0.0133020056	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	7935.1439973	-1.08797779869908	0.0004224455	0.0147411233
NS	13555.109115	-1.13947532488193	0.0004577468	0.0151743077
NS	18.423401802	1.98908957148289	0.0031900244	0.0384542942
0.0065872994	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	NS	NS	NS	NS
7.950316E-07	NS	NS	NS	NS
0.0080151275	NS	NS	NS	NS
0.029620989	56.987459598	2.74233217461578	0.0005319709	0.0153260998
0.0120982136	NS	NS	NS	NS
0.0002572232	NS	NS	NS	NS
NS	NS	NS	NS	NS
0.005103239	455.03935471	2.49321779601402	0.0013107628	0.0208339666
NS	6177.3979546	1.6373440148326	0.0010870559	0.0194788672
NS	NS	NS	NS	NS
0.0192416626	NS	NS	NS	NS
NS	730157.42313	1.07075447060004	0.0038098504	0.042812387
0.0007105585	283.29456171	2.32987995777694	0.0048193389	0.0489549229
0.0001716629	NS	NS	NS	NS
5.970974E-05	2131.6999901	2.46077986815116	0.0047882795	0.0489549229
0.0179346273	NS	NS	NS	NS
0.0446743057	NS	NS	NS	NS
NS	NS	NS	NS	NS
NS	7.5173009804	-3.30525010333344	0.0012347391	0.020465801
0.0004749334	18.055955896	-2.49359304150227	0.0021922307	0.0284989988
0.0041682704	NS	NS	NS	NS
NS	227.52118965	1.51837500404978	0.0001176643	0.0070919461
NS	344.71249682	1.21452755409091	0.0007151954	0.0165818439
NS	NS	NS	NS	NS

NS	NS	NS	NS	NS
NS	104.81285172	-1.14408198448589	0.0051761162	0.0496944925
NS	940.87135974	-1.57843880864229	0.0007628666	0.0168119152
0.0446743057	NS	NS	NS	NS
NS	170495.71447	-2.08403749209316	0.0007252994	0.0165818439
NS	78372.441065	0.536771232320134	0.0015479712	0.0223109755
NS	1300.9925288	-1.70048799753224	0.000881478	0.0177096942
NS	3244.0224945	-2.68594727248037	1.0171571E-08	6.743752E-06
NS	3747.7714388	-2.02025705011229	0.0002373334	0.0110407853
0.0242408645	NS	NS	NS	NS
NS	NS	NS	NS	NS
0.0016475261	NS	NS	NS	NS
0.0446743057	NS	NS	NS	NS
0.0136497335	NS	NS	NS	NS
0.0011146056	354.47711391	2.71938137032654	0.0005547909	0.0153260998

Genus	baseMean	log2FoldChange.M2	pvalue.M2	FDR.M2
Dethiosulfovibrio	1.1203645551	-2.57332818203556	0.0020165228	0.0264668619
Deferribacter	1.4984664473	-2.34777503563961	0.0010251273	0.0177170255
Bartonella	3.1243402888	-2.48419332186266	0.0013148206	0.0207084237
unclassified Enterobacteriaceae	3.2410831199	3.24743164099598	0.0018961554	0.025969085
Acetivibrio	10.822518919	-0.594923855290991	0.0037684567	0.0429157311
Hippea	11.287841117	-1.46935901438464	0.0038147317	0.0429157311
Pseudogulbenkiana	12.092268316	-1.46681620707047	0.0037525383	0.0429157311
Pectobacterium	13.125717311	1.93358101667685	0.0015770498	0.0225804851
Pantoea	15.288386849	1.97777543097888	0.0001773271	0.0050780023
Serratia	17.532798551	1.79657457534688	0.0015136224	0.0225804851
Raphidiopsis	19.412425251	2.56859619313044	0.0006013002	0.0120609161
Dickeya	23.154493933	2.01139947920503	0.0004340833	0.0108526409
Helicobacter	29.178933175	1.92272118664129	0.0045114771	0.0490039749
Shewanella	39.711673629	1.79157682903309	0.0035818208	0.0429157311
Erwinia	41.689116024	2.51838701629822	1.55E-05	0.0006097553
Cronobacter	50.613102405	2.38072104379463	0.0001143755	0.0036028274
Rheinheimera	60.640284203	2.09183723698107	0.0007855383	0.0145555619
Dermacoccus	106.6722814	2.43536048708067	9.70E-05	0.0033947073
Yersinia	112.43494894	1.98415655990265	0.0004478868	0.0108526409
Bacillus	231.15271172	1.42979593898023	0.0005403586	0.0120609161
Pseudomonas	538.71280102	1.84864057656334	0.000612618	0.0120609161
Salmonella	838.75023335	2.54294598912405	3.31E-06	0.0002084253
Klebsiella	1314.8072541	2.99459444432131	1.29E-06	0.0002014192
Enterobacter	2064.670143	2.75451599443617	2.56E-06	0.0002014192
Citrobacter	2269.1567261	2.49053409912659	6.27E-06	0.000329183
Pseudoflavonifractor	13810.776864	-0.47177726733599	0.001068646	0.0177170255
Subdoligranulum	14645.794829	-0.589060651890544	8.07E-06	0.0003632692
Intestinibacter	40828.129982	-1.69927114303397	1.17E-06	0.0002014192
Escherichia	64517.118438	2.63807660647505	2.36E-06	0.0002014192
Achromobacter	NS	NS	NS	NS
Ralstonia	NS	NS	NS	NS
Listeria	NS	NS	NS	NS
Coriobacterium	NS	NS	NS	NS
Olsenella	NS	NS	NS	NS
Burkholderia	NS	NS	NS	NS
Riemerella	NS	NS	NS	NS
Slackia	NS	NS	NS	NS
Fusobacterium	NS	NS	NS	NS
Brachyspira	NS	NS	NS	NS
Oribacterium	NS	NS	NS	NS
Rothia	NS	NS	NS	NS
Veillonella	NS	NS	NS	NS
Porphyromonas	NS	NS	NS	NS
Streptococcus	NS	NS	NS	NS
Collinsella	NS	NS	NS	NS
Bifidobacterium	NS	NS	NS	NS
Bacteroides	NS	NS	NS	NS

Photorhabdus	NS	NS	NS	NS
Xanthomonas	NS	NS	NS	NS
Edwardsiella	NS	NS	NS	NS
Methylobacillus	NS	NS	NS	NS
Desulfurispirillum	NS	NS	NS	NS
Rahnella	NS	NS	NS	NS
Xenorhabdus	NS	NS	NS	NS
Providencia	NS	NS	NS	NS
Alkaliphilus	NS	NS	NS	NS
Acinetobacter	NS	NS	NS	NS
Holdemania	NS	NS	NS	NS

baseMean	log2FoldChange.M4	pvalue.M4	FDR.M4	baseMean	log2FoldChange.P/M6
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
NS	NS	NS	NS	NS	NS
13.125717311	2.29405713712304	0.0001734827	0.0023739732	NS	NS
15.288386849	2.36547100448097	6.91E-06	0.0001797709	NS	NS
17.532798551	1.91729592834407	0.0007064186	0.0079856015	NS	NS
NS	NS	NS	NS	NS	NS
23.154493933	2.40760957107512	2.44E-05	0.0005287831	NS	NS
NS	NS	NS	NS	NS	NS
39.711673629	2.92213579109827	1.75E-06	6.49E-05	NS	NS
41.689116024	2.97539284016915	3.10E-07	1.61E-05	NS	NS
50.613102405	2.84290908117312	3.89E-06	0.000112333	NS	NS
60.640284203	2.24641239342111	0.0003094774	0.00365746	385.52126051	2.41120346718811
106.6722814	2.32108521725282	0.0002040524	0.0026526807	557.44380344	2.33815575473702
112.43494894	2.2305899749061	7.82E-05	0.0012705358	353.47371186	2.53135321106484
NS	NS	NS	NS	919.86915476	1.30814962523106
538.71280102	3.19691957150476	2.80E-09	2.43E-07	NS	NS
838.75023335	2.7299106368497	5.94E-07	2.57E-05	2468.7294315	2.3249018878589
1314.8072541	4.47439221983451	4.52E-13	1.18E-10	NS	NS
2064.670143	2.39136336706601	4.45E-05	0.0008895503	NS	NS
2269.1567261	2.84736039893435	2.41E-07	1.57E-05	10791.804455	2.16138680300606
NS	NS	NS	NS	NS	NS
14645.794829	-0.408035395947533	0.0019904982	0.0207011808	76376.769627	0.357179353638895
40828.129982	-2.1196349337939	1.33E-09	1.73E-07	61094.040144	-1.04249112437843
64517.118438	2.46179407958598	1.06E-05	0.0002505165	301428.61607	2.37707119362075
NS	NS	NS	NS	78.351458173	-1.20845561937365
NS	NS	NS	NS	83.734550709	-1.31471573698494
NS	NS	NS	NS	96.214445203	-1.72692680820829
NS	NS	NS	NS	117.68168767	1.26303448525741
NS	NS	NS	NS	398.24889255	1.79264355849396
NS	NS	NS	NS	434.38819896	-1.07316378559191
NS	NS	NS	NS	508.59638397	-0.866049537435811
NS	NS	NS	NS	522.30810222	1.15842178740998
NS	NS	NS	NS	1361.7811447	-1.95930952717181
NS	NS	NS	NS	3954.578138	0.899366680795127
NS	NS	NS	NS	4373.9970927	-0.591529256125902
NS	NS	NS	NS	6837.4067277	1.31785334574673
NS	NS	NS	NS	9555.0281672	-2.13724681082723
NS	NS	NS	NS	15184.460217	-1.1990701142485
NS	NS	NS	NS	433545.3203	-1.3679337064167
NS	NS	NS	NS	666194.20863	1.25536785935027
NS	NS	NS	NS	2187577.8701	1.56422460791659
NS	NS	NS	NS	24025555.665	-1.05772082412784

2.3316978805	3.18688182854961	0.0001060376	0.001621752	NS	NS
3.87511727	2.65069371744059	5.40E-05	0.0009822346	NS	NS
6.5005830742	1.98375620109614	0.0023105314	0.0224691114	NS	NS
7.1915848397	2.79444601758884	0.0054924068	0.0492422681	NS	NS
10.524726612	2.07081122257176	0.0027851535	0.0258621397	NS	NS
10.771366696	2.60813376960162	2.63E-06	8.54E-05	NS	NS
11.918054766	2.46308703032416	0.0002414496	0.0029893764	NS	NS
13.077809252	2.44326122217054	0.0001422285	0.0020544117	NS	NS
13.874604426	-1.39022962640062	5.67E-05	0.0009822346	NS	NS
127.15355893	1.49117162013494	0.0008134273	0.0088121287	NS	NS
11637.273218	-0.358171079474317	0.0023333308	0.0224691114	NS	NS

pvalue.P/M6	FDR.P/M6
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
NS	NS
0.0025493456	0.0305921476
0.0036547166	0.0375913707
0.0018043096	0.0236200524
0.0173669846	0.0937767267
NS	NS
0.01153647	0.0722283336
NS	NS
NS	NS
0.0067212864	0.0537702913
NS	NS
0.0103687396	0.0716583997
0.0104501833	0.0716583997
0.0053509444	0.0481584997
0.011418342	0.0722283336
0.0175831363	0.0937767267
0.0014181113	0.0226897811
0.0002215414	0.0085088806
1.80E-05	0.001295046
0.0073276922	0.0555361936
0.0162441934	0.0935665538
0.0003494389	0.0085088806
0.0003168421	0.0085088806
0.0058289095	0.0493742921
0.0016860309	0.0236200524
0.0048675926	0.046728889
2.36E-06	0.0003399428
0.0007765226	0.0139774069
0.0005987198	0.0123165208
0.0003545367	0.0085088806
0.0035079562	0.0375913707
0.0161305426	0.0935665538

[illegible]

Supplementary Table 4

Sheet1

Sheet2

List of KOs significantly affected in the fecal metagenomes across all sampling points and corre

List of KOs;

KEGG pathway annotations for all KOs listed in Sheet1 (for KOs only significant after 2 and 4 months o

KO	Function	baseMean
K00003	E1.1.1.3; homoserine dehydrogenase [EC:1.1.1.3]	NA
K00005	E1.1.1.6, gldA; glycerol dehydrogenase [EC:1.1.1.6]	NA
K00020	E1.1.1.31, mmsB; 3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]	NA
K00024	mdh; malate dehydrogenase [EC:1.1.1.37]	NA
K00029	E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	NA
K00030	IDH3; isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]	NA
K00033	PGD, gnd; 6-phosphogluconate dehydrogenase [EC:1.1.1.44]	2919.514417
K00043	E1.1.1.61; 4-hydroxybutyrate dehydrogenase [EC:1.1.1.61]	NA
K00065	kduD; 2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]	698.2214032
K00068	srlD; sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]	382.6625487
K00090	E1.1.1.215; gluconate 2-dehydrogenase [EC:1.1.1.215]	NA
K00094	E1.1.1.251, gatD; galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]	16.36855478
K00100	E1.1.1.-	4847.248272
K00101	E1.1.2.3, lldD; L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]	29.8046841
K00102	E1.1.2.4, dld; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	NA
K00104	glcD; glycolate oxidase [EC:1.1.3.15]	NA
K00108	E1.1.99.1, betA, CHDH; choline dehydrogenase [EC:1.1.99.1]	35.63493489
K00116	mqq; malate dehydrogenase (quinone) [EC:1.1.5.4]	22.81672463
K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]	51.27410398
K00129	E1.2.1.5; aldehyde dehydrogenase (naD(P)+) [EC:1.2.1.5]	3.390080527
K00135	gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrog	184.2718633
K00137	prp; aminobutyraldehyde dehydrogenase [EC:1.2.1.19]	24.95510203
K00138	aldB; aldehyde dehydrogenase [EC:1.2.1.-]	40.89908546
K00140	mmsA, iolA, ALDH6A1; malonate-semialdehyde dehydrogenase (acetylating) / me	NA
K00163	aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]	81.23184643
K00164	OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	316.1296252
K00174	korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]	NA
K00175	korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]	NA
K00208	fabI; enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]	NA
K00216	entA; 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [EC:1.3.1.28]	NA
K00228	CPOX, hemF; coproporphyrinogen III oxidase [EC:1.3.3.3]	15.21887791
K00241	sdhC; succinate dehydrogenase cytochrome b556 subunit	NA
K00242	sdhD; succinate dehydrogenase membrane anchor subunit	6.954790002
K00247	frdD; fumarate reductase subunit D	16.17629129
K00257	E1.3.99.-	NA
K00259	ald; alanine dehydrogenase [EC:1.4.1.1]	NA
K00299	ssuE; FMN reductase [EC:1.5.1.38]	22.28983935
K00309	E1.5.3.-	8.079161178
K00329	E1.6.5.3; naDH dehydrogenase [EC:1.6.5.3]	2.036109793
K00330	nuoA; NADH-quinone oxidoreductase subunit A [EC:1.6.5.3]	NA
K00337	nuoH; NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]	NA
K00338	nuoI; NADH-quinone oxidoreductase subunit I [EC:1.6.5.3]	NA
K00339	nuoJ; NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]	NA
K00340	nuoK; NADH-quinone oxidoreductase subunit K [EC:1.6.5.3]	NA
K00341	nuoL; NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]	NA
K00343	nuoN; NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]	NA
K00346	nqrA; Na+-transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.6.5.-]	NA

K00347	nqrB; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit B [EC:1.6.5.-]	NA
K00348	nqrC; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit C [EC:1.6.5.-]	NA
K00349	nqrD; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit D [EC:1.6.5.-]	NA
K00351	nqrF; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit F [EC:1.6.5.-]	NA
K00362	nirB; nitrite reductase (naDH) large subunit [EC:1.7.1.15]	NS
K00363	nirD; nitrite reductase (naDH) small subunit [EC:1.7.1.15]	NS
K00372	nasA; assimilatory nitrate reductase catalytic subunit [EC:1.7.99.4]	70.25381818
K00380	cysJ; sulfite reductase (naDPH) flavoprotein alpha-component [EC:1.8.1.2]	71.91710792
K00381	cysI; sulfite reductase (naDPH) hemoprotein beta-component [EC:1.8.1.2]	45.91719966
K00383	GSR, gor; glutathione reductase (naDPH) [EC:1.8.1.7]	284.21138
K00394	aprA; adenylylsulfate reductase, subunit A [EC:1.8.99.2]	NA
K00395	aprB; adenylylsulfate reductase, subunit B [EC:1.8.99.2]	NA
K00427	lldP, lctP; L-lactate permease	42.8289479
K00432	E1.11.1.9; glutathione peroxidase [EC:1.11.1.9]	NA
K00433	cpo; non-heme chloroperoxidase [EC:1.11.1.10]	NS
K00441	frhB; coenzyme F420 hydrogenase subunit beta [EC:1.12.98.1]	NA
K00510	HMOX, hmuO, ho; heme oxygenase [EC:1.14.99.3]	9.878843776
K00525	E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1A]	NA
K00526	E1.17.4.1B, nrdB, nrdF; ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1B]	NA
K00528	E1.18.1.2, fpr; ferredoxin--NADP ⁺ reductase [EC:1.18.1.2]	NA
K00568	ubiG; 2-polyprenyl-6-hydroxyphenyl methylase / 3-demethylubiquinone-9 3-methyltransferase [EC:2.3.1.18]	15.39365526
K00575	cheR; chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	1023.387138
K00620	argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35]	NA
K00631	plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]	235.3588381
K00632	E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]	44.5898857
K00634	ptb; phosphate butyryltransferase [EC:2.3.1.19]	NA
K00656	E2.3.1.54, pflD; formate C-acetyltransferase [EC:2.3.1.54]	27057.17497
K00667	FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]	NA
K00673	astA; arginine N-succinyltransferase [EC:2.3.1.109]	18.00603769
K00677	lpxA; UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]	NA
K00687	pbp2B, penA; penicillin-binding protein 2B [EC:2.3.2.-]	NA
K00690	E2.4.1.7; sucrose phosphorylase [EC:2.4.1.7]	NA
K00693	GYS; glycogen(starch) synthase [EC:2.4.1.11]	3.430152127
K00697	otsA; trehalose 6-phosphate synthase [EC:2.4.1.15]	30.61565546
K00713	waaD; UDP-glucose:(glucosyl)LPS alpha-1,2-glucosyltransferase [EC:2.4.1.-]	NA
K00725	B4GALNT1, GALGT; (N-Acetylneuraminy)-galactosylglucosylceramide N-acetylglucosyltransferase [EC:2.4.1.25]	2.020024515
K00756	E2.4.2.2, pdp; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]	3184.122286
K00786	E2.4.-.-	607.724309
K00812	aspB; aspartate aminotransferase [EC:2.6.1.1]	NA
K00823	puuE; 4-aminobutyrate aminotransferase [EC:2.6.1.19]	NA
K00835	avtA; valine--pyruvate aminotransferase [EC:2.6.1.66]	58.94561117
K00840	astC; succinylornithine aminotransferase [EC:2.6.1.81]	20.03896043
K00851	E2.7.1.12, gntK, idnK; gluconokinase [EC:2.7.1.12]	NA
K00853	araB; L-ribulokinase [EC:2.7.1.16]	1917.37665
K00855	PRK, prkB; phosphoribulokinase [EC:2.7.1.19]	20.78767382
K00857	tdk, TK; thymidine kinase [EC:2.7.1.21]	NA
K00860	cysC; adenylylsulfate kinase [EC:2.7.1.25]	NA
K00863	E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]	NS

K00872	thrB1; homoserine kinase [EC:2.7.1.39]	NA
K00882	fruK; 1-phosphofructokinase [EC:2.7.1.56]	NA
K00884	naGK, nagK; N-acetylglucosamine kinase [EC:2.7.1.59]	24.65399978
K00885	nanK; N-acylmannosamine kinase [EC:2.7.1.60]	28.20302826
K00892	gsk; inosine kinase [EC:2.7.1.73]	29.1755452
K00895	E2.7.1.90, pfk; pyrophosphate--fructose-6-phosphate 1-phosphotransferase [EC:2.7.1.90]	NA
K00903	E2.7.10.-; protein-tyrosine kinase [EC:2.7.10.-]	71.01949038
K00906	aceK; isocitrate dehydrogenase kinase/phosphatase [EC:2.7.11.5 3.1.3.-]	43.92264243
K00912	lpxK; tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]	NA
K00924	E2.7.1.-	355.0757223
K00932	E2.7.2.15, tdcD, pduW; propionate kinase [EC:2.7.2.15]	28.36277294
K00934	E2.7.3.3; arginine kinase [EC:2.7.3.3]	27.78658206
K00938	E2.7.4.2, mvaK2; phosphomevalonate kinase [EC:2.7.4.2]	NA
K00940	E2.7.4.6, ndk; nucleoside-diphosphate kinase [EC:2.7.4.6]	NA
K00943	E2.7.4.9, tmk; dTMP kinase [EC:2.7.4.9]	2563.373184
K00946	thiL; thiamine-monophosphate kinase [EC:2.7.4.16]	NA
K00961	E2.7.7.7; Dna polymerase [EC:2.7.7.7]	33.75941033
K00971	manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]	NA
K00978	rfbF; glucose-1-phosphate cytidyltransferase [EC:2.7.7.33]	NA
K00983	E2.7.7.43, neuA, CMAS; N-acylneuraminate cytidyltransferase [EC:2.7.7.43]	NA
K00989	rph; ribonuclease PH [EC:2.7.7.56]	NA
K00997	acpS; holo-[acyl-carrier protein] synthase [EC:2.7.8.7]	NA
K01008	selD, SEPHS; selenide, water dikinase [EC:2.7.9.3]	NA
K01034	atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]	351.687113
K01035	atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]	304.1141396
K01048	pldB; lysophospholipase [EC:3.1.1.5]	NA
K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]	NA
K01060	E3.1.1.41; cephalosporin-C deacetylase [EC:3.1.1.41]	NA
K01061	E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]	40.19333776
K01070	frmB, ESD, fghA; S-formylglutathione hydrolase [EC:3.1.2.12]	30.96270239
K01087	otsB; trehalose 6-phosphate phosphatase [EC:3.1.3.12]	19.08542985
K01089	hisB; imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:4.2.1.1]	NA
K01091	E3.1.3.18, gph; phosphoglycolate phosphatase [EC:3.1.3.18]	13022.1139
K01114	plcC; phospholipase C [EC:3.1.4.3]	NS
K01119	cpdB; 2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.4.16]	NA
K01126	E3.1.4.46, glpQ, ugpQ; glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]	NA
K01133	E3.1.6.6, betC; choline-sulfatase [EC:3.1.6.6]	24.6857774
K01139	spoT, HDDC3; guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.11.5]	NS
K01144	E3.1.11.5; exodeoxyribonuclease V [EC:3.1.11.5]	NA
K01146	xni; protein Xni	15.76919632
K01155	E3.1.21.4; type II restriction enzyme [EC:3.1.21.4]	NA
K01167	E3.1.27.3; ribonuclease T1 [EC:3.1.27.3]	NA
K01169	rna; ribonuclease I (enterobacter ribonuclease) [EC:3.1.27.6]	16.17473466
K01173	ENDOG; endonuclease G, mitochondrial	NA
K01201	GBA, srfJ; glucosylceramidase [EC:3.2.1.45]	NA
K01205	NAGLU; alpha-N-acetylglucosaminidase [EC:3.2.1.50]	NA
K01206	FUCA; alpha-L-fucosidase [EC:3.2.1.51]	NA
K01207	E3.2.1.52, nagZ; beta-N-acetylhexosaminidase [EC:3.2.1.52]	4685.800509

K01210	E3.2.1.58; glucan 1,3-beta-glucosidase [EC:3.2.1.58]	NA
K01212	sacC; levanase [EC:3.2.1.65]	NA
K01238	E3.2.1.-	556.0884093
K01239	iunH; purine nucleosidase [EC:3.2.2.1]	NA
K01241	amn; AMP nucleosidase [EC:3.2.2.4]	NA
K01247	alkA; Dna-3-methyladenine glycosylase II [EC:3.2.2.21]	702.9464609
K01252	entB, dhbB, vibB, mxrF; bifunctional isochorismate lyase / aryl carrier protein [EC:3.2.2.22]	11.09280992
K01261	pepA; glutamyl aminopeptidase [EC:3.4.11.7]	NA
K01263	E3.4.11.14; cytosol alanyl aminopeptidase [EC:3.4.11.14]	22.977788
K01266	dmpA; D-aminopeptidase [EC:3.4.11.19]	NS
K01269	E3.4.11.-; aminopeptidase [EC:3.4.11.-]	3902.826567
K01277	E3.4.14.4, DPP3; dipeptidyl-peptidase III [EC:3.4.14.4]	NA
K01278	DPP4; dipeptidyl-peptidase 4 [EC:3.4.14.5]	NA
K01305	iadA; beta-aspartyl-dipeptidase (metallo-type) [EC:3.4.19.-]	2390.321971
K01354	ptrB; oligopeptidase B [EC:3.4.21.83]	NA
K01355	ompT; omptin [EC:3.4.23.49]	19.02638398
K01369	LGMM; legumain [EC:3.4.22.34]	NA
K01387	colA; microbial collagenase [EC:3.4.24.3]	18.27710765
K01407	ptr; protease III [EC:3.4.24.55]	72.81603497
K01412	PMPCA, MAS2; mitochondrial-processing peptidase subunit alpha [EC:3.4.24.64]	26.73271914
K01417	E3.4.24.-; putative zinc metalloprotease [EC:3.4.24.-]	NS
K01421	yhgE; putative membrane protein	NA
K01424	E3.5.1.1, ansA, ansB; L-asparaginase [EC:3.5.1.1]	NA
K01433	purU; formyltetrahydrofolate deformylase [EC:3.5.1.10]	NA
K01438	argE; acetylornithine deacetylase [EC:3.5.1.16]	NA
K01449	E3.5.1.28C, cwjJ, sleB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	1578.625326
K01460	gsp; glutathionylspermidine amidase/synthetase [EC:3.5.1.78 6.3.1.8]	72.08724975
K01464	DPYS, dht, hydA; dihydropyrimidinase [EC:3.5.2.2]	NA
K01468	hutI, AMDHD1; imidazolonepropionase [EC:3.5.2.7]	NA
K01470	E3.5.2.10; creatinine amidohydrolase [EC:3.5.2.10]	1600.179402
K01484	astB; succinylarginine dihydrolase [EC:3.5.3.23]	20.88363982
K01487	E3.5.4.3, guaD; guanine deaminase [EC:3.5.4.3]	NA
K01497	ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]	36.83464287
K01506	E3.5.-.-	2.169051691
K01507	ppa; inorganic pyrophosphatase [EC:3.6.1.1]	1013.433879
K01509	E3.6.1.3; adenosinetriphosphatase [EC:3.6.1.3]	9.930339573
K01521	cdh; CDP-diacylglycerol pyrophosphatase [EC:3.6.1.26]	24.80796699
K01552	E3.6.3.-	NA
K01553	E3.6.4.1; myosin ATPase [EC:3.6.4.1]	NA
K01574	adc; acetoacetate decarboxylase [EC:4.1.1.4]	23.61151997
K01585	E4.1.1.19S, speA; arginine decarboxylase [EC:4.1.1.19]	NA
K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]	NA
K01597	MVD, mvaD; diphosphomevalonate decarboxylase [EC:4.1.1.33]	NA
K01608	gcl; tartronate-semialdehyde synthase [EC:4.1.1.47]	47.62448348
K01631	dgoA; 2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]	23.63464499
K01632	E4.1.2.22; fructose-6-phosphate phosphoketolase [EC:4.1.2.22]	NA
K01633	folB; dihydroneopterin aldolase [EC:4.1.2.25]	NA
K01637	E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]	32.89565441

K01638	E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]	64.56773857
K01639	E4.1.3.3, nana, NPL; N-acetylneuraminate lyase [EC:4.1.3.3]	2791.710083
K01664	pabA; para-aminobenzoate synthetase component II [EC:2.6.1.85]	NA
K01666	E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]	3054.633237
K01669	E4.1.99.3, phrB; deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]	NS
K01671	E4.1.-.-	7.990764732
K01674	cah; carbonic anhydrase [EC:4.2.1.1]	NA
K01676	E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]	NA
K01682	acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]	182.1544329
K01690	edd; phosphogluconate dehydratase [EC:4.2.1.12]	38.12452893
K01693	E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]	NA
K01697	E4.2.1.22, CBS; cystathionine beta-synthase [EC:4.2.1.22]	NA
K01698	hemB, ALAD; porphobilinogen synthase [EC:4.2.1.24]	NA
K01706	gudD; glucarate dehydratase [EC:4.2.1.40]	292.7574011
K01708	garD; galactarate dehydratase [EC:4.2.1.42]	385.1424748
K01712	hutU, UROC1; urocanate hydratase [EC:4.2.1.49]	NA
K01716	fabA; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]	30.43235118
K01719	hemD, UROS; uroporphyrinogen-III synthase [EC:4.2.1.75]	NA
K01729	algL; poly(beta-D-mannuronate) lyase [EC:4.2.2.3]	NA
K01730	ogl; oligogalacturonide lyase [EC:4.2.2.6]	NA
K01737	queD, ptpS, PTS; 6-pyruvoyltetrahydropterin/6-carboxytetrahydropterin synthase	NA
K01745	hutH, HAL; histidine ammonia-lyase [EC:4.3.1.3]	NA
K01749	hemC, HMBS; hydroxymethylbilane synthase [EC:2.5.1.61]	NA
K01751	E4.3.1.15; diaminopropionate ammonia-lyase [EC:4.3.1.15]	1131.44489
K01761	E4.4.1.11; methionine-gamma-lyase [EC:4.4.1.11]	724.2625629
K01766	csdA; cysteine sulfinatase desulfinate [EC:4.4.1.-]	33.35776054
K01782	fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyry	44.30224564
K01785	E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]	NA
K01786	araD; L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	NA
K01787	RENBP; N-acylglucosamine 2-epimerase [EC:5.1.3.8]	NA
K01788	nanE; N-acylglucosamine-6-phosphate 2-epimerase [EC:5.1.3.9]	1377.96103
K01791	wecB; UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]	NA
K01807	rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]	908.3777131
K01811	yicI; alpha-D-xyloside xylohydrolase [EC:3.2.1.177]	NA
K01815	kduI; 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase [EC:5.3.1.17]	NA
K01818	fucl; L-fucose isomerase [EC:5.3.1.25]	5629.081473
K01819	E5.3.1.26, lacA, lacB; galactose-6-phosphate isomerase [EC:5.3.1.26]	NA
K01825	fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyry	62.34503267
K01840	manB; phosphomannomutase [EC:5.4.2.8]	NA
K01841	pepM; phosphoenolpyruvate phosphomutase [EC:5.4.2.9]	NA
K01847	MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]	NA
K01858	E5.5.1.4, INO1; myo-inositol-1-phosphate synthase [EC:5.5.1.4]	NA
K01895	ACSS, acs; acetyl-CoA synthetase [EC:6.2.1.1]	NA
K01897	ACSL, fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	NA
K01908	E6.2.1.17, prpE; propionyl-CoA synthetase [EC:6.2.1.17]	37.67680437
K01960	E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]	NA
K01961	accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	8363.594381
K01990	ABC-2.A; ABC-2 type transport system ATP-binding protein	NA

K01991	ABC-2.OM, wza; polysaccharide export outer membrane protein	NA
K01993	ABC-2.TX; HlyD family secretion protein	NA
K01994	gerE; LuxR family transcriptional regulator, transcriptional regulator of spore coat	12.91440241
K02018	modB; molybdate transport system permease protein	NA
K02024	lamB; maltoporin	206.3038438
K02032	ABC.PE.A1; peptide/nickel transport system ATP-binding protein	NA
K02033	ABC.PE.P; peptide/nickel transport system permease protein	NA
K02045	cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]	NA
K02046	cysU; sulfate transport system permease protein	NA
K02047	cysW; sulfate transport system permease protein	NA
K02048	cysP, sbp; sulfate transport system substrate-binding protein	NA
K02053	ABC.SP.P; putative spermidine/putrescine transport system permease protein	NA
K02054	ABC.SP.P1; putative spermidine/putrescine transport system permease protein	NA
K02055	ABC.SP.S; putative spermidine/putrescine transport system substrate-binding protein	NA
K02062	thiQ; thiamine transport system ATP-binding protein	21.69807208
K02063	thiP; thiamine transport system permease protein	61.00608502
K02064	thiB, tbpA; thiamine transport system substrate-binding protein	39.79373385
K02065	ABC.X1.A; putative ABC transport system ATP-binding protein	NA
K02066	ABC.X1.P; putative ABC transport system permease protein	NA
K02074	ABC.ZM.A; zinc/manganese transport system ATP-binding protein	NA
K02077	ABC.ZM.S; zinc/manganese transport system substrate-binding protein	NA
K02079	agaA; N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]	20.96730863
K02100	araE; MFS transporter, SP family, arabinose:H ⁺ symporter	317.0204741
K02102	K02102	23.63962854
K02133	ATPeF1B, ATP5B; F-type H ⁺ -transporting ATPase subunit beta [EC:3.6.3.14]	33.09630589
K02167	betI; TetR/AcrR family transcriptional regulator, transcriptional repressor of bet g	12.88338673
K02169	bioC; malonyl-CoA O-methyltransferase [EC:2.1.1.197]	NA
K02170	bioH; pimeloyl-[acyl-carrier protein] methyl ester esterase [EC:3.1.1.85]	16.4940342
K02196	ccmD; heme exporter protein D	3.43246033
K02248	comGF; competence protein ComGF	NA
K02255	ftnB; ferritin-like protein 2	7.184833615
K02280	cpaC, rcpA; pilus assembly protein CpaC	44.17466412
K02297	cyoA; cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]	20.80080501
K02298	cyoB; cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]	45.17722481
K02299	cyoC; cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]	11.84247949
K02301	cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]	17.48076027
K02317	dnaT; Dna replication protein DnaT	NS
K02336	DPO2, polB; Dna polymerase II [EC:2.7.7.7]	52.36600299
K02344	DPO3P, holD; Dna polymerase III subunit psi [EC:2.7.7.7]	9.226052399
K02345	DPO3T, holE; Dna polymerase III subunit theta [EC:2.7.7.7]	4.401835396
K02361	entC; isochorismate synthase [EC:5.4.4.2]	NA
K02362	entD; enterobactin synthetase component D [EC:2.7.8.-]	14.81324405
K02364	entF; enterobactin synthetase component F [EC:2.7.7.-]	90.54066
K02381	fdrA; FdrA protein	NS
K02402	flhC; flagellar transcriptional activator FlhC	11.95643553
K02403	flhD; flagellar transcriptional activator FlhD	NS
K02419	fliP; flagellar biosynthetic protein FliP	929.4808684
K02423	fliT; flagellar protein FliT	NA

K02425	fliz; Fliz protein	12.31512164
K02429	fucP; MFS transporter, FHS family, L-fucose permease	NA
K02430	fucR; DeoR family transcriptional regulator, L-fucose operon activator	18.17746563
K02433	gatA, QRSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A	NA
K02434	gatB, PET112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit E	NA
K02435	gatC, GATC; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C	NA
K02436	gatR; DeoR family transcriptional regulator, galactitol utilization operon repressor	14.35603921
K02439	glpE; thiosulfate sulfurtransferase [EC:2.8.1.1]	NA
K02444	glpR; DeoR family transcriptional regulator, glycerol-3-phosphate regulon repress	781.7180673
K02445	glpT; MFS transporter, OPA family, glycerol-3-phosphate transporter	NA
K02452	gspC; general secretion pathway protein C	29.63984578
K02457	gspH; general secretion pathway protein H	14.37383549
K02458	gspI; general secretion pathway protein I	14.25667334
K02459	gspJ; general secretion pathway protein J	18.20780847
K02461	gspL; general secretion pathway protein L	45.00261089
K02462	gspM; general secretion pathway protein M	12.30792752
K02467	gutQ; GutQ protein	22.13156672
K02468	srlR, gutR; DeoR family transcriptional regulator, glucitol operon repressor	13.59680488
K02472	wecC; UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.336]	NA
K02474	wbpO; UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.-]	NA
K02475	K02475; two-component system, CitB family, response regulator	2.822946308
K02476	K02476; two-component system, CitB family, sensor kinase [EC:2.7.13.3]	8.24780701
K02485	rssB, hnr; two-component system, unclassified family, response regulator	20.25164818
K02492	hemA; glutamyl-tRNA reductase [EC:1.2.1.70]	NA
K02495	hemN, hemZ; oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]	18258.98924
K02499	yabN; tetrapyrrole methylase family protein / MazG family protein	2188.114785
K02502	hisZ; ATP phosphoribosyltransferase regulatory subunit	NA
K02504	hofB; protein transport protein HofB	44.99371512
K02505	hofC; protein transport protein HofC	37.9806253
K02521	ilvY; LysR family transcriptional regulator, positive regulator for ilvC	75.27820974
K02523	ispB; octaprenyl-diphosphate synthase [EC:2.5.1.90]	NA
K02525	kdgR; LacI family transcriptional regulator, kdg operon repressor	NA
K02526	kdgT; 2-keto-3-deoxygluconate permease	NA
K02527	kdtA, waaA; 3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12 2.4.99.1]	NA
K02531	lacT; transcriptional antiterminator	25.92949041
K02538	manR; activator of the mannose operon, transcriptional antiterminator	70.15821789
K02550	glcA; glycolate permease	29.34787784
K02551	menD; 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	NA
K02553	rraA, menG; regulator of ribonuclease activity A	15.57847118
K02560	msbB; lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase [EC:2.3.1.-]	28.52240291
K02562	mtlR1, mtlR; mannitol operon repressor	12.78110088
K02565	nagC; N-acetylglucosamine repressor	NS
K02589	nifHD1, nifH1; nitrogen regulatory protein PII 1	78.67353042
K02594	nifV; homocitrate synthase NifV [EC:2.3.3.14]	72.23467912
K02603	ORC1; origin recognition complex subunit 1	NA
K02621	parC; topoisomerase IV subunit A [EC:5.99.1.-]	NA
K02622	parE; topoisomerase IV subunit B [EC:5.99.1.-]	NA
K02652	pilB; type IV pilus assembly protein PilB	3887.200508

K02669	pilT; twitching motility protein PilT	NA
K02679	ppdA; prepilin peptidase dependent protein A	14.9571351
K02680	ppdB; prepilin peptidase dependent protein B	18.4990022
K02681	ppdC; prepilin peptidase dependent protein C	NA
K02682	ppdD; prepilin peptidase dependent protein D	15.65178181
K02742	sprT; SprT protein	11.64330756
K02744	PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component [EC:2.7.1.6]	424.830231
K02757	PTS-Bgl-EIIC, bglF; PTS system, beta-glucosides-specific IIC component	NA
K02763	PTS-Dgl-EIIA, gamP; PTS system, D-glucosamine-specific IIA component [EC:2.7.1.6]	11.38287011
K02773	PTS-Gat-EIIA, gatA; PTS system, galactitol-specific IIA component [EC:2.7.1.69]	355.259407
K02774	PTS-Gat-EIIB, gatB; PTS system, galactitol-specific IIB component [EC:2.7.1.69]	141.7738971
K02777	PTS-Glc-EIIA, crr; PTS system, glucose-specific IIA component [EC:2.7.1.69]	405.8026451
K02779	PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component	966.3690865
K02794	PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]	2164.940074
K02795	PTS-Man-EIIC, manY; PTS system, mannose-specific IIC component	2745.353138
K02796	PTS-Man-EIID, manZ; PTS system, mannose-specific IID component	2689.578829
K02800	PTS-Mtl-EIIC, mtlA; PTS system, mannitol-specific IIC component	2104.227519
K02812	PTS-Sor-EIIA, sorF; PTS system, sorbose-specific IIA component [EC:2.7.1.69]	5.400092215
K02813	PTS-Sor-EIIB, sorB; PTS system, sorbose-specific IIB component [EC:2.7.1.69]	10.37528475
K02814	PTS-Sor-EIIC, sorA; PTS system, sorbose-specific IIC component	13.33764966
K02821	PTS-Ula-EIIA, ulaC, sgaA; PTS system, ascorbate-specific IIA component [EC:2.7.1.6]	190.2852941
K02822	PTS-Ula-EIIB, ulaB, sgaB; PTS system, ascorbate-specific IIB component [EC:2.7.1.6]	96.55502466
K02840	waaB, rfaB; UDP-D-galactose:(glucosyl)LPS alpha-1,6-D-galactosyltransferase [EC:2.4.1.1]	NA
K02843	waaF, rfaF; heptosyltransferase II [EC:2.4.-.-]	1361.6278
K02844	waaG, rfaG; UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]	103.4380992
K02846	solA; N-methyl-L-tryptophan oxidase [EC:1.5.3.-]	20.506025
K02847	waaL, rfaL; O-antigen ligase [EC:6.-.-.-]	40.06885115
K02848	waaP, rfaP; heptose (I) phosphotransferase [EC:2.7.1.-]	NA
K02850	waaY, rfaY; heptose (II) phosphotransferase [EC:2.7.1.-]	22.87843966
K02852	rffM; UDP-N-acetyl-D-mannosaminuronic acid transferase [EC:2.4.1.-]	NA
K02853	wzyE, rffT; 4-alpha-L-fucosyltransferase [EC:2.4.1.-]	96.63774351
K02856	K02856, rhaT; L-rhamnose-H ⁺ transport protein	NA
K02902	RP-L28, MRPL28, rpmB; large subunit ribosomal protein L28	NA
K03072	secD; preprotein translocase subunit SecD	2858.14801
K03078	ulaD, sgaH; 3-dehydro-L-gulonate-6-phosphate decarboxylase [EC:4.1.1.85]	NA
K03081	sgbH; 3-dehydro-L-gulonate-6-phosphate decarboxylase [EC:4.1.1.85]	19.14807623
K03088	SIG3.2, rpoE; RNA polymerase sigma-70 factor, ECF subfamily	NA
K03092	SIG54, rpoN; RNA polymerase sigma-54 factor	NA
K03113	EIF1, SUI1; translation initiation factor 1	NA
K03119	tauD; taurine dioxygenase [EC:1.14.11.17]	17.46930261
K03126	TAF12; transcription initiation factor TFIID subunit 12	NA
K03177	truB, PUS4, TRUB1; tRNA pseudouridine55 synthase [EC:5.4.99.25]	6885.939195
K03181	ubiC; chorismate--pyruvate lyase [EC:4.1.3.40]	10.97780546
K03182	ubiD; 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]	NA
K03184	ubiF; 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase [EC:1.14.13.-]	22.36099938
K03185	ubiH; 2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]	25.31761455
K03195	virB10, lvhB10; type IV secretion system protein VirB10	NS
K03200	virB5, lvhB5; type IV secretion system protein VirB5	94.87076686

K03207	wcaH; colanic acid biosynthesis protein WcaH [EC:3.6.1.-]	11.2528994
K03212	rumB; 23S rRNA (uracil747-C5)-methyltransferase [EC:2.1.1.189]	31.20068389
K03214	yfiF, trmG; RNA methyltransferase, TrmH family [EC:2.1.1.-]	32.13937209
K03218	rlmB; 23S rRNA (guanosine2251-2'-O)-methyltransferase [EC:2.1.1.185]	NS
K03219	yscC; type III secretion protein SctC	48.18839235
K03223	yscL; type III secretion protein SctL	13.43730754
K03224	yscN; ATP synthase in type III secretion protein SctN [EC:3.6.3.14]	39.63829367
K03269	lpxH; UDP-2,3-diacylglucosamine hydrolase [EC:3.6.1.54]	NA
K03281	TC.CIC; chloride channel protein, CIC family	NA
K03286	TC.OOP; OmpA-OmpF porin, OOP family	NA
K03290	nanT; MFS transporter, SHS family, sialic acid transporter	29.67771247
K03291	MFS.SET; MFS transporter, SET family, sugar efflux transporter	60.17067265
K03293	TC.AAT; amino acid transporter, AAT family	NA
K03294	TC.APA; basic amino acid/polyamine antiporter, APA family	5236.288037
K03304	tehA; tellurite resistance protein	25.96821872
K03305	TC.POT; proton-dependent oligopeptide transporter, POT family	NA
K03314	nhaB; Na ⁺ :H ⁺ antiporter, NhaB family	108.4087837
K03316	TC.CPA1; monovalent cation:H ⁺ antiporter, CPA1 family	NA
K03321	TC.SULP; sulfate permease, SulP family	NA
K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	NA
K03328	TC.PST; polysaccharide transporter, PST family	NA
K03329	yahN; amino acid exporter	12.1711945
K03337	iolB; 5-deoxy-glucuronate isomerase [EC:5.3.1.-]	NA
K03394	cobI-cbiL; precorrin-2/cobalt-factor-2 C20-methyltransferase [EC:2.1.1.130 2.1.1.131]	2346.945233
K03425	tatE; sec-independent protein translocase protein TatE	1.745344153
K03435	fruR1, fruR; LacI family transcriptional regulator, fructose operon transcriptional	28.13613326
K03444	MFS.SP; MFS transporter, SP family, sugar porter, other	NA
K03445	nepl; MFS transporter, DHA1 family, purine ribonucleoside efflux pump	37.00088261
K03455	TC.KEF; monovalent cation:H ⁺ antiporter-2, CPA2 family	NA
K03468	aaeB; p-hydroxybenzoic acid efflux pump subunit AaeB	53.60545011
K03472	epd; D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]	25.95910383
K03473	pdxB; erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]	NA
K03474	pdxJ; pyridoxine 5-phosphate synthase [EC:2.6.99.2]	NA
K03475	PTS-Ula-EIIC, ulaA, sgaT; PTS system, ascorbate-specific IIC component	820.5114906
K03476	ulaG; L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]	225.0622309
K03477	ulaR; DeoR family transcriptional regulator, ulaG and ulaABCDEF operon transcrip	19.73897123
K03480	glcT; transcriptional antiterminator	NA
K03483	mtlR2, mtlR; mannitol operon transcriptional antiterminator	1274.504459
K03485	treR1, treR; LacI family transcriptional regulator, trehalose operon repressor	23.0047414
K03486	treR2, treR; GntR family transcriptional regulator, trehalose operon transcriptional	NA
K03489	yydK; GntR family transcriptional regulator, transcriptional regulator of bglA	NS
K03518	coxS; carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]	NA
K03527	E1.17.1.2, lytB, ispH; 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.1.1.171]	10669.71294
K03528	zipA; cell division protein ZipA	65.31308595
K03530	hupB; DNA-binding protein HU-beta	NA
K03534	rhaM; L-rhamnose mutarotase [EC:5.1.3.-]	NA
K03548	perM; putative permease	72.05851703
K03554	rdgC; recombination associated protein RdgC	64.3608763

K03558	cvpA; membrane protein required for colicin V production	NA
K03561	exbB; biopolymer transport protein ExbB	NA
K03566	gcvA; LysR family transcriptional regulator, glycine cleavage system transcriptiona	30.36815992
K03568	tldD; TldD protein	NA
K03576	metR; LysR family transcriptional regulator, regulator for metE and methH	28.81445612
K03590	ftsA; cell division protein FtsA	NA
K03591	ftsN; cell division protein FtsN	35.49365366
K03597	rseA; sigma-E factor negative regulatory protein RseA	20.96958568
K03598	rseB; sigma-E factor negative regulatory protein RseB	81.75650456
K03606	wcaJ; putative colanic acid biosynthesis UDP-glucose lipid carrier transferase	NA
K03607	proQ; ProP effector	42.20599746
K03632	mukB; chromosome partition protein MukB	148.8186333
K03633	mukF; chromosome partition protein MukF	39.61781933
K03637	moaC; molybdenum cofactor biosynthesis protein C	NA
K03638	moaB; molybdenum cofactor biosynthesis protein B	NS
K03639	MOCS1, moaA; molybdenum cofactor biosynthesis protein	NA
K03640	pal; peptidoglycan-associated lipoprotein	NA
K03645	seqA; negative modulator of initiation of replication	20.33636296
K03649	MUG, TDG; TDG/mug DNA glycosylase family protein [EC:3.2.2.-]	NA
K03651	icc; lcc protein	72.32204908
K03652	MPG; Dna-3-methyladenine glycosylase [EC:3.2.2.21]	253.8538106
K03656	rep; ATP-dependent Dna helicase Rep [EC:3.6.4.12]	188.2725423
K03658	helD; DNA helicase IV [EC:3.6.4.12]	NA
K03666	hfq; host factor-I protein	237.4756198
K03672	trxC; thioredoxin 2 [EC:1.8.1.8]	10.39672948
K03675	grxB; glutaredoxin 2	NA
K03676	grxC, GLRX, GLRX2; glutaredoxin 3	NS
K03683	rnt; ribonuclease T [EC:3.1.13.-]	18.10131404
K03688	ubiB, aarF; ubiquinone biosynthesis protein	NA
K03690	yigP; hypothetical protein	12.81725737
K03693	pbp; penicillin-binding protein	NA
K03707	tena; thiaminase (transcriptional activator Tena) [EC:3.5.99.2]	NS
K03710	K03710; GntR family transcriptional regulator	4262.505487
K03711	fur; Fur family transcriptional regulator, ferric uptake regulator	NA
K03716	spIB; spore photoproduct lyase [EC:4.1.99.14]	663.6340103
K03718	asnC; Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	NA
K03720	trpR; TrpR family transcriptional regulator, trp operon repressor	9.722191411
K03721	tyrR; transcriptional regulator of aroF, aroG, tyrA and aromatic amino acid transpo	285.2636573
K03724	lhr; ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]	NA
K03727	helY; ATP-dependent RNA helicase HelY [EC:3.6.4.-]	NA
K03732	rhIB; ATP-dependent Rna helicase RhIB [EC:3.6.4.13]	52.84270774
K03733	xerC; integrase/recombinase XerC	NA
K03742	cina; competence/damage-inducible protein Cina	5479.837214
K03744	lemA; LemA protein	NA
K03746	hns; Dna-binding protein H-na	NS
K03747	smg; Smg protein	9.859551852
K03750	moeA; molybdopterin molybdotransferase [EC:2.10.1.1]	2000.359411
K03755	adiY; AraC family transcriptional regulator, transcriptional activator of adiA	20.29059503

K03761	kgtP; MFS transporter, MHS family, alpha-ketoglutarate permease	32.25205102
K03764	metJ; transcriptional repressor of met regulon (beta-ribbon, MetJ family)	8.232828285
K03770	ppiD; peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]	NA
K03771	surA; peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]	NA
K03773	fklB; FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]	NA
K03774	slpA; FKBP-type peptidyl-prolyl cis-trans isomerase SlpA [EC:5.2.1.8]	5.49925623
K03775	slyD; FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]	NA
K03776	aer; aerotaxis receptor	94.47659967
K03777	dld; D-lactate dehydrogenase [EC:1.1.1.28]	43.59243327
K03782	katG; catalase-peroxidase [EC:1.11.1.21]	53.24360398
K03787	surE; 5'-nucleotidase [EC:3.1.3.5]	NA
K03788	aphA; acid phosphatase (class B) [EC:3.1.3.2]	34.93715181
K03802	cphA; cyanophycin synthetase [EC:6.3.2.29 6.3.2.30]	47.90269551
K03803	rseC; sigma-E factor negative regulatory protein RseC	NA
K03804	mukE; chromosome partition protein MukE	20.92017973
K03807	ampE; AmpE protein	18.51333783
K03808	pqiA; paraquat-inducible protein A	94.38936766
K03811	pnuC; nicotinamide mononucleotide transporter	NA
K03814	mtgA; monofunctional biosynthetic peptidoglycan transglycosylase [EC:2.4.1.-]	NA
K03818	wcaF; putative colanic acid biosynthesis acetyltransferase WcaF [EC:2.3.1.-]	NA
K03819	wcaB; putative colanic acid biosynthesis acetyltransferase WcaB [EC:2.3.1.-]	8.130841555
K03832	tonB; periplasmic protein TonB	NA
K03834	tyrP; tyrosine-specific transport protein	62.76755541
K03835	mtr; tryptophan-specific transport protein	65.39524515
K03836	tnaB; low affinity tryptophan permease	12.57928624
K03837	sdaC; serine transporter	62.85122667
K03838	tdcC; threonine transporter	35.43518226
K03839	fldA, nifF, isiB; flavodoxin I	NA
K03840	fldB; flavodoxin II	9.020230972
K03855	fixX; ferredoxin like protein	7.628080688
K03885	ndh; NADH dehydrogenase [EC:1.6.99.3]	NA
K03892	arsR; ArsR family transcriptional regulator	NA
K03894	iucA; N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]	17.06235425
K03895	iucC; aerobactin synthase [EC:6.3.2.39]	16.61657845
K03897	iucD; lysine N6-hydroxylase [EC:1.14.13.59]	12.38557439
K03919	alkB; alkylated Dna repair protein (Dna oxidative demethylase) [EC:1.14.11.33]	2.370038578
K03930	estA; putative tributyrin esterase [EC:3.1.1.-]	NA
K03931	ygjK; putative isomerase	NA
K03970	pspB; phage shock protein B	2.108017841
K03971	pspD; phage shock protein D	NA
K03972	pspE; phage shock protein E	11.40986683
K03974	pspF; psp operon transcriptional activator	14.76297897
K03975	dedA; membrane-associated protein	1165.826229
K04013	nrfB; cytochrome c-type protein NrfB	22.99046639
K04016	nrfE; cytochrome c-type biogenesis protein NrfE	54.7051283
K04018	nrfG; formate-dependent nitrite reductase complex subunit NrfG	56.99926941
K04022	eutG; alcohol dehydrogenase	21.67870019
K04025	eutK; ethanolamine utilization protein EutK	8.995934255

K04028	eutN; ethanolamine utilization protein EutN	NA
K04031	eutS; ethanolamine utilization protein EutS	438.6656235
K04033	eutR; AraC family transcriptional regulator, ethanolamine operon transcriptional a	19.53269961
K04058	yscW; type III secretion protein SctW	26.60271421
K04065	osmY; hyperosmotically inducible periplasmic protein	15.40706927
K04067	priC; primosomal replication protein N"	14.37024216
K04070	pflX; putative pyruvate formate lyase activating enzyme [EC:1.97.1.4]	3421.711932
K04076	lonB; Lon-like ATP-dependent protease [EC:3.4.21.-]	156.4583698
K04080	ibpA; molecular chaperone IbpA	NS
K04081	ibpB; molecular chaperone IbpB	12.72049742
K04086	clpL; ATP-dependent Clp protease ATP-binding subunit ClpL	NA
K04091	ssuD; alkanesulfonate monooxygenase [EC:1.14.14.5]	26.25531352
K04092	tyrA1; chorismate mutase [EC:5.4.99.5]	NA
K04094	trmFO, gid; methylenetetrahydrofolate--tRna-(uracil-5-)-methyltransferase [EC:2.	3865.852616
K04335	csgB; minor curlin subunit	8.462291003
K04336	csgC; curli production protein	7.300934011
K04337	csgE; curli production assembly/transport component CsgE	6.990373814
K04338	csgF; curli production assembly/transport component CsgF	5.989463105
K04516	ARO1, aroA; chorismate mutase [EC:5.4.99.5]	NA
K04517	tyrA2; prephenate dehydrogenase [EC:1.3.1.12]	NA
K04518	pheA2; prephenate dehydratase [EC:4.2.1.51]	NA
K04564	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	NA
K04568	poxA; lysyl-tRna synthetase, class II [EC:6.1.1.6]	43.67187778
K04654	hypD; hydrogenase expression/formation protein HypD	NA
K04655	hypE; hydrogenase expression/formation protein HypE	NA
K04656	hypF; hydrogenase maturation protein HypF	NA
K04691	hhoB, degS; serine protease DegS [EC:3.4.21.-]	80.44620946
K04753	sufl; suppressor of ftsI	51.20324078
K04757	rsbW; serine/threonine-protein kinase RsbW [EC:2.7.11.1]	NA
K04759	feoB; ferrous iron transport protein B	35233.07835
K04761	oxyR; LysR family transcriptional regulator, hydrogen peroxide-inducible genes ac	NA
K04770	lonH; Lon-like ATP-dependent protease [EC:3.4.21.-]	109.8186108
K04771	degP, htrA; serine protease Do [EC:3.4.21.107]	NS
K04773	sppA; protease IV [EC:3.4.21.-]	NA
K04774	sohB; serine protease SohB [EC:3.4.21.-]	70.72950777
K04775	ydgD; protease YdgD [EC:3.4.21.-]	12.51706754
K04781	mbtI, irp9, ybtS; salicylate synthetase [EC:5.4.4.2 4.2.99.21]	NS
K04785	irp3, ybtU; yersiniabactin synthetase, thiazolanyl reductase component	NA
K04786	irp1, HMWP1; yersiniabactin nonribosomal peptide/polyketide synthase	NA
K04954	HCN1; hyperpolarization activated cyclic nucleotide-gated potassium channel 1	1.901876271
K05245	caiT; L-carnitine/gamma-butyrobetaine antiporter	34.37064594
K05286	PIGB; phosphatidylinositol glycan, class B [EC:2.4.1.-]	NS
K05311	cggR; central glycolytic genes regulator	NS
K05346	K05346, deoR; deoxyribonucleoside regulator	397.7888924
K05364	E2.4.1.129; peptidoglycan glycosyltransferase [EC:2.4.1.129]	NA
K05365	mrcB; penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]	193.5933071
K05368	fre, ubiB; aquacobalamin reductase / naD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.	16.86490885
K05372	ybtA; AraC family transcriptional regulator	NA

K05373	ybtX, irp8; MFS transporter, putative signal transducer	NA
K05374	irp4, ybtT; yersiniabactin synthetase, thioesterase component	NA
K05515	mrda; penicillin-binding protein 2	20234.86122
K05517	tsx; nucleoside-specific channel-forming protein	27.1408686
K05522	nei; endonuclease VIII [EC:3.2.2.- 4.2.99.18]	16.66187262
K05526	astE; succinylglutamate desuccinylase [EC:3.5.1.96]	16.04712135
K05540	dusB; tRNA-dihydrouridine synthase B [EC:1.-.-.-]	NS
K05541	dusC; tRNA-dihydrouridine synthase C [EC:1.-.-.-]	84.5738509
K05590	srnB; ATP-dependent RNA helicase SrmB [EC:2.7.7.-]	99.28791608
K05595	marC; multiple antibiotic resistance protein	NA
K05596	iciA; LysR family transcriptional regulator, chromosome initiation inhibitor	27.39101513
K05739	seaA; hypothetical protein	20.86872776
K05774	phnN; ribose 1,5-bisphosphokinase [EC:2.7.4.23]	20.2656714
K05775	malM; maltose operon periplasmic protein	20.92061825
K05776	modF; molybdate transport system ATP-binding protein	NA
K05777	ABC.VB1X.S; putative thiamine transport system substrate-binding protein	15.26623323
K05778	ABC.VB1X.P; putative thiamine transport system permease protein	25.35713582
K05779	ABC.VB1X.A; putative thiamine transport system ATP-binding protein	11.55845545
K05782	benE; benzoate membrane transport protein	25.36531763
K05789	wzzB; chain length determinant protein (polysaccharide antigen chain regulator)	20.1300394
K05790	wzzE; lipopolysaccharide biosynthesis protein WzzE	31.48122156
K05798	leuO; LysR family transcriptional regulator, transcriptional activator for leuABCD	27.87189185
K05800	ybaO; Lrp/AsnC family transcriptional regulator	12.73595763
K05801	djlA; DnaJ like chaperone protein	NA
K05802	kefA, bspA, aefA; potassium efflux system protein	382.5726268
K05803	nlpI; lipoprotein NlpI	80.5660937
K05804	rob; right origin-binding protein	23.77007554
K05807	bamD; outer membrane protein assembly factor BamD	NA
K05813	ugpB; sn-glycerol 3-phosphate transport system substrate-binding protein	NS
K05814	ugpA; sn-glycerol 3-phosphate transport system permease protein	NS
K05815	ugpE; sn-glycerol 3-phosphate transport system permease protein	NS
K05816	ugpC; sn-glycerol 3-phosphate transport system ATP-binding protein [EC:3.6.3.20]	157.9983545
K05823	E3.5.1.47; N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]	NA
K05838	ybbN; putative thioredoxin	NA
K05839	hha; haemolysin expression modulating protein	NS
K05851	E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]	250.6616293
K05874	tsr; methyl-accepting chemotaxis protein I, serine sensor receptor	42.72516586
K05875	tar; methyl-accepting chemotaxis protein II, aspartate sensor receptor	34.03978145
K05876	trg; methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor	20.30075686
K05878	dhaK; dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]	1163.991581
K05879	dhaL; dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]	701.6511939
K05880	dhaR; transcriptional activator for dhaKLM operon	35.53542438
K05881	dhaM; PTS hybrid protein	35.26657274
K05910	E1.11.1.1; NADH peroxidase [EC:1.11.1.1]	43.59147539
K05982	E3.1.21.7, nfi; deoxyribonuclease V [EC:3.1.21.7]	NA
K05984	cho; excinuclease Cho [EC:3.1.25.-]	11.56525168
K05995	pepE; dipeptidase E [EC:3.4.13.21]	NS
K06006	cpxP; periplasmic protein CpxP	11.45673118

K06048	ybdK; carboxylate-amine ligase [EC:6.3.-.-]	23.08458165
K06062	PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]	NS
K06074	ABC.VB12.A, btuD; vitamin B12 transport system ATP-binding protein [EC:3.6.3.33]	12.25974621
K06075	slyA; MarR family transcriptional regulator, transcriptional regulator for hemolysin	NS
K06076	fadL; long-chain fatty acid transport protein	NA
K06080	rcsF; RcsF protein	19.37373918
K06084	LMO7, FBXO20; F-box protein 20	NS
K06113	abnA_B; arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]	NA
K06120	dhaB; glycerol dehydratase large subunit [EC:4.2.1.30]	3.270634543
K06132	ybhO; putative cardiolipin synthase [EC:2.7.8.-]	24.19359737
K06136	pqqB; pyrroloquinoline quinone biosynthesis protein B	1.751662539
K06139	pqqE; pyrroloquinoline quinone biosynthesis protein E	NA
K06141	tsgA; MFS transporter, TsgA protein	24.22097612
K06142	hlpA, ompH; outer membrane protein	NA
K06144	uspB; universal stress protein B	NS
K06145	gntR; LacI family transcriptional regulator, gluconate utilization system Gnt-I trans	26.02797021
K06149	uspA; universal stress protein A	13.71065328
K06155	gntT; Gnt-I system high-affinity gluconate transporter	251.4724996
K06156	gntU; Gnt-I system low-affinity gluconate transporter	30.78724606
K06159	yojI; putative ATP-binding cassette transporter	32.89199884
K06167	phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]	NA
K06177	rluA; tRNA pseudouridine32 synthase / 23S rRNA pseudouridine746 synthase [EC:NA	NA
K06181	rluE; 23S rRNA pseudouridine2457 synthase [EC:5.4.99.20]	34.91578842
K06194	nlpD; lipoprotein NlpD	NS
K06201	cutC; copper homeostasis protein	3123.851399
K06205	mioC; MioC protein	15.07356588
K06212	focA; formate transporter	71.18111252
K06214	csgG; curli production assembly/transport component CsgG	14.11042785
K06219	smtA; S-adenosylmethionine-dependent methyltransferase	14.84461129
K06222	dkgB; 2,5-diketo-D-gluconate reductase B [EC:1.1.1.346]	16.16253249
K06276	PDPK1; 3-phosphoinositide dependent protein kinase-1 [EC:2.7.11.1]	NA
K06295	gerKA; spore germination protein KA	2519.718018
K06298	gerM; germination protein M	1123.67647
K06307	yfkQ; spore germination protein	2.552608821
K06310	yndD; spore germination protein	NA
K06311	yndE; spore germination protein	NS
K06328	cotE; spore coat protein E	45.83523531
K06386	spolIQ; stage II sporulation protein Q	197.5027611
K06401	spolVFA; stage IV sporulation protein FA	40.15376964
K06402	spolVFB; stage IV sporulation protein FB [EC:3.4.24.-]	358.4128467
K06415	spoVR; stage V sporulation protein R	23.62968333
K06426	sspl; small acid-soluble spore protein I (minor)	7.890086367
K06436	yabG; spore coat assembly protein	243.6167151
K06445	fadE; acyl-CoA dehydrogenase [EC:1.3.99.-]	52.8514425
K06447	astD; succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]	31.33012069
K06601	flbT; flagellar protein FlbT	30.49421585
K06602	flaF; flagellar protein FlaF	25.34180541
K06608	iolR; DeoR family transcriptional regulator, myo-inositol catabolism operon repres	NA

K06858	ABC.VB12.S1, btuF; vitamin B12 transport system substrate-binding protein	18.31563766
K06861	lptB; lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]	NA
K06864	K06864; uncharacterized protein	NA
K06866	grcA; autonomous glycyl radical cofactor	12.51318126
K06887	K06887	47.94187644
K06898	K06898	NA
K06899	ndpA; nucleoid-associated protein	35.84312608
K06902	UMF1; MFS transporter, UMF1 family	NA
K06910	K06910	NA
K06916	K06916	23.21053016
K06918	K06918	36.7191324
K06920	queC; 7-cyano-7-deazaguanine synthase [EC:6.3.4.20]	NA
K06927	DPH6; diphthine-ammonia ligase [EC:6.3.1.14]	55.64098871
K06937	K06937	NA
K06957	tmcA; tRna(Met) cytidine acetyltransferase [EC:2.3.1.193]	60.7779784
K06968	rlmM; 23S rRna (cytidine2498-2'-O)-methyltransferase [EC:2.1.1.186]	61.2924596
K06999	K06999; phospholipase/carboxylesterase	NA
K07001	K07001; NTE family protein	NA
K07011	K07011	NA
K07026	E3.1.3.70; mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]	14.32281127
K07028	K07028	7.628174818
K07033	K07033	NA
K07034	K07034	63.38908222
K07038	K07038; inner membrane protein	NA
K07069	K07069	NA
K07080	K07080	NA
K07084	K07084	NS
K07085	K07085; putative transport protein	NA
K07091	lptF; lipopolysaccharide export system permease protein	NA
K07104	K07104	NA
K07105	K07105	NA
K07114	yfbK; Ca-activated chloride channel homolog	NA
K07115	rlmJ; 23S rRNA (adenine2030-N6)-methyltransferase [EC:2.1.1.266]	NA
K07124	K07124	3147.857863
K07126	K07126	7639.234607
K07132	K07132	NA
K07136	K07136	3.978387015
K07137	K07137	19609.38495
K07140	K07140	20.86094476
K07141	mocA; molybdenum cofactor cytidyltransferase [EC:2.7.7.76]	NA
K07145	isdG, isdI; heme oxygenase (staphylobilin-producing) [EC:1.14.99.48]	NA
K07147	yedY; sulfoxide reductase catalytic subunit YedY [EC:1.8.-.-]	25.95733951
K07148	K07148; uncharacterized protein	NA
K07153	hflD; high frequency lysogenization protein	41.24490358
K07156	pcoC	8.347793041
K07160	K07160; UPF0271 protein	NA
K07164	K07164	NA
K07165	fecR; transmembrane sensor	11.37008653

K07169	K07169; FHA domain-containing protein	17.23894712
K07170	K07170; GAF domain-containing protein	NA
K07175	phoH2; PhoH-like ATPase	2370.50168
K07214	fes; enterochelin esterase and related enzymes	NA
K07219	K07219; putative molybdopterin biosynthesis protein	NA
K07221	oprO_P; phosphate-selective porin OprO and OprP	NA
K07224	efeO; iron uptake system component EfeO	NS
K07225	hmuS; putative hemin transport protein	14.85662036
K07229	yqjH; ferric-chelate reductase (naDPH) [EC:1.16.1.9]	16.87519741
K07232	chaC; cation transport protein ChaC	10.19474475
K07235	tusD, dsrE; tRNA 2-thiouridine synthesizing protein D [EC:2.8.1.-]	9.449264705
K07238	TC.ZIP, zupT, ZRT3, ZIP2; zinc transporter, ZIP family	5616.350622
K07245	pcoD; putative copper resistance protein D	20.75500942
K07251	thiK; thiamine kinase [EC:2.7.1.89]	13.98092632
K07261	mepA; penicillin-insensitive murein endopeptidase [EC:3.4.24.-]	45.81923587
K07263	pqqL; zinc protease [EC:3.4.24.-]	NA
K07265	kpsS, lipB; capsular polysaccharide export protein	123.3779208
K07266	kpsC, lipA; capsular polysaccharide export protein	185.467302
K07269	ytfB; hypothetical protein	12.45483267
K07270	K07270; glycosyl transferase, family 25	129.1783523
K07271	licD; lipopolysaccharide cholinephosphotransferase [EC:2.7.8.-]	NA
K07273	acm; lysozyme	NA
K07277	SAM50, TOB55, bamA; outer membrane protein insertion porin family	NA
K07278	ytfM; outer membrane protein	NS
K07279	yfaL; autotransporter family porin	102.1510212
K07283	ydiY; putative salt-induced outer membrane protein	13.90462384
K07284	srtA; sortase A [EC:3.4.22.70]	NA
K07285	slp; outer membrane lipoprotein	33.41321477
K07286	yajG; uncharacterized lipoprotein	24.78187624
K07304	msrA; peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]	NA
K07310	ynfF; Tat-targeted selenate reductase subunit YnfF [EC:1.97.1.9]	41.91985149
K07311	ynfG; Tat-targeted selenate reductase subunit YnfG	30.72545047
K07312	ynfH; Tat-targeted selenate reductase subunit YnfH	13.75210891
K07314	pphB; serine/threonine protein phosphatase 2 [EC:3.1.3.16]	16.21623902
K07318	K07318; adenine-specific Dna-methyltransferase [EC:2.1.1.72]	203.7631911
K07322	ytfE, scdA; regulator of cell morphogenesis and NO signaling	NA
K07334	higA; proteic killer suppression protein	NA
K07335	bmpA, bmpB, tmpC; basic membrane protein A and related proteins	6711.77377
K07345	fimA; major type 1 subunit fimbrin (pilin)	30.56338783
K07346	fimC; fimbrial chaperone protein	32.06549842
K07347	fimD, fimC, mrkC, htrE, cssD; outer membrane usher protein	432.9501144
K07349	fimG; minor fimbrial subunit	10.49448448
K07350	fimH; minor fimbrial subunit	10.51757962
K07357	fimB; type 1 fimbriae regulatory protein FimB	22.61109661
K07358	fimE; type 1 fimbriae regulatory protein FimE	12.7961191
K07386	pepO; putative endopeptidase [EC:3.4.24.-]	NA
K07400	nfuA; Fe/S biogenesis protein NfuA	44.72286201
K07402	xdhC; xanthine dehydrogenase accessory factor	NA

K07405	E3.2.1.1A; alpha-amylase [EC:3.2.1.1]	NA
K07442	TRM61, GCD14; tRNA (adenine57-N1/adenine58-N1)-methyltransferase [EC:2.1.1.1]	NA
K07467	rstA1; phage replication initiation protein	NA
K07469	mop; aldehyde oxidoreductase [EC:1.2.99.7]	NA
K07479	yrdD; putative Dna topoisomerase	36.83447721
K07480	insB; insertion element IS1 protein InsB	NS
K07489	K07489; transposase	5.224771449
K07506	K07506; AraC family transcriptional regulator	14.29032041
K07507	mgtC; putative Mg ²⁺ transporter-C (MgtC) family protein	NS
K07552	bcr; MFS transporter, DHA1 family, bicyclomycin/chloramphenicol resistance prot	NA
K07566	tsaC, rimN, SUA5; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]	NS
K07570	GSP13; general stress protein 13	92.18286623
K07588	argK; LAO/AO transport system kinase [EC:2.7.-.-]	NA
K07591	tdcR; threonine dehydratase operon activator protein	NA
K07592	tdcA; LysR family transcriptional regulator, tdc operon transcriptional activator	33.27951651
K07637	phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]	28.4552161
K07639	rstB; two-component system, OmpR family, sensor histidine kinase RstB [EC:2.7.13.3]	25.77313925
K07640	cpxA; two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]	59.94702249
K07641	creC; two-component system, OmpR family, sensor histidine kinase CreC [EC:2.7.13.3]	NS
K07647	torS; two-component system, OmpR family, sensor histidine kinase TorS [EC:2.7.13.3]	67.13956203
K07648	arcB; two-component system, OmpR family, aerobic respiration control sensor his	81.47585046
K07657	phoB; two-component system, OmpR family, phosphate regulon response regulat	490.5446427
K07660	phoP; two-component system, OmpR family, response regulator PhoP	12.07259953
K07661	rstA; two-component system, OmpR family, response regulator RstA	10.47287453
K07662	cpxR; two-component system, OmpR family, response regulator CpxR	52.48097111
K07664	baeR; two-component system, OmpR family, response regulator BaeR	13.15777601
K07670	mtrA; two-component system, OmpR family, response regulator MtrA	29.15112491
K07674	narQ; two-component system, narL family, nitrate/nitrite sensor histidine kinase	73.78605305
K07675	uhpB; two-component system, NarL family, sensor histidine kinase UhpB [EC:2.7.13.3]	NA
K07676	rcsD; two-component system, narL family, sensor histidine kinase RcsD [EC:2.7.13.3]	61.61087756
K07677	rcsC; two-component system, narL family, capsular synthesis sensor histidine kina	65.52822487
K07678	barA; two-component system, narL family, sensor histidine kinase BarA [EC:2.7.13.3]	53.67168456
K07686	uhpA; two-component system, narL family, uhpT operon response regulator Uhp	13.06795013
K07687	rcsB; two-component system, narL family, captular synthesis response regulator	13.69776379
K07689	uvrY; two-component system, narL family, invasion response regulator UvrY	14.19010093
K07690	evgA, bvgA; two-component system, narL family, response regulator EvgA	13.72638347
K07697	kinB; two-component system, sporulation sensor kinase B [EC:2.7.13.3]	66.93365065
K07700	dpiB, citA; two-component system, CitB family, cit operon sensor histidine kinase	38.20751154
K07701	dcuS; two-component system, CitB family, sensor histidine kinase DcuS [EC:2.7.13.3]	14.00308077
K07702	dpiA, citB; two-component system, CitB family, response regulator CitB	13.83723175
K07703	dcuR; two-component system, CitB family, response regulator DcuR	19.77262701
K07711	glrK, qseE; two-component system, NtrC family, sensor histidine kinase GlrK [EC:2.7.13.3]	34.387692
K07713	zraR, hydG; two-component system, NtrC family, response regulator HydG	NA
K07714	atoC; two-component system, NtrC family, response regulator AtoC	68.91255587
K07715	glrR, qseF; two-component system, NtrC family, response regulator GlrR	33.61109317
K07723	ydcD; CopG family transcriptional regulator	4.935455387
K07739	ELP3, KAT9; elongator complex protein 3 [EC:2.3.1.48]	NA
K07742	K07742; hypothetical protein	968.4922818

K07751	pepB; PepB aminopeptidase [EC:3.4.11.23]	100.513657
K07768	senX3; two-component system, OmpR family, sensor histidine kinase SenX3 [EC:2.7.1.1]	NA
K07771	basR; two-component system, OmpR family, response regulator BasR	14.47626159
K07772	torR; two-component system, OmpR family, torCAD operon response regulator TorR	10.2728424
K07773	arcA; two-component system, OmpR family, aerobic respiration control protein ArcA	26.04445043
K07776	regX3; two-component system, OmpR family, response regulator RegX3	NA
K07781	rcsA; LuxR family transcriptional regulator, capsular biosynthesis positive transcription factor RcsA	12.5077547
K07782	sdiA; LuxR family transcriptional regulator	13.62023921
K07783	uhpC; MFS transporter, OPA family, sugar phosphate sensor protein UhpC	NA
K07784	uhpT; MFS transporter, OPA family, hexose phosphate transport protein UhpT	37.59834507
K07786	emrY; MFS transporter, multidrug resistance protein Y	35.89800658
K07794	tctB; putative tricarboxylic transport membrane protein	NS
K07796	cusC, silC; Cu(I)/Ag(I) efflux system outer membrane protein CusC/SilC	34.94519702
K07797	emrK; multidrug resistance protein K	23.83709039
K07811	torA; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]	46.35234548
K07813	agrB; accessory gene regulator B	3798.458066
K07821	torY; trimethylamine-N-oxide reductase (cytochrome c), cytochrome c-type subunit TorY	26.6467447
K08094	hxlB; 6-phospho-3-hexuloisomerase [EC:5.3.1.27]	NA
K08137	galP; MFS transporter, SP family, galactose:H ⁺ symporter	87.11470165
K08138	xylE; MFS transporter, SP family, xylose:H ⁺ symporter	NA
K08153	blt, norA; MFS transporter, DHA1 family, multidrug resistance protein	NA
K08154	emrD; MFS transporter, DHA1 family, 2-module integral membrane pump EmrD	32.7405639
K08160	cmr, mdFA; MFS transporter, DHA1 family, multidrug/chloramphenicol efflux transporter	23.09582823
K08162	mdtH; MFS transporter, DHA1 family, multidrug resistance protein	27.68306886
K08163	mdtL; MFS transporter, DHA1 family, multidrug resistance protein	31.51885105
K08172	shiA; MFS transporter, MHS family, shikimate and dehydroshikimate transport protein	26.2250608
K08191	exuT; MFS transporter, ACS family, hexuronate transporter	NA
K08194	dgoT; MFS transporter, ACS family, D-galactonate transporter	16.24027132
K08218	ampG; MFS transporter, PAT family, beta-lactamase induction signal transducer	NA
K08219	UMF2; MFS transporter, UMF2 family, putative MFS family transporter protein	38.73882716
K08225	entS; MFS transporter, ENTS family, enterobactin (siderophore) exporter	25.22444696
K08227	lplT; MFS transporter, LPLT family, lysophospholipid transporter	23.18336918
K08276	eco; ecotin	5.624014075
K08307	mltD, dniR; membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]	NA
K08308	mltE; membrane-bound lytic murein transglycosylase E [EC:3.2.1.-]	11.11237504
K08316	rsmD; 16S rRNA (guanine966-N2)-methyltransferase [EC:2.1.1.171]	NA
K08317	ybdH; uncharacterized oxidoreductase [EC:1.1.-.-]	29.74436064
K08318	yihU; putative dehydrogenase [EC:1.1.-.-]	23.76972408
K08319	ygbJ; putative dehydrogenase [EC:1.1.-.-]	NA
K08321	lsrF; putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]	304.6970887
K08324	sad; succinate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.24]	22.88173541
K08326	ypdF; aminopeptidase [EC:3.4.11.-]	26.13237939
K08345	K08345	69.14714659
K08346	K08346	26.1639492
K08347	K08347	9.099256122
K08348	fdnG; formate dehydrogenase-N, alpha subunit [EC:1.1.5.6]	98.04129451
K08349	fdnH; formate dehydrogenase-N, beta subunit	15.01046198
K08350	fdnI; formate dehydrogenase-N, gamma subunit	16.38901358

K08351	bisC; biotin/methionine sulfoxide reductase [EC:1.-.-.]	48.99354193
K08352	phsA, psrA; thiosulfate reductase / polysulfide reductase chain A	NA
K08354	phsC; thiosulfate reductase cytochrome b subunit	11.60357306
K08361	K08361	13.32596889
K08369	ydjE; MFS transporter, putative metabolite:H ⁺ symporter	NA
K08372	pepD; putative serine protease PepD [EC:3.4.21.-]	NA
K08587	cloSI; clostripain [EC:3.4.22.8]	2.248079147
K08589	E3.4.22.37; gingipain R [EC:3.4.22.37]	20.89242787
K08590	mtnU; carbon-nitrogen hydrolase family protein	NA
K08591	plsY; glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]	NA
K08602	pepF, pepB; oligoendopeptidase F [EC:3.4.24.-]	4630.477972
K08641	vanX; D-alanyl-D-alanine dipeptidase [EC:3.4.13.22]	NA
K08659	pepDA, pepDB; dipeptidase [EC:3.4.-.-]	NA
K08676	tri; tricorn protease [EC:3.4.21.-]	NA
K08682	acpH; acyl carrier protein phosphodiesterase [EC:3.1.4.14]	NA
K08693	E3.1.3.6; 3'-nucleotidase [EC:3.1.3.6]	20.34000042
K08717	utp; urea transporter	NA
K08722	yfbR; 5'-nucleotidase [EC:3.1.3.5]	1200.481461
K08723	yjjG; 5'-nucleotidase [EC:3.1.3.5]	14.2409373
K08726	EPHX2; soluble epoxide hydrolase [EC:3.3.2.10]	NA
K08900	BCS1; mitochondrial chaperone BCS1	NA
K08970	rcna; nickel/cobalt exporter	14.95605981
K08978	TC.BAT1; bacterial/archaeal transporter family protein	NA
K08994	yneE; putative membrane protein	13.34342725
K08997	ydiU; hypothetical protein	26.58988888
K08999	K08999; hypothetical protein	NA
K09009	K09009; hypothetical protein	NA
K09011	cimA; D-citramalate synthase [EC:2.3.1.182]	NA
K09016	rutG; putative pyrimidine permease RutG	19.92263275
K09018	rutA; pyrimidine oxygenase [EC:1.14.99.46]	22.42877719
K09019	rutE; 3-hydroxypropanoate dehydrogenase [EC:1.1.1.-]	10.39154019
K09020	rutB; ureidoacrylate peracid hydrolase [EC:3.5.1.110]	NA
K09021	rutC; aminoacrylate peracid reductase	5.694508111
K09022	yjgF; UPF0076 protein YjgF	NA
K09023	rutD; aminoacrylate hydrolase [EC:3.5.1.-]	14.54049964
K09116	K09116; hypothetical protein	377.4539051
K09121	K09121; hypothetical protein	NA
K09155	K09155; hypothetical protein	NA
K09159	K09159; hypothetical protein	NS
K09161	K09161; hypothetical protein	9.549605717
K09251	E2.6.1.82; putrescine aminotransferase [EC:2.6.1.82]	NA
K09456	aidB; putative acyl-CoA dehydrogenase	40.90389168
K09457	queF1, queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]	NA
K09471	puuB, ordL; gamma-glutamylputrescine oxidase [EC:1.4.3.-]	26.28827704
K09473	puuD; gamma-glutamyl-gamma-aminobutyrate hydrolase [EC:3.5.1.94]	NS
K09475	ompC; outer membrane pore protein C	19.34769782
K09477	citT; citrate:succinate antiporter	38.93109723
K09607	ina; immune inhibitor A [EC:3.4.24.-]	5.110895323

K09612	iap; alkaline phosphatase isozyme conversion protein [EC:3.4.11.-]	23.75351094
K09667	OGT; polypeptide N-acetylglucosaminyltransferase [EC:2.4.1.-]	12.33631351
K09680	coaW; type II pantothenate kinase [EC:2.7.1.33]	NA
K09684	pucR; purine catabolism regulatory protein	1268.154099
K09688	ABC-2.CPSE.P; capsular polysaccharide transport system permease protein	41.4885474
K09689	ABC-2.CPSE.A; capsular polysaccharide transport system ATP-binding protein	50.14385714
K09696	natB; sodium transport system permease protein	1024.946447
K09697	natA; sodium transport system ATP-binding protein	362.866164
K09704	K09704; hypothetical protein	NA
K09748	rimP; ribosome maturation factor RimP	3649.020384
K09781	K09781; hypothetical protein	21.68410656
K09789	bioG; biotin synthesis protein BioG	NA
K09797	K09797; hypothetical protein	NA
K09802	K09802; hypothetical protein	10.40469392
K09808	ABC.LPT.P, lolC, lolE; lipoprotein-releasing system permease protein	NA
K09823	zur; Fur family transcriptional regulator, zinc uptake regulator	11.73595203
K09835	crtISO, crtH; polycopene isomerase [EC:5.2.1.13]	92.46991879
K09891	K09891; hypothetical protein	40.36377018
K09892	K09892; hypothetical protein	8.200532757
K09893	K09893; hypothetical protein	14.0972473
K09894	K09894; hypothetical protein	25.33108221
K09895	K09895; hypothetical protein	36.25527967
K09896	K09896; hypothetical protein	11.26278248
K09897	K09897; hypothetical protein	21.05927874
K09899	K09899; hypothetical protein	28.34362203
K09900	K09900; hypothetical protein	4.908018246
K09901	K09901; hypothetical protein	7.571921995
K09902	K09902; hypothetical protein	15.74949728
K09906	K09906; hypothetical protein	12.91694084
K09907	K09907; hypothetical protein	15.18685514
K09908	K09908; hypothetical protein	12.26372378
K09910	K09910; hypothetical protein	9.232353086
K09912	K09912; hypothetical protein	NA
K09913	K09913; hypothetical protein	5.559607789
K09914	K09914; putative lipoprotein	12.12649805
K09915	K09915; hypothetical protein	9.446987976
K09921	K09921; hypothetical protein	20.18186677
K09922	K09922; hypothetical protein	NA
K09923	K09923; hypothetical protein	9.609680057
K09933	K09933; hypothetical protein	13.79953745
K09934	K09934; hypothetical protein	9.760760918
K09951	cas2; CRISPR-associated protein Cas2	NA
K09952	K09952; hypothetical protein	NA
K09962	K09962; hypothetical protein	NA
K09979	K09979; hypothetical protein	7.999147769
K09980	K09980; hypothetical protein	NA
K09982	K09982; hypothetical protein	3.28085635
K09985	K09985; hypothetical protein	46.2010249

K09992	K09992; hypothetical protein	39.19375859
K09996	artJ; arginine transport system substrate-binding protein	17.51617479
K09998	artM; arginine transport system permease protein	16.09307197
K09999	artQ; arginine transport system permease protein	16.37862743
K10000	artP; arginine transport system ATP-binding protein [EC:3.6.3.-]	22.23490083
K10005	gluB; glutamate transport system substrate-binding protein	NA
K10006	gluC; glutamate transport system permease protein	NA
K10007	gluD; glutamate transport system permease protein	NA
K10008	gluA; glutamate transport system ATP-binding protein [EC:3.6.3.-]	NA
K10013	ABC.ARG.S, argT; lysine/arginine/ornithine transport system substrate-binding protein	16.09568315
K10014	hisJ; histidine transport system substrate-binding protein	16.40766951
K10015	hisM; histidine transport system permease protein	13.7290348
K10017	hisP; histidine transport system ATP-binding protein [EC:3.6.3.21]	13.54680944
K10038	glnQ; glutamine transport system ATP-binding protein [EC:3.6.3.-]	NA
K10107	ABC-2.CPSE.P1; capsular polysaccharide transport system permease protein	78.18193412
K10108	malE; maltose/maltodextrin transport system substrate-binding protein	76.34966302
K10109	malF; maltose/maltodextrin transport system permease protein	104.0040456
K10111	malK, mtlK, thuK; multiple sugar transport system ATP-binding protein [EC:3.6.3.-]	73.24932079
K10124	bglH; carbohydrate-specific outer membrane porin	41.89008788
K10125	dctB; two-component system, NtrC family, C4-dicarboxylate transport sensor histidine kinase	37.57965026
K10126	dctD; two-component system, NtrC family, C4-dicarboxylate transport response regulator	NA
K10213	rihB; ribosylpyrimidine nucleosidase [EC:3.2.2.8]	NA
K10355	ACTF; actin, other eukaryote	NS
K10536	E3.5.3.12; agmatine deiminase [EC:3.5.3.12]	NA
K10543	xylF; D-xylose transport system substrate-binding protein	NS
K10544	xylH; D-xylose transport system permease protein	NA
K10555	lsrB; AI-2 transport system substrate-binding protein	100.5395493
K10673	strA; streptomycin 3"-kinase [EC:2.7.1.87]	NS
K10680	nemaA; N-ethylmaleimide reductase [EC:1.-.-.-]	19.41754725
K10748	tus, tau; Dna replication terminus site-binding protein	21.54277492
K10805	tesB; acyl-CoA thioesterase II [EC:3.1.2.-]	NA
K10806	yciA; acyl-CoA thioesterase YciA [EC:3.1.2.-]	NS
K10819	E2.7.13.3; histidine kinase	NA
K10844	ERCC2, XPD; Dna excision repair protein ERCC-2 [EC:3.6.4.12]	15.27619077
K10857	exoX; exodeoxyribonuclease X [EC:3.1.11.-]	NS
K10908	POLRMT, RPO41; DNA-directed RNA polymerase, mitochondrial [EC:2.7.7.6]	NA
K10939	acfD; accessory colonization factor AcfD	81.64781688
K10941	flrA; sigma-54 specific transcriptional regulator, flagellar regulatory protein A	NA
K10954	zot; zona occludens toxin	NA
K10975	allP; allantoin permease	33.39535475
K10979	ku; Dna end-binding protein Ku	34.93890452
K11057	cpb2; beta2-toxin	1.716411949
K11059	K11059, entA; probable enterotoxin A	3.757422558
K11060	K11060, entB; probable enterotoxin B	14.63274744
K11073	potF; putrescine transport system substrate-binding protein	97.34551058
K11075	potH; putrescine transport system permease protein	47.89972509
K11102	gltP, gltT; proton glutamate symport protein	NS
K11103	dctA; aerobic C4-dicarboxylate transport protein	NS

K11106	ttdT; L-tartrate/succinate antiporter	30.54987605
K11139	hlyE, clyA, sheA; hemolysin E	NS
K11192	PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component	24.11124644
K11201	PTS-Fru2-EIIA; PTS system, fructose-specific IIA-like component [EC:2.7.1.69]	133.6383236
K11203	PTS-Fru2-EIIC; PTS system, fructose-specific IIC-like component	NA
K11211	kdkA; 3-deoxy-D-manno-octulosonic acid kinase [EC:2.7.1.166]	NA
K11214	SHPK; sedoheptulokinase [EC:2.7.1.14]	89.89120402
K11263	bccA; acetyl-/propionyl-CoA carboxylase, biotin carboxylase, biotin carboxyl carrier	NA
K11358	yhdR; aspartate aminotransferase [EC:2.6.1.1]	NA
K11391	rlmG; 23S rRNA (guanine1835-N2)-methyltransferase [EC:2.1.1.174]	23.92355159
K11472	glcE; glycolate oxidase FAD binding subunit	NA
K11474	glcC; GntR family transcriptional regulator, glc operon transcriptional activator	16.50894482
K11477	glcG; glc operon protein GlcG	NA
K11498	CENPE; centromeric protein E	NS
K11533	fas; fatty acid synthase, bacteria type [EC:2.3.1.-]	NA
K11535	nupC; nucleoside transport protein	160.0098403
K11605	sitC; manganese/iron transport system permease protein	24.27828834
K11606	sitD; manganese/iron transport system permease protein	16.06504199
K11607	sitB; manganese/iron transport system ATP-binding protein	25.66056626
K11617	liaS; two-component system, NarL family, sensor histidine kinase LiaS [EC:2.7.13.3]	NA
K11631	bceA; bacitracin transport system ATP-binding protein	20.71432414
K11693	femX, fmhB; peptidoglycan pentaglycine glycine transferase (the first glycine) [EC:2.3.1.11]	12.26288315
K11695	femB; peptidoglycan pentaglycine glycine transferase (the fourth and fifth glycine)	15.08917709
K11707	troA, mntA, znuA; manganese/zinc/iron transport system substrate-binding protein	NA
K11709	troD, mntD, znuB; manganese/zinc/iron transport system permease protein	NA
K11710	troB, mntB, znuC; manganese/zinc/iron transport system ATP-binding protein	101.2247233
K11720	lptG; lipopolysaccharide export system permease protein	NA
K11732	pheP; phenylalanine-specific permease	32.76225934
K11734	aroP; aromatic amino acid transport protein AroP	259.8768693
K11735	gabP; GABA permease	25.21412006
K11736	proY; proline-specific permease ProY	30.64707945
K11737	cycA; D-serine/D-alanine/glycine transporter	50.27764095
K11738	ansP; L-asparagine permease	30.12587036
K11739	nfrA; bacteriophage N4 adsorption protein A	59.24701984
K11740	nfrB; bacteriophage N4 adsorption protein B	46.01399305
K11744	tqsA; AI-2 transport protein TqsA	39.02309153
K11745	kefC; glutathione-regulated potassium-efflux system ancillary protein KefC	48.92400026
K11746	kefF; glutathione-regulated potassium-efflux system ancillary protein KefF	10.64576501
K11747	kefB; glutathione-regulated potassium-efflux system protein KefB	71.43310862
K11748	kefG; glutathione-regulated potassium-efflux system ancillary protein KefG	12.9627303
K11750	frsA; esterase FrsA [EC:3.1.-.-]	78.39530426
K11891	impL, vasK, icmF; type VI secretion system protein ImpL	138.8472884
K11892	impK, ompA, vasF, dotU; type VI secretion system protein ImpK	21.09773539
K11893	impJ, vasE; type VI secretion system protein ImpJ	53.44240607
K11894	impI, vasC; type VI secretion system protein ImpI	21.43942586
K11895	impH, vasB; type VI secretion system protein ImpH	34.37637301
K11896	impG, vasA; type VI secretion system protein ImpG	84.51506253
K11900	impC; type VI secretion system protein ImpC	61.8184953

K11901	impB; type VI secretion system protein ImpB	20.93304209
K11903	K11903, hcp; type VI secretion system secreted protein Hcp	18.6810188
K11904	vgrG; type VI secretion system secreted protein VgrG	71.57501818
K11905	K11905; type VI secretion system protein	9.899705224
K11906	vasD, lip; type VI secretion system protein VasD	14.34005465
K11907	vasG, clpV; type VI secretion system protein VasG	106.4327457
K11909	vasI; type VI secretion system protein VasI	11.70443829
K11910	vasJ; type VI secretion system protein VasJ	44.30801592
K11911	vasL; type VI secretion system protein VasL	40.91103491
K11922	mngR, farR; GntR family transcriptional regulator, mannosyl-D-glycerate transpo	53.12527554
K11923	cueR; MerR family transcriptional regulator, copper efflux regulator	NS
K11925	sgrR; SgrR family transcriptional regulator	39.45349082
K11929	phoE; outer membrane pore protein E	25.81325001
K11930	torT; periplasmic protein TorT	18.67784132
K11931	pgaB; biofilm PGA synthesis lipoprotein PgaB [EC:3.-.-.]	68.8369081
K11932	uspG; universal stress protein G	NS
K11933	hcr; naDH oxidoreductase Hcr [EC:1.-.-.]	2.648134991
K11934	ompX; outer membrane protein X	NA
K11935	pgaA; biofilm PGA synthesis protein PgaA	40.51843596
K11938	cof; HMP-PP phosphatase [EC:3.6.1.-]	19.85576091
K11941	mdoC; glucans biosynthesis protein C [EC:2.1.-.-]	22.72809932
K12055	K12055, parA; chromosome partitioning related protein ParA	NA
K12056	traG; conjugal transfer mating pair stabilization protein TraG	NS
K12057	traF; conjugal transfer pilus assembly protein TraF	NS
K12071	traD; conjugal transfer pilus assembly protein TraD	NA
K12072	traH; conjugative transfer pilus assembly protein TraH	NS
K12113	ebgR; LacI family transcriptional regulator, ebg operon repressor	NS
K12138	hyfC; hydrogenase-4 component C [EC:1.-.-.]	NA
K12147	msyB; acidic protein MsyB	8.385047846
K12148	bssS; biofilm regulator BssS	3.254534402
K12150	K12150	6.664070113
K12228	trbB; TrbB protein	NS
K12255	gbuA; guanidinobutyrase [EC:3.5.3.7]	NS
K12262	cybB; cytochrome b561	8.66259537
K12264	norV; anaerobic nitric oxide reductase flavorubredoxin	34.24483161
K12265	norW; nitric oxide reductase FIRd-naD(+) reductase [EC:1.18.1.-]	24.61950231
K12266	norR; anaerobic nitric oxide reductase transcription regulator	39.8296691
K12271	SRP43, CAO; signal recognition particle 43 kDa protein	NA
K12284	mshN; MSHA biogenesis protein MshN	NA
K12288	hofM; pilus assembly protein HofM	17.96110562
K12289	hofN; pilus assembly protein HofN	9.408252009
K12292	ABCC-BAC.COMA, comA; ATP-binding cassette, subfamily C, bacterial, competence	NA
K12296	comX1_2; competence protein ComX	NA
K12299	garP; MFS transporter, ACS family, probable galactarate transporter	32.61064027
K12340	tolC; outer membrane channel protein	NA
K12368	dppA; dipeptide transport system substrate-binding protein	119.9251568
K12369	dppB; dipeptide transport system permease protein	65.31784158
K12370	dppC; dipeptide transport system permease protein	48.52754933

K12371	dppD; dipeptide transport system ATP-binding protein	63.3366972
K12372	dppF; dipeptide transport system ATP-binding protein	53.33201619
K12373	HEXA_B; hexosaminidase [EC:3.2.1.52]	NA
K12454	rfbE; CDP-paratose 2-epimerase [EC:5.1.3.10]	NA
K12500	tesC; thioesterase III [EC:3.1.2.-]	NS
K12516	bigA; putative surface-exposed virulence protein	114.7469942
K12524	thrA; bifunctional aspartokinase / homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.	NA
K12525	metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.	60.52414453
K12527	ygfK; putative selenate reductase [EC:1.97.1.9]	NA
K12542	lapC; membrane fusion protein LapC	42.37338111
K12553	pbp3; penicillin-binding protein 3 [EC:3.4.-.-]	NA
K12556	pbp2X; penicillin-binding protein 2X [EC:2.3.2.-]	NA
K12581	CNOT7_8, CAF1, POP2; CCR4-NOT transcription complex subunit 7/8	9.358179905
K12680		NA
K12687	flu; antigen 43	85.71419989
K12942	abgT; aminobenzoyl-glutamate transport protein	NA
K12943	ygeR; lipoprotein YgeR	13.76868779
K12945	nudK; GDP-mannose pyrophosphatase NudK [EC:3.6.1.-]	12.35411573
K12950	ctpC; cation-transporting P-type ATPase C [EC:3.6.3.-]	NS
K12957	yjgB; uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.-]	22.90997137
K12961	diaA; DnaA initiator-associating protein	15.02099316
K12972	ghrA; glyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]	18.71428674
K12974	lpxP; palmitoleoyl transferase [EC:2.3.1.-]	15.64319749
K12975	eptB; phosphoethanolamine transferase	50.18921449
K12982	opsX; heptosyltransferase I [EC:2.4.-.-]	NA
K12984	waaE, kdtX; (heptosyl)LPS beta-1,4-glucosyltransferase [EC:2.4.1.-]	NA
K12995	wbpZ; rhamnosyltransferase [EC:2.4.1.-]	NA
K12997	rgpB; rhamnosyltransferase [EC:2.4.1.-]	NA
K12998	rgpE; glucosyltransferase [EC:2.4.1.-]	NA
K13010	per, rfbE; perosamine synthetase [EC:2.6.1.102]	NA
K13014	arnD; undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]	NS
K13025	EIF4A3, FAL1; ATP-dependent Rna helicase [EC:3.6.4.13]	12.13687332
K13043	argF2; N-succinyl-L-ornithine transcarbamylase [EC:2.1.3.11]	NA
K13053	sulA; cell division inhibitor SulA	8.850176345
K13069	E2.7.7.65; diguanylate cyclase [EC:2.7.7.65]	44.70054616
K13118	DGCR14; protein DGCR14	NA
K13243	dos; c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]	45.9881066
K13244	yahA; c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]	23.66844634
K13255	fhuF; ferric iron reductase protein FhuF	18.66924869
K13274	wprA; cell wall-associated protease [EC:3.4.21.-]	4.942730626
K13275	isp; major intracellular serine protease [EC:3.4.21.-]	40.9062389
K13281	uvrE, UVE1; UV Dna damage endonuclease [EC:3.-.-.-]	95.50832097
K13282	cphB; cyanophycinase [EC:3.4.15.6]	28.15030019
K13288	orn, REX2, REXO2; oligoribonuclease [EC:3.1.-.-]	NA
K13301	secM; secretion monitor	16.1306403
K13378	nuoCD; NADH-quinone oxidoreductase subunit C/D [EC:1.6.5.3]	NA
K13381	chiA; bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]	43.11669809
K13498	trpCF; indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomer	NS

K13527	mpa; proteasome-associated ATPase	NA
K13542	cobA-hemD; uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75]	NA
K13543	hemDX; uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75]	NA
K13570	pup; prokaryotic ubiquitin-like protein Pup	NA
K13571	pafA; proteasome accessory factor A [EC:6.3.2.-]	NA
K13573	pafC; proteasome accessory factor C	NA
K13611	pksJ; polyketide synthase PksJ	NA
K13620	wcaD; putative colanic acid polymerase	25.21267286
K13629	dsdX; D-serine transporter	28.35560017
K13631	soxS; AraC family transcriptional regulator, transcriptional activator of the super	4.827213437
K13632	marA; AraC family transcriptional regulator, multiple antibiotic resistance protei	5.443739251
K13634	cysB; LysR family transcriptional regulator, cys regulon transcriptional activator	23.0044135
K13635	cbl; LysR family transcriptional regulator, cys regulon transcriptional activator	20.91718607
K13637	uxuR; GntR family transcriptional regulator, uxuAB operon transcriptional repress	16.53074832
K13640	hspR; MerR family transcriptional regulator, heat shock protein HspR	NA
K13671	K13671; alpha-1,2-mannosyltransferase [EC:2.4.1.-]	3.195988505
K13683	wcaE; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]	13.0575268
K13684	wcaC; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]	23.24388738
K13694	spr; lipoprotein Spr	NA
K13695	nlpC; probable lipoprotein NlpC	11.53371268
K13735	yeeJ; adhesin/invasin	233.6086044
K13745	ddc; L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]	2.895161435
K13787	idsA; geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.29]	NA
K13820	flhR-flhB; flagellar biosynthetic protein FlhR/FlhB	31.95159445
K13829	aroKB; shikimate kinase / 3-dehydroquinate synthase [EC:2.7.1.71 4.2.3.4]	NA
K13918	gudX; glucarate dehydratase-related protein	27.15951584
K13921	pduQ; 1-propanol dehydrogenase	10.60870191
K13922	pduP; propionaldehyde dehydrogenase	NA
K13926	rbbA; ribosome-dependent ATPase	71.14223683
K13938	folM; dihydromonapterin reductase / dihydrofolate reductase [EC:1.5.1.- 1.5.1.3]	12.5628035
K13979	yahK; uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.-]	60.09563144
K13993	HSP20; HSP20 family protein	NA
K14051	gmr; cyclic di-GMP phosphodiesterase Gmr [EC:3.1.4.52]	35.83705153
K14053	ompG; outer membrane protein G	NA
K14055	uspE; universal stress protein E	137.9961572
K14056	puuR; HTH-type transcriptional regulator, repressor for puuD	NS
K14062	ompN; outer membrane protein N	23.14100924
K14064	uspC; universal stress protein C	11.45265634
K14088	echC; ech hydrogenase subunit C	NA
K14138	acsB; acetyl-CoA synthase [EC:2.3.1.169]	NA
K14154	THI6; thiamine-phosphate diphosphorylase / hydroxyethylthiazole kinase [EC:2.5.1.10]	NA
K14194	sdrC_D_E; serine-aspartate repeat-containing protein C/D/E	NS
K14287	ybdL; methionine aminotransferase [EC:2.6.1.-]	23.51253772
K14348	lldR; GntR family transcriptional regulator, L-lactate dehydrogenase operon regula	18.63683617
K14392	panF; sodium/pantothenate symporter	1306.670556
K14393	actP; cation/acetate symporter	37.68904387
K14567	UTP14; U3 small nucleolar Rna-associated protein 14	2.787372169
K14587	sgcE; protein sgcE [EC:5.1.3.-]	10.75797296

K14588	cueO; blue copper oxidase	39.13958017
K14645	K14645; serine protease [EC:3.4.21.-]	45.89417451
K14665	amhX; amidohydrolase [EC:3.5.1.-]	NA
K14681	argHA; argininosuccinate lyase / amino-acid N-acetyltransferase [EC:4.3.2.1 2.3.1.1]	NA
K14744	rzpD; prophage endopeptidase [EC:3.4.-.-]	13.64028548
K14762	yibL; ribosome-associated protein	7.825976605
K14767	UTP3, SAS10; U3 small nucleolar Rna-associated protein 3	NS
K14977	ylbA; ureidoglycine aminohydrolase [EC:3.5.3.-]	103.9513421
K14982	ciaH; two-component system, OmpR family, sensor histidine kinase CiaH [EC:2.7.1.1]	NA
K15152	MED21, SRB7; mediator of Rna polymerase II transcription subunit 21	16.93029427
K15176	CTR9; Rna polymerase-associated protein CTR9	4.09662621
K15257	cmoB; tRNA (mo5U34)-methyltransferase [EC:2.1.1.-]	29.34153576
K15268	eamA; O-acetylserine/cysteine efflux transporter	13.99588179
K15342	cas1; CRISP-associated protein Cas1	NA
K15396	trmJ; tRNA (cytidine32/uridine32-2'-O)-methyltransferase [EC:2.1.1.200]	22.23984348
K15460	yfiC, trmX; tRNA1Val (adenine37-N6)-methyltransferase [EC:2.1.1.223]	NA
K15475	lpnE; enhanced entry protein LpnE	24.53839168
K15518	dgk; deoxyguanosine kinase [EC:2.7.1.113]	8.685584231
K15519	dck; deoxyadenosine/deoxycytidine kinase [EC:2.7.1.76 2.7.1.74]	6.918390982
K15533	K15533; 1,3-beta-galactosyl-N-acetylhexosamine phosphorylase [EC:2.4.1.211]	NA
K15536	cybC; soluble cytochrome b562	5.476911389
K15540	ecpD; chaperone protein EcpD	16.48284115
K15547	mdtO; multidrug resistance protein MdtO	47.00463356
K15548	aaeA; p-hydroxybenzoic acid efflux pump subunit AaeA	23.10062103
K15549	mdtN; multidrug resistance protein MdtN	26.03051412
K15550	mdtP; multidrug resistance outer membrane protein MdtP	25.60678407
K15552	tauC; taurine transport system permease protein	80.4241955
K15598	thiY; putative hydroxymethylpyrimidine transport system substrate-binding protein	175.8995778
K15635	apgM; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.1]	NA
K15661	ituA, mycA, bmyA; iturin family lipopeptide synthetase A	NA
K15721	fyuA; pesticin/yersiniabactin receptor	27.76755026
K15723	syd; SecY interacting protein Syd	12.11841345
K15735	csiR; GntR family transcriptional regulator, carbon starvation induced regulator	9.430932506
K15737	csiD; protein CsiD	24.0703774
K15780	tilS-hprT; bifunctional protein TilS/HprT [EC:6.3.4.19 2.4.2.8]	38.58109043
K15827	hycB; formate hydrogenlyase subunit 2	9.164536685
K15828	hycC; formate hydrogenlyase subunit 3	31.9831242
K15829	hycD; formate hydrogenlyase subunit 4	15.73579328
K15830	hycE; formate hydrogenlyase subunit 5	34.25395312
K15831	hycF; formate hydrogenlyase subunit 6	NS
K15833	hycA; formate hydrogenlyase regulatory protein HycA	11.04942385
K15836	fhlA; formate hydrogenlyase transcriptional activator	52.89521052
K15894	pseB; UDP-N-acetylglucosamine 4,6-dehydratase [EC:4.2.1.115]	NA
K15895	pseC; UDP-4-amino-4,6-dideoxy-L-N-acetyl-beta-L-altrosamine transaminase [EC:2.4.1.116]	NS
K15898	psel, neuB3; pseudaminic acid synthase [EC:2.5.1.97]	NA
K15924	xynC; glucuronoarabinoxylan endo-1,4-beta-xylanase [EC:3.2.1.136]	138.7616598
K15974	emrR, mprA; MarR family transcriptional regulator, negative regulator of the mu operon	11.64797887
K15984	rsmJ; 16S rRNA (guanine1516-N2)-methyltransferase [EC:2.1.1.242]	NA

K16012	cydC; ATP-binding cassette, subfamily C, bacterial CydC	382.7274072
K16013	cydD; ATP-binding cassette, subfamily C, bacterial CydD	421.451002
K16053	mscM; miniconductance mechanosensitive channel	NA
K16055	TPS; trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	NA
K16066	ydfG; malonic semialdehyde reductase [EC:1.1.1.-]	20.64896513
K16076	nmpC, ompD; outer membrane porin protein LC	35.77782223
K16077	scrY; sucrose porin	14.8962425
K16090	fiu; catecholate siderophore receptor	46.90750581
K16136	mall; LacI family transcriptional regulator, maltose regulon regulatory protein	21.35298157
K16138	uidR; TetR/AcrR family transcriptional regulator, repressor for uid operon	NS
K16140	uidC, gusC; putative glucuronide porin	23.95529231
K16147	glgE; starch synthase (maltosyl-transferring) [EC:2.4.99.16]	NA
K16148	glgA; starch synthase [EC:2.4.1.21]	NA
K16211	malY, malT; maltose/moltooligosaccharide transporter	NA
K16263	yjeH; amino acid efflux transporter	29.52087787
K16291	erfK; L,D-transpeptidase	96.03823969
K16301	efeB; deferrochelataase/peroxidase EfeB [EC:1.11.1.-]	NS
K16321	gntP; high-affinity gluconate transporter	63.79291791
K16322	pit; low-affinity inorganic phosphate transporter	70.23391654
K16324	psuT; putative pseudouridine transporter	25.36078507
K16326	yeiL; CRP/FNR family transcriptional regulator, putative post-exponential-phase ni	15.28730801
K16345	xanP; xanthine permease XanP	NA
K16346	xanQ; xanthine permease XanQ	40.72330745
K16363	lpxC-fabZ; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase / 3-hy	NA
K16568	exoZ; exopolysaccharide production protein ExoZ	6.827996629
K16619	plc, cpa; phospholipase C / alpha-toxin [EC:3.1.4.3]	4.194873423
K16692	etk-wzc; tyrosine-protein kinase Etk/Wzc [EC:2.7.10.-]	63.66058421
K16693	wzxE; O-antigen flippase	32.45835715
K16695	wxC; lipopolysaccharide exporter	23.74398934
K16697	K16697, tuaC; teichuronic acid biosynthesis glycosyltransferase TuaC [EC:2.4.-.-]	55.1998709
K16703	wcaL, amsK; colanic acid/amylovoran biosynthesis glycosyltransferase [EC:2.4.-.-]	55.34194431
K16704	rffC, wecD; dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase [EC:2.3.1.210]	NS
K16711	wcaM; colanic acid biosynthesis protein WcaM	21.89986489
K16783	bioN; biotin transport system permease protein	NA
K16784	bioM; biotin transport system ATP-binding protein [EC:3.6.3.-]	NA
K16787	ecfA2; energy-coupling factor transport system ATP-binding protein [EC:3.6.3.-]	NA
K16905	K16905; fluoroquinolones transport system permease protein	NA
K16906	K16906; fluoroquinolones transport system permease protein	NA
K16907	K16907; fluoroquinolones transport system ATP-binding protein [EC:3.6.3.-]	NA

[illegible]

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NS	NS	NS	28.52178859	1.323825036	0.004909034
NS	NS	NS	5.602312509	2.218527487	0.003284125
	-2.853418719	2.21E-08	5.93E-05	70.25381818	-1.943061301 0.000119253
	1.402386871	0.000444246	0.009262221	71.91710792	1.279625721 0.00136165
	1.925834478	2.52E-05	0.002654065	45.91719966	1.89588544 3.38E-05
	1.244347564	0.000898258	0.013438841	284.21138	1.074627956 0.004178059
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.715898805	7.57E-06	0.002258858	42.8289479	2.488353013 4.15E-05
NA	NA	NA	NA	NA	NA
NS	NS	NS	4.186661119	-1.804655461	0.002351669
NA	NA	NA	NA	NA	NA
	-1.552335428	0.003228952	0.029049747	9.878843776	-2.214597632 4.58E-05
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.174884849	0.000426557	0.009112422	15.39365526	1.764475835 0.004414917
	-0.487309269	0.002472607	0.024684703	NS	NS
NA	NA	NA	NA	NA	NA
	1.541290482	0.003348175	0.029687323	235.3588381	1.52106705 0.003790057
	2.074120481	0.00025464	0.007115616	44.5898857	1.77670072 0.001752744
NA	NA	NA	NA	NA	NA
	0.092466648	0.003083124	0.028162347	NS	NS
NA	NA	NA	NA	NA	NA
	2.122743466	0.000710731	0.011673804	18.00603769	2.425801248 0.00010443
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-3.740038016	4.76E-05	0.002992269	NS	NS
	1.955100246	0.001181029	0.015547325	30.61565546	2.019651504 0.000803697
NA	NA	NA	NA	NA	NA
	-2.901269764	0.003343431	0.029687323	NS	NS
	-0.231674412	0.001060375	0.014678539	3184.122286	-0.235997093 0.000854805
	-0.518052913	0.006136149	0.045270956	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.536666282	0.00373411	0.031936154	58.94561117	1.559074472 0.003230108
	1.886588392	0.000565832	0.010443578	20.03896043	1.945167838 0.000377331
NA	NA	NA	NA	NA	NA
	0.415278267	0.00610778	0.045123642	NS	NS
	1.653261582	0.006348871	0.046520852	20.78767382	1.907527114 0.001609009
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NS	NS	NS	233.2800351	0.818172228	0.001497933

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.587310054	0.002756545	0.02625071	24.65399978	1.496885191 0.004807864
	2.007287734	0.000127768	0.004804346	28.20302826	1.641073555 0.001785333
	2.463577916	9.94E-05	0.004202658	29.1755452	2.320568119 0.00024828
NA	NA	NA	NA	NA	NA
	-1.443590105	0.005571287	0.042335671	NS	NS
	2.409598932	2.45E-05	0.002654065	43.92264243	2.36294369 3.51E-05
NA	NA	NA	NA	NA	NA
	-0.677833642	0.001724496	0.019706957	355.0757223	-0.761613936 0.000428759
	1.81937835	0.002283502	0.023444537	28.36277294	1.713323578 0.004085637
	-1.161164484	0.006212037	0.045705277	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.258514	0.002545373	0.025129528	NS	NS
NA	NA	NA	NA	NA	NA
	-1.086390598	0.000388979	0.008786906	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.59445115	0.002167151	0.022689605	NS	NS
	-0.588558146	0.004789522	0.038166947	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.10077554	0.000446713	0.009263696	40.19333776	2.253148096 0.000164262
	1.495500402	0.005019984	0.039476331	30.96270239	1.698377847 0.001428586
	1.924934358	0.001115879	0.014983467	19.08542985	1.985454831 0.000770142
NA	NA	NA	NA	NA	NA
	-0.096050514	0.00366421	0.031388309	NS	NS
NS	NS	NS	21.72990349	-2.15285691	1.44E-05
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-1.005808621	0.005417664	0.041628434	24.6857774	-1.176346865 0.001229833
NS	NS	NS	210.1332104	0.849293043	0.001225733
NA	NA	NA	NA	NA	NA
	1.957087812	0.00346153	0.030279933	15.76919632	2.077111892 0.001904494
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.08300274	0.002117692	0.022272198	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.243538781	0.000550401	0.010269078	NS	NS

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.555244576	0.005102448	0.04000766	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.370034918	0.001545936	0.018575445	702.9464609	-0.367031756 0.001693433
	2.996591538	4.97E-06	0.001736561	11.09280992	2.881457911 1.17E-05
NA	NA	NA	NA	NA	NA
	2.809523884	0.000339908	0.008151433	NS	NS
NS	NS	NS	899.8883012	-0.295059135	0.002824348
	-0.225901417	0.006942292	0.049481516	3902.826567	-0.234522124 0.005075316
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	0.292272908	0.00065699	0.011273785	2390.321971	0.253517601 0.003131216
NA	NA	NA	NA	NA	NA
	2.226612893	0.000920293	0.013579373	NS	NS
NA	NA	NA	NA	NA	NA
	-1.874210668	0.002185579	0.02283802	NS	NS
	2.457326866	7.88E-05	0.003909894	72.81603497	2.534299947 4.65E-05
	-1.448165294	0.001424344	0.017667787	NS	NS
NS	NS	NS	2779.803569	-0.377688863	0.000750681
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.23960665	0.006616854	0.047641684	NS	NS
	2.187735672	4.04E-05	0.002842415	72.08724975	1.939919325 0.00027486
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	0.300640517	0.001653907	0.019269273	NS	NS
	2.578547773	1.27E-05	0.002342972	20.88363982	2.501442018 2.31E-05
NA	NA	NA	NA	NA	NA
	1.805461679	0.001563725	0.018705489	36.83464287	1.807667498 0.001546033
	-2.517086527	0.000464222	0.009462135	NS	NS
	-0.319265396	0.002207615	0.022984687	NS	NS
	0.961650213	0.002630383	0.025455475	9.930339573	0.927433331 0.003861094
	2.103244897	0.00063705	0.011191419	24.80796699	2.070081709 0.000774706
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-2.01378007	0.001974465	0.021423944	23.61151997	-2.223392682 0.000818952
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.578684693	0.002959942	0.027611929	47.62448348	1.499009521 0.004782177
	1.886353553	0.000755332	0.012110117	23.63464499	1.684025999 0.002689019
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.914115207	0.002765605	0.026290349	32.89565441	2.088350953 0.001081833

	2.051981201	0.000389366	0.008786906	64.56773857	2.039642965	0.000421231
	0.282385648	0.000122486	0.004767197	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-0.324948488	0.001471819	0.018048269	NS	NS	NS
NS	NS	NS	62.1864098	1.665177489	0.002018734	
	2.480993894	0.001634642	0.019221911	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.831064244	0.00095322	0.013950265	182.1544329	1.579374178	0.004404152
	2.034568835	0.002535571	0.02508021	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	0.943303966	3.98E-05	0.002842415	NS	NS	NS
	0.726604391	0.000764385	0.012218791	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.533172613	0.0062866	0.046127501	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	0.43494606	0.000860445	0.013140749	NS	NS	NS
	-0.405940909	0.006063146	0.044979497	NS	NS	NS
	2.301651772	2.80E-05	0.002781952	33.35776054	2.264650557	3.76E-05
	1.910337679	0.001388603	0.017323567	44.30224564	2.013667996	0.000749894
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	0.341566196	0.004445533	0.036163656	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	0.389981092	0.002235854	0.02309379	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	0.194047411	0.006448453	0.046866905	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.420231514	3.16E-05	0.002842415	62.34503267	2.425423337	3.02E-05
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.371609446	0.000443405	0.009262221	37.67680437	2.083574383	0.002055247
NA	NA	NA	NA	NA	NA	NA
	0.188957181	0.002450296	0.024553242	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA

NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-0.986881578	0.006533693	0.047338503	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.771714198	0.003983757	0.033196607	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.558098943	0.004033324	0.033379017	NS	NS	NS
	2.085315098	3.51E-05	0.002842415	61.00608502	1.787313443	0.000397325
	2.162547632	1.05E-05	0.002342972	39.79373385	1.996790831	4.80E-05
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.206901915	0.000407449	0.009043008	20.96730863	2.132315706	0.000641587
	2.039366722	1.97E-05	0.002519772	317.0204741	2.273846896	1.91E-06
	-1.039038896	0.001903534	0.020780244	NS	NS	NS
	-1.0740891	0.003927918	0.033067159	33.09630589	-1.19170893	0.00142296
	2.347492872	0.000435591	0.009210867	12.88338673	2.277832555	0.00064908
NA	NA	NA	NA	NA	NA	NA
	1.902856625	0.001300559	0.016767934	NS	NS	NS
	1.66736382	0.003028889	0.027904228	3.43246033	1.602126743	0.00459605
NA	NA	NA	NA	NA	NA	NA
	2.043858677	0.003491312	0.03048235	7.184833615	2.094668476	0.002748757
	-0.994473398	0.005613404	0.042503624	NS	NS	NS
	2.529717629	0.000109982	0.004441464	20.80080501	2.217600827	0.000711889
	2.413737961	6.99E-05	0.003828827	45.17722481	2.302047001	0.000149479
	2.078500298	0.000911218	0.01355721	11.84247949	1.900394401	0.002462245
	2.390856279	9.89E-05	0.004202658	17.48076027	2.219884405	0.000304705
NS	NS	NS	NS	9.626960116	1.785382332	0.005195463
	2.560406801	2.63E-05	0.002666731	52.36600299	2.501620119	4.03E-05
	1.75244142	0.005181487	0.040391534	NS	NS	NS
	2.131103429	0.003501696	0.03048235	4.401835396	2.207063294	0.002486023
NA	NA	NA	NA	NA	NA	NA
	1.809458128	0.003555015	0.03074716	14.81324405	1.798656343	0.003774697
	2.528175592	1.25E-05	0.002342972	90.54066	2.297850188	7.23E-05
NS	NS	NS	NS	88.19903731	0.840875341	0.003910364
	1.976606213	0.004084517	0.033696301	11.95643553	2.205283835	0.001324916
NS	NS	NS	NS	5.272832991	1.942144181	0.002754117
	-0.436804798	0.006528166	0.047338503	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA

	1.921370598	0.001504398	0.018280824	12.31512164	1.855122808	0.002208197
NA	NA	NA	NA	NA	NA	NA
	1.945474017	0.00137089	0.017243678	18.17746563	1.706614373	0.005075775
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.542869828	6.20E-05	0.003543329	14.35603921	2.579356741	4.86E-05
NA	NA	NA	NA	NA	NA	NA
	0.432721085	0.003653321	0.031367652	781.7180673	0.419525579	0.004839531
NA	NA	NA	NA	NA	NA	NA
	2.930299077	8.37E-07	0.000499444	29.63984578	2.18719589	0.000257147
	2.520550632	5.31E-05	0.003136928	14.37383549	2.030831011	0.001191931
	2.396385131	0.000488321	0.009732409	14.25667334	2.157896934	0.00173853
	2.337254668	0.000273611	0.007384746	18.20780847	1.907086157	0.003090938
	2.412344905	5.31E-05	0.003136928	45.00261089	1.846195006	0.002040859
	1.894045552	0.003409616	0.029888671	12.30792752	1.890171445	0.003487935
	2.284155756	0.000336341	0.008137336	22.13156672	2.302064181	0.000301509
	1.648181329	0.005577118	0.042335671	13.59680488	1.741278041	0.003397236
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-2.184683149	0.001302786	0.016767934	NS	NS	NS
	-3.1777542	8.43E-06	0.002342972	8.24780701	-1.94160548	0.004534268
	2.264838253	0.000357531	0.008277146	20.25164818	1.798067701	0.004749566
NA	NA	NA	NA	NA	NA	NA
	-0.056381866	0.003955603	0.033158962	NS	NS	NS
	-0.2914289	0.001104951	0.014978202	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.098817931	0.00010314	0.004294321	44.99371512	1.826715847	0.0007377
	2.180772346	0.000170719	0.005695218	37.9806253	1.974752427	0.000672017
	1.749991238	0.000678824	0.011393639	75.27820974	1.802471473	0.000462494
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.404285991	0.006090889	0.045060832	NS	NS	NS
	1.707825724	0.005235308	0.040590032	NS	NS	NS
	2.028302296	0.001102393	0.014978202	29.34787784	1.738976569	0.005207876
NA	NA	NA	NA	NA	NA	NA
	1.845885752	0.003511226	0.030515853	NS	NS	NS
	2.045116193	0.000182785	0.005984569	28.52240291	1.774122091	0.001197934
	1.968009465	0.002352457	0.023884773	12.78110088	1.928175006	0.002892485
NS	NS	NS	NS	26.54967697	1.738676448	0.00172386
	-0.71258487	0.003861433	0.032764232	NS	NS	NS
	-2.645117319	1.57E-05	0.002459639	72.23467912	-2.209241433	0.000296963
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-0.289908244	0.00174808	0.019856859	NS	NS	NS

NA	NA	NA	NA	NA	NA
	1.655870274	0.00294953	0.027611929	14.9571351	1.579488951 0.004616996
	1.732932262	0.002230441	0.02309379	NS	NS
NA	NA	NA	NA	NA	NA
	1.772594257	0.001842231	0.020443431	NS	NS
	1.847779165	0.00423963	0.034711974	NS	NS
	0.560089583	0.000700685	0.011557946	NS	NS
NA	NA	NA	NA	NA	NA
	-1.756250213	0.000211452	0.006318861	11.38287011	-1.465497406 0.001841866
	0.691605918	0.000584393	0.010676111	355.259407	0.602071543 0.002773694
	0.636604109	0.002816924	0.026656848	141.7738971	0.654439533 0.002148001
	0.410792794	0.005785336	0.043402352	NS	NS
	0.562842981	0.001980054	0.021441275	NS	NS
	0.423293584	0.004478923	0.03622936	NS	NS
	0.462260048	0.000992388	0.014076723	NS	NS
	0.399104425	0.005502944	0.041923844	NS	NS
	0.476978216	0.000183123	0.005984569	NS	NS
	2.319120959	0.002706758	0.025960712	5.400092215	2.355497563 0.00232311
	1.934963195	0.002961175	0.027611929	NS	NS
	2.663493717	0.000345389	0.00824482	13.33764966	2.203812892 0.003182016
	0.623867826	0.000356044	0.008277146	NS	NS
	0.656897081	0.00061936	0.011015178	NS	NS
NA	NA	NA	NA	NA	NA
	0.371424386	0.005368102	0.041306696	NS	NS
	0.918916758	0.003070053	0.028095857	NS	NS
	2.052004176	0.000512976	0.009910778	20.506025	1.97531226 0.000831807
	2.216908283	0.000522432	0.010057292	40.06885115	2.149280753 0.000772195
NA	NA	NA	NA	NA	NA
	2.302606352	0.00016235	0.005662218	22.87843966	2.248893196 0.000230904
NA	NA	NA	NA	NA	NA
	0.933537885	0.004969868	0.039197007	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.270849761	0.00232898	0.023691199	NS	NS
NA	NA	NA	NA	NA	NA
	1.668376255	0.003758389	0.0320927	NS	NS
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.5016624	7.06E-05	0.00382975	17.46930261	2.407539391 0.000132561
NA	NA	NA	NA	NA	NA
	-0.095527191	0.000743923	0.012071328	NS	NS
	1.873885897	0.002624368	0.02544311	10.97780546	2.026317145 0.001120172
NA	NA	NA	NA	NA	NA
	2.525020496	7.83E-05	0.003909894	22.36099938	2.287422963 0.000354732
	2.419467007	0.000310379	0.00775371	25.31761455	2.331293922 0.0005134
NS	NS	NS		228.3722379	1.260655922 0.000966285
	1.178127558	0.004255258	0.034786894	NS	NS

	1.656013468	0.001895951	0.020767207	11.2528994	1.612467705	0.002533374
	2.110861288	2.99E-05	0.002842415	31.20068389	1.870263497	0.000222101
	2.155438503	0.00021267	0.006318861	32.13937209	1.667296119	0.004266925
NS	NS	NS	5707.610624		-0.132463316	0.005320236
	0.936852161	0.003009245	0.027904228	NS	NS	NS
	0.914242931	0.003925479	0.033067159	NS	NS	NS
	0.849812579	0.003902849	0.033011346	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.134101908	0.000737853	0.012009113	29.67771247	2.068825591	0.001071707
	2.187115631	3.28E-05	0.002842415	60.17067265	2.272220774	1.59E-05
	NA	NA	NA	NA	NA	NA
	0.269423134	0.006371589	0.046560282	NS	NS	NS
	1.790254462	0.000726198	0.011855342	25.96821872	1.68664141	0.001483156
	NA	NA	NA	NA	NA	NA
	1.851200673	0.000424253	0.009112422	108.4087837	1.487429279	0.004670579
	NA	NA	NA	NA	NA	NA
	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.224760316	0.003182503	0.028824999	NS	NS	NS
	NA	NA	NA	NA	NA	NA
	0.192027227	0.003613983	0.031106893	NS	NS	NS
	2.118639568	0.006539782	0.047338503	NS	NS	NS
	2.216439471	1.84E-05	0.002519772	28.13613326	2.06652549	6.64E-05
	NA	NA	NA	NA	NA	NA
	1.723151669	0.001617806	0.019146762	37.00088261	1.552211885	0.004562915
	NA	NA	NA	NA	NA	NA
	2.477092453	3.38E-05	0.002842415	53.60545011	2.175587522	0.000274456
	2.099913682	0.001172999	0.015479551	25.95910383	2.289537719	0.000397559
	NA	NA	NA	NA	NA	NA
	NA	NA	NA	NA	NA	NA
	0.724126002	4.23E-05	0.002842415	NS	NS	NS
	0.634448452	0.002619239	0.025439302	NS	NS	NS
	2.033799886	0.001111173	0.014978202	19.73897123	2.013988783	0.001242641
NA	NA	NA	NA	NA	NA	NA
	0.554609427	0.000285859	0.007563282	1274.504459	0.460045589	0.002625379
	2.213498162	0.000353242	0.00826066	23.0047414	2.269912257	0.00024648
	NA	NA	NA	NA	NA	NA
NS	NS	NS	69.2895774		-1.570994509	0.000571713
NA	NA	NA	NA	NA	NA	NA
	-0.144159584	0.000688847	0.011525847	NS	NS	NS
	1.569663525	0.002819045	0.026656848	NS	NS	NS
	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.798223818	0.002261645	0.023270683	NS	NS	NS
	1.650126657	0.002069164	0.021970999	64.3608763	1.529305129	0.004332097

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.966673171	0.000271412	0.007384746	30.36815992	1.747507323 0.001236403
NA	NA	NA	NA	NA	NA
	1.81100148	0.000353613	0.00826066	28.81445612	1.824046141 0.00032033
NA	NA	NA	NA	NA	NA
	1.62962365	0.002430594	0.024457561	NS	NS
	2.166547589	0.00011291	0.004517615	20.96958568	1.854711387 0.000974863
	1.664473501	0.000888225	0.013344651	NS	NS
NA	NA	NA	NA	NA	NA
	1.767490063	0.001640171	0.019234405	42.20599746	1.75300688 0.001799692
	2.093131012	5.71E-05	0.003330886	148.8186333	1.931576972 0.000204904
	1.994364242	0.000429239	0.009112422	39.61781933	1.866754367 0.000988161
NA	NA	NA	NA	NA	NA
NS	NS	NS		20.32861915	1.394501277 0.0034767
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.200638116	9.38E-05	0.004131544	20.33636296	2.027958099 0.000324233
NA	NA	NA	NA	NA	NA
	1.410842771	0.00243164	0.024457561	NS	NS
	-0.679446024	0.003222214	0.029037773	NS	NS
	1.494551269	0.000701525	0.011557946	188.2725423	1.347829506 0.002249717
NA	NA	NA	NA	NA	NA
	-0.497255931	0.001033553	0.014456287	NS	NS
	1.979017065	0.00304348	0.027968582	10.39672948	2.251334868 0.000726772
NA	NA	NA	NA	NA	NA
NS	NS	NS		4.99617931	2.018301077 0.000370161
	1.851853894	0.001290279	0.016699003	NS	NS
NA	NA	NA	NA	NA	NA
	2.079584394	0.002735169	0.026139849	12.81725737	2.284089264 0.000985747
NA	NA	NA	NA	NA	NA
NS	NS	NS		723.8221332	-0.393418571 0.002240459
	0.238424556	0.000552553	0.010269078	NS	NS
NA	NA	NA	NA	NA	NA
	-0.659317802	0.000542333	0.010256579	NS	NS
NA	NA	NA	NA	NA	NA
	1.675333226	0.003172594	0.028783785	9.722191411	1.782236367 0.001683851
	1.619407969	0.000262436	0.007228429	285.2636573	1.787411933 5.60E-05
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.345057952	0.001957904	0.021287249	52.84270774	1.352297277 0.001857608
NA	NA	NA	NA	NA	NA
	-0.158468175	0.002851387	0.026868069	5479.837214	-0.160181715 0.00256955
NA	NA	NA	NA	NA	NA
NS	NS	NS		36.4490007	1.163589531 0.004943705
	1.960857315	0.001509981	0.01829729	9.859551852	2.162420788 0.000454542
	0.242960183	0.006368148	0.046560282	NS	NS
	1.983141481	0.001515974	0.01829729	20.29059503	2.024257685 0.001203807

	2.166557297	0.000206124	0.006254759	NS	NS	NS
	1.816921442	0.002328523	0.023691199	8.232828285	1.897378661	0.001475966
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.183378199	0.000665254	0.011332433	5.49925623	2.254132866	0.00043933
NA	NA	NA	NA	NA	NA	NA
	1.687354786	0.006837742	0.048938573	NS	NS	NS
	1.871663806	0.000154114	0.005445713	NS	NS	NS
	2.150042729	0.000105876	0.00437429	53.24360398	1.866180538	0.0007758
NA	NA	NA	NA	NA	NA	NA
	1.86215559	0.000404864	0.009043008	34.93715181	1.837279468	0.000485654
	-3.232619176	6.74E-07	0.000452653	47.90269551	-3.334301296	3.21E-07
NA	NA	NA	NA	NA	NA	NA
	1.603628864	0.004935934	0.03898662	20.92017973	1.975224686	0.000516684
	1.722469922	0.005706736	0.042988607	NS	NS	NS
	2.283190519	2.48E-05	0.002654065	94.38936766	1.868594862	0.00056599
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.855336522	0.000811232	0.012702999	8.130841555	1.649975804	0.00305766
NA	NA	NA	NA	NA	NA	NA
	2.026556988	0.000203378	0.006206502	62.76755541	1.558839515	0.004369229
	1.296395921	9.46E-05	0.004131544	65.39524515	1.035510514	0.001850574
	1.986479376	0.00332556	0.029621196	NS	NS	NS
	1.663756619	0.000632739	0.011179077	62.85122667	1.512337518	0.00191133
	2.27332206	0.000309934	0.00775371	35.43518226	2.117110796	0.000790339
NA	NA	NA	NA	NA	NA	NA
	1.96802627	0.003349566	0.029687323	9.020230972	2.175913216	0.001147526
	1.787086477	0.005360257	0.041306696	7.628080688	1.795182875	0.005179927
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.503570415	0.000471093	0.009512186	17.06235425	2.218759899	0.001978663
	1.872001978	0.004813718	0.038302936	NS	NS	NS
	2.107984191	0.002074753	0.021979284	NS	NS	NS
	3.108032543	0.000167056	0.005686707	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.05662889	0.004768326	0.038054503	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.393534079	0.001387204	0.017323567	11.40986683	1.608473833	0.000215176
	1.82605915	0.002510832	0.024927318	NS	NS	NS
	0.311483064	0.007003918	0.04981387	NS	NS	NS
	1.746546428	0.00131558	0.016823758	NS	NS	NS
	1.847213741	0.000477087	0.009597138	54.7051283	1.676668264	0.001536959
	0.97793153	0.004403423	0.035943442	NS	NS	NS
	2.183212419	0.00071953	0.011782301	21.67870019	2.151269067	0.000864051
	1.903621073	0.00533193	0.04120546	NS	NS	NS

NA	NA	NA	NA	NA	NA
	0.42217565	0.006596373	0.047619782	NS	NS
	2.027996102	0.002689429	0.025840647	19.53269961	2.364182683
	1.286471236	1.93E-05	0.002519772	26.60271421	0.919225262
	2.005981253	0.003202314	0.02892173	15.40706927	2.170006843
	2.133876406	0.000135458	0.004983179	14.37024216	1.829189938
	-0.235520951	0.003954514	0.033158962	NS	NS
	-1.143285961	3.77E-05	0.002842415	156.4583698	-1.16975515
NS	NS	NS	15.00967893	1.72321045	0.003256634
	2.054238867	0.003539826	0.03071471	12.72049742	1.988719563
NA	NA	NA	NA	NA	NA
	2.115089561	0.001102378	0.014978202	26.25531352	2.072962813
NA	NA	NA	NA	NA	NA
	-0.314182738	0.003874034	0.032819297	NS	NS
	1.845667134	0.005440065	0.041697812	8.462291003	2.1275947
	2.410230072	0.000184963	0.005984569	7.300934011	2.009621512
	2.259681228	0.001347273	0.01702636	6.990373814	2.412075653
	2.044927967	0.002250198	0.023197334	5.989463105	2.082311866
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.329539269	0.004606635	0.036983912	43.67187778	1.455307985
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.361901817	0.003655958	0.031367652	NS	NS
	1.655102919	0.000701205	0.011557946	51.20324078	1.378278939
NA	NA	NA	NA	NA	NA
	-0.066274655	0.001098861	0.014978202	NS	NS
NA	NA	NA	NA	NA	NA
	1.89483096	0.000453548	0.009369249	109.8186108	1.715432403
NS	NS	NS	33.53021677	1.853912369	0.001295812
NA	NA	NA	NA	NA	NA
	1.621381304	0.004981216	0.0392289	NS	NS
	2.238752253	0.000983664	0.014051222	12.51706754	2.177160422
NS	NS	NS	13.89648353	2.054943969	0.001316388
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-2.002651194	0.003153554	0.028659453	NS	NS
	2.03515123	0.000753333	0.012110117	34.37064594	1.881436609
NS	NS	NS	17.96551549	-1.379014169	0.001034207
NS	NS	NS	288.0728137	-0.668577289	0.002854128
	0.585707417	0.001099376	0.014978202	NS	NS
NA	NA	NA	NA	NA	NA
	1.659466319	0.001461699	0.017965181	193.5933071	1.656990862
	1.928396618	0.001719313	0.019689617	16.86490885	2.035700623
NA	NA	NA	NA	NA	NA

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	-0.091366595	0.005033806	0.039527155	NS	NS
	2.188963662	0.000367453	0.008434138	27.1408686	1.87008482
	2.582199919	1.91E-05	0.002519772	16.66187262	2.293002988
	2.207740334	0.00130497	0.016767934	16.04712135	2.275517539
NS	NS	NS	794.8220746	-0.336846409	0.001287848
	1.160438557	0.001891929	0.020767207	84.5738509	1.1386244
	1.742909968	0.000466444	0.009462135	NS	NS
NA	NA	NA	NA	NA	NA
	2.29602244	9.19E-05	0.004131544	27.39101513	2.053320307
	-2.199498436	0.000308105	0.00775371	20.86872776	-3.45135798
	1.21583878	0.003810039	0.032430618	20.2656714	1.317367422
	2.125594724	0.0006023	0.010783181	20.92061825	1.861039597
NA	NA	NA	NA	NA	NA
	1.888192786	0.004561287	0.036784795	15.26623323	1.970878964
	2.217240223	0.000275525	0.007399217	25.35713582	2.293087427
	1.812018499	0.003550763	0.03074716	NS	NS
	1.727139065	0.001366861	0.017233357	NS	NS
	2.305767856	0.000889478	0.013344651	20.1300394	2.29400371
	2.01313753	0.000311969	0.007757341	31.48122156	1.950498163
	2.176136764	0.0005952	0.01072876	27.87189185	2.061201044
	1.876119263	0.003920168	0.033067159	NS	NS
NA	NA	NA	NA	NA	NA
	1.970772923	8.11E-05	0.003933706	382.5726268	1.739093012
	1.712696473	0.001042739	0.014471714	NS	NS
	2.415953165	7.65E-05	0.003909894	23.77007554	2.621685157
NA	NA	NA	NA	NA	NA
NS	NS	NS	1289.712219	0.407675201	0.001429073
NS	NS	NS	884.185141	0.360523202	0.002145348
NS	NS	NS	765.9903512	0.39285111	0.002900013
	0.513209918	0.004560269	0.036784795	157.9983545	0.597747498
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NS	NS	NS	4.642118393	2.335082042	0.000854595
	1.792149752	0.000455506	0.009373657	250.6616293	1.520113629
	2.812033526	4.37E-06	0.001677938	42.72516586	2.816682476
	2.162771944	0.00056449	0.010443578	34.03978145	1.887980102
	1.979505323	0.00340953	0.029888671	NS	NS
	0.414179081	0.000315525	0.007809606	1163.991581	0.351354263
	0.477737492	9.88E-05	0.004202658	701.6511939	0.393396889
	2.223707065	0.0001649	0.005686707	35.53542438	2.186985827
	1.815525206	0.001390143	0.017323567	35.26657274	1.700203763
	1.974448534	0.004756294	0.038014965	NS	NS
NA	NA	NA	NA	NA	NA
	2.253699539	0.001808904	0.020240885	NS	NS
NS	NS	NS	2178.954079	-0.335566187	0.002774905
	1.823945331	0.003972391	0.033181513	11.45673118	1.901766564

	2.126324097	6.16E-05	0.003543329	23.08458165	2.010432686	0.000153955
NS	NS	NS		15.83682802	-1.710160882	0.001393647
	2.129489227	0.000767988	0.012239957	12.25974621	1.913864129	0.002545248
NS	NS	NS		76.93358475	1.309973953	0.004656966
NA	NA	NA	NA	NA	NA	
	1.807667252	0.006390605	0.046635787	NS	NS	NS
NS	NS	NS		4.85237749	-2.311603526	0.004548268
NA	NA	NA	NA	NA	NA	NA
	-2.461547848	0.001014005	0.014257117	NS	NS	NS
	2.149380008	0.000596337	0.01072876	24.19359737	2.031942215	0.001175306
	3.041896438	0.001884464	0.020767207	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.739392789	1.15E-05	0.002342972	24.22097612	2.59892251	3.18E-05
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		5.870314813	2.049587017	0.002836457
	1.69321299	0.001139626	0.015188409	26.02797021	1.881839838	0.000292858
	1.822506178	0.001797168	0.020193699	13.71065328	1.629540016	0.005331306
	0.84782847	0.006017653	0.044833287	251.4724996	0.986653009	0.001379768
	1.901181187	0.000957572	0.013975864	30.78724606	1.98959328	0.000544079
	2.72880023	1.21E-05	0.002342972	32.89199884	2.686250795	1.66E-05
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.323725473	0.00111041	0.014978202	34.91578842	1.344889903	0.00093227
NS	NS	NS		151.4367276	0.783403026	0.003673805
	0.174863748	0.001246301	0.016207953	NS	NS	NS
	1.650710038	0.003299014	0.029482536	15.07356588	1.617768498	0.004008428
	1.732408809	0.000782722	0.012437871	71.18111252	1.530652637	0.003016299
	1.846095716	0.004199538	0.034436211	14.11042785	1.828408266	0.004591098
	2.057595211	0.001987512	0.021478722	14.84461129	2.431449921	0.000247369
	2.438251304	3.83E-05	0.002842415	16.16253249	2.345759826	7.57E-05
NA	NA	NA	NA	NA	NA	NA
	-0.425396064	0.001627076	0.019206654	NS	NS	NS
	-0.385489254	0.002672826	0.025727152	NS	NS	NS
	-2.499980773	0.000238657	0.006928804	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		15.44161733	-1.171159183	0.001679278
	-2.376092076	5.18E-07	0.000397803	NS	NS	NS
	-0.877303737	0.000379437	0.00867215	NS	NS	NS
	-2.483471789	6.64E-05	0.003698	NS	NS	NS
	-0.497393602	0.004477398	0.03622936	NS	NS	NS
	-2.914056064	3.89E-05	0.002842415	23.62968333	-3.368671341	2.45E-06
	-2.83706729	5.74E-06	0.001814338	NS	NS	NS
	-0.837761951	0.002826574	0.026681071	243.6167151	-0.955132612	0.00066207
	2.550458963	1.60E-05	0.002459639	52.8514425	2.440817787	3.66E-05
	2.228210332	0.000255691	0.007115616	31.33012069	2.606347667	1.82E-05
	-2.100489427	0.000861207	0.013140749	NS	NS	NS
	-1.890098014	0.001635527	0.019221911	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA

	2.402982091	9.36E-05	0.004131544	18.31563766	2.553102327	3.26E-05
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.886530377	0.001381489	0.017323567	NS	NS	NS
	1.547860648	0.006424192	0.046753839	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.506484471	0.003070614	0.028095857	35.84312608	1.427188483	0.005043643
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.068228253	0.000253528	0.007115616	23.21053016	1.991079136	0.000431337
	2.005437474	0.000360757	0.008315997	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-1.214115651	0.00011355	0.004517615	55.64098871	-0.935644195	0.002852549
NA	NA	NA	NA	NA	NA	NA
	1.979813658	8.90E-05	0.004122792	60.7779784	1.705002976	0.000748831
	1.16577216	0.000489983	0.009732409	61.2924596	1.061016537	0.001528654
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.417186698	0.000534549	0.010181075	14.32281127	2.351259432	0.000760718
	-2.812498682	0.000676341	0.011393639	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-0.940784041	0.006016485	0.044833287	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		305.884758	0.618579365	0.003821378
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-0.244163887	0.000995537	0.014076723	3147.857863	-0.273349189	0.000229289
	-0.328118395	0.001121942	0.015027306	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.095185648	0.001755117	0.019881181	3.978387015	1.965033712	0.003495955
	-0.075727339	0.002638676	0.0254898	19609.38495	-0.077859081	0.001995041
	2.36350453	0.000262311	0.007228429	20.86094476	1.979416257	0.002304641
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.263135741	0.000532338	0.010175037	25.95733951	2.009554436	0.002130601
NA	NA	NA	NA	NA	NA	NA
	1.505488517	0.006617147	0.047641684	NS	NS	NS
	1.983776329	0.003364669	0.02970678	8.347793041	2.028209125	0.002702228
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.541695397	0.000198578	0.006129675	11.37008653	1.939972686	0.004722543

	2.273585563	0.001659548	0.019293144	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	0.305896767	0.000842736	0.013006059	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	80.31027419		1.209883145	0.003757176
	3.012780868	4.79E-05	0.002992269	14.85662036	2.729058329	0.000237183
	2.045697451	0.001486391	0.018144102	16.87519741	2.469310097	0.000120081
	2.150912424	0.000641772	0.011191419	10.19474475	1.864377813	0.003195044
	1.732726193	0.006842835	0.048938573	NS	NS	NS
	-0.23657351	0.000589876	0.010712096	NS	NS	NS
	1.87267502	0.004934796	0.03898662	20.75500942	2.177282464	0.001055844
	2.242617824	0.000937473	0.013794978	13.98092632	2.181670553	0.00129472
	1.833478682	0.000491412	0.009732409	45.81923587	1.723291831	0.0010621
NA	NA	NA	NA	NA	NA	NA
	1.038246979	0.0006752	0.011393639	NS	NS	NS
	0.977532781	0.000420065	0.009097461	NS	NS	NS
	2.100337746	0.000501506	0.009805209	12.45483267	1.81610723	0.002713208
	1.054584369	0.000233979	0.006829886	129.1783523	0.877900458	0.002226142
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	431.2077144		0.68145624	0.00404849
	1.398076841	0.004436051	0.036154825	NS	NS	NS
	1.849723396	0.006818793	0.048896847	13.90462384	2.032597928	0.002916627
NA	NA	NA	NA	NA	NA	NA
	2.231064917	1.73E-05	0.002519772	33.41321477	1.913094653	0.000236188
	2.049213326	0.000419104	0.009097461	24.78187624	1.822978311	0.001733691
NA	NA	NA	NA	NA	NA	NA
	1.468216785	0.002027073	0.02173335	NS	NS	NS
	0.841919652	0.002610149	0.025439302	30.72545047	1.271372138	4.73E-06
	2.083965913	0.003963518	0.033158962	NS	NS	NS
	2.098192804	0.00206988	0.021970999	NS	NS	NS
	-1.350144061	4.53E-07	0.000397803	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-0.209588135	0.003806805	0.032430618	6711.77377	-0.216792788	0.002763199
	2.412422951	4.14E-05	0.002842415	30.56338783	2.285538912	0.000103983
	2.710674223	3.03E-05	0.002842415	32.06549842	2.040347035	0.001758468
	2.680637049	2.45E-06	0.001011179	432.9501144	2.486971572	1.23E-05
	1.812459458	0.005580647	0.042335671	10.49448448	1.825822534	0.005234211
	1.981688501	0.000998554	0.014076723	10.51757962	1.745134704	0.003865105
	1.964539629	0.002549915	0.025129528	22.61109661	2.26305577	0.000497103
	1.970265434	0.003028875	0.027904228	12.7961191	1.918568579	0.00390823
NA	NA	NA	NA	NA	NA	NA
	1.534921947	0.004715246	0.03774305	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA

NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	1.55313138	0.002715643	0.025999497	36.83447721	1.53245531 0.003115123
NS	NS	NS	165.9763283	1.705863705	0.002588084
	-2.018884367	0.001898473	0.020767207	5.224771449	-2.320209995 0.000471809
	-1.116479642	0.00175825	0.019881181	NS	NS
NS	NS	NS	2448.042303	-0.221842437	0.00508282
NA	NA	NA	NA	NA	NA
NS	NS	NS	7961.913435	-0.097026369	0.004358169
	-0.867940476	0.001092184	0.014978202	92.18286623	-0.827620203 0.001851744
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
	2.007753249	0.000917752	0.013579186	33.27951651	2.200331709 0.000275646
	2.383689477	4.23E-05	0.002842415	28.4552161	1.96324211 0.000771064
	2.174460231	0.00053111	0.010175037	25.77313925	2.011623282 0.001366371
	1.9380246	0.000131431	0.004894508	59.94702249	1.888754724 0.000195291
NS	NS	NS	32.57135029	1.423095404	0.004376221
	1.390840943	0.004078388	0.033696301	67.13956203	1.386656483 0.00418741
	2.070648678	8.76E-05	0.004122792	81.47585046	1.803961854 0.000637651
	-0.519158431	0.00658087	0.047571808	NS	NS
	2.307314849	0.000272949	0.007384746	12.07259953	2.493708388 8.18E-05
	2.18453219	0.000590352	0.010712096	10.47287453	2.034856532 0.001407661
	1.305733181	0.00521104	0.040509784	NS	NS
	2.672850573	1.77E-05	0.002519772	13.15777601	2.252613152 0.000318003
	-1.071855994	0.001339028	0.016987841	NS	NS
	1.427544141	0.002035352	0.02173335	NS	NS
NA	NA	NA	NA	NA	NA
	2.072679093	0.000241409	0.006971017	61.61087756	2.074562904 0.000237391
	2.201373442	9.88E-06	0.002342972	65.52822487	2.103725644 2.41E-05
	2.293357115	8.84E-05	0.004122792	53.67168456	2.36105714 5.41E-05
	2.210551951	0.000857675	0.013140749	13.06795013	2.157355998 0.001147129
	2.174623872	0.00050898	0.009869072	13.69776379	2.52064564 5.32E-05
	1.847361987	0.003277274	0.029386039	14.19010093	2.152853469 0.000588218
	2.215319222	0.000640443	0.011191419	13.72638347	2.330335147 0.000326259
	-1.081429185	0.001525475	0.018370683	NS	NS
	2.130613136	0.000440972	0.009262221	38.20751154	2.467284744 4.58E-05
	2.323690806	0.00010928	0.004441464	14.00308077	2.355502131 8.74E-05
	1.936127179	0.002874247	0.027036044	13.83723175	2.077621824 0.001363121
	2.614357431	0.00024764	0.007037427	19.77262701	2.501338105 0.000457682
	2.115883142	0.000823127	0.012814531	NS	NS
NA	NA	NA	NA	NA	NA
	1.3310131	0.001698135	0.019572286	68.91255587	1.265643239 0.002868295
	1.783344023	0.001653681	0.019269273	33.61109317	1.587599472 0.00514066
	-2.194017301	4.19E-05	0.002842415	4.935455387	-2.925576951 3.14E-07
NA	NA	NA	NA	NA	NA
	-0.288866391	0.00210584	0.022262645	NS	NS

	1.804015652	0.00026677	0.007310309	100.513657	1.391938083	0.004989309
NA	NA	NA	NA	NA	NA	NA
	2.058426757	0.000405516	0.009043008	14.47626159	1.970125555	0.000722265
	1.917344327	0.004450601	0.036163656	10.2728424	2.043264695	0.00242136
	1.679723377	0.001907618	0.020782591	26.04445043	1.732933378	0.001362739
NA	NA	NA	NA	NA	NA	NA
	2.081557785	0.000969607	0.01404635	12.5077547	1.903086286	0.002593692
	2.055039264	0.001998749	0.021513585	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.50896353	4.70E-05	0.002992269	37.59834507	2.384034281	0.000110601
	2.167900591	0.000748809	0.012110117	35.89800658	2.075473768	0.001250298
NS	NS	NS		94.72494587	-0.544217826	0.003666758
	2.322959996	0.000196897	0.006112918	34.94519702	2.423942498	0.000101934
	2.446458533	9.69E-05	0.004196106	23.83709039	1.967882957	0.001772779
	2.060032876	0.000191813	0.006044097	46.35234548	1.990573256	0.000313684
	-0.354552589	0.002296002	0.023444537	NS	NS	NS
	2.181120509	7.47E-05	0.003896956	26.6467447	1.754050139	0.001515256
NA	NA	NA	NA	NA	NA	NA
	1.963845222	0.00123792	0.01613803	87.11470165	1.735198085	0.004355256
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.075672891	0.001040856	0.014471714	32.7405639	1.962409519	0.001941382
	1.854546733	0.003118623	0.028390042	23.09582823	1.910237433	0.002323154
	1.739922766	0.00168152	0.019422462	NS	NS	NS
	2.458445367	4.06E-05	0.002842415	31.51885105	2.217337366	0.00021757
	2.282476747	0.000120943	0.004741509	26.2250608	2.279200772	0.000123212
NA	NA	NA	NA	NA	NA	NA
	1.750040605	0.005136396	0.040098235	16.24027132	2.089120174	0.000807993
NA	NA	NA	NA	NA	NA	NA
	1.726525225	0.0004867	0.009732409	38.73882716	1.739829907	0.000437649
	1.80972665	0.004706268	0.037727409	NS	NS	NS
	2.581558025	2.47E-05	0.002654065	23.18336918	2.386496137	9.85E-05
	2.042127948	0.00335654	0.029700129	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.026838906	0.002617948	0.025439302	11.11237504	2.088725601	0.001916725
NA	NA	NA	NA	NA	NA	NA
	1.926134685	0.000502035	0.009805209	NS	NS	NS
	2.123169672	0.000810835	0.012702999	23.76972408	2.550562767	5.50E-05
NA	NA	NA	NA	NA	NA	NA
	0.431644216	0.002109791	0.022262645	NS	NS	NS
	2.293227222	5.23E-05	0.003136928	22.88173541	1.953067498	0.0005892
	2.024126923	0.001831474	0.020408399	26.13237939	1.979483348	0.002311846
	1.986369062	0.000628025	0.011132411	69.14714659	1.820011148	0.001735213
	2.217234832	0.000169405	0.005686707	26.1639492	2.300425447	9.48E-05
	2.047645996	0.002882561	0.027066841	9.099256122	1.9469304	0.004659393
	2.211495105	3.49E-05	0.002842415	98.04129451	1.952546506	0.000260037
	2.632877603	0.000125696	0.004788027	15.01046198	2.576358324	0.000176227
	1.995027574	0.000914191	0.013563868	16.38901358	1.960557933	0.001131254

	1.769633514	0.000607931	0.010847836	48.99354193	1.588274959	0.002111738
NA	NA	NA	NA	NA	NA	NA
	1.968630976	0.00164636	0.019264921	11.60357306	1.989720507	0.001471813
	2.24828723	0.000293326	0.007647834	13.32596889	2.030631317	0.001099624
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-2.996918425	0.000983337	0.014051222	NS	NS	NS
	-1.891355103	0.005465511	0.041697812	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-0.284849107	0.00058025	0.010667159	4630.477972	-0.322382227	9.88E-05
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-2.27205801	0.000328803	0.008063929	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-0.456022546	0.000167769	0.005686707	1200.481461	-0.353724899	0.003509631
	1.928201305	0.002231925	0.02309379	14.2409373	2.22788548	0.000398662
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.044145133	0.001885338	0.020767207	14.95605981	2.044575916	0.00188551
NA	NA	NA	NA	NA	NA	NA
	2.083823279	0.000656464	0.011273785	13.34342725	2.047213217	0.000820095
	2.493384477	6.68E-05	0.003698	26.58988888	2.416634808	0.000112113
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.436364479	2.51E-05	0.002654065	19.92263275	1.911199575	0.000998993
	1.673438471	0.002293826	0.023444537	22.42877719	1.912326548	0.000480626
	1.892116918	0.006053601	0.044970804	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.956871251	0.003046289	0.027968582	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.070938239	0.000644104	0.011195734	14.54049964	2.056948951	0.000703483
	0.458843743	0.004012982	0.033313334	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		11.86042611	1.731866051	0.005363135
	1.826977434	0.006685296	0.048067904	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.312827071	8.76E-05	0.004122792	40.90389168	2.024891331	0.000602141
NA	NA	NA	NA	NA	NA	NA
	1.723568502	0.002751211	0.026246451	NS	NS	NS
NS	NS	NS		6.633815341	1.950259771	0.004627993
	2.103504537	0.00086488	0.013159406	19.34769782	2.164801288	0.000601433
	1.895671522	0.000800057	0.012675835	38.93109723	1.917338833	0.000697157
	-2.045858825	0.00086862	0.013178971	5.110895323	-2.59936567	4.26E-05

	2.730136134	4.79E-05	0.002992269	23.75351094	2.564043659	0.000135973
	-3.306702398	4.78E-07	0.000397803	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	0.341696024	0.003010542	0.027904228	NS	NS	NS
	1.183701623	0.00050615	0.009849753	NS	NS	NS
	1.050844129	0.001438457	0.01776081	NS	NS	NS
	-0.577070044	0.000213055	0.006318861	NS	NS	NS
	-0.851260442	0.00113246	0.01513045	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-0.125795414	0.005308719	0.041085198	NS	NS	NS
	1.85826612	0.000444918	0.009262221	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.192362232	0.00019243	0.006044097	10.40469392	1.872993555	0.001511707
NA	NA	NA	NA	NA	NA	NA
	1.98631967	0.001485898	0.018144102	11.73595203	1.943190152	0.001893213
	-1.835052691	9.81E-06	0.002342972	92.46991879	-1.310539444	0.001532961
	1.846224338	0.001153518	0.015262279	40.36377018	1.686556749	0.003018282
	1.689137767	0.004844835	0.038469604	8.200532757	1.782282893	0.002928004
	1.876300979	0.001865898	0.020663381	NS	NS	NS
	1.790405246	0.001992637	0.021490872	25.33108221	1.846736402	0.001429239
	1.858054202	0.000878134	0.013248475	36.25527967	1.669937241	0.002828666
	1.72703251	0.002504846	0.024925317	NS	NS	NS
	1.801072732	0.000810579	0.012702999	NS	NS	NS
	1.481971879	0.00694639	0.049481516	28.34362203	1.549246179	0.004752026
	2.184752434	0.002400472	0.024234845	4.908018246	2.304075343	0.001354082
	1.889677197	0.000980937	0.014051222	NS	NS	NS
	1.777210588	0.005785903	0.043402352	NS	NS	NS
	2.305630589	6.38E-05	0.003608504	12.91694084	2.208540923	0.000131201
	2.357365253	5.25E-05	0.003136928	15.18685514	2.08099625	0.000372775
	1.74644414	0.002585305	0.025338819	NS	NS	NS
	1.805050395	0.004031174	0.033379017	9.232353086	1.83883056	0.003411443
NA	NA	NA	NA	NA	NA	NA
	1.543708477	0.001596818	0.018974584	NS	NS	NS
	2.1215633	0.00131505	0.016823758	12.12649805	1.990524879	0.002610664
	2.069745364	0.003368354	0.02970678	9.446987976	2.494208277	0.000388375
	1.916594619	0.000352594	0.00826066	20.18186677	1.672838591	0.001859809
NA	NA	NA	NA	NA	NA	NA
	1.715123642	0.006018395	0.044833287	NS	NS	NS
	2.137112345	0.000982138	0.014051222	13.79953745	2.13708317	0.000988487
	2.257195127	0.001017975	0.014275567	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.841188132	0.005669853	0.042830913	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	1.960631002	0.002059386	0.021946351	NS	NS	NS
	-1.424033705	0.00399274	0.033196607	NS	NS	NS

	-0.802775203	0.003991224	0.033196607	39.19375859	-0.791969498	0.004602077
	1.569528144	0.00250599	0.024925317	NS	NS	NS
	1.750227002	0.00523718	0.040590032	16.09307197	1.793089822	0.004238717
	1.719446685	0.00203344	0.02173335	16.37862743	1.705808294	0.0022317
	1.84777786	0.001514317	0.01829729	22.23490083	1.733819442	0.002942598
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.187684567	0.000998222	0.014076723	16.09568315	2.245245228	0.000726823
	2.586796065	0.000127913	0.004804346	16.40766951	2.410095261	0.000364867
	1.753566508	0.005775641	0.043402352	13.7290348	1.868883811	0.003238066
	1.952397686	0.00330786	0.029512484	13.54680944	1.921059069	0.003846473
NA	NA	NA	NA	NA	NA	NA
	1.004552113	0.001193594	0.015598041	NS	NS	NS
	1.589778242	0.005362929	0.041306696	NS	NS	NS
	2.020763966	0.000901043	0.013443054	NS	NS	NS
	1.843431842	0.002595182	0.025389298	73.24932079	1.743981671	0.004397854
	1.91640259	0.001326643	0.016924942	41.89008788	2.071285563	0.00051596
	1.448948881	0.000815108	0.012726581	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		3.304592046	-3.265326955	0.000916116
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		676.2672781	0.41663971	0.004074292
NA	NA	NA	NA	NA	NA	NA
	0.720868149	0.002959394	0.027611929	NS	NS	NS
NS	NS	NS		8.712622793	2.295776878	0.000843352
	1.883207049	0.002289702	0.023444537	NS	NS	NS
	1.979350694	0.00211899	0.022272198	21.54277492	2.008483208	0.001814804
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		51.32384548	0.953539325	0.000369153
NA	NA	NA	NA	NA	NA	NA
	-1.190036736	0.007011597	0.04981387	NS	NS	NS
NS	NS	NS		18.84147134	2.040977936	0.000851108
NA	NA	NA	NA	NA	NA	NA
	1.704788637	0.000551635	0.010269078	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.040768769	0.001594728	0.018974584	NS	NS	NS
	-0.865603368	0.004586025	0.036928847	NS	NS	NS
	-3.118554087	0.001264864	0.016409622	NS	NS	NS
	-2.850238309	1.31E-05	0.002342972	NS	NS	NS
	-2.565280257	0.000412114	0.009097461	14.63274744	-2.786638145	0.000133153
	1.710347456	0.004598668	0.036975221	NS	NS	NS
	1.683981295	0.004848989	0.038469604	NS	NS	NS
NS	NS	NS		194.9148943	1.341339342	0.001774555
NS	NS	NS		258.7681722	0.647199267	0.003223962

NS	2.390740604	7.40E-05	0.003896956	30.54987605	2.247569289	0.000197021
	NS	NS		11.71182119	1.942272936	0.004895625
	2.069576619	0.000973862	0.014051222	24.11124644	1.832943027	0.003536948
	2.045269483	0.000125391	0.004788027	133.6383236	1.750422273	0.001036996
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	0.591795051	0.001887712	0.020767207	89.89120402	0.609918671	0.001370368
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.967777946	0.002439367	0.024489425	23.92355159	1.904397327	0.003372714
NA	NA	NA	NA	NA	NA	NA
	1.992595544	0.003816514	0.032434329	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS		11.31464581	-1.233098337	0.001713396
NA	NA	NA	NA	NA	NA	NA
	1.777871117	0.000310325	0.00775371	160.0098403	1.778733998	0.000308547
	2.236731844	8.13E-05	0.003933706	24.27828834	1.704374509	0.002793908
	2.276446827	3.98E-05	0.002842415	16.06504199	1.880619329	0.000720796
	2.210603221	0.00028336	0.007534289	25.66056626	1.953709991	0.001361303
NA	NA	NA	NA	NA	NA	NA
	2.051327797	0.005122267	0.040057882	NS	NS	NS
	-1.775261789	0.00264754	0.025529513	NS	NS	NS
	-4.046441763	1.27E-06	0.000652408	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-1.328507525	0.000213432	0.006318861	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.552576222	1.44E-05	0.002342972	32.76225934	2.431789363	3.61E-05
	1.606087828	0.000638412	0.011191419	259.8768693	1.32878456	0.004793438
	2.087921108	0.000581917	0.010667159	25.21412006	2.180747722	0.000325365
	2.590334136	3.14E-05	0.002842415	30.64707945	2.370447506	0.000140722
	1.94658956	0.000184634	0.005984569	50.27764095	1.90947202	0.000244664
	2.056606311	0.000114423	0.004518862	30.12587036	1.710509926	0.001364786
	2.327763315	2.59E-05	0.002666731	59.24701984	1.64257896	0.003089135
	2.062154561	9.39E-05	0.004131544	NS	NS	NS
	1.885928682	0.000305298	0.00775371	39.02309153	1.731318644	0.000926505
	1.864074652	0.001681419	0.019422462	NS	NS	NS
	1.828881961	0.006177178	0.045511144	NS	NS	NS
	2.043185731	7.37E-05	0.003896956	71.43310862	1.811699607	0.000445024
	2.115859041	0.000806709	0.012702999	12.9627303	2.289896838	0.000280884
	2.136799533	0.000597263	0.01072876	78.39530426	1.919139506	0.002066322
	1.695189823	3.21E-05	0.002842415	NS	NS	NS
	2.255016701	0.000249212	0.007044824	NS	NS	NS
	1.896333788	1.93E-05	0.002519772	NS	NS	NS
	2.329636814	0.000348567	0.00826066	NS	NS	NS
	1.627696188	0.000414981	0.009097461	NS	NS	NS
	1.791382628	3.96E-05	0.002842415	NS	NS	NS
	1.741812032	0.0002011	0.006172046	NS	NS	NS

	1.58079855	0.001337318	0.016987841	NS	NS	NS
	1.444402214	0.00038294	0.00871514	NS	NS	NS
	2.234693864	0.000215295	0.006318861	NS	NS	NS
	2.073582003	0.001618438	0.019146762	NS	NS	NS
	2.029786075	0.001412741	0.017564426	NS	NS	NS
	2.111036422	0.000101712	0.004267911	NS	NS	NS
	2.174154762	0.001100926	0.014978202	NS	NS	NS
	2.319722503	4.59E-05	0.002992269	44.30801592	1.705391821	0.002856598
	2.680057898	3.05E-05	0.002842415	40.91103491	1.86813438	0.003827991
	-1.142378662	0.000694557	0.011557946	NS	NS	NS
NS	NS	NS	5.273865857	1.928278546	0.005036723	
	2.305490294	0.000123537	0.004773495	39.45349082	2.209937784	0.000234931
	1.940940074	0.001730677	0.019735602	25.81325001	2.334244402	0.000158317
	1.776274115	0.006414821	0.046748984	NS	NS	NS
	1.723720354	0.000750886	0.012110117	NS	NS	NS
NS	NS	NS	7.58353095	1.847060274	0.004149443	
	2.879336179	0.001794202	0.020193699	NS	NS	NS
NA	NA	NA	NA	NA	NA	
	2.983164904	9.44E-06	0.002342972	40.51843596	2.565606183	0.000141878
	2.286249214	0.0004062	0.009043008	19.85576091	2.217835933	0.000606768
	2.116417737	0.000835615	0.012971348	22.72809932	2.088291932	0.000979523
NA	NA	NA	NA	NA	NA	
NS	NS	NS	173.3105252	0.991932175	0.003273351	
NS	NS	NS	52.00938016	1.105617458	0.002561916	
NA	NA	NA	NA	NA	NA	
NS	NS	NS	77.1845063	1.276912771	0.001033077	
NS	NS	NS	20.77174399	1.795796654	0.004573839	
NA	NA	NA	NA	NA	NA	
	2.006044061	0.002363545	0.023952072	8.385047846	2.020396443	0.002207348
	2.225023437	0.001092933	0.014978202	3.254534402	2.312752064	0.000685033
	2.068781964	0.002209999	0.022984687	6.664070113	1.90305679	0.005000284
NS	NS	NS	8.01044239	1.984459655	0.005076745	
NS	NS	NS	10.59416011	-2.624020669	0.001325866	
	1.793620871	0.005706386	0.042988607	8.66259537	1.951301939	0.002596535
	2.501097601	2.29E-05	0.002654065	34.24483161	2.512595378	2.09E-05
	2.339723923	0.000319011	0.007859671	24.61950231	2.061297681	0.001549431
	1.226784613	0.003499893	0.03048235	NS	NS	NS
NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	
	2.34324694	0.000339959	0.008151433	17.96110562	2.189744843	0.000822178
	1.972135142	0.006749776	0.048466638	NS	NS	NS
NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	
	1.997256182	0.002034236	0.02173335	NS	NS	NS
NA	NA	NA	NA	NA	NA	
	1.686027307	0.000149092	0.005303144	119.9251568	1.56769145	0.00042313
	1.688712981	0.000845115	0.013006059	NS	NS	NS
	1.928080983	0.000191036	0.006044097	48.52754933	1.705399918	0.000981293

	1.810448389	0.000183416	0.005984569	63.3366972	1.398529104	0.003919429
	1.878321702	0.00024677	0.007037427	53.33201619	1.53053199	0.002862487
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	5.882910382	1.912793846	0.003018191	
	2.158570073	0.000215268	0.006318861	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.282890121	0.000142133	0.005191394	60.52414453	2.075470368	0.000545362
NA	NA	NA	NA	NA	NA	NA
	0.917814797	0.004859939	0.038499604	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	-2.628932951	0.000331757	0.008081068	9.358179905	-3.318230248	1.29E-05
NA	NA	NA	NA	NA	NA	NA
	2.592409432	1.10E-05	0.002342972	85.71419989	2.126839894	0.000315432
NA	NA	NA	NA	NA	NA	NA
	1.922358764	0.003612205	0.031106893	13.76868779	1.946390802	0.003205537
	1.850985813	0.003961627	0.033158962	NS	NS	NS
NS	NS	NS	291.2312439	-1.122732814	0.004149531	
	2.62924949	3.93E-05	0.002842415	22.90997137	2.640551107	3.62E-05
	2.060702491	0.002555783	0.025141223	15.02099316	2.104374692	0.002059604
	2.1601703	0.000332511	0.008081068	NS	NS	NS
	2.153639251	0.000546865	0.010269078	15.64319749	2.273757037	0.000258255
	2.111548079	0.000876419	0.013248475	50.18921449	2.122095669	0.000823812
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	19.44908778	1.453045362	0.003828395	
	-2.536233087	0.005461799	0.041697812	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	2.256592927	0.001715884	0.019689617	8.850176345	2.288998937	0.00146627
	1.71296065	0.001748705	0.019856859	44.70054616	1.891456015	0.000538072
NA	NA	NA	NA	NA	NA	NA
	2.110549996	0.000498214	0.009801853	45.9881066	1.960813992	0.001224165
	1.911652914	0.002520008	0.024972254	NS	NS	NS
	1.821269759	0.006030822	0.044863638	18.66924869	2.131482989	0.001284531
	-2.444605462	0.001827784	0.020408399	4.942730626	-3.107621022	0.000117249
	-2.276457296	2.15E-05	0.002654065	40.9062389	-2.425698205	6.83E-06
	-2.496736376	2.56E-07	0.000343348	95.50832097	-2.109910733	1.26E-05
	-2.481574793	1.26E-08	5.93E-05	28.15030019	-1.897715812	9.81E-06
NA	NA	NA	NA	NA	NA	NA
	2.182979702	0.000662878	0.011332433	16.1306403	2.004772008	0.001792703
NA	NA	NA	NA	NA	NA	NA
	2.046773863	0.00214252	0.022475532	NS	NS	NS
NS	NS	NS	401.5491484	0.863149289	0.002119141	

NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.556790597	0.000143051	0.005191394	25.21267286	2.749372645	4.26E-05
	1.869451352	0.002467184	0.024676432	28.35560017	2.274554774	0.000219873
	2.010965847	0.006223	0.045723304	NS	NS	NS
	2.2598268	0.001501742	0.018280824	NS	NS	NS
	1.754741609	0.000545184	0.010269078	NS	NS	NS
	2.099387478	0.000301413	0.00775371	20.91718607	1.968352719	0.00070902
	1.945902465	0.001041336	0.014471714	16.53074832	1.784710805	0.00267585
	NA	NA	NA	NA	NA	NA
	1.963486405	0.005462512	0.041697812	NS	NS	NS
	2.24298146	0.000282696	0.007534289	13.0575268	2.093204099	0.000719109
	2.014342334	0.000168428	0.005686707	23.24388738	2.012610026	0.000172517
	NA	NA	NA	NA	NA	NA
	1.671779845	0.00358713	0.030975039	NS	NS	NS
	1.927495854	7.57E-05	0.00390919	NS	NS	NS
	2.512782296	0.005618613	0.042503624	NS	NS	NS
	NA	NA	NA	NA	NA	NA
	-2.558141455	9.01E-05	0.004131544	31.95159445	-3.011533265	5.13E-06
	NA	NA	NA	NA	NA	NA
	2.243054845	0.000147119	0.005303144	27.15951584	2.336973551	7.60E-05
	1.942381141	0.001112698	0.014978202	10.60870191	2.027226734	0.000667705
	NA	NA	NA	NA	NA	NA
	1.338248362	0.005211741	0.040509784	NS	NS	NS
	2.179427926	0.003394203	0.029885682	NS	NS	NS
	1.212862493	0.00300824	0.027904228	NS	NS	NS
	NA	NA	NA	NA	NA	NA
	2.454930077	8.71E-05	0.004122792	35.83705153	2.284063462	0.000263724
	NA	NA	NA	NA	NA	NA
	1.490174115	0.005956669	0.04462102	NS	NS	NS
NS	NS	NS	NS	4.676008955	2.17773615	0.002360096
	2.86715829	1.34E-06	0.000652408	23.14100924	2.921973492	8.23E-07
	1.934380903	0.002398036	0.024234845	11.45265634	1.812093154	0.004514511
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	NS	20.69337631	-1.530200643	0.000467836
	2.41379254	0.000165375	0.005686707	23.51253772	2.144353815	0.000831714
	2.315805309	0.000309887	0.00775371	18.63683617	2.193302768	0.000641916
	0.428392467	0.000108183	0.004435492	1306.670556	0.456769847	3.67E-05
	1.961287637	0.000156158	0.005481861	37.68904387	1.881358226	0.000288196
	-4.161046763	3.84E-05	0.002842415	NS	NS	NS
	1.776821952	0.001573187	0.018776859	NS	NS	NS

	2.397653096	7.88E-05	0.003909894	39.13958017	1.965175292	0.001241446
	0.630328163	0.006078616	0.045032066	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	2.288811949	0.000414995	0.009097461	13.64028548	2.231743145	0.000578333
	1.865150531	0.003411237	0.029888671	NS	NS	NS
NS	NS	NS	13.12837737	-2.022136535	0.002541564	
	0.675248389	0.002585063	0.025338819	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
	-1.408407448	0.000987759	0.014072294	NS	NS	NS
	-2.507542678	0.000537605	0.010203096	4.09662621	-3.266931579	1.48E-05
	1.916585217	0.000678622	0.011393639	29.34153576	1.652270719	0.003472433
	2.364286189	0.000353743	0.00826066	13.99588179	2.552096774	0.000113109
NA	NA	NA	NA	NA	NA	NA
	2.07732776	0.000132136	0.004894508	22.23984348	1.636138631	0.002722293
NA	NA	NA	NA	NA	NA	NA
	-1.641505365	1.40E-05	0.002342972	24.53839168	-1.153550271	0.001936758
	-2.018280218	0.001428061	0.017673079	8.685584231	-2.442109058	0.000152164
	-2.540660274	4.20E-05	0.002842415	6.918390982	-2.925788816	4.06E-06
NA	NA	NA	NA	NA	NA	NA
	2.116655333	0.00311063	0.028365353	NS	NS	NS
	2.208173391	0.000952255	0.013950265	NS	NS	NS
	2.1743028	0.000427807	0.009112422	47.00463356	2.212943294	0.000335561
	2.210024588	0.000188469	0.006044097	23.10062103	1.980940628	0.000830398
	2.219905902	0.000419425	0.009097461	26.03051412	2.233520906	0.00038538
	2.112758799	0.000696195	0.011557946	25.60678407	1.946382356	0.001800612
	0.855425329	0.005123769	0.040057882	NS	NS	NS
	0.413224225	0.00261661	0.025439302	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
	1.741097963	0.006005989	0.044833287	27.76755026	2.316726446	0.000239418
	1.899727956	0.003285834	0.029413691	12.11841345	1.834244287	0.004569027
	2.019231456	0.000666738	0.011332433	NS	NS	NS
	1.982329286	0.000966916	0.01404635	24.0703774	2.078173804	0.000536916
	-3.377723892	1.24E-07	0.000222032	38.58109043	-2.5501328	4.58E-05
	2.119834175	0.0016796	0.019422462	NS	NS	NS
	2.168685854	0.000649832	0.011238058	31.9831242	1.940801524	0.002299458
	2.355454025	0.000247003	0.007037427	15.73579328	2.209015003	0.000600558
	2.374937003	2.31E-05	0.002654065	34.25395312	2.353614491	2.71E-05
NS	NS	NS	8.376971611	2.281660209	0.000809946	
	1.982420403	0.001717014	0.019689617	11.04942385	1.97676808	0.001772733
	2.048829086	0.000295656	0.007671336	52.89521052	1.975411251	0.000484116
NA	NA	NA	NA	NA	NA	NA
NS	NS	NS	18.03684598	-2.762840688	0.001861052	
NA	NA	NA	NA	NA	NA	NA
	-1.024828604	0.003258674	0.029268121	NS	NS	NS
	2.062285138	0.003013569	0.027904228	NS	NS	NS
NA	NA	NA	NA	NA	NA	NA

[illegible]

FDR.M4	baseMean	log2FoldChange.P/M6	pvalue.P/M6	padj.P/M6
NA	38079.898744	0.263964942714753	0.0066697105	0.0849464324
NA	12476.365093	0.446258932141667	0.0030532584	0.0741810097
NA	1231.4469428	0.776519670727606	0.0056149021	0.0812209105
NA	19940.198843	-0.728820578742522	0.0036246179	0.0760045841
NA	28718.040569	-0.691933728773723	0.008120686	0.0899438649
NA	5253.4515479	0.555026917550347	0.0012685537	0.0567917067
NS	NA	NA	NA	NA
NA	34.531754584	-1.25634397619443	0.0094443012	0.0937130433
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	117.10676575	1.76840483666356	0.0070729321	0.086324584
0.022098145	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.021055924	134.66209521	2.35217009488896	0.0052835145	0.0799649767
NA	970.25356559	1.28716892568542	0.0001857223	0.0205518861
NA	6722.6026015	0.654619335708293	0.0046812098	0.0776531914
0.022270245	NA	NA	NA	NA
0.008625038	NA	NA	NA	NA
0.006864913	250.77427432	2.66891723854741	0.0006377084	0.040588267
0.006357212	23.156322502	-2.73370186232222	0.0002122994	0.0216705609
NS	NA	NA	NA	NA
0.045144762	NA	NA	NA	NA
0.020609428	NA	NA	NA	NA
NA	1360.6982921	0.738735131873548	0.0036919371	0.0766575554
0.010646931	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	34733.808428	-0.531299000986649	0.0061282102	0.0832617833
NA	20788.285703	-0.52304496344305	0.0067674515	0.0849464324
NA	12089.290943	-0.660229791519088	0.0060566869	0.0829536098
NA	61.762814281	2.42263909124175	0.003618446	0.0760045841
0.022927484	NA	NA	NA	NA
NA	8754.0803523	-0.650143363289467	0.0111293841	0.0991014749
0.01603898	27.926150001	2.28665535656556	0.0098873243	0.0951681068
NS	NA	NA	NA	NA
NA	8191.5513921	-0.710486698984018	0.0031452127	0.0741810097
NA	15127.689462	-0.58770623296543	0.009568408	0.0937130433
0.011803806	39.19735029	2.38562162653127	0.0069080443	0.0853253879
0.004877096	12.773361658	-3.85739909490389	0.0001351848	0.0192460483
NS	4.3698683901	-4.54007842268768	5.26E-05	0.011847285
NA	3299.6462965	-0.731271164312322	0.0052662171	0.0799649767
NA	12910.606809	-0.683289972679587	0.0075661737	0.0877930649
NA	4666.0432294	-0.763699860568804	0.0035988088	0.0760045841
NA	5592.1676245	-0.703236793062188	0.0078208347	0.0885454245
NA	1970.9170052	-0.678769916795284	0.0111679349	0.0991014749
NA	23786.969596	-0.671069253020636	0.0084512125	0.0909070202
NA	18369.100949	-0.656443753375106	0.006627169	0.0849464324
NA	16700.495414	-0.748242396951001	0.0055890536	0.0812209105

NA	13958.351149	-0.661516600110513	0.0103170723	0.0957381838
NA	7040.3599789	-0.789318344943308	0.0033548355	0.075869171
NA	6530.1705089	-0.772783706046363	0.005241614	0.0799649767
NA	15013.637282	-0.80591230610735	0.0031358995	0.0741810097
0.047179186	NA	NA	NA	NA
0.036429193	NA	NA	NA	NA
0.008063027	91.334611858	-3.10972735447061	9.73E-10	2.63E-06
0.022927484	NA	NA	NA	NA
0.004980849	NA	NA	NA	NA
0.04329363	NA	NA	NA	NA
NA	11798.835354	0.591458640927481	0.000185879	0.0205518861
NA	1287.2971889	0.585251796694255	0.0020405669	0.0656986937
0.005086178	204.07659171	2.35950760080067	0.0063209595	0.084369207
NA	3346.1608558	-0.985527349859587	0.0004776537	0.036395868
0.030426599	14.080916048	-2.0245961786639	0.0032782475	0.075469442
NA	901.91536372	-1.11622646298965	0.0035580553	0.0760045841
0.005086178	17.938823017	-2.14606110182431	4.78E-05	0.0113116848
NA	50287.545093	-0.363979399513312	0.0106867427	0.0974250132
NA	9209.7089399	-0.219949447712332	0.0094552851	0.0937130433
NA	20005.106223	0.344624423304997	0.0017872327	0.0648921401
0.044645625	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	25313.771253	0.330788249207968	0.0015222814	0.0607210796
0.040696648	NA	NA	NA	NA
0.02627029	222.24637097	1.92883928390021	0.0099946059	0.0951730623
NA	6958.3735041	-0.414115787637828	0.0020616733	0.0656986937
NS	NA	NA	NA	NA
NA	356.13752425	2.67772586169459	8.14E-06	0.0033863292
0.007733946	NA	NA	NA	NA
NA	17225.18836	-0.673599819670529	0.005608618	0.0812209105
NA	517.58826943	-1.44156139781639	0.001317291	0.0578814445
NA	7633.5471823	0.631343261566401	0.0004553427	0.0357015041
NS	NA	NA	NA	NA
0.018212962	NA	NA	NA	NA
NA	4.7196518662	-3.15007184239467	0.007455383	0.087302212
NS	NA	NA	NA	NA
0.018396576	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	34123.851849	-0.573739580940589	0.0051011291	0.0795305713
NA	1109.1623774	0.746564517986782	0.0065661015	0.0849464324
0.036148496	NA	NA	NA	NA
0.012926802	NA	NA	NA	NA
NA	1126.972053	1.14489690423824	0.0007340556	0.0441248952
NS	NA	NA	NA	NA
0.024932218	NA	NA	NA	NA
NA	10922.596855	-0.395827878569355	0.0061407489	0.0832617833
NA	2936.8254469	-0.715513114944813	0.0059017788	0.081920912
0.023872128	NA	NA	NA	NA

NA	7781.1301716	0.301230034573892	0.0069266926	0.085360836
NA	17593.870336	0.31062293044179	0.0109097261	0.0986983586
0.046562314	NA	NA	NA	NA
0.02636012	90.327368304	2.30188336351725	0.0091904211	0.0929394342
0.010778769	128.73211695	2.12192190309888	0.0098774643	0.0951681068
NA	18328.490016	-0.855853686784792	0.0010871764	0.0538898364
NS	NA	NA	NA	NA
0.004980849	NA	NA	NA	NA
NA	17340.602196	-0.697769781089741	0.0049082303	0.0785607278
0.013924436	NA	NA	NA	NA
0.042598896	126.41843847	2.24812350573256	0.0085414844	0.0909838909
NS	NA	NA	NA	NA
NA	244.94430444	-1.43599647328228	0.004341393	0.0776531914
NA	2722.2601888	-0.514206743397428	0.0023973812	0.0717591277
NS	NA	NA	NA	NA
NA	17361.56445	-0.62856517145614	0.010079416	0.0951730623
NS	NA	NA	NA	NA
NA	24804.344401	-0.530713785051008	0.0088356726	0.0922276335
NA	7747.0583264	-0.617439907565844	0.0008143354	0.0453871889
NA	6274.4697491	-0.737880924973103	0.0043906095	0.0776531914
NA	3509.5049794	0.614485746492867	0.0011752659	0.0552885952
NA	3242.2103873	0.413874150597123	0.0061155247	0.0832617833
NA	12290.601252	0.462352687096037	0.0007816416	0.0447907708
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	6354.2229918	0.484101653014782	0.0012807002	0.0567917067
NA	16787.381626	-0.686810509842855	0.0027635815	0.0741810097
NA	1102.4977722	0.86430782711051	0.0071638904	0.0868983122
0.009191392	NA	NA	NA	NA
0.023218213	NA	NA	NA	NA
0.01783985	96.024291197	2.49565864144356	0.0012352398	0.0564135344
NA	11231.233561	-0.857398661168517	0.0024130562	0.0717591277
NS	NA	NA	NA	NA
0.004144754	229.674196	-1.70378889029316	0.0050920667	0.0795305713
NA	22459.642319	-0.598912698914923	0.0047279634	0.0776531914
NA	40665.879608	-0.419594090881798	0.0089159062	0.0922276335
0.022270245	NA	NA	NA	NA
0.022270245	NA	NA	NA	NA
NA	6238.9040859	-0.691434981447522	0.006498817	0.0849464324
0.026941101	77.023707767	2.53312303413448	0.0088936074	0.0922276335
NA	8227.4153968	-0.678499912437881	0.008416295	0.0909070202
NA	4.0427132708	-4.66556928258856	0.0002009993	0.0209116536
NS	NA	NA	NA	NA
NA	16968.114444	-0.727643713157419	0.0037691146	0.0766575554
NA	14846.676247	-0.4414057971343	0.0087019364	0.0917689584
NA	14246.767334	-0.892051728193553	0.0039116802	0.0769534172
NA	78053.499266	-0.498649597824469	0.0110194199	0.098908935
NS	NA	NA	NA	NA

NA	983.23002554	0.984206804201046	0.0073145884	0.087302212
NA	36309.815492	-0.642599097404511	0.0044575256	0.0776531914
NS	NA	NA	NA	NA
NA	2595.506139	0.742370126227309	0.0036200312	0.0760045841
NA	3857.3481454	-0.793892855114226	0.0046078177	0.0776531914
0.026000399	NA	NA	NA	NA
0.004071762	NA	NA	NA	NA
NA	326.48324283	-1.26328337734873	0.0090115465	0.092614995
NS	NA	NA	NA	NA
0.033670712	NA	NA	NA	NA
0.047934606	17148.782384	0.358640150231614	0.0058072375	0.0819152788
NA	26354.520844	-0.825684591055847	0.0010993846	0.0538898364
NA	56913.343147	-0.659110737694637	0.0111741034	0.0991014749
0.035435512	NA	NA	NA	NA
NA	3036.9107469	1.6695689516203	1.76E-05	0.0052779869
NS	NA	NA	NA	NA
NA	8.1268724362	4.15298019166437	0.0007217599	0.0438732697
NS	NA	NA	NA	NA
0.005086178	338.82717393	2.21188432132462	0.0108281107	0.0981240851
NS	NA	NA	NA	NA
0.017748498	NA	NA	NA	NA
NA	80915.537763	0.456587934767086	0.0005352064	0.036575624
NA	35807.981368	-0.306979271367527	0.0067343576	0.0849464324
NA	4388.5816499	-1.08929987589516	0.0011678999	0.0552885952
NA	11644.151396	-0.730696532024012	0.0044541404	0.0776531914
NS	NA	NA	NA	NA
0.011285813	NA	NA	NA	NA
NA	9320.191103	0.47564113926986	0.0037216648	0.0766575554
NA	11203.142761	-0.581374679871662	0.0078009503	0.0885454245
NS	NA	NA	NA	NA
0.004812758	NA	NA	NA	NA
NA	8016.8308825	0.396160173837043	0.0104305331	0.0957596847
0.024083131	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.040978249	NA	NA	NA	NA
0.01783985	NA	NA	NA	NA
NA	25267.572931	0.504779008323384	0.0073824955	0.087302212
NA	22.650523571	1.53944974693918	0.0095964928	0.0937130433
0.018212962	NA	NA	NA	NA
NA	27821.178937	-0.740865910272553	0.004187001	0.0772557863
NA	7031.9495542	1.1319409081704	0.0031959308	0.0741810097
NA	249.86376304	-1.43553418047347	0.0031483501	0.0741810097
0.046492358	239.55956732	2.05971381127113	0.0093358828	0.0937052429
0.033029025	105.9609266	1.66434397839951	0.0097760092	0.0947215911
NA	2590.4400548	1.30699709356416	0.0009026054	0.04787348
NA	4571.6883749	-0.615273850234459	0.0084857755	0.0909070202
0.020873992	165.08446521	2.43839843010671	0.0092655656	0.0933458288

0.013836894	350.71360415	2.15073901578273	0.0091606436	0.0929394342
NS	NA	NA	NA	NA
NA	910.19585435	1.0883746215974	0.0025113172	0.0717717548
NS	NA	NA	NA	NA
0.027852997	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	114.95488154	-1.62544615617175	0.0029835193	0.0741810097
NA	22135.762798	-0.652540734489326	0.008112744	0.0899438649
0.044626373	NA	NA	NA	NA
NS	175.73108043	2.27319313852303	0.0084718398	0.0909070202
NA	9184.2480639	0.384355171364138	0.0004748183	0.036395868
NA	1227.3526035	1.27533970616202	0.0061176974	0.0832617833
NA	7253.6447637	0.3371963996343	0.000896997	0.04787348
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	18363.713279	-0.575942185078623	0.0074500199	0.087302212
NS	NA	NA	NA	NA
NA	11797.677469	-0.831222273535384	0.0007607341	0.044253455
NA	2108.3407808	-1.12350099191261	0.0005071086	0.036575624
NA	2765.3213785	-1.03277088122775	0.0084051149	0.0909070202
NA	4567.6316656	-0.47147270251503	0.0064842613	0.0849464324
NA	20095.008161	-0.52431206355677	0.0111337601	0.0991014749
NA	7652.9389276	0.468457580446029	7.66E-05	0.0138132698
NS	4563.2938189	0.479741588779065	0.0107443443	0.0975283599
NS	NA	NA	NA	NA
0.004980849	NA	NA	NA	NA
0.017748498	195.34410953	2.29357782841839	0.0076687936	0.0879264902
NA	48941.049975	-0.444011703478575	0.0096611231	0.0941741912
NA	8469.8834288	0.414072222700565	0.0040871538	0.0772557863
NA	10276.382086	-0.65423879059455	0.0038292724	0.0769534172
NS	NA	NA	NA	NA
NA	34383.239552	-0.521818214893529	0.0013967212	0.0594087473
NS	NA	NA	NA	NA
NA	82352.215757	-0.534322959441065	0.0072374655	0.087204206
NA	14528.087598	-0.643550608856712	0.0066122405	0.0849464324
NS	NA	NA	NA	NA
NA	574.71667241	1.12526871194617	0.0058297814	0.0819197857
0.004980849	NA	NA	NA	NA
NA	26572.93463	-0.696967099736981	0.0029640147	0.0741810097
NA	3110.0867633	-0.895277600109009	0.0025110394	0.0717717548
NA	39517.787491	-0.521896338909906	0.0086392927	0.0914533127
NA	13105.744719	-0.781347361705175	0.0043085029	0.0776531914
NA	23060.678304	-0.528627105222554	0.0041194417	0.0772557863
NA	110244.19329	-0.411638235013073	0.0047305879	0.0776531914
0.028185237	NA	NA	NA	NA
NA	26402.867895	-0.776853050411173	0.0031837237	0.0741810097
NS	NA	NA	NA	NA
NA	52842.34883	-0.225127454817512	0.0018245758	0.0653852737

NA	15503.024572	-0.68204092919455	0.0074112852	0.087302212
NA	23865.248127	-0.710193814759763	0.0068664126	0.0851688714
NS	NA	NA	NA	NA
NA	7766.5245063	0.356558600497524	0.0064680434	0.0849464324
NS	NA	NA	NA	NA
NA	32209.797476	0.379635380290665	0.0076067378	0.0877930649
NA	35716.298919	0.355174748604362	0.0099870373	0.0951730623
NA	7183.8993612	0.578647824777341	0.0001721063	0.0205518861
NA	5081.5746307	0.552362418156656	0.0006680021	0.04131669
NA	5063.370142	0.579371798186718	0.0004009398	0.034429913
NA	7178.2620159	0.575954376086998	2.23E-05	0.0063532844
NA	2354.4718714	0.597942704710524	0.0101506002	0.0951730623
NA	1897.2849964	0.647052630700947	0.007823422	0.0885454245
NA	3638.1196646	0.532553659127475	0.0064094006	0.0849464324
NS	NA	NA	NA	NA
0.013208292	NA	NA	NA	NA
0.00510015	NA	NA	NA	NA
NA	11607.044115	-0.630823643123414	0.0067276439	0.0849464324
NA	11718.957387	-0.568791552309275	0.0106677078	0.0974250132
NA	846.50497133	1.76884061398448	0.0004406511	0.0355454483
NA	2054.8554359	1.62053116100262	8.95E-05	0.0156190368
0.016749673	96.862467636	3.13938790817497	0.0001527266	0.0201524654
0.001919291	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.023218213	NA	NA	NA	NA
0.016849312	NA	NA	NA	NA
NA	5189.4690522	-0.850013399640566	0.0084171602	0.0909070202
NS	NA	NA	NA	NA
0.045622169	NA	NA	NA	NA
NA	108.25141924	-1.16002830113907	0.0101068637	0.0951730623
0.033340709	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.017597508	NA	NA	NA	NA
0.008810452	NA	NA	NA	NA
0.031392065	NA	NA	NA	NA
0.011803806	NA	NA	NA	NA
0.048723184	NA	NA	NA	NA
0.005086178	263.51519443	2.24481413488459	0.0054613423	0.0805064356
NS	NA	NA	NA	NA
0.031615176	NA	NA	NA	NA
NA	9952.8613921	-0.841107003461079	0.0066192131	0.0849464324
0.040618316	67.160591753	2.45962238841923	0.0087231608	0.0918138127
0.006615778	433.01497289	2.4668715787004	0.0032065068	0.0741810097
0.041284264	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
0.033340709	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	25.286074152	2.40283579583001	0.0047113108	0.0776531914

0.029497294	46.803977015	2.63007246479788	0.0037275639	0.0766575554
NA	35318.305921	-0.898392035271578	0.000827029	0.0453871889
0.047934606	NA	NA	NA	NA
NA	29013.250388	0.374851132740141	0.0020481947	0.0656986937
NA	28219.076798	0.379685648134465	0.0026605363	0.0741810097
NA	4326.6380484	0.528652725653035	7.31E-05	0.0137626308
0.00510015	NA	NA	NA	NA
NA	360.40455066	0.964031727075026	0.0014165857	0.0594087473
0.046779034	2417.1705477	0.648613717366664	0.0086376896	0.0914533127
NA	8901.2645893	-0.56621179765228	0.0079274398	0.0889781106
0.011004609	131.94695215	2.40514275799098	0.0047072527	0.0776531914
0.022098145	70.291035566	2.60473312052232	0.0034384715	0.0759443488
0.026135029	NA	NA	NA	NA
0.03513761	86.363842284	2.58617664654553	0.0031904845	0.0741810097
0.028081326	192.12384471	2.45248295118099	0.0058994493	0.081920912
0.038102475	60.527580093	2.29918077222861	0.0100471188	0.0951730623
0.011803806	NA	NA	NA	NA
0.0374365	NA	NA	NA	NA
NA	6699.840779	-0.602425649706349	0.0060064761	0.0828809395
NA	10088.007141	-0.669388682561079	0.0043666536	0.0776531914
NS	NA	NA	NA	NA
0.045577993	NA	NA	NA	NA
0.046378303	77.852161911	2.3941377782088	0.0107149506	0.0974250132
NA	9133.425008	0.292538080435825	0.0038988559	0.0769534172
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	22434.144923	0.288133730271751	0.0086551009	0.0914533127
0.017748498	NA	NA	NA	NA
0.017179068	NA	NA	NA	NA
0.014289086	NA	NA	NA	NA
NA	14853.553693	-0.693847807836343	0.0068796297	0.0851688714
NA	736.23330995	0.848461896235537	0.0094983248	0.0937130433
NA	1549.0079153	0.879077129303156	0.0058143192	0.0819152788
NA	18638.460025	-0.628743754684951	0.0098875123	0.0951681068
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.048748821	159.58187517	2.5975596904092	0.0039569909	0.0770531926
NA	21514.424869	-0.649741211608553	0.0104238855	0.0957596847
NS	NA	NA	NA	NA
0.022098145	NA	NA	NA	NA
0.033853584	NA	NA	NA	NA
0.026135029	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.01177564	NA	NA	NA	NA
NA	13.333599989	1.90553939032556	0.0001427712	0.019711881
NA	45908.179354	-0.643350331198688	0.0023091485	0.0709800746
NA	33439.224799	-0.610702160680865	0.0034064198	0.075869171
NS	NA	NA	NA	NA

NA	16674.738637	0.349350759936815	0.0094380975	0.0937130433
0.045680145	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	30.411736405	2.26175341133514	0.0080905848	0.0899438649
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	16633.929568	0.503920970229982	0.003759493	0.0766575554
0.026625735	22.722401718	-1.3803311699241	0.0072325935	0.087204206
0.033351837	NA	NA	NA	NA
0.028846219	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	8974.5634229	0.592753674816264	0.0100830645	0.0951730623
NS	8890.7592538	0.568324101845476	0.0093264572	0.0937052429
NS	NA	NA	NA	NA
0.030153097	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.035929664	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	36.653245845	-3.8539603962957	3.86E-07	0.0004172574
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.018212962	NA	NA	NA	NA
0.01783985	NA	NA	NA	NA
NA	106.41804206	1.56951112675603	0.0085434042	0.0909838909
0.010765265	NA	NA	NA	NA
NA	1842.7259559	-0.863309480081945	6.07E-05	0.0127609166
NS	NA	NA	NA	NA
NA	7809.1577095	-0.8687054963773	0.0078818425	0.0886912879
NA	3408.5353473	-0.42193762099045	0.0054811418	0.0805787417
NS	NA	NA	NA	NA
NA	109.07139556	1.65247428911038	0.0042038992	0.0772557863
NS	69.431653314	2.48042488906448	0.0029939235	0.0741810097
NA	176948.13499	-0.301899397132375	0.0011109827	0.0538898364
NA	29991.623434	-0.490405653816404	0.0095581179	0.0937130433
NA	2339.3637515	-0.644013986332476	0.0079661919	0.0892279466
0.008488085	NA	NA	NA	NA
NA	30.962866905	1.62382527298874	0.0047309747	0.0776531914
NS	NA	NA	NA	NA
0.021287496	NA	NA	NA	NA
NA	5693.6560755	0.554396383754753	0.0029836016	0.0741810097
0.012580498	108.97395937	2.56783853808004	0.0026198394	0.0738194341
0.014868684	129.61703139	2.3583039729051	0.0102965627	0.0957120348
0.019912092	NA	NA	NA	NA
NS	NA	NA	NA	NA

0.032124983	NA	NA	NA	NA
0.010652396	NA	NA	NA	NA
0.043853541	NA	NA	NA	NA
0.049616131	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	9702.1495626	-0.771278072313424	0.0034078019	0.075869171
NA	23147.108449	-0.672553120848814	0.0077737863	0.0885393345
NA	5403.4312307	-0.850972211061877	0.0057932471	0.0819152788
0.020758149	154.52070814	2.4247415767004	0.0020075251	0.0656986937
0.004156046	NA	NA	NA	NA
NA	5885.3313735	1.35893903811351	0.0002727816	0.0262653424
NS	NA	NA	NA	NA
0.023711663	NA	NA	NA	NA
NA	23161.530968	-0.657785871346511	0.0032041844	0.0741810097
0.045849969	NA	NA	NA	NA
NA	4268.82931	0.987970458399719	0.0046741506	0.0776531914
NA	35794.210141	-0.449316085215844	0.0074551318	0.087302212
NA	33842.502035	-0.649115195660882	0.0065992883	0.0849464324
NA	7230.6788623	-0.706634399259418	0.0010841093	0.0538898364
NS	NA	NA	NA	NA
NA	2371.933607	0.517230309527568	0.0016970292	0.0641231239
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.006312946	NA	NA	NA	NA
NA	1474.7566764	-0.916988478063243	0.0052946626	0.0799649767
0.045611592	NA	NA	NA	NA
NA	32845.084091	-0.590270834078933	0.0074258582	0.087302212
0.011285813	241.14974802	2.36159548530992	0.0109890704	0.098908935
0.013208292	NA	NA	NA	NA
NA	9253.4383431	-0.744500964799327	0.0043251551	0.0776531914
NA	6548.9213857	-0.64845445906498	0.0102914918	0.0957120348
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.022270245	NA	NA	NA	NA
NA	1445.2784777	0.702303327217332	0.0044061729	0.0776531914
0.032565051	NA	NA	NA	NA
0.010778769	NA	NA	NA	NA
NA	1622.7908866	0.62936269281234	0.0028488437	0.0741810097
0.0159069	NA	NA	NA	NA
NA	5417.3611445	0.376472436167716	0.0095005782	0.0937130433
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	14091.489517	-0.379739525176207	0.0030132724	0.0741810097
NA	3073.2455787	-0.644161011007426	0.008059002	0.0898952599
NS	NA	NA	NA	NA
0.044432669	NA	NA	NA	NA

NA	4010.7009176	-0.645217209541603	0.0095830799	0.0937130433
NA	24247.186295	-0.752189975837829	0.0017849657	0.0648921401
0.022270245	NA	NA	NA	NA
NA	9388.8617241	-0.474789511635028	0.0068516716	0.0851688714
0.011820436	NA	NA	NA	NA
NA	26937.720625	-0.630159469610216	0.002835479	0.0741810097
NS	NA	NA	NA	NA
0.019912092	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	10929.445801	-0.822952481937778	0.0044733379	0.0776531914
0.02636012	NA	NA	NA	NA
0.010529572	NA	NA	NA	NA
0.019912092	NA	NA	NA	NA
NA	5828.8358972	0.405926322811483	0.0029159385	0.0741810097
0.038062309	NA	NA	NA	NA
NA	13498.974725	0.340014112078034	0.0055150645	0.0808576451
NA	2611.498026	-0.643588067480474	0.0039441426	0.0770531926
0.011820436	NA	NA	NA	NA
NA	86.801359841	1.42314768488398	0.0078679402	0.0886912879
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.029736411	NA	NA	NA	NA
NA	12974.128339	-0.579780486958792	0.0055300053	0.0808576451
NS	NA	NA	NA	NA
0.017597508	NA	NA	NA	NA
NA	58.112862129	2.21394638326071	0.007563349	0.0877930649
0.012856089	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	12663.975361	0.741258302252212	0.0001895197	0.0205518861
0.019912092	NA	NA	NA	NA
NA	750.06016524	-1.20274981152018	0.0028585715	0.0741810097
0.029691977	NA	NA	NA	NA
NS	17310.018076	0.350339656850521	0.0005880797	0.0387989187
NA	16330.058162	-0.337044255995034	0.0066793035	0.0849464324
NS	NA	NA	NA	NA
NA	10361.476259	-0.903238324822323	0.0004091267	0.0345839936
0.02593234	NA	NA	NA	NA
0.005418557	NA	NA	NA	NA
NA	9870.7562367	0.627279853738607	0.0091908683	0.0929394342
NA	2147.9562623	1.60972555212239	0.0017067892	0.0641231239
0.026625735	NA	NA	NA	NA
NA	15757.754041	-0.643207321603347	0.000486548	0.0365586748
0.032269958	NA	NA	NA	NA
NA	12243.089019	-0.440774842507236	0.0019247647	0.0656855737
0.047421903	NA	NA	NA	NA
0.014227703	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.022125448	87.267253428	2.49608956893845	0.006304395	0.084369207

NS	132.3259383	2.33436925010334	0.0050472043	0.0795305713
0.023711663	NA	NA	NA	NA
NA	28615.684351	-0.684458147344529	0.0040787181	0.0772557863
NA	26765.184183	-0.738217136628459	0.0027989943	0.0741810097
NA	7757.5282206	-0.788983954959338	0.0034015452	0.075869171
0.014002961	NA	NA	NA	NA
NA	6495.3465828	-0.79442372792451	0.0025118714	0.0717717548
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.01783985	289.15408782	2.17458388894453	0.0091616511	0.0929394342
NA	11798.280207	-0.598893473294954	0.0053658856	0.0801918262
0.014386787	NA	NA	NA	NA
0.000538829	70.698716948	-3.0180045373356	3.39E-05	0.008740021
NA	3661.7664351	-0.619562620693024	0.0058566287	0.081920912
0.014868684	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.01583515	NA	NA	NA	NA
NA	6126.8815755	-0.702446332099727	0.0066869581	0.0849464324
NA	6114.2972419	-0.902096107717267	0.0014829428	0.0603416563
NA	1268.4078231	-0.79719500682239	0.0020643647	0.0656986937
0.034916953	NA	NA	NA	NA
NA	24323.192422	-0.841826331804306	0.001220028	0.0564135344
0.044522528	NA	NA	NA	NA
0.026625735	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.026962068	NA	NA	NA	NA
0.018091573	NA	NA	NA	NA
NA	6824.4983817	-0.844342558298418	0.0012208532	0.0564135344
0.021563218	NA	NA	NA	NA
0.048668117	NA	NA	NA	NA
NA	11091.613547	-0.965350372713159	0.0001315149	0.0192296165
NA	4525.5330806	0.281524013356925	0.0063315893	0.084369207
0.027450542	62.382182432	2.18794295202909	0.0099970496	0.0951730623
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	758.58566165	-1.38812442993854	5.53E-07	0.0004274219
NA	17598.908069	-0.919374541204858	0.0057667898	0.0819152788
NS	NA	NA	NA	NA
NA	4.5172128273	2.93437691944872	0.0019073728	0.0656855737
0.010646931	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.02403766	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.018516439	NA	NA	NA	NA
NS	NA	NA	NA	NA

NA	488.73801144	0.712394264457159	0.000416577	0.0346720235
NS	NA	NA	NA	NA
0.014227703	NA	NA	NA	NA
0.031118107	NA	NA	NA	NA
0.023218213	NA	NA	NA	NA
0.021287496	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.004812758	NA	NA	NA	NA
0.03628409	NA	NA	NA	NA
0.046481838	NA	NA	NA	NA
NA	705.24228413	-1.22017476981397	0.004059738	0.0772557863
0.023086863	118.99110533	2.36926657611626	0.004822823	0.0776531914
NA	402.33963745	1.51031990717131	0.0034049339	0.075869171
NS	NA	NA	NA	NA
0.022889046	NA	NA	NA	NA
0.027148592	NA	NA	NA	NA
0.016150098	NA	NA	NA	NA
0.026633361	NA	NA	NA	NA
NA	12432.025233	-0.718580793340758	0.0060207411	0.0828809395
NA	18480.07648	0.289772308688514	0.0058757379	0.081920912
NA	10041.717359	-0.657193932597746	0.0034493927	0.0759443488
NA	7275.8089965	-0.443298580647414	0.0095658357	0.0937130433
0.027040604	NA	NA	NA	NA
NA	6508.9744346	0.404441260728155	0.0037596611	0.0766575554
NA	6642.8315261	0.285075141108813	0.0059776525	0.0827086954
NA	15056.408547	0.373705809621105	0.0029822341	0.0741810097
NS	NA	NA	NA	NA
0.046853007	NA	NA	NA	NA
NA	95.818299424	-1.13256238850259	0.0032085686	0.0741810097
NS	NA	NA	NA	NA
NA	8036.2144741	-0.680540560803271	0.0069631536	0.0856151387
0.023921101	NA	NA	NA	NA
0.022817162	NA	NA	NA	NA
NA	27115.761639	-0.691685634993439	0.0027643266	0.0741810097
NS	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
0.022927484	41.215498784	2.8382911230202	0.0040646189	0.0772557863
NA	46.509966076	2.70052847099427	0.0027440056	0.0741810097
NA	215.13371993	2.31065368962365	0.0014074513	0.0594087473
NS	NA	NA	NA	NA
0.026625735	157.59825183	2.17123744284723	0.008315555	0.0908306813
0.020479663	NA	NA	NA	NA
0.033670712	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	18313.03215	0.449812104350495	0.0071006358	0.086324584
0.023711663	NA	NA	NA	NA
0.019441167	78.142790442	2.55742682897732	0.0028560886	0.0741810097
NA	37.008494378	2.31833075651852	0.0090110414	0.092614995

NA	52.16405355	2.68272269252395	0.0010193994	0.0535432094
NA	28.449331965	2.90878714808059	0.0005466121	0.036575624
NS	NA	NA	NA	NA
0.030647627	NA	NA	NA	NA
0.008810452	NA	NA	NA	NA
0.019437119	NA	NA	NA	NA
0.022817162	NA	NA	NA	NA
0.030153097	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	7776.3906436	-0.810145388510403	0.0006098992	0.0392804134
0.014386787	109.5694588	2.3780325698961	0.0042234964	0.0772557863
0.000228166	29.290238606	-3.0272114862107	2.38E-06	0.0012864694
0.026076418	NA	NA	NA	NA
0.033187882	84.200563349	2.24720591652347	0.0082162923	0.0907145743
NA	13573.618422	-0.87078110462764	0.0037597931	0.0766575554
0.034916953	NA	NA	NA	NA
0.009243617	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.019672212	NA	NA	NA	NA
0.014386787	NA	NA	NA	NA
0.021595027	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	7666.8992403	-0.948776254087067	0.0066479121	0.0849464324
0.014838446	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.004156046	NA	NA	NA	NA
NA	10590.432129	-0.684971330647058	0.0035245762	0.0759679575
0.023218213	NA	NA	NA	NA
0.028846219	NA	NA	NA	NA
0.033853584	NA	NA	NA	NA
0.019743726	NA	NA	NA	NA
NA	277.5521836	-1.81169306176702	0.0001190248	0.0183697595
NA	1786.6031391	1.13794636272551	0.0041203449	0.0772557863
0.018396576	NA	NA	NA	NA
0.034162206	NA	NA	NA	NA
0.002584934	181.87579836	2.35890902493506	0.005396897	0.0802121223
0.03269983	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.029745694	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
0.010646931	NA	NA	NA	NA
0.033373008	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	74.549289499	2.65077609975002	0.000663576	0.04131669
NS	NA	NA	NA	NA
0.033351837	NA	NA	NA	NA
0.033029025	NA	NA	NA	NA

0.008810452	103.12900918	2.15386917465017	0.0097873141	0.0947215911
0.023086863	NA	NA	NA	NA
0.032124983	NA	NA	NA	NA
0.045829502	NA	NA	NA	NA
NA	17591.005765	-0.771609098034686	0.002966115	0.0741810097
NS	NA	NA	NA	NA
0.045611592	NA	NA	NA	NA
NA	6073.0088496	-1.00054791701692	0.0076712206	0.0879264902
NS	4.4129943239	-2.62505313528537	0.0024386598	0.0717591277
0.021921635	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	253.23822895	-1.74092600099204	0.0091304764	0.0929394342
0.004980849	96.62757841	2.15833940262154	0.0110190919	0.098908935
NA	19871.022785	-0.735654112681985	0.0015622628	0.0616922747
0.033670712	NA	NA	NA	NA
0.011705024	NA	NA	NA	NA
0.049627463	NA	NA	NA	NA
0.023008321	NA	NA	NA	NA
0.015343249	NA	NA	NA	NA
0.004156046	160.51079226	2.35890777232465	0.0038643424	0.0769534172
NA	9906.4535217	-0.57684125061015	0.0073298526	0.087302212
NA	19682.139472	-0.776096437015208	0.0050917829	0.0795305713
0.019480963	NA	NA	NA	NA
0.039702317	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.042055091	NA	NA	NA	NA
0.034624299	NA	NA	NA	NA
0.045622169	NA	NA	NA	NA
0.010778769	68.507279013	2.41261291237858	0.0047200162	0.0776531914
0.006712702	NA	NA	NA	NA
NA	24.576051644	-2.19377208477259	0.0048079691	0.0776531914
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	5.8667720979	-2.71437815677528	0.001956964	0.0656855737
NA	10966.601893	0.572700879054966	0.0076171413	0.0877930649
0.02593234	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.002057538	29.72775155	-3.16915072409194	6.13E-05	0.0127609166
NS	NA	NA	NA	NA
0.017098373	NA	NA	NA	NA
0.004980849	265.29862597	2.41796604010402	0.0034651322	0.0759443488
0.004166124	161.24689261	2.42219320834868	0.0044731135	0.0776531914
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	1057.0340694	0.732578346214311	0.0039006495	0.0769534172

0.004980849	NA	NA	NA	NA
NA	12375.763685	-0.623396049165207	0.0088891285	0.0922276335
NA	7394.7153545	0.329685115961634	0.0028420365	0.0741810097
NS	NA	NA	NA	NA
NS	184.19439026	2.04982146746003	0.0101295235	0.0951730623
NA	6253.4460612	0.358384226586565	0.001103028	0.0538898364
0.047924128	NA	NA	NA	NA
NA	13348.756456	0.466115895465077	0.000446782	0.0355454483
NA	1087.9345524	0.717427840994015	0.0027376784	0.0741810097
0.013924436	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	10933.194882	-0.515051558402893	0.0101506205	0.0951730623
0.033670712	NA	NA	NA	NA
NA	3411.2624984	0.727656440142885	0.0040507211	0.0772557863
0.017748498	NA	NA	NA	NA
0.02403766	NA	NA	NA	NA
NA	1718.8536095	1.20417454811797	0.0003006912	0.0280472303
NA	47222.243911	-0.658087860098425	0.0001761304	0.0205518861
NA	16380.333759	-0.732665818223731	0.001663464	0.0634011992
0.01783985	67.300088973	2.41990004663196	0.0072898203	0.087302212
NS	NA	NA	NA	NA
NA	4952.1228415	0.32157633503343	0.0084572423	0.0909070202
NS	NA	NA	NA	NA
NA	1296.868656	0.615827752412785	2.27E-06	0.0012864694
NA	84.311974436	0.90848912266491	0.0103799064	0.0957596847
NA	12050.172498	0.293496449658792	0.0035186319	0.0759679575
0.040847026	NA	NA	NA	NA
NA	53209.384939	-0.773793044998113	0.0033686325	0.075869171
NA	26650.594715	-0.765951859384276	0.0014834455	0.0603416563
NA	74.560774919	-1.97958793205817	0.0021326585	0.0666918067
NA	7590.81972	0.305554941222847	0.0053214505	0.0799649767
NA	30877.503874	-0.475314415636415	0.0038427759	0.0769534172
NA	1038.2392283	-0.948940068964173	0.0083275449	0.0908306813
0.010765265	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	3797.1184025	-0.770048050278223	0.0068186225	0.084997114
0.038107418	NA	NA	NA	NA
0.027601723	NA	NA	NA	NA
0.030153097	NA	NA	NA	NA
NA	5448.4563871	0.463694040751686	0.005674822	0.0818687648
NA	427.70168396	-0.767898335964944	0.0045432981	0.0776531914
0.028765973	NA	NA	NA	NA
NA	10503.847107	-0.787001379660932	0.0055916375	0.0812209105
NS	NA	NA	NA	NA
0.033110515	NA	NA	NA	NA
NA	3963.3001363	0.56042252040945	0.0037592383	0.0766575554
NA	10355.431925	-0.601365172333582	0.0100806421	0.0951730623
0.046269898	NA	NA	NA	NA

NS	NA	NA	NA	NA
NA	3716.0999885	-0.678951400507997	0.0030500202	0.0741810097
NS	NA	NA	NA	NA
NA	8447.4940146	-0.814855806205746	0.0051309283	0.0795367389
NA	2864.8923791	0.747986327532962	0.0038087503	0.0769534172
NA	8462.8167492	-0.747353684148272	0.0042173399	0.0772557863
0.040516353	NA	NA	NA	NA
0.010765265	NA	NA	NA	NA
0.008063027	82.041420634	2.44882497982757	0.0050036823	0.0795305713
0.035996071	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.020609428	NA	NA	NA	NA
0.022817162	61.608774087	2.5073028659381	0.0042062357	0.0772557863
0.020651498	NA	NA	NA	NA
NA	46378.973014	-0.619643878632908	0.007089757	0.086324584
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.033164356	NA	NA	NA	NA
0.029653933	NA	NA	NA	NA
NA	20360.463216	-0.384910791925106	0.0067111884	0.0849464324
NA	4945.8463486	-0.65527352390691	0.0026657418	0.0741810097
NA	40683.625808	-0.599502907503566	0.0085407165	0.0909838909
0.042387105	NA	NA	NA	NA
NS	385.80844366	2.14246624404216	0.0024538704	0.0717591277
0.033921792	NA	NA	NA	NA
NA	14513.175345	0.511367194072538	0.0105202789	0.0963023841
0.010765265	NA	NA	NA	NA
0.026135029	NA	NA	NA	NA
NA	3508.9695368	-0.635104338879956	0.0089449327	0.0923513092
NS	189.16205448	2.29971743862721	0.0031965786	0.0741810097
0.002584934	NA	NA	NA	NA
NS	58.215074169	2.25933866478028	0.0051651746	0.0798388411
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	7412.4395474	-0.715035670439972	0.0017503104	0.0648921401
NA	1437.9195304	-0.875356218591997	0.0005115714	0.036575624
0.033351837	NA	NA	NA	NA
0.007733946	NA	NA	NA	NA
0.026277875	NA	NA	NA	NA
0.004071762	NA	NA	NA	NA
0.048904425	NA	NA	NA	NA
0.040978249	NA	NA	NA	NA
0.014639835	NA	NA	NA	NA
0.041284264	NA	NA	NA	NA
NA	36476.923655	-0.576910747442195	0.0102729376	0.0957120348
NS	NA	NA	NA	NA
NA	20790.309662	0.478716139292728	0.000757157	0.044253455

NA	11641.51218	-0.843151923004905	0.0005476202	0.036575624
NA	1020.6907178	1.27917886286361	0.0002561446	0.0256618925
NA	4011.7722154	0.733274837544324	0.0046184144	0.0776531914
NA	24.292492024	1.21120085724509	0.0097681877	0.0947215911
0.035332787	NA	NA	NA	NA
0.032366713	NA	NA	NA	NA
0.014386787	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.047934606	NA	NA	NA	NA
NA	7065.6915448	-0.730309721709035	0.0011156491	0.0538898364
0.044518739	NA	NA	NA	NA
0.026625735	NA	NA	NA	NA
NA	10457.362452	-0.495674936699974	0.0099899405	0.0951730623
NA	30.9774917	2.40711304042333	0.0073611659	0.087302212
0.011285813	NA	NA	NA	NA
0.01783985	132.52126558	2.32845729606891	0.0094919422	0.0937130433
0.022927484	NA	NA	NA	NA
0.010228864	NA	NA	NA	NA
0.044522528	173.31650936	1.83565682263181	0.011067701	0.0989926947
0.043301426	302.65467892	1.76607258404915	0.0066532449	0.0849464324
0.016749673	297.41498786	1.92182068792293	0.0095079139	0.0937130433
NS	NA	NA	NA	NA
0.006864913	NA	NA	NA	NA
0.023218213	51.022137551	2.1785104019477	0.0082533796	0.0908306813
NS	NA	NA	NA	NA
0.011820436	65.168576983	2.26104572028712	0.009176551	0.0929394342
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	449.55518883	2.40355418924294	0.0020982777	0.0659981548
0.010765265	NA	NA	NA	NA
0.004812758	288.533417	2.07168021391304	0.0030237035	0.0741810097
0.005418557	NA	NA	NA	NA
0.021563218	70.573594306	2.20959402231036	0.0104432928	0.0957596847
0.005418557	NA	NA	NA	NA
0.01603898	NA	NA	NA	NA
0.011820436	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.005086178	NA	NA	NA	NA
0.007217797	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
0.014227703	84.988292941	2.52120224204589	0.0049029241	0.0785607278
NS	NA	NA	NA	NA
NA	5067.8978915	-0.722152088611085	0.0088722267	0.0922276335
0.033670712	NA	NA	NA	NA
0.048389469	NA	NA	NA	NA
0.000538829	NA	NA	NA	NA
NA	1509.4766892	1.00949579104451	0.0018249864	0.0653852737
NS	NA	NA	NA	NA

0.047677724	NA	NA	NA	NA
NA	1609.5223894	1.51541831844046	0.0001566158	0.0201736056
0.017597508	67.296430285	2.19582823574544	0.004819841	0.0776531914
0.03102791	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
NA	849.86624296	1.28597607342863	0.001947611	0.0656855737
0.032366713	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	6307.1303668	-0.698249695358852	0.0050303399	0.0795305713
0.007911379	185.63912559	2.15173010113489	0.0095885956	0.0937130433
0.022328023	NA	NA	NA	NA
0.039702317	NA	NA	NA	NA
0.007733946	NA	NA	NA	NA
0.026284292	NA	NA	NA	NA
0.011820436	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.023921101	NA	NA	NA	NA
NA	1011.2053049	0.719232760159815	0.0102886062	0.0957120348
0.044518739	NA	NA	NA	NA
NA	13471.556536	-0.898737245956257	0.002995443	0.0741810097
NA	85.572028816	-0.997056090173539	0.0004971263	0.036575624
0.027082547	156.64841055	2.3919812363478	0.007999256	0.0894131713
0.030153097	113.76681475	2.16203582182876	0.007437402	0.087302212
NS	NA	NA	NA	NA
0.010646931	NA	NA	NA	NA
0.008164406	NA	NA	NA	NA
NA	15766.286054	-0.882187003369627	0.0012408892	0.0564135344
0.018212962	NA	NA	NA	NA
NA	22653.902734	-0.68797439633388	0.0095611709	0.0937130433
0.014002961	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.007657973	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	18802.634384	-0.724461683078922	0.0035156023	0.0759679575
0.026962644	NA	NA	NA	NA
NA	3140.6033867	0.604045338134595	0.0003210106	0.0294350422
NS	NA	NA	NA	NA
0.005418557	NA	NA	NA	NA
NA	86.725352096	2.51371754914627	0.003086831	0.0741810097
NS	NA	NA	NA	NA
0.01603898	118.95817172	2.42515592793003	0.0053199591	0.0799649767
0.030153097	122.73087591	2.43487968425804	0.0073879182	0.087302212
0.026135029	331.4234475	2.19962353419471	0.0110244155	0.098908935
0.007576766	139.5261871	2.55665699163779	0.0019433347	0.0656855737
0.045829502	NA	NA	NA	NA
0.011004609	NA	NA	NA	NA
0.009542808	NA	NA	NA	NA
0.021417284	NA	NA	NA	NA

0.028664997	NA	NA	NA	NA
NA	1442.2313916	0.837835642457482	0.0008487504	0.0459173961
0.023711663	NA	NA	NA	NA
0.021055924	62.767087815	2.73457236479277	0.0013469808	0.0582973284
NA	4261.660994	0.738403077248814	0.0025440072	0.0720580039
NA	3979.9338875	1.00490482914781	0.0007881598	0.0447907708
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	8000.2427077	-0.49161298063932	0.0057484939	0.0819152788
NA	15943.507409	0.309586559064617	0.0050574986	0.0795305713
0.007657973	NA	NA	NA	NA
NA	5043.5160118	-0.530884841828474	0.0014513867	0.0603416563
NA	14409.648973	0.451697706328135	0.0104035417	0.0957596847
NA	13361.163058	-0.776798650442591	0.0065010349	0.0849464324
NA	53.691741087	2.20137428417135	0.0091839798	0.0929394342
NS	NA	NA	NA	NA
NA	2622.7679812	-0.755172108512914	0.0063311084	0.084369207
0.038173875	NA	NA	NA	NA
0.013208292	74.736558924	2.60266837363416	0.0024423341	0.0717591277
NA	17.677158586	3.61175933471927	0.0020049594	0.0656986937
NA	45.440897813	2.75099662291093	0.0103651977	0.0957596847
0.026823249	NA	NA	NA	NA
NA	7062.9006278	0.361139116705598	0.0053349731	0.0799649767
0.018212962	NA	NA	NA	NA
0.007911379	NA	NA	NA	NA
NA	4455.3252272	-0.751964315626833	0.0046749953	0.0776531914
NA	438.04023671	1.69419862505267	0.0033679047	0.075869171
NA	16643.031224	-0.893831174127512	0.0015012562	0.0606104195
0.020043544	NA	NA	NA	NA
0.014386787	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	61.892317038	2.30377320259744	0.0090272611	0.092614995
NS	25.967909457	2.23194538548294	0.0112840084	0.0999124145
NA	1231.3094944	0.53421867397817	0.0045038335	0.0776531914
0.017597508	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	12199.081377	0.33762670029062	0.0016558204	0.0634011992
NA	3677.0887031	-0.970795988209073	2.65E-05	0.0071719353
0.049831635	NA	NA	NA	NA
NS	47.394934891	2.57980603932555	0.0030743895	0.0741810097
NA	1055.5010425	1.18429150831748	0.0031383937	0.0741810097
0.016129705	NA	NA	NA	NA
NA	5873.5273685	-0.540946527949842	0.0051297896	0.0795367389
NS	NA	NA	NA	NA
0.045699159	NA	NA	NA	NA
0.016129705	94.127283257	2.49788238476406	0.0029103971	0.0741810097
0.017554423	NA	NA	NA	NA
0.005086178	18.282110387	-2.74470578433023	0.0017866965	0.0648921401

0.008559493	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	7582.7923918	-0.811216979971305	0.0018918375	0.0656855737
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	10886.144039	-0.459860778745193	0.010256189	0.0957120348
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	3737.1602261	-1.03281816768091	0.0039762985	0.0771031356
NA	7031.9588749	-0.814430106714427	0.004563684	0.0776531914
0.023921101	NA	NA	NA	NA
NA	34595.086471	-0.671822662771373	0.0066594456	0.0849464324
0.026856958	NA	NA	NA	NA
0.02403766	NA	NA	NA	NA
0.034624299	NA	NA	NA	NA
0.033975635	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.023218213	NA	NA	NA	NA
0.033670712	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.046378303	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.008488085	NA	NA	NA	NA
0.012858193	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.037510978	NA	NA	NA	NA
NA	61.012942441	2.34931426375002	0.0083050885	0.0908306813
NS	NA	NA	NA	NA
0.032462474	NA	NA	NA	NA
0.013126552	NA	NA	NA	NA
0.026625735	NA	NA	NA	NA
NA	3643.545372	-0.687920093898894	0.0038830165	0.0769534172
NS	NA	NA	NA	NA
0.019912092	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	1683.4066462	-0.946999468199415	5.44E-07	0.0004274219
NA	43150.503745	-0.697356427290111	7.38E-05	0.0137626308
NA	118.5557364	-2.08544800563463	0.0001794938	0.0205518861
NS	NA	NA	NA	NA
NA	34.171698168	2.57627634379854	0.0030943319	0.0741810097
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA

0.045622169	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.043652721	NA	NA	NA	NA
0.029653933	NA	NA	NA	NA
0.034066493	NA	NA	NA	NA
NA	1485.8402218	1.30129015163815	0.0003786017	0.0333193347
NA	882.29972308	1.45033622955781	0.0001172317	0.0183697595
NA	1567.360901	1.43824980906556	6.65E-05	0.0133288866
NA	1080.1597287	1.44245934958477	4.81E-05	0.0113116848
0.017597508	NA	NA	NA	NA
0.012849439	NA	NA	NA	NA
0.036157211	NA	NA	NA	NA
0.040953142	NA	NA	NA	NA
NA	118.37226074	1.16197908979708	0.0052748266	0.0799649767
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.044626373	NA	NA	NA	NA
0.014868684	207.64697551	2.43177584538834	0.0035914758	0.0760045841
NS	NA	NA	NA	NA
NA	35.411976322	2.78152532879147	0.0045262604	0.0776531914
NA	259.91143602	1.03557857897822	0.0066339551	0.0849464324
0.019437119	NA	NA	NA	NA
NA	9456.5798316	0.446214259272607	0.0003421176	0.0308475992
0.042568748	NA	NA	NA	NA
NA	180.16114537	1.36024004990322	0.0060421704	0.0829536098
NS	NA	NA	NA	NA
0.018385803	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.026490875	NA	NA	NA	NA
NA	1209.6184011	1.64208296475924	0.0001222387	0.0183697595
0.012856089	NA	NA	NA	NA
NA	3371.2754511	-0.459906595241408	0.0039594801	0.0770531926
NS	NA	NA	NA	NA
0.018396576	NA	NA	NA	NA
NA	98.310712392	3.05110116057612	1.20E-05	0.0043406817
NS	NA	NA	NA	NA
NA	808.97300282	-2.47027361972157	0.0052800992	0.0799649767
NA	16.284670336	3.23501470208109	0.009683088	0.0942185359
NS	119.85442568	2.26798841319463	0.0077234959	0.0881521365
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.008488085	21.520962185	-3.00641937311829	9.20E-06	0.0035533125
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.026284292	NA	NA	NA	NA
0.036148496	NA	NA	NA	NA

[illegible]

NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	270.54784907	1.92428315946173	0.008576959	0.0911617844
NS	NA	NA	NA	NA
0.033670712	NA	NA	NA	NA
0.040847026	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.047924128	NA	NA	NA	NA
0.010765265	NA	NA	NA	NA
0.008958241	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.043086676	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	857.89457476	-1.01870158913573	0.0042490263	0.0772557863
0.008608407	NA	NA	NA	NA
0.016150098	79.111866019	2.40412115695852	0.00623752	0.084347671
0.019912092	NA	NA	NA	NA
NA	7.7449863351	-3.30352840650889	0.0006720645	0.04131669
0.036389838	NA	NA	NA	NA
0.032254527	NA	NA	NA	NA
NA	1968.8960906	-1.02899897509595	0.0049678823	0.0792809543
0.020479663	NA	NA	NA	NA
0.045611592	NA	NA	NA	NA
NA	552.24951576	1.08092224181819	0.001785454	0.0648921401
0.029497294	NA	NA	NA	NA
0.017335813	NA	NA	NA	NA
0.047692104	NA	NA	NA	NA
0.047934606	NA	NA	NA	NA
0.022927484	NA	NA	NA	NA
0.032366713	36.388260076	2.2823001835083	0.0099038159	0.0951681068
0.004582102	164.12629404	2.29952165734665	0.0093717595	0.0937130433
0.024083131	119.95293865	2.43220237988111	0.0104030441	0.0957596847
NS	NA	NA	NA	NA
NA	10.348350254	-4.06955753164944	0.0005250294	0.036575624
NA	108.1794894	1.23450031189772	0.0016121618	0.0627467306
0.018212962	84.782996718	2.47242365972544	0.0041546189	0.0772557863
NS	NA	NA	NA	NA
NA	98.598582697	-3.33886422351825	2.30E-06	0.0012864694
NA	133.2719175	-1.58283588498707	0.0005998371	0.0390978143
NS	145.43390395	2.17452477614417	0.0070047667	0.0859314912
NA	26757.989253	-0.756478638406718	0.0038280154	0.0769534172
0.013836894	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.019912092	NA	NA	NA	NA

0.041293403	NA	NA	NA	NA
0.033670712	NA	NA	NA	NA
NA	126159.767	-0.590644269866568	0.0057812706	0.0819152788
NA	462.86061415	-2.75027588577606	0.000145744	0.019711881
0.034624299	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	28530.923166	-0.864559721670539	0.0025206346	0.0717717548
0.015343249	NA	NA	NA	NA
NA	14148.828568	0.461513556914349	0.0047012088	0.0776531914
NS	NA	NA	NA	NA
NA	24.057687593	-3.11403380117605	0.0057421745	0.0819152788
NA	587.16163602	-1.33915945169709	0.0042184687	0.0772557863
0.004071762	NA	NA	NA	NA
NA	32.755181367	-2.36790025046624	0.0001143705	0.0183697595
0.011820436	470.85261774	3.78624024001311	4.53E-06	0.0020438675
NA	9299.2454694	-0.865205322047731	0.0001672767	0.0205518861
0.036033668	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.043086676	NA	NA	NA	NA
0.004980849	81.701203932	2.43749857236375	0.0054466011	0.0805064356
0.028185237	61.74784047	2.25557415668178	0.0109578139	0.098908935
NS	NA	NA	NA	NA
0.011004609	NA	NA	NA	NA
0.018212962	NA	NA	NA	NA
NA	648.07379137	-2.61986455936185	0.0018466829	0.0656855737
NA	8.3808749806	-2.66679147478753	0.003395187	0.075869171
NA	1567.985396	-1.13773866800523	0.0010792874	0.0538898364
NA	389.00921431	-1.699657512819	1.56E-05	0.0049570843
NA	13.218529252	-3.15814152156326	0.001664135	0.0634011992
NA	485.37599873	-1.97290258324045	0.0066829045	0.0849464324
0.040847026	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	10385.733101	-0.77594501491427	0.0070951355	0.086324584
0.023711663	NA	NA	NA	NA
0.0153092	NA	NA	NA	NA
NA	34.789290022	1.42449137094837	0.0090389496	0.092614995
0.022270245	198.7809014	2.49812982848692	0.0054261899	0.0804265401
NS	NA	NA	NA	NA
0.022817162	NA	NA	NA	NA
0.008063027	5.4869939747	-2.82593677691465	0.0020644691	0.0656986937
0.003126712	49.692384018	-3.82572586349373	8.74E-10	2.63E-06
0.004071762	203.93374154	-1.46068968726325	0.0074755827	0.0873496816
0.004071762	94.060833407	-1.38000882578426	0.008802491	0.0922276335
NA	1077.5877335	0.914285804051834	0.0019841738	0.0656986937
0.02636012	NA	NA	NA	NA
NA	19314.833091	-0.751437279340473	0.0042554943	0.0772557863
NS	107.04047465	2.47248808837254	0.0088695931	0.0922276335
0.028688153	NA	NA	NA	NA

NA	1664.2059408	1.61770831679262	0.0014761011	0.0603416563
NA	12189.542019	0.590886402685989	1.36E-05	0.0046073347
NA	17.689228532	-1.94276611182416	0.0076271239	0.0877930649
NA	130.25070477	1.64191436693845	0.0050943459	0.0795305713
NA	3004.2275602	1.69283843777697	0.0013266727	0.0578814445
NA	469.45446513	1.25665286591466	0.0110703476	0.0989926947
NA	8.4882273364	-2.26765234955947	0.0082951512	0.0908306813
0.005086178	NA	NA	NA	NA
0.010646931	68.900396061	2.51121068489109	0.008479791	0.0909070202
NS	20.779289347	2.67552110121199	0.0042292775	0.0772557863
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.017597508	NA	NA	NA	NA
0.033028381	NA	NA	NA	NA
NA	973.34843245	1.38861499016051	0.000102647	0.01735376
NS	NA	NA	NA	NA
0.017597508	NA	NA	NA	NA
0.00944343	106.573766	2.30759037580187	0.0007467809	0.044253455
NA	1603.3277417	-0.837180324890408	0.0081298614	0.0899438649
NS	NA	NA	NA	NA
NS	1088.814548	2.14852699901843	0.0011260459	0.0539106929
NS	NA	NA	NA	NA
NA	1890.9706936	1.09906616269413	0.0008305604	0.0453871889
0.002584934	69.227232691	-4.66380286710301	7.83E-09	1.06E-05
NA	1773.8701402	1.09275457055066	0.0025189639	0.0717717548
0.006712702	130.11565863	2.24195831124582	0.0015264449	0.0607210796
0.017155927	NA	NA	NA	NA
NA	4580.5816943	0.564700658100327	0.0053359254	0.0799649767
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	9685.4852532	-0.631770999435092	0.002180549	0.0677975283
0.011067629	NA	NA	NA	NA
NA	58.591671083	2.54702820830929	0.0076007407	0.0877930649
NS	NA	NA	NA	NA
0.030426599	NA	NA	NA	NA
0.001036188	NA	NA	NA	NA
0.04547016	42.235860181	2.45015297689557	0.0047831998	0.0776531914
NA	296.77607764	1.28924889253197	0.0019417039	0.0656855737
NA	9076.0771809	0.606209460924949	0.0089145492	0.0922276335
NA	50.310881997	1.56108729839214	0.002402076	0.0717591277
0.01436598	NA	NA	NA	NA
0.018212962	105.08502341	2.42149287318747	0.0062837974	0.084369207
0.016749673	NA	NA	NA	NA
0.004980849	NA	NA	NA	NA
0.011610825	NA	NA	NA	NA
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA

0.022270245	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	754.01443866	-0.674907519583138	0.0005222591	0.036575624
NA	22.591069174	-3.7314729088548	0.0005346325	0.036575624
0.016002658	60.821368558	2.48994978928774	0.004796895	0.0776531914
NS	NA	NA	NA	NA
0.032124983	5.7049821567	-2.07590380812827	0.0002679895	0.0262653424
NS	NA	NA	NA	NA
NA	208.94333959	-1.53428166727822	0.0002767328	0.0262653424
NS	NA	NA	NA	NA
0.004144754	NA	NA	NA	NA
0.038062309	NA	NA	NA	NA
0.007911379	NA	NA	NA	NA
NA	18294.842557	-0.519386514445645	0.0001937424	0.0205518861
0.033187882	NA	NA	NA	NA
NA	5156.3925888	-0.704206108586986	0.0003818482	0.0333193347
0.027082547	NA	NA	NA	NA
0.008810452	18.17311418	-4.26341605572242	1.65E-09	2.98E-06
0.002584934	10.439386239	-2.93534107295944	3.15E-06	0.0015505804
NA	19785.156158	0.393319870960612	0.0034813676	0.0759443488
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.011985007	237.66578492	2.49224779199943	0.0023335266	0.0713241761
0.018212962	105.46981138	2.37046571831053	0.0082627617	0.0908306813
0.013113341	NA	NA	NA	NA
0.02636012	142.77868248	2.4305433306636	0.0047748873	0.0776531914
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	17993.813061	-0.460038781272551	0.0051921006	0.0799649767
NA	58.279908005	-2.16619342369595	0.0063868173	0.084896023
0.010765265	82.933865302	2.68077240327243	0.0019021408	0.0656855737
0.045611592	NA	NA	NA	NA
NS	42.520030234	2.30688392673141	0.0101091543	0.0951730623
0.0153092	NA	NA	NA	NA
0.005086178	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.030153097	NA	NA	NA	NA
0.016129705	NA	NA	NA	NA
0.004877096	169.73302835	2.1998523364751	0.0092579773	0.0933458288
0.018212962	NA	NA	NA	NA
0.026284292	NA	NA	NA	NA
0.014386787	NA	NA	NA	NA
NA	606.9786476	-2.43140324053043	0.0015786696	0.0618884238
0.026625735	NA	NA	NA	NA
NA	1897.4402396	-1.0007124461666	0.0067834837	0.084950572
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
NA	1709.8761433	0.585063391821406	0.0067559461	0.0849464324

0.02842194	NA	NA	NA	NA
0.017748498	NA	NA	NA	NA
NA	14541.767789	-0.757009505570835	0.0019669248	0.0656855737
NA	10372.640465	-0.857531829266197	0.0088715938	0.0922276335
0.030426599	NA	NA	NA	NA
0.020609428	102.5711219	2.48693659112115	0.0075677667	0.0877930649
0.010001822	NA	NA	NA	NA
0.011820436	196.7521778	2.43556308081415	0.0062520178	0.084347671
0.047624419	91.687966669	2.13413039759165	0.0059055741	0.081920912
0.020135906	NA	NA	NA	NA
0.041644545	NA	NA	NA	NA
NA	2548.8326431	1.64465815395638	0.0045604414	0.0776531914
NA	1113.2119662	1.74931595674905	0.002084695	0.065954386
NA	13671.781881	-0.878900558006334	0.0027259349	0.0741810097
0.0435491	NA	NA	NA	NA
0.017182907	NA	NA	NA	NA
0.033853584	NA	NA	NA	NA
0.011985007	NA	NA	NA	NA
0.006864913	344.00516626	2.43339823812276	0.0045131561	0.0776531914
0.018717307	106.76787244	2.61248196789075	0.0034683173	0.0759443488
0.026076418	61.512162137	2.22281689670814	0.0056991965	0.0819152788
NA	6283.7613046	-0.763151872558869	0.0107097391	0.0974250132
NS	NA	NA	NA	NA
NA	17785.404969	-0.686100119583317	0.0057323021	0.0819152788
NS	NA	NA	NA	NA
NS	NA	NA	NA	NA
0.010228864	368.13931274	2.38280925822119	0.0001916595	0.0205518861
0.007576766	NA	NA	NA	NA
0.010646931	116.77206176	2.41036508876161	0.0042354492	0.0772557863
0.007911379	296.9871694	1.1756177316964	0.0078854916	0.0886912879
NS	101.66699762	2.11239164679766	0.0019525153	0.0656855737
0.036654238	NA	NA	NA	NA
0.008608407	NA	NA	NA	NA
NA	23.650928745	3.39645429008792	0.0040065701	0.0772557863
NA	682.98775691	1.64074649450172	0.0101274134	0.0951730623
NA	89561.268521	0.274638410875868	0.0111640179	0.0991014749
NA	222.07439593	-1.84409876019803	0.0007948085	0.0447907708
NA	112.22424081	-1.51642848947753	0.0036043122	0.0760045841
NA	224.63164984	-1.7514927121763	0.0012781602	0.0567917067

KEGG pathway
ko02020

Annotation
Two-component system

Number of KOs in category
67

ko02010

ABC transporters

54

ko03070

Bacterial secretion system

21

ko02060

Phosphotransferase system (PTS)

17

ko01503	Cationic antimicrobial peptide (CAMP) resistance	10
---------	--	----

ko00520	Amino sugar and nucleotide sugar metabolism	17
---------	---	----

ko00920	Sulfur metabolism	13
---------	-------------------	----

ko02030	Bacterial chemotaxis	7
---------	-----------------------------	---

ko00540	Lipopolysaccharide biosynthesis	8
---------	--	---

ko00620	Pyruvate metabolism	12
---------	----------------------------	----

ko00330	Arginine and proline metabolism	12
---------	--	----

ko00051	Fructose and mannose metabolism	12
---------	--	----

ko00650	Butanoate metabolism	11
---------	-----------------------------	----

ko00640	Propanoate metabolism	11
---------	------------------------------	----

ko00310	Lysine degradation	9
---------	---------------------------	---

Other Significant KOs

Enrichment category	FDR	KO
metformin	1.19583E-20	K00247
		K00575
		K01034
		K01035
		K02402
		K02403
		K03776
		K04771
		K05874
		K05875
		K05876
		K06080
		K07637
		K07639
		K07640
		K07641
		K07647
		K07648
		K07657
		K07660
		K07661
		K07662
		K07664
		K07670
		K07674
		K07676
		K07677
		K07678
		K07686
		K07687
		K07689
		K07690
		K07697
		K07700
		K07701
		K07702
		K07703
		K07711
		K07714
		K07715
		K07768
		K07771
		K07772
		K07773
		K07781
		K07782
		K07784

		K07786
		K07794
		K07796
		K07797
		K07811
		K07813
		K08348
		K08349
		K08350
		K08372
		K09475
		K09477
		K09696
		K09697
		K10125
		K11103
		K11631
		K12292
		K12296
		K14982
metformin	2.071475E-12	K02045
		K02046
		K02047
		K02048
		K02062
		K02063
		K02064
		K02196
		K05813
		K05814
		K05815
		K05816
		K06074
		K06159
		K06858
		K09688
		K09689
		K09696
		K09697
		K09996
		K09998
		K09999
		K10000
		K10005
		K10006
		K10007
		K10008
		K10013

		K10014
		K10015
		K10017
		K10107
		K10108
		K10109
		K10111
		K10543
		K10555
		K11073
		K11075
		K11605
		K11606
		K11607
		K11631
		K11710
		K12368
		K12369
		K12370
		K12371
		K12372
		K15552
		K15598
		K16012
		K16013
		K16905
metformin	1.562405E-11	K02452
		K02457
		K02458
		K02459
		K02461
		K02462
		K03072
		K03195
		K03200
		K03219
		K03223
		K03224
		K03425
		K04058
		K11891
		K11892
		K11903
		K11904
		K11906
		K11907
		K13301
metformin	6.622338E-07	K02744

		K02763
		K02773
		K02774
		K02777
		K02779
		K02794
		K02795
		K02796
		K02800
		K02812
		K02813
		K02814
		K02821
		K02822
		K03475
		K11192
metformin	0.0015541873	K04771
		K07637
		K07640
		K07660
		K07662
		K07771
		K08589
		K12975
		K13014
		K13632
metformin	0.0015541873	K00884
		K00885
		K00978
		K01207
		K01639
		K01788
		K02763
		K02777
		K02779
		K02794
		K02795
		K02796
		K11192
		K12454
		K13014
		K13381
		K15895
metformin	0.0015541873	K00299
		K00380
		K00381
		K00394
		K02045

		K02046
		K02047
		K02048
		K03119
		K04091
		K08352
		K08354
		K15552
metformin	0.0015541873	K00575
		K03776
		K05874
		K05875
		K05876
		K10108
		K12368
metformin	0.0025850273	K02560
		K02840
		K02843
		K02844
		K02847
		K02850
		K11211
		K12975
metformin	0.0065615129	K00101
		K00102
		K00116
		K00138
		K00163
		K00247
		K00656
		K01638
		K01961
		K02594
		K03777
		K12972
metformin	0.0066047255	K00137
		K00673
		K00840
		K00934
		K01470
		K01484
		K05526
		K06447
		K09471
		K09473
		K10536
		K12255
metformin	0.0081461317	K00068

		K00100
		K01729
		K01818
		K02794
		K02795
		K02796
		K02800
		K02812
		K02813
		K02814
		K07026
metformin	0.0092252483	K00100
		K00135
		K00242
		K00247
		K00656
		K01034
		K01035
		K01782
		K01825
		K08318
		K08324
metformin	0.020331504	K00656
		K00932
		K01034
		K01035
		K01574
		K01682
		K01782
		K01825
		K01908
		K01961
		K13921
metformin	0.0329899572	K00135
		K00164
		K01034
		K01035
		K01782
		K01825
		K03894
		K03895
		K03897
		K00129
		K00138
		K00163
		K02777
		K02779
		K04022

K00116
K00163
K00164
K00242
K00247
K01682
K00033
K00117
K00851
K01690
K01807
K05774
K00065
K00853
K03081
K00094
K01631
K02079
K02744
K02773
K02774
K01706
K01708
K02821
K02822
K03475
K03476
K00667
K01716
K01961
K00632
K01782
K01825
K06445
K01574
K00568
K03181
K03184
K03185
K00242
K00247
K00329
K01507
K02133
K02297
K02298
K02299
K02301

K03885
K14681
K00892
K01139
K01509
K02344
K02345
K05851
K08693
K08723
K14977
K15518
K15519
K15780
K00756
K00943
K02344
K02345
K08693
K08723
K09018
K09019
K09021
K09023
K15519
K16066
K00135
K08324
K14681
K01961
K00108
K12525
K12972
K13745
K16066
K12525
K01761
K12525
K00632
K01782
K01825
K00632
K01782
K01825
K00835
K05823
K12525
K00129

K01693
K00129
K00135
K00129
K01666
K03782
K01061
K00632
K01666
K01782
K01825
K00100
K01061
K00164
K01782
K01825
K03782
K13498
K00129
K00137
K01782
K01825
K03119
K01008
K01761
K07310
K00033
K00383
K00432
K01460
K07751
K00690
K00693
K00697
K00978
K01087
K02777
K07405
K09667
K01207
K05365
K05515
K11693
K11695
K00631
K00863
K05878
K05879

K06120
K01114
K16619
K05286
K00631
K01114
K01521
K06132
K16619
K01114
K16619
K00432
K00100
K00632
K00725
K01666
K01666
K01061
K00100
K01034
K01035
K03788
K01091
K01608
K01637
K01638
K01682
K12972
K10680
K00632
K13938
K00863
K01070
K00855
K01807
K11214
K00242
K00247
K01682
K01961
K03707
K07251
K00299
K01497
K05368
K03472
K03742
K08693

K08723
K02170
K08351
K13938
K00228
K00510
K01698
K01719
K01749
K02301
K02495
K03394
K05368
K13542
K03527
K13787
K01782
K01825
K09835
K00362
K00363
K00372
K01782
K01825
K03782
K02435
K04568
K00129
K00129
K01782
K01825
K10805
K10806
K01252
K02364
K04781
K00033
K00116
K00163
K00164
K00242
K00247
K00851
K00855
K00863
K01070
K01637
K01638

K01682
K01690
K01782
K01807
K01825
K01961
K08318
K01682
K14681
K00632
K00667
K01716
K01782
K01825
K01961
K06445
K01666
K01682
K01693
K01807
K05823
K12525
K13498
K14681
K01207
K05515
K09475
K02402
K02403
K02419
K13820
K14567
K13025
K13025
K03666
K03732
K12581
K10844
K02344
K02345
K13025
K03072
K03425
K13301
K01247
K03652
K05522
K10844

K02344
K02345
K10857
K02317
K02344
K02345
K04067
K10979
K02603
K02603
K02603
K07235
K01369
K00693
K00693
K06062
K06084
K01369
K00863
K00693
K00383
K00432
K01114
K06062
K00693
K00693
K09667
K00510
K02133
K02133
K02133
K13735
K05851
K10939
K12264
K12265
K12266
K07345
K07347
K07690
K15475
K01354
K01354
K14194
K06062
K06062
K00129
K00309

K00427
K00433
K00786
K00903
K00906
K00924
K00961
K01133
K01146
K01167
K01169
K01238
K01263
K01266
K01269
K01305
K01355
K01387
K01407
K01412
K01417
K01421
K01449
K01506
K01632
K01669
K01671
K01751
K01766
K01994
K02024
K02074
K02077
K02100
K02102
K02167
K02255
K02280
K02336
K02362
K02381
K02425
K02429
K02430
K02436
K02444
K02467
K02468

K02475
K02476
K02485
K02499
K02504
K02505
K02521
K02531
K02538
K02550
K02553
K02562
K02565
K02589
K02652
K02679
K02680
K02682
K02742
K02846
K02852
K02853
K03177
K03207
K03212
K03214
K03218
K03290
K03291
K03293
K03294
K03304
K03314
K03329
K03435
K03445
K03468
K03477
K03483
K03485
K03489
K03528
K03548
K03554
K03566
K03576
K03591
K03597

K03598
K03607
K03632
K03633
K03638
K03645
K03651
K03656
K03672
K03676
K03683
K03688
K03690
K03710
K03716
K03718
K03720
K03721
K03733
K03746
K03747
K03750
K03755
K03761
K03764
K03774
K03802
K03804
K03807
K03808
K03819
K03834
K03835
K03836
K03837
K03838
K03840
K03855
K03919
K03930
K03970
K03972
K03974
K03975
K04013
K04016
K04018
K04025

K04028
K04031
K04033
K04065
K04070
K04076
K04080
K04081
K04094
K04335
K04336
K04337
K04338
K04691
K04753
K04759
K04770
K04774
K04775
K04954
K05245
K05311
K05346
K05374
K05517
K05540
K05541
K05590
K05595
K05596
K05739
K05775
K05777
K05778
K05779
K05782
K05789
K05790
K05798
K05800
K05802
K05803
K05804
K05839
K05880
K05881
K05910
K05982

K05984
K05995
K06006
K06048
K06075
K06136
K06141
K06144
K06145
K06149
K06155
K06156
K06181
K06194
K06201
K06205
K06212
K06214
K06219
K06222
K06295
K06298
K06307
K06311
K06328
K06386
K06401
K06402
K06415
K06426
K06436
K06601
K06602
K06866
K06887
K06899
K06902
K06916
K06918
K06927
K06957
K06968
K06999
K07001
K07028
K07034
K07038
K07084

K07124
K07126
K07136
K07137
K07140
K07147
K07153
K07156
K07165
K07169
K07175
K07224
K07225
K07229
K07232
K07238
K07245
K07261
K07265
K07266
K07269
K07270
K07278
K07279
K07283
K07285
K07286
K07311
K07312
K07314
K07318
K07334
K07335
K07346
K07349
K07350
K07357
K07358
K07400
K07402
K07442
K07479
K07480
K07489
K07506
K07507
K07566
K07570

K07592
K07723
K07742
K07821
K08137
K08153
K08154
K08160
K08162
K08163
K08172
K08194
K08219
K08225
K08227
K08276
K08308
K08316
K08317
K08321
K08326
K08345
K08346
K08347
K08361
K08587
K08602
K08722
K08970
K08994
K08997
K09016
K09116
K09155
K09159
K09161
K09456
K09607
K09612
K09684
K09748
K09781
K09802
K09823
K09891
K09892
K09893
K09894

K09895
K09896
K09897
K09899
K09900
K09901
K09902
K09906
K09907
K09908
K09910
K09913
K09914
K09915
K09921
K09923
K09933
K09934
K09951
K09952
K09962
K09979
K09982
K09985
K09992
K10124
K10355
K10673
K10748
K10908
K10975
K11057
K11059
K11060
K11102
K11106
K11139
K11201
K11391
K11474
K11498
K11535
K11732
K11734
K11735
K11736
K11737
K11738

K11739
K11740
K11744
K11745
K11746
K11747
K11748
K11750
K11893
K11894
K11895
K11896
K11900
K11901
K11905
K11909
K11910
K11911
K11922
K11923
K11925
K11929
K11930
K11931
K11932
K11933
K11935
K11938
K11941
K12055
K12056
K12057
K12072
K12113
K12147
K12148
K12150
K12228
K12262
K12271
K12288
K12289
K12299
K12500
K12516
K12542
K12680
K12687

K12942
K12943
K12945
K12950
K12957
K12961
K12974
K12997
K13053
K13069
K13243
K13244
K13255
K13274
K13275
K13281
K13282
K13620
K13629
K13631
K13634
K13635
K13637
K13640
K13671
K13683
K13684
K13695
K13918
K13926
K13979
K14051
K14055
K14056
K14062
K14064
K14287
K14348
K14392
K14393
K14587
K14588
K14645
K14665
K14744
K14762
K14767
K15152

K15176
K15257
K15268
K15342
K15396
K15460
K15536
K15540
K15547
K15548
K15549
K15550
K15721
K15723
K15735
K15737
K15827
K15828
K15829
K15830
K15831
K15833
K15836
K15924
K15974
K16076
K16077
K16090
K16136
K16138
K16140
K16263
K16291
K16301
K16321
K16322
K16324
K16326
K16346
K16568
K16692
K16693
K16695
K16697
K16703
K16704
K16711

Definition

frdD; fumarate reductase subunit D

cheR; chemotaxis protein methyltransferase CheR [EC:2.1.1.80]

atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]

atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]

flhC; flagellar transcriptional activator FlhC

flhD; flagellar transcriptional activator FlhD

aer; aerotaxis receptor

degP, htrA; serine protease Do [EC:3.4.21.107]

tsr; methyl-accepting chemotaxis protein I, serine sensor receptor

tar; methyl-accepting chemotaxis protein II, aspartate sensor receptor

trg; methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor

rscF; RcsF protein

phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]

rstB; two-component system, OmpR family, sensor histidine kinase RstB [EC:2.7.13.3]

cpxA; two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]

creC; two-component system, OmpR family, sensor histidine kinase CreC [EC:2.7.13.3]

torS; two-component system, OmpR family, sensor histidine kinase TorS [EC:2.7.13.3]

arcB; two-component system, OmpR family, aerobic respiration control sensor histidine kinase ArcB [EC:2.7.13.3]

phoB; two-component system, OmpR family, phosphate regulon response regulator PhoB

phoP; two-component system, OmpR family, response regulator PhoP

rstA; two-component system, OmpR family, response regulator RstA

cpxR; two-component system, OmpR family, response regulator CpxR

baeR; two-component system, OmpR family, response regulator BaeR

mtrA; two-component system, OmpR family, response regulator MtrA

narQ; two-component system, NarL family, nitrate/nitrite sensor histidine kinase NarQ [EC:2.7.13.3]

rscD; two-component system, NarL family, sensor histidine kinase RcsD [EC:2.7.13.3]

rscC; two-component system, NarL family, capsular synthesis sensor histidine kinase RcsC [EC:2.7.13.3]

barA; two-component system, NarL family, sensor histidine kinase BarA [EC:2.7.13.3]

uhpA; two-component system, NarL family, uhpT operon response regulator UhpA

rscB; two-component system, NarL family, capsular synthesis response regulator RcsB

uvrY; two-component system, NarL family, invasion response regulator UvrY

evgA, bvgA; two-component system, NarL family, response regulator EvgA

kinB; two-component system, sporulation sensor kinase B [EC:2.7.13.3]

dpiB, citA; two-component system, CitB family, cit operon sensor histidine kinase CitA [EC:2.7.13.3]

dcuS; two-component system, CitB family, sensor histidine kinase DcuS [EC:2.7.13.3]

dpiA, citB; two-component system, CitB family, response regulator CitB

dcuR; two-component system, CitB family, response regulator DcuR

glrK, qseE; two-component system, NtrC family, sensor histidine kinase GlrK [EC:2.7.13.3]

atoC; two-component system, NtrC family, response regulator AtoC

glrR, qseF; two-component system, NtrC family, response regulator GlrR

senX3; two-component system, OmpR family, sensor histidine kinase SenX3 [EC:2.7.13.3]

basR; two-component system, OmpR family, response regulator BasR

torR; two-component system, OmpR family, torCAD operon response regulator TorR

arcA; two-component system, OmpR family, aerobic respiration control protein ArcA

rscA; LuxR family transcriptional regulator, capsular biosynthesis positive transcription factor

sdiA; LuxR family transcriptional regulator

uhpT; MFS transporter, OPA family, hexose phosphate transport protein UhpT

emrY; MFS transporter, multidrug resistance protein Y
tctB; putative tricarboxylic transport membrane protein
cusC, silC; Cu(I)/Ag(I) efflux system outer membrane protein CusC/SilC
emrK; multidrug resistance protein K
torA; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]
agrB; accessory gene regulator B
fdnG; formate dehydrogenase-N, alpha subunit [EC:1.1.5.6]
fdnH; formate dehydrogenase-N, beta subunit
fdnI; formate dehydrogenase-N, gamma subunit
pepD; putative serine protease PepD [EC:3.4.21.-]
ompC; outer membrane pore protein C
citT; citrate:succinate antiporter
natB; sodium transport system permease protein
natA; sodium transport system ATP-binding protein
dctB; two-component system, NtrC family, C4-dicarboxylate transport sensor histidine kinase DctB [EC:2.7.13.3]
dctA; aerobic C4-dicarboxylate transport protein
bceA; bacitracin transport system ATP-binding protein
ABCC-BAC.COMA, comA; ATP-binding cassette, subfamily C, bacterial, competence factor transporting protein [EC:3.4.22.-]
comX1_2; competence protein ComX
ciaH; two-component system, OmpR family, sensor histidine kinase CiaH [EC:2.7.13.3]
cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]
cysU; sulfate transport system permease protein
cysW; sulfate transport system permease protein
cysP, sbp; sulfate transport system substrate-binding protein
thiQ; thiamine transport system ATP-binding protein
thiP; thiamine transport system permease protein
thiB, tbpA; thiamine transport system substrate-binding protein
ccmD; heme exporter protein D
ugpB; sn-glycerol 3-phosphate transport system substrate-binding protein
ugpA; sn-glycerol 3-phosphate transport system permease protein
ugpE; sn-glycerol 3-phosphate transport system permease protein
ugpC; sn-glycerol 3-phosphate transport system ATP-binding protein [EC:3.6.3.20]
ABC.VB12.A, btuD; vitamin B12 transport system ATP-binding protein [EC:3.6.3.33]
yojI; putative ATP-binding cassette transporter
ABC.VB12.S1, btuF; vitamin B12 transport system substrate-binding protein
ABC-2.CPSE.P; capsular polysaccharide transport system permease protein
ABC-2.CPSE.A; capsular polysaccharide transport system ATP-binding protein
natB; sodium transport system permease protein
natA; sodium transport system ATP-binding protein
artJ; arginine transport system substrate-binding protein
artM; arginine transport system permease protein
artQ; arginine transport system permease protein
artP; arginine transport system ATP-binding protein [EC:3.6.3.-]
gluB; glutamate transport system substrate-binding protein
gluC; glutamate transport system permease protein
gluD; glutamate transport system permease protein
gluA; glutamate transport system ATP-binding protein [EC:3.6.3.-]
ABC.ARG.S, argT; lysine/arginine/ornithine transport system substrate-binding protein

hisJ; histidine transport system substrate-binding protein
hisM; histidine transport system permease protein
hisP; histidine transport system ATP-binding protein [EC:3.6.3.21]
ABC-2.CPSE.P1; capsular polysaccharide transport system permease protein
malE; maltose/maltodextrin transport system substrate-binding protein
malF; maltose/maltodextrin transport system permease protein
malK, mtlK, thuK; multiple sugar transport system ATP-binding protein [EC:3.6.3.-]
xylF; D-xylose transport system substrate-binding protein
lsrB; AI-2 transport system substrate-binding protein
potF; putrescine transport system substrate-binding protein
potH; putrescine transport system permease protein
sitC; manganese/iron transport system permease protein
sitD; manganese/iron transport system permease protein
sitB; manganese/iron transport system ATP-binding protein
bceA; bacitracin transport system ATP-binding protein
troB, mntB, znuC; manganese/zinc/iron transport system ATP-binding protein
dppA; dipeptide transport system substrate-binding protein
dppB; dipeptide transport system permease protein
dppC; dipeptide transport system permease protein
dppD; dipeptide transport system ATP-binding protein
dppF; dipeptide transport system ATP-binding protein
tauC; taurine transport system permease protein
thiY; putative hydroxymethylpyrimidine transport system substrate-binding protein
cydC; ATP-binding cassette, subfamily C, bacterial CydC
cydD; ATP-binding cassette, subfamily C, bacterial CydD
K16905; fluoroquinolones transport system permease protein
gspC; general secretion pathway protein C
gspH; general secretion pathway protein H
gspI; general secretion pathway protein I
gspJ; general secretion pathway protein J
gspL; general secretion pathway protein L
gspM; general secretion pathway protein M
secD; preprotein translocase subunit SecD
virB10, lvhB10; type IV secretion system protein VirB10
virB5, lvhB5; type IV secretion system protein VirB5
yscC; type III secretion protein SctC
yscL; type III secretion protein SctL
yscN; ATP synthase in type III secretion protein SctN [EC:3.6.3.14]
tatE; sec-independent protein translocase protein TatE
yscW; type III secretion protein SctW
impL, vasK, icmF; type VI secretion system protein ImpL
impK, ompA, vasF, dotU; type VI secretion system protein ImpK
K11903, hcp; type VI secretion system secreted protein Hcp
vgrG; type VI secretion system secreted protein VgrG
vasD, lip; type VI secretion system protein VasD
vasG, clpV; type VI secretion system protein VasG
secM; secretion monitor
PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component [EC:2.7.1.69]

PTS-Dgl-EIIA, gamP; PTS system, D-glucosamine-specific IIA component [EC:2.7.1.69]
 PTS-Gat-EIIA, gatA; PTS system, galactitol-specific IIA component [EC:2.7.1.69]
 PTS-Gat-EIIB, gatB; PTS system, galactitol-specific IIB component [EC:2.7.1.69]
 PTS-Glc-EIIA, crr; PTS system, glucose-specific IIA component [EC:2.7.1.69]
 PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component
 PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]
 PTS-Man-EIIC, manY; PTS system, mannose-specific IIC component
 PTS-Man-EIID, manZ; PTS system, mannose-specific IID component
 PTS-Mtl-EIIC, mtlA; PTS system, mannitol-specific IIC component
 PTS-Sor-EIIA, sorF; PTS system, sorbose-specific IIA component [EC:2.7.1.69]
 PTS-Sor-EIIB, sorB; PTS system, sorbose-specific IIB component [EC:2.7.1.69]
 PTS-Sor-EIIC, sorA; PTS system, sorbose-specific IIC component
 PTS-Ula-EIIA, ulaC, sgaA; PTS system, ascorbate-specific IIA component [EC:2.7.1.69]
 PTS-Ula-EIIB, ulaB, sgaB; PTS system, ascorbate-specific IIB component [EC:2.7.1.69]
 PTS-Ula-EIIC, ulaA, sgaT; PTS system, ascorbate-specific IIC component
 PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
 degP, htrA; serine protease Do [EC:3.4.21.107]
 phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]
 cpxA; two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]
 phoP; two-component system, OmpR family, response regulator PhoP
 cpxR; two-component system, OmpR family, response regulator CpxR
 basR; two-component system, OmpR family, response regulator BasR
 E3.4.22.37; gingipain R [EC:3.4.22.37]
 eptB; phosphoethanolamine transferase
 arnD; undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]
 marA; AraC family transcriptional regulator, multiple antibiotic resistance protein MarA
 NAGK, nagK; N-acetylglucosamine kinase [EC:2.7.1.59]
 nanK; N-acylmannosamine kinase [EC:2.7.1.60]
 rfbF; glucose-1-phosphate cytidyltransferase [EC:2.7.7.33]
 E3.2.1.52, nagZ; beta-N-acetylhexosaminidase [EC:3.2.1.52]
 E4.1.3.3, nanA, NPL; N-acetylneuraminate lyase [EC:4.1.3.3]
 nanE; N-acylglucosamine-6-phosphate 2-epimerase [EC:5.1.3.9]
 PTS-Dgl-EIIA, gamP; PTS system, D-glucosamine-specific IIA component [EC:2.7.1.69]
 PTS-Glc-EIIA, crr; PTS system, glucose-specific IIA component [EC:2.7.1.69]
 PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component
 PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]
 PTS-Man-EIIC, manY; PTS system, mannose-specific IIC component
 PTS-Man-EIID, manZ; PTS system, mannose-specific IID component
 PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
 rfbE; CDP-paratose 2-epimerase [EC:5.1.3.10]
 arnD; undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]
 chiA; bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]
 pseC; UDP-4-amino-4,6-dideoxy-L-N-acetyl-beta-L-altrosamine transaminase [EC:2.6.1.92]
 ssuE; FMN reductase [EC:1.5.1.38]
 cysJ; sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]
 cysI; sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]
 aprA; adenylylsulfate reductase, subunit A [EC:1.8.99.2]
 cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]

cysU; sulfate transport system permease protein
cysW; sulfate transport system permease protein
cysP, sbp; sulfate transport system substrate-binding protein
tauD; taurine dioxygenase [EC:1.14.11.17]
ssuD; alkanesulfonate monooxygenase [EC:1.14.14.5]
phsA, psrA; thiosulfate reductase / polysulfide reductase chain A
phsC; thiosulfate reductase cytochrome b subunit
tauC; taurine transport system permease protein
cheR; chemotaxis protein methyltransferase CheR [EC:2.1.1.80]
aer; aerotaxis receptor
tsr; methyl-accepting chemotaxis protein I, serine sensor receptor
tar; methyl-accepting chemotaxis protein II, aspartate sensor receptor
trg; methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
malE; maltose/maltodextrin transport system substrate-binding protein
dppA; dipeptide transport system substrate-binding protein
msbB; lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase [EC:2.3.1.-]
waaB, rfaB; UDP-D-galactose:(glucosyl)LPS alpha-1,6-D-galactosyltransferase [EC:2.4.1.-]
waaF, rfaF; heptosyltransferase II [EC:2.4.-.-]
waaG, rfaG; UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]
waaL, rfaL; O-antigen ligase [EC:6.-.-.-]
waaY, rfaY; heptose (II) phosphotransferase [EC:2.7.1.-]
kdsA; 3-deoxy-D-manno-octulosonic acid kinase [EC:2.7.1.166]
eptB; phosphoethanolamine transferase
E1.1.2.3, lldD; L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]
E1.1.2.4, dld; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]
mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]
aldB; aldehyde dehydrogenase [EC:1.2.1.-]
aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
frdD; fumarate reductase subunit D
E2.3.1.54, pfkD; formate C-acetyltransferase [EC:2.3.1.54]
E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]
accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
nifV; homocitrate synthase NifV [EC:2.3.3.14]
dld; D-lactate dehydrogenase [EC:1.1.1.28]
ghrA; glyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]
prf; aminobutyraldehyde dehydrogenase [EC:1.2.1.19]
astA; arginine N-succinyltransferase [EC:2.3.1.109]
astC; succinylornithine aminotransferase [EC:2.6.1.81]
E2.7.3.3; arginine kinase [EC:2.7.3.3]
E3.5.2.10; creatinine amidohydrolase [EC:3.5.2.10]
astB; succinylarginine dihydrolase [EC:3.5.3.23]
astE; succinylglutamate desuccinylase [EC:3.5.1.96]
astD; succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]
puuB, ordL; gamma-glutamylputrescine oxidase [EC:1.4.3.-]
puuD; gamma-glutamyl-gamma-aminobutyrate hydrolase [EC:3.5.1.94]
E3.5.3.12; agmatine deiminase [EC:3.5.3.12]
gbuA; guanidinobutyrase [EC:3.5.3.7]
srlD; sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]

E1.1.1.1.-

algL; poly(beta-D-mannuronate) lyase [EC:4.2.2.3]

fucI; L-fucose isomerase [EC:5.3.1.25]

PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]

PTS-Man-EIIC, manY; PTS system, mannose-specific IIC component

PTS-Man-EIID, manZ; PTS system, mannose-specific IID component

PTS-Mtl-EIIC, mtlA; PTS system, mannitol-specific IIC component

PTS-Sor-EIIA, sorF; PTS system, sorbose-specific IIA component [EC:2.7.1.69]

PTS-Sor-EIIB, sorB; PTS system, sorbose-specific IIB component [EC:2.7.1.69]

PTS-Sor-EIIC, sorA; PTS system, sorbose-specific IIC component

E3.1.3.70; mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]

E1.1.1.1.-

gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]

sdhD; succinate dehydrogenase membrane anchor subunit

frdD; fumarate reductase subunit D

E2.3.1.54, pfID; formate C-acetyltransferase [EC:2.3.1.54]

atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]

atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]

fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]

fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase

yihU; putative dehydrogenase [EC:1.1.-.-]

sad; succinate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.24]

E2.3.1.54, pfID; formate C-acetyltransferase [EC:2.3.1.54]

E2.7.2.15, tdcD, pduW; propionate kinase [EC:2.7.2.15]

atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]

atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]

adc; acetoacetate decarboxylase [EC:4.1.1.4]

acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]

fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]

fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase

E6.2.1.17, prpE; propionyl-CoA synthetase [EC:6.2.1.17]

accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]

pduQ; 1-propanol dehydrogenase

gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]

OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]

atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]

atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]

fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]

fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase

iucA; N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]

iucC; aerobactin synthase [EC:6.3.2.39]

iucD; lysine N6-hydroxylase [EC:1.14.13.59]

E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]

aldB; aldehyde dehydrogenase [EC:1.2.1.-]

aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]

PTS-Glc-EIIA, crr; PTS system, glucose-specific IIA component [EC:2.7.1.69]

PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component

eutG; alcohol dehydrogenase

mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]
 aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 sdhD; succinate dehydrogenase membrane anchor subunit
 frdD; fumarate reductase subunit D
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 PGD, gnd; 6-phosphogluconate dehydrogenase [EC:1.1.1.44]
 gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
 E2.7.1.12, gntK, idnK; gluconokinase [EC:2.7.1.12]
 edd; phosphogluconate dehydratase [EC:4.2.1.12]
 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
 phnN; ribose 1,5-bisphosphokinase [EC:2.7.4.23]
 kduD; 2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]
 araB; L-ribulokinase [EC:2.7.1.16]
 sgbH; 3-dehydro-L-gulonate-6-phosphate decarboxylase [EC:4.1.1.85]
 E1.1.1.251, gatD; galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]
 dgoA; 2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]
 agaA; N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]
 PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component [EC:2.7.1.69]
 PTS-Gat-EIIA, gatA; PTS system, galactitol-specific IIA component [EC:2.7.1.69]
 PTS-Gat-EIIB, gatB; PTS system, galactitol-specific IIB component [EC:2.7.1.69]
 gudD; glucarate dehydratase [EC:4.2.1.40]
 garD; galactarate dehydratase [EC:4.2.1.42]
 PTS-Ula-EIIA, ulaC, sgaA; PTS system, ascorbate-specific IIA component [EC:2.7.1.69]
 PTS-Ula-EIIB, ulaB, sgaB; PTS system, ascorbate-specific IIB component [EC:2.7.1.69]
 PTS-Ula-EIIC, ulaA, sgaT; PTS system, ascorbate-specific IIC component
 ulaG; L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]
 FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]
 fabA; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
 accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
 E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 fadE; acyl-CoA dehydrogenase [EC:1.3.99.-]
 adc; acetoacetate decarboxylase [EC:4.1.1.4]
 ubiG; 2-polyprenyl-6-hydroxyphenyl methylase / 3-demethylubiquinone-9 3-methyltransferase [EC:2.1.1.222 2.1.1.64]
 ubiC; chorismate--pyruvate lyase [EC:4.1.3.40]
 ubiF; 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase [EC:1.14.13.-]
 ubiH; 2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]
 sdhD; succinate dehydrogenase membrane anchor subunit
 frdD; fumarate reductase subunit D
 E1.6.5.3; NADH dehydrogenase [EC:1.6.5.3]
 ppa; inorganic pyrophosphatase [EC:3.6.1.1]
 ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
 cyoA; cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]
 cyoB; cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]
 cyoC; cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]
 cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]

ndh; NADH dehydrogenase [EC:1.6.99.3]
 argHA; argininosuccinate lyase / amino-acid N-acetyltransferase [EC:4.3.2.1 2.3.1.1]
 gsk; inosine kinase [EC:2.7.1.73]
 spoT, HDDC3; guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]
 E3.6.1.3; adenosinetriphosphatase [EC:3.6.1.3]
 DPO3P, holD; DNA polymerase III subunit psi [EC:2.7.7.7]
 DPO3T, holE; DNA polymerase III subunit theta [EC:2.7.7.7]
 E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]
 E3.1.3.6; 3'-nucleotidase [EC:3.1.3.6]
 yjjG; 5'-nucleotidase [EC:3.1.3.5]
 ylbA; ureidoglycine aminohydrolase [EC:3.5.3.-]
 dgk; deoxyguanosine kinase [EC:2.7.1.113]
 dck; deoxyadenosine/deoxycytidine kinase [EC:2.7.1.76 2.7.1.74]
 tilS-hprT; bifunctional protein TilS/HprT [EC:6.3.4.19 2.4.2.8]
 E2.4.2.2, pdp; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]
 E2.7.4.9, tmk; dTMP kinase [EC:2.7.4.9]
 DPO3P, holD; DNA polymerase III subunit psi [EC:2.7.7.7]
 DPO3T, holE; DNA polymerase III subunit theta [EC:2.7.7.7]
 E3.1.3.6; 3'-nucleotidase [EC:3.1.3.6]
 yjjG; 5'-nucleotidase [EC:3.1.3.5]
 rutA; pyrimidine oxygenase [EC:1.14.99.46]
 rutE; 3-hydroxypropanoate dehydrogenase [EC:1.1.1.-]
 rutC; aminoacrylate peracid reductase
 rutD; aminoacrylate hydrolase [EC:3.5.1.-]
 dck; deoxyadenosine/deoxycytidine kinase [EC:2.7.1.76 2.7.1.74]
 ydfG; malonic semialdehyde reductase [EC:1.1.1.-]
 gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]
 sad; succinate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.24]
 argHA; argininosuccinate lyase / amino-acid N-acetyltransferase [EC:4.3.2.1 2.3.1.1]
 accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
 E1.1.99.1, betA, CHDH; choline dehydrogenase [EC:1.1.99.1]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 ghrA; glyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]
 ddc; L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]
 ydfG; malonic semialdehyde reductase [EC:1.1.1.-]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 E4.4.1.11; methionine-gamma-lyase [EC:4.4.1.11]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.3.1.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.3.1.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 avtA; valine--pyruvate aminotransferase [EC:2.6.1.66]
 E3.5.1.47; N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]

E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]
 gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]
 E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
 katG; catalase-peroxidase [EC:1.11.1.21]
 E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
 E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
 E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.3.1.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 E1.1.1.-
 E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.3.1.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 katG; catalase-peroxidase [EC:1.11.1.21]
 trpCF; indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomerase [EC:4.1.1.48 5.3.1.24]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]
 prr; aminobutyraldehyde dehydrogenase [EC:1.2.1.19]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.3.1.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 tauD; taurine dioxygenase [EC:1.14.11.17]
 selD, SEPHS; selenide, water dikinase [EC:2.7.9.3]
 E4.4.1.11; methionine-gamma-lyase [EC:4.4.1.11]
 ynfF; Tat-targeted selenate reductase subunit YnfF [EC:1.97.1.9]
 PGD, gnd; 6-phosphogluconate dehydrogenase [EC:1.1.1.44]
 GSR, gor; glutathione reductase (NADPH) [EC:1.8.1.7]
 E1.11.1.9; glutathione peroxidase [EC:1.11.1.9]
 gsp; glutathionylspermidine amidase/synthetase [EC:3.5.1.78 6.3.1.8]
 pepB; PepB aminopeptidase [EC:3.4.11.23]
 E2.4.1.7; sucrose phosphorylase [EC:2.4.1.7]
 GYS; glycogen(starch) synthase [EC:2.4.1.11]
 otsA; trehalose 6-phosphate synthase [EC:2.4.1.15]
 rfbF; glucose-1-phosphate cytidyltransferase [EC:2.7.7.33]
 otsB; trehalose 6-phosphate phosphatase [EC:3.1.3.12]
 PTS-Glc-EIIA, crr; PTS system, glucose-specific IIA component [EC:2.7.1.69]
 E3.2.1.1A; alpha-amylase [EC:3.2.1.1]
 OGT; polypeptide N-acetylglucosaminyltransferase [EC:2.4.1.-]
 E3.2.1.52, nagZ; beta-N-acetylhexosaminidase [EC:3.2.1.52]
 mrcB; penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]
 mrdA; penicillin-binding protein 2
 femX, fmhB; peptidoglycan pentaglycine glycine transferase (the first glycine) [EC:2.3.2.16]
 femB; peptidoglycan pentaglycine glycine transferase (the fourth and fifth glycine) [EC:2.3.2.18]
 plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]
 E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
 dhaK; dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]
 dhaL; dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]

dhaB; glycerol dehydratase large subunit [EC:4.2.1.30]
plcC; phospholipase C [EC:3.1.4.3]
plc, cpa; phospholipase C / alpha-toxin [EC:3.1.4.3]
PIGB; phosphatidylinositol glycan, class B [EC:2.4.1.-]
plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]
plcC; phospholipase C [EC:3.1.4.3]
cdh; CDP-diacylglycerol pyrophosphatase [EC:3.6.1.26]
ybhO; putative cardiolipin synthase [EC:2.7.8.-]
plc, cpa; phospholipase C / alpha-toxin [EC:3.1.4.3]
plcC; phospholipase C [EC:3.1.4.3]
plc, cpa; phospholipase C / alpha-toxin [EC:3.1.4.3]
E1.11.1.9; glutathione peroxidase [EC:1.11.1.9]
E1.1.1.-
E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
B4GALNT1, GALGT; (N-Acetylneuraminy)-galactosylglucosylceramide N-acetylgalactosaminyltransferase [EC:2.4.1.92]
E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
E1.1.1.-
atoD; acetate CoA/acetoacetate CoA-transferase alpha subunit [EC:2.8.3.8 2.8.3.9]
atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]
aphA; acid phosphatase (class B) [EC:3.1.3.2]
E3.1.3.18, gph; phosphoglycolate phosphatase [EC:3.1.3.18]
gcl; tartronate-semialdehyde synthase [EC:4.1.1.47]
E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]
E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
ghrA; glyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]
nemA; N-ethylmaleimide reductase [EC:1.-.-.-]
E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
folM; dihydromonapterin reductase / dihydrofolate reductase [EC:1.5.1.- 1.5.1.3]
E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
frmB, ESD, fghA; S-formylglutathione hydrolase [EC:3.1.2.12]
PRK, prkB; phosphoribulokinase [EC:2.7.1.19]
rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
SHPK; sedoheptulokinase [EC:2.7.1.14]
sdhD; succinate dehydrogenase membrane anchor subunit
frdD; fumarate reductase subunit D
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
tenA; thiaminase (transcriptional activator TenA) [EC:3.5.99.2]
thiK; thiamine kinase [EC:2.7.1.89]
ssuE; FMN reductase [EC:1.5.1.38]
ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]
fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.41]
epd; D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]
cinA; competence/damage-inducible protein CinA
E3.1.3.6; 3'-nucleotidase [EC:3.1.3.6]

yjjG; 5'-nucleotidase [EC:3.1.3.5]
 bioH; pimeloyl-[acyl-carrier protein] methyl ester esterase [EC:3.1.1.85]
 bisC; biotin/methionine sulfoxide reductase [EC:1.-.-.-]
 folM; dihydromonapterin reductase / dihydrofolate reductase [EC:1.5.1.- 1.5.1.3]
 CPOX, hemF; coproporphyrinogen III oxidase [EC:1.3.3.3]
 HMOX, hmuO, ho; heme oxygenase [EC:1.14.99.3]
 hemB, ALAD; porphobilinogen synthase [EC:4.2.1.24]
 hemD, UROS; uroporphyrinogen-III synthase [EC:4.2.1.75]
 hemC, HMBS; hydroxymethylbilane synthase [EC:2.5.1.61]
 cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]
 hemN, hemZ; oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]
 cobI-cbiL; precorrin-2/cobalt-factor-2 C20-methyltransferase [EC:2.1.1.130 2.1.1.151]
 fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.41]
 cobA-hemD; uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75]
 E1.17.1.2, lytB, ispH; 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.17.1.2]
 idsA; geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.29]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 crtISO, crtH; polycopene isomerase [EC:5.2.1.13]
 nirB; nitrite reductase (NADH) large subunit [EC:1.7.1.15]
 nirD; nitrite reductase (NADH) small subunit [EC:1.7.1.15]
 nasA; assimilatory nitrate reductase catalytic subunit [EC:1.7.99.4]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 katG; catalase-peroxidase [EC:1.11.1.21]
 gatC, GATC; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C [EC:6.3.5.6 6.3.5.7]
 poxA; lysyl-tRNA synthetase, class II [EC:6.1.1.6]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]
 E1.2.1.5; aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 tesB; acyl-CoA thioesterase II [EC:3.1.2.-]
 yciA; acyl-CoA thioesterase YciA [EC:3.1.2.-]
 entB, dhbB, vibB, mxCF; bifunctional isochorismate lyase / aryl carrier protein [EC:3.3.2.1]
 entF; enterobactin synthetase component F [EC:2.7.7.-]
 mbtI, irp9, ybtS; salicylate synthetase [EC:5.4.4.2 4.2.99.21]
 PGD, gnd; 6-phosphogluconate dehydrogenase [EC:1.1.1.44]
 mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]
 aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 sdhD; succinate dehydrogenase membrane anchor subunit
 frdD; fumarate reductase subunit D
 E2.7.1.12, gntK, idnK; gluconokinase [EC:2.7.1.12]
 PRK, prkB; phosphoribulokinase [EC:2.7.1.19]
 E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
 frmB, ESD, fghA; S-formylglutathione hydrolase [EC:3.1.2.12]
 E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]
 E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]

acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 edd; phosphogluconate dehydratase [EC:4.2.1.12]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
 yihU; putative dehydrogenase [EC:1.1.-.-]
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 argHA; argininosuccinate lyase / amino-acid N-acetyltransferase [EC:4.3.2.1 2.3.1.1]
 E2.3.1.16, fadA; acetyl-CoA acyltransferase [EC:2.3.1.16]
 FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]
 fabA; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
 fadJ; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.3.1]
 fadB; 3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase
 accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
 fadE; acyl-CoA dehydrogenase [EC:1.3.99.-]
 E4.1.3.39, mhpE; 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]
 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
 E3.5.1.47; N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 trpCF; indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomerase [EC:4.1.1.48 5.3.1.24]
 argHA; argininosuccinate lyase / amino-acid N-acetyltransferase [EC:4.3.2.1 2.3.1.1]
 E3.2.1.52, nagZ; beta-N-acetylhexosaminidase [EC:3.2.1.52]
 mrdA; penicillin-binding protein 2
 ompC; outer membrane pore protein C
 flhC; flagellar transcriptional activator FlhC
 flhD; flagellar transcriptional activator FlhD
 fliP; flagellar biosynthetic protein FliP
 fliR-flhB; flagellar biosynthetic protein FliR/FlhB
 UTP14; U3 small nucleolar RNA-associated protein 14
 EIF4A3, FAL1; ATP-dependent RNA helicase [EC:3.6.4.13]
 EIF4A3, FAL1; ATP-dependent RNA helicase [EC:3.6.4.13]
 hfq; host factor-I protein
 rhIB; ATP-dependent RNA helicase RhIB [EC:3.6.4.13]
 CNOT7_8, CAF1, POP2; CCR4-NOT transcription complex subunit 7/8
 ERCC2, XPD; DNA excision repair protein ERCC-2 [EC:3.6.4.12]
 DPO3P, holD; DNA polymerase III subunit psi [EC:2.7.7.7]
 DPO3T, holE; DNA polymerase III subunit theta [EC:2.7.7.7]
 EIF4A3, FAL1; ATP-dependent RNA helicase [EC:3.6.4.13]
 secD; preprotein translocase subunit SecD
 tatE; sec-independent protein translocase protein TatE
 secM; secretion monitor
 alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]
 MPG; DNA-3-methyladenine glycosylase [EC:3.2.2.21]
 nei; endonuclease VIII [EC:3.2.2.- 4.2.99.18]
 ERCC2, XPD; DNA excision repair protein ERCC-2 [EC:3.6.4.12]

DPO3P, holD; DNA polymerase III subunit psi [EC:2.7.7.7]
DPO3T, holE; DNA polymerase III subunit theta [EC:2.7.7.7]
exoX; exodeoxyribonuclease X [EC:3.1.11.-]
dnaT; DNA replication protein DnaT
DPO3P, holD; DNA polymerase III subunit psi [EC:2.7.7.7]
DPO3T, holE; DNA polymerase III subunit theta [EC:2.7.7.7]
priC; primosomal replication protein N"
ku; DNA end-binding protein Ku
ORC1; origin recognition complex subunit 1
ORC1; origin recognition complex subunit 1
ORC1; origin recognition complex subunit 1
tusD, dsrE; tRNA 2-thiouridine synthesizing protein D [EC:2.8.1.-]
LGMN; legumain [EC:3.4.22.34]
GYS; glycogen(starch) synthase [EC:2.4.1.11]
GYS; glycogen(starch) synthase [EC:2.4.1.11]
PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]
LMO7, FBXO20; F-box protein 20
LGMN; legumain [EC:3.4.22.34]
E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
GYS; glycogen(starch) synthase [EC:2.4.1.11]
GSR, gor; glutathione reductase (NADPH) [EC:1.8.1.7]
E1.11.1.9; glutathione peroxidase [EC:1.11.1.9]
plcC; phospholipase C [EC:3.1.4.3]
PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]
GYS; glycogen(starch) synthase [EC:2.4.1.11]
GYS; glycogen(starch) synthase [EC:2.4.1.11]
OGT; polypeptide N-acetylglucosaminyltransferase [EC:2.4.1.-]
HMOX, hmuO, ho; heme oxygenase [EC:1.14.99.3]
ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
yeeJ; adhesin/invasin
E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]
acfD; accessory colonization factor AcfD
norV; anaerobic nitric oxide reductase flavorubredoxin
norW; nitric oxide reductase FIRD-NAD(+) reductase [EC:1.18.1.-]
norR; anaerobic nitric oxide reductase transcription regulator
fimA; major type 1 subunit fimbrin (pilin)
fimD, fimC, mrkC, htrE, cssD; outer membrane usher protein
evgA, bvgA; two-component system, NarL family, response regulator EvgA
lpnE; enhanced entry protein LpnE
ptrB; oligopeptidase B [EC:3.4.21.83]
ptrB; oligopeptidase B [EC:3.4.21.83]
sdrC_D_E; serine-aspartate repeat-containing protein C/D/E
PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]
PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]
E1.2.1.5; aldehyde dehydrogenase (NAD(P)⁺) [EC:1.2.1.5]
E1.5.3.-

lldP, lctP; L-lactate permease
 cpo; non-heme chloroperoxidase [EC:1.11.1.10]
 E2.4.-.-
 E2.7.10.-; protein-tyrosine kinase [EC:2.7.10.-]
 aceK; isocitrate dehydrogenase kinase/phosphatase [EC:2.7.11.5 3.1.3.-]
 E2.7.1.-
 E2.7.7.7; DNA polymerase [EC:2.7.7.7]
 E3.1.6.6, betC; choline-sulfatase [EC:3.1.6.6]
 xni; protein Xni
 E3.1.27.3; ribonuclease T1 [EC:3.1.27.3]
 rna; ribonuclease I (enterobacter ribonuclease) [EC:3.1.27.6]
 E3.2.1.-
 E3.4.11.14; cytosol alanyl aminopeptidase [EC:3.4.11.14]
 dmpA; D-aminopeptidase [EC:3.4.11.19]
 E3.4.11.-; aminopeptidase [EC:3.4.11.-]
 iadA; beta-aspartyl-dipeptidase (metallo-type) [EC:3.4.19.-]
 ompT; ompT [EC:3.4.23.49]
 colA; microbial collagenase [EC:3.4.24.3]
 ptr; protease III [EC:3.4.24.55]
 PMPCA, MAS2; mitochondrial-processing peptidase subunit alpha [EC:3.4.24.64]
 E3.4.24.-; putative zinc metalloprotease [EC:3.4.24.-]
 yhgE; putative membrane protein
 E3.5.1.28C, cwIJ, sleB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
 E3.5.-.-
 E4.1.2.22; fructose-6-phosphate phosphoketolase [EC:4.1.2.22]
 E4.1.99.3, phrB; deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]
 E4.1.-.-
 E4.3.1.15; diaminopropionate ammonia-lyase [EC:4.3.1.15]
 csdA; cysteine sulfinatase desulfinate [EC:4.4.1.-]
 gerE; LuxR family transcriptional regulator, transcriptional regulator of spore coat protein
 lamB; maltoporin
 ABC.ZM.A; zinc/manganese transport system ATP-binding protein
 ABC.ZM.S; zinc/manganese transport system substrate-binding protein
 araE; MFS transporter, SP family, arabinose:H⁺ symporter
 NA
 betI; TetR/AcrR family transcriptional regulator, transcriptional repressor of bet genes
 ftnB; ferritin-like protein 2
 cpaC, rcpA; pilus assembly protein CpaC
 DPO2, polB; DNA polymerase II [EC:2.7.7.7]
 entD; enterobactin synthetase component D [EC:2.7.8.-]
 fdrA; FdrA protein
 fliZ; FlhZ protein
 fucP; MFS transporter, FHS family, L-fucose permease
 fucR; DeoR family transcriptional regulator, L-fucose operon activator
 gatR; DeoR family transcriptional regulator, galactitol utilization operon repressor
 glpR; DeoR family transcriptional regulator, glycerol-3-phosphate regulon repressor
 gutQ; GutQ protein
 srlR, gutR; DeoR family transcriptional regulator, glucitol operon repressor

K02475; two-component system, CitB family, response regulator
K02476; two-component system, CitB family, sensor kinase [EC:2.7.13.3]
rssB, hnr; two-component system, unclassified family, response regulator
yabN; tetrapyrrole methylase family protein / MazG family protein
hofB; protein transport protein HofB
hofC; protein transport protein HofC
ilvY; LysR family transcriptional regulator, positive regulator for ilvC
lacT; transcriptional antiterminator
manR; activator of the mannose operon, transcriptional antiterminator
glcA; glycolate permease
rraA, menG; regulator of ribonuclease activity A
mtlR1, mtlR; mannitol operon repressor
nagC; N-acetylglucosamine repressor
nifHD1, nif1; nitrogen regulatory protein PII 1
pilB; type IV pilus assembly protein PilB
ppdA; prepilin peptidase dependent protein A
ppdB; prepilin peptidase dependent protein B
ppdD; prepilin peptidase dependent protein D
sprT; SprT protein
solA; N-methyl-L-tryptophan oxidase [EC:1.5.3.-]
rffM; UDP-N-acetyl-D-mannosaminuronic acid transferase [EC:2.4.1.-]
wzyE, rffT; 4-alpha-L-fucosyltransferase [EC:2.4.1.-]
truB, PUS4, TRUB1; tRNA pseudouridine55 synthase [EC:5.4.99.25]
wcaH; colanic acid biosynthesis protein WcaH [EC:3.6.1.-]
rumB; 23S rRNA (uracil747-C5)-methyltransferase [EC:2.1.1.189]
yfiF, trmG; RNA methyltransferase, TrmH family [EC:2.1.1.-]
rlmB; 23S rRNA (guanosine2251-2'-O)-methyltransferase [EC:2.1.1.185]
nanT; MFS transporter, SHS family, sialic acid transporter
MFS.SET; MFS transporter, SET family, sugar efflux transporter
TC.AAT; amino acid transporter, AAT family
TC.APA; basic amino acid/polyamine antiporter, APA family
tehA; tellurite resistance protein
nhaB; Na⁺:H⁺ antiporter, NhaB family
yahN; amino acid exporter
fruR1, fruR; LacI family transcriptional regulator, fructose operon transcriptional repressor
nepl; MFS transporter, DHA1 family, purine ribonucleoside efflux pump
aaeB; p-hydroxybenzoic acid efflux pump subunit AaeB
ulaR; DeoR family transcriptional regulator, ulaG and ulaABCDEF operon transcriptional repressor
mtlR2, mtlR; mannitol operon transcriptional antiterminator
treR1, treR; LacI family transcriptional regulator, trehalose operon repressor
yydK; GntR family transcriptional regulator, transcriptional regulator of bglA
zipA; cell division protein ZipA
perM; putative permease
rdgC; recombination associated protein RdgC
gcvA; LysR family transcriptional regulator, glycine cleavage system transcriptional activator
metR; LysR family transcriptional regulator, regulator for metE and metH
ftsN; cell division protein FtsN
rseA; sigma-E factor negative regulatory protein RseA

rseB; sigma-E factor negative regulatory protein RseB
proQ; ProP effector
mukB; chromosome partition protein MukB
mukF; chromosome partition protein MukF
moaB; molybdenum cofactor biosynthesis protein B
seqA; negative modulator of initiation of replication
icc; Icc protein
rep; ATP-dependent DNA helicase Rep [EC:3.6.4.12]
trxC; thioredoxin 2 [EC:1.8.1.8]
grxC, GLRX, GLRX2; glutaredoxin 3
rnt; ribonuclease T [EC:3.1.13.-]
ubiB, aarF; ubiquinone biosynthesis protein
yigP; hypothetical protein
K03710; GntR family transcriptional regulator
splB; spore photoproduct lyase [EC:4.1.99.14]
asnC; Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA
trpR; TrpR family transcriptional regulator, trp operon repressor
tyrR; transcriptional regulator of aroF, aroG, tyrA and aromatic amino acid transport
xerC; integrase/recombinase XerC
hns; DNA-binding protein H-NS
smg; Smg protein
moeA; molybdopterin molybdotransferase [EC:2.10.1.1]
adiY; AraC family transcriptional regulator, transcriptional activator of adiA
kgtP; MFS transporter, MHS family, alpha-ketoglutarate permease
metJ; transcriptional repressor of met regulon (beta-ribbon, MetJ family)
slpA; FKBP-type peptidyl-prolyl cis-trans isomerase SlpA [EC:5.2.1.8]
cphA; cyanophycin synthetase [EC:6.3.2.29 6.3.2.30]
mukE; chromosome partition protein Muke
ampE; AmpE protein
pqiA; paraquat-inducible protein A
wcaB; putative colanic acid biosynthesis acetyltransferase WcaB [EC:2.3.1.-]
tyrP; tyrosine-specific transport protein
mtr; tryptophan-specific transport protein
tnaB; low affinity tryptophan permease
sdaC; serine transporter
tdcC; threonine transporter
fldB; flavodoxin II
fixX; ferredoxin like protein
alkB; alkylated DNA repair protein (DNA oxidative demethylase) [EC:1.14.11.33]
estA; putative tributyrin esterase [EC:3.1.1.-]
pspB; phage shock protein B
pspE; phage shock protein E
pspF; psp operon transcriptional activator
dedA; membrane-associated protein
nrfB; cytochrome c-type protein NrfB
nrfE; cytochrome c-type biogenesis protein NrfE
nrfG; formate-dependent nitrite reductase complex subunit NrfG
eutK; ethanolamine utilization protein EutK

eutN; ethanolamine utilization protein EutN
eutS; ethanolamine utilization protein EutS
eutR; AraC family transcriptional regulator, ethanolamine operon transcriptional activator
osmY; hyperosmotically inducible periplasmic protein
pflX; putative pyruvate formate lyase activating enzyme [EC:1.97.1.4]
lonB; Lon-like ATP-dependent protease [EC:3.4.21.-]
ibpA; molecular chaperone IbpA
ibpB; molecular chaperone IbpB
trmFO, gid; methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase [EC:2.1.1.74]
csgB; minor curlin subunit
csgC; curli production protein
csgE; curli production assembly/transport component CsgE
csgF; curli production assembly/transport component CsgF
hhoB, degS; serine protease DegS [EC:3.4.21.-]
sufI; suppressor of ftsI
feoB; ferrous iron transport protein B
lonH; Lon-like ATP-dependent protease [EC:3.4.21.-]
sohB; serine protease SohB [EC:3.4.21.-]
ydgD; protease YdgD [EC:3.4.21.-]
HCN1; hyperpolarization activated cyclic nucleotide-gated potassium channel 1
caiT; L-carnitine/gamma-butyrobetaine antiporter
cggR; central glycolytic genes regulator
K05346, deoR; deoxyribonucleoside regulator
irp4, ybtT; yersiniabactin synthetase, thioesterase component
tsx; nucleoside-specific channel-forming protein
dusB; tRNA-dihydrouridine synthase B [EC:1.-.-.-]
dusC; tRNA-dihydrouridine synthase C [EC:1.-.-.-]
srmB; ATP-dependent RNA helicase SrmB [EC:2.7.7.-]
marC; multiple antibiotic resistance protein
iciA; LysR family transcriptional regulator, chromosome initiation inhibitor
seaA; hypothetical protein
malM; maltose operon periplasmic protein
ABC.VB1X.S; putative thiamine transport system substrate-binding protein
ABC.VB1X.P; putative thiamine transport system permease protein
ABC.VB1X.A; putative thiamine transport system ATP-binding protein
benE; benzoate membrane transport protein
wzzB; chain length determinant protein (polysaccharide antigen chain regulator)
wzzE; lipopolysaccharide biosynthesis protein WzzE
leuO; LysR family transcriptional regulator, transcriptional activator for leuABCD operon
ybaO; Lrp/AsnC family transcriptional regulator
kefA, bspA, aefA; potassium efflux system protein
nlpI; lipoprotein NlpI
rob; right origin-binding protein
hha; haemolysin expression modulating protein
dhaR; transcriptional activator for dhaKLM operon
dhaM; PTS hybrid protein
E1.11.1.1; NADH peroxidase [EC:1.11.1.1]
E3.1.21.7, nfi; deoxyribonuclease V [EC:3.1.21.7]

cho; excinuclease Cho [EC:3.1.25.-]
pepE; dipeptidase E [EC:3.4.13.21]
cpxP; periplasmic protein CpxP
ybdK; carboxylate-amine ligase [EC:6.3.-.-]
slyA; MarR family transcriptional regulator, transcriptional regulator for hemolysin
pqqB; pyrroloquinoline quinone biosynthesis protein B
tsgA; MFS transporter, TsgA protein
uspB; universal stress protein B
gntR; LacI family transcriptional regulator, gluconate utilization system Gnt-I transcriptional repressor
uspA; universal stress protein A
gntT; Gnt-I system high-affinity gluconate transporter
gntU; Gnt-I system low-affinity gluconate transporter
rluE; 23S rRNA pseudouridine²⁴⁵⁷ synthase [EC:5.4.99.20]
nlpD; lipoprotein NlpD
cutC; copper homeostasis protein
mioC; MioC protein
focA; formate transporter
csgG; curli production assembly/transport component CsgG
smtA; S-adenosylmethionine-dependent methyltransferase
dlkB; 2,5-diketo-D-gluconate reductase B [EC:1.1.1.346]
gerKA; spore germination protein KA
gerM; germination protein M
yfkQ; spore germination protein
yndE; spore germination protein
cotE; spore coat protein E
spolIQ; stage II sporulation protein Q
spolVFA; stage IV sporulation protein FA
spolVFB; stage IV sporulation protein FB [EC:3.4.24.-]
spoVR; stage V sporulation protein R
sspl; small acid-soluble spore protein I (minor)
yabG; spore coat assembly protein
flbT; flagellar protein FlbT
flaF; flagellar protein FlaF
grcA; autonomous glycyl radical cofactor
K06887
ndpA; nucleoid-associated protein
UMF1; MFS transporter, UMF1 family
K06916
K06918
DPH6; diphthine-ammonia ligase [EC:6.3.1.14]
tmcA; tRNA(Met) cytidine acetyltransferase [EC:2.3.1.193]
rlmM; 23S rRNA (cytidine^{2498-2'}-O)-methyltransferase [EC:2.1.1.186]
K06999; phospholipase/carboxylesterase
K07001; NTE family protein
K07028
K07034
K07038; inner membrane protein
K07084

K07124
K07126
K07136
K07137
K07140
yedY; sulfoxide reductase catalytic subunit YedY [EC:1.8.-.-]
hflD; high frequency lysogenization protein
pcoC
fecR; transmembrane sensor
K07169; FHA domain-containing protein
phoH2; PhoH-like ATPase
efeO; iron uptake system component EfeO
hmuS; putative heme transport protein
yqjH; ferric-chelate reductase (NADPH) [EC:1.16.1.9]
chaC; cation transport protein ChaC
TC.ZIP, zupT, ZRT3, ZIP2; zinc transporter, ZIP family
pcoD; putative copper resistance protein D
mepA; penicillin-insensitive murein endopeptidase [EC:3.4.24.-]
kpsS, lipB; capsular polysaccharide export protein
kpsC, lipA; capsular polysaccharide export protein
ytfB; hypothetical protein
K07270; glycosyl transferase, family 25
ytfM; outer membrane protein
yfaL; autotransporter family porin
ydiY; putative salt-induced outer membrane protein
slp; outer membrane lipoprotein
yajG; uncharacterized lipoprotein
ynfG; Tat-targeted selenate reductase subunit YnfG
ynfH; Tat-targeted selenate reductase subunit YnfH
pphB; serine/threonine protein phosphatase 2 [EC:3.1.3.16]
K07318; adenine-specific DNA-methyltransferase [EC:2.1.1.72]
higA; proteic killer suppression protein
bmpA, bmpB, tmpC; basic membrane protein A and related proteins
fimC; fimbrial chaperone protein
fimG; minor fimbrial subunit
fimH; minor fimbrial subunit
fimB; type 1 fimbriae regulatory protein FimB
fimE; type 1 fimbriae regulatory protein FimE
nfuA; Fe/S biogenesis protein NfuA
xdhC; xanthine dehydrogenase accessory factor
TRM61, GCD14; tRNA (adenine57-N1/adenine58-N1)-methyltransferase [EC:2.1.1.219 2.1.1.220]
yrdD; putative DNA topoisomerase
insB; insertion element IS1 protein InsB
K07489; transposase
K07506; AraC family transcriptional regulator
mgtC; putative Mg²⁺ transporter-C (MgtC) family protein
tsaC, rimN, SUA5; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]
GSP13; general stress protein 13

tdcA; LysR family transcriptional regulator, tdc operon transcriptional activator
ydcD; CopG family transcriptional regulator
K07742; hypothetical protein
torY; trimethylamine-N-oxide reductase (cytochrome c), cytochrome c-type subunit TorY
galP; MFS transporter, SP family, galactose:H⁺ symporter
blt, norA; MFS transporter, DHA1 family, multidrug resistance protein
emrD; MFS transporter, DHA1 family, 2-module integral membrane pump EmrD
cmr, mdfA; MFS transporter, DHA1 family, multidrug/chloramphenicol efflux transport protein
mdtH; MFS transporter, DHA1 family, multidrug resistance protein
mdtL; MFS transporter, DHA1 family, multidrug resistance protein
shiA; MFS transporter, MHS family, shikimate and dehydroshikimate transport protein
dgoT; MFS transporter, ACS family, D-galactonate transporter
UMF2; MFS transporter, UMF2 family, putative MFS family transporter protein
entS; MFS transporter, ENTs family, enterobactin (siderophore) exporter
lplT; MFS transporter, LPLT family, lysophospholipid transporter
eco; ecotin
mltE; membrane-bound lytic murein transglycosylase E [EC:3.2.1.-]
rsmD; 16S rRNA (guanine966-N2)-methyltransferase [EC:2.1.1.171]
ybdH; uncharacterized oxidoreductase [EC:1.1.-.-]
lsrF; putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]
ypdF; aminopeptidase [EC:3.4.11.-]
NA
NA
NA
NA
cloSI; clostripain [EC:3.4.22.8]
pepF, pepB; oligoendopeptidase F [EC:3.4.24.-]
yfbR; 5'-nucleotidase [EC:3.1.3.5]
rcnA; nickel/cobalt exporter
yneE; putative membrane protein
ydiU; hypothetical protein
rutG; putative pyrimidine permease RutG
K09116; hypothetical protein
K09155; hypothetical protein
K09159; hypothetical protein
K09161; hypothetical protein
aidB; putative acyl-CoA dehydrogenase
ina; immune inhibitor A [EC:3.4.24.-]
iap; alkaline phosphatase isozyme conversion protein [EC:3.4.11.-]
pucR; purine catabolism regulatory protein
rimP; ribosome maturation factor RimP
K09781; hypothetical protein
K09802; hypothetical protein
zur; Fur family transcriptional regulator, zinc uptake regulator
K09891; hypothetical protein
K09892; hypothetical protein
K09893; hypothetical protein
K09894; hypothetical protein

K09895; hypothetical protein
K09896; hypothetical protein
K09897; hypothetical protein
K09899; hypothetical protein
K09900; hypothetical protein
K09901; hypothetical protein
K09902; hypothetical protein
K09906; hypothetical protein
K09907; hypothetical protein
K09908; hypothetical protein
K09910; hypothetical protein
K09913; hypothetical protein
K09914; putative lipoprotein
K09915; hypothetical protein
K09921; hypothetical protein
K09923; hypothetical protein
K09933; hypothetical protein
K09934; hypothetical protein
cas2; CRISPR-associated protein Cas2
K09952; hypothetical protein
K09962; hypothetical protein
K09979; hypothetical protein
K09982; hypothetical protein
K09985; hypothetical protein
K09992; hypothetical protein
bglH; carbohydrate-specific outer membrane porin
ACTF; actin, other eukaryote
strA; streptomycin 3"-kinase [EC:2.7.1.87]
tus, tau; DNA replication terminus site-binding protein
POLRMT, RPO41; DNA-directed RNA polymerase, mitochondrial [EC:2.7.7.6]
allP; allantoin permease
cpb2; beta2-toxin
K11059, entA; probable enterotoxin A
K11060, entB; probable enterotoxin B
gltP, gltT; proton glutamate symport protein
ttdT; L-tartrate/succinate antiporter
hlyE, clyA, sheA; hemolysin E
PTS-Fru2-EIIA; PTS system, fructose-specific IIA-like component [EC:2.7.1.69]
rlmG; 23S rRNA (guanine1835-N2)-methyltransferase [EC:2.1.1.174]
glcC; GntR family transcriptional regulator, glc operon transcriptional activator
CENPE; centromeric protein E
nupC; nucleoside transport protein
pheP; phenylalanine-specific permease
aroP; aromatic amino acid transport protein AroP
gabP; GABA permease
proY; proline-specific permease ProY
cycA; D-serine/D-alanine/glycine transporter
ansP; L-asparagine permease

nfrA; bacteriophage N4 adsorption protein A
nfrB; bacteriophage N4 adsorption protein B
tqsA; AI-2 transport protein TqsA
kefC; glutathione-regulated potassium-efflux system ancillary protein KefC
kefF; glutathione-regulated potassium-efflux system ancillary protein KefF
kefB; glutathione-regulated potassium-efflux system protein KefB
kefG; glutathione-regulated potassium-efflux system ancillary protein KefG
frsA; esterase FrsA [EC:3.1.-.-]
impJ, vasE; type VI secretion system protein ImpJ
impl, vasC; type VI secretion system protein Impl
impH, vasB; type VI secretion system protein ImpH
impG, vasA; type VI secretion system protein ImpG
impC; type VI secretion system protein ImpC
impB; type VI secretion system protein ImpB
K11905; type VI secretion system protein
vasI; type VI secretion system protein VasI
vasJ; type VI secretion system protein VasJ
vasL; type VI secretion system protein VasL
mngR, farR; GntR family transcriptional regulator, mannosyl-D-glycerate transport/metabolism system repressor
cueR; MerR family transcriptional regulator, copper efflux regulator
sgrR; SgrR family transcriptional regulator
phoE; outer membrane pore protein E
torT; periplasmic protein TorT
pgaB; biofilm PGA synthesis lipoprotein PgaB [EC:3.-.-]
uspG; universal stress protein G
hcr; NADH oxidoreductase Hcr [EC:1.-.-]
pgaA; biofilm PGA synthesis protein PgaA
cof; HMP-PP phosphatase [EC:3.6.1.-]
mdoC; glucans biosynthesis protein C [EC:2.1.-.-]
K12055, parA; chromosome partitioning related protein ParA
traG; conjugal transfer mating pair stabilization protein TraG
traF; conjugal transfer pilus assembly protein TraF
traH; conjugative transfer pilus assembly protein TraH
ebgR; LacI family transcriptional regulator, ebg operon repressor
msyB; acidic protein MsyB
bssS; biofilm regulator BssS
NA
trbB; TrbB protein
cybB; cytochrome b561
SRP43, CAO; signal recognition particle 43 kDa protein
hofM; pilus assembly protein HofM
hofN; pilus assembly protein HofN
garP; MFS transporter, ACS family, probable galactarate transporter
tesC; thioesterase III [EC:3.1.2.-]
bigA; putative surface-exposed virulence protein
lapC; membrane fusion protein LapC
NA
flu; antigen 43

abgT; aminobenzoyl-glutamate transport protein
ygeR; lipoprotein YgeR
nudK; GDP-mannose pyrophosphatase NudK [EC:3.6.1.-]
ctpC; cation-transporting P-type ATPase C [EC:3.6.3.-]
yjbB; uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.-]
diaA; DnaA initiator-associating protein
lpxP; palmitoleoyl transferase [EC:2.3.1.-]
rgpB; rhamnosyltransferase [EC:2.4.1.-]
suaA; cell division inhibitor Sula
E2.7.7.65; diguanylate cyclase [EC:2.7.7.65]
dos; c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]
yahA; c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]
fhuF; ferric iron reductase protein FhuF
wprA; cell wall-associated protease [EC:3.4.21.-]
isp; major intracellular serine protease [EC:3.4.21.-]
uvrE, UVE1; UV DNA damage endonuclease [EC:3.-.-.-]
cphB; cyanophycinase [EC:3.4.15.6]
wcaD; putative colanic acid polymerase
dsdX; D-serine transporter
soxS; AraC family transcriptional regulator, transcriptional activator of the superoxide response regulon
cysB; LysR family transcriptional regulator, cys regulon transcriptional activator
cbl; LysR family transcriptional regulator, cys regulon transcriptional activator
uxuR; GntR family transcriptional regulator, uxuAB operon transcriptional repressor
hspR; MerR family transcriptional regulator, heat shock protein HspR
K13671; alpha-1,2-mannosyltransferase [EC:2.4.1.-]
wcaE; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]
wcaC; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]
nlpC; probable lipoprotein NlpC
gudX; glucarate dehydratase-related protein
rbbA; ribosome-dependent ATPase
yahK; uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.-]
gmr; cyclic di-GMP phosphodiesterase Gmr [EC:3.1.4.52]
uspE; universal stress protein E
puuR; HTH-type transcriptional regulator, repressor for puuD
ompN; outer membrane protein N
uspC; universal stress protein C
ybdL; methionine aminotransferase [EC:2.6.1.-]
lldR; GntR family transcriptional regulator, L-lactate dehydrogenase operon regulator
panF; sodium/pantothenate symporter
actP; cation/acetate symporter
sgcE; protein sgcE [EC:5.1.3.-]
cueO; blue copper oxidase
K14645; serine protease [EC:3.4.21.-]
amhX; amidohydrolase [EC:3.5.1.-]
rzpD; prophage endopeptidase [EC:3.4.-.-]
yibL; ribosome-associated protein
UTP3, SAS10; U3 small nucleolar RNA-associated protein 3
MED21, SRB7; mediator of RNA polymerase II transcription subunit 21

CTR9; RNA polymerase-associated protein CTR9
cmoB; tRNA (mo5U34)-methyltransferase [EC:2.1.1.-]
eamA; O-acetylserine/cysteine efflux transporter
cas1; CRISP-associated protein Cas1
trmJ; tRNA (cytidine32/uridine32-2'-O)-methyltransferase [EC:2.1.1.200]
yfiC, trmX; tRNA1Val (adenine37-N6)-methyltransferase [EC:2.1.1.223]
cybC; soluble cytochrome b562
ecpD; chaperone protein EcpD
mdtO; multidrug resistance protein MdtO
aaeA; p-hydroxybenzoic acid efflux pump subunit AaeA
mdtN; multidrug resistance protein MdtN
mdtP; multidrug resistance outer membrane protein MdtP
fyuA; pesticin/yersiniabactin receptor
syd; SecY interacting protein Syd
csiR; GntR family transcriptional regulator, carbon starvation induced regulator
csiD; protein CsiD
hycB; formate hydrogenlyase subunit 2
hycC; formate hydrogenlyase subunit 3
hycD; formate hydrogenlyase subunit 4
hycE; formate hydrogenlyase subunit 5
hycF; formate hydrogenlyase subunit 6
hycA; formate hydrogenlyase regulatory protein HycA
fhIA; formate hydrogenlyase transcriptional activator
xynC; glucuronoarabinoxylan endo-1,4-beta-xylanase [EC:3.2.1.136]
emrR, mprA; MarR family transcriptional regulator, negative regulator of the multidrug operon emrRAB
nmpC, ompD; outer membrane porin protein LC
scrY; sucrose porin
fiu; catecholate siderophore receptor
mall; LacI family transcriptional regulator, maltose regulon regulatory protein
uidR; TetR/AcrR family transcriptional regulator, repressor for uid operon
uidC, gusC; putative glucuronide porin
yjeH; amino acid efflux transporter
erfK; L,D-transpeptidase
efeB; deferriochelatase/peroxidase EfeB [EC:1.11.1.-]
gntP; high-affinity gluconate transporter
pit; low-affinity inorganic phosphate transporter
psuT; putative pseudouridine transporter
yeiL; CRP/FNR family transcriptional regulator, putative post-exponential-phase nitrogen-starvation regulator
xanQ; xanthine permease XanQ
exoZ; exopolysaccharide production protein ExoZ
etk-wzc; tyrosine-protein kinase Etk/Wzc [EC:2.7.10.-]
wzxE; O-antigen flippase
wzxC; lipopolysaccharide exporter
K16697, tuaC; teichuronic acid biosynthesis glycosyltransferase TuaC [EC:2.4.-.-]
wcaL, amsK; colanic acid/amylovoran biosynthesis glycosyltransferase [EC:2.4.-.-]
rffC, wecD; dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase [EC:2.3.1.210]
wcaM; colanic acid biosynthesis protein WcaM

Bacteria

Akkermansia muciniphila ATCC BAA-835
Clostridium symbiosum WAL-14163
Clostridium hiranonis DSM 13275
Clostridium sp. 7_2_43FAA
Faecalibacterium cf. prausnitzii KLE1255
Faecalibacterium prausnitzii SL3/3
Faecalibacterium prausnitzii A2-165
Collinsella stercoris DSM 13279
Collinsella intestinalis DSM 13280
Lachnoanaerobaculum saburreum DSM 3986
Prevotella oris C735
Prevotella melaninogenica D18
Porphyromonas uenonis 60-3
Dyadobacter fermentans DSM 18053
Alistipes shahii WAL 8301
Parabacteroides sp. 20_3
Ruminococcus bromii L2-63
Alistipes sp. HGB5
Clostridium perfringens E str. JGS1987
[Clostridium] sticklandii
Clostridium beijerinckii NCIMB 8052
Clostridium ljungdahlii DSM 13528
Peptostreptococcus stomatis DSM 17678
Alkaliphilus metalliredigens QYMF
Clostridium butyricum E4 str. BoNT E BL5262
Verrucomicrobium spinosum DSM 4136
Pedosphaera parvula Ellin514
Verrucomicrobiae bacterium DG1235
Bilophila wadsworthia 3_1_6
Bacteroides uniformis ATCC 8492
Coprobacillus sp. D7
Ahrensia sp. R2A130
Bulleidia extructa W1219
Clostridium botulinum C str. Eklund
Clostridium botulinum E1 str. 'BoNT E Beluga'
Clostridium difficile QCD-63q42
Cytophaga hutchinsonii ATCC 33406
Deinococcus proteolyticus MRP
Desulfobacterium autotrophicum HRM2
Eubacterium hallii DSM 3353
Lactobacillus acidophilus ATCC 4796
Leadbetterella byssophila DSM 17132
Mahella australiensis 50-1 BON
marine actinobacterium PHSC20C1
Nitratifractor salsuginis DSM 16511

[illegible]

Parvibaculum lavamentivorans DS-1	-	-	-
Peptostreptococcus anaerobius 653-L	-	-	-
Pseudoalteromonas tunicata D2	-	-	-
Runella slithyformis DSM 19594	-	-	-
Sphingobacterium sp. 21	-	-	-
Subdoligranulum variabile DSM 15176	-	-	-
Sutterella wadsworthensis 3_1_45B	-	-	-
Lachnospiraceae bacterium 3_1_57FAA_CT1	-	-	-
Bacteroides sp. 2_2_4	-	-	-
Eggerthella lenta DSM 2243	-	-	-
Prevotella copri DSM 18205	-	-	-
Bacillus cereus SJ1	-	-	-
Bacillus weihenstephanensis KBAB4	-	-	-
Veillonella atypica ACS-134-V-Col7a	-	-	-
Fusobacterium nucleatum subsp. animalis 7_1	-	-	-
Bacillus cytotoxicus NVH 391-98	-	-	-
Sporosarcina newyorkensis 2681	-	-	-
Candidatus Regiella insecticola LSR1	-	-	-
Prevotella bryantii B14	-	-	-
Prevotella oulorum F0390	-	-	-
Fusobacterium nucleatum subsp. vincentii 4_1_13	-	-	-

[illegible]

[illegible]

[illegible]

-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	-	-	-	-	-
-	-	953559.753	1.462	0.000	-	-
-	-	711778.165	1.015	0.019	-	-
-	-	25666.191	1.959	0.049	-	-
-	-	15170.719	2.158	0.029	-	-
-	-	4849.745	-2.969	0.000	-	-
-	-	912.873	-3.392	0.000	-	-
-	-	419.109	-1.668	0.045	-	-
-	-	256.664	2.500	0.033	-	-
-	-	138.456	-3.620	0.000	-	-
-	-	124.307	-2.676	0.012	-	-
-	-	109.713	-2.502	0.012	-	-
-	-	108.953	2.767	0.026	-	-
-	-	52.365	2.724	0.033	-	-
-	-	29.060	3.050	0.019	-	-

[illegible]

Supplementary Table 6

Sheet1

Sheet2

Sheet3

List of KOs significantly enriched or depleted in the metagenome and metatranscriptome from the samples from donors 13 and 49 and corresponding KEGG pathway annotations.

List of KOs in both donors.

KEGG pathway annotations for all KOs derived from donor 13.

KEGG pathway annotations for all KOs derived from donor 49.

KO	Annotation	baseMean
K00001	E1.1.1.1, adh; alcohol dehydrogenase [EC:1.1.1.1]	NA
K00012	UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	11461.242938
K00013	hisD; histidinol dehydrogenase [EC:1.1.1.23]	8121.642553
K00019	E1.1.1.30, bdh; 3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]	NA
K00024	mdh; malate dehydrogenase [EC:1.1.1.37]	23541.440302
K00029	E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(N	10892.496112
K00052	leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]	9405.2529023
K00053	ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]	20208.50401
K00057	gpsA; glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]	NA
K00060	tdh; threonine 3-dehydrogenase [EC:1.1.1.103]	NA
K00065	kduD; 2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]	864.22713165
K00074	paaH, hbd, fadB, mmgB; 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.115]	10088.362787
K00077	panE, apbA; 2-dehydropantoate 2-reductase [EC:1.1.1.169]	NA
K00088	guaB; IMP dehydrogenase [EC:1.1.1.205]	NA
K00097	pdxA; 4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]	5839.7604366
K00099	dxr; 1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]	NA
K00100	E1.1.1.-	NA
K00104	glcD; glycolate oxidase [EC:1.1.3.15]	4514.1280428
K00108	E1.1.99.1, betA, CHDH; choline dehydrogenase [EC:1.1.99.1]	10.046673347
K00117	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]	28.744807501
K00134	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	NA
K00138	aldB; aldehyde dehydrogenase [EC:1.2.1.-]	10.950800086
K00140	mmsA, iolA, ALDH6A1; malonate-semialdehyde dehydrogenase (acetylating)	NA
K00145	argC; N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]	NA
K00156	poxB; pyruvate dehydrogenase (quinone) [EC:1.2.5.1]	NA
K00161	PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.1.12]	1343.1992837
K00162	PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.1.13]	1388.5368074
K00163	aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]	91.721345668
K00164	OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	4317.7591633
K00171	porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]	NA
K00174	korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]	21459.120063
K00175	korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]	11060.903546
K00177	korG; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]	3605.0716562
K00179	iorA; indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]	9497.0799649
K00184	K00184; prokaryotic molybdopterin-containing oxidoreductase family, iron	2890.5417442
K00185	K00185; prokaryotic molybdopterin-containing oxidoreductase family, me	3071.4305914
K00194	cdhD, acsD; acetyl-CoA decarbonylase/synthase complex subunit delta [EC:1.2.1.18]	NA
K00208	fabI; enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]	7029.2400288
K00226	pyrD; dihydroorotate dehydrogenase (fumarate) [EC:1.3.98.1]	10757.509065
K00228	CPOX, hemF; coproporphyrinogen III oxidase [EC:1.3.3.3]	NA
K00239	sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]	35394.209674
K00240	sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]	13192.052749
K00241	sdhC; succinate dehydrogenase cytochrome b556 subunit	8964.1761644
K00244	frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]	4049.5453502
K00248	ACADS, bcd; butyryl-CoA dehydrogenase [EC:1.3.8.1]	9696.2144192
K00262	E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	38548.354455
K00265	gltB; glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]	NA

K00275	pdxH, PNPO; pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]	NA
K00276	AOC3, AOC2, tynA; primary-amine oxidase [EC:1.4.3.21]	NA
K00278	nadB; L-aspartate oxidase [EC:1.4.3.16]	6561.2027953
K00281	GLDC, gcvP; glycine dehydrogenase [EC:1.4.4.2]	15446.459237
K00285	dadA; D-amino-acid dehydrogenase [EC:1.4.99.1]	NA
K00290	LYS1; saccharopine dehydrogenase (NAD ⁺ , L-lysine forming) [EC:1.5.1.7]	NA
K00293	LYS9; saccharopine dehydrogenase (NADP ⁺ , L-glutamate forming) [EC:1.5.1.1]	NA
K00294	E1.2.1.88; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.2.1.88]	NA
K00297	metF, MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	NA
K00299	ssuE; FMN reductase [EC:1.5.1.38]	NA
K00313	fixC; electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]	NA
K00322	sthA, udhA; NAD(P) transhydrogenase [EC:1.6.1.1]	NA
K00324	pntA; NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]	NA
K00325	pntB; NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]	NA
K00330	nuoA; NADH-quinone oxidoreductase subunit A [EC:1.6.5.3]	NA
K00331	nuoB; NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]	1509.7244743
K00332	nuoC; NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]	560.771222
K00333	nuoD; NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]	951.91750125
K00337	nuoH; NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]	2960.9401579
K00338	nuoI; NADH-quinone oxidoreductase subunit I [EC:1.6.5.3]	NA
K00339	nuoJ; NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]	1090.1114256
K00340	nuoK; NADH-quinone oxidoreductase subunit K [EC:1.6.5.3]	NA
K00341	nuoL; NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]	5222.786168
K00342	nuoM; NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]	4085.5543807
K00343	nuoN; NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]	4281.5544898
K00346	nqrA; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.1.1.1]	11679.721802
K00347	nqrB; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit B [EC:1.1.1.1]	9872.1873632
K00348	nqrC; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit C [EC:1.1.1.1]	3972.7214372
K00349	nqrD; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit D [EC:1.1.1.1]	3833.3274298
K00350	nqrE; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit E [EC:1.1.1.1]	4654.9697869
K00351	nqrF; Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit F [EC:1.1.1.1]	10897.400517
K00359	E1.6.-.-; NADH oxidase [EC:1.6.-.-]	NA
K00376	nosZ; nitrous-oxide reductase [EC:1.7.2.4]	NA
K00380	cysJ; sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]	3691.8759191
K00382	DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]	NA
K00385	asrC; anaerobic sulfite reductase subunit C	NA
K00425	cydA; cytochrome d ubiquinol oxidase subunit I [EC:1.10.3.-]	16669.857615
K00426	cydB; cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]	8675.9116041
K00428	E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]	6216.7491081
K00441	frhB; coenzyme F420 hydrogenase subunit beta [EC:1.12.98.1]	278.2302861
K00455	hpaD, hpcB; 3,4-dihydroxyphenylacetate 2,3-dioxygenase [EC:1.13.11.15]	NA
K00520	merA; mercuric reductase [EC:1.16.1.1]	NA
K00525	E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain	23157.483819
K00526	E1.17.4.1B, nrdB, nrdF; ribonucleoside-diphosphate reductase beta chain	825.08766506
K00527	nrdD; ribonucleoside-triphosphate reductase [EC:1.17.4.2]	NA
K00529	hcaD; ferredoxin--NAD ⁺ reductase [EC:1.18.1.3]	NA
K00533	E1.12.7.2L; ferredoxin hydrogenase large subunit [EC:1.12.7.2]	NA
K00537	ARSC1, arsC; arsenate reductase [EC:1.20.4.1]	NA

K00547	mmuM; homocysteine S-methyltransferase [EC:2.1.1.10]	429.70872526
K00554	trmD; tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]	5764.4216011
K00556	trmH; tRNA (guanosine-2'-O-)-methyltransferase [EC:2.1.1.34]	363.42101855
K00558	DNMT1, dcm; DNA (cytosine-5)-methyltransferase 1 [EC:2.1.1.37]	NA
K00563	rlmA1; 23S rRNA (guanine745-N1)-methyltransferase [EC:2.1.1.187]	460.38603818
K00564	rsmC; 16S rRNA (guanine1207-N2)-methyltransferase [EC:2.1.1.172]	14.283850203
K00566	mnmA, trmU, TRMU; tRNA-specific 2-thiouridylase [EC:2.8.1.-]	NA
K00567	E2.1.1.63, MGMT, ogt; methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]	2710.5308042
K00571	E2.1.1.72; site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.72]	NA
K00602	purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP dehydrogenase [EC:2.3.1.20]	14023.558782
K00605	gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]	6763.4976775
K00606	panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]	2852.1150975
K00609	pyrB, PYR2; aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]	NA
K00611	OTC, argF, argI; ornithine carbamoyltransferase [EC:2.1.3.3]	NA
K00613	GATM; glycine amidinotransferase [EC:2.1.4.1]	NA
K00619	argA; amino-acid N-acetyltransferase [EC:2.3.1.1]	NA
K00620	argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.1]	NA
K00626	E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	11568.095092
K00627	DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.16]	2499.6164694
K00631	plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]	33.688406302
K00639	kbl, GCAT; glycine C-acetyltransferase [EC:2.3.1.29]	14933.149273
K00640	cysE; serine O-acetyltransferase [EC:2.3.1.30]	NA
K00641	metX; homoserine O-acetyltransferase [EC:2.3.1.31]	1126.4229705
K00645	fabD; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	NA
K00647	fabB; 3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]	2966.5609404
K00656	E2.3.1.54, pflD; formate C-acetyltransferase [EC:2.3.1.54]	NA
K00658	DLST, sucB; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.55]	NA
K00661	maa; maltose O-acetyltransferase [EC:2.3.1.79]	4057.5653994
K00667	FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]	NA
K00674	dapD; 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC:2.3.1.90]	582.99662061
K00684	aat; leucyl/phenylalanyl-tRNA--protein transferase [EC:2.3.2.6]	740.38195361
K00689	E2.4.1.5; dextransucrase [EC:2.4.1.5]	NA
K00691	E2.4.1.8, mapA; maltose phosphorylase [EC:2.4.1.8]	858.10360691
K00697	otsA; trehalose 6-phosphate synthase [EC:2.4.1.15]	NA
K00700	glgB; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	NA
K00737	MGAT3; beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [EC:2.4.1.22]	NA
K00748	lpxB; lipid-A-disaccharide synthase [EC:2.4.1.182]	4019.039499
K00756	E2.4.2.2, pdp; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]	598.05581014
K00758	deoA, TYMP; thymidine phosphorylase [EC:2.4.2.4]	14.48268447
K00762	pyrE; orotate phosphoribosyltransferase [EC:2.4.2.10]	NA
K00764	purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]	NA
K00765	hisG; ATP phosphoribosyltransferase [EC:2.4.2.17]	NA
K00767	nadC, QPRT; nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.8.1.18]	5745.0167016
K00782	ykgG; hypothetical protein	NA
K00788	thiE; thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]	NA
K00793	ribE, RIB5; riboflavin synthase [EC:2.5.1.9]	2617.2245893
K00794	ribH, RIB4; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]	2322.6316403
K00795	ispA; farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]	NA

K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]	NA
K00801	FDFT1; farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]	742.60774563
K00812	aspB; aspartate aminotransferase [EC:2.6.1.1]	11514.493844
K00813	aspC; aspartate aminotransferase [EC:2.6.1.1]	38.841074044
K00817	hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]	8440.7437802
K00819	E2.6.1.13, rocD; ornithine--oxo-acid transaminase [EC:2.6.1.13]	NA
K00831	serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]	11871.082877
K00832	tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]	3860.5419532
K00833	bioA; adenosylmethionine-8-amino-7-oxononanoate aminotransferase [EC:2.6.1.52]	5122.4509895
K00835	avtA; valine--pyruvate aminotransferase [EC:2.6.1.66]	1196.6209741
K00839	E2.6.1.-B; aminotransferase [EC:2.6.1.-]	1165.7842115
K00845	glk; glucokinase [EC:2.7.1.2]	16234.968526
K00849	galK; galactokinase [EC:2.7.1.6]	NA
K00850	pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]	NA
K00853	araB; L-ribulokinase [EC:2.7.1.16]	1029.8177812
K00855	PRK, prkB; phosphoribulokinase [EC:2.7.1.19]	NA
K00863	E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]	NA
K00873	PK, pyk; pyruvate kinase [EC:2.7.1.40]	NA
K00878	thiM; hydroxyethylthiazole kinase [EC:2.7.1.50]	NA
K00879	fucK; L-fuculokinase [EC:2.7.1.51]	NA
K00886	ppgK; polyphosphate glucokinase [EC:2.7.1.63]	NA
K00892	gsk; inosine kinase [EC:2.7.1.73]	9.9816029254
K00912	lpxK; tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]	5029.6448113
K00924	E2.7.1.-	2086.9142582
K00927	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]	NA
K00930	argB; acetylglutamate kinase [EC:2.7.2.8]	5398.8295038
K00936	E2.7.3.-	NA
K00937	ppk; polyphosphate kinase [EC:2.7.4.1]	NA
K00941	thiD; hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [EC:2.7.1.13]	NA
K00946	thiL; thiamine-monophosphate kinase [EC:2.7.4.16]	5032.5979777
K00948	PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	NA
K00954	E2.7.7.3A, coaD, kdtB; pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]	3527.4458664
K00958	sat, met3; sulfate adenylyltransferase [EC:2.7.7.4]	NA
K00962	pnp, PNPT1; polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	NA
K00963	UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	NA
K00965	galT, GALT; UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.3]	3289.1555954
K00966	GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]	1132.6187557
K00968	PCYT1; choline-phosphate cytidylyltransferase [EC:2.7.7.15]	1250.6005864
K00969	nadD; nicotinate-nucleotide adenylyltransferase [EC:2.7.7.18]	5779.3355626
K00970	pcnB; poly(A) polymerase [EC:2.7.7.19]	2967.3115472
K00971	manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]	NA
K00973	E2.7.7.24, rfbA, rffH; glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]	NA
K00975	glgC; glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]	18596.42579
K00979	kdsB; 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase) [EC:2.7.7.27]	3216.4848747
K00981	E2.7.7.41, CDS1, CDS2, cdsA; phosphatidate cytidylyltransferase [EC:2.7.7.41]	NA
K00989	rph; ribonuclease PH [EC:2.7.7.56]	1106.5973377
K00997	acpS; holo-[acyl-carrier protein] synthase [EC:2.7.8.7]	NA
K00998	pssA; CDP-diacylglycerol---serine O-phosphatidyltransferase [EC:2.7.8.8]	4566.8997679

K01006	ppdK; pyruvate,orthophosphate dikinase [EC:2.7.9.1]	NA
K01039	gctA; glutaconate CoA-transferase, subunit A [EC:2.8.3.12]	NA
K01040	gctB; glutaconate CoA-transferase, subunit B [EC:2.8.3.12]	NA
K01061	E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]	13.261677168
K01077	E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]	9270.1981381
K01079	serB, PSPH; phosphoserine phosphatase [EC:3.1.3.3]	2505.5295022
K01081	E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]	NA
K01082	E3.1.3.7, cysQ, MET22, BPNT1; 3'(2'), 5'-bisphosphate nucleotidase [EC:3.1.3.7]	2424.5602064
K01085	agp; glucose-1-phosphatase [EC:3.1.3.10]	NA
K01089	hisB; imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:3.1.3.11]	4222.9537029
K01091	E3.1.3.18, gph; phosphoglycolate phosphatase [EC:3.1.3.18]	6705.6274134
K01092	E3.1.3.25, IMPA, suhB; myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	3805.839923
K01104	E3.1.3.48; protein-tyrosine phosphatase [EC:3.1.3.48]	NA
K01134	ARSA; arylsulfatase A [EC:3.1.6.8]	1058.4625869
K01139	spoT, HDDC3; guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.6.1]	59.514132563
K01141	E3.1.11.1, sbcB; exodeoxyribonuclease I [EC:3.1.11.1]	NA
K01142	E3.1.11.2, xthA; exodeoxyribonuclease III [EC:3.1.11.2]	NA
K01146	xni; protein Xni	NA
K01151	nfo; deoxyribonuclease IV [EC:3.1.21.2]	3751.9583275
K01153	hsdR; type I restriction enzyme, R subunit [EC:3.1.21.3]	7349.8742061
K01154	hsdS; type I restriction enzyme, S subunit [EC:3.1.21.3]	NA
K01169	rna; ribonuclease I (enterobacter ribonuclease) [EC:3.1.27.6]	NA
K01173	ENDOG; endonuclease G, mitochondrial	5677.9970441
K01176	E3.2.1.1, amyA, malS; alpha-amylase [EC:3.2.1.1]	NA
K01179	E3.2.1.4; endoglucanase [EC:3.2.1.4]	NA
K01186	NEU1; sialidase-1 [EC:3.2.1.18]	NA
K01187	E3.2.1.20, malZ; alpha-glucosidase [EC:3.2.1.20]	18043.057377
K01190	lacZ; beta-galactosidase [EC:3.2.1.23]	NA
K01194	E3.2.1.28, treA, treF; alpha,alpha-trehalase [EC:3.2.1.28]	45.534075854
K01197	hya; hyaluronoglucosaminidase [EC:3.2.1.35]	NA
K01198	xynB; xylan 1,4-beta-xylosidase [EC:3.2.1.37]	NA
K01218	E3.2.1.78; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]	3255.9421809
K01220	E3.2.1.85, lacG; 6-phospho-beta-galactosidase [EC:3.2.1.85]	53.3200995
K01222	E3.2.1.86A, celF; 6-phospho-beta-glucosidase [EC:3.2.1.86]	38.933916693
K01226	treC; trehalose-6-phosphate hydrolase [EC:3.2.1.93]	990.8429765
K01246	tag; DNA-3-methyladenine glycosylase I [EC:3.2.2.20]	2377.632647
K01247	alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]	196.29577
K01251	E3.3.1.1, ahcY; adenosylhomocysteinase [EC:3.3.1.1]	6381.4394017
K01258	pepT; tripeptide aminopeptidase [EC:3.4.11.4]	8101.7615474
K01259	pip; proline iminopeptidase [EC:3.4.11.5]	280.66476982
K01269	E3.4.11.-; aminopeptidase [EC:3.4.11.-]	NA
K01277	E3.4.14.4, DPP3; dipeptidyl-peptidase III [EC:3.4.14.4]	7841.1788743
K01278	DPP4; dipeptidyl-peptidase 4 [EC:3.4.14.5]	7919.3428094
K01284	dcp; peptidyl-dipeptidase Dcp [EC:3.4.15.5]	13238.723556
K01299	E3.4.17.19; carboxypeptidase Taq [EC:3.4.17.19]	1001.1532719
K01322	E3.4.21.26, PREP; prolyl oligopeptidase [EC:3.4.21.26]	4520.8490463
K01338	lon; ATP-dependent Lon protease [EC:3.4.21.53]	20281.866952
K01354	ptrB; oligopeptidase B [EC:3.4.21.83]	17.138354145

K01362	E3.4.21.-	NA
K01414	prlC; oligopeptidase A [EC:3.4.24.70]	2952.5028747
K01417	E3.4.24.-; putative zinc metalloprotease [EC:3.4.24.-]	312.49252917
K01421	yhgE; putative membrane protein	NA
K01434	E3.5.1.11; penicillin amidase [EC:3.5.1.11]	NA
K01438	argE; acetylornithine deacetylase [EC:3.5.1.16]	1230.432292
K01443	E3.5.1.25, nagA, AMDHD2; N-acetylglucosamine-6-phosphate deacetylase	NA
K01447	E3.5.1.28A, cwIA, xlyA, xlyB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28A]	1552.4626232
K01460	gsp; glutathionylspermidine amidase/synthetase [EC:3.5.1.78 6.3.1.8]	30.501284133
K01462	PDF, def; peptide deformylase [EC:3.5.1.88]	3550.3628679
K01465	URA4, pyrC; dihydroorotase [EC:3.5.2.3]	9018.889222
K01467	ampC; beta-lactamase class C [EC:3.5.2.6]	4604.9981101
K01468	hutI, AMDHD1; imidazolonepropionase [EC:3.5.2.7]	4810.4969814
K01473	hyuA; N-methylhydantoinase A [EC:3.5.2.14]	91.26051159
K01474	hyuB; N-methylhydantoinase B [EC:3.5.2.14]	63.914260667
K01476	E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]	1716.9870273
K01478	E3.5.3.6, arcA; arginine deiminase [EC:3.5.3.6]	471.64229997
K01479	hutG; formiminoglutamase [EC:3.5.3.8]	NA
K01480	E3.5.3.11, speB; agmatinase [EC:3.5.3.11]	2459.2509546
K01483	allA; ureidoglycolate hydrolase [EC:3.5.3.19]	NA
K01493	comEB; dCMP deaminase [EC:3.5.4.12]	NA
K01496	hisI; phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]	977.77740372
K01497	ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]	11.328546387
K01515	nudF; ADP-ribose pyrophosphatase [EC:3.6.1.13]	NA
K01524	ppx-gppA; exopolyphosphatase / guanosine-5'-triphosphate,3'-diphosphate	NA
K01533	copB; Cu ²⁺ -exporting ATPase [EC:3.6.3.4]	NA
K01537	E3.6.3.8; Ca ²⁺ -transporting ATPase [EC:3.6.3.8]	15176.688603
K01546	kdpA; K ⁺ -transporting ATPase ATPase A chain [EC:3.6.3.12]	5621.0317147
K01547	kdpB; K ⁺ -transporting ATPase ATPase B chain [EC:3.6.3.12]	NA
K01548	kdpC; K ⁺ -transporting ATPase ATPase C chain [EC:3.6.3.12]	NA
K01572	E4.1.1.3B, oadB; oxaloacetate decarboxylase, beta subunit [EC:4.1.1.3]	NA
K01581	E4.1.1.17, ODC1, speC, speF; ornithine decarboxylase [EC:4.1.1.17]	NA
K01582	E4.1.1.18, ldcC, cadA; lysine decarboxylase [EC:4.1.1.18]	10.370001257
K01584	E4.1.1.19A, adi; arginine decarboxylase [EC:4.1.1.19]	NA
K01585	E4.1.1.19S, speA; arginine decarboxylase [EC:4.1.1.19]	8832.988899
K01586	lysA; diaminopimelate decarboxylase [EC:4.1.1.20]	NA
K01588	purE; 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]	NA
K01589	purK; 5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	494.74391106
K01591	pyrF; orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]	NA
K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]	245.10760282
K01596	E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	10767.640664
K01598	PPCDC, coaC; phosphopantothienoylcysteine decarboxylase [EC:4.1.1.36]	NA
K01607	pcaC; 4-carboxymuconolactone decarboxylase [EC:4.1.1.44]	2773.8419047
K01609	trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]	2818.4551932
K01615	E4.1.1.70; glutaconyl-CoA decarboxylase [EC:4.1.1.70]	549.46090911
K01626	E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	NA
K01627	kdsA; 2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:3.5.1.25]	3849.2427327
K01631	dgoA; 2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]	6.6952504657

K01632	E4.1.2.22; fructose-6-phosphate phosphoketolase [EC:4.1.2.22]	NA
K01637	E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]	13.574554705
K01638	E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]	23.680292639
K01639	E4.1.3.3, nanA, NPL; N-acetylneuraminate lyase [EC:4.1.3.3]	NA
K01644	citE; citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.6 4.1.3.34]	NA
K01649	leuA; 2-isopropylmalate synthase [EC:2.3.3.13]	13872.931447
K01652	E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	NA
K01653	E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]	NA
K01654	E2.5.1.56, neuB; N-acetylneuraminate synthase [EC:2.5.1.56]	NA
K01657	trpE; anthranilate synthase component I [EC:4.1.3.27]	NA
K01658	trpG; anthranilate synthase component II [EC:4.1.3.27]	NA
K01661	menB; naphthoate synthase [EC:4.1.3.36]	2571.1472543
K01664	pabA; para-aminobenzoate synthetase component II [EC:2.6.1.85]	NA
K01665	pabB; para-aminobenzoate synthetase component I [EC:2.6.1.85]	NA
K01667	tnaA; tryptophanase [EC:4.1.99.1]	6487.5394269
K01676	E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]	11549.487102
K01678	E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]	1392.5493319
K01682	acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.24]	68.23309858
K01689	ENO, eno; enolase [EC:4.2.1.11]	31164.945524
K01693	E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]	NA
K01695	trpA; tryptophan synthase alpha chain [EC:4.2.1.20]	NA
K01696	trpB; tryptophan synthase beta chain [EC:4.2.1.20]	NA
K01698	hemB, ALAD; porphobilinogen synthase [EC:4.2.1.24]	NA
K01699	pduC; propanediol dehydratase large subunit [EC:4.2.1.28]	2525.56322
K01703	leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.29]	13117.031652
K01704	leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.29]	3211.203358
K01711	gmd, GMDS; GDPmannose 4,6-dehydratase [EC:4.2.1.47]	NA
K01716	fabA; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]	NA
K01735	aroB; 3-dehydroquinate synthase [EC:4.2.3.4]	7251.7710699
K01737	queD, ptpS, PTS; 6-pyruvoyltetrahydropterin/6-carboxytetrahydropterin synthase [EC:4.1.1.61]	NA
K01738	cysK; cysteine synthase A [EC:2.5.1.47]	NA
K01740	E2.5.1.49, metY; O-acetylhomoserine (thiol)-lyase [EC:2.5.1.49]	NA
K01744	aspA; aspartate ammonia-lyase [EC:4.3.1.1]	NA
K01752	E4.3.1.17, sdaA; L-serine dehydratase [EC:4.3.1.17]	NA
K01753	dsdA; D-serine dehydratase [EC:4.3.1.18]	NA
K01754	E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]	NA
K01755	argH, ASL; argininosuccinate lyase [EC:4.3.2.1]	NA
K01756	purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]	NA
K01766	csdA; cysteine sulfinatase desulfinate [EC:4.4.1.-]	19.007498356
K01775	alr; alanine racemase [EC:5.1.1.1]	8149.4392551
K01777	E5.1.1.4; proline racemase [EC:5.1.1.4]	2430.5403468
K01784	galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]	NA
K01785	E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]	16599.997074
K01792	E5.1.3.15; glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	572.64856324
K01799	nicE, maiA; maleate isomerase [EC:5.2.1.1]	15.813586118
K01803	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]	NA
K01809	E5.3.1.8, manA; mannose-6-phosphate isomerase [EC:5.3.1.8]	8021.9872399
K01814	hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.20]	NA

K01817	trpF; phosphoribosylanthranilate isomerase [EC:5.3.1.24]	NA
K01818	fucl; L-fucose isomerase [EC:5.3.1.25]	NA
K01839	deoB; phosphopentomutase [EC:5.4.2.7]	3120.9220149
K01847	MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]	41821.019278
K01866	YARS, tyrS; tyrosyl-tRNA synthetase [EC:6.1.1.1]	11853.83906
K01868	TARS, thrS; threonyl-tRNA synthetase [EC:6.1.1.3]	25493.614055
K01870	IARS, ileS; isoleucyl-tRNA synthetase [EC:6.1.1.5]	NA
K01872	AARS, alaS; alanyl-tRNA synthetase [EC:6.1.1.7]	NA
K01873	VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]	NA
K01874	MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]	17347.962255
K01875	SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]	NA
K01881	PARS, proS; prolyl-tRNA synthetase [EC:6.1.1.15]	13495.763025
K01886	QARS, glnS; glutaminyl-tRNA synthetase [EC:6.1.1.18]	15393.171846
K01887	RARS, argS; arginyl-tRNA synthetase [EC:6.1.1.19]	16187.709076
K01890	FARSB, pheT; phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	19279.398484
K01893	NARS, asnS; asparaginyl-tRNA synthetase [EC:6.1.1.22]	15557.432792
K01894	gluQ; glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]	515.21928538
K01902	sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	4270.165376
K01903	sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]	NA
K01911	menE; O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]	NA
K01915	glnA; glutamine synthetase [EC:6.3.1.2]	91694.422357
K01918	panC; pantoate--beta-alanine ligase [EC:6.3.2.1]	3332.4825746
K01921	ddl; D-alanine-D-alanine ligase [EC:6.3.2.4]	NA
K01922	PPCS, coaB; phosphopantothenate-cysteine ligase [EC:6.3.2.5]	414.50330045
K01923	purC; phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]	NA
K01925	murD; UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]	NA
K01932	E6.3.2.-	25.965958375
K01935	bioD; dethiobiotin synthetase [EC:6.3.3.3]	NA
K01937	E6.3.4.2, pyrG; CTP synthase [EC:6.3.4.2]	30381.985643
K01938	fhs; formate--tetrahydrofolate ligase [EC:6.3.4.3]	NA
K01939	E6.3.4.4, purA; adenylosuccinate synthase [EC:6.3.4.4]	NA
K01940	E6.3.4.5, argG; argininosuccinate synthase [EC:6.3.4.5]	NA
K01945	purD; phosphoribosylamine--glycine ligase [EC:6.3.4.13]	NA
K01951	guaA, GMPS; GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	NA
K01955	carB, CPA2; carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	NA
K01960	E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]	23598.839149
K01966	PCCB, pccB; propionyl-CoA carboxylase beta chain [EC:6.4.1.3]	NA
K01972	E6.5.1.2, ligA, ligB; DNA ligase (NAD+) [EC:6.5.1.2]	NA
K01990	ABC-2.A; ABC-2 type transport system ATP-binding protein	NA
K01991	ABC-2.OM, wza; polysaccharide export outer membrane protein	2009.5634667
K01992	ABC-2.P; ABC-2 type transport system permease protein	NA
K01993	ABC-2.TX; HlyD family secretion protein	6714.7597388
K02001	proW; glycine betaine/proline transport system permease protein	NA
K02007	cblM; cobalt/nickel transport system permease protein	NA
K02014	TC.FEV.OM; iron complex outer membrane receptor protein	NA
K02022	ABC.MR.TX; HlyD family secretion protein	1137.2055148
K02023		696.10553972
K02030	ABC.PA.S; polar amino acid transport system substrate-binding protein	NA

K02031	ABC.PE.A; peptide/nickel transport system ATP-binding protein	NA
K02032	ABC.PE.A1; peptide/nickel transport system ATP-binding protein	NA
K02039	phoU; phosphate transport system protein	NA
K02045	cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]	NA
K02046	cysU; sulfate transport system permease protein	NA
K02047	cysW; sulfate transport system permease protein	NA
K02048	cysP, sbp; sulfate transport system substrate-binding protein	NA
K02065	ABC.X1.A; putative ABC transport system ATP-binding protein	3256.5299654
K02066	ABC.X1.P; putative ABC transport system permease protein	3401.6358906
K02067	ABC.X1.S; putative ABC transport system substrate-binding protein	4561.82431
K02077	ABC.ZM.S; zinc/manganese transport system substrate-binding protein	NA
K02079	agaA; N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]	NA
K02082	agaS; tagatose-6-phosphate ketose/aldose isomerase [EC:5.-.-.]	855.51359835
K02109	ATPF0B, atpF; F-type H ⁺ -transporting ATPase subunit b [EC:3.6.3.14]	NA
K02110	ATPF0C, atpE; F-type H ⁺ -transporting ATPase subunit c [EC:3.6.3.14]	NA
K02111	ATPF1A, atpA; F-type H ⁺ -transporting ATPase subunit alpha [EC:3.6.3.14]	NA
K02112	ATPF1B, atpD; F-type H ⁺ -transporting ATPase subunit beta [EC:3.6.3.14]	NA
K02113	ATPF1D, atpH; F-type H ⁺ -transporting ATPase subunit delta [EC:3.6.3.14]	NA
K02114	ATPF1E, atpC; F-type H ⁺ -transporting ATPase subunit epsilon [EC:3.6.3.14]	NA
K02115	ATPF1G, atpG; F-type H ⁺ -transporting ATPase subunit gamma [EC:3.6.3.14]	NA
K02133	ATPeF1B, ATP5B; F-type H ⁺ -transporting ATPase subunit beta [EC:3.6.3.14]	241.03935124
K02173	yggC; hypothetical protein	NA
K02192	bfd; bacterioferritin-associated ferredoxin	NA
K02193	ccmA; heme exporter protein A [EC:3.6.3.41]	280.51866683
K02255	ftnB; ferritin-like protein 2	NA
K02279	cpaB, rcpC; pilus assembly protein CpaB	437.33230145
K02291	crtB; phytoene synthase [EC:2.5.1.32]	945.93734812
K02300	cyoD; cytochrome o ubiquinol oxidase operon protein cyoD	NA
K02301	cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]	NA
K02313	dnaA; chromosomal replication initiator protein	9277.6111767
K02317	dnaT; DNA replication protein DnaT	NA
K02334	dpo; DNA polymerase bacteriophage-type [EC:2.7.7.7]	NA
K02335	DPO1, polA; DNA polymerase I [EC:2.7.7.7]	NA
K02336	DPO2, polB; DNA polymerase II [EC:2.7.7.7]	NA
K02338	DPO3B, dnaN; DNA polymerase III subunit beta [EC:2.7.7.7]	14156.593717
K02340	DPO3D1, holA; DNA polymerase III subunit delta [EC:2.7.7.7]	NA
K02342	DPO3E, dnaQ; DNA polymerase III subunit epsilon [EC:2.7.7.7]	4524.3431091
K02346	DPO4, dinB; DNA polymerase IV [EC:2.7.7.7]	NA
K02348	elaA; ElaA protein	299.27314029
K02357	tsf, TSFM; elongation factor Ts	NA
K02364	entF; enterobactin synthetase component F [EC:2.7.7.-]	NA
K02377	TSTA3, fcl; GDP-L-fucose synthase [EC:1.1.1.271]	NA
K02396	flgK; flagellar hook-associated protein 1 FlgK	NA
K02402	flhC; flagellar transcriptional activator FlhC	9.5419935779
K02403	flhD; flagellar transcriptional activator FlhD	NA
K02407	fliD; flagellar hook-associated protein 2	NA
K02419	fliP; flagellar biosynthetic protein FliP	NA
K02421	fliR; flagellar biosynthetic protein FliR	NA

K02423	fliT; flagellar protein FliT	NA
K02426	sufE; cysteine desulfuration protein SufE	NA
K02428	rdgB; dITP/XTP pyrophosphatase [EC:3.6.1.19]	5777.6800144
K02431	fucU; L-fucose mutarotase [EC:5.1.3.-]	NA
K02433	gatA, QRSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase	NA
K02434	gatB, PET112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase	NA
K02453	gspD; general secretion pathway protein D	37797.033274
K02461	gspL; general secretion pathway protein L	12.641000979
K02466	gutM; glucitol operon activator protein	NA
K02467	gutQ; GutQ protein	9.1213328548
K02469	gyrA; DNA gyrase subunit A [EC:5.99.1.3]	NA
K02470	gyrB; DNA gyrase subunit B [EC:5.99.1.3]	NA
K02472	wecC; UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.3]	1888.2428687
K02477	K02477; two-component system, LytT family, response regulator	NA
K02478	K02478; two-component system, LytT family, sensor kinase [EC:2.7.13.3]	NA
K02482	K02482; two-component system, NtrC family, sensor kinase [EC:2.7.13.3]	NA
K02485	rssB, hnr; two-component system, unclassified family, response regulator	NA
K02493	hemK, prnC; release factor glutamine methyltransferase [EC:2.1.1.-]	NA
K02498	hemY; HemY protein	13.642962017
K02500	hisF; cyclase [EC:4.1.3.-]	NA
K02501	hisH; glutamine amidotransferase [EC:2.4.2.-]	NA
K02511	hpaX; MFS transporter, ACS family, 4-hydroxyphenylacetate permease	NA
K02517	htrB; lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]	NA
K02519	infB, MTIF2; translation initiation factor IF-2	NA
K02520	infC, MTIF3; translation initiation factor IF-3	6929.6174948
K02523	ispB; octaprenyl-diphosphate synthase [EC:2.5.1.90]	3806.8055453
K02527	kdtA, waaA; 3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12]	24773.3280817
K02528	ksgA; 16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase [EN	NA
K02536	lpxD; UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.5.5]	1.3752101
K02548	menA; 1,4-dihydroxy-2-naphthoate octaprenyltransferase [EC:2.5.1.74]	2.5.2998.4890732
K02549	menC; O-succinylbenzoate synthase [EC:4.2.1.113]	908.41797245
K02551	menD; 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate sy	4930.6348547
K02552	menF; menaquinone-specific isochorismate synthase [EC:5.4.4.2]	NA
K02554	mhpD; 2-keto-4-pentenoate hydratase [EC:4.2.1.80]	NA
K02558	mpl; UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopi	1349.8671919
K02560	msbB; lipid A biosynthesis (KDO)2-(lauroyl)-lipid iva acyltransferase [EC:2.3.6.3]	422069306
K02562	mtlR1, mtlR; mannitol operon repressor	NA
K02564	nagB, GNPD; glucosamine-6-phosphate deaminase [EC:3.5.99.6]	18074.928291
K02565	nagC; N-acetylglucosamine repressor	NA
K02569	napC; cytochrome c-type protein NapC	NA
K02572	napF; ferredoxin-type protein NapF	NA
K02584	nifA; Nif-specific regulatory protein	1751.4629135
K02594	nifV; homocitrate synthase NifV [EC:2.3.3.14]	78.148711635
K02598	nirC; nitrite transporter NirC	NA
K02600	nusA; N utilization substance protein A	13670.475612
K02601	nusG; transcriptional antiterminator NusG	24142.197434
K02613	paaE; ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE	NA
K02617	paaY; phenylacetic acid degradation protein	NA

K02619	pabC; 4-amino-4-deoxychorismate lyase [EC:4.1.3.38]	NA
K02621	parC; topoisomerase IV subunit A [EC:5.99.1.-]	9246.9136313
K02622	parE; topoisomerase IV subunit B [EC:5.99.1.-]	7067.1513426
K02652	pilB; type IV pilus assembly protein PilB	7664.7771983
K02653	pilC; type IV pilus assembly protein PilC	NA
K02654	pilD, pppA; leader peptidase (prepilin peptidase) / N-methyltransferase [EC:NA]	NA
K02663	pilN; type IV pilus assembly protein PilN	NA
K02669	pilT; twitching motility protein PilT	5926.5594103
K02686	priB; primosomal replication protein N	86.533224827
K02744	PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component	101.81915273
K02745	PTS-Aga-EIIB, agaV; PTS system, N-acetylgalactosamine-specific IIB component	1230.6403493
K02746	PTS-Aga-EIIC, agaW; PTS system, N-acetylgalactosamine-specific IIC component	2511.7697537
K02747	PTS-Aga-EIID, agaE; PTS system, N-acetylgalactosamine-specific IID component	3128.2309682
K02750	PTS-Arb-EIIC, glvC; PTS system, arbutin-like IIC component	54.002118791
K02753	PTS-Asc-EIIC, ascF; PTS system, arbutin-, cellobiose-, and salicin-specific IIC component	NA
K02760	PTS-Cel-EIIB, celA; PTS system, cellobiose-specific IIB component [EC:2.7.1.1]	55.759353286
K02765	PTS-Dgl-EIIC, gamP; PTS system, D-glucosamine-specific IIC component	1597.6150799
K02779	PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component	103.68753908
K02788	PTS-Lac-EIIC, lacE; PTS system, lactose-specific IIC component	60.213378283
K02794	PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.1]	467.3069329
K02804	PTS-Nag-EIIC, nagE; PTS system, N-acetylglucosamine-specific IIC component	8171.0094008
K02805	rffA, wecE; dTDP-4-amino-4,6-dideoxygalactose transaminase [EC:2.6.1.59]	NA
K02806	PTS-Ntr-EIIA, ptsN; PTS system, nitrogen regulatory IIA component [EC:2.7.1.1]	776.84472891
K02825	pyrR; pyrimidine operon attenuation protein / uracil phosphoribosyltransferase	NA
K02834	rbfA; ribosome-binding factor A	NA
K02835	prfA, MTRF1, MRF1; peptide chain release factor 1	NA
K02836	prfB; peptide chain release factor 2	NA
K02846	solA; N-methyl-L-tryptophan oxidase [EC:1.5.3.-]	8.8354563954
K02853	wzyE, rfft; 4-alpha-L-fucosyltransferase [EC:2.4.1.-]	23.9017057
K02854	rhaR; AraC family transcriptional regulator, L-rhamnose operon transcription factor	NA
K02863	RP-L1, MRPL1, rplA; large subunit ribosomal protein L1	NA
K02867	RP-L11, MRPL11, rplK; large subunit ribosomal protein L11	NA
K02874	RP-L14, MRPL14, rplN; large subunit ribosomal protein L14	NA
K02878	RP-L16, MRPL16, rplP; large subunit ribosomal protein L16	NA
K02885	RP-L19e, RPL19; large subunit ribosomal protein L19e	7.7527789374
K02886	RP-L2, MRPL2, rplB; large subunit ribosomal protein L2	NA
K02887	RP-L20, MRPL20, rplT; large subunit ribosomal protein L20	NA
K02890	RP-L22, MRPL22, rplV; large subunit ribosomal protein L22	NA
K02892	RP-L23, MRPL23, rplW; large subunit ribosomal protein L23	NA
K02895	RP-L24, MRPL24, rplX; large subunit ribosomal protein L24	NA
K02897	RP-L25, rplY; large subunit ribosomal protein L25	8154.9582807
K02904	RP-L29, rpmC; large subunit ribosomal protein L29	NA
K02914	RP-L34, MRPL34, rpmH; large subunit ribosomal protein L34	NA
K02916	RP-L35, MRPL35, rpml; large subunit ribosomal protein L35	NA
K02926	RP-L4, MRPL4, rplD; large subunit ribosomal protein L4	NA
K02931	RP-L5, MRPL5, rplE; large subunit ribosomal protein L5	NA
K02935	RP-L7, MRPL12, rplL; large subunit ribosomal protein L7/L12	NA
K02939	RP-L9, MRPL9, rplI; large subunit ribosomal protein L9	7914.5615948

K02945	RP-S1, rpsA; small subunit ribosomal protein S1	59872.459481
K02954	RP-S14, MRPS14, rpsN; small subunit ribosomal protein S14	4818.4226653
K02961	RP-S17, MRPS17, rpsQ; small subunit ribosomal protein S17	NA
K02965	RP-S19, rpsS; small subunit ribosomal protein S19	NA
K02982	RP-S3, rpsC; small subunit ribosomal protein S3	NA
K02986	RP-S4, rpsD; small subunit ribosomal protein S4	NA
K02996	RP-S9, MRPS9, rpsI; small subunit ribosomal protein S9	9861.3805874
K03043	rpoB; DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]	NA
K03046	rpoC; DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]	NA
K03070	secA; preprotein translocase subunit SecA	NA
K03072	secD; preprotein translocase subunit SecD	NA
K03074	secF; preprotein translocase subunit SecF	NA
K03075	secG; preprotein translocase subunit SecG	4963.0881923
K03092	SIG54, rpoN; RNA polymerase sigma-54 factor	6504.8660417
K03098	APOD; apolipoprotein D and lipocalin family protein	NA
K03100	lepB; signal peptidase I [EC:3.4.21.89]	10054.211717
K03101	lspA; signal peptidase II [EC:3.4.23.36]	NA
K03106	SRP54, ffh; signal recognition particle subunit SRP54	13634.579163
K03110	ftsY; fused signal recognition particle receptor	6062.5847371
K03112	damX; DamX protein	30.189771708
K03113	EIF1, SUI1; translation initiation factor 1	561.96187432
K03116	tatA; sec-independent protein translocase protein TatA	NA
K03119	tauD; taurine dioxygenase [EC:1.14.11.17]	NA
K03147	thiC; thiamine biosynthesis protein ThiC	NA
K03149	thiG; thiamine biosynthesis ThiG	NA
K03150	thiH; thiamine biosynthesis ThiH	NA
K03152	thiJ; 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	NA
K03154	thiS; sulfur carrier protein	NA
K03169	topB; DNA topoisomerase III [EC:5.99.1.2]	19951.186165
K03179	ubiA; 4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]	755.92282935
K03181	ubiC; chorismate--pyruvate lyase [EC:4.1.3.40]	NA
K03182	ubiD; 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]	1407.0477146
K03183	ubiE; ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.13]	3080.4063649
K03205	virD4, lvhD4; type IV secretion system protein VirD4	4855.1460594
K03210	yajC; preprotein translocase subunit YajC	NA
K03214	yfiF, trmG; RNA methyltransferase, TrmH family [EC:2.1.1.-]	15.453850787
K03216	trmL, cspR; tRNA (cytidine/uridine-2'-O-)-methyltransferase [EC:2.1.1.207]	NA
K03218	rlmB; 23S rRNA (guanosine2251-2'-O-)-methyltransferase [EC:2.1.1.185]	NA
K03222	yscJ; type III secretion protein SctJ	274.08963361
K03229	yscU; type III secretion protein SctU	115.98857352
K03271	gmhA, lpcA; D-sedoheptulose 7-phosphate isomerase [EC:5.3.1.28]	NA
K03272	gmhC, hldE, waaE, rfaE; D-beta-D-heptose 7-phosphate kinase / D-beta-D-	12681.0953941
K03273	gmhB; D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.1.13]	NA
K03274	gmhD, rfaD; ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]	NA
K03281	TC.CIC; chloride channel protein, CIC family	6077.558258
K03282	mscL; large conductance mechanosensitive channel	3965.4464636
K03284	corA; magnesium transporter	NA
K03291	MFS.SET; MFS transporter, SET family, sugar efflux transporter	NA

K03296	TC.HAE1; hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 f	69731.399367
K03301	TC.AAA; ATP:ADP antiporter, AAA family	777.35395408
K03303	TC.LCTP; lactate transporter, LctP family	NA
K03305	TC.POT; proton-dependent oligopeptide transporter, POT family	6379.5012474
K03310	TC.AGCS; alanine or glycine:cation symporter, AGCS family	NA
K03313	nhaA; Na ⁺ :H ⁺ antiporter, NhaA family	2337.7295241
K03314	nhaB; Na ⁺ :H ⁺ antiporter, NhaB family	9.7001829386
K03316	TC.CPA1; monovalent cation:H ⁺ antiporter, CPA1 family	NA
K03321	TC.SULP; sulfate permease, SulP family	5817.7382023
K03322	mntH; manganese transport protein	1222.7958157
K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE f	5131.4061148
K03329	yahN; amino acid exporter	NA
K03340	dapdh; diaminopimelate dehydrogenase [EC:1.4.1.16]	NA
K03386	E1.11.1.15, PRDX, ahpC; peroxiredoxin (alkyl hydroperoxide reductase sub	7880.0361156
K03389	hdrB; heterodisulfide reductase subunit B [EC:1.8.98.1]	2465.9268572
K03413	cheY; two-component system, chemotaxis family, response regulator CheY	NA
K03424	tatD; TatD DNase family protein [EC:3.1.21.-]	5638.2161643
K03427	hsdM; type I restriction enzyme M protein [EC:2.1.1.72]	NA
K03429	ugtP; 1,2-diacylglycerol 3-glucosyltransferase [EC:2.4.1.157]	317.95731316
K03435	fruR1, fruR; LacI family transcriptional regulator, fructose operon transcrip	21.725940746
K03436	fruR2, fruR; DeoR family transcriptional regulator, fructose operon transcri	NA
K03446	emrB; MFS transporter, DHA2 family, multidrug resistance protein B	596.7985929
K03449	MFS.CP; MFS transporter, CP family, cyanate transporter	2011.6029271
K03453	TC.BASS; bile acid:Na ⁺ symporter, BASS family	2607.2837167
K03455	TC.KEF; monovalent cation:H ⁺ antiporter-2, CPA2 family	NA
K03457	TC.NCS1; nucleobase:cation symporter-1, NCS1 family	35.142991893
K03459	focB; formate transporter	NA
K03468	aaeB; p-hydroxybenzoic acid efflux pump subunit AaeB	15.418566
K03470	rnhB; ribonuclease HII [EC:3.1.26.4]	2642.5426198
K03471	rnhC; ribonuclease HIII [EC:3.1.26.4]	NA
K03472	epd; D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]	17.739469178
K03473	pdxB; erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]	2088.6887055
K03474	pdxJ; pyridoxine 5-phosphate synthase [EC:2.6.99.2]	4696.8071532
K03477	ulaR; DeoR family transcriptional regulator, ulaG and ulaABCDEF operon tr	NA
K03482	yidP; GntR family transcriptional regulator, glv operon transcriptional regul	NA
K03485	treR1, treR; LacI family transcriptional regulator, trehalose operon repress	NA
K03488	licT, bglG; beta-glucoside operon transcriptional antiterminator	626.26274871
K03489	yydK; GntR family transcriptional regulator, transcriptional regulator of bgl	NA
K03491	licR; lichenan operon transcriptional antiterminator	NA
K03492	ydhQ; GntR family transcriptional regulator	NA
K03500	rsmB, sun; 16S rRNA (cytosine967-C5)-methyltransferase [EC:2.1.1.176]	NA
K03517	nadA; quinolinate synthase [EC:2.5.1.72]	4356.5365076
K03524	birA; BirA family transcriptional regulator, biotin operon repressor / biotin	NA
K03526	E1.17.7.1, gcpE, ispG; (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synth	12157.200705
K03528	zipA; cell division protein ZipA	17.608678987
K03535	gudP; MFS transporter, ACS family, glucarate transporter	6.8823897135
K03536	rnpA; ribonuclease P protein component [EC:3.1.26.5]	2233.681488
K03544	clpX, CLPX; ATP-dependent Clp protease ATP-binding subunit ClpX	NA

K03545	tig; trigger factor	NA
K03547	sbcD; exonuclease SbcD	NA
K03549	kup; KUP system potassium uptake protein	NA
K03550	ruvA; holliday junction DNA helicase RuvA [EC:3.6.4.12]	NA
K03551	ruvB; holliday junction DNA helicase RuvB [EC:3.6.4.12]	6155.2625262
K03555	mutS; DNA mismatch repair protein MutS	17073.831788
K03558	cvpA; membrane protein required for colicin V production	626.83179828
K03559	exbD; biopolymer transport protein ExbD	NA
K03561	exbB; biopolymer transport protein ExbB	21448.604137
K03566	gcvA; LysR family transcriptional regulator, glycine cleavage system transcr	NA
K03568	tldD; TldD protein	2100.4289892
K03572	mutL; DNA mismatch repair protein MutL	10746.380904
K03574	mutT, NUDT15, MTH2; 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	NA
K03578	hrpA; ATP-dependent helicase HrpA [EC:3.6.4.13]	3104.8145001
K03579	hrpB; ATP-dependent helicase HrpB [EC:3.6.4.13]	2237.3534564
K03583	recC; exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]	28.737665766
K03585	acrA; membrane fusion protein	10748.442558
K03587	ftsI; cell division protein FtsI (penicillin-binding protein 3) [EC:2.4.1.129]	8284.5723964
K03590	ftsA; cell division protein FtsA	8128.7180634
K03593	mrp; ATP-binding protein involved in chromosome partitioning	4861.837297
K03596	lepA; GTP-binding protein LepA	NA
K03597	rseA; sigma-E factor negative regulatory protein RseA	NA
K03598	rseB; sigma-E factor negative regulatory protein RseB	24.963982217
K03600	sspB; stringent starvation protein B	NA
K03603	fadR; GntR family transcriptional regulator, negative regulator for fad regu	NA
K03605	hyaD, hybD; hydrogenase maturation protease [EC:3.4.23.-]	926.83905412
K03607	proQ; ProP effector	13.952538959
K03625	nusB; N utilization substance protein B	5226.2070438
K03628	rho; transcription termination factor Rho	17062.908539
K03629	recF; DNA replication and repair protein RecF	5748.4063003
K03631	recN; DNA repair protein RecN (Recombination protein N)	9477.9974748
K03642	rlpA; rare lipoprotein A	1187.3855088
K03644	lipA; lipoic acid synthetase [EC:2.8.1.8]	4116.4626515
K03647	nrdI; protein involved in ribonucleotide reduction	NA
K03650	mnme, trmE, MSS1; tRNA modification GTPase [EC:3.6.-.-]	NA
K03651	icc; lcc protein	32.652427564
K03654	recQ; ATP-dependent DNA helicase RecQ [EC:3.6.4.12]	23321.886964
K03656	rep; ATP-dependent DNA helicase Rep [EC:3.6.4.12]	18.424578903
K03665	hflX; GTP-binding protein HflX	8629.5777839
K03669	mdoH; membrane glycosyltransferase [EC:2.4.1.-]	NA
K03670	mdoG; periplasmic glucans biosynthesis protein	NA
K03675	grxB; glutaredoxin 2	NA
K03683	rnt; ribonuclease T [EC:3.1.13.-]	NA
K03684	rnd; ribonuclease D [EC:3.1.13.5]	826.2132566
K03688	ubiB, aarF; ubiquinone biosynthesis protein	824.38403674
K03690	yigP; hypothetical protein	7.3628230998
K03696	clpC; ATP-dependent Clp protease ATP-binding subunit ClpC	NA
K03698	cbf; CMP-binding protein	NA

K03699	tlyC; putative hemolysin	10766.117814
K03701	uvrA; excinuclease ABC subunit A	32613.064117
K03704	cspA; cold shock protein (beta-ribbon, CspA family)	5692.1198527
K03723	mfd; transcription-repair coupling factor (superfamily II helicase) [EC:3.6.4.NA	NA
K03724	lhr; ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]	NA
K03732	rhIB; ATP-dependent RNA helicase RhIB [EC:3.6.4.13]	NA
K03733	xerC; integrase/recombinase XerC	14284.125474
K03738	aor; aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]	NA
K03746	hns; DNA-binding protein H-NS	40.211146891
K03747	smg; Smg protein	24.035249636
K03748	sanA; SanA protein	1114.2255464
K03759	adiC; arginine:agmatine antiporter	10.182257954
K03760	eptA; phosphoethanolamine transferase	2285.5137196
K03764	metJ; transcriptional repressor of met regulon (beta-ribbon, MetJ family)	3.634932564
K03768	PPIB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]	4007.9395771
K03770	ppiD; peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]	10658.799649
K03771	surA; peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]	8654.4758081
K03772	fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]	25.814293013
K03773	fklB; FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]	5454.7106057
K03776	aer; aerotaxis receptor	11.593523995
K03777	dld; D-lactate dehydrogenase [EC:1.1.1.28]	20.282352264
K03781	katE, CAT, catB, srpA; catalase [EC:1.11.1.6]	20178.239673
K03785	aroD; 3-dehydroquinate dehydratase I [EC:4.2.1.10]	NA
K03787	surE; 5'-nucleotidase [EC:3.1.3.5]	2082.8301186
K03788	aphA; acid phosphatase (class B) [EC:3.1.3.2]	NA
K03797	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]	18916.234576
K03801	lipB; lipoyl(octanoyl) transferase [EC:2.3.1.181]	2933.3561786
K03806	ampD; AmpD protein	NA
K03807	ampE; AmpE protein	7.2454265409
K03808	pqiA; paraquat-inducible protein A	NA
K03812	rmf; ribosome modulation factor	19.990314353
K03817	rimL; ribosomal-protein-serine acetyltransferase [EC:2.3.1.-]	156.6752937
K03818	wcaF; putative colanic acid biosynthesis acetyltransferase WcaF [EC:2.3.1.-]	NA
K03820	Int; apolipoprotein N-acyltransferase [EC:2.3.1.-]	2128.7674165
K03826	yiaC; putative acetyltransferase [EC:2.3.1.-]	NA
K03828	yjgM; putative acetyltransferase [EC:2.3.1.-]	78.975896672
K03832	tonB; periplasmic protein TonB	22813.286808
K03834	tyrP; tyrosine-specific transport protein	NA
K03838	tdcC; threonine transporter	NA
K03840	fldB; flavodoxin II	8.7329587864
K03851	tpa; taurine-pyruvate aminotransferase [EC:2.6.1.77]	NA
K03892	arsR; ArsR family transcriptional regulator	1901.1323264
K03894	iucA; N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]	21.475280891
K03895	iucC; aerobactin synthase [EC:6.3.2.39]	11.633821209
K03896	iucB; acetyl CoA:N6-hydroxylysine acetyl transferase [EC:2.3.1.102]	NA
K03918	lat; L-lysine 6-transaminase [EC:2.6.1.36]	NA
K03923	mdaB; modulator of drug activity B	NA
K03924	moxR; MoxR-like ATPase [EC:3.6.3.-]	16836.068087

K03932	lpqC; polyhydroxybutyrate depolymerase	508.51706418
K03933	cpbD; chitin-binding protein	20.415232493
K03974	pspF; psp operon transcriptional activator	6.6440307928
K03979	obg; GTP-binding protein	NA
K03980	mviN; virulence factor	1470.2647598
K03981	dsbC; thiol:disulfide interchange protein DsbC [EC:5.3.4.1]	NA
K04022	eutG; alcohol dehydrogenase	NA
K04032	eutT; ethanolamine utilization cobalamin adenosyltransferase [EC:2.5.1.17]	NA
K04047	dps; starvation-inducible DNA-binding protein	1703.1357535
K04062	osmB; osmotically inducible lipoprotein OsmB	NA
K04063	osmC; osmotically inducible protein OsmC	3.7423909883
K04067	priC; primosomal replication protein N"	NA
K04072	adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10]	NA
K04075	tisJ; mesJ; tRNA(Ile)-lysine synthase [EC:6.3.4.19]	6525.4398955
K04077	groEL, HSPD1; chaperonin GroEL	NA
K04079	htpG, HSP90A; molecular chaperone HtpG	NA
K04080	ibpA; molecular chaperone IbpA	37.70375614
K04081	ibpB; molecular chaperone IbpB	27.61635457
K04083	hslO; molecular chaperone Hsp33	NA
K04092	tyrA1; chorismate mutase [EC:5.4.99.5]	NA
K04096	smf; DNA processing protein	4510.3911854
K04335	csgB; minor curlin subunit	3.7669886869
K04486	E3.1.3.15B; histidinol-phosphatase (PHP family) [EC:3.1.3.15]	NA
K04517	tyrA2; prephenate dehydrogenase [EC:1.3.1.12]	3705.0509224
K04562	flhG, fleN; flagellar biosynthesis protein FlhG	15.533487639
K04564	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	12381.334443
K04568	poxA; lysyl-tRNA synthetase, class II [EC:6.1.1.6]	11.572557802
K04651	hypA, hybF; hydrogenase nickel incorporation protein HypA/HybF	NA
K04652	hypB; hydrogenase nickel incorporation protein HypB	NA
K04653	hypC; hydrogenase expression/formation protein HypC	NA
K04654	hypD; hydrogenase expression/formation protein HypD	NA
K04655	hypE; hydrogenase expression/formation protein HypE	NA
K04656	hypF; hydrogenase maturation protein HypF	NA
K04691	hhoB, degS; serine protease DegS [EC:3.4.21.-]	26.788844144
K04744	lptD, imp, ostA; LPS-assembly protein	3072.4079727
K04749	rsbV; anti-sigma B factor antagonist	16.962631155
K04757	rsbW; serine/threonine-protein kinase RsbW [EC:2.7.11.1]	NA
K04759	feoB; ferrous iron transport protein B	25962.836062
K04760	greB; transcription elongation factor GreB	NA
K04767	acuB; acetoin utilization protein AcuB	NA
K04774	sohB; serine protease SohB [EC:3.4.21.-]	9.9079196817
K04775	ydgD; protease YdgD [EC:3.4.21.-]	14.666150071
K04786	irp1, HMWP1; yersiniabactin nonribosomal peptide/polyketide synthase	26.233568758
K04835	E4.3.1.2; methylaspartate ammonia-lyase [EC:4.3.1.2]	172.40791289
K05305	FUK; fucokinase [EC:2.7.1.52]	NA
K05340	glcU; glucose uptake protein	1551.0021193
K05365	mrcB; penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]	28.01884539
K05367	pbpC; penicillin-binding protein 1C [EC:2.4.1.-]	3445.4270479

K05368	fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.-]	11.332526058
K05499	cytR; LacI family transcriptional regulator, repressor for deo operon, udp,	NA
K05515	mrdA; penicillin-binding protein 2	NA
K05517	tsx; nucleoside-specific channel-forming protein	NA
K05521	draG; ADP-ribosylglycohydrolase [EC:3.2.-.-]	NA
K05527	bolA; BolA protein	NA
K05539	dusA; tRNA-dihydrouridine synthase A [EC:1.-.-.-]	NA
K05541	dusC; tRNA-dihydrouridine synthase C [EC:1.-.-.-]	805.95683569
K05566	mnhB, mrpB; multicomponent Na ⁺ :H ⁺ antiporter subunit B	NA
K05591	dbpA; ATP-independent RNA helicase DbpA [EC:3.6.4.13]	8.2199611845
K05592	deaD; ATP-dependent RNA helicase DeaD [EC:3.6.4.13]	8981.0991209
K05595	marC; multiple antibiotic resistance protein	NA
K05596	iciA; LysR family transcriptional regulator, chromosome initiation inhibitor	NA
K05606	MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]	2114.8610041
K05712	mhpA; 3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.127]	NA
K05713	mhpB; 2,3-dihydroxyphenylpropionate 1,2-dioxygenase [EC:1.13.11.16]	NA
K05714	mhpC; 2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase [EC:3.7.1.-]	NA
K05775	malM; maltose operon periplasmic protein	NA
K05787	hupA; DNA-binding protein HU-alpha	22.167048345
K05789	wzzB; chain length determinant protein (polysaccharide antigen chain regu	12.180901992
K05800	ybaO; Lrp/AsnC family transcriptional regulator	NA
K05802	kefA, bspA, aefA; potassium efflux system protein	51.856513901
K05803	nlpI; lipoprotein NlpI	86.831219776
K05804	rob; right origin-binding protein	25.3981825
K05807	bamD; outer membrane protein assembly factor BamD	5107.5869392
K05808	yhbH; putative sigma-54 modulation protein	NA
K05809	raiA; ribosome-associated inhibitor A	25.735075945
K05831	argE1, lysK; LysW-gamma-L-lysine carboxypeptidase	NA
K05835	rhtC; threonine efflux protein	NA
K05836	hutC; GntR family transcriptional regulator, histidine utilization repressor	26.374714023
K05838	ybbN; putative thioredoxin	NA
K05844	rimK; ribosomal protein S6 modification protein	NA
K05851	E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]	53.34980037
K05874	tsr; methyl-accepting chemotaxis protein I, serine sensor receptor	NA
K05880	dhaR; transcriptional activator for dhaKLM operon	10.46835773
K05881	dhaM; PTS hybrid protein	NA
K05916	hmp, YHB1; nitric oxide dioxygenase [EC:1.14.12.17]	11.836187176
K05939	aas; acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase / long-chain	1816.2607773
K05945	E2.4.1.58	NA
K05966	citG; triphosphoribosyl-dephospho-CoA synthase [EC:2.4.2.52]	44.257020565
K05970	E3.1.1.53, SIAE; sialate O-acetyltransferase [EC:3.1.1.53]	14644.575616
K05984	cho; excinuclease Cho [EC:3.1.25.-]	NA
K05989	E3.2.1.40; alpha-L-rhamnosidase [EC:3.2.1.40]	NA
K05995	pepE; dipeptidase E [EC:3.4.13.21]	780.26320275
K05997	sufA; Fe-S cluster assembly protein SufA	NA
K06001	K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]	6501.4690827
K06041	E5.3.1.13; arabinose-5-phosphate isomerase [EC:5.3.1.13]	3631.8554646
K06045	shc, sqhC; squalene-hopene/tetraprenyl-beta-curcumene cyclase [EC:5.4.9	1925.6113203

K06048	ybdK; carboxylate-amine ligase [EC:6.3.-.-]	7.5000326917
K06073	ABC.VB12.P, btuC; vitamin B12 transport system permease protein	NA
K06074	ABC.VB12.A, btuD; vitamin B12 transport system ATP-binding protein [EC:3.6.3.-]	NA
K06077	slyB; outer membrane lipoprotein SlyB	1842.6858683
K06113	abnA_B; arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]	407.34553785
K06131	cls; cardiolipin synthase [EC:2.7.8.-]	NA
K06140	rnk; regulator of nucleoside diphosphate kinase	NA
K06141	tsgA; MFS transporter, TsgA protein	18.859336437
K06142	hlpA, ompH; outer membrane protein	11218.796017
K06144	uspB; universal stress protein B	8.381956421
K06145	gntR; LacI family transcriptional regulator, gluconate utilization system GntR	13.236475991
K06149	uspA; universal stress protein A	29.880699621
K06158	ABCF3; ATP-binding cassette, subfamily F, member 3	13665.333756
K06159	yojI; putative ATP-binding cassette transporter	NA
K06167	phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]	2371.5656718
K06168	miaB; bifunctional enzyme involved in thiolation and methylation of tRNA	9639.6704908
K06181	rluE; 23S rRNA pseudouridine2457 synthase [EC:5.4.99.20]	368.2601371
K06183	rsuA; 16S rRNA pseudouridine516 synthase [EC:5.4.99.19]	NA
K06186	bamE, smpA; outer membrane protein assembly factor BamE	NA
K06194	nlpD; lipoprotein NlpD	17.685155028
K06195	apaG; ApaG protein	347.56088762
K06199	crcB; CrcB protein	1082.6019783
K06203	cysZ; CysZ protein	NA
K06204	dksA; DnaK suppressor protein	578.13871295
K06205	mioC; MioC protein	NA
K06212	focA; formate transporter	20.591078432
K06215	pdxS, pdx1; pyridoxal 5'-phosphate synthase pdxS subunit [EC:4.3.3.6]	NA
K06218	relE; RelE protein	508.47655199
K06281	hyaB, hybC; hydrogenase large subunit [EC:1.12.99.6]	5610.4096945
K06282	hyaA, hybO; hydrogenase small subunit [EC:1.12.99.6]	4316.5261105
K06346	jag; spoIIJ-associated protein	NA
K06350	kipA; antagonist of KipI	8044.4425355
K06442	tlyA; 23S rRNA (cytidine1920-2'-O)/16S rRNA (cytidine1409-2'-O)-methyltransferase	NA
K06447	astD; succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]	NA
K06858	ABC.VB12.S1, btuF; vitamin B12 transport system substrate-binding protein	NA
K06859	pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]	402.96838587
K06861	lptB; lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]	3049.5984464
K06864	K06864; uncharacterized protein	NA
K06867	K06867	NA
K06879	queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]	NA
K06889	K06889	13942.003355
K06894	K06894	12722.595902
K06898	K06898	NA
K06901	pbuG; putative MFS transporter, AGZA family, xanthine/uracil permease	7190.2959026
K06906	K06906	14.063235789
K06908	K06908	32.011157543
K06916	K06916	8.6625855635
K06918	K06918	12.155327033

K06920	queC; 7-cyano-7-deazaguanine synthase [EC:6.3.4.20]	1718.8329047
K06940	K06940	NA
K06941	rlmN; 23S rRNA (adenine2503-C2)-methyltransferase [EC:2.1.1.192]	NA
K06951	K06951	87.965211566
K06956	K06956	655.81562073
K06957	tmcA; tRNA(Met) cytidine acetyltransferase [EC:2.3.1.193]	13.229538705
K06966	K06966	NA
K06969	rlmI; 23S rRNA (cytosine1962-C5)-methyltransferase [EC:2.1.1.191]	10832.409652
K06973	K06973	NA
K06978	K06978	2007.2413721
K06997	K06997	NA
K07000	K07000	50.663946871
K07005	K07005	NA
K07016	K07016	NA
K07026	E3.1.3.70; mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]	NA
K07032	K07032	NA
K07037	K07037	6125.4440532
K07051	K07051	1145.0771844
K07054	K07054	NA
K07071	K07071	4654.1153164
K07079	K07079	5413.7878385
K07080	K07080	NA
K07081	K07081	283.78577408
K07083	K07083	487.22457961
K07084	K07084	NA
K07091	lptF; lipopolysaccharide export system permease protein	5661.0537262
K07096	K07096	445.57564913
K07098	K07098	7771.3179028
K07102	K07102	653.40178601
K07107	ybgC; acyl-CoA thioester hydrolase [EC:3.1.2.-]	3097.3175225
K07109	K07109	1068.7641134
K07113	fxsA; UPF0716 protein FxsA	NA
K07114	yfbK; Ca-activated chloride channel homolog	11171.107141
K07121	K07121	24.399470543
K07124	K07124	2179.1178341
K07132	K07132	562.8876328
K07136	K07136	NA
K07137	K07137	NA
K07138	K07138	NA
K07140	K07140	8.8002131245
K07145	isdG, isdI; heme oxygenase (staphylobilin-producing) [EC:1.14.99.48]	118.40842447
K07146	K07146; UPF0176 protein	6.4436635922
K07147	yedY; sulfoxide reductase catalytic subunit YedY [EC:1.8.-.-]	19.11952395
K07148	K07148; uncharacterized protein	2219.8547276
K07151	STT3; dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.3.3.73]	73755637
K07164	K07164	5114.6886081
K07165	fecR; transmembrane sensor	7.5573646875
K07180	prkA; serine protein kinase	27.175009194

K07185	tspO; tryptophan-rich sensory protein	246.53545853
K07192	FLOT; flotillin	NA
K07219	K07219; putative molybdopterin biosynthesis protein	NA
K07221	oprO_P; phosphate-selective porin OprO and OprP	NA
K07224	efeO; iron uptake system component EfeO	11.920141146
K07229	yqjH; ferric-chelate reductase (NADPH) [EC:1.16.1.9]	NA
K07235	tusD, dsrE; tRNA 2-thiouridine synthesizing protein D [EC:2.8.1.-]	4.7513723
K07236	tusC, dsrF; tRNA 2-thiouridine synthesizing protein C	3.2758671223
K07239	TC.HME; heavy-metal exporter, HME family	NA
K07243	FTR, efeU; high-affinity iron transporter	15.41747698
K07251	thiK; thiamine kinase [EC:2.7.1.89]	NA
K07257	spsF; spore coat polysaccharide biosynthesis protein SpsF	460.82744598
K07261	mepA; penicillin-insensitive murein endopeptidase [EC:3.4.24.-]	NA
K07263	pqqL; zinc protease [EC:3.4.24.-]	26614.367694
K07264	arnT, pmrK; 4-amino-4-deoxy-L-arabinose transferase [EC:2.4.2.43]	NA
K07267	oprB; porin	1726.8595878
K07269	ytfB; hypothetical protein	NA
K07275	ompW; outer membrane protein	8.8068340138
K07276	K07276; hypothetical protein	685.02128979
K07277	SAM50, TOB55, bamA; outer membrane protein insertion porin family	17490.331846
K07279	yfaL; autotransporter family porin	23.495734405
K07283	ydiY; putative salt-induced outer membrane protein	5.341658219
K07285	slp; outer membrane lipoprotein	23.999402858
K07287	bamC; outer membrane protein assembly factor BamC	112.3200015
K07309	ynfE; Tat-targeted selenate reductase subunit YnfE [EC:1.97.1.9]	NA
K07311	ynfG; Tat-targeted selenate reductase subunit YnfG	NA
K07313	pphA; serine/threonine protein phosphatase 1 [EC:3.1.3.16]	66.556437516
K07322	ytfE, scdA; regulator of cell morphogenesis and NO signaling	1462.9126188
K07335	bmpA, bmpB, tmpC; basic membrane protein A and related proteins	15398.947444
K07337	K07337; hypothetical protein	8.8966227705
K07340	K07340; hypothetical protein	NA
K07349	fimG; minor fimbrial subunit	5.9129786784
K07358	fimE; type 1 fimbriae regulatory protein FimE	NA
K07386	pepO; putative endopeptidase [EC:3.4.24.-]	11894.881139
K07391	comM; magnesium chelatase family protein	6077.0686178
K07396	K07396; putative protein-disulfide isomerase	NA
K07397	yhfA; putative redox protein	184.79871493
K07400	nfuA; Fe/S biogenesis protein NfuA	NA
K07403	nfeD; membrane-bound serine protease (ClpP class)	1140.8101256
K07405	E3.2.1.1A; alpha-amylase [EC:3.2.1.1]	NA
K07462	recJ; single-stranded-DNA-specific exonuclease [EC:3.1.-.-]	12294.93455
K07467	rstA1; phage replication initiation protein	156.81803384
K07470	sbmC; DNA gyrase inhibitor	3.5779417276
K07478	ycaJ; putative ATPase	NA
K07479	yrdD; putative DNA topoisomerase	NA
K07480	insB; insertion element IS1 protein InsB	NA
K07492	K07492; putative transposase	NA
K07566	tsaC, rimN, SUA5; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]	NA

K07588	argK; LAO/AO transport system kinase [EC:2.7.-.-]	5207.5426885
K07637	phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ	NA
K07638	envZ; two-component system, OmpR family, osmolarity sensor histidine kinase	NA
K07639	rstB; two-component system, OmpR family, sensor histidine kinase RstB [E	15.874297666
K07640	cpxA; two-component system, OmpR family, sensor histidine kinase CpxA	NA
K07645	qseC; two-component system, OmpR family, sensor histidine kinase QseC	4.7482216994
K07646	kdpD; two-component system, OmpR family, sensor histidine kinase KdpD	NA
K07647	torS; two-component system, OmpR family, sensor histidine kinase TorS	ENA
K07657	phoB; two-component system, OmpR family, phosphate regulon response	770.76857642
K07659	ompR; two-component system, OmpR family, phosphate regulon response	52.317605996
K07660	phoP; two-component system, OmpR family, response regulator PhoP	NA
K07664	baeR; two-component system, OmpR family, response regulator BaeR	NA
K07674	narQ; two-component system, NarL family, nitrate/nitrite sensor histidine	NA
K07675	uhpB; two-component system, NarL family, sensor histidine kinase UhpB	ENA
K07676	rdsD; two-component system, NarL family, sensor histidine kinase RdsD	ECNA
K07677	rdsC; two-component system, NarL family, capsular synthesis sensor histidine	20.041712875
K07678	barA; two-component system, NarL family, sensor histidine kinase BarA	ENA
K07679	evgS, bvgS; two-component system, NarL family, sensor histidine kinase Ev	NA
K07685	narP; two-component system, NarL family, nitrate/nitrite response regulator	NA
K07687	rdsB; two-component system, NarL family, capsular synthesis response reg	NA
K07689	uvrY; two-component system, NarL family, invasion response regulator Uvr	NA
K07690	evgA, bvgA; two-component system, NarL family, response regulator EvgA	NA
K07696	nreC; two-component system, NarL family, response regulator NreC	NA
K07702	dpiA, citB; two-component system, CitB family, response regulator CitB	3.5602623102
K07703	dcuR; two-component system, CitB family, response regulator DcuR	7.1834696003
K07710	atoS; two-component system, NtrC family, sensor histidine kinase AtoS	EC102.27226649
K07717	ycbA, glnK; two-component system, sensor histidine kinase YcbA [EC:2.7.1:	103.15172562
K07735	algH; putative transcriptional regulator	NA
K07739	ELP3, KAT9; elongator complex protein 3 [EC:2.3.1.48]	NA
K07746	K07746; hypothetical protein	45.997358349
K07749	frc; formyl-CoA transferase [EC:2.8.3.16]	351.59252349
K07757	E3.1.3.23; sugar-phosphatase [EC:3.1.3.23]	NA
K07771	basR; two-component system, OmpR family, response regulator BasR	5.8455091058
K07773	arcA; two-component system, OmpR family, aerobic respiration control pr	39.142353234
K07775	resD; two-component system, OmpR family, response regulator ResD	143.32238358
K07783	uhpC; MFS transporter, OPA family, sugar phosphate sensor protein UhpC	1610.1659682
K07784	uhpT; MFS transporter, OPA family, hexose phosphate transport protein U	NA
K07795	tctC; putative tricarboxylic transport membrane protein	NA
K07806	arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransfe	5.1363577115
K07811	torA; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]	NA
K07812	torZ; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]	521.59615665
K08156	araJ; MFS transporter, DHA1 family, arabinose polymer transporter	1860.1411804
K08159	sotB; MFS transporter, DHA1 family, L-arabinose/isopropyl-beta-D-thiogal	NA
K08161	mdtG; MFS transporter, DHA1 family, multidrug resistance protein	NA
K08162	mdtH; MFS transporter, DHA1 family, multidrug resistance protein	NA
K08218	ampG; MFS transporter, PAT family, beta-lactamase induction signal tran	3523.8133385
K08219	UMF2; MFS transporter, UMF2 family, putative MFS family transporter pro	NA
K08222	yqgE; MFS transporter, YQGE family, putative transporter	1529.3374175

K08227	lplT; MFS transporter, LPLT family, lysophospholipid transporter	NA
K08277	caiF; transcriptional activator CaiF	4.4329099677
K08282	E2.7.11.1; non-specific serine/threonine protein kinase [EC:2.7.11.1]	1890.656953
K08289	purT; phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]	3545.667018
K08296	sixA; phosphohistidine phosphatase [EC:3.1.3.-]	NA
K08298	caiB; crotonobetainyl-CoA:carnitine CoA-transferase [EC:2.8.3.-]	NA
K08300	rne; ribonuclease E [EC:3.1.26.12]	NA
K08301	rng, cafA; ribonuclease G [EC:3.1.26.-]	NA
K08302	gatY-kbaY; tagatose 1,6-diphosphate aldolase GatY/KbaY [EC:4.1.2.40]	976.32034241
K08303	K08303; putative protease [EC:3.4.-.-]	NA
K08307	mltD, dniR; membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]	3588.4710398
K08312	nudE; ADP-ribose diphosphatase [EC:3.6.1.-]	NA
K08315	hycl; hydrogenase 3 maturation protease [EC:3.4.23.51]	7.5521941802
K08318	yihU; putative dehydrogenase [EC:1.1.-.-]	NA
K08351	bisC; biotin/methionine sulfoxide reductase [EC:1.-.-.-]	NA
K08352	phsA, psrA; thiosulfate reductase / polysulfide reductase chain A	NA
K08476	pgtA; two-component system, NtrC family, phosphoglycerate transport sys	NA
K08483	PTS-EI.PTSl, ptsI; phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	NA
K08484	PTS-EI.PTSP, ptsP; phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]	32.427803604
K08641	vanX; D-alanyl-D-alanine dipeptidase [EC:3.4.13.22]	NA
K08679	E5.1.3.6; UDP-glucuronate 4-epimerase [EC:5.1.3.6]	NA
K08680	menH; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [E	746.31723515
K08681	pdxT, pdx2; 5'-phosphate synthase pdxT subunit [EC:4.3.3.6]	NA
K08682	acpH; acyl carrier protein phosphodiesterase [EC:3.1.4.14]	8.285943273
K08723	yjjG; 5'-nucleotidase [EC:3.1.3.5]	NA
K08930	pucA; light-harvesting protein B-800-850 alpha chain	NA
K08969	mtnE, mtnV; aminotransferase [EC:2.6.1.-]	NA
K08984	yjdF; putative membrane protein	NA
K08992	yciS; putative membrane protein	5.6260284741
K08997	ydiU; hypothetical protein	NA
K08999	K08999; hypothetical protein	NA
K09002	K09002; hypothetical protein	NA
K09007	GCH4, folE; GTP cyclohydrolase I [EC:3.5.4.16]	NA
K09011	cimA; D-citramalate synthase [EC:2.3.1.182]	5770.5107166
K09013	sufC; Fe-S cluster assembly ATP-binding protein	5491.2213658
K09015	sufD; Fe-S cluster assembly protein SufD	6090.5991983
K09016	rutG; putative pyrimidine permease RutG	5.8056793655
K09117	K09117; hypothetical protein	NA
K09118	K09118; hypothetical protein	12.087267636
K09121	K09121; hypothetical protein	NA
K09123	K09123; hypothetical protein	NA
K09124	K09124; hypothetical protein	120.34185225
K09125	K09125; hypothetical protein	NA
K09131	K09131; hypothetical protein	NA
K09136	ycaO; ribosomal protein S12 methylthiotransferase	15.22011851
K09158	K09158; hypothetical protein	NA
K09181	yfiQ; hypothetical protein	1568.5168492
K09384	K09384; hypothetical protein	345.1611437

K09456	aidB; putative acyl-CoA dehydrogenase	NA
K09457	queF1, queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]	NA
K09458	fabF; 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	NA
K09475	ompC; outer membrane pore protein C	222.58423529
K09477	citT; citrate:succinate antiporter	6.4143420287
K09582	PDIA4, ERP72; protein disulfide-isomerase A4 [EC:5.3.4.1]	3.9496191011
K09612	iap; alkaline phosphatase isozyme conversion protein [EC:3.4.11.-]	11.513799298
K09680	coaW; type II pantothenate kinase [EC:2.7.1.33]	729.93301366
K09690	ABC-2.LPSE.P; lipopolysaccharide transport system permease protein	794.80917014
K09700	K09700; hypothetical protein	NA
K09704	K09704; hypothetical protein	4202.6284289
K09706	K09706; hypothetical protein	NA
K09740	K09740; hypothetical protein	80.09321553
K09747	K09747; hypothetical protein	NA
K09760	rmuC; DNA recombination protein RmuC	2173.2216495
K09761	rsmE; 16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]	NA
K09769	K09769; hypothetical protein	1528.4830809
K09778	K09778; hypothetical protein	833.13531121
K09781	K09781; hypothetical protein	NA
K09786	K09786; hypothetical protein	NA
K09793	K09793; hypothetical protein	478.59643702
K09806	K09806; hypothetical protein	NA
K09808	ABC.LPT.P, lolC, lolE; lipoprotein-releasing system permease protein	7727.9970243
K09810	ABC.LPT.A, lolD; lipoprotein-releasing system ATP-binding protein [EC:3.6.3.18]	1814.5700709
K09819	ABC.MN.P; manganese/iron transport system permease protein	1092.2990053
K09820	ABC.MN.A; manganese/iron transport system ATP-binding protein	361.69436052
K09825	perR; Fur family transcriptional regulator, peroxide stress response regulator	NA
K09891	K09891; hypothetical protein	7.7438404182
K09893	K09893; hypothetical protein	NA
K09894	K09894; hypothetical protein	9.4127004173
K09896	K09896; hypothetical protein	2.6922771058
K09901	K09901; hypothetical protein	4.1415026507
K09902	K09902; hypothetical protein	NA
K09907	K09907; hypothetical protein	NA
K09908	K09908; hypothetical protein	NA
K09909	K09909; hypothetical protein	NA
K09911	K09911; hypothetical protein	2.4797307643
K09912	K09912; hypothetical protein	NA
K09914	K09914; putative lipoprotein	NA
K09920	K09920; hypothetical protein	NA
K09921	K09921; hypothetical protein	6.3686408528
K09922	K09922; hypothetical protein	549.31198875
K09928	K09928; hypothetical protein	426.79140067
K09940	K09940; hypothetical protein	600.86591557
K09949	K09949; hypothetical protein	NA
K09951	cas2; CRISPR-associated protein Cas2	275.75973271
K09952	K09952; hypothetical protein	7188.234564
K09954	K09954; hypothetical protein	239.94441762

K09971	aapM, bztC; general L-amino acid transport system permease protein	NA
K09974	K09974; hypothetical protein	NA
K09992	K09992; hypothetical protein	NA
K10005	gluB; glutamate transport system substrate-binding protein	NA
K10006	gluC; glutamate transport system permease protein	10.441430249
K10007	gluD; glutamate transport system permease protein	NA
K10008	gluA; glutamate transport system ATP-binding protein [EC:3.6.3.-]	NA
K10010	ABC.CYST.A; cystine transport system ATP-binding protein [EC:3.6.3.-]	NA
K10016	hisQ; histidine transport system permease protein	NA
K10022	aotJ; arginine/ornithine transport system substrate-binding protein	58.019161908
K10109	malF; maltose/maltodextrin transport system permease protein	NA
K10112	msmX, msmK, malK, sugC, ggtA, msik; multiple sugar transport system ATP	13152.176396
K10530	lctO; lactate oxidase [EC:1.13.12.-]	12.853822188
K10536	E3.5.3.12; agmatine deiminase [EC:3.5.3.12]	NA
K10541	mgIC; methyl-galactoside transport system permease protein	3875.6737157
K10542	mgIA; methyl-galactoside transport system ATP-binding protein [EC:3.6.3.1	5116.673669
K10546	ABC.GGU.S, chvE; putative multiple sugar transport system substrate-binding	NA
K10549	alsB; D-allose transport system substrate-binding protein	189.36590796
K10679	nfnB, nfsB; nitroreductase / dihydropteridine reductase [EC:1.-.-. 1.5.1.34]	1496.3042838
K10716	kch, trkA, mthK, pch; voltage-gated potassium channel	2258.7273632
K10763	hda; DnaA-homolog protein	31.687108432
K10796	prdE; D-proline reductase (dithiol) PrdE [EC:1.21.4.1]	71.356519911
K10797	enr; 2-enoate reductase [EC:1.3.1.31]	NA
K10800	SMUG1; single-strand selective monofunctional uracil DNA glycosylase [EC:5	513.60120131
K10806	yciA; acyl-CoA thioesterase YciA [EC:3.1.2.-]	460.54041714
K10819	E2.7.13.3; histidine kinase	NA
K10823	oppF; oligopeptide transport system ATP-binding protein	4754.3300889
K10852	E2.3.1.164; isopenicillin-N N-acyltransferase [EC:2.3.1.164]	NA
K10907	K10907; aminotransferase [EC:2.6.1.-]	NA
K10939	acfD; accessory colonization factor AcfD	24.628845903
K10973	allR; lclR family transcriptional regulator, negative regulator of allantoin a	NA
K11005	hlyA1, hlyA; hemolysin A	39.55737413
K11066	E3.5.1.28D, amiD; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	NA
K11085	msbA; ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]	7761.0354012
K11106	ttdT; L-tartrate/succinate antiporter	NA
K11180	dsrA; sulfite reductase alpha subunit [EC:1.8.99.3 1.8.99.1]	NA
K11192	PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC compo	8.3405637134
K11201	PTS-Fru2-EIIA; PTS system, fructose-specific IIA-like component [EC:2.7.1.6	30.690337579
K11208	yncG; GST-like protein	NA
K11214	SHPK; sedoheptulokinase [EC:2.7.1.14]	NA
K11250	leuE; leucine efflux protein	NA
K11261	fwdE, fmdE; formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]	NA
K11264	mmcD; methylmalonyl-CoA decarboxylase [EC:4.1.1.41]	NA
K11337	bchC; 3-hydroxyethyl bacteriochlorophyllide a dehydrogenase [EC:1.-.-.]	NA
K11382	pgtP; MFS transporter, OPA family, phosphoglycerate transporter protein	NA
K11391	rlmG; 23S rRNA (guanine1835-N2)-methyltransferase [EC:2.1.1.174]	9.1592347399
K11473	glcF; glycolate oxidase iron-sulfur subunit	NA
K11474	glcC; GntR family transcriptional regulator, glc operon transcriptional activ	NA

K11537	xapB; MFS transporter, NHS family, xanthosine permease	4997.9502844
K11605	sitC; manganese/iron transport system permease protein	NA
K11606	sitD; manganese/iron transport system permease protein	NA
K11607	sitB; manganese/iron transport system ATP-binding protein	NA
K11614	yufL, malK; two-component system, CitB family, sensor histidine kinase	31.627107231
K11646	K11646; 3-dehydroquinate synthase II [EC:1.4.1.24]	NA
K11719	lptC; lipopolysaccharide export system protein LptC	NA
K11720	lptG; lipopolysaccharide export system permease protein	4240.6558118
K11732	pheP; phenylalanine-specific permease	13.814344631
K11733	lysP; lysine-specific permease	11.951334225
K11734	aroP; aromatic amino acid transport protein AroP	13.069043994
K11737	cycA; D-serine/D-alanine/glycine transporter	21.450878283
K11739	nfrA; bacteriophage N4 adsorption protein A	18.483202793
K11744	tqsA; AI-2 transport protein TqsA	NA
K11747	kefB; glutathione-regulated potassium-efflux system protein KefB	15.437012265
K11748	kefG; glutathione-regulated potassium-efflux system ancillary protein KefG	NA
K11749	rseP; regulator of sigma E protease [EC:3.4.24.-]	NA
K11750	frsA; esterase FrsA [EC:3.1.-.-]	20.030129504
K11751	ushA; 5'-nucleotidase / UDP-sugar diphosphatase [EC:3.1.3.5 3.6.1.45]	15.082651248
K11752	ribD; diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amin	NA
K11754	folC; dihydrofolate synthase / folypolyglutamate synthase [EC:6.3.2.12 6.3	NA
K11894	impl, vasC; type VI secretion system protein Impl	NA
K11902	impA; type VI secretion system protein ImpA	146.31177666
K11910	vasJ; type VI secretion system protein VasJ	NA
K11912	ppkA; serine/threonine-protein kinase PpkA [EC:2.7.11.1]	NA
K11923	cueR; MerR family transcriptional regulator, copper efflux regulator	NA
K11925	sgrR; SgrR family transcriptional regulator	NA
K11927	rhIE; ATP-dependent RNA helicase RhIE [EC:3.6.4.13]	4600.6126054
K11932	uspG; universal stress protein G	21.397475016
K11934	ompX; outer membrane protein X	136.89795266
K11935	pgaA; biofilm PGA synthesis protein PgaA	12.424012923
K11938	cof; HMP-PP phosphatase [EC:3.6.1.-]	NA
K11940	hspQ; heat shock protein HspQ	NA
K11991	tadA; tRNA(adenine34) deaminase [EC:3.5.4.33]	NA
K12072	traH; conjugative transfer pilus assembly protein TraH	NA
K12112	ebgC; evolved beta-galactosidase subunit beta	NA
K12138	hyfC; hydrogenase-4 component C [EC:1.-.-.-]	NA
K12144	hyfI; hydrogenase-4 component I [EC:1.-.-.-]	NA
K12146	hyfR; hydrogenase-4 transcriptional activator	NA
K12148	bssS; biofilm regulator BssS	26.857807335
K12204	dotC, tral; defect in organelle trafficking protein DotC	11.516967746
K12209	icmE, dotG; intracellular multiplication protein IcmE	NA
K12211	icmG, dotF; intracellular multiplication protein IcmG	NA
K12218	icmP, trbA; intracellular multiplication protein IcmP	NA
K12251	aguB; N-carbamoylputrescine amidase [EC:3.5.1.53]	NA
K12264	norV; anaerobic nitric oxide reductase flavorubredoxin	NA
K12267	msrAB; peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11 1.	5771.6953574
K12288	hofM; pilus assembly protein HofM	NA

K12297	rlmL, rlmK; 23S rRNA (guanine2445-N2)-methyltransferase / 23S rRNA (guanine2445-N2)-methyltransferase	61.975991809
K12308	bgaB, lacA; beta-galactosidase [EC:3.2.1.23]	NA
K12339	cysM; cysteine synthase B [EC:2.5.1.47]	414.05653392
K12343	SRD5A1; 3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.1.22]	2008.2943275
K12373	HEXA_B; hexosaminidase [EC:3.2.1.52]	48167.709972
K12506	ispDF; 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase / 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	NA
K12516	bigA; putative surface-exposed virulence protein	40.391258431
K12518	papC; outer membrane usher protein PapC	NA
K12525	metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.1]	NA
K12542	lapC; membrane fusion protein LapC	813.60687169
K12543	lapE; outer membrane protein LapE	936.49463726
K12573	rnr, vacB; ribonuclease R [EC:3.1.-.-]	NA
K12582	wecF, rfft; TDP-Fuc4NAc transferase [EC:2.4.1.-]	NA
K12684	esp, sigA, sepA; serine protease autotransporter [EC:3.4.21.-]	38.563862118
K12687	flu; antigen 43	52.804583106
K12943	ygeR; lipoprotein YgeR	NA
K12960	mtaD; 5-methylthioadenosine/S-adenosylhomocysteine deaminase [EC:3.5.1.10]	53634.1493981
K12962	arnE; undecaprenyl phosphate-alpha-L-ara4N flippase subunit ArnE	NA
K12974	lpxP; palmitoleoyl transferase [EC:2.3.1.-]	NA
K12975	eptB; phosphoethanolamine transferase	18.735718736
K12994	wbpY; alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]	NA
K12995	wbpZ; rhamnosyltransferase [EC:2.4.1.-]	275.96077649
K12996	rgpA; rhamnosyltransferase [EC:2.4.1.-]	68.419519009
K12997	rgpB; rhamnosyltransferase [EC:2.4.1.-]	15.515026663
K13014	arnD; undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]	NA
K13015	wbpA; UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.136]	21.266246488
K13021	ttuB; MFS transporter, ACS family, tartrate transporter	NA
K13069	E2.7.7.65; diguanylate cyclase [EC:2.7.7.65]	14.065236586
K13085	ipgD, sopB; phosphatidylinositol-4,5-bisphosphate 4-phosphatase [EC:3.1.3.60]	NA
K13098	TLS, FUS; RNA-binding protein FUS	6.0287666812
K13255	fhuF; ferric iron reductase protein FhuF	NA
K13301	secM; secretion monitor	NA
K13381	chiA; bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]	17.543407409
K13409	raxB, cvaB; ATP-binding cassette, subfamily B, bacterial RaxB	NA
K13481	xdhA; xanthine dehydrogenase small subunit [EC:1.17.1.4]	NA
K13483	yagT; xanthine dehydrogenase YagT iron-sulfur-binding subunit	NA
K13497	trpGD; anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27 2.4.2.14]	25.5738072
K13525	VCP, CDC48; transitional endoplasmic reticulum ATPase	NA
K13527	mpa; proteasome-associated ATPase	NA
K13541	cbiGH-cobJ; cobalt-precorrin 5A hydrolase / precorrin-3B C17-methyltransferase	13.753503227
K13542	cobA-hemD; uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.11]	NA
K13571	pafA; proteasome accessory factor A [EC:6.3.2.-]	8.7802230826
K13598	ntrY; two-component system, NtrC family, nitrogen regulation sensor histidine kinase	304.90206151
K13631	soxS; AraC family transcriptional regulator, transcriptional activator of the sox operon	11.872063034
K13640	hspR; MerR family transcriptional regulator, heat shock protein HspR	23.523045063
K13643	iscR; Rrf2 family transcriptional regulator, iron-sulfur cluster assembly transcription factor	44.638618272
K13655	mqsA; HTH-type transcriptional regulator / antitoxin for MqsR toxin	NA
K13683	wcaE; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]	NA

K13695	nlpC; probable lipoprotein NlpC	7.7528073018
K13730	inlA; internalin A	NA
K13735	yeeJ; adhesin/invasin	NA
K13747	nspC; carboxynorspermidine decarboxylase [EC:4.1.1.-]	5041.9658285
K13771	nsrR; Rrf2 family transcriptional regulator, nitric oxide-sensitive transcript	NA
K13789	GGPS; geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10 2.5.1.11]	NA
K13821	putA; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase	5556.7551086
K13892	gsiA; glutathione transport system ATP-binding protein	583.90261545
K13893	yejA; microcin C transport system substrate-binding protein	NA
K13894	yejB; microcin C transport system permease protein	900.96400315
K13895	yejE; microcin C transport system permease protein	1204.091077
K13919	pduD; propanediol dehydratase medium subunit [EC:4.2.1.28]	1778.9986173
K13926	rbbA; ribosome-dependent ATPase	NA
K13990	FTCD; glutamate formiminotransferase / formiminotetrahydrofolate cyclohydrolase	1360.6818036
K14051	gmr; cyclic di-GMP phosphodiesterase Gmr [EC:3.1.4.52]	NA
K14054	mpaA; protein MpaA	9.1039526258
K14055	uspE; universal stress protein E	35.308572898
K14061	uspF; universal stress protein F	NA
K14063	fear; AraC family transcriptional regulator, positive regulator of tynA and fliC	NA
K14064	uspC; universal stress protein C	6.411085584
K14065	uspD; universal stress protein D	7.8551676596
K14170	pheA; chorismate mutase / prephenate dehydratase [EC:5.4.99.5 4.2.1.51]	NA
K14192	clfB; clumping factor B	NA
K14260	alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]	NA
K14347	SLC10A7, P7; solute carrier family 10 (sodium/bile acid cotransporter), member 7	766.682099
K14393	actP; cation/acetate symporter	NA
K14441	rimO; ribosomal protein S12 methylthiotransferase [EC:2.-.-.-]	NA
K14445	SLC13A2_3_5; solute carrier family 13 (sodium-dependent dicarboxylate transporter) member 5	4935.7533855
K14475	ICP; inhibitor of cysteine peptidase	NA
K14587	sgcE; protein sgcE [EC:5.1.3.-]	7.9832951939
K14588	cueO; blue copper oxidase	11.196650516
K14652	ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase	6355.753386
K14682	argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]	746.08798571
K14762	yibL; ribosome-associated protein	NA
K14836	NOP8; nucleolar protein 8	221.72084975
K14986	fixL; two-component system, LuxR family, sensor kinase FixL [EC:2.7.13.3]	533.59647805
K15342	cas1; CRISP-associated protein Cas1	2060.9255865
K15396	trmJ; tRNA (cytidine32/uridine32'-O)-methyltransferase [EC:2.1.1.200]	21.601330294
K15524	mngB; mannosylglycerate hydrolase [EC:3.2.1.170]	NA
K15533	K15533; 1,3-beta-galactosyl-N-acetylhexosamine phosphorylase [EC:2.4.1.100]	4664.9284456
K15547	mdtO; multidrug resistance protein MdtO	NA
K15548	aaeA; p-hydroxybenzoic acid efflux pump subunit AaeA	6.0267559481
K15724	erpA; iron-sulfur cluster insertion protein	NA
K15773	hipB; HTH-type transcriptional regulator, antitoxin HipB	NA
K15778	pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.9]	NA
K15830	hycE; formate hydrogenlyase subunit 5	9.5891455557
K15835	murR; RpiR family transcriptional regulator, murPQ operon repressor	NA
K15922	yihQ; alpha-glucosidase [EC:3.2.1.20]	27.740030628

K15977	K15977; putative oxidoreductase	2333.8487286
K15986	ppaC; manganese-dependent inorganic pyrophosphatase [EC:3.6.1.1]	NA
K15987	hppA; K(+)-stimulated pyrophosphate-energized sodium pump [EC:3.6.1.1]	20093.022334
K16012	cydC; ATP-binding cassette, subfamily C, bacterial CydC	13.126185019
K16066	ydfG; malonic semialdehyde reductase [EC:1.1.1.-]	12.894554437
K16076	nmpC, ompD; outer membrane porin protein LC	35.315941139
K16091	fecA; Fe(3+) dicitrate transport protein	23.341531035
K16138	uidR; TetR/AcrR family transcriptional regulator, repressor for uid operon	9.3787677016
K16139	uidB, gusB; glucuronide carrier protein	NA
K16140	uidC, gusC; putative glucuronide porin	7.0566706554
K16147	glgE; starch synthase (maltosyl-transferring) [EC:2.4.99.16]	NA
K16153	K16153; phosphorylase / glycogen(starch) synthase [EC:2.4.1.1 2.4.1.11]	8619.7634879
K16181	pylC; pyrrolysine biosynthesis protein PylC	122.82478167
K16201	dppC1; dipeptide transport system permease protein	10.17623137
K16263	yjeH; amino acid efflux transporter	10.402801394
K16264	czcD, zitB; cobalt-zinc-cadmium efflux system protein	1264.607404
K16291	erfK; L,D-transpeptidase	39.06840973
K16301	efeB; deferrochelataase/peroxidase EfeB [EC:1.11.1.-]	NA
K16322	pit; low-affinity inorganic phosphate transporter	36.145045385
K16363	lpxC-fabZ; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	6404.6716937
K16371	gatZ-kbaZ; D-tagatose-1,6-bisphosphate aldolase subunit GatZ/KbaZ	697.41498029
K16693	wzxE; O-antigen flippase	10.250716177
K16704	rffC, wecD; dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase [EC:2.3.5.3064017028]	
K16784	bioM; biotin transport system ATP-binding protein [EC:3.6.3.-]	NA
K16792	aksD; methanogen homoaconitase large subunit [EC:4.2.1.114]	NA
K16846	suyB; (2R)-sulfolactate sulfo-lyase subunit beta [EC:4.4.1.24]	232.49103008
K16850	uxaA2; altronate dehydratase large subunit [EC:4.2.1.7]	NA

log2FoldChange (donor 13)	pvalue (donor 13)	padj (donor 13)	baseMean
NA	NA	NA	8240.6329252
0.436957814382456	0.00129174689241	0.016394281177	17112.691461
0.5407195639405270	0.004535991257897	0.033581798915	13022.849152
NA	NA	NA	53.777068508
0.690183743191102	4.58E-05	0.002885854632	NA
0.541269555359360	0.001193863739666	0.015402024285	19488.795254
0.7557711596912860	0.000764321460678	0.012484461142	18106.57093
0.467855175317477	0.00115415966891	0.015056805454	31166.353684
NA	NA	NA	10388.33912
NA	NA	NA	3254.5463378
0.8821305385035710	0.001174022564907	0.015246691715	NA
-0.7871947054922540	0.003447007002207	0.028426899518	NA
NA	NA	NA	6165.1143598
NA	NA	NA	27220.831956
0.570348502459180	0.001961235393976	0.020776339174	NA
NA	NA	NA	12124.637465
NA	NA	NA	5995.6168566
0.935111753685545	3.52E-05	0.002416879689	29132.366609
-1.262078986623750	0.006097190798766	0.03978951391	NA
-1.273547825507470	0.005733619143655	0.038257599991	NA
NA	NA	NA	75563.298643
-1.20874596971334	0.00681451063554	0.041941288739	120.00402195
NA	NA	NA	5298.968211
NA	NA	NA	10029.274212
NA	NA	NA	4845.7228926
0.9890298161203520	0.000572498089947	0.010561228305	3061.4240396
1.093724543511120	0.000961972841747	0.013691245012	3738.4693663
-1.320576230662690	0.003266325095857	0.02745820387	NA
1.20217672294865	6.21E-05	0.003237738974	7335.860566
NA	NA	NA	99.969002727
0.613096526094609	0.00076650567257	0.012484461142	NA
0.4930838216561370	0.006609713875773	0.041472506485	NA
0.5908343070484150	0.000983942907315	0.013835369873	NA
0.5428425223715540	0.002731307483047	0.024375983907	NA
1.110504534270570	0.000155358672149	0.005235319392	4931.4201282
1.13752476054086	2.85E-05	0.002188001309	9390.8703434
NA	NA	NA	398.19155296
0.6827298478060450	0.000121905696469	0.004718112549	12355.638601
0.5360565818822110	0.000375779073904	0.008743573809	NA
NA	NA	NA	72.713637726
0.6138024754327380	0.000524978847572	0.010157469952	NA
0.6276883838589970	0.000317650586837	0.007858836354	22622.891142
0.784688235064697	2.51E-05	0.002005503415	NA
-0.7525305470724170	0.000286475388416	0.007382051048	NA
-0.785223063122212	3.40E-05	0.002415114557	NA
0.5974405412309590	0.000341262033652	0.008225835743	55892.930007
NA	NA	NA	13554.557723

NA	NA	NA	1385.4735773
NA	NA	NA	31.864151469
	0.5567860956039230.000194696655108	0.006040231943	11247.836121
	0.745198257193147	9.41E-05 0.004087548262	NA
NA	NA	NA	141.53021424
NA	NA	NA	8189.9276488
NA	NA	NA	268.51470236
NA	NA	NA	1164.3115982
NA	NA	NA	7616.0156382
NA	NA	NA	16.923649126
NA	NA	NA	170.0566575
NA	NA	NA	18.991691128
NA	NA	NA	531.47319061
NA	NA	NA	769.40959442
NA	NA	NA	1130.9037335
	0.7189098799855050.001440238741768	0.017313829233	2197.5610827
	1.048398035625550.000556158165492	0.010412050908	934.32979709
	0.9119185181897840.005344190755717	0.036570598914	1838.3117004
	0.7472342019661490.004088795244262	0.031649704178	6598.3559385
NA	NA	NA	1751.5459081
	0.7583413944264650.003607860249257	0.02907860972	1963.5879803
NA	NA	NA	713.04581655
	0.7147605570489880.003894192396985	0.030690318709	9628.5860968
	0.7657989382930950.001774407081193	0.019504863295	6604.4076277
	0.6873884915609390.003955836623935	0.030926730726	7695.4165697
	0.507056764527053 0.00229805210051	0.022799709799	NA
	0.5231406284406850.002386541075849	0.02297780558	NA
	0.7051301401638330.000549867147792	0.010383723095	NA
	0.7283635904195440.000841201707093	0.012870852446	NA
	0.5894657861029190.005753082323482	0.038311411929	NA
	0.5230077775968230.004984324685778	0.035296603617	NA
NA	NA	NA	7108.7287214
NA	NA	NA	72.104555833
	1.37792278429781	2.19E-06 0.000371587584	5898.5850202
NA	NA	NA	22117.791385
NA	NA	NA	875.81344425
	0.694862103573179	4.38E-05 0.002885854632	NA
	0.6321977753078990.000431709743886	0.009427672563	18155.451148
	0.845347343231081 0.00025496864852	0.006979570965	7401.6521171
	0.9736905360052270.000448219587205	0.009676385474	NA
NA	NA	NA	18.270984783
NA	NA	NA	3.2456140032
	0.550729622075360.001418684213391	0.017116162315	28920.396052
	-1.050840216683140.000469174997981	0.009747450927	NA
NA	NA	NA	38632.217882
NA	NA	NA	20.481574489
NA	NA	NA	35.129466488
NA	NA	NA	504.02827343

	-0.9123643341669780.000153436861558	0.005235319392	NA
	0.5771188775474480.005390035932674	0.036570598914	NA
	1.54926441079477	8.45E-10	5.51E-07 NA
NA	NA	NA	10073.53739
	-1.32609979946630.000665620828598	0.011462166603	NA
	-1.527811035149290.000920545896355	0.01339994932	110.09114922
NA	NA	NA	13140.165057
	0.5615439748457590.001139208417397	0.014993823918	NA
NA	NA	NA	1631.6447154
	0.4716051119455270.001389952464631	0.016979138076	25841.524491
	0.5755919424840730.002647992852898	0.023876340917	15084.486798
	0.6187007305670480.005380964356051	0.036570598914	NA
NA	NA	NA	9131.8973774
NA	NA	NA	6682.6699785
NA	NA	NA	2213.5079912
NA	NA	NA	1323.2305181
NA	NA	NA	6697.890279
	-0.6913736892701360.001641413448479	0.018810043984	NA
	1.054710715164240.000590707418728	0.010671861592	9443.0074884
	-1.578830508725420.000508883900567	0.010034110177	297.2973154
	0.718485274825220.001604509026385	0.018501550986	NA
NA	NA	NA	7626.2148003
	1.63831006799265	6.67E-08	2.30E-05 NA
NA	NA	NA	10717.209807
	0.5698904487418290.008119918339278	0.047374269833	NA
NA	NA	NA	174049.10333
NA	NA	NA	4224.7074536
	0.5396419300247220.000453000394429	0.009676385474	NA
NA	NA	NA	60.251376255
	1.37300455833714	1.01E-06	0.000207426541 NA
	1.016520026172270.000527492044088	0.010157469952	NA
NA	NA	NA	10.949510413
	0.930146524198830.005373951450192	0.036570598914	NA
NA	NA	NA	61.72459424
NA	NA	NA	31229.562786
NA	NA	NA	93.318878399
	0.614370686974320.000495916841342	0.009941225296	7333.009347
	-1.118866099881670.002425710744001	0.023131362287	NA
	-1.523650257232790.000933517810267	0.013483162483	NA
NA	NA	NA	9046.0853586
NA	NA	NA	22051.080283
NA	NA	NA	6350.6374939
	0.472853505832470.003705823102771	0.029563392875	NA
NA	NA	NA	4154.0710876
NA	NA	NA	5117.4150042
	0.5333974426281660.006254112405142	0.040342121108	NA
	0.7238587378207510.002319230545586	0.022940345502	NA
NA	NA	NA	105.07624333

NA	NA	NA	83.735106693
	1.115848418179070.001538693173503	0.017954482434	1057.6718822
	0.4177020414974010.005602248575284	0.037627473678	NA
	-1.80031558696296	5.83E-05	0.003131643275 NA
	0.5417277432172790.008498436067083	0.048997620334	12446.820698
NA	NA	NA	1268.4825631
	0.3718683250755430.005430034905284	0.036638411574	NA
	-0.4780528846170290.000621503722292	0.010943504732	NA
	0.549592765701990.004526926709646	0.033578285594	6864.3540997
	1.28009068506308	5.47E-05	0.003131643275 2183.9349876
	0.8950114048367840.005246138845919	0.036348859553	2273.2032499
	0.594858309067779	2.67E-05	0.002089397236 NA
NA	NA	NA	22847.384902
NA	NA	NA	49879.768492
	0.8686003422714320.000297213855127	0.007544214024	NA
NA	NA	NA	64.362236837
NA	NA	NA	140.05503798
NA	NA	NA	20675.589266
NA	NA	NA	2809.4060402
NA	NA	NA	5868.1406202
NA	NA	NA	59.020139228
	-1.29981682138850.004270420418696	0.032366852519	NA
	0.929107484932765	7.64E-05	0.003599543986 NA
	-1.613947965197790.000461953057484	0.009747450927	NA
NA	NA	NA	39870.173372
	0.4330392147100660.006814804316602	0.041941288739	7115.0823101
NA	NA	NA	6217.9704711
NA	NA	NA	19120.570372
NA	NA	NA	5214.2426702
	0.833526567035171	8.92E-06	0.001035687245 NA
NA	NA	NA	20294.368296
	0.3652498103506420.004437349113421	0.033102285657	3097.7985314
NA	NA	NA	32681.312929
NA	NA	NA	46741.289338
NA	NA	NA	8283.4420801
	-0.8552143829326240.000816210567188	0.012711422738	NA
	0.660724824858922	0.00573327345491	0.038257599991 1509.508988
	1.1520753805220.000657858187314	0.011378617939	1670.1723794
	0.511186388251273	0.00297535763229	0.025903503307 NA
	0.5288382431095120.006440261588044	0.040861724865	5748.5477593
NA	NA	NA	6225.9022505
NA	NA	NA	9571.089357
	-0.476320786785558	0.00830694797874	0.048106458739 NA
	0.5600758128059560.003997435604558	0.031065558207	NA
NA	NA	NA	7017.2524226
	0.9746883980266080.001894679594812	0.020319435713	2450.3151209
NA	NA	NA	999.94941249
	0.6320281752613140.002048428759268	0.021458108235	NA

NA	NA	NA	78027.009211
NA	NA	NA	1480.9792743
NA	NA	NA	918.61590352
	-1.32618613195377	0.00390874376684	0.03072333052 NA
	0.6363722277481320	0.001535232293244	0.017954482434 11304.735648
	0.756951012929170	0.001495738226223	0.017610966043 NA
NA	NA	NA	3466.5814941
	0.7081963332407890	0.000128009129806	0.004765597032 NA
NA	NA	NA	92.656191412
	0.6997259350795850	0.001786002989416	0.019555982313 NA
	0.460506447386140	0.002287103944426	0.022768048493 NA
	0.805750836625997	4.88E-05	0.002933793783 NA
NA	NA	NA	5452.9281038
	0.978442076521660	0.002816359821246	0.024810888519 1359.9270045
	-1.400581498190890	0.000130134642928	0.004799021879 NA
NA	NA	NA	106.3562077
NA	NA	NA	5605.4953887
NA	NA	NA	38.608036593
	0.5176421321714480	0.008604095329472	0.049460895063 NA
	0.4289410245557530	0.007788138693148	0.046065409327 18384.812368
NA	NA	NA	8592.8332705
NA	NA	NA	50.733436354
	0.791036193909680	0.000510818092902	0.010034110177 NA
NA	NA	NA	3830.1267021
NA	NA	NA	17681.683868
NA	NA	NA	14140.166182
	0.7664580282133880	0.000206396071866	0.006158795763 NA
NA	NA	NA	101632.65849
	-1.308047993771050	0.001682405899622	0.018926245257 NA
NA	NA	NA	34999.394761
NA	NA	NA	1232.467296
	0.890576270587970	0.003171045980748	0.027104537921 NA
	-1.14735125294756	0.00770570541743	0.045777511363 NA
	-1.282255809442160	0.001835890349141	0.019976361508 244.64669726
	-0.7103712312853450	0.007295311386845	0.044076309445 NA
	0.6171491528011090	0.001756113018073	0.019391654767 NA
	-0.9458265661789480	0.000852727603127	0.012946781116 NA
	0.716673231988415	3.09E-06	0.000463946149 NA
	0.4054111519906480	0.003604771466367	0.02907860972 11274.753567
	-1.066986157871340	0.003201702420399	0.027159494389 262.96257008
NA	NA	NA	3934.5198618
	0.7101425032016120	0.000170600267542	0.005557303715 NA
	0.5750033188327920	0.002352054549724	0.02297780558 NA
	0.7221489902768260	0.001341177029706	0.016558853745 NA
	-1.035731017997330	0.002058529185969	0.021458108235 NA
	0.6182630627392310	0.005057926752653	0.035496293853 NA
	0.3565820215477480	0.005213373057745	0.036197291799 NA
	-1.72089026858940	0.000187358070308	0.005859061575 205.80398658

NA	NA	NA	14400.833069
	1.048834184378020.000215618838016	0.006243363243	8097.8716912
	-1.118651310461820.000759761196707	0.012484461142	NA
NA	NA	NA	6111.6177454
NA	NA	NA	10.829373856
	1.0078317420054	2.09E-05	0.001739192918 NA
NA	NA	NA	17989.818044
	0.8169181228040190.004579039474005	0.033645611473	2233.1404366
	-1.571546666526160.000593449271767	0.010671861592	NA
	0.4877719357581940.001476127148846	0.017560235107	NA
	0.4745814751421280.001451445265581	0.017350763129	15335.995511
	0.8025156628756760.000102700043822	0.004363635558	2862.1883468
	0.7033322151758230.002079602437981	0.02156277435	NA
	1.353255352779770.000492729541202	0.009941225296	NA
	1.310475326027540.001503035578093	0.017643741966	NA
	0.9892108662296630.001364325875388	0.016770911468	1671.6036488
	-1.059523496356240.004105768494117	0.031718278742	NA
NA	NA	NA	394.01011474
	0.824880893181262	0.00218193336978	0.022072217929 NA
NA	NA	NA	53.450242805
NA	NA	NA	3642.0952516
	1.177663333547730.000135835793374	0.004916501077	1745.9592989
	-1.353898760807560.003175717157253	0.027104537921	76.406497919
NA	NA	NA	1959.6280154
NA	NA	NA	10207.52149
NA	NA	NA	21585.695076
	0.4704477005168130.000536706706899	0.010234080572	NA
	0.7157725713983520.000282371561173	0.007382051048	8118.0707898
NA	NA	NA	10166.058285
NA	NA	NA	2042.7384002
NA	NA	NA	84777.712541
NA	NA	NA	366.09457856
	-1.355014396382280.002516022259885	0.023141484739	NA
NA	NA	NA	299.64248049
	0.743065328857491	0.00011379841584	0.004682505342 NA
NA	NA	NA	11394.10918
NA	NA	NA	5934.6647133
	1.004127390090530.000963185566212	0.013691245012	1623.6766892
NA	NA	NA	8666.5597679
	-1.401167699680170.000791391209605	0.012688384014	2120.2281348
	0.922427603318256	1.44E-05	0.001389800975 64635.100564
NA	NA	NA	514.0298524
	0.678841017729207	1.06E-05	0.00114859848 5299.2115366
	0.712263999608787	0.00501746169233	0.035444739018 4173.7001658
	1.193774617969010.000244623123636	0.006830227074	NA
NA	NA	NA	4212.0981653
	0.662909937099680.001342838740653	0.016558853745	6262.2848401
	-1.7882865222697	6.77E-05	0.003365374882 44.110690765

NA	NA	NA	6017.3027143
	-1.205085550369680.007068692888615	0.042906087735	NA
	-1.63847791497111	6.98E-05	0.003368326615 NA
NA	NA	NA	5934.3820814
NA	NA	NA	1934.4825613
	0.701940158352598	5.53E-05	0.003131643275 25553.931329
NA	NA	NA	32865.066628
NA	NA	NA	4999.6913025
NA	NA	NA	1115.7293183
NA	NA	NA	6777.899692
NA	NA	NA	2003.1304779
	0.4987646566924030.002831315433399	0.024871038268	4169.512903
NA	NA	NA	64.983854608
NA	NA	NA	2820.0017824
	1.20285739742188	2.99E-06	0.000463946149 13645.082419
	0.6542543814003030.000118298125173	0.004718112549	NA
	-0.661610570878009	0.00874618043564	0.049837929042 NA
	-1.556728805315650.000473293565888	0.009747450927	NA
	0.5803232083720170.000201602226114	0.006109016294	57797.200044
NA	NA	NA	3344.9514097
NA	NA	NA	3117.193098
NA	NA	NA	8062.3282986
NA	NA	NA	8405.7309419
	0.4620996908539430.003619208996191	0.029110057543	NA
	0.7882423733605950.006551913828705	0.041175934335	23254.81154
	0.7451858749511830.008699804118647	0.049718617397	5703.5313787
NA	NA	NA	5647.4604124
NA	NA	NA	50.338917607
	0.5103824593219960.004130596308129	0.031751141989	9607.7350265
NA	NA	NA	1778.2950611
NA	NA	NA	11759.23194
NA	NA	NA	23301.671025
NA	NA	NA	13759.191906
NA	NA	NA	15933.069954
NA	NA	NA	1238.5377472
NA	NA	NA	8216.6497048
NA	NA	NA	15551.90847
NA	NA	NA	19506.857836
	-1.49582439030423	0.00069352281241	0.011838343553 122.23529535
	0.6306218069708210.000616032849349	0.01089625524	16481.789984
	-0.6167000736961590.002496678705315	0.023139164847	1592.8645918
NA	NA	NA	26450.956154
	0.4187961210309730.003237456639755	0.027333084244	22992.180463
	1.05976252428814	0.00381738464361	0.030268066069 879.56156665
	1.530790137207540.000808017195349	0.012688384014	NA
NA	NA	NA	18025.391811
	0.5144909442857710.005253800370266	0.036348859553	NA
NA	NA	NA	5351.4008084

NA	NA	NA	2016.1747204
NA	NA	NA	21702.095857
	-0.5732621404787790.001135417097027	0.014993823918 NA	
	0.77107063169219	1.47E-05 0.001389800975	75743.673126
	0.4290106269235830.003108233521789	0.026762301402 NA	
	0.4237611035468070.004789009331086	0.034543610623 NA	
NA	NA	NA	39833.257204
NA	NA	NA	34549.945064
NA	NA	NA	31489.321449
	0.3504130218353330.000995422403721	0.013881074201 NA	
NA	NA	NA	20028.263742
	0.3970681332691980.001669771142121	0.018864553163 NA	
	0.3760258740689560.004736505212912	0.034414496054 NA	
	0.3628584989542630.006213946622686	0.04019822813 21398.225556	
	0.5436723667399920.001914321305027	0.020389869159 34956.549518	
	0.386398733181370.001012875173295	0.01392437606 NA	
	1.046934656389490.004451890808497	0.033147506991 778.92044114	
	0.5704434235652280.000572775748434	0.010561228305 6092.2564329	
NA	NA	NA	4591.7523482
NA	NA	NA	2314.5229269
	0.6033330841317160.005210744329654	0.036197291799 40769.67787	
	0.6738378209496540.002530051551053	0.023215895571 5834.9711756	
NA	NA	NA	12748.472072
	1.11653053565960.001206676441002	0.015513139947 540.32695168	
NA	NA	NA	13145.689051
NA	NA	NA	14213.725134
	1.264398244678820.005735214529158	0.038257599991 28.042813375	
NA	NA	NA	2196.9797277
	0.5761698009283390.003107690698776	0.026762301402 NA	
NA	NA	NA	24368.595417
NA	NA	NA	19547.93951
NA	NA	NA	15508.804581
NA	NA	NA	16489.04817
NA	NA	NA	33432.145393
NA	NA	NA	60088.848746
	0.863207434808904 0.00216274009002	0.022045257534 NA	
NA	NA	NA	12890.727728
NA	NA	NA	22575.260407
NA	NA	NA	15865.099688
	1.16618852359475	5.70E-06 0.000742971837 NA	
NA	NA	NA	16817.966394
	0.5721826380162440.006936897840395	0.042303172634 NA	
NA	NA	NA	918.27697893
NA	NA	NA	4406.6998228
NA	NA	NA	117370.33974
	0.8032543430891350.006891125598381	0.042155571149 1769.7383842	
	-1.09877115118536 0.00582905750137	0.038619975886 NA	
NA	NA	NA	28805.038232

NA	NA	NA	8002.0579516
NA	NA	NA	16503.050713
NA	NA	NA	3481.910481
NA	NA	NA	84.272550693
NA	NA	NA	57.969619652
NA	NA	NA	55.96839731
NA	NA	NA	138.44684955
	0.5141343981474990.005436244234583	0.036638411574 NA	
	0.5999755581433260.000740442915652	0.012316558967 NA	
	0.7939002037003610.000410541266234	0.009170318913 NA	
NA	NA	NA	923.73875017
NA	NA	NA	48.530000443
	-1.424721835398530.001153176792251	0.015056805454 NA	
NA	NA	NA	14923.069533
NA	NA	NA	8773.8817339
NA	NA	NA	80082.190004
NA	NA	NA	59829.867136
NA	NA	NA	14190.157744
NA	NA	NA	10925.78547
NA	NA	NA	31064.132573
	-1.401346210039450.000934749816517	0.013483162483 NA	
NA	NA	NA	46.124642677
NA	NA	NA	182.85780723
	1.13817709664111 0.00586301127184	0.038779206534 NA	
NA	NA	NA	36.244576633
	-1.27205549144813 0.00431711934711	0.032574465302 NA	
	1.266428656731330.000437687073073	0.00950510427 1636.8902218	
NA	NA	NA	14.560349726
NA	NA	NA	42.282910477
	0.5338933129974590.003536815156333	0.028863069825 NA	
NA	NA	NA	25.874450134
NA	NA	NA	4856.8369512
NA	NA	NA	27083.100833
NA	NA	NA	182.28759572
	0.4510142289119790.006416829744007	0.040861724865 NA	
NA	NA	NA	6877.7884725
	0.6876365429893970.005410224419679	0.036589216707 NA	
NA	NA	NA	8116.9101467
	1.272032835205410.000860065391965	0.01294678116 NA	
NA	NA	NA	29420.340641
NA	NA	NA	209.70747392
NA	NA	NA	5367.6413801
NA	NA	NA	1141.273275
	-1.286221315284770.004860715423359	0.03486336989 49.113472066	
NA	NA	NA	20.72714536
NA	NA	NA	2144.4455937
NA	NA	NA	836.58133482
NA	NA	NA	808.42396582

NA	NA	NA	10.7618161
NA	NA	NA	1485.9630412
	0.686448838707098	9.11E-05 0.004047244675	8960.027942
NA	NA	NA	1010.087579
NA	NA	NA	7926.5775229
NA	NA	NA	6273.8293767
	1.043819950986530.000459098053502	0.009747450927	93653.894651
	-1.38154251673626	0.00250104979506 0.023139164847	NA
NA	NA	NA	14.522548072
	-1.243421816150680.006401046597156	0.040861724865	NA
NA	NA	NA	46998.497182
NA	NA	NA	38332.614261
	0.879264447130446	0.00031558604025 0.007857489372	NA
NA	NA	NA	2533.5787731
NA	NA	NA	197.39821215
NA	NA	NA	770.9712189
NA	NA	NA	57.597298091
NA	NA	NA	6613.5424493
	-1.288282614964030.005120062273163	0.035803798615	NA
NA	NA	NA	6392.0674071
NA	NA	NA	4495.606081
NA	NA	NA	24.155269028
NA	NA	NA	5636.1880643
NA	NA	NA	58380.192812
	0.421221901485390.005023378208217	0.035444739018	12328.64381
	0.930209641852026	8.29E-05 0.003857179156	NA
	0.7017944884195830.000401070034782	0.009128698828	6685.5237324
NA	NA	NA	10139.294762
	0.5258638196512340.004117536321924	0.031746448683	10213.427521
	0.8592315458716110.000306507078827	0.00769777306	NA
	1.172529046037920.000388879657486	0.008941944595	1657.3543706
	0.5047030046288590.005875670125019	0.038797288038	6838.3328985
NA	NA	NA	750.26719369
NA	NA	NA	15.200859345
	1.125176656111580.000282890842638	0.007382051048	2572.9836985
	-1.240828410150670.005368907091432	0.036570598914	NA
NA	NA	NA	101.66855929
	0.4709331285416620.000887908333259	0.013147097253	NA
NA	NA	NA	81.169490809
NA	NA	NA	48.063603233
NA	NA	NA	39.084339287
	0.998085830817941	0.00038296927793 0.008858147381	4077.0070194
	-1.24904475613671	0.00166664102088 0.018864553163	NA
NA	NA	NA	187.97546144
	0.5576143827092770.000799807447229	0.012688384014	20701.460565
	0.5443181472677090.003385748988045	0.028133744233	25332.952468
NA	NA	NA	18.72521552
NA	NA	NA	8.8990939912

NA	NA	NA	933.21667128
	0.677369399021707	8.45E-05	0.00388617427 13679.667858
	0.6525085611470410.004413757794898	0.032989252811	NA
	0.867112479410729	0.00185214617944	0.020055510846 14504.653046
NA	NA	NA	12000.963856
NA	NA	NA	4105.6998916
NA	NA	NA	155.19323589
	0.79728448826502	0.00100233410543	0.013894056802 10483.385581
	-1.41186512800750.000287048288381	0.007382051048	NA
	-1.82942203624747	3.09E-05	0.002239449958 NA
	-1.59031119301949	0.00049363335715	0.009941225296 NA
	-1.33480785663940.003741000663631	0.029783241536	NA
	-1.84644588312099	3.50E-05	0.002416879689 NA
	-1.342329208740340.002433424995441	0.023131362287	NA
NA	NA	NA	43.31459029
	-1.093248772595210.008384378778861	0.048483042377	NA
	-1.003078668448730.005317506104409	0.036570598914	NA
	-1.17411239300740.000205216217555	0.006158795763	NA
	-1.467257048103620.000861131517446	0.01294678116	NA
	-1.285670510208530.000808056344379	0.012688384014	NA
	-0.7095402986252080.007850930728596	0.046308865617	8802.9318312
NA	NA	NA	2324.2629443
	1.260495520108480.000170374054063	0.005557303715	1270.4144467
NA	NA	NA	2197.0957791
NA	NA	NA	3159.3546178
NA	NA	NA	11007.401741
NA	NA	NA	11108.63156
	-1.194374187884140.007552878305546	0.045277787368	NA
	-1.287142813239690.005195773548815	0.036197291799	NA
NA	NA	NA	60.13342201
NA	NA	NA	31999.969916
NA	NA	NA	18372.439769
NA	NA	NA	9366.0615079
NA	NA	NA	12176.796884
	-1.325594521437180.002365751173571	0.02297780558	NA
NA	NA	NA	34662.377352
NA	NA	NA	10315.432547
NA	NA	NA	11070.472928
NA	NA	NA	7307.5424916
NA	NA	NA	8118.6398129
	0.668358612315902	5.98E-05	0.00316007441 15405.810887
NA	NA	NA	4743.8288739
NA	NA	NA	1343.5392839
NA	NA	NA	5638.5146142
NA	NA	NA	20019.360406
NA	NA	NA	20239.039974
NA	NA	NA	19040.256514
	0.5758753373206530.002147951518502	0.02203764432	NA

	0.472657519087780.001411895904669	0.017087000283	78414.429556
	0.8385424008953220.000556694458871	0.010412050908	NA
NA	NA	NA	7010.7129922
NA	NA	NA	7107.1008759
NA	NA	NA	24748.147353
NA	NA	NA	28856.440021
	0.5239076855337380.000763286462946	0.012484461142	NA
NA	NA	NA	104365.09831
NA	NA	NA	113420.10396
NA	NA	NA	48424.753561
NA	NA	NA	7397.0473868
NA	NA	NA	3132.6239062
	0.6291393824560410.001477952762905	0.017560235107	NA
	0.6602067512741550.004698712583454	0.034203477633	NA
NA	NA	NA	843.33654327
	0.5222792337219950.002348749649261	0.02297780558	NA
NA	NA	NA	3761.2374836
	0.4778978533981990.001190797367695	0.015402024285	NA
	0.3753847956309640.008016695705558	0.047123704531	9493.5986305
	-1.464667457497330.001093690706008	0.014691535979	NA
	0.8446978530400520.003874079617064	0.03065541948	NA
NA	NA	NA	1169.8151605
NA	NA	NA	38.372065513
NA	NA	NA	14634.194483
NA	NA	NA	2824.5126594
NA	NA	NA	8528.8516017
NA	NA	NA	6790.010881
NA	NA	NA	1015.7241653
	0.4652331722280170.005795430747249	0.03852778706	28234.265669
	1.49219899559344	7.05E-08	2.30E-05 1516.3371457
NA	NA	NA	56.250579893
	0.7992040795508660.002102214680251	0.021739569273	NA
	0.667037935571404	0.00017224150981	0.005564397205 NA
	-0.5471126283632440.006090319254016	0.03978951391	NA
NA	NA	NA	7323.7981903
	-1.37586740710240.002767495354781	0.024530928213	NA
NA	NA	NA	2226.2599878
NA	NA	NA	6953.6648948
	0.850997059327110.004466046561658	0.033189688231	NA
	0.9826703558775440.003404262221061	0.028133744233	NA
NA	NA	NA	2712.8691569
	0.7039885403959990.006035070371651	0.03971563987	3849.8907014
NA	NA	NA	1137.0438234
NA	NA	NA	2659.2319033
	0.7875791989199610.000248639313611	0.006893128205	8645.6953831
	0.5581466802086030.002850522823416	0.024983618199	4766.648909
NA	NA	NA	6918.0980315
NA	NA	NA	88.144895195

	0.4810881115228270.002282919226045	0.022768048493	NA
	1.195868460957830.000350298894852	0.008298899273	1403.1186924
NA	NA	NA	27957.351646
	0.816870457317820.000270902802695	0.007303165902	NA
NA	NA	NA	19167.203529
	1.085152532204760.000527297460762	0.010157469952	NA
	-1.219040030567910.008143554901933	0.047431127006	NA
NA	NA	NA	350.00398005
	0.6971200349300640.000337641723064	0.008225835743	NA
	0.7033725225432770.003102958938354	0.026762301402	NA
	0.6582103661290580.001493125339894	0.017610966043	NA
NA	NA	NA	37.668630188
NA	NA	NA	12874.818768
	0.90015020441403	4.47E-05	0.002885854632 19723.643431
	0.74986032581270.000781821741698	0.012628682596	NA
NA	NA	NA	1235.9873122
	0.461838768130144	0.00238060534297	0.02297780558 NA
NA	NA	NA	10132.670914
	-1.369484882267550.002110220890426	0.021764784857	NA
	-1.89114518946549	2.14E-05	0.001739192918 236.67172081
NA	NA	NA	2062.4779088
	1.04883638502371	1.86E-05	0.001620000291 NA
	1.066569357356140.000132929426155	0.004856272213	2131.8134231
	0.6217295638960860.002369444700321	0.02297780558	NA
NA	NA	NA	11798.105659
	1.16212405351558	0.00765574481464	0.045619369635 NA
NA	NA	NA	14.842538822
	-1.218870942987990.008109963900549	0.047374269833	101.24413146
	0.493666670987390.008228608098773	0.047794396817	4234.9669859
NA	NA	NA	916.3259893
	-2.00686219275489	3.89E-06	0.000543450874 117.74528461
	0.5634028230737650.004639464338645	0.033898441308	NA
	0.8701596717490250.000473682639358	0.009747450927	6583.4796351
NA	NA	NA	60.936263865
NA	NA	NA	14.804216133
NA	NA	NA	53.149398044
	-0.8134375464017730.003986843407046	0.031044961909	1973.7793109
NA	NA	NA	2.775859896
NA	NA	NA	1513.4795114
NA	NA	NA	40.856564011
NA	NA	NA	8463.4339958
	0.4584896713043610.004324929007834	0.032574465302	NA
NA	NA	NA	8914.249501
	0.40102717261920.003476981924107	0.028553618364	NA
	-1.715657234893370.000126932394584	0.004765597032	135.11854783
	-1.327561555145610.003765896456157	0.0299205066	NA
	0.4956145517827510.001979721264293	0.020915487627	NA
NA	NA	NA	18301.387437

NA	NA	NA	28866.850075
NA	NA	NA	5534.7194835
NA	NA	NA	474.38435792
NA	NA	NA	5192.0789652
	0.4225297369641340.004824210069495	0.034728981882 NA	
	0.664862471759080.000810352432602	0.012688384014 28823.287512	
	1.09563494621239	4.17E-05 0.00281133197 NA	
NA	NA	NA	5942.6815269
	0.787474309221540.000218414212699	0.006277802628 NA	
NA	NA	NA	48.941734225
	0.8359464915665730.002481085595737	0.023139164847 NA	
	0.4844212757397750.000960331227971	0.013691245012 NA	
NA	NA	NA	2133.8963066
	1.096652850249980.000359073962673	0.008455542892 5055.5088483	
	1.30753969731815	1.67E-06 0.000310559649 4681.1100244	
	-1.226688615553470.007789520482263	0.046065409327 232.90377647	
	0.782149735898582	4.79E-06 0.000645548092 NA	
	0.6654024420674910.000181580794157	0.005770726214 NA	
	0.823112577337863	6.80E-05 0.003365374882 NA	
	0.619359454175756	0.00034835486326 0.008298899273 NA	
NA	NA	NA	17058.164791
NA	NA	NA	677.0379278
	-1.469329240875090.001082863318011	0.014596250725 186.28761337	
NA	NA	NA	85.766940266
NA	NA	NA	61.431365227
	1.08839255870780.001023786579292	0.013992943141 1996.9617659	
	-1.4683602039890.001330841913244	0.016558853745 NA	
	0.679167743749774	0.00019965654295 0.006097323644 NA	
	0.7235890680253890.000296949041768	0.007544214024 25601.812446	
	0.4222556089009340.004408214602569	0.032989252811 NA	
	0.4169736696118710.001489847877239	0.017610966043 NA	
	1.235787701179150.000120959309181	0.004718112549 3490.1396753	
	1.021564381792220.000451032682609	0.009676385474 NA	
NA	NA	NA	59.383390428
NA	NA	NA	11493.499151
	-1.391887329900680.002455747083431	0.023131362287 297.95899904	
	0.4818467917715170.001684915157192	0.018926245257 NA	
	-1.433049376553580.001873522089296	0.020230933279 NA	
	0.455719726729640.001911016906721	0.020389869159 12597.63521	
NA	NA	NA	238.08877897
NA	NA	NA	253.19023078
NA	NA	NA	59.841006172
NA	NA	NA	23.634196015
	0.908530291602280.002289036341242	0.022768048493 1540.9823276	
	-1.04742666327713	0.00130232406904 0.016421886406 NA	
	-1.393021940894950.002515260699385	0.023141484739 63.72519633	
NA	NA	NA	35687.135812
NA	NA	NA	5241.0014

	0.4733768420328930.005328949739499	0.036570598914	NA
	0.4741833754453030.000731795906326	0.01223508864	43164.733114
	-0.7559623697015770.006825604341052	0.041941288739	4345.0554641
NA	NA	NA	23373.054005
NA	NA	NA	6357.4476175
NA	NA	NA	178.10159883
	0.660152142737325 0.00025532838269	0.006979570965	NA
NA	NA	NA	1909.3377562
	-1.479518809423270.000428885405988	0.009418612652	NA
	-1.49940503024360.001102208697472	0.014755252734	181.79544717
	0.9997874639393760.001398418154485	0.017029335096	1096.7766823
	-1.627171434315110.000343000268969	0.008225835743	NA
	1.71917315525359 6.21E-08	2.30E-05	NA
	-1.207898116483890.006832390347236	0.041941288739	NA
	0.3900425267091130.004674075936213	0.034087617229	8245.2558788
	1.10948772233409 5.68E-07	0.000123404968	NA
	0.7080255267787190.000832602414992	0.012813554489	NA
	-1.7542286663867 0.00013855051377	0.004968751911	152.52738795
	0.6785622237448580.004037166594453	0.031312071861	6859.7672113
	-1.37149175894079 0.00240985267114	0.0231136167	67.914893907
	-1.28868611581170.004413204356804	0.032989252811	NA
	0.587453806956920.000922124934027	0.01339994932	22637.782301
NA	NA	NA	2943.6260562
	0.5501236253302260.003202999977845	0.027159494389	NA
NA	NA	NA	48.202603011
	0.4814184116527110.000307201994718	0.00769777306	NA
	0.9566877475873510.000179401170466	0.005748189962	3567.4438538
NA	NA	NA	41.492304639
	-1.306490926137590.003403266496748	0.028133744233	NA
NA	NA	NA	100.28444316
	-1.516027096160730.000988298943809	0.013846812084	NA
	1.60905514154148 2.51E-07	6.76E-05	NA
NA	NA	NA	425.29172303
	1.35830255215403 2.84E-07	6.95E-05	5624.143427
NA	NA	NA	918.80320235
	1.319081694335110.003473716648834	0.028553618364	NA
	0.825828774527360.000183167193939	0.005774198073	NA
NA	NA	NA	72.052410101
NA	NA	NA	54.522433177
	-1.196833632085490.006785563934871	0.041941288739	NA
NA	NA	NA	48789.786395
	0.869595129871433 5.62E-05	0.003131643275	3080.6441753
	-1.266457202686220.003273491172394	0.027459392689	12.931341674
	-1.461740095290360.001411513448527	0.017087000283	11.065032541
NA	NA	NA	5.7297522376
NA	NA	NA	2141.1873007
NA	NA	NA	59.942828416
	0.6379905001885530.004789623166515	0.034543610623	22695.455848

	1.74652612236355	2.32E-11	2.27E-08 NA
	-1.77694539243638	9.29E-05	0.004078425746 NA
	-1.23161778932304	0.00619360242175	0.040150566943 NA
NA	NA	NA	11610.470116
	0.7135932159715610	0.005382526299591	0.036570598914 NA
NA	NA	NA	63.486735721
NA	NA	NA	52.906281076
NA	NA	NA	13922.048761
	1.017087930286530	0.006077807857822	0.03978951391 NA
NA	NA	NA	28.612339495
	-1.374665963490190	0.002124604194758	0.021855467888 NA
NA	NA	NA	30.324694597
NA	NA	NA	18532.258637
	0.3100846932773050	0.005052674842657	0.035496293853 NA
NA	NA	NA	180873.25805
NA	NA	NA	31069.991385
	-1.641086237893790	0.000150545707241	0.005226885873 NA
	-1.553114944762630	0.000589794141804	0.010671861592 96.855609337
NA	NA	NA	2750.6906901
NA	NA	NA	14.238967975
	0.598817116727840	0.001550447559295	0.018037796159 NA
	-1.48210229007430	0.000724254094003	0.01223508864 NA
NA	NA	NA	8167.2334702
	0.4294734394584230	0.002756108708497	0.024485520322 NA
	-1.287753383187880	0.002650890754181	0.023876340917 NA
	0.509335162409450	0.003287965370128	0.027521748676 NA
	-1.27769495572768	0.00419307118577	0.0318885511 NA
NA	NA	NA	1959.7875122
NA	NA	NA	3964.4765177
NA	NA	NA	414.94671403
NA	NA	NA	2840.2788626
NA	NA	NA	4054.0418596
NA	NA	NA	7140.2416326
	-1.582561912328160	0.000121191241468	0.004718112549 88.728509899
	0.9360698612033060	0.000571149807587	0.010561228305 5225.7921372
	-1.278743862450750	0.005270562547826	0.036400404593 NA
NA	NA	NA	4.0584599425
	0.5320783305268180	0.006324203628618	0.040660052606 NA
NA	NA	NA	31.262801088
NA	NA	NA	6133.5509292
	-1.649629348292710	0.000276721346367	0.007382051048 NA
	-1.475444583344380	0.001332028914171	0.016558853745 NA
	-1.419619321011760	0.001795814685174	0.019608490515 165.92744086
	2.31479286802271	3.09E-08	1.34E-05 NA
NA	NA	NA	658.73627382
	0.6535275656540570	0.003354142956284	0.028015694052 NA
	-1.490383535095390	0.001048976204782	0.014287275207 NA
	0.6337258040705430	0.005398116033167	0.036570598914 NA

	-1.511814676379050.000604111705845	0.010782980174	66.344976865
NA	NA	NA	598.09421873
NA	NA	NA	20034.160479
NA	NA	NA	92.015738901
NA	NA	NA	2088.7209022
NA	NA	NA	56.069430542
NA	NA	NA	58.021430986
	1.381239499306820.000615335083258	0.01089625524	1227.714104
NA	NA	NA	534.64513648
	-1.302873656962850.004638932368278	0.033898441308	NA
	0.6219277963410020.000407503650526	0.009154780287	13672.048401
NA	NA	NA	2992.4271753
NA	NA	NA	94.0715517
	0.815574090671699 0.00073241512965	0.01223508864	NA
NA	NA	NA	30.172945637
NA	NA	NA	16.097345136
NA	NA	NA	11.629351683
NA	NA	NA	56.521656147
	-1.500464694550280.001117384868385	0.014882004406	NA
	-1.329238768785840.003574265930124	0.029075395577	51.627114774
NA	NA	NA	84.483347944
	-1.57710613584884 2.97E-05	0.002234610916	NA
	-1.396671488610940.002171252021087	0.022045257534	388.97594934
	-1.511807362742610.000589652388635	0.010671861592	304.2413603
	0.782427828425665 4.52E-05	0.002885854632	NA
NA	NA	NA	11020.12431
	-2.09081257523745 3.68E-06	0.000532290273	310.65479856
NA	NA	NA	26.4120253
NA	NA	NA	88.725223091
	-1.57570073638083 0.00047667161484	0.009755546295	NA
NA	NA	NA	451.92892367
NA	NA	NA	56.140379331
	-1.661677941265840.000151096982259	0.005226885873	381.27256258
NA	NA	NA	83.685811647
	-1.96657445400453 1.95E-05	0.001658624996	NA
NA	NA	NA	101.4521224
	-1.387471277811060.002257122657379	0.022681471639	NA
	1.035078958733190.000595156261724	0.010671861592	3738.8404468
NA	NA	NA	325.18826187
	-1.96759762352105 1.65E-06	0.000310559649	NA
	0.6327231768451410.000972097270925	0.013747903611	NA
NA	NA	NA	97.665853035
NA	NA	NA	7905.3900119
	0.8083742705858590.001015207771067	0.01392437606	NA
NA	NA	NA	14.986314888
	0.4972274841696340.000799007597767	0.012688384014	10246.805649
	0.900737692849751 2.04E-06	0.000362611923	6724.8251744
	1.034593939665640.000236273219454	0.006644546869	2517.6119121

	-1.374110764235810.002755880301562	0.024485520322	NA
NA	NA	NA	38.803887053
NA	NA	NA	32.291652167
	0.8257990600663970.003229137152014	0.027321855254	6681.9675982
	1.41694045091938	6.90E-05	0.003368326615 NA
NA	NA	NA	13511.481943
NA	NA	NA	35.135348528
	-1.79795951088386	9.63E-05	0.00413517426 NA
	0.5998439666338470.000508681117525	0.010034110177	NA
	-1.555831836131870.000726438082704	0.01223508864	64.253873431
	-1.342787783509220.003581105080008	0.029075395577	150.38354566
	-1.92324823612245	1.30E-05	0.001336893121 NA
	0.4161192378868890.000643263018076	0.011175622834	20036.882789
NA	NA	NA	79.785783438
	0.5900177919289970.006743719639231	0.041941288739	3896.429823
	0.486774287875820.000401672089628	0.009128698828	NA
	1.149828244646160.002985515173521	0.025934175141	598.59289043
NA	NA	NA	2072.921681
NA	NA	NA	108.04697066
	-1.204151354109430.007942624775936	0.046758614833	NA
	1.026954959841880.004750179281653	0.034449815978	561.53118227
	0.678893727097987	0.00259635807312	0.023547943638 NA
NA	NA	NA	24.763769717
	0.8438448036339950.007854381658821	0.046308865617	NA
NA	NA	NA	40.439676696
	-1.229507085791030.006699721062011	0.041769074372	NA
NA	NA	NA	1554.5463194
	-1.269862568648650.003200213412409	0.027159494389	NA
	0.762134379928360.007563672333456	0.045277787368	21723.469983
	0.8326679884343690.002265919115116	0.022711481592	23075.322746
NA	NA	NA	6859.3353441
	-0.4352047059090750.000593193420638	0.010671861592	NA
NA	NA	NA	3139.9126172
NA	NA	NA	63.657836673
NA	NA	NA	35.036412153
	0.924695611089506	0.00604716192123	0.039728329328 NA
	0.6575736851836640.000283518643601	0.007382051048	NA
NA	NA	NA	3806.3895706
NA	NA	NA	42.406077301
NA	NA	NA	45.777701711
	0.4720989383474670.000957274278146	0.013691245012	NA
	0.5639419181273990.002550190660081	0.02334589061	NA
NA	NA	NA	3650.8329221
	-0.4316028171401490.006444432780516	0.040861724865	NA
	-2.5382196785056	3.05E-08	1.34E-05 NA
	-1.611557654304070.000420013257942	0.009275886019	NA
	-1.42078644343930.001890332985493	0.020319435713	56.85773543
	-1.211049435124050.007269608426008	0.043989008262	107.97387248

	0.6809356820986460.008092920240409	0.047358121586	3171.4711856
NA	NA	NA	1404.9253152
NA	NA	NA	10441.145737
	1.005033274346760.006769238408579	0.041941288739	NA
	-1.080878169462140.001124521718213	0.014900865751	NA
	-1.305877889368580.003648788722069	0.029226935431	112.05324308
NA	NA	NA	5188.2094348
	0.571905023427404	1.30E-05	0.001336893121 NA
NA	NA	NA	11697.074779
	0.7384498793360720.006361460369305	0.040765489481	NA
NA	NA	NA	6111.174837
	-1.449605115242230.000121044424939	0.004718112549	NA
NA	NA	NA	2484.3770788
NA	NA	NA	268.8297546
NA	NA	NA	43.056826025
NA	NA	NA	235.40600098
	0.6745715327465890.001666745436762	0.018864553163	11039.295378
	1.38204903816237	9.09E-05	0.004047244675 1623.5703395
NA	NA	NA	92.548919225
	0.3840466751800730.005980625980717	0.039423721684	4218.683208
	0.3789934579678420.002359235503828	0.02297780558	NA
NA	NA	NA	22268.50509
	1.45844952231688	7.88E-06	0.000962194074 NA
	1.59150889062937	2.96E-06	0.000463946149 NA
NA	NA	NA	811.31595097
	0.7322869590947380.000533423954984	0.010221344314	NA
	0.9843876390031870.003656170740752	0.029226935431	NA
	0.50622881458318	0.0065403333952	0.041169344995 11731.387169
	0.9183918050282120.008153931273426	0.047431127006	905.43134104
	0.6474053301436020.002503931115489	0.023139164847	NA
	1.66846632061427	2.11E-11	2.27E-08 NA
NA	NA	NA	126.60616609
	0.497711722504583	0.00509207353401	0.035671891477 16267.869954
	-1.555417181265710.000543365029616	0.010310747091	194.27971326
	0.6846190235376320.000842910776742	0.012870852446	NA
	-2.02148488707585	5.25E-07	0.000120709814 NA
NA	NA	NA	11.197988499
NA	NA	NA	16450.0196
NA	NA	NA	13382.705183
	-1.535753700607760.000832379514147	0.012813554489	73.695580768
	1.28095534806245	5.19E-05	0.003071173289 5.6671379842
	-1.17850493106630.008266427819586	0.047942828408	76.502576702
	-1.404458974874890.002075400667383	0.02156277435	NA
	1.19918237138558	1.68E-05	0.001492342105 NA
	0.9827402009370130.001082782856766	0.014596250725	NA
	0.743799321267852	0.00012672190524	0.004765597032 7753.9832699
	-1.276025848580880.005321215548208	0.036570598914	2.2177375282
	-1.555937938447940.000472626916573	0.009747450927	175.82248518

	1.085942174403130.004884888977388	0.034972584272	NA
NA	NA	NA	16002.004615
NA	NA	NA	1761.37551
NA	NA	NA	2369.3760667
	-1.624331408109160.000415380970371	0.009225705757	45.37513377
NA	NA	NA	33.766720113
	-1.1548766599411 0.00864712310126	0.049506305839	25.87675253
	-1.395409852839810.000806971144908	0.012688384014	15.607275161
NA	NA	NA	4239.2143421
	-1.501289948798240.000997846469779	0.013881074201	54.538027986
NA	NA	NA	35.805107849
	1.02955454351752 7.45E-05	0.003549313162	695.26817836
NA	NA	NA	43.14793734
	0.7895789436708030.000213674997538	0.006236122641	41745.206454
NA	NA	NA	73.170627006
	0.878508625363760.006528348378744	0.041160183569	1683.4982224
NA	NA	NA	79.484537481
	-1.421683425951210.001998441947107	0.020999756912	97.270637064
	1.078044754233650.001577330063616	0.018296092637	1514.8573134
	0.5348155233480110.000777627823703	0.012613058767	23401.345951
	-1.491259317230320.001119291198618	0.014882004406	NA
	-1.202628513589580.006845367668392	0.041941288739	22.636235992
	-1.39577657897389 0.00241247265633	0.0231136167	218.53508194
	-1.061634599302130.000721890254926	0.01223508864	329.33814168
NA	NA	NA	167.02650905
NA	NA	NA	18.213545821
	-1.104833345383240.001593936687434	0.018434019264	NA
	1.146654940566940.000159227319325	0.005319825566	NA
	-0.671526304690328 0.00128710178152	0.016388537016	NA
	-1.486541431717740.001210413835744	0.015513139947	NA
NA	NA	NA	72.946860321
	-1.404128945575560.002323964394727	0.022940345502	NA
NA	NA	NA	16.315828243
	0.577188592786053 5.37E-05	0.003131643275	NA
	0.5489447354844360.005544872666056	0.037306208695	NA
NA	NA	NA	149.50692666
	1.29323752846362 1.53E-05	0.001389800975	NA
NA	NA	NA	75.384622826
	0.958937816864110.002336409525721	0.02297780558	2677.4044135
NA	NA	NA	7818.5275621
	0.537917463736020.006185091015682	0.040150566943	NA
	-1.04894497173390.006480794323148	0.040926373197	NA
	-1.45375417353630.000873561207867	0.013057454583	NA
NA	NA	NA	16588.292388
NA	NA	NA	73.150247389
NA	NA	NA	402.47895267
NA	NA	NA	872.46957903
NA	NA	NA	11776.032196

	0.7904222256383970	0.000162308227404	0.005376803906	NA
NA	NA	NA	98.045502558	
NA	NA	NA	160.39831281	
	-1.695590806644420	0.000209605674898	0.006207186236	120.43310205
NA	NA	NA	126.17436428	
	-1.200484233275960	0.007582444931357	0.045320760301	NA
NA	NA	NA	14957.325485	
NA	NA	NA	138.70896829	
	1.33763365859458	8.99E-08	2.70E-05	NA
	-1.094449927609870	0.006992435186231	0.042509221062	NA
NA	NA	NA	65.417986289	
NA	NA	NA	45.577606861	
NA	NA	NA	113.73114027	
NA	NA	NA	72.603876066	
NA	NA	NA	177.39655269	
	-1.37057419550557	0.00244003436834	0.023131362287	138.49988743
NA	NA	NA	84.133510415	
NA	NA	NA	125.44735593	
NA	NA	NA	49.622357733	
NA	NA	NA	89.981205775	
NA	NA	NA	64.960043598	
NA	NA	NA	20.499451735	
NA	NA	NA	18.347505226	
	-1.199538903501620	0.006813191192475	0.041941288739	NA
	-1.47100461310977	0.00137689627117	0.016872374683	NA
	-0.9855584871786350	0.004561963390507	0.033595840423	NA
	0.9677491390071840	0.008071120049311	0.047301361728	NA
NA	NA	NA	1833.8239996	
NA	NA	NA	13.218023274	
	1.502368648233940	0.000146071694788	0.005144092387	NA
	0.8864711651326450	0.002612936955848	0.023643450371	NA
NA	NA	NA	38.188279249	
	-1.276937778243480	0.004969316601119	0.035254189825	NA
	-1.38189302498911	0.00272108028013	0.024340281041	480.20572022
	-1.408450665037150	0.001338551460539	0.016558853745	NA
	0.8790995404435930	0.006460103854324	0.040861724865	NA
NA	NA	NA	91.811051252	
NA	NA	NA	1048.0558872	
	-1.317693253625810	0.003918009485686	0.03072333052	63.073500683
NA	NA	NA	99.46229465	
	-0.723635980821265	0.00248941004357	0.023139164847	195.78175129
	0.697933759935440	0.003394387459803	0.028133744233	NA
NA	NA	NA	69.159671466	
NA	NA	NA	172.56261736	
NA	NA	NA	143.08646738	
	0.579678571790115	0.00669768383312	0.041769074372	NA
NA	NA	NA	1233.6799956	
	0.5960939613579520	0.002428555222777	0.023131362287	NA

NA	NA	NA	46.703971809
	-1.214065680597350.007511559449957	0.045103972181	48.505750922
	1.083006220932060.000824942404989	0.01279642802	3920.2120544
	0.6064497221949890.002058298546687	0.021458108235	NA
NA	NA	NA	168.19701365
NA	NA	NA	68.752987052
NA	NA	NA	4879.6114996
NA	NA	NA	12091.303633
	-1.226368651044460.000912958663241	0.013366125148	NA
NA	NA	NA	30959.272089
	0.6456949751123550.001332462924426	0.016558853745	NA
NA	NA	NA	42.852533233
	-1.376742162744540.002382375685152	0.02297780558	NA
NA	NA	NA	14.48362776
NA	NA	NA	103.67096022
NA	NA	NA	2693.8272235
NA	NA	NA	4.3556589792
NA	NA	NA	13857.528465
	-1.25693968068266	0.00619093029657	0.040150566943
			256.87928699
NA	NA	NA	2423.1883807
NA	NA	NA	2076.480222
	1.31450516299525	4.77E-05	0.002933793783
			1055.0284731
NA	NA	NA	735.91954145
	-1.698175883431380.000229575180646	0.00650296653	32.606724206
NA	NA	NA	41.277812686
NA	NA	NA	75.79496493
NA	NA	NA	2.3837730209
NA	NA	NA	20.94362989
	-1.31753550330929	0.00415582700473	0.031767578694
			NA
NA	NA	NA	60.125395011
NA	NA	NA	2179.9033036
NA	NA	NA	137.82280811
NA	NA	NA	2206.2636155
	1.015323059494120.001727035114352	0.019233562	NA
	0.5148411140120730.001776344674605	0.019504863295	NA
	0.6429815906615930.000108093920659	0.004543431568	8338.7612104
	-1.26121243588786	0.00538831244597	0.036570598914
			NA
NA	NA	NA	6782.9201564
	-1.194971060619680.007356975359682	0.044345009325	NA
NA	NA	NA	6962.7345103
NA	NA	NA	1319.8532009
	-1.186445880726930.005169652512161	0.036086020839	NA
NA	NA	NA	1424.1488416
NA	NA	NA	278.39027777
	-1.21772818204299	0.00698081386637	0.042504675084
			NA
NA	NA	NA	48.375769308
	0.8914307984371150.001155549152262	0.015056805454	NA
	-1.240839083169920.002882730862747	0.025209384659	NA

NA	NA	NA	99.068885487
NA	NA	NA	1916.1653791
NA	NA	NA	38851.028165
	-1.628662329433250.000325469552718	0.008001638249	NA
	-1.278593358493390.004921321576336	0.035166760197	NA
	-1.280419395499190.004846720981206	0.034826897639	NA
	-1.272520418377570.004947996446227	0.035166760197	60.165059226
	0.8040014468330990.008630285154658	0.049506305839	NA
	-0.7227741321326770.002706225323668	0.024262923831	NA
NA	NA	NA	115.86341259
	0.698301150188656	3.06E-05	0.002239449958 NA
NA	NA	NA	6.1419427867
	1.084895705595660.004272523893581	0.032366852519	NA
NA	NA	NA	2480.3086605
	0.6896839515228150.000898079145108	0.013247514635	NA
NA	NA	NA	6585.0233452
	1.25620191532736	6.15E-06	0.000775465934 4127.0377154
	1.152948801910620.001666054259291	0.018864553163	1580.0914704
NA	NA	NA	35.465612801
NA	NA	NA	55.183879491
	0.9725883593275770.001299026012795	0.016421886406	NA
NA	NA	NA	53.887448216
	0.793215167899296	0.0001118499372	0.004651291537 NA
	0.7248276340940170.001645698399173	0.018810043984	NA
	1.14692009955595	0.00081148529128	0.012688384014 1617.1971824
	1.278792986747780.000624971524757	0.010955218342	536.37875483
NA	NA	NA	5796.1131423
	-1.324185227547320.003921960074116	0.03072333052	NA
NA	NA	NA	87.127845456
	-1.597233047987060.000526823046817	0.010157469952	63.810577395
	-1.194220884309640.006120767645052	0.039876801208	NA
	-1.324500187915690.002909046934717	0.025382733187	NA
NA	NA	NA	17.191198252
NA	NA	NA	21.850744582
NA	NA	NA	97.413097505
NA	NA	NA	23.702838977
	-1.151538758571010.006084243369078	0.03978951391	NA
NA	NA	NA	32.566211363
NA	NA	NA	46.751754623
NA	NA	NA	44.012498983
	-1.236165079794930.005811784632052	0.038570910232	48.882545968
	0.68686718135925	0.00860119898887	0.049460895063 NA
	1.06870728074747	0.00171647362552	0.019170558292 541.06137964
	0.8861221284089520.008720143376536	0.04976210286	1367.0818096
NA	NA	NA	4851.6366828
	1.104081891422590.000905574028751	0.013307852926	NA
	0.8070082489457280.000875173471637	0.013057454583	10317.250711
	0.9548331102010670.008048894572472	0.047241935261	337.31172782

NA	NA	NA	42.961994232
NA	NA	NA	650.77257984
NA	NA	NA	111.8116283
NA	NA	NA	122.64635484
	-1.206775356058720.008649988971025	0.049506305839	75.112882287
NA	NA	NA	215.11533744
NA	NA	NA	58.322279029
NA	NA	NA	203.10879236
NA	NA	NA	40.226962646
	0.9686406785507740.006675211842831	0.041769074372	NA
NA	NA	NA	94.460273329
	-0.9343101697477470.002188983397504	0.022072217929	NA
	-1.15817196269930.008463951426908	0.048870880543	NA
NA	NA	NA	1817.9320494
	-0.8447932869301380.004602705950914	0.033756055464	NA
	-0.839865081361590.002780913085584	0.024594093329	NA
NA	NA	NA	16235.34015
	-1.329527033715280.000126152764213	0.004765597032	NA
	1.073509955934310.000259832487036	0.007053369388	2050.2219593
	0.4185963779605290.004558888594019	0.033595840423	2693.9362697
	-1.205609777640220.002164828078811	0.022045257534	70.436035405
	-1.138241059569590.003090048618428	0.026762301402	NA
NA	NA	NA	795.26034601
	1.228110173531710.000858789034368	0.01294678116	747.76102186
	0.956916498729610.006221521621527	0.04019822813	563.62482024
NA	NA	NA	599.78583977
	-0.5430038948395560.006924850796878	0.042295690258	NA
NA	NA	NA	827.82963328
NA	NA	NA	7887.7001121
	-1.445095863509020.001707476858762	0.019124719315	123.05857491
NA	NA	NA	167.18004488
	-1.58108440083245	0.00049120036355	0.009941225296 NA
NA	NA	NA	98.220537333
	1.13179895599937	2.59E-07	6.76E-05 11157.911531
NA	NA	NA	63.788893781
NA	NA	NA	101874.96372
	-1.669994995124990.000286075660775	0.007382051048	61.765262037
	-1.464770376364030.000343006197516	0.008225835743	264.01358381
NA	NA	NA	14.017994524
NA	NA	NA	48.85739005
NA	NA	NA	31.437487132
NA	NA	NA	3660.486754
NA	NA	NA	11.369150736
NA	NA	NA	27.141711146
NA	NA	NA	4.4207185224
	-1.339903941844540.003645896338916	0.029226935431	NA
NA	NA	NA	14412.885233
NA	NA	NA	36.097708134

	0.8903779187519650.002704622932509	0.024262923831	NA
NA	NA	NA	19.489223508
NA	NA	NA	13.629600403
NA	NA	NA	21.692892582
	1.322637581896820.002818120875481	0.024810888519	NA
NA	NA	NA	688.15318726
NA	NA	NA	53.0787777
	0.52118943635921	0.00637968685214	0.040815377913 NA
	-1.207333840637630.007499096877373	0.045098414913	79.706175541
	-1.375628680287530.002582184464957	0.023528575929	NA
	-1.20557123174970.006685773768893	0.041769074372	134.28515998
	-1.305492837652910.004403740859917	0.032989252811	109.34671605
	-1.292538020352560.004294514112776	0.032470513862	153.37479042
NA	NA	NA	1149.278739
	-1.349302455214290.002494271756559	0.023139164847	82.722498946
NA	NA	NA	33.085912798
NA	NA	NA	10765.37518
	-1.29963888343546	0.00247925087539	0.023139164847 128.0084679
	-1.22926156602290.007667524046602	0.045620017501	NA
NA	NA	NA	5956.8351406
NA	NA	NA	10610.275744
NA	NA	NA	46.76011762
	0.9600611188150640.003493389503415	0.028628217125	NA
NA	NA	NA	86.386487302
NA	NA	NA	1887.8967134
NA	NA	NA	33.892267256
NA	NA	NA	95.741320913
	0.861847394616718	8.74E-05	0.003972746637 7594.644249
	-1.83919052173359	6.39E-05	0.003287045506 214.05879627
	-1.405044056914220.001062671789914	0.014423555649	NA
	-1.639806401634770.000369417083198	0.008647014241	NA
NA	NA	NA	64.285510113
NA	NA	NA	375.15910197
NA	NA	NA	29.419095661
NA	NA	NA	84.088203258
NA	NA	NA	27.968090785
NA	NA	NA	19.859789996
NA	NA	NA	9.5747594302
NA	NA	NA	9.0707501813
	-1.33792497736159	0.00325323782185	0.027407126391 128.44871042
	-1.226235699743810.007766951218515	0.046065409327	54.640125519
NA	NA	NA	100.38380221
NA	NA	NA	40.354524137
NA	NA	NA	75.675222464
NA	NA	NA	3571.5918277
NA	NA	NA	71.540134586
	0.693787233334579	9.27E-06	0.001035687245 6981.1033537
NA	NA	NA	35.947713958

	-1.68511796450772	4.88E-05	0.002933793783	NA
NA	NA	NA	28840.739043	
	1.95294325568593	3.30E-10	2.58E-07	NA
	0.548616009648880.006430554821497	0.040861724865	NA	
	0.5295992668250850.000631960142513	0.011028268737	NA	
NA	NA	NA	1010.9886476	
	-1.319479918133190.004134390195089	0.031751141989	NA	
NA	NA	NA	6.5051656346	
NA	NA	NA	208.54539275	
	0.7253077008146220.003585147267422	0.029075395577	NA	
	0.7609462237370330.006336871021528	0.040674595769	NA	
NA	NA	NA	22448.967664	
NA	NA	NA	113.68545749	
	-1.91792398414112	1.52E-05	0.001389800975	NA
	-1.4884361307164 0.00011784895788	0.004718112549	5.9929133585	
NA	NA	NA	37.013216713	
	0.716455324379047	5.85E-05	0.003131643275	NA
NA	NA	NA	10.650406644	
NA	NA	NA	220.64127624	
	-1.292704557468630.005037505415273	0.035480375979	127.19059101	
NA	NA	NA	5.5184573892	
	1.241933078449010.004563671339081	0.033595840423	NA	
	-1.294832162190310.004169037572282	0.031767578694	NA	
	-1.298151992191180.004145111538263	0.031767578694	NA	
NA	NA	NA	39.900921028	
	1.741238035838180.000144423112397	0.00513227224	NA	
NA	NA	NA	14.37001331	
	-1.69683401161150.000213773454569	0.006236122641	97.802962095	
NA	NA	NA	305.20579269	
	-1.84124982123616	5.75E-05	0.003131643275	NA
NA	NA	NA	115.74249533	
NA	NA	NA	108.43793866	
	-1.233121193358240.007166988498685	0.043435283785	NA	
NA	NA	NA	8.7569191054	
NA	NA	NA	576.02319397	
NA	NA	NA	3.1603471151	
	1.213229122391680.000154330145844	0.005235319392	4003.5107819	
NA	NA	NA	3.742678658	
NA	NA	NA	146.17452402	
	1.288169055133160.004785749683198	0.034543610623	NA	
NA	NA	NA	9904.6789593	
	-1.29282171312463 0.00416507053043	0.031767578694	97.896550124	
	0.8017461509912570.007362474047514	0.044345009325	NA	
	-1.245318217669 0.00677187994157	0.041941288739	48.315071103	
	-1.399258687181240.001922788079665	0.020424398379	NA	
	-1.246531475653530.001009125558451	0.01392437606	NA	
NA	NA	NA	16.206182961	
NA	NA	NA	370.39051076	

	-1.714818472307350.000198115381638	0.006097323644	35.146844376
NA	NA	NA	1028.8084066
NA	NA	NA	298.82209852
	0.6017739517385860.002578889244727	0.023528575929	6731.7477404
NA	NA	NA	32.4112037
NA	NA	NA	9980.6808583
	0.645334606608992 0.0013102436337	0.016468624965	13434.975786
	0.7116104688561010.004941821345808	0.035166760197	NA
NA	NA	NA	2069.2726337
	1.15099213466125 0.00050642494518	0.010034110177	1213.3998689
	1.073341202210060.003129121117674	0.026882932855	1608.6553365
	0.5405168670173050.003165082268284	0.027104537921	NA
NA	NA	NA	175.4605057
	1.84188140297585 9.66E-13	1.89E-09	NA
NA	NA	NA	107.51022831
	-1.405257575200230.002167841459601	0.022045257534	50.625764812
	-2.57942357776211 2.24E-09	1.25E-06	304.80604259
NA	NA	NA	83.146751571
NA	NA	NA	19.051407454
	-1.255089525550440.004943361165995	0.035166760197	28.968786978
	-1.437912651840080.001755638829942	0.019391654767	NA
NA	NA	NA	5091.7585574
NA	NA	NA	11.502506027
NA	NA	NA	343.22295171
	1.043841294008390.002190846906242	0.022072217929	1120.1178823
NA	NA	NA	80.337091672
NA	NA	NA	15359.057647
	0.8516351241932840.001229139928408	0.015701660066	9453.6797315
NA	NA	NA	12.257294924
	-1.373832732135980.002493021333646	0.023139164847	NA
	-1.342337824684540.003599491059251	0.02907860972	NA
	0.452288137017759 0.00760705992294	0.045398469067	9408.8964755
	1.112834951373510.002372300977537	0.02297780558	1470.2684852
NA	NA	NA	17.630456225
	-1.97113293762805 9.13E-06	0.001035687245	NA
	0.9528103540914880.002588776480571	0.023533784332	NA
	0.5281768890438970.003883539354646	0.030668192601	NA
	-1.44808837308990.001645368584236	0.018810043984	NA
NA	NA	NA	136.86107793
	-1.096522027712820.000672702552653	0.011533308238	NA
NA	NA	NA	103.65635976
	-1.44958043141582 0.00144392640829	0.017313829233	NA
NA	NA	NA	117.43861621
NA	NA	NA	119.9042164
NA	NA	NA	2164.9281544
	-1.630574203497480.000404550019187	0.009140959682	NA
NA	NA	NA	18.158879703
	1.413194350605650.001897312365088	0.020319435713	NA

	0.882608692568366	1.37E-05	0.001373370707	2582.7315613
NA	NA	NA		11208.437677
	0.550811966340871	6.57E-05	0.00333350372	NA
	-1.374448738132040	0.002445831671368	0.023131362287	NA
	-1.40978207049640	0.001996472626007	0.020999756912	NA
	-1.22518503926210	0.006837455923684	0.041941288739	76.211685164
	-1.310860641128570	0.003985560165372	0.031044961909	NA
	-1.33425007042050	0.003386726398065	0.028133744233	NA
NA	NA	NA		128.06985867
	-1.443234703115850	0.001742468944604	0.019350315638	NA
NA	NA	NA		243.16472041
	1.57964007543024	4.63E-20	1.81E-16	NA
	1.042289560776290	0.002454650135926	0.023131362287	NA
	-1.530826094297830	0.000764831385518	0.012484461142	NA
	-1.60254616951580	0.000473782470235	0.009747450927	NA
	0.8179175974081220	0.006276893673053	0.040422367987	NA
	-1.40339995881990	0.001839726309282	0.019976361508	239.87035679
NA	NA	NA		47.283271113
	-1.43022695711009	0.00088038441248	0.013085257294	NA
	0.6947067741830380	0.000221772159588	0.006327791035	NA
	-1.424991670807370	0.000974205500158	0.013747903611	NA
	-1.247190466918730	0.005731902591111	0.038257599991	75.118344769
	-1.218763194985990	0.006456137178595	0.040861724865	NA
NA	NA	NA		31.91573414
NA	NA	NA		1329.754333
	0.8953208130382820	0.003511336991419	0.028715096861	NA
NA	NA	NA		2224.0084773

log2FoldChange (donor 49)	pvalue (donor 49)	padj (donor 49)
1.21694912912973	2.03E-08	6.29E-07
0.4440294674417660	0.007906213957333	0.040976191442
0.5854771843450050	0.000184246492709	0.002159368895
1.462589833144730	0.005455553948089	0.031634354682
NA	NA	NA
0.579297793783979	4.67E-05	0.000682525112
0.7707421503906650	0.002964920709758	0.019864064816
0.553507639861872	1.10E-05	0.000196102636
0.3678158905158790	0.001231130543541	0.010151629904
2.08212817456168	2.61E-19	3.10E-17
NA	NA	NA
NA	NA	NA
0.4277155593132150	0.001010624247875	0.008760736823
0.356783408669519	1.21E-06	2.76E-05
NA	NA	NA
0.51897022356996	3.73E-07	8.90E-06
0.5522383173317660	0.000197907697678	0.002288958767
0.930247393293101	1.51E-05	0.000259044934
NA	NA	NA
NA	NA	NA
0.3354350567045820	0.003740763428099	0.023931084813
-0.9529601780399080	0.000953130210319	0.008411661193
0.3465064401600540	0.004008151403557	0.025237572233
0.3666712041408310	0.000123167700512	0.001520567539
1.47981577231642	1.88E-10	8.24E-09
2.94334929889416	1.06E-19	1.33E-17
2.76209700350076	1.09E-13	6.87E-12
NA	NA	NA
3.05950000428133	3.19E-15	2.50E-13
0.9155404825071810	0.009707227660029	0.047828773056
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
3.94555069383966	9.15E-24	1.75E-21
1.40171396814637	5.76E-06	0.000113979352
-0.8264376640966790	0.009520407970104	0.047119586744
0.656653328593549	0.00086143346146	0.007742331417
NA	NA	NA
-1.254450286894310	0.000809446339034	0.007335085897
NA	NA	NA
0.5751548103298870	0.000735700515616	0.006764443025
NA	NA	NA
NA	NA	NA
NA	NA	NA
0.5100171367650210	0.005652201372308	0.032472451021
0.7720354383528040	0.002854745650304	0.019243262474

	1.001399645082520.000227038901684	0.002545499931
	-1.629811974044110.000302217706706	0.003231528722
	0.409709113657599	4.70E-06 9.56E-05
NA	NA	NA
	-0.7959496362264490.005231969499282	0.030700274966
	0.939118668863268	4.20E-10 1.74E-08
	1.506665967209260.000145980675947	0.001762596348
	0.736717321973494	2.08E-05 0.000335242742
	0.420183783595509	1.86E-06 4.06E-05
	-1.169523269679590.008780700944937	0.044544226132
	-1.01712317569322	1.11E-05 0.000197194161
	-1.226366230591650.002988324584081	0.019975077889
	-1.133741731368210.002872758938683	0.019335031448
	-1.274182366593440.001109709318684	0.009379177799
	1.30378234181191	1.94E-05 0.000313957766
	1.096074679937810.000606226458149	0.005792098443
	4.12235306094391	8.47E-29 2.19E-26
	4.08828847711298	2.48E-26 5.45E-24
	1.27000676073261	9.00E-05 0.001156149349
	1.148059575601640.000229520269971	0.002566772485
	1.025792824000710.002021632526163	0.01485798487
	1.300188110578780.000518025505851	0.005104299733
	1.067981525912860.000111172966109	0.001384150669
	0.967568482848701	1.79E-05 0.000296398299
	1.01327827744184	9.67E-06 0.000177171304
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.3442361884559340.008504743403023	0.043412714583
	-1.601083555760890.000864653129798	0.007755409195
	1.931735869678720.000217954692281	0.002462495816
	0.3426142211224080.001788255773944	0.013528004181
	-0.674019054448250.005586041538074	0.032261041472
NA	NA	NA
	0.457769897702058	4.05E-08 1.19E-06
	1.26657611582302	8.60E-09 2.88E-07
NA	NA	NA
	-1.392491715329610.003884205244095	0.024598100933
	-1.53212648725964 0.00391768378054	0.024738822149
	0.533983930686929	1.72E-05 0.000289175539
NA	NA	NA
	0.542670188933059	1.20E-07 3.21E-06
	-1.102288089812520.007071030001814	0.037916736549
	-1.084649022355780.006708779547968	0.036718662657
	1.85029561628973	3.03E-13 1.80E-11

NA	NA	NA
NA	NA	NA
NA	NA	NA
	1.04357138181226	3.62E-06 7.51E-05
NA	NA	NA
	-0.8342084548512030.004207686439214	0.026082908181
	0.3943775171978540.001561338178377	0.012203366192
NA	NA	NA
	1.474744925306750.000734320453947	0.006764443025
	0.561615815685592 0.00020180155224	0.002321774403
	0.4289623771171380.001030961107301	0.008849754036
NA	NA	NA
	0.7996513382095690.000984342294698	0.008600764185
	1.050209006378590.000143937532189	0.001742714749
	1.410360919270570.007088492511522	0.037946314967
	0.4617340724000480.004367536896277	0.026846607915
	1.1257977182729	4.00E-11 1.95E-09
NA	NA	NA
	2.2463316754378	2.61E-12 1.40E-10
	-1.11094835177405	1.42E-06 3.19E-05
NA	NA	NA
	0.3985476651874430.001604866196402	0.01246181437
NA	NA	NA
	0.5024338777163760.000297108162496	0.003184854571
NA	NA	NA
	0.4069371235572010.000198576376817	0.002290664504
	0.999797298862645	7.78E-11 3.68E-09
NA	NA	NA
	-1.570569896355420.001844939309241	0.013813472341
NA	NA	NA
NA	NA	NA
	-1.25905307587191 0.00986096827209	0.04836937004
NA	NA	NA
	-1.196604323865390.000961335465683	0.008467072889
	0.444332797180935	1.91E-09 7.11E-08
	1.12735167518146	3.43E-05 0.000513854178
	0.3951824145734440.006124438826363	0.034245430842
NA	NA	NA
NA	NA	NA
	0.4706889088792830.001153392281101	0.009655541096
	0.418178009027470.007424555594333	0.039168697278
	0.797473432992996	7.82E-05 0.001039706133
NA	NA	NA
	0.611756206696357	6.75E-05 0.000926541437
	0.700793377157172	1.54E-14 1.07E-12
NA	NA	NA
NA	NA	NA
	-0.6888544914477050.009788454368284	0.048121092784

	-1.203276277730920.000302932840382	0.003231528722
	3.65831394506258	9.33E-34
		5.13E-31
NA	NA	NA
NA	NA	NA
	0.5646241126082710.002032840959771	0.014915419062
	0.9239998820678540.000193350065574	0.002250519416
NA	NA	NA
NA	NA	NA
	0.4949628545460870.004187276147955	0.026047897087
	3.18620940811332	4.26E-29
	3.89350997334784	4.61E-29
		1.27E-26
NA	NA	NA
	0.411614125560333	0.00195897200687
	0.461871157035443	0.014445775118
		2.00E-07
		5.11E-06
NA	NA	NA
	-1.238758740405030.000205329606015	0.002350061506
	1.549584526740210.000165670653642	0.001962594401
	0.35991552963048	1.67E-06
	1.35092362208877	3.66E-05
	1.35092362208877	6.54E-09
	2.07827069108013	2.26E-07
		9.44E-08
		2.64E-06
	-1.223438134641640.004196111749221	0.026047897087
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.407729166819417	8.61E-06
	0.4092655211738170.005435502412662	0.000162439375
	1.03992187581409	0.031599250137
		1.34E-07
	0.680818346934617	3.56E-06
		1.64E-13
	0.776756715358377	1.00E-11
		2.64E-06
		5.67E-05
NA	NA	NA
	0.3834646636737320.006377652138817	0.035391137816
	0.483853109729563	3.27E-05
	0.663480258065818	0.000497444962
		8.76E-06
	0.3693641636651870.001015056037988	0.000162533048
	1.38098679873018	0.008770287862
		1.26E-09
		4.80E-08
NA	NA	NA
	1.66545370054591	9.52E-12
	2.06138487600083	4.98E-10
		4.80E-07
		1.13E-05
NA	NA	NA
	0.917562418255528	8.69E-06
	0.771492435739618	0.000162533048
		1.12E-05
	0.3420411310808850.001584403360639	0.000198306971
		0.012324695168
NA	NA	NA
NA	NA	NA
	0.44861120421010.000724890362218	0.006707143457
	1.8347441990468	5.71E-14
		3.69E-12
	0.662359879026749	0.00743910263284
		0.039168697278
NA	NA	NA

	0.635167466397613	2.41E-07	6.04E-06
	0.9137387015311940.002505418084235	0.017340649575	
	0.8978014478058650.004672381868575	0.028168886574	
NA	NA	NA	
	0.352226322374920.009995033223326	0.048754906789	
NA	NA	NA	
	0.8859410961010680.000254819798359	0.002778990109	
NA	NA	NA	
	-1.15614171537665	2.88E-05	0.000449256896
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	0.43325550629490.000923491465086	0.008216082974	
	3.14958656407096	2.63E-14	1.78E-12
NA	NA	NA	
	-1.20820669476326	2.58E-07	6.34E-06
	0.5206372119085970.002600100181756	0.017911348431	
	-1.162765732791780.000461316232008	0.004639553409	
NA	NA	NA	
	0.880335255682896	2.27E-07	5.77E-06
	0.686563180459382	5.62E-06	0.000112802401
	-0.9206032128939190.002456418364416	0.017136442399	
NA	NA	NA	
	1.80663829277782	1.46E-07	3.82E-06
	1.200135348831460.001495438040247	0.011736518191	
	0.7324254015187140.001736649361116	0.013320373372	
NA	NA	NA	
	0.6642380881612390.003707987806917	0.023790666294	
NA	NA	NA	
	0.689457412384738	0.00706345688744	0.037916736549
	0.4757039521228650.000241681125942	0.002648849248	
NA	NA	NA	
NA	NA	NA	
	-0.6245319054217660.005156959987579	0.030381821911	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	0.304813584132518	0.00933299944235	0.046506272731
	0.6883485627883250.010249421546278	0.049665058099	
	1.07978807848473	4.27E-05	0.000628369647
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	-1.26084252455265	4.00E-05	0.000592100482

	0.988381712501687	2.05E-05	0.000330784192
	3.40563862915673	4.33E-31	1.73E-28
NA	NA	NA	
	-0.6597807883685230.004562886808877	0.027661783484	
	-2.96661577549989	1.22E-08	4.00E-07
NA	NA	NA	
	0.5136756452820690.007765935145196	0.040392053211	
	2.25450043588276	1.82E-12	9.86E-11
NA	NA	NA	
NA	NA	NA	
	0.934350077023893	5.79E-08	1.68E-06
	0.747600388905107	8.80E-08	2.50E-06
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	1.19171165264862	1.61E-06	3.56E-05
NA	NA	NA	
	1.013822107169320.007048422351874	0.037916543741	
NA	NA	NA	
	-1.236164469554610.000122528431312	0.001516936495	
	0.454830954902096	7.23E-05	0.000977165573
	2.26233149280616	1.14E-21	1.62E-19
	-0.6957309539571090.007236825133917	0.038552541168	
	0.7585814570305190.001812745319698	0.013618830222	
	0.960899508261725	7.91E-09	2.67E-07
	0.3618337199103240.000769300715748	0.007029265376	
NA	NA	NA	
	0.4985118832951310.007710815014714	0.04024825652	
	0.761380964093104	2.78E-05	0.000436098218
	0.973859165032411	1.54E-06	3.44E-05
	0.606608177883132	6.52E-06	0.00012672809
	-0.737273345280525	2.94E-05	0.000454585422
NA	NA	NA	
	-1.335978895581510.002788076986913	0.018877631976	
NA	NA	NA	
	0.3402384450076360.003220725750695	0.021126999514	
	0.354955549932695	7.83E-05	0.001039706133
	-0.9929265813004010.007412156178231	0.039168697278	
	0.34704770308583	2.81E-05	0.00043923088
	-1.40921830050226	2.56E-08	7.76E-07
	2.6418168137084	6.45E-36	5.67E-33
	3.19517856014967	8.34E-15	6.11E-13
	0.645779657068142	2.22E-08	6.79E-07
	1.63336248388975	2.51E-07	6.21E-06
NA	NA	NA	
	1.02893263026438	5.51E-09	1.94E-07
	0.786077002403799	7.21E-09	2.46E-07
	-1.137660444750670.005576541482237	0.032248552387	

	-1.79103293301446	2.02E-08	6.29E-07
NA	NA	NA	
NA	NA	NA	
	0.680407001599710.009311804738793	0.04645332784	
	0.6137311356652950.007683316129105	0.040152407119	
	0.5407338511423830.000240892066304	0.002646801579	
	0.400520748615898 0.00211330971609	0.015199735219	
	0.716110331087663 1.24E-05	0.000217405544	
	0.5094504794743490.001694892624605	0.013022820079	
	1.101447786258030.001784613480623	0.013528004181	
	1.395179634731970.000727516474504	0.006717300222	
	1.74930173445869 5.12E-18	5.12E-16	
	-1.212562752343420.001015717069782	0.008770287862	
	1.10359450546106 8.51E-06	0.000161851966	
	1.20792951815306 4.71E-05	0.000685240724	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	0.391656302840506 0.00831245790315	0.042529979609	
	0.79912548203981 3.57E-06	7.43E-05	
	1.00036733722233 5.74E-06	0.000113979352	
	0.6539423785069420.000706764549077	0.006553228256	
	0.8382080800989280.004538088160302	0.027624511724	
NA	NA	NA	
	0.848233343152656 7.29E-05	0.000982995095	
	0.585736050312930.000519140382396	0.005104299733	
	0.710340296626697 1.52E-05	0.000259346103	
	-0.9935153848050760.008797357970974	0.044544226132	
	0.898086180817293 3.39E-15	2.61E-13	
	0.929274771968929 1.39E-09	5.23E-08	
	0.4593066168675050.001467895878516	0.011582410029	
	0.4026842023479480.008622032634798	0.043858603507	
	0.31441215667839 0.00734331421431	0.038978099	
	0.502362555581049 8.02E-05	0.001055100137	
	0.5696864162565110.007008129590139	0.037745992094	
	0.910579117701365 6.52E-05	0.000906524872	
	0.465432002185879 6.29E-09	2.20E-07	
	0.5165421676310510.001180221088592	0.009823999402	
	-0.949591892290977 3.05E-05	0.000467168101	
	0.389891928319856 0.00470642274957	0.028305618266	
	0.6067800998141330.000489883438313	0.004887562174	
	0.772575724661154 1.10E-07	3.01E-06	
	0.7303084383277740.000596432837222	0.005757687755	
	2.02928883174276 5.96E-08	1.71E-06	
NA	NA	NA	
	0.3010013628322930.006905847143653	0.037378339129	
NA	NA	NA	
	0.560796161572201 9.47E-09	3.13E-07	

	1.03565732097461	9.78E-06	0.000177614527
	1.047963091937160.000127519443587	0.001552487409	
NA	NA	NA	
	0.666978144607812	8.34E-14	5.31E-12
NA	NA	NA	
NA	NA	NA	
	0.496924588479029	2.72E-05	0.000429635006
	0.467251538931616	6.46E-06	0.000126650882
	0.4041270505564470.002361011375537	0.016576110216	
NA	NA	NA	
	0.3504244743703290.008797072060845	0.044544226132	
NA	NA	NA	
NA	NA	NA	
	0.4823284032729	2.95E-05	0.000455167523
	0.634184080232794	4.83E-08	1.41E-06
NA	NA	NA	
	2.35417050047551	3.20E-13	1.88E-11
	1.3378324345916	7.28E-06	0.000140350538
	0.950412446596294	3.04E-07	7.34E-06
	0.88928382656268	2.33E-05	0.00037439575
	0.517907331734284	5.81E-05	0.000823202294
	0.566455149582597	7.69E-10	3.02E-08
	0.4553634239431030.001419190501872	0.011320040392	
	2.89212178004687	1.33E-10	5.92E-09
	0.4832922024568120.000165067810754	0.001960737914	
	0.3349156783052640.002305524311342	0.016271045518	
	1.480562223699720.002371889629394	0.016599450511	
	0.803432663634567	1.43E-11	7.37E-10
NA	NA	NA	
	0.3451278423900490.008735715672694	0.044385514892	
	0.352800576043966	8.46E-05	0.001106554149
	0.5320750602414540.003301689095737	0.021465863278	
	0.6061968116615890.002730023381978	0.018547455933	
	0.2907281913290120.001191065605789	0.009895526158	
	0.852732645544252	8.74E-06	0.000162533048
NA	NA	NA	
	1.96046706287966	1.20E-13	7.43E-12
	0.4318393116994560.004349184977517	0.026771243664	
	0.821883704575422	6.83E-11	3.26E-09
NA	NA	NA	
	0.502297700226821	9.75E-06	0.000177614527
NA	NA	NA	
	0.6190949613479090.002061441898459	0.015074937011	
	0.8658716231494530.005538253284674	0.032069332261	
	0.4742788632469190.006935014188651	0.037490021352	
	3.39227972827087	3.14E-22	5.11E-20
NA	NA	NA	
	0.5401851045208990.000514280352054	0.00507924078	

	0.6783741409004840.001088342790282	0.009251966273
	0.2962720827561190.008420379232999	0.043032054336
	0.768968506353466	1.15E-09 4.43E-08
	-0.875181566855240.001227122263223	0.010137598396
	-1.5300737666086	1.51E-05 0.000259044934
	-1.33733011019272	2.98E-05 0.000458544053
	-1.29814879974799	1.09E-05 0.000193898242
NA	NA	NA
NA	NA	NA
NA	NA	NA
	3.40212220729452	1.24E-27 2.87E-25
	-1.076836439896890.001357039853008	0.011085855305
NA	NA	NA
	0.564015940009884	2.57E-09 9.34E-08
	0.373800924350204	9.42E-05 0.001200298015
	0.4261421258354280.001373878097381	0.011120063053
	0.418609768819575	2.42E-07 6.04E-06
	0.350446507288882 0.00578915239067	0.032872512606
	0.3205817893813190.004569386759801	0.027661783484
	0.400038029423001 0.00183516737869	0.01376375534
NA	NA	NA
	-1.006765302829120.001880297557604	0.014030403677
	-0.7357586983920250.001004282220415	0.008728050054
NA	NA	NA
	-1.412411887196540.000471668737801	0.004732840417
NA	NA	NA
	4.07465466387905	4.78E-43 2.10E-39
	-1.29489363230401 0.00190110116539	0.014161592579
	-0.9895747443340870.009016726057225	0.04523802628
NA	NA	NA
	-1.265894278347820.004474195074521	0.027349217458
	1.83078942646311	3.19E-06 6.74E-05
	0.3129888333656490.003276950140096	0.021399993857
	-0.957148613443544	1.00E-05 0.000180958353
NA	NA	NA
	0.4334003125045760.009652809436857	0.047614026347
NA	NA	NA
	0.4169084963417010.002087349449949	0.015180791256
NA	NA	NA
	0.457324325405666 0.00045264896911	0.004573315447
	-0.7074432829618180.003217717932538	0.021126999514
	1.09703309218599	1.59E-08 5.13E-07
	-0.8107104242165990.002432073201364	0.016993579841
	-1.6277663333396	2.70E-05 0.000427641181
	-1.645874912910650.000155373566448	0.001855616371
	-0.5381187654043920.004432926598003	0.027208525382
	-0.5176688385117960.008904241427846	0.044827194817
	-0.7896663314737240.002700902875926	0.018461070202

	-1.42136936264698	0.00344810571157	0.02231874021
	0.844220032030670	0.003881036558758	0.024598100933
	0.629108149474024	1.36E-05	0.00023602947
	0.8808621076723120	0.009397039286812	0.046613981564
	0.858926584352849	4.97E-05	0.000716833333
	0.943681594184735	7.22E-05	0.000977165573
	2.52817482457985	2.75E-07	6.70E-06
NA	NA	NA	
	-1.427928742572070	0.000787862613054	0.007183933992
NA	NA	NA	
	0.505155513274562	9.15E-07	2.10E-05
	0.406786518270516	6.65E-05	0.000919533565
NA	NA	NA	
	0.5768286283864090	0.003174755866565	0.020919118491
	-1.13484062241731	1.79E-06	3.92E-05
	0.741121608455697	5.81E-06	0.000114412692
	-1.15594330615980	0.001004867651317	0.008728050054
	0.3667391332576990	0.000645922497376	0.006105009411
NA	NA	NA	
	0.4029708298815340	0.008993527346361	0.045173203071
	0.40832272406001	0.00536177646136	0.031305379363
	-1.491685095189710	0.000925558907705	0.008217841211
	0.6347723719101890	0.003821897500026	0.024308595532
	0.515576570622149	6.74E-05	0.000926541437
	0.4627517709387120	0.000101730641781	0.001281106506
NA	NA	NA	
	0.4891078527496950	0.000416115976939	0.004293027509
	0.695401648614201	4.11E-14	2.69E-12
	0.5027572112423640	0.001928214134077	0.014294710505
NA	NA	NA	
	2.30828490393612	1.27E-07	3.37E-06
	1.09266762949899	1.12E-18	1.23E-16
	2.30836962863762	3.07E-17	2.65E-15
	-1.328065616168080	0.001353069688411	0.011074006109
	2.46478193580206	1.74E-25	3.64E-23
NA	NA	NA	
	-0.8247212458790890	0.002908724847497	0.019547164686
NA	NA	NA	
	-0.8440916846781810	0.008881750494887	0.044813476347
	-0.998103774019294	0.00137208970088	0.011120063053
	-1.3815975393928	8.55E-05	0.001112213832
	1.2496107959175	1.87E-05	0.000305782709
NA	NA	NA	
	-1.22972358728874	5.18E-09	1.84E-07
	0.610732827611504	6.10E-12	3.23E-10
	0.425194023513779	8.26E-06	0.000157786787
	-1.598015687415920	0.000702564161854	0.006528053893
	-1.28529915753341	0.00794820594371	0.041096900144

	0.684250487014012	7.10E-06	0.000137409389
	0.3456183253111340.007888552735734	0.040932927123	
NA	NA	NA	
	2.42021905071126	1.53E-12	8.42E-11
	1.34659123748597	2.52E-05	0.000400628189
	1.35582302878003	1.15E-10	5.33E-09
	1.098062968282020.005999011946929	0.033672614951	
	1.80293300668718	1.31E-14	9.43E-13
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	-1.426470399462140.001774147783869	0.013502080794	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	-1.093020922418780.002057229798862	0.015069208277	
	1.75167415742183	5.48E-18	5.35E-16
	2.95419916346145	1.78E-17	1.63E-15
	1.00469926904995 0.00192826968601	0.014294710505	
	0.819820401226742	1.61E-06	3.56E-05
	0.463703143710846	7.15E-09	2.45E-07
	0.457439870384871	1.68E-08	5.35E-07
NA	NA	NA	
NA	NA	NA	
	-1.082107132367280.002240485629457	0.015933550714	
	0.344547903958042	6.99E-05	0.000954210079
	0.3554941309503260.000226222235608	0.0025428305	
	0.479106865742568	8.82E-10	3.43E-08
	0.417891840994928	1.16E-07	3.14E-06
NA	NA	NA	
	0.396159744412364	8.74E-06	0.000162533048
	0.3771309731190840.004195472450199	0.026047897087	
	0.3115508742540850.001282301169073	0.010514391116	
	0.3400280891153290.000124226251623	0.001523040248	
	0.281173175495320.006621799992396	0.036378513708	
	0.641499636044221	2.21E-09	8.17E-08
	0.312384979023243 0.00700385919098	0.037745992094	
	0.4865559963569550.001141800968138	0.009613439186	
	0.528757592062856	2.78E-05	0.000436098218
	0.403685172919183	5.64E-05	0.00080150495
	0.3616255610567980.000448016827227	0.00454742253	
	0.485460152324484	1.75E-08	5.52E-07
NA	NA	NA	

	0.64002664832815	5.37E-05	0.000768639351
NA	NA	NA	
	0.3751782678294540.000153482152396		0.001838021961
	0.460959900143387	2.34E-07	5.91E-06
	0.364423349631270.002143221493383		0.015316192623
	0.4347332421623720.006472249476244		0.035691618557
NA	NA	NA	
	0.3576693181973820.005755468228837		0.032765910448
	0.3754410643792410.000672803903805		0.006304846817
	0.430352231625801	4.13E-09	1.48E-07
	0.4948455327423170.001092217010256		0.009266976371
	0.4648099939288310.007745854085321		0.040369817426
NA	NA	NA	
NA	NA	NA	
	1.44421733855191	6.09E-05	0.000858010024
NA	NA	NA	
	0.494193961376889	6.59E-05	0.000914308811
NA	NA	NA	
	0.2439737843422550.004646317077869		0.028050224667
NA	NA	NA	
NA	NA	NA	
	0.5867220048495680.000558487016977		0.005406498766
	-1.370843877305420.005779690499281		0.032861241584
	0.858168606172755	2.60E-09	9.38E-08
	0.918763876064099	3.64E-05	0.000544616133
	0.621056719862155	8.55E-06	0.000161993321
	0.6677356086944320.002067457480179		0.01509139956
	1.01075158682676	5.08E-10	2.03E-08
	0.5476219694711430.002315297331489		0.016307262455
	1.31939178098619	8.40E-07	1.93E-05
	-0.8890537888729450.005228013744034		0.030700274966
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	0.433394118107529	5.89E-05	0.000832490693
NA	NA	NA	
	0.5897107341267640.008280497931052		0.042465330697
	0.3372097240524090.000270969818619		0.002933281657
NA	NA	NA	
NA	NA	NA	
	0.777796326590568	0.00010158688631	0.001281106506
	2.03117866083263	2.26E-10	9.85E-09
	0.5865130269459980.007152676709088		0.038196858003
	1.185973757239670.000849319495278		0.007649096684
	0.485795386076888	3.36E-08	1.00E-06
	0.5793530259831710.000494515843667		0.004917188084
	0.369935074745354	5.34E-06	0.00010763226
	-1.100951264435030.000212579277835		0.002420756541

NA	NA	NA
	3.96438120078366	3.69E-39
	0.4434223956595630.002346920739392	8.12E-36
NA	NA	NA
	0.555011538309476	0.00082390340029
NA	NA	NA
NA	NA	NA
	-0.970645889235368	0.00080803221858
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-1.162317277453920.002137395728283	0.01529943685
	0.559944204357188	3.06E-05
	0.999704385795877	0.000467168101
		8.19E-05
NA	NA	NA
	1.85531122534804	0.001074009785
NA	NA	NA
	0.829175716995411	3.53E-08
NA	NA	NA
	-1.22399690919656	1.05E-06
	1.417253427848450.000605162071018	4.54E-10
NA	NA	NA
	2.88330434363118	1.86E-08
NA	NA	NA
	0.774898993698121	1.29E-06
NA	NA	NA
	-1.425872581133350.002306453096128	2.93E-05
	-0.859333357592430.005600762636245	0.005792098443
	0.3289853363986680.008186160704475	
	2.34602008490232	0.042129012056
	-0.9191298042867920.001952555691526	2.49E-13
NA	NA	NA
	0.8586313762850430.001484373936053	1.50E-11
	-0.7584308002843690.006403605358012	0.014422659268
	-1.526171567009390.001795661849137	
	-0.8804266050874840.003049220286781	0.016271045518
	-1.151903236836850.002114757339255	0.032303611268
	-1.918985474568830.000304424910601	0.042129012056
	-0.4962005090514890.001365060080658	
	-1.143218898986970.000443745069851	0.011691439873
	0.704872392438009	0.035445649305
NA	NA	NA
	0.6022442280361470.000230592457033	0.013560023758
NA	NA	NA
	-0.9641000571898020.003536912972383	0.020243690575
NA	NA	NA
NA	NA	NA
	0.3219105721123720.004450449956513	0.015199735219
		0.003239292346
		0.011103187491
		0.004514489773
		1.10E-07
		3.02E-06
NA	NA	NA
	0.6022442280361470.000230592457033	
NA	NA	NA
	-0.9641000571898020.003536912972383	
NA	NA	NA
NA	NA	NA
	0.3219105721123720.004450449956513	
		0.022792862923
		0.027241960388

	0.3962368945636040.001571165284341	0.012243389051
	0.3819009846509950.000219678336685	0.002475605871
	-0.7891124100961020.001788343669845	0.013528004181
	0.422465917674924	2.50E-05 0.000399063376
NA	NA	NA
	0.449387526235108	2.17E-11 1.10E-09
NA	NA	NA
	1.77607822386099	1.24E-08 4.03E-07
NA	NA	NA
	-0.949317474191660.001751501047664	0.01336431789
NA	NA	NA
NA	NA	NA
	0.8180976211153310.000266355097583	0.002890446059
	2.16721281820108	1.02E-10 4.78E-09
	1.187245964522120.001388958061169	0.011159909833
	-0.779472373061907 0.00430992859347	0.026604123832
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.461916719084736	2.06E-06 4.47E-05
	-1.289378349944420.000436006053426	0.004456387453
	-1.356080154680090.001032996546082	0.00884994117
	-0.7532272322089170.004788721087779	0.028629174121
	-1.208825219145030.001388555921929	0.011159909833
	2.54091614900117	3.18E-23 5.60E-21
NA	NA	NA
NA	NA	NA
	0.649181193454416	3.92E-05 0.000582394989
NA	NA	NA
NA	NA	NA
	1.15961823069822	5.25E-05 0.000753780062
NA	NA	NA
	-0.8179476425524650.006189106894107	0.034545623023
	0.629230512278488	3.31E-05 0.000499625568
	-1.61237761503465	1.82E-08 5.70E-07
NA	NA	NA
NA	NA	NA
	0.540872900508865	4.38E-06 8.95E-05
	-1.203651981127390.000245067636526	0.002679284235
	-1.35431278414805	1.38E-07 3.63E-06
	-0.933153130705050.004522982243713	0.027570744745
	-1.259288101964790.005399276299965	0.031471908937
	2.59021294626587	7.28E-18 6.95E-16
NA	NA	NA
	-0.7313981955773170.009081554409331	0.045511324548
	0.9047883261013290.007603776334837	0.039831462445
	0.73204343114825	4.90E-07 1.15E-05

NA	NA	NA
	0.6106383609280290.000161396629124	0.001922325705
	-0.4401368076873250.007454112719457	0.039168697278
	0.354502592453486	0.00076593087616
	0.007013054585	
	-0.580345905432113	0.00534302941719
	0.031268461103	
	-1.38816865341157	9.42E-08
		2.64E-06
NA	NA	NA
	0.72267018314428	8.55E-05
	0.001112213832	
NA	NA	NA
	-0.9942689262310690.006997138905043	0.037745992094
	1.4616777804134	7.89E-06
	0.000151486097	
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.390079425773426	0.00193649720382
	0.01432812325	
NA	NA	NA
NA	NA	NA
	-0.9143623672200110.000967416527552	0.008503591277
	1.45721976380259	1.30E-05
	0.000227378903	
	-1.046490604344060.001146943087128	0.009631830932
NA	NA	NA
	1.29376908270991	1.19E-10
	5.45E-09	
	1.46305165926465	4.09E-21
	5.45E-19	
NA	NA	NA
	-1.008578732544470.004158490763452	0.025997961459
NA	NA	NA
	0.560410635292951	1.72E-05
	0.000289175539	
	-0.9907620198249820.001196794418244	0.009924361261
NA	NA	NA
	-0.89116021255313	0.00044129482257
	0.004499978527	
NA	NA	NA
NA	NA	NA
	1.211704073943110.004069155120048	0.025548481075
	0.698756433883924	0.00197571120357
	0.014544808609	
	1.03917628971701	5.27E-06
	0.000106707981	
NA	NA	NA
NA	NA	NA
	-0.9204724328093090.000951393142144	0.008411661193
	-1.296763752955580.000125001915766	0.001526065055
NA	NA	NA
	0.4886933952450350.001394772411849	0.011186176551
	1.42062389819268	9.78E-13
	5.44E-11	
	-3.44356481856178	1.65E-11
	8.43E-10	
	-2.78123975498499	2.21E-08
	6.79E-07	
	-1.97496575403138	0.0002025987954
	0.002324860851	
	0.9815772791976450.005947694675882	0.033509637153
	-0.9356385893812260.004564625018663	0.027661783484
	1.066910534051020.000233008022341	0.002586036006

NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.3773861895500110.000362192100736	0.003790081626
NA	NA	NA
	-0.8669885799967750.006511897772655	0.035819512779
	-0.8688422731388090.010247614703331	0.049665058099
	0.4364566864482210.003779512810414	0.024108793616
NA	NA	NA
	-1.146869182588170.002503873820623	0.017340649575
NA	NA	NA
	-1.320717872816980.001363449729705	0.011103187491
	-0.564200856743589 0.0082144944718	0.042225383864
NA	NA	NA
	0.8820431167049370.005911277465327	0.033436376397
	0.7687539809506640.005828018163762	0.033050503006
NA	NA	NA
	-1.043755827419410.006393175312608	0.035432541613
	0.736263573091683 0.00012151840959	0.00150868195
	-1.486443276979660.004083502380734	0.025601987109
NA	NA	NA
NA	NA	NA
	0.4882542424328430.000314473542357	0.003322382737
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.7304205584106980.007438805061394	0.039168697278
	1.42716971818579 1.32E-10	5.92E-09
	0.7191621382897750.003374262132191	0.021872982406
	1.02945961394081 9.05E-05	0.001159515284
	1.71757150542663 1.79E-18	1.92E-16
	1.42941502650763 1.36E-14	9.65E-13
	-0.9574838581645340.009379496923002	0.046579535567
	1.169038139792690.001441051726149	0.011453821746
NA	NA	NA
	1.562833959494760.003301626475106	0.021465863278
NA	NA	NA
	-1.168892543239490.002254724140338	0.015989629118
	0.3640023957060420.009227855970258	0.046139279851
NA	NA	NA
NA	NA	NA
	-0.78332577407141 0.00067743677952	0.006322711214
NA	NA	NA
	0.8563741323656250.000371360519521	0.003867605411
NA	NA	NA
NA	NA	NA
NA	NA	NA

	-0.980273892248750.002113385861216	0.015199735219
	0.649585113040014 0.00350158689786	0.022631580024
	0.804576026618778 3.54E-08	1.05E-06
	-0.8214822643219470.005627992287323	0.032414087537
	0.4891046003717250.007995651890649	0.041245176126
	-1.126271413563860.000677587481641	0.006322711214
	-1.06066946994640.005363583768068	0.031305379363
	3.23902492905074 3.49E-19	4.04E-17
	0.5525158250428250.007419846662361	0.039168697278
NA	NA	NA
	0.520641609433756 0.00019272896787	0.002250519416
	0.7240566647299 2.43E-09	8.89E-08
	-0.9619195703184060.000654723014697	0.006163597925
NA	NA	NA
	-1.295732727777320.004122954584384	0.025812514812
	-1.455278376729650.003137286359094	0.020703263586
	-1.359683535784930.007408119435373	0.039168697278
	-1.022806436637670.004268070968878	0.026382801559
NA	NA	NA
	-1.12898088879540.000182701739921	0.002146989698
	-0.908680464111360.010113323156219	0.049222652571
NA	NA	NA
	-0.9813093552557590.000434758570767	0.004453995148
	-0.9133888068319340.000106774956307	0.00133696847
NA	NA	NA
	0.6533358611290690.000240275059401	0.002646638812
	-0.871976251424309 0.00177570027278	0.013502080794
	1.338948068360440.004733575949155	0.028343414573
	-0.954574702888933 0.00023132097894	0.002573811905
NA	NA	NA
	-0.966176151301711 1.73E-05	0.000289606981
	-0.9118589082901280.003785417093641	0.024111461053
	-1.010597866372020.000697392396146	0.006493727926
	-0.8972443327662390.007459431085697	0.039168697278
NA	NA	NA
	-1.17325540892794 3.79E-05	0.000564143204
NA	NA	NA
	2.32873177649599 4.72E-13	2.73E-11
	0.9299310348569570.004169648499815	0.026030689143
NA	NA	NA
NA	NA	NA
	-1.2228478950030.002089733494881	0.015180791256
	0.50309839833357 7.15E-07	1.66E-05
NA	NA	NA
	-1.074089956073340.007923003472681	0.041014841299
	0.5681811520839930.001387129506579	0.011159909833
	0.737471176783229 3.93E-10	1.66E-08
	3.45357079367854 5.69E-15	4.24E-13

NA	NA	NA
	-1.46769708430174	6.36E-05 0.000893300747
	-1.324851851933820	0.000427382777309 0.004398939827
	2.35261218995742	1.10E-21 1.62E-19
NA	NA	NA
	0.278043752555037	0.00985504379723 0.04836937004
	-0.8933338279176930	0.005145233304223 0.030353423318
NA	NA	NA
NA	NA	NA
	-1.181682578685430	0.001164464989467 0.009711240282
	-1.15800715336162	6.50E-05 0.000906524872
NA	NA	NA
	0.501842685286087	1.91E-07 4.91E-06
	-1.166718844049190	0.000103630504607 0.001301303051
	0.4364829880244560	0.007197408372423 0.038389089559
NA	NA	NA
	2.82086840226461	2.07E-21 2.84E-19
	0.928043635008393	1.03E-05 0.000185844061
	-1.011724732928930	0.004049004514905 0.025458333109
NA	NA	NA
	2.88951712115611	4.19E-29 1.25E-26
NA	NA	NA
	-1.287820978791510	0.003734839078469 0.023928014213
NA	NA	NA
	-0.8542643727786960	0.007074339924988 0.037916736549
NA	NA	NA
	0.619567286480670	0.001405198556927 0.011249267136
NA	NA	NA
	1.39621257467047	3.42E-18 3.58E-16
	1.37649899417067	2.73E-14 1.82E-12
	0.4586913400111510	0.002659732319152 0.018207980596
NA	NA	NA
	0.6890147578440450	0.000497469864794 0.00493539516
	-1.276882823565920	0.007255544198705 0.038605468224
	-1.145253221516480	0.001109534472363 0.009379177799
NA	NA	NA
NA	NA	NA
	0.888695689714696	8.00E-05 0.001055100137
	-1.399409864955930	0.002619326738782 0.018015557147
	-0.9376387829944590	0.003583282560171 0.023057872404
NA	NA	NA
NA	NA	NA
	1.18400787475626	2.92E-10 1.26E-08
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-0.9254507469718210	0.001465970017007 0.011582410029
	-0.9230421215801750	0.000949936628909 0.008411661193

	1.09277098230177	4.34E-07	1.03E-05
	0.49133718832301	0.00459634768568	0.027786723629
	0.2909661627982220	0.003071974120442	0.020324192957
NA	NA	NA	
NA	NA	NA	
	-0.93535537162377	5.47E-05	0.000780750819
	1.0464352732098	9.06E-13	5.17E-11
NA	NA	NA	
	0.6701492756388580	0.000294134546172	0.003164102332
NA	NA	NA	
	0.5817193442866060	0.000378382079196	0.003926512368
NA	NA	NA	
	0.4573562014392230	0.005954727330305	0.033509637153
	1.166745311062310	0.002725507883697	0.018547455933
	-1.146006091413960	0.000490424327379	0.004887562174
	1.731286185039020	0.000365162486628	0.003812088192
	0.851346301344424	1.35E-09	5.11E-08
	4.18629311289421	4.42E-36	4.85E-33
	-1.19992599142049	4.13E-06	8.52E-05
	1.075739299599110	0.001742041551288	0.013329479491
NA	NA	NA	
	0.5026436817946230	0.000171703221737	0.002028590483
NA	NA	NA	
NA	NA	NA	
	0.972925817676385	4.34E-06	8.91E-05
NA	NA	NA	
NA	NA	NA	
	0.5336445118454220	0.003075219184656	0.020324192957
	2.9805805440542	1.99E-17	1.78E-15
NA	NA	NA	
NA	NA	NA	
	-0.9780158374096060	0.002725712382695	0.018547455933
	0.515615025935505	9.92E-08	2.74E-06
	-0.6766726616426160	0.006440123712116	0.035602948069
NA	NA	NA	
NA	NA	NA	
	-1.14993996553184	0.00745707570085	0.039168697278
	0.3503308098017220	0.000233759705517	0.002587843591
	0.456656961822363	2.76E-06	5.87E-05
	-0.9729172093711810	0.000894739700896	0.008008922577
	1.389362346624770	0.006478796918428	0.035691618557
	-0.8833143023506710	0.009921251217476	0.048556680513
NA	NA	NA	
NA	NA	NA	
NA	NA	NA	
	0.586328319949022	3.32E-10	1.42E-08
	-1.80256288583555	0.00050788227827	0.005027348227
	-1.125716485771250	0.000100068981875	0.001267444309

NA	NA	NA
0.86675710466822	6.40E-05	0.000895789513
0.4836734550713340.008601180574528	0.043803231315	
2.4750455704333	4.82E-31	1.77E-28
-1.25937973546680.000217948192187	0.002462495816	
-1.262629428469330.000615958259774	0.005872313561	
-1.034354996845810.003251002501556	0.021293824135	
-1.240470561736260.009439294534742	0.046770799865	
3.83369015715834	1.88E-19	2.29E-17
-0.870320119220530.006762183018124	0.036918999211	
-0.9836166517941430.004181184131236	0.026047897087	
0.4161212539501280.005736645698509	0.032703118211	
-1.19838257882565	9.23E-05	0.001179477974
1.07502559491169	1.44E-15	1.15E-13
-0.9877947419275090.004551383513272	0.027661783484	
3.80286261444652	8.13E-21	1.05E-18
-0.914929136872207 0.00162149480138	0.012568729545	
-1.005486408432290.002070560622277	0.01509139956	
3.09836517873042	1.81E-36	2.65E-33
0.535960966103053	1.76E-05	0.000292550416
NA	NA	NA
-1.20970081745590.002120008575442	0.015199735219	
-0.9113123595752030.007790005108513	0.04046935278	
-0.6955248415445640.010308699895531	0.049842393884	
-1.45208609886124	1.25E-10	5.66E-09
-1.236373229469470.004833197166256	0.028822118787	
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
-0.9566099722770490.006271628542473	0.034890895499	
NA	NA	NA
-1.161706958160560.005634667321594	0.032414087537	
NA	NA	NA
NA	NA	NA
0.7094147349565820.006677479230355	0.036592919224	
NA	NA	NA
-0.9769160619836360.006804690336698	0.037104980186	
2.83398060739229	1.10E-29	3.71E-27
1.52517267205937	1.06E-15	8.60E-14
NA	NA	NA
NA	NA	NA
NA	NA	NA
0.5782627589987870.000124407610669	0.001523040248	
-0.9838898944179870.006074049553904	0.034006939859	
-1.109359592669590.003345627095062	0.021719395986	
0.5948632436495150.006884063548954	0.037352418886	
0.3782562945084180.007137456203482	0.038161946489	

NA	NA	NA
	-0.813902442676836	0.00397458159512 0.025062103458
	-0.6575348480725770	0.004721861214663 0.028311841799
	-1.35817074822633	1.77E-07 4.57E-06
	-0.833828404512789	0.00596268371992 0.033511502492
NA	NA	NA
	0.5443631807206240	0.002255647338629 0.015989629118
	-1.19401820880089	1.87E-05 0.000305782709
NA	NA	NA
NA	NA	NA
	-0.8128106268867460	0.002110975847459 0.015199735219
	-1.193528437558840	0.000110495459591 0.001379623707
	-1.350156555492280	0.000330258449452 0.003472454271
	-1.05573537028140	0.000597384668109 0.005757687755
	-1.02968701479061	3.33E-05 0.000501064138
	-1.16083082951872	6.48E-06 0.000126650882
	-0.9303249472952960	0.000543387587142 0.005283602756
	-1.123850698064330	0.002368849830948 0.016599450511
	-1.142030268459950	0.005141673376628 0.030353423318
	-1.085998445735430	0.000974995421226 0.008553103545
	-0.936240318967230	0.001366740485274 0.011103187491
	-1.334867065363570	0.002194037313654 0.015653886353
	1.550142034376540	0.002932480533945 0.019676720529
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.985651280689773	3.49E-06 7.31E-05
	-1.504847025912640	0.001001309301414 0.008728050054
NA	NA	NA
NA	NA	NA
	-0.9687332172961680	0.008919737598308 0.044853829227
NA	NA	NA
	-0.901357587312095	1.75E-05 0.00029116478
NA	NA	NA
NA	NA	NA
	-1.1632102510208	7.31E-05 0.000983150795
	0.5366685736688250	0.005697244257374 0.032560973357
	-1.33980708511240	0.000261551581268 0.002845344554
	-1.06112884427760	0.000805334757859 0.007328046089
	-0.7987155449376980	0.009641806080869 0.047613188456
NA	NA	NA
	-0.9331524138961580	0.000455730068173 0.004593884517
	-0.8929650085636590	0.008011507049489 0.04127851522
	-1.91701966141333	3.31E-05 0.000499625568
NA	NA	NA
	1.471463394562910	0.001133641353322 0.009563059017
NA	NA	NA

	-1.201922635731430.003015418647624	0.020049568769
	-1.1152046681680.001441174840817	0.011453821746
	1.66133734026585	7.73E-05 0.001032147172
NA	NA	NA
	-1.082808964041430.000670772498872	0.006299241736
	-0.7269037251280270.008848732229466	0.044701354194
	-0.7923848132857720.009969256382015	0.048683201999
	0.4101761044317970.006851965399722	0.037252857134
NA	NA	NA
	0.3679361158734360.010199261641194	0.049586012072
NA	NA	NA
	-1.36698347635896	1.31E-05 0.000228088385
NA	NA	NA
	-1.42988107814395	0.00425658781714 0.026348878108
	-0.8846075294875290.005335598340114	0.031266606273
	0.4732427766120970.004988099670439	0.029632042156
	-2.28540805405104	1.51E-05 0.000259044934
	0.829156971187362	9.94E-05 0.001262300537
	-0.9200747985361990.006670781799689	0.036592919224
	0.502155509241420.006857238093639	0.037252857134
	0.4929116430950810.002272120905682	0.016080469212
	2.79813383365607	3.47E-11 1.73E-09
	0.503235211875886	0.00766818476846 0.040121038164
	-1.393512098500730.000238432098978	0.002632937374
	-1.02181026917860.006730692457022	0.036792777797
	0.9465100577751750.002527086652908	0.017463122389
	-1.786176407923750.000744254392493	0.00682880596
	-1.08954861395060.007296352038515	0.038775655634
NA	NA	NA
	-1.049037753976830.008311515198779	0.042529979609
	1.281165535960090.000340561689535	0.003572240156
	1.056155078906070.001021918801672	0.008806535556
	1.4928440377624	7.46E-07 1.73E-05
NA	NA	NA
NA	NA	NA
	0.754309865950557	2.89E-05 0.000449449394
NA	NA	NA
	0.4980225433433880.002107065909048	0.015199735219
NA	NA	NA
	0.956939168366612	1.87E-05 0.000305782709
	0.887522971486080.005054147479809	0.029912469607
NA	NA	NA
	1.040478638829180.009370027007788	0.046579535567
	2.70673955953202	5.34E-15 4.04E-13
NA	NA	NA
	-1.029536755785630.000911157947959	0.008139307279
NA	NA	NA
NA	NA	NA

	-1.282017303751930.000216981371412	0.002462495816
	0.663767065405633	6.37E-10
	0.491825290406392	5.69E-06
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-0.8975273839442110.003011648486927	0.020049568769
NA	NA	NA
NA	NA	NA
	1.368787185224570.000413989577045	0.004281139273
NA	NA	NA
	-2.08835933383161	4.16E-05
NA	NA	NA
	0.7238177195922690.000197789176536	0.002288958767
NA	NA	NA
	0.451661807310485	1.31E-06
	2.34891169248839	4.90E-17
	2.01445497736905	2.87E-17
	-1.355285054784310.001449663225496	0.011500487141
	-1.200147249122270.004438796973614	0.027208525382
NA	NA	NA
	-1.352341483490210.001059948634771	0.009028050872
NA	NA	NA
NA	NA	NA
	4.02904059811883	1.25E-35
	3.89373653836367	3.48E-34
	0.521122068729842	4.62E-05
NA	NA	NA
	-1.128465664370260.000311336427586	0.003297165299
	-0.8264816956211120.001803233838061	0.013593846858
NA	NA	NA
NA	NA	NA
	-1.172679076912220.003516796724701	0.022696507496
	-1.073109128859310.003849988402137	0.024451877207
	-0.7946734590940050.004328287133334	0.026679974686
	-1.018581270088060.007474082895195	0.03919879991
NA	NA	NA
	-1.116326060862080.004989240317493	0.029632042156
	-0.9855392759631080.001464663668981	0.011582410029
	-1.07218753857299	0.00279191371658
	-0.918815572943120.002094988225065	0.015193850246
NA	NA	NA
	3.83838063354755	3.55E-22
	4.05085011633054	2.13E-23
	2.23587590365439	1.17E-17
NA	NA	NA
	1.1657742525666	9.06E-09
	3.65484349642372	1.15E-22

	-1.053981554100440.004875966282597	0.029037766683
	1.87430290686589	4.02E-10
	1.035879894067530.008836215462277	0.044689490169
	-1.62167645714787	2.84E-07
	-1.79501381840405	8.73E-05
	-1.395633264838840.000131303278117	0.001594137866
	-1.293400507194160.001869140872092	0.013970874376
	-0.8484423375861160.000378803468499	0.003926512368
	-1.012011519257390.001522916729726	0.011930871706
NA	NA	NA
	-1.254767116345130.008589601604644	0.043795010502
NA	NA	NA
NA	NA	NA
	2.33901185985294	5.09E-19
NA	NA	NA
NA	NA	NA
	-0.9228167811233730.000451072506176	0.004567888628
NA	NA	NA
	3.14338669145324	1.03E-16
	1.16476196565472	3.62E-11
	-1.376857012269230.000922386806136	0.008216082974
NA	NA	NA
	0.4334769534044620.002486525679694	0.017264265975
	3.875648109042	6.95E-24
	3.16523677396975	1.04E-32
	0.4546728623187580.006905850141756	0.037378339129
NA	NA	NA
	0.5624713444246220.006480525963331	0.035691618557
	0.7638862548122640.001743902322449	0.013329479491
	-1.072426916977370.000522746021746	0.005128278495
	-0.7888788939538	0.00021260796924
NA	NA	NA
	-1.002267613934190.002631309167117	0.01806301459
	0.833387812611928	2.72E-06
	-1.242898344716840.000149434749888	0.001794441874
	0.4361916759854560.000429026683239	0.004405542694
	-1.123752193411150.000294452298935	0.003164102332
	-1.10940157055389	2.37E-06
	-1.521775399116020.001670204792282	0.012878158004
	1.032611014129140.005736997529204	0.032703118211
	-0.904522837473370.005426557615479	0.031589034066
	0.3510448196456670.001148368466092	0.009631830932
	-1.340239529867140.005938896159875	0.033509637153
	-1.080860316852270.006073605564825	0.034006939859
	-2.036205808896860.000123590435731	0.001521512507
NA	NA	NA
	0.4434319709397560.003917396006864	0.024738822149
	-0.917446411394420.006815807342238	0.037119545563

NA	NA	NA
	-1.321176157328430.001489575061352	0.011711417522
	-1.622346065132210.000534425063369	0.005219551452
	-0.999464732567274	0.00975432609567 0.048007013651
NA	NA	NA
	0.511549781812270.004710492206904	0.028305618266
	-1.01818346079320.005455936484363	0.031634354682
NA	NA	NA
	-1.19781598884591	0.00048899791068 0.004887562174
NA	NA	NA
	-0.6538359213867670.005908440008906	0.033436376397
	-0.9985736481974850.000305134705664	0.003239292346
	-0.9745465424812520.000626060561195	0.005942842692
	1.77441900186624	1.53E-05 0.000260452643
	-1.002508511528210.001046321018779	0.008929283257
	-1.21195815844270.000283983458994	0.003066602708
	0.406976003060815	0.00127413436797 0.010466954294
	-1.06565179995336	1.88E-05 0.000306126997
NA	NA	NA
	0.633443860262728	9.74E-08 2.71E-06
	0.392073567035005	9.15E-06 0.000168351722
	-1.146095626992150.005682826066996	0.032560973357
NA	NA	NA
	-1.072505942317930.002781501401352	0.018865275708
	0.4184297137127970.009297769392917	0.046436018729
	-1.35174558589679	7.14E-05 0.000971249614
	-0.7836525787222630.009591105436143	0.047416094929
	0.471658633365371	3.32E-06 6.97E-05
	-1.34075694226172	8.64E-08 2.47E-06
NA	NA	NA
NA	NA	NA
	-1.2633872907766	4.80E-05 0.000693561819
	-0.9288228593826480.000654926104893	0.006163597925
	-1.20250209932928	0.00032059321942 0.003378914147
	-1.197770172698590.001806742215226	0.013596972664
	-1.476651029826210.003274148044698	0.021399993857
	-1.407638059859070.001217604518445	0.010077913105
	-1.98052568802717	8.92E-05 0.001151129754
	-1.47459666178679	0.00299507101276 0.019975077889
	-1.0254412651670.008891319994304	0.044813476347
	-0.9589683018632180.005679260591144	0.032560973357
	-1.127853043916930.000600255658595	0.005764232296
	-1.140804025213320.002730421840426	0.018547455933
	-0.9295198227877150.005220545063452	0.030700274966
	0.96059840975532	5.16E-22 7.81E-20
	-1.038028334674530.002117571551589	0.015199735219
	0.754022453069681	1.63E-08 5.22E-07
	-1.099684599678660.007752474609246	0.040369817426

NA	NA	NA
	0.5875487726687050	0.009364180274265 0.046579535567
NA	NA	NA
NA	NA	NA
NA	NA	NA
	0.5766514325281540	0.001160988662013 0.009700656216
NA	NA	NA
	-1.360878631616570	0.009126145210903 0.045682697269
	-0.721514637226476	0.00823929906905 0.042303410524
NA	NA	NA
NA	NA	NA
	0.3935235569192720	0.006193845493138 0.034545623023
	-1.22336785950495	7.96E-05 0.001053971416
NA	NA	NA
	-1.708228899657670	0.000977139116743 0.008554833502
	-1.246552179876530	0.001244977683458 0.01024658599
NA	NA	NA
	-1.1822360182181	0.01022287364704 0.049645889148
	-1.39264521047050	0.000639086391617 0.006053415283
	-1.76033232912213	1.17E-05 0.000205485412
	-1.9819544187440	0.000193560031652 0.002250519416
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-1.260713191948990	0.001685836213862 0.01297591972
NA	NA	NA
	-1.274784065194640	0.010053271384501 0.048984620549
	-1.621133632839120	0.000529476399873 0.005182736698
	0.7058190883820540	0.005046890094767 0.029912469607
NA	NA	NA
	-1.2112498371702	6.71E-07 1.57E-05
	-1.26188683977173	7.61E-05 0.001020048122
NA	NA	NA
	-2.7949089813522	1.12E-07 3.03E-06
	1.266098929256580	0.004794328135013 0.028629174121
	-1.681106429223230	0.001563252597519 0.012203366192
	2.46949004045148	9.69E-13 5.44E-11
	-1.645483776904920	0.001928728857672 0.014294710505
	-1.92025136971888	4.79E-05 0.000693561819
NA	NA	NA
	0.7857669986508210	0.003682378511121 0.023660897012
	-1.436022010780020	0.001029979566797 0.008849754036
NA	NA	NA
	-1.209175672097650	0.001630358923529 0.012593018399
NA	NA	NA
NA	NA	NA
	-1.407666767050880	0.000624434877483 0.00594024088
	2.30582961971878	3.38E-07 8.12E-06

	-1.282986319833960.001035777113297	0.008856498858
	-0.4714388664096950.006327206942517	0.035155593568
	-0.772007057223441 0.00375552513396	0.023990600238
	0.659977937923548 2.47E-07	6.13E-06
	-1.165149547263630.002225259223117	0.015850914563
	0.342044791527053 0.00299512544454	0.019975077889
	1.95364509651096 4.53E-18	4.63E-16
NA	NA	NA
	2.5302536573942 2.03E-14	1.39E-12
	3.31192120900107 4.07E-28	9.93E-26
	3.43255914800359 4.22E-31	1.73E-28
NA	NA	NA
	-1.20465387760759 6.77E-05	0.000926541437
NA	NA	NA
	-1.253235076180690.001624660090224	0.01257109348
	-0.8847050877318430.002634446496587	0.01806301459
	-1.12435584410948 0.00014657628651	0.001764939121
	-1.270719062963580.003298096432572	0.021465863278
	-1.189538517838340.005948016275772	0.033509637153
	-1.01517859174270.009944463884306	0.048616149913
NA	NA	NA
	0.6007964749474310.003059792429917	0.020283239411
	1.340983748976560.010290252055258	0.049807993153
	-0.711599594333524 0.0047143828374	0.028305618266
	1.79237900157278 8.94E-06	0.000165104215
	-1.101922044822510.002590904711937	0.017876022306
	0.466309723445353 2.83E-08	8.51E-07
	1.96876886243778 1.60E-07	4.17E-06
	1.519016360318040.002830755189438	0.019110858767
NA	NA	NA
NA	NA	NA
	0.383818236335286 1.70E-05	0.000287920379
	2.11061081718873 4.95E-10	1.99E-08
	-1.255436314116740.004516654655833	0.027570412795
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-1.02000335195240.001384801695912	0.011159909833
NA	NA	NA
	-1.252608490987110.007994784078167	0.041245176126
NA	NA	NA
	-0.9308677268621530.005056874839088	0.029912469607
	0.9726974042118350.000600686778563	0.005764232296
	0.4561582435354910.009918317824674	0.048556680513
NA	NA	NA
	-1.645382719564590.000829609833983	0.007486930637
NA	NA	NA

	0.652494505131070.001409479575779	0.011263023156
	0.7989013333720390.000555518816598	0.005389636201
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-1.2820408359466	1.05E-05 0.000188122678
NA	NA	NA
NA	NA	NA
	-1.451097152893910.003209707960085	0.021117764198
NA	NA	NA
	-1.25582512850930.006215004081324	0.03461969954
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-0.807508822533424	8.93E-05 0.001151129754
	-1.174259899446350.002484711246136	0.017264265975
NA	NA	NA
NA	NA	NA
NA	NA	NA
	-1.107491223576070.000177392655779	0.002090189604
NA	NA	NA
	-1.487371156615170.000535643235837	0.005219849272
	1.430935934739830.002468953929934	0.017196596707
NA	NA	NA
	0.5965726132587460.005692309497679	0.032560973357

KEGG pathway**Annotation**

ko01210

2-Oxocarboxylic acid metabolism

ko00520

Amino sugar and nucleotide sugar metabolism

ko00970

Aminoacyl-tRNA biosynthesis

ko00330

Arginine and proline metabolism

ko00220

Arginine biosynthesis

ko03070

Bacterial secretion system

ko01230

Biosynthesis of amino acids

ko00650

Butanoate metabolism

ko00660

C5-Branched dibasic acid metabolism

ko00720

Carbon fixation pathways in prokaryotes

ko01200

Carbon metabolism

ko00020

Citrate cycle (TCA cycle)

ko00270

Cysteine and methionine metabolism

ko00052

Galactose metabolism

ko00010

Glycolysis / Gluconeogenesis

ko00630

Glyoxylate and dicarboxylate metabolism

ko00340

Histidine metabolism

ko00540

Lipopolysaccharide biosynthesis

ko00401

Novobiocin biosynthesis

ko00190

Oxidative phosphorylation

ko00770

Pantothenate and CoA biosynthesis

ko00400

Phenylalanine, tyrosine and tryptophan biosynthesis

ko02060

Phosphotransferase system (PTS)

ko00620

Pyruvate metabolism

ko00740

Riboflavin metabolism

ko00500

Starch and sucrose metabolism

ko00960

Tropane, piperidine and pyridine alkaloid biosynthesis

ko02020

Two-component system

ko00130

Ubiquinone and other terpenoid-quinone biosynthesis

ko00290

Valine, leucine and isoleucine biosynthesis

ko00750

Vitamin B6 metabolism

Other significant K

Number of KOs in FDR		KO
12	0.00030474562070388	K00052
		K00053
		K00812
		K00813
		K00930
		K01438
		K01649
		K01682
		K01703
		K01704
		K09011
		K14682
		K00012
		K00845
		K00965
		K00966
		K00975
		K01809
		K02472
19	2.8796377834678E-05	K02564
		K02765
		K02779
		K02794
		K02804
		K06859
		K07102
		K07806
		K11192
		K12373
		K13015
		K13381
		K01866
9	0.0063611243524591	K01868
		K01874
		K01881
		K01886
		K01887
		K01890
		K01893
		K04568
		K00812
12	0.00258146198811406	K00813
		K01259
		K01473
		K01474
		K01476
		K01480

		K01585
		K01777
		K10796
		K13747
		K13821
		K00262
		K00812
		K00813
		K00930
9	0.00321229834835604	K01438
		K01476
		K01478
		K01915
		K14682
		K02453
		K02461
		K03075
8	0.0488791677301393	K03106
		K03110
		K03205
		K03222
		K03229
		K00013
		K00052
		K00053
		K00674
		K00812
		K00813
		K00817
		K00831
		K00832
		K00930
		K01079
		K01089
		K01438
		K01476
30	3.0825764942532E-08	K01496
		K01609
		K01649
		K01682
		K01689
		K01703
		K01704
		K01735
		K01915
		K01960
		K04517
		K06001

		K09011
		K12339
		K13497
		K14682
		K00074
		K00174
		K00175
		K00239
		K00240
11	0.00373166645369643	K00241
		K00244
		K00248
		K00626
		K01615
		K01799
		K00052
		K01703
6	0.00373166645369643	K01704
		K01902
		K04835
		K09011
		K00024
		K00174
		K00175
		K00177
		K00239
		K00240
		K00241
		K00244
17	7.4557068250431E-06	K00626
		K01595
		K01676
		K01678
		K01682
		K01847
		K01902
		K01960
		K05606
		K00024
		K00029
		K00161
		K00162
		K00163
		K00164
		K00174
		K00175
		K00177
		K00239

		K00240
		K00241
		K00244
		K00248
		K00281
		K00605
		K00626
		K00627
37	5.3280508987188E-08	K00831
		K00845
		K01079
		K01595
		K01637
		K01638
		K01676
		K01678
		K01682
		K01689
		K01847
		K01902
		K01960
		K03389
		K03781
		K04835
		K05606
		K06859
		K12339
		K00024
		K00161
		K00162
		K00163
		K00164
		K00174
		K00175
		K00177
		K00239
19	1.1380629006833E-11	K00240
		K00241
		K00244
		K00627
		K01596
		K01676
		K01678
		K01682
		K01902
		K01960
		K00024
		K00547

		K00641
		K00812
10	0.0201869248460279	K00813
		K00832
		K01251
		K12339
		K12960
		K16846
		K00845
		K00965
		K01187
		K01220
		K01631
		K01785
14	9.0523508408146E-06	K02744
		K02745
		K02746
		K02747
		K02788
		K08302
		K15922
		K16371
		K00138
		K00161
		K00162
		K00163
		K00174
		K00175
		K00627
16	9.0523508408146E-06	K00845
		K01222
		K01596
		K01689
		K01785
		K01792
		K02750
		K02779
		K06859
		K00024
		K00104
		K00281
		K00605
		K00626
		K01091
14	0.00014009450411553	K01637
		K01638
		K01682
		K01847

		K01915
		K03781
		K04835
		K05606
		K00013
		K00817
6	0.0440068930965138	K01089
		K01468
		K01496
		K13990
		K00748
		K00912
		K00979
		K01627
		K02527
11	2.9163920965115E-06	K02536
		K02560
		K03272
		K06041
		K12975
		K16363
		K00812
		K00813
5	0.0440068930965138	K00817
		K00832
		K04517
		K00239
		K00240
		K00241
		K00244
		K00331
		K00332
		K00333
16	0.0440068930965138	K00337
		K00339
		K00341
		K00342
		K00343
		K00425
		K00426
		K02133
		K15987
		K00053
		K00606
		K00954
7	0.00400348581159221	K01918
		K01922
		K08682

		K09680
		K00812
		K00813
		K00817
		K00832
9	0.0140274179725372	K01609
		K01735
		K04517
		K06001
		K13497
		K02744
		K02745
		K02746
		K02747
		K02750
		K02760
14	2.8796377834678E-05	K02765
		K02779
		K02788
		K02794
		K02804
		K02806
		K08484
		K11192
		K00024
		K00029
		K00138
		K00161
		K00162
		K00163
		K00174
		K00175
		K00244
20	8.7910525089003E-09	K00626
		K00627
		K01595
		K01596
		K01638
		K01649
		K01676
		K01678
		K01960
		K02594
		K03777
		K00793
		K00794
5	0.0260406517341956	K01497
		K05368

		K14652
		K00012
		K00691
		K00845
		K00975
10	0.0391249349913255	K01187
		K01194
		K01226
		K06859
		K15922
		K16153
		K00812
		K00813
5	0.0225025243650138	K00817
		K00832
		K01582
		K00244
		K00425
		K00426
		K00626
		K01077
		K01467
		K01546
		K01915
		K02313
		K02402
		K02584
		K03092
		K03776
		K05966
		K07639
		K07645
33	0.00119648775443431	K07657
		K07659
		K07677
		K07702
		K07703
		K07710
		K07717
		K07771
		K07773
		K07775
		K07783
		K07806
		K09475
		K09477
		K11614
		K13598

Os

		K14986
		K01661
		K02548
		K02549
8	0.0102788741831309	K02551
		K03179
		K03182
		K03183
		K08680
		K00052
		K00053
		K00835
7	2.8796377834678E-05	K01649
		K01703
		K01704
		K09011
		K00097
		K00831
5	0.0163948884517566	K03472
		K03473
		K03474
		K00012
		K00024
		K00029
		K00065
		K00074
		K00108
		K00117
		K00161
		K00162
		K00164
		K00179
		K00184
		K00185
		K00208
		K00226
		K00239
		K00248
		K00262
		K00278
		K00281
		K00346
		K00347
		K00348
		K00349
		K00350
		K00351
		K00380

K00428
K00441
K00525
K00526
K00554
K00556
K00563
K00564
K00567
K00602
K00605
K00626
K00631
K00639
K00647
K00661
K00674
K00684
K00756
K00758
K00767
K00801
K00812
K00813
K00817
K00831
K00832
K00833
K00839
K00845
K00853
K00892
K00924
K00946
K00965
K00966
K00968
K00969
K00970
K00989
K00998
K01061
K01077
K01079
K01082
K01092
K01134
K01139

K01151
K01153
K01173
K01218
K01246
K01247
K01258
K01277
K01278
K01284
K01299
K01322
K01338
K01354
K01414
K01417
K01447
K01460
K01462
K01465
K01467
K01476
K01537
K01582
K01589
K01595
K01596
K01607
K01615
K01667
K01682
K01689
K01699
K01766
K01775
K01799
K01809
K01839
K01847
K01874
K01894
K01902
K01915
K01918
K01932
K01937
K01991
K01993

K02022
K02023
K02065
K02066
K02067
K02082
K02133
K02193
K02279
K02291
K02313
K02338
K02342
K02348
K02402
K02428
K02467
K02498
K02520
K02523
K02558
K02600
K02601
K02621
K02622
K02652
K02669
K02686
K02794
K02846
K02853
K02885
K02897
K02939
K02945
K02954
K02996
K03075
K03092
K03100
K03106
K03110
K03112
K03113
K03169
K03214
K03281
K03282

K03296
K03301
K03305
K03313
K03314
K03321
K03322
K03327
K03386
K03389
K03424
K03429
K03435
K03446
K03449
K03453
K03457
K03468
K03470
K03488
K03517
K03526
K03528
K03535
K03536
K03551
K03555
K03558
K03561
K03568
K03572
K03578
K03579
K03583
K03585
K03587
K03590
K03593
K03598
K03605
K03607
K03625
K03628
K03629
K03631
K03642
K03644
K03651

K03654
K03656
K03665
K03684
K03688
K03690
K03699
K03701
K03704
K03733
K03746
K03747
K03748
K03759
K03760
K03764
K03768
K03770
K03771
K03772
K03773
K03776
K03781
K03787
K03797
K03801
K03807
K03812
K03817
K03820
K03828
K03832
K03840
K03892
K03894
K03895
K03924
K03932
K03933
K03974
K03980
K04047
K04063
K04075
K04080
K04081
K04096
K04335

K04562
K04564
K04691
K04744
K04749
K04759
K04774
K04775
K04786
K05340
K05365
K05367
K05368
K05541
K05591
K05592
K05606
K05787
K05789
K05802
K05803
K05804
K05807
K05809
K05836
K05851
K05880
K05916
K05939
K05970
K05995
K06001
K06045
K06048
K06077
K06113
K06141
K06142
K06144
K06145
K06149
K06158
K06167
K06168
K06181
K06194
K06195
K06199

K06204
K06212
K06218
K06281
K06282
K06350
K06859
K06861
K06889
K06894
K06901
K06906
K06908
K06916
K06918
K06920
K06951
K06956
K06957
K06969
K06978
K07000
K07037
K07051
K07071
K07079
K07081
K07083
K07091
K07096
K07098
K07107
K07109
K07114
K07121
K07124
K07132
K07140
K07145
K07146
K07147
K07148
K07151
K07164
K07165
K07180
K07185
K07224

K07235
K07236
K07243
K07257
K07263
K07267
K07275
K07276
K07277
K07279
K07283
K07285
K07287
K07313
K07322
K07335
K07337
K07349
K07386
K07391
K07397
K07403
K07462
K07467
K07470
K07588
K07746
K07749
K07771
K07806
K07812
K08156
K08218
K08222
K08277
K08282
K08289
K08307
K08315
K08992
K09013
K09015
K09016
K09118
K09124
K09136
K09181
K09384

K09475
K09582
K09612
K09690
K09704
K09740
K09760
K09769
K09778
K09793
K09808
K09810
K09819
K09820
K09891
K09894
K09896
K09901
K09911
K09921
K09922
K09928
K09940
K09951
K09952
K09954
K10006
K10022
K10112
K10530
K10541
K10542
K10549
K10679
K10716
K10763
K10800
K10806
K10823
K10939
K11005
K11085
K11201
K11391
K11537
K11720
K11732
K11733

K11734
K11737
K11739
K11747
K11750
K11751
K11902
K11927
K11932
K11934
K11935
K12148
K12204
K12267
K12297
K12339
K12343
K12373
K12516
K12542
K12543
K12684
K12687
K12975
K12995
K12996
K12997
K13069
K13098
K13541
K13571
K13631
K13640
K13643
K13695
K13821
K13892
K13894
K13895
K13919
K13990
K14054
K14055
K14064
K14065
K14347
K14445
K14587

K14588
K14836
K15342
K15396
K15533
K15548
K15830
K15977
K16012
K16066
K16076
K16091
K16138
K16140
K16181
K16201
K16263
K16264
K16291
K16322
K16363
K16693
K16704

Definition

leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
aspB; aspartate aminotransferase [EC:2.6.1.1]
aspC; aspartate aminotransferase [EC:2.6.1.1]
argB; acetylglutamate kinase [EC:2.7.2.8]
argE; acetylornithine deacetylase [EC:3.5.1.16]
leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
cimA; D-citramalate synthase [EC:2.3.1.182]
argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
glk; glucokinase [EC:2.7.1.2]
galT, GALT; UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]
GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
glgC; glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]
E5.3.1.8, manA; mannose-6-phosphate isomerase [EC:5.3.1.8]
wecC; UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.336]
nagB, GNPDH; glucosamine-6-phosphate deaminase [EC:3.5.99.6]
PTS-Dgl-EIIC, gamP; PTS system, D-glucosamine-specific IIC component
PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component
PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]
PTS-Nag-EIIC, nagE; PTS system, N-acetylglucosamine-specific IIC component
pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]
K07102
arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]
PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
HEXA_B; hexosaminidase [EC:3.2.1.52]
wbpA; UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.136]
chiA; bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]
YARS, tyrS; tyrosyl-tRNA synthetase [EC:6.1.1.1]
TARS, thrS; threonyl-tRNA synthetase [EC:6.1.1.3]
MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]
PARS, proS; prolyl-tRNA synthetase [EC:6.1.1.15]
QARS, glnS; glutaminyl-tRNA synthetase [EC:6.1.1.18]
RARS, argS; arginyl-tRNA synthetase [EC:6.1.1.19]
FARSB, pheT; phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
NARS, asnS; asparaginylyl-tRNA synthetase [EC:6.1.1.22]
poxA; lysyl-tRNA synthetase, class II [EC:6.1.1.6]
aspB; aspartate aminotransferase [EC:2.6.1.1]
aspC; aspartate aminotransferase [EC:2.6.1.1]
pip; proline iminopeptidase [EC:3.4.11.5]
hyuA; N-methylhydantoinase A [EC:3.5.2.14]
hyuB; N-methylhydantoinase B [EC:3.5.2.14]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
E3.5.3.11, speB; agmatinase [EC:3.5.3.11]

E4.1.1.19S, speA; arginine decarboxylase [EC:4.1.1.19]
E5.1.1.4; proline racemase [EC:5.1.1.4]
prdE; D-proline reductase (dithiol) PrdE [EC:1.21.4.1]
nspC; carboxynorspermidine decarboxylase [EC:4.1.1.-]
putA; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.5.2 1.2.1.88]
E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
aspB; aspartate aminotransferase [EC:2.6.1.1]
aspC; aspartate aminotransferase [EC:2.6.1.1]
argB; acetylglutamate kinase [EC:2.7.2.8]
argE; acetylornithine deacetylase [EC:3.5.1.16]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
E3.5.3.6, arcA; arginine deiminase [EC:3.5.3.6]
glnA; glutamine synthetase [EC:6.3.1.2]
argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
gspD; general secretion pathway protein D
gspL; general secretion pathway protein L
secG; preprotein translocase subunit SecG
SRP54, ffh; signal recognition particle subunit SRP54
ftsY; fused signal recognition particle receptor
virD4, lvhD4; type IV secretion system protein VirD4
yscJ; type III secretion protein SctJ
yscU; type III secretion protein SctU
hisD; histidinol dehydrogenase [EC:1.1.1.23]
leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
dapD; 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC:2.3.1.117]
aspB; aspartate aminotransferase [EC:2.6.1.1]
aspC; aspartate aminotransferase [EC:2.6.1.1]
hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
argB; acetylglutamate kinase [EC:2.7.2.8]
serB, PSPH; phosphoserine phosphatase [EC:3.1.3.3]
hisB; imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:4.2.1.19 3.1.3.15]
argE; acetylornithine deacetylase [EC:3.5.1.16]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
hisI; phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]
leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
ENO, eno; enolase [EC:4.2.1.11]
leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
aroB; 3-dehydroquinate synthase [EC:4.2.3.4]
glnA; glutamine synthetase [EC:6.3.1.2]
E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]
tyrA2; prephenate dehydrogenase [EC:1.3.1.12]
K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]

cimA; D-citramalate synthase [EC:2.3.1.182]
 cysM; cysteine synthase B [EC:2.5.1.47]
 trpGD; anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27 2.4.2.18]
 argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
 paaH, hbd, fadB, mmgB; 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
 korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
 korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 sdhC; succinate dehydrogenase cytochrome b556 subunit
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 ACADS, bcd; butyryl-CoA dehydrogenase [EC:1.3.8.1]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 E4.1.1.70; glutaconyl-CoA decarboxylase [EC:4.1.1.70]
 nicE, maiA; maleate isomerase [EC:5.2.1.1]
 leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
 leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
 sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
 E4.3.1.2; methylaspartate ammonia-lyase [EC:4.3.1.2]
 cimA; D-citramalate synthase [EC:2.3.1.182]
 mdh; malate dehydrogenase [EC:1.1.1.37]
 korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
 korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
 korG; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 sdhC; succinate dehydrogenase cytochrome b556 subunit
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
 E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]
 E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]
 sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
 E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]
 MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]
 mdh; malate dehydrogenase [EC:1.1.1.37]
 E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
 korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
 korG; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]

sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 sdhC; succinate dehydrogenase cytochrome b556 subunit
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 ACADS, bcd; butyryl-CoA dehydrogenase [EC:1.3.8.1]
 GLDC, gcvP; glycine dehydrogenase [EC:1.4.4.2]
 gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
 serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
 glk; glucokinase [EC:2.7.1.2]
 serB, PSPH; phosphoserine phosphatase [EC:3.1.3.3]
 ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
 E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]
 E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]
 E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]
 E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 ENO, eno; enolase [EC:4.2.1.11]
 MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]
 sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
 E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]
 hdrB; heterodisulfide reductase subunit B [EC:1.8.98.1]
 katE, CAT, catB, srpA; catalase [EC:1.11.1.6]
 E4.3.1.2; methylaspartate ammonia-lyase [EC:4.3.1.2]
 MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]
 pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]
 cysM; cysteine synthase B [EC:2.5.1.47]
 mdh; malate dehydrogenase [EC:1.1.1.37]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
 korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
 korG; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 sdhC; succinate dehydrogenase cytochrome b556 subunit
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
 E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
 E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]
 E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]
 acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
 sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
 E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]
 mdh; malate dehydrogenase [EC:1.1.1.37]
 mmuM; homocysteine S-methyltransferase [EC:2.1.1.10]

metX; homoserine O-acetyltransferase [EC:2.3.1.31]
aspB; aspartate aminotransferase [EC:2.6.1.1]
aspC; aspartate aminotransferase [EC:2.6.1.1]
tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
E3.3.1.1, ahcY; adenosylhomocysteinase [EC:3.3.1.1]
cysM; cysteine synthase B [EC:2.5.1.47]
mtaD; 5-methylthioadenosine/S-adenosylhomocysteine deaminase [EC:3.5.4.31 3.5.4.28]
suyB; (2R)-sulfolactate sulfo-lyase subunit beta [EC:4.4.1.24]
glk; glucokinase [EC:2.7.1.2]
galT, GALT; UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]
E3.2.1.20, malZ; alpha-glucosidase [EC:3.2.1.20]
E3.2.1.85, lacG; 6-phospho-beta-galactosidase [EC:3.2.1.85]
dgoA; 2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]
E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]
PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component [EC:2.7.1.69]
PTS-Aga-EIIB, agaV; PTS system, N-acetylgalactosamine-specific IIB component [EC:2.7.1.69]
PTS-Aga-EIIC, agaW; PTS system, N-acetylgalactosamine-specific IIC component
PTS-Aga-EIID, agaE; PTS system, N-acetylgalactosamine-specific IID component
PTS-Lac-EIIC, lacE; PTS system, lactose-specific IIC component
gatY-kbaY; tagatose 1,6-diphosphate aldolase GatY/KbaY [EC:4.1.2.40]
yihQ; alpha-glucosidase [EC:3.2.1.20]
gatZ-kbaZ; D-tagatose-1,6-bisphosphate aldolase subunit GatZ/KbaZ
aldB; aldehyde dehydrogenase [EC:1.2.1.-]
PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
glk; glucokinase [EC:2.7.1.2]
E3.2.1.86A, celF; 6-phospho-beta-glucosidase [EC:3.2.1.86]
E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
ENO, eno; enolase [EC:4.2.1.11]
E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]
E5.1.3.15; glucose-6-phosphate 1-epimerase [EC:5.1.3.15]
PTS-Arb-EIIC, glvC; PTS system, arbutin-like IIC component
PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component
pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]
mdh; malate dehydrogenase [EC:1.1.1.37]
glcD; glycolate oxidase [EC:1.1.3.15]
GLDC, gcvP; glycine dehydrogenase [EC:1.4.4.2]
gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
E3.1.3.18, gph; phosphoglycolate phosphatase [EC:3.1.3.18]
E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]
E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]

glnA; glutamine synthetase [EC:6.3.1.2]
 katE, CAT, catB, srpA; catalase [EC:1.11.1.6]
 E4.3.1.2; methylaspartate ammonia-lyase [EC:4.3.1.2]
 MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]
 hisD; histidinol dehydrogenase [EC:1.1.1.23]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 hisB; imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:4.2.1.19 3.1.3.15]
 hutI, AMDHD1; imidazolonepropionase [EC:3.5.2.7]
 hisI; phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
 FTCD; glutamate formiminotransferase / formiminotetrahydrofolate cyclodeaminase [EC:2.1.2.5 4.3.1.4]
 lpxB; lipid-A-disaccharide synthase [EC:2.4.1.182]
 lpxK; tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]
 kdsB; 3-deoxy-manno-octulosonate cytidyltransferase (CMP-KDO synthetase) [EC:2.7.7.38]
 kdsA; 2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:2.5.1.55]
 kdtA, waaA; 3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12 2.4.99.13 2.4.99.14 2.4.99.15]
 lpxD; UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.191]
 msbB; lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase [EC:2.3.1.-]
 gmhC, hldE, waaE, rfaE; D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate adenosyltransferase [EC:2.7.1.13 5.3.1.13; arabinose-5-phosphate isomerase [EC:5.3.1.13]
 eptB; phosphoethanolamine transferase
 lpxC-fabZ; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase / 3-hydroxyacyl-[acyl-carrier-protein] dehydratase
 aspB; aspartate aminotransferase [EC:2.6.1.1]
 aspC; aspartate aminotransferase [EC:2.6.1.1]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
 tyrA2; prephenate dehydrogenase [EC:1.3.1.12]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 sdhC; succinate dehydrogenase cytochrome b556 subunit
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 nuoB; NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]
 nuoC; NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]
 nuoD; NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]
 nuoH; NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]
 nuoJ; NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]
 nuoL; NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]
 nuoM; NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]
 nuoN; NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]
 cydA; cytochrome d ubiquinol oxidase subunit I [EC:1.10.3.-]
 cydB; cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]
 ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
 hppA; K⁽⁺⁾-stimulated pyrophosphate-energized sodium pump [EC:3.6.1.1]
 ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
 panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]
 E2.7.7.3A, coaD, kdtB; pantetheine-phosphate adenyltransferase [EC:2.7.7.3]
 panC; pantoate--beta-alanine ligase [EC:6.3.2.1]
 PPCS, coaB; phosphopantothenate-cysteine ligase [EC:6.3.2.5]
 acpH; acyl carrier protein phosphodiesterase [EC:3.1.4.14]

coaW; type II pantothenate kinase [EC:2.7.1.33]
 aspB; aspartate aminotransferase [EC:2.6.1.1]
 aspC; aspartate aminotransferase [EC:2.6.1.1]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
 trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]
 aroB; 3-dehydroquinate synthase [EC:4.2.3.4]
 tyrA2; prephenate dehydrogenase [EC:1.3.1.12]
 K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]
 trpGD; anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27 2.4.2.18]
 PTS-Aga-EIIA, agaF; PTS system, N-acetylgalactosamine-specific IIA component [EC:2.7.1.69]
 PTS-Aga-EIIB, agaV; PTS system, N-acetylgalactosamine-specific IIB component [EC:2.7.1.69]
 PTS-Aga-EIIC, agaW; PTS system, N-acetylgalactosamine-specific IIC component
 PTS-Aga-EIID, agaE; PTS system, N-acetylgalactosamine-specific IID component
 PTS-Arb-EIIC, glvC; PTS system, arbutin-like IIC component
 PTS-Cel-EIIB, celA; PTS system, cellobiose-specific IIB component [EC:2.7.1.69]
 PTS-Dgl-EIIC, gamP; PTS system, D-glucosamine-specific IIC component
 PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component
 PTS-Lac-EIIC, lacE; PTS system, lactose-specific IIC component
 PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]
 PTS-Nag-EIIC, nagE; PTS system, N-acetylglucosamine-specific IIC component
 PTS-Ntr-EIIA, ptsN; PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]
 PTS-El.PTSP, ptsP; phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]
 PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
 mdh; malate dehydrogenase [EC:1.1.1.37]
 E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
 aldB; aldehyde dehydrogenase [EC:1.2.1.-]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 aceE; pyruvate dehydrogenase E1 component [EC:1.2.4.1]
 korA; 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
 korB; 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
 ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
 E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
 E2.3.3.9, aceB, glcB; malate synthase [EC:2.3.3.9]
 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
 E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2]
 E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]
 E6.4.1.1B, pycB; pyruvate carboxylase subunit B [EC:6.4.1.1]
 nifV; homocitrate synthase NifV [EC:2.3.3.14]
 dld; D-lactate dehydrogenase [EC:1.1.1.28]
 ribE, RIB5; riboflavin synthase [EC:2.5.1.9]
 ribH, RIB4; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]
 ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]
 fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.41]

ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II [EC:4.1.99.12 3.5.4.25]
 UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
 E2.4.1.8, mapA; maltose phosphorylase [EC:2.4.1.8]
 glk; glucokinase [EC:2.7.1.2]
 glgC; glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]
 E3.2.1.20, malZ; alpha-glucosidase [EC:3.2.1.20]
 E3.2.1.28, treA, treF; alpha,alpha-trehalase [EC:3.2.1.28]
 treC; trehalose-6-phosphate hydrolase [EC:3.2.1.93]
 pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]
 yihQ; alpha-glucosidase [EC:3.2.1.20]
 K16153; phosphorylase / glycogen(starch) synthase [EC:2.4.1.1 2.4.1.11]
 aspB; aspartate aminotransferase [EC:2.6.1.1]
 aspC; aspartate aminotransferase [EC:2.6.1.1]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
 E4.1.1.18, ldcC, cadA; lysine decarboxylase [EC:4.1.1.18]
 frdA; fumarate reductase flavoprotein subunit [EC:1.3.99.1]
 cydA; cytochrome d ubiquinol oxidase subunit I [EC:1.10.3.-]
 cydB; cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]
 ampC; beta-lactamase class C [EC:3.5.2.6]
 kdpA; K⁺-transporting ATPase ATPase A chain [EC:3.6.3.12]
 glnA; glutamine synthetase [EC:6.3.1.2]
 dnaA; chromosomal replication initiator protein
 flhC; flagellar transcriptional activator FlhC
 nifA; Nif-specific regulatory protein
 SIG54, rpoN; RNA polymerase sigma-54 factor
 aer; aerotaxis receptor
 citG; triphosphoribosyl-dephospho-CoA synthase [EC:2.4.2.52]
 rstB; two-component system, OmpR family, sensor histidine kinase RstB [EC:2.7.13.3]
 qseC; two-component system, OmpR family, sensor histidine kinase QseC [EC:2.7.13.3]
 phoB; two-component system, OmpR family, phosphate regulon response regulator PhoB
 ompR; two-component system, OmpR family, phosphate regulon response regulator OmpR
 rcsC; two-component system, NarL family, capsular synthesis sensor histidine kinase RcsC [EC:2.7.13.3]
 dpiA, citB; two-component system, CitB family, response regulator CitB
 dcuR; two-component system, CitB family, response regulator DcuR
 atoS; two-component system, NtrC family, sensor histidine kinase AtoS [EC:2.7.13.3]
 ycbA, glnK; two-component system, sensor histidine kinase YcbA [EC:2.7.13.3]
 basR; two-component system, OmpR family, response regulator BasR
 arcA; two-component system, OmpR family, aerobic respiration control protein ArcA
 resD; two-component system, OmpR family, response regulator ResD
 uhpC; MFS transporter, OPA family, sugar phosphate sensor protein UhpC
 arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]
 ompC; outer membrane pore protein C
 citT; citrate:succinate antiporter
 yufL, malK; two-component system, CitB family, sensor histidine kinase MalK [EC:2.7.13.3]
 ntrY; two-component system, NtrC family, nitrogen regulation sensor histidine kinase NtrY [EC:2.7.13.3]

fixL; two-component system, LuxR family, sensor kinase FixL [EC:2.7.13.3]
 menB; naphthoate synthase [EC:4.1.3.36]
 menA; 1,4-dihydroxy-2-naphthoate octaprenyltransferase [EC:2.5.1.74 2.5.1.-]
 menC; O-succinylbenzoate synthase [EC:4.2.1.113]
 menD; 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase [EC:2.2.1.9]
 ubiA; 4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]
 ubiD; 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]
 ubiE; ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.163 2.1.1.201]
 menH; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [EC:4.2.99.20]
 leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
 ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
 avtA; valine--pyruvate aminotransferase [EC:2.6.1.66]
 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
 leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
 cimA; D-citramalate synthase [EC:2.3.1.182]
 pdxA; 4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]
 serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
 epd; D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]
 pdxB; erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]
 pdxJ; pyridoxine 5-phosphate synthase [EC:2.6.99.2]
 UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
 mdh; malate dehydrogenase [EC:1.1.1.37]
 E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
 kduD; 2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]
 paaH, hbd, fadB, mmgB; 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
 E1.1.99.1, betA, CHDH; choline dehydrogenase [EC:1.1.99.1]
 gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 iorA; indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]
 K00184; prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit
 K00185; prokaryotic molybdopterin-containing oxidoreductase family, membrane subunit
 fabI; enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]
 pyrD; dihydroorotate dehydrogenase (fumarate) [EC:1.3.98.1]
 sdhA; succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
 ACADS, bcd; butyryl-CoA dehydrogenase [EC:1.3.8.1]
 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
 nadB; L-aspartate oxidase [EC:1.4.3.16]
 GLDC, gcvP; glycine dehydrogenase [EC:1.4.4.2]
 nqrA; Na+-transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.6.5.-]
 nqrB; Na+-transporting NADH:ubiquinone oxidoreductase subunit B [EC:1.6.5.-]
 nqrC; Na+-transporting NADH:ubiquinone oxidoreductase subunit C [EC:1.6.5.-]
 nqrD; Na+-transporting NADH:ubiquinone oxidoreductase subunit D [EC:1.6.5.-]
 nqrE; Na+-transporting NADH:ubiquinone oxidoreductase subunit E [EC:1.6.5.-]
 nqrF; Na+-transporting NADH:ubiquinone oxidoreductase subunit F [EC:1.6.5.-]
 cysJ; sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]

E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]
 frhB; coenzyme F420 hydrogenase subunit beta [EC:1.12.98.1]
 E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
 E1.17.4.1B, nrdB, nrdF; ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]
 trmD; tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]
 trmH; tRNA (guanosine-2'-O-)-methyltransferase [EC:2.1.1.34]
 rlmA1; 23S rRNA (guanine745-N1)-methyltransferase [EC:2.1.1.187]
 rsmC; 16S rRNA (guanine1207-N2)-methyltransferase [EC:2.1.1.172]
 E2.1.1.63, MGMT, ogt; methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]
 purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
 gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
 E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
 plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]
 kbl, GCAT; glycine C-acetyltransferase [EC:2.3.1.29]
 fabB; 3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]
 maa; maltose O-acetyltransferase [EC:2.3.1.79]
 dapD; 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC:2.3.1.117]
 aat; leucyl/phenylalanyl-tRNA--protein transferase [EC:2.3.2.6]
 E2.4.2.2, pdp; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]
 deoA, TYMP; thymidine phosphorylase [EC:2.4.2.4]
 nadC, QPRT; nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19]
 FDFT1; farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]
 aspB; aspartate aminotransferase [EC:2.6.1.1]
 aspC; aspartate aminotransferase [EC:2.6.1.1]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
 tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]
 bioA; adenosylmethionine-8-amino-7-oxononanoate aminotransferase [EC:2.6.1.62]
 E2.6.1.-B; aminotransferase [EC:2.6.1.-]
 glk; glucokinase [EC:2.7.1.2]
 araB; L-ribulokinase [EC:2.7.1.16]
 gsk; inosine kinase [EC:2.7.1.73]
 E2.7.1.-
 thiL; thiamine-monophosphate kinase [EC:2.7.4.16]
 galT, GALT; UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]
 GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
 PCYT1; choline-phosphate cytidylyltransferase [EC:2.7.7.15]
 nadD; nicotinate-nucleotide adenyllyltransferase [EC:2.7.7.18]
 pcnB; poly(A) polymerase [EC:2.7.7.19]
 rph; ribonuclease PH [EC:2.7.7.56]
 pssA; CDP-diacylglycerol---serine O-phosphatidyltransferase [EC:2.7.8.8]
 E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
 E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]
 serB, PSPH; phosphoserine phosphatase [EC:3.1.3.3]
 E3.1.3.7, cysQ, MET22, BPNT1; 3'(2'), 5'-bisphosphate nucleotidase [EC:3.1.3.7]
 E3.1.3.25, IMPA, suhB; myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
 ARSA; arylsulfatase A [EC:3.1.6.8]
 spoT, HDDC3; guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]

nfo; deoxyribonuclease IV [EC:3.1.21.2]
hsdR; type I restriction enzyme, R subunit [EC:3.1.21.3]
ENDOG; endonuclease G, mitochondrial
E3.2.1.78; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]
tag; DNA-3-methyladenine glycosylase I [EC:3.2.2.20]
alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]
pepT; tripeptide aminopeptidase [EC:3.4.11.4]
E3.4.14.4, DPP3; dipeptidyl-peptidase III [EC:3.4.14.4]
DPP4; dipeptidyl-peptidase 4 [EC:3.4.14.5]
dcp; peptidyl-dipeptidase Dcp [EC:3.4.15.5]
E3.4.17.19; carboxypeptidase Taq [EC:3.4.17.19]
E3.4.21.26, PREP; prolyl oligopeptidase [EC:3.4.21.26]
lon; ATP-dependent Lon protease [EC:3.4.21.53]
ptrB; oligopeptidase B [EC:3.4.21.83]
prlC; oligopeptidase A [EC:3.4.24.70]
E3.4.24.-; putative zinc metalloprotease [EC:3.4.24.-]
E3.5.1.28A, cwIA, xlyA, xlyB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
gsp; glutathionylspermidine amidase/synthetase [EC:3.5.1.78 6.3.1.8]
PDF, def; peptide deformylase [EC:3.5.1.88]
URA4, pyrC; dihydroorotase [EC:3.5.2.3]
ampC; beta-lactamase class C [EC:3.5.2.6]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
E3.6.3.8; Ca²⁺-transporting ATPase [EC:3.6.3.8]
E4.1.1.18, ldcC, cadA; lysine decarboxylase [EC:4.1.1.18]
purK; 5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]
ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
E4.1.1.32, pckA, PEPC; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
pcaC; 4-carboxymuconolactone decarboxylase [EC:4.1.1.44]
E4.1.1.70; glutaconyl-CoA decarboxylase [EC:4.1.1.70]
tnaA; tryptophanase [EC:4.1.99.1]
acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99]
ENO, eno; enolase [EC:4.2.1.11]
pduC; propanediol dehydratase large subunit [EC:4.2.1.28]
csdA; cysteine sulfinic acid desulfurase [EC:4.4.1.-]
alr; alanine racemase [EC:5.1.1.1]
nicE, maiA; maleate isomerase [EC:5.2.1.1]
E5.3.1.8, manA; mannose-6-phosphate isomerase [EC:5.3.1.8]
deoB; phosphopentomutase [EC:5.4.2.7]
MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]
MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]
gluQ; glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]
sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
glnA; glutamine synthetase [EC:6.3.1.2]
panC; pantoate--beta-alanine ligase [EC:6.3.2.1]
E6.3.2.-
E6.3.4.2, pyrG; CTP synthase [EC:6.3.4.2]
ABC-2.OM, wza; polysaccharide export outer membrane protein
ABC-2.TX; HlyD family secretion protein

ABC.MR.TX; HlyD family secretion protein
NA
ABC.X1.A; putative ABC transport system ATP-binding protein
ABC.X1.P; putative ABC transport system permease protein
ABC.X1.S; putative ABC transport system substrate-binding protein
agaS; tagatose-6-phosphate ketose/aldose isomerase [EC:5.-.-.]
ATPeF1B, ATP5B; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
ccmA; heme exporter protein A [EC:3.6.3.41]
cpaB, rcpC; pilus assembly protein CpaB
crtB; phytoene synthase [EC:2.5.1.32]
dnaA; chromosomal replication initiator protein
DPO3B, dnaN; DNA polymerase III subunit beta [EC:2.7.7.7]
DPO3E, dnaQ; DNA polymerase III subunit epsilon [EC:2.7.7.7]
elaA; ElaA protein
flhC; flagellar transcriptional activator FlhC
rdgB; dITP/XTP pyrophosphatase [EC:3.6.1.19]
gutQ; GutQ protein
hemY; HemY protein
infC, MTIF3; translation initiation factor IF-3
ispB; octaprenyl-diphosphate synthase [EC:2.5.1.90]
mpl; UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [EC:6.3.2.-]
nusA; N utilization substance protein A
nusG; transcriptional antiterminator NusG
parC; topoisomerase IV subunit A [EC:5.99.1.-]
parE; topoisomerase IV subunit B [EC:5.99.1.-]
pilB; type IV pilus assembly protein PilB
pilT; twitching motility protein PilT
priB; primosomal replication protein N
PTS-Man-IIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]
solA; N-methyl-L-tryptophan oxidase [EC:1.5.3.-]
wzyE, rffT; 4-alpha-L-fucosyltransferase [EC:2.4.1.-]
RP-L19e, RPL19; large subunit ribosomal protein L19e
RP-L25, rplY; large subunit ribosomal protein L25
RP-L9, MRPL9, rplI; large subunit ribosomal protein L9
RP-S1, rpsA; small subunit ribosomal protein S1
RP-S14, MRPS14, rpsN; small subunit ribosomal protein S14
RP-S9, MRPS9, rpsI; small subunit ribosomal protein S9
secG; preprotein translocase subunit SecG
SIG54, rpoN; RNA polymerase sigma-54 factor
lepB; signal peptidase I [EC:3.4.21.89]
SRP54, ffh; signal recognition particle subunit SRP54
ftsY; fused signal recognition particle receptor
damX; DamX protein
EIF1, SUI1; translation initiation factor 1
topB; DNA topoisomerase III [EC:5.99.1.2]
yfiF, trmG; RNA methyltransferase, TrmH family [EC:2.1.1.-]
TC.CIC; chloride channel protein, CIC family
mscL; large conductance mechanosensitive channel

TC.HAE1; hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family
 TC.AAA; ATP:ADP antiporter, AAA family
 TC.POT; proton-dependent oligopeptide transporter, POT family
 nhaA; Na⁺:H⁺ antiporter, NhaA family
 nhaB; Na⁺:H⁺ antiporter, NhaB family
 TC.SULP; sulfate permease, SulP family
 mntH; manganese transport protein
 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
 E1.11.1.15, PRDX, ahpC; peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
 hdrB; heterodisulfide reductase subunit B [EC:1.8.98.1]
 tatD; TatD DNase family protein [EC:3.1.21.-]
 ugtP; 1,2-diacylglycerol 3-glucosyltransferase [EC:2.4.1.157]
 fruR1, fruR; LacI family transcriptional regulator, fructose operon transcriptional repressor
 emrB; MFS transporter, DHA2 family, multidrug resistance protein B
 MFS.CP; MFS transporter, CP family, cyanate transporter
 TC.BASS; bile acid:Na⁺ symporter, BASS family
 TC.NCS1; nucleobase:cation symporter-1, NCS1 family
 aaeB; p-hydroxybenzoic acid efflux pump subunit AaeB
 rnhB; ribonuclease HII [EC:3.1.26.4]
 licT, bglG; beta-glucoside operon transcriptional antiterminator
 nadA; quinolinate synthase [EC:2.5.1.72]
 E1.17.7.1, gcpE, ispG; (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [EC:1.17.7.1]
 zipA; cell division protein ZipA
 gudP; MFS transporter, ACS family, glucarate transporter
 rnpA; ribonuclease P protein component [EC:3.1.26.5]
 ruvB; holliday junction DNA helicase RuvB [EC:3.6.4.12]
 mutS; DNA mismatch repair protein MutS
 cvpA; membrane protein required for colicin V production
 exbB; biopolymer transport protein ExbB
 tldD; TldD protein
 mutL; DNA mismatch repair protein MutL
 hrpA; ATP-dependent helicase HrpA [EC:3.6.4.13]
 hrpB; ATP-dependent helicase HrpB [EC:3.6.4.13]
 recC; exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]
 acrA; membrane fusion protein
 ftsI; cell division protein FtsI (penicillin-binding protein 3) [EC:2.4.1.129]
 ftsA; cell division protein FtsA
 mrp; ATP-binding protein involved in chromosome partitioning
 rseB; sigma-E factor negative regulatory protein RseB
 hyaD, hybD; hydrogenase maturation protease [EC:3.4.23.-]
 proQ; ProP effector
 nusB; N utilization substance protein B
 rho; transcription termination factor Rho
 recF; DNA replication and repair protein RecF
 recN; DNA repair protein RecN (Recombination protein N)
 rlpA; rare lipoprotein A
 lipA; lipoic acid synthetase [EC:2.8.1.8]
 icc; Icc protein

recQ; ATP-dependent DNA helicase RecQ [EC:3.6.4.12]
rep; ATP-dependent DNA helicase Rep [EC:3.6.4.12]
hflX; GTP-binding protein HflX
rnd; ribonuclease D [EC:3.1.13.5]
ubiB, aarF; ubiquinone biosynthesis protein
yigP; hypothetical protein
tlyC; putative hemolysin
uvrA; excinuclease ABC subunit A
cspA; cold shock protein (beta-ribbon, CspA family)
xerC; integrase/recombinase XerC
hns; DNA-binding protein H-NS
smg; Smg protein
sanA; SanA protein
adiC; arginine:agmatine antiporter
eptA; phosphoethanolamine transferase
metJ; transcriptional repressor of met regulon (beta-ribbon, MetJ family)
PPIB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
ppiD; peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]
surA; peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]
fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]
fkIB; FKBP-type peptidyl-prolyl cis-trans isomerase FkIB [EC:5.2.1.8]
aer; aerotaxis receptor
katE, CAT, catB, srpA; catalase [EC:1.11.1.6]
surE; 5'-nucleotidase [EC:3.1.3.5]
E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]
lipB; lipoyl(octanoyl) transferase [EC:2.3.1.181]
ampE; AmpE protein
rmf; ribosome modulation factor
rimL; ribosomal-protein-serine acetyltransferase [EC:2.3.1.-]
Int; apolipoprotein N-acyltransferase [EC:2.3.1.-]
yjiM; putative acetyltransferase [EC:2.3.1.-]
tonB; periplasmic protein TonB
fldB; flavodoxin II
arsR; ArsR family transcriptional regulator
iucA; N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]
iucC; aerobactin synthase [EC:6.3.2.39]
moxR; MoxR-like ATPase [EC:3.6.3.-]
lpqC; polyhydroxybutyrate depolymerase
cpbD; chitin-binding protein
pspF; psp operon transcriptional activator
mviN; virulence factor
dps; starvation-inducible DNA-binding protein
osmC; osmotically inducible protein OsmC
tis, mesJ; tRNA(Ile)-lysine synthase [EC:6.3.4.19]
ibpA; molecular chaperone IbpA
ibpB; molecular chaperone IbpB
smf; DNA processing protein
csgB; minor curlin subunit

flhG, fleN; flagellar biosynthesis protein FlhG
SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
hhoB, degS; serine protease DegS [EC:3.4.21.-]
lptD, imp, ostA; LPS-assembly protein
rsbV; anti-sigma B factor antagonist
feoB; ferrous iron transport protein B
sohB; serine protease SohB [EC:3.4.21.-]
ydgD; protease YdgD [EC:3.4.21.-]
irp1, HMWP1; yersiniabactin nonribosomal peptide/polyketide synthase
glcU; glucose uptake protein
mrcB; penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]
pbpC; penicillin-binding protein 1C [EC:2.4.1.-]
fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.41]
dusC; tRNA-dihydrouridine synthase C [EC:1.-.-.-]
dbpA; ATP-independent RNA helicase DbpA [EC:3.6.4.13]
deaD; ATP-dependent RNA helicase DeaD [EC:3.6.4.13]
MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]
hupA; DNA-binding protein HU-alpha
wzzB; chain length determinant protein (polysaccharide antigen chain regulator)
kefA, bspA, aefA; potassium efflux system protein
nlpI; lipoprotein NlpI
rob; right origin-binding protein
bamD; outer membrane protein assembly factor BamD
raiA; ribosome-associated inhibitor A
hutC; GntR family transcriptional regulator, histidine utilization repressor
E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]
dhaR; transcriptional activator for dhaKLM operon
hmp, YHB1; nitric oxide dioxygenase [EC:1.14.12.17]
aas; acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase / long-chain-fatty-acid--[acyl-carrier-protein] ligase [EC:2.3.1.53, SIAE; sialate O-acetyltransferase [EC:3.1.1.53]
pepE; dipeptidase E [EC:3.4.13.21]
K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]
shc, sqhC; squalene-hopene/tetraprenyl-beta-curcumen cyclase [EC:5.4.99.17 4.2.1.129]
ybdK; carboxylate-amine ligase [EC:6.3.-.-]
slyB; outer membrane lipoprotein SlyB
abnA_B; arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]
tsgA; MFS transporter, TsgA protein
hlpA, ompH; outer membrane protein
uspB; universal stress protein B
gntR; LacI family transcriptional regulator, gluconate utilization system Gnt-I transcriptional repressor
uspA; universal stress protein A
ABCF3; ATP-binding cassette, subfamily F, member 3
phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]
miaB; bifunctional enzyme involved in thiolation and methylation of tRNA
rluE; 23S rRNA pseudouridine2457 synthase [EC:5.4.99.20]
nlpD; lipoprotein NlpD
apaG; ApaG protein
crcB; CrcB protein

dkmA; DnaK suppressor protein
focA; formate transporter
relE; RelE protein
hyaB, hybC; hydrogenase large subunit [EC:1.12.99.6]
hyaA, hybO; hydrogenase small subunit [EC:1.12.99.6]
kipA; antagonist of Kipl
pgi1; glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]
lptB; lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]
K06889
K06894
pbuG; putative MFS transporter, AGZA family, xanthine/uracil permease
K06906
K06908
K06916
K06918
queC; 7-cyano-7-deazaguanine synthase [EC:6.3.4.20]
K06951
K06956
tmcA; tRNA(Met) cytidine acetyltransferase [EC:2.3.1.193]
rlmI; 23S rRNA (cytosine1962-C5)-methyltransferase [EC:2.1.1.191]
K06978
K07000
K07037
K07051
K07071
K07079
K07081
K07083
lptF; lipopolysaccharide export system permease protein
K07096
K07098
ybgC; acyl-CoA thioester hydrolase [EC:3.1.2.-]
K07109
yfbK; Ca-activated chloride channel homolog
K07121
K07124
K07132
K07140
isdG, isdI; heme oxygenase (staphylobilin-producing) [EC:1.14.99.48]
K07146; UPF0176 protein
yedY; sulfoxide reductase catalytic subunit YedY [EC:1.8.-.-]
K07148; uncharacterized protein
STT3; dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.4.99.18]
K07164
fecR; transmembrane sensor
prkA; serine protein kinase
tspO; tryptophan-rich sensory protein
efeO; iron uptake system component EfeO

tusD, dsrE; tRNA 2-thiouridine synthesizing protein D [EC:2.8.1.-]
tusC, dsrF; tRNA 2-thiouridine synthesizing protein C
FTR, efeU; high-affinity iron transporter
spsF; spore coat polysaccharide biosynthesis protein SpsF
pqqL; zinc protease [EC:3.4.24.-]
oprB; porin
ompW; outer membrane protein
K07276; hypothetical protein
SAM50, TOB55, bamA; outer membrane protein insertion porin family
yfaL; autotransporter family porin
ydiY; putative salt-induced outer membrane protein
slp; outer membrane lipoprotein
bamC; outer membrane protein assembly factor BamC
pphA; serine/threonine protein phosphatase 1 [EC:3.1.3.16]
ytfE, scdA; regulator of cell morphogenesis and NO signaling
bmpA, bmpB, tmpC; basic membrane protein A and related proteins
K07337; hypothetical protein
fimG; minor fimbrial subunit
pepO; putative endopeptidase [EC:3.4.24.-]
comM; magnesium chelatase family protein
yhfA; putative redox protein
nfeD; membrane-bound serine protease (ClpP class)
recJ; single-stranded-DNA-specific exonuclease [EC:3.1.-.-]
rstA1; phage replication initiation protein
sbmC; DNA gyrase inhibitor
argK; LAO/AO transport system kinase [EC:2.7.-.-]
K07746; hypothetical protein
frc; formyl-CoA transferase [EC:2.8.3.16]
basR; two-component system, OmpR family, response regulator BasR
arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]
torZ; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]
araJ; MFS transporter, DHA1 family, arabinose polymer transporter
ampG; MFS transporter, PAT family, beta-lactamase induction signal transducer AmpG
yqgE; MFS transporter, YQGE family, putative transporter
caiF; transcriptional activator CaiF
E2.7.11.1; non-specific serine/threonine protein kinase [EC:2.7.11.1]
purT; phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]
mltD, dniR; membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]
hycl; hydrogenase 3 maturation protease [EC:3.4.23.51]
yciS; putative membrane protein
sufC; Fe-S cluster assembly ATP-binding protein
sufD; Fe-S cluster assembly protein SufD
rutG; putative pyrimidine permease RutG
K09118; hypothetical protein
K09124; hypothetical protein
ycaO; ribosomal protein S12 methylthiotransferase
yfiQ; hypothetical protein
K09384; hypothetical protein

ompC; outer membrane pore protein C
PDIA4, ERP72; protein disulfide-isomerase A4 [EC:5.3.4.1]
iap; alkaline phosphatase isozyme conversion protein [EC:3.4.11.-]
ABC-2.LPSE.P; lipopolysaccharide transport system permease protein
K09704; hypothetical protein
K09740; hypothetical protein
rmuC; DNA recombination protein RmuC
K09769; hypothetical protein
K09778; hypothetical protein
K09793; hypothetical protein
ABC.LPT.P, lolC, lolE; lipoprotein-releasing system permease protein
ABC.LPT.A, lolD; lipoprotein-releasing system ATP-binding protein [EC:3.6.3.-]
ABC.MN.P; manganese/iron transport system permease protein
ABC.MN.A; manganese/iron transport system ATP-binding protein
K09891; hypothetical protein
K09894; hypothetical protein
K09896; hypothetical protein
K09901; hypothetical protein
K09911; hypothetical protein
K09921; hypothetical protein
K09922; hypothetical protein
K09928; hypothetical protein
K09940; hypothetical protein
cas2; CRISPR-associated protein Cas2
K09952; hypothetical protein
K09954; hypothetical protein
gluC; glutamate transport system permease protein
aotJ; arginine/ornithine transport system substrate-binding protein
msmX, msmK, malK, sugC, ggtA, msiK; multiple sugar transport system ATP-binding protein
lctO; lactate oxidase [EC:1.13.12.-]
mglC; methyl-galactoside transport system permease protein
mglA; methyl-galactoside transport system ATP-binding protein [EC:3.6.3.17]
alsB; D-allose transport system substrate-binding protein
nfnB, nfsB; nitroreductase / dihydropteridine reductase [EC:1.-.- 1.5.1.34]
kch, trkA, mthK, pch; voltage-gated potassium channel
hda; DnaA-homolog protein
SMUG1; single-strand selective monofunctional uracil DNA glycosylase [EC:3.2.2.-]
yciA; acyl-CoA thioesterase YciA [EC:3.1.2.-]
oppF; oligopeptide transport system ATP-binding protein
acfD; accessory colonization factor AcfD
hlyA1, hlyA; hemolysin A
msbA; ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]
PTS-Fru2-EIIA; PTS system, fructose-specific IIA-like component [EC:2.7.1.69]
rlmG; 23S rRNA (guanine1835-N2)-methyltransferase [EC:2.1.1.174]
xapB; MFS transporter, NHS family, xanthosine permease
lptG; lipopolysaccharide export system permease protein
pheP; phenylalanine-specific permease
lysP; lysine-specific permease

aroP; aromatic amino acid transport protein AroP
cycA; D-serine/D-alanine/glycine transporter
nfrA; bacteriophage N4 adsorption protein A
kefB; glutathione-regulated potassium-efflux system protein KefB
frsA; esterase FrsA [EC:3.1.-.-]
ushA; 5'-nucleotidase / UDP-sugar diphosphatase [EC:3.1.3.5 3.6.1.45]
impA; type VI secretion system protein ImpA
rhIE; ATP-dependent RNA helicase RhIE [EC:3.6.4.13]
uspG; universal stress protein G
ompX; outer membrane protein X
pgaA; biofilm PGA synthesis protein PgaA
bssS; biofilm regulator BssS
dotC, tral; defect in organelle trafficking protein DotC
msrAB; peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11 1.8.4.12]
rlmL, rlmK; 23S rRNA (guanine2445-N2)-methyltransferase / 23S rRNA (guanine2069-N7)-methyltransferase [EC:2.1.1.173]
cysM; cysteine synthase B [EC:2.5.1.47]
SRD5A1; 3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.1.22]
HEXA_B; hexosaminidase [EC:3.2.1.52]
bigA; putative surface-exposed virulence protein
lapC; membrane fusion protein LapC
lapE; outer membrane protein LapE
esp, sigA, sepA; serine protease autotransporter [EC:3.4.21.-]
flu; antigen 43
eptB; phosphoethanolamine transferase
wbpZ; rhamnosyltransferase [EC:2.4.1.-]
rgpA; rhamnosyltransferase [EC:2.4.1.-]
rgpB; rhamnosyltransferase [EC:2.4.1.-]
E2.7.7.65; diguanylate cyclase [EC:2.7.7.65]
TLS, FUS; RNA-binding protein FUS
cbiGH-cobJ; cobalt-precorrin 5A hydrolase / precorrin-3B C17-methyltransferase [EC:3.7.1.12 2.1.1.131]
pafA; proteasome accessory factor A [EC:6.3.2.-]
soxS; AraC family transcriptional regulator, transcriptional activator of the superoxide response regulon
hspR; MerR family transcriptional regulator, heat shock protein HspR
iscR; Rrf2 family transcriptional regulator, iron-sulfur cluster assembly transcription factor
nlpC; probable lipoprotein NlpC
putA; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.5.2 1.2.1.88]
gsiA; glutathione transport system ATP-binding protein
yejB; microcin C transport system permease protein
yejE; microcin C transport system permease protein
pduD; propanediol dehydratase medium subunit [EC:4.2.1.28]
FTCD; glutamate formiminotransferase / formiminotetrahydrofolate cyclodeaminase [EC:2.1.2.5 4.3.1.4]
mpaA; protein MpaA
uspE; universal stress protein E
uspC; universal stress protein C
uspD; universal stress protein D
SLC10A7, P7; solute carrier family 10 (sodium/bile acid cotransporter), member 7
SLC13A2_3_5; solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5
sgcE; protein sgcE [EC:5.1.3.-]

cueO; blue copper oxidase
NOP8; nucleolar protein 8
cas1; CRISP-associated protein Cas1
trmJ; tRNA (cytidine32/uridine32-2'-O)-methyltransferase [EC:2.1.1.200]
K15533; 1,3-beta-galactosyl-N-acetylhexosamine phosphorylase [EC:2.4.1.211]
aaeA; p-hydroxybenzoic acid efflux pump subunit AaeA
hycE; formate hydrogenlyase subunit 5
K15977; putative oxidoreductase
cydC; ATP-binding cassette, subfamily C, bacterial CydC
ydfG; malonic semialdehyde reductase [EC:1.1.1.-]
nmpC, ompD; outer membrane porin protein LC
fecA; Fe(3+) dicitrate transport protein
uidR; TetR/AcrR family transcriptional regulator, repressor for uid operon
uidC, gusC; putative glucuronide porin
pylC; pyrrolysine biosynthesis protein PylC
dppC1; dipeptide transport system permease protein
yjeH; amino acid efflux transporter
czcD, zitB; cobalt-zinc-cadmium efflux system protein
erfK; L,D-transpeptidase
pit; low-affinity inorganic phosphate transporter
lpxC-fabZ; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase / 3-hydroxyacyl-[acyl-carrier-protein] dehydratase
wzxE; O-antigen flippase
rffC, wecD; dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase [EC:2.3.1.210]

KEGG pathway	Annotation	Number of KOs in category
ko01210	2-Oxocarboxylic acid metabolism	15
ko00250	Alanine, aspartate and glutamate metabolism	15
ko00520	Amino sugar and nucleotide sugar metabolism	21

ko00330

Arginine and proline metabolism

13

ko00220

Arginine biosynthesis

13

ko01230

Biosynthesis of amino acids

59

ko00780

Biotin metabolism

6

ko00650	Butanoate metabolism	11
---------	-----------------------------	----

ko00660	C5-Branched dibasic acid metabolism	7
---------	--	---

ko00710	Carbon fixation in photosynthetic organisms	8
---------	--	---

ko01200	Carbon metabolism	38
---------	--------------------------	----

ko01503	Cationic antimicrobial peptide (CAMP) resistance	8
---------	--	---

ko00020	Citrate cycle (TCA cycle)	11
---------	---------------------------	----

ko02040	Flagellar assembly	7
---------	--------------------	---

ko00790	Folate biosynthesis	10
---------	---------------------	----

ko00051	Fructose and mannose metabolism	12
---------	--	----

ko00052	Galactose metabolism	11
---------	-----------------------------	----

ko00260	Glycine, serine and threonine metabolism	12
---------	---	----

ko00010	Glycolysis / Gluconeogenesis	23
---------	-------------------------------------	----

ko00340	Histidine metabolism	10
---------	-----------------------------	----

ko00540	Lipopolysaccharide biosynthesis	11
---------	--	----

ko00633	Nitrotoluene degradation	5
---------	---------------------------------	---

ko00190	Oxidative phosphorylation	24
---------	----------------------------------	----

ko00770	Pantothenate and CoA biosynthesis	10
---------	--	----

ko00360	Phenylalanine metabolism	10
---------	---------------------------------	----

ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	15
---------	--	----

ko03060

Protein export

8

ko00230

Purine metabolism

32

ko00620

Pyruvate metabolism

16

ko03010

Ribosome

21

ko03018

RNA degradation

12

ko00500	Starch and sucrose metabolism	12
---------	--------------------------------------	----

ko00920	Sulfur metabolism	13
---------	--------------------------	----

ko00730	Thiamine metabolism	7
---------	----------------------------	---

ko02020

Two-component system

43

ko00130

Quinone and other terpenoid-quinone biosynthesis

8

ko00290

Valine, leucine and isoleucine biosynthesis

10

ko00750

Vitamin B6 metabolism

5

Other significant KOs

FDR	KO
	K00052
	K00053
	K00145
	K00619
	K00620
	K00930
	K01649
0.0001183616	K01652
	K01653
	K01703
	K01704
	K05831
	K14260
	K14682
	K16792
	K00262
	K00265
	K00278
	K00294
	K00609
	K00764
	K01744
5.402501E-05	K01755
	K01756
	K01915
	K01939
	K01940
	K01955
	K13821
	K14260
	K00012
	K00849
	K00886
	K00963
	K00966
	K00971
	K01198
	K01443
	K01639
	K01654
0.0002509366	K01711
	K01784
	K02377
	K02804
	K05305
	K07102
	K07806

K08679
K11192
K13014
K15778
K00294
K00613
K00819
K01259
K01476
K01581
0.0096178115 K01584
K01777
K06447
K10536
K12251
K13747
K13821
K00145
K00262
K00611
K00619
K00620
K00930
0.0001099218 K01476
K01755
K01915
K01940
K05831
K14260
K14682
K00013
K00052
K00053
K00134
K00145
K00265
K00290
K00293
K00611
K00619
K00620
K00640
K00765
K00817
K00850
K00873
K00927
K00930

	K00948
	K01476
	K01496
	K01586
	K01609
	K01626
	K01649
	K01652
	K01653
	K01657
	K01658
7.535892E-25	K01689
	K01693
	K01695
	K01696
	K01703
	K01704
	K01735
	K01738
	K01752
	K01754
	K01755
	K01803
	K01814
	K01817
	K01915
	K01940
	K02500
	K02501
	K03340
	K03785
	K04092
	K04486
	K05831
	K06001
	K12525
	K13497
	K14170
	K14260
	K14682
	K16792
	K00208
	K00833
0.0096178115	K01935
	K03524
	K08351
	K09458
	K00019

	K00100
	K00171
	K00240
	K00656
0.0357540522	K01039
	K01040
	K01652
	K01653
	K04072
	K08318
	K00052
	K01652
	K01653
0.0025942959	K01703
	K01704
	K01902
	K01903
	K00029
	K00134
	K00855
0.004811555	K00927
	K01006
	K01595
	K01803
	K11214
	K00029
	K00134
	K00140
	K00161
	K00162
	K00164
	K00171
	K00194
	K00240
	K00297
	K00382
	K00605
	K00627
	K00640
	K00658
	K00850
	K00855
	K00863
8.525989E-05	K00873
	K00886
	K00927
	K00948
	K01006

	K01595
	K01689
	K01738
	K01752
	K01754
	K01803
	K01847
	K01902
	K01903
	K01938
	K01966
	K03738
	K03781
	K08318
	K11261
	K07264
	K07637
	K07640
0.0461362504	K07660
	K07806
	K12962
	K12975
	K13014
	K00161
	K00162
	K00164
	K00171
	K00240
0.0020189848	K00382
	K00627
	K00658
	K01596
	K01902
	K01903
	K02396
	K02402
	K02403
0.0381671129	K02407
	K02419
	K02421
	K02423
	K01077
	K01664
	K01665
	K01737
0.0016031828	K02619
	K06879
	K06920

	K09007
	K09457
	K11754
	K00100
	K00850
	K00879
	K00966
	K00971
0.0351559868	K01711
	K01803
	K01818
	K02377
	K05305
	K07026
	K15778
	K00849
	K00850
	K00963
	K01190
	K01631
0.011794551	K01784
	K01785
	K02079
	K12112
	K12308
	K15778
	K00060
	K00276
	K00382
	K00605
	K00613
0.0232012665	K01695
	K01696
	K01752
	K01753
	K01754
	K06001
	K12525
	K00001
	K00134
	K00138
	K00161
	K00162
	K00171
	K00382
	K00627
	K00850
	K00873

	K00886
2.988763E-08	K00927
	K01085
	K01222
	K01596
	K01689
	K01785
	K01792
	K01803
	K02753
	K04022
	K04072
	K15778
	K00013
	K00765
	K00817
	K01479
0.000751687	K01496
	K01693
	K01814
	K02500
	K02501
	K04486
	K00748
	K01627
	K02517
	K02527
	K02536
8.525989E-05	K03271
	K03272
	K03273
	K03274
	K06041
	K12975
	K00171
	K06281
0.0137849853	K06282
	K10679
	K11180
	K00240
	K00330
	K00331
	K00332
	K00333
	K00337
	K00338
	K00339
	K00340

	K00341
	K00342
0.0024110224	K00343
	K00426
	K00937
	K02109
	K02110
	K02111
	K02112
	K02113
	K02114
	K02115
	K02300
	K02301
	K15986
	K00053
	K00077
	K00954
	K00997
0.0001807423	K01598
	K01652
	K01653
	K01918
	K01922
	K08682
	K00276
	K00285
	K00529
	K00817
0.0381671129	K02554
	K02613
	K05712
	K05713
	K05714
	K10797
	K00817
	K01609
	K01626
	K01657
	K01658
	K01695
	K01696
8.525989E-05	K01735
	K01817
	K03785
	K04092
	K06001
	K11646

	K13497
	K14170
	K03070
	K03072
	K03074
0.0075907959	K03101
	K03110
	K03116
	K03210
	K13301
	K00088
	K00525
	K00527
	K00602
	K00764
	K00839
	K00873
	K00948
	K00958
	K00962
	K01081
	K01483
	K01515
	K01524
	K01588
9.372675E-05	K01589
	K01756
	K01923
	K01939
	K01945
	K01951
	K02335
	K02340
	K02428
	K03043
	K03046
	K05851
	K08312
	K08723
	K13481
	K13483
	K15778
	K00029
	K00138
	K00156
	K00161
	K00162
	K00171

	K00382
	K00627
0.0002977522	K00656
	K00873
	K01006
	K01572
	K01595
	K01596
	K01649
	K04072
	K02863
	K02867
	K02874
	K02878
	K02886
	K02887
	K02890
	K02892
	K02895
	K02897
0.0001807423	K02904
	K02914
	K02916
	K02926
	K02931
	K02935
	K02945
	K02961
	K02965
	K02982
	K02986
	K00850
	K00937
	K00962
	K00970
	K01689
0.0061091055	K03628
	K03732
	K04077
	K05592
	K08300
	K11927
	K12573
	K00012
	K00689
	K00697
	K00700
	K00963

0.0434618043	K01176
	K01179
	K01198
	K07405
	K08679
	K15778
	K16147
	K00299
	K00380
	K00385
	K00640
	K00958
K01738	
0.0075907959	K02045
	K02046
	K02047
	K02048
	K03119
	K08352
	K11180
	K00788
0.0021540339	K00878
	K00941
0.0021540339	K03147
	K03149
	K03150
	K07251
	K00426
	K00689
	K01077
	K01467
	K01546
	K01547
	K01548
	K01644
	K01915
	K02402
	K02403
	K02584
	K03413
	K03776
	K05874
	K07637
	K07638
	K07639
	K07640
	K07646
	K07647

0.0005452202 K07660

K07664

K07674

K07675

K07676

K07677

K07678

K07679

K07685

K07687

K07689

K07690

K07696

K07773

K07784

K07795

K07806

K07811

K08476

K08641

K08930

K11382

K01661

K01911

K02549

0.0498574059 K02551

K02552

K03179

K03181

K08680

K00052

K00053

K00835

K01649

1.280108E-07 K01652

K01653

K01703

K01704

K01754

K14260

K00275

K03472

0.0461362504 K03474

K06215

K08681

K00001

K00012

K00019



K00057
K00088
K00099
K00100
K00104
K00134
K00140
K00161
K00162
K00164
K00171
K00184
K00185
K00194
K00208
K00228
K00240
K00262
K00265
K00276
K00278
K00290
K00293
K00297
K00299
K00313
K00322
K00324
K00325
K00359
K00376
K00382
K00428
K00455
K00520
K00525
K00527
K00529
K00533
K00537
K00558
K00564
K00566
K00571
K00602
K00605
K00609
K00631

K00640
K00645
K00656
K00658
K00667
K00737
K00762
K00782
K00795
K00799
K00801
K00817
K00850
K00863
K00873
K00936
K00948
K00958
K00962
K00963
K00968
K00973
K00981
K00989
K01006
K01039
K01040
K01077
K01081
K01104
K01134
K01141
K01142
K01146
K01153
K01154
K01169
K01176
K01186
K01190
K01197
K01258
K01269
K01354
K01362
K01414
K01421
K01434

K01447
K01465
K01467
K01476
K01493
K01497
K01533
K01581
K01586
K01591
K01595
K01596
K01607
K01632
K01667
K01689
K01698
K01716
K01738
K01740
K01752
K01766
K01775
K01803
K01847
K01870
K01872
K01873
K01875
K01887
K01890
K01894
K01902
K01903
K01915
K01918
K01921
K01925
K01932
K01938
K01951
K01955
K01966
K01972
K01990
K01992
K02001
K02007

K02014
K02022
K02030
K02031
K02032
K02039
K02045
K02046
K02047
K02048
K02077
K02109
K02110
K02111
K02112
K02113
K02114
K02115
K02173
K02192
K02255
K02291
K02301
K02317
K02334
K02335
K02336
K02340
K02346
K02357
K02364
K02426
K02431
K02433
K02434
K02453
K02466
K02469
K02470
K02477
K02478
K02482
K02485
K02493
K02511
K02519
K02520
K02528

K02552
K02554
K02558
K02562
K02565
K02569
K02572
K02598
K02600
K02601
K02617
K02621
K02652
K02653
K02654
K02663
K02669
K02753
K02804
K02805
K02806
K02825
K02834
K02835
K02836
K02854
K03043
K03046
K03070
K03072
K03074
K03098
K03110
K03116
K03119
K03152
K03154
K03169
K03210
K03216
K03218
K03281
K03282
K03284
K03291
K03301
K03303
K03310

K03316
K03329
K03340
K03386
K03413
K03427
K03435
K03436
K03449
K03455
K03459
K03468
K03470
K03471
K03477
K03482
K03485
K03488
K03489
K03491
K03492
K03500
K03528
K03544
K03545
K03547
K03549
K03550
K03555
K03559
K03566
K03574
K03578
K03579
K03583
K03596
K03597
K03598
K03600
K03603
K03605
K03642
K03647
K03650
K03651
K03665
K03669
K03670

K03675
K03683
K03684
K03690
K03696
K03698
K03701
K03704
K03723
K03724
K03738
K03747
K03748
K03768
K03772
K03773
K03776
K03781
K03788
K03801
K03806
K03808
K03818
K03820
K03826
K03834
K03838
K03851
K03892
K03894
K03895
K03896
K03918
K03923
K03924
K03979
K03981
K04032
K04062
K04067
K04072
K04077
K04079
K04081
K04083
K04651
K04652
K04653

K04654
K04655
K04656
K04691
K04744
K04757
K04760
K04767
K04786
K05368
K05499
K05515
K05517
K05521
K05527
K05539
K05541
K05566
K05595
K05596
K05712
K05713
K05714
K05775
K05789
K05800
K05803
K05804
K05808
K05809
K05831
K05835
K05838
K05844
K05851
K05874
K05881
K05939
K05945
K05984
K05989
K05997
K06045
K06073
K06074
K06077
K06131
K06140

K06144
K06145
K06158
K06159
K06167
K06181
K06183
K06186
K06195
K06203
K06205
K06346
K06442
K06858
K06864
K06867
K06898
K06916
K06918
K06940
K06941
K06957
K06966
K06973
K06997
K07005
K07016
K07032
K07037
K07051
K07054
K07071
K07080
K07084
K07098
K07113
K07114
K07121
K07136
K07137
K07138
K07140
K07145
K07146
K07164
K07165
K07180
K07192

K07219
K07221
K07224
K07229
K07235
K07236
K07239
K07243
K07257
K07261
K07263
K07267
K07269
K07275
K07276
K07277
K07283
K07285
K07287
K07309
K07311
K07340
K07358
K07396
K07400
K07403
K07478
K07479
K07480
K07492
K07566
K07679
K07690
K07735
K07739
K07757
K07812
K08159
K08161
K08162
K08219
K08227
K08277
K08282
K08296
K08298
K08301
K08303

K08483
K08484
K08641
K08723
K08969
K08984
K08997
K08999
K09002
K09015
K09117
K09121
K09123
K09125
K09131
K09158
K09456
K09458
K09612
K09700
K09706
K09747
K09761
K09769
K09778
K09781
K09786
K09806
K09819
K09820
K09825
K09893
K09894
K09902
K09907
K09908
K09909
K09912
K09914
K09920
K09921
K09928
K09940
K09949
K09952
K09954
K09971
K09974

K09992
K10005
K10006
K10007
K10008
K10010
K10016
K10109
K10546
K10716
K10763
K10800
K10806
K10819
K10852
K10907
K10939
K10973
K11066
K11085
K11106
K11192
K11201
K11208
K11250
K11261
K11264
K11337
K11473
K11474
K11605
K11606
K11607
K11719
K11732
K11734
K11737
K11739
K11744
K11747
K11748
K11749
K11750
K11752
K11894
K11910
K11912
K11923

K11925
K11932
K11938
K11940
K11991
K12072
K12112
K12138
K12144
K12146
K12148
K12204
K12209
K12211
K12218
K12264
K12267
K12288
K12506
K12518
K12525
K12582
K12687
K12943
K12974
K12994
K13021
K13069
K13085
K13255
K13301
K13409
K13525
K13527
K13542
K13571
K13631
K13655
K13683
K13695
K13730
K13735
K13771
K13789
K13893
K13894
K13895
K13926

K14051
K14054
K14055
K14061
K14063
K14064
K14192
K14347
K14393
K14441
K14445
K14475
K14652
K14762
K15524
K15547
K15724
K15773
K15778
K15835
K15977
K16076
K16139
K16291
K16301
K16693
K16784
K16792
K16850

Definition

leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
argC; N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]
argA; amino-acid N-acetyltransferase [EC:2.3.1.1]
argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]
argB; acetylglutamate kinase [EC:2.7.2.8]
leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
argE1, lysK; LysW-gamma-L-lysine carboxypeptidase
alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
aksD; methanogen homoaconitase large subunit [EC:4.2.1.114]
E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
gltB; glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]
nadB; L-aspartate oxidase [EC:1.4.3.16]
E1.2.1.88; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.2.1.88]
pyrB, PYR2; aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]
purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]
aspA; aspartate ammonia-lyase [EC:4.3.1.1]
argH, ASL; argininosuccinate lyase [EC:4.3.2.1]
purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]
glnA; glutamine synthetase [EC:6.3.1.2]
E6.3.4.4, purA; adenylosuccinate synthase [EC:6.3.4.4]
E6.3.4.5, argG; argininosuccinate synthase [EC:6.3.4.5]
carB, CPA2; carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]
putA; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.5.2 1.2.1.88]
alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
galK; galactokinase [EC:2.7.1.6]
ppgK; polyphosphate glucokinase [EC:2.7.1.63]
UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
xynB; xylan 1,4-beta-xylosidase [EC:3.2.1.37]
E3.5.1.25, nagA, AMDHD2; N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]
E4.1.3.3, nanA, NPL; N-acetylneuraminate lyase [EC:4.1.3.3]
E2.5.1.56, neuB; N-acetylneuraminate synthase [EC:2.5.1.56]
gmd, GMDS; GDPmannose 4,6-dehydratase [EC:4.2.1.47]
galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]
TSTA3, fcl; GDP-L-fucose synthase [EC:1.1.1.271]
PTS-Nag-EIIC, nagE; PTS system, N-acetylglucosamine-specific IIC component
FUK; fucokinase [EC:2.7.1.52]
K07102
arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]

E5.1.3.6; UDP-glucuronate 4-epimerase [EC:5.1.3.6]
PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
arnD; undecaprenyl phosphate- α -L-ara4FN deformylase [EC:3.5.-.-]
pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
E1.2.1.88; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.2.1.88]
GATM; glycine amidinotransferase [EC:2.1.4.1]
E2.6.1.13, rocD; ornithine--oxo-acid transaminase [EC:2.6.1.13]
pip; proline iminopeptidase [EC:3.4.11.5]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
E4.1.1.17, ODC1, speC, speF; ornithine decarboxylase [EC:4.1.1.17]
E4.1.1.19A, adi; arginine decarboxylase [EC:4.1.1.19]
E5.1.1.4; proline racemase [EC:5.1.1.4]
astD; succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]
E3.5.3.12; agmatine deiminase [EC:3.5.3.12]
aguB; N-carbamoylputrescine amidase [EC:3.5.1.53]
nspC; carboxynorspermidine decarboxylase [EC:4.1.1.-]
putA; proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.5.2 1.2.1.88]
argC; N-acetyl- γ -glutamyl-phosphate reductase [EC:1.2.1.38]
E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
OTC, argF, argI; ornithine carbamoyltransferase [EC:2.1.3.3]
argA; amino-acid N-acetyltransferase [EC:2.3.1.1]
argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]
argB; acetylglutamate kinase [EC:2.7.2.8]
E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
argH, ASL; argininosuccinate lyase [EC:4.3.2.1]
glnA; glutamine synthetase [EC:6.3.1.2]
E6.3.4.5, argG; argininosuccinate synthase [EC:6.3.4.5]
argE1, lysK; LysW- γ -L-lysine carboxypeptidase
alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
hisD; histidinol dehydrogenase [EC:1.1.1.23]
leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
argC; N-acetyl- γ -glutamyl-phosphate reductase [EC:1.2.1.38]
gltB; glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]
LYS1; saccharopine dehydrogenase (NAD⁺, L-lysine forming) [EC:1.5.1.7]
LYS9; saccharopine dehydrogenase (NADP⁺, L-glutamate forming) [EC:1.5.1.10]
OTC, argF, argI; ornithine carbamoyltransferase [EC:2.1.3.3]
argA; amino-acid N-acetyltransferase [EC:2.3.1.1]
argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]
cysE; serine O-acetyltransferase [EC:2.3.1.30]
hisG; ATP phosphoribosyltransferase [EC:2.4.2.17]
hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
PK, pyk; pyruvate kinase [EC:2.7.1.40]
PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
argB; acetylglutamate kinase [EC:2.7.2.8]

PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
 E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
 hisI; phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
 lysA; diaminopimelate decarboxylase [EC:4.1.1.20]
 trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]
 E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]
 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
 E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
 E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
 trpE; anthranilate synthase component I [EC:4.1.3.27]
 trpG; anthranilate synthase component II [EC:4.1.3.27]
 ENO, eno; enolase [EC:4.2.1.11]
 E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]
 trpA; tryptophan synthase alpha chain [EC:4.2.1.20]
 trpB; tryptophan synthase beta chain [EC:4.2.1.20]
 leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
 aroB; 3-dehydroquinate synthase [EC:4.2.3.4]
 cysK; cysteine synthase A [EC:2.5.1.47]
 E4.3.1.17, sdaA; L-serine dehydratase [EC:4.3.1.17]
 E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]
 argH, ASL; argininosuccinate lyase [EC:4.3.2.1]
 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
 hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.16]
 trpF; phosphoribosylanthranilate isomerase [EC:5.3.1.24]
 glnA; glutamine synthetase [EC:6.3.1.2]
 E6.3.4.5, argG; argininosuccinate synthase [EC:6.3.4.5]
 hisF; cyclase [EC:4.1.3.-]
 hisH; glutamine amidotransferase [EC:2.4.2.-]
 dapdh; diaminopimelate dehydrogenase [EC:1.4.1.16]
 aroD; 3-dehydroquinate dehydratase I [EC:4.2.1.10]
 tyrA1; chorismate mutase [EC:5.4.99.5]
 E3.1.3.15B; histidinol-phosphatase (PHP family) [EC:3.1.3.15]
 argE1, lysK; LysW-gamma-L-lysine carboxypeptidase
 K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 trpGD; anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27 2.4.2.18]
 pheA; chorismate mutase / prephenate dehydratase [EC:5.4.99.5 4.2.1.51]
 alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
 argAB; amino-acid N-acetyltransferase [EC:2.3.1.1]
 aksD; methanogen homoaconitase large subunit [EC:4.2.1.114]
 fabI; enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]
 bioA; adenosylmethionine-8-amino-7-oxononanoate aminotransferase [EC:2.6.1.62]
 bioD; dethiobiotin synthetase [EC:6.3.3.3]
 birA; BirA family transcriptional regulator, biotin operon repressor / biotin-[acetyl-CoA-carboxylase] ligase [EC:6.3.4.15]
 bisC; biotin/methionine sulfoxide reductase [EC:1.-.-.-]
 fabF; 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]
 E1.1.1.30, bdh; 3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]

E1.1.1.-

porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
E2.3.1.54, pfID; formate C-acetyltransferase [EC:2.3.1.54]
gctA; glutaconate CoA-transferase, subunit A [EC:2.8.3.12]
gctB; glutaconate CoA-transferase, subunit B [EC:2.8.3.12]
E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]
yihU; putative dehydrogenase [EC:1.1.-.-]
leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
PRK, prkB; phosphoribulokinase [EC:2.7.1.19]
PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
ppdK; pyruvate, orthophosphate dikinase [EC:2.7.9.1]
ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
SHPK; sedoheptulokinase [EC:2.7.1.14]
E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
mmsA, iolA, ALDH6A1; malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.12]
PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
cdhD, acsD; acetyl-CoA decarbonylase/synthase complex subunit delta [EC:2.1.1.245]
sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
metF, MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]
DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
cysE; serine O-acetyltransferase [EC:2.3.1.30]
DLST, sucB; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
PRK, prkB; phosphoribulokinase [EC:2.7.1.19]
E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
PK, pyk; pyruvate kinase [EC:2.7.1.40]
ppgK; polyphosphate glucokinase [EC:2.7.1.63]
PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
ppdK; pyruvate, orthophosphate dikinase [EC:2.7.9.1]

ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
ENO, eno; enolase [EC:4.2.1.11]
cysK; cysteine synthase A [EC:2.5.1.47]
E4.3.1.17, sdaA; L-serine dehydratase [EC:4.3.1.17]
E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]
TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]
sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
fhs; formate--tetrahydrofolate ligase [EC:6.3.4.3]
PCCB, pccB; propionyl-CoA carboxylase beta chain [EC:6.4.1.3]
aor; aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
katE, CAT, catB, srpA; catalase [EC:1.11.1.6]
yihU; putative dehydrogenase [EC:1.1.-.-]
fwdE, fmdE; formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]
arnT, pmrK; 4-amino-4-deoxy-L-arabinose transferase [EC:2.4.2.43]
phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]
cpxA; two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]
phoP; two-component system, OmpR family, response regulator PhoP
arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]
arnE; undecaprenyl phosphate-alpha-L-ara4N flippase subunit ArnE
eptB; phosphoethanolamine transferase
arnD; undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]
PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
DLST, sucB; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
E4.1.1.32, pckA, PEPC; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
flgK; flagellar hook-associated protein 1 FlgK
flhC; flagellar transcriptional activator FlhC
flhD; flagellar transcriptional activator FlhD
fliD; flagellar hook-associated protein 2
fliP; flagellar biosynthetic protein FliP
fliR; flagellar biosynthetic protein FliR
fliT; flagellar protein FliT
E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]
pabA; para-aminobenzoate synthetase component II [EC:2.6.1.85]
pabB; para-aminobenzoate synthetase component I [EC:2.6.1.85]
queD, ptpS, PTS; 6-pyruvoyltetrahydropterin/6-carboxytetrahydropterin synthase [EC:4.2.3.12 4.1.2.50]
pabC; 4-amino-4-deoxychorismate lyase [EC:4.1.3.38]
queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]
queC; 7-cyano-7-deazaguanine synthase [EC:6.3.4.20]

GCH4, folE; GTP cyclohydrolase I [EC:3.5.4.16]
queF1, queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]
folC; dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2.17]
E1.1.1.-
pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
fucK; L-fuculokinase [EC:2.7.1.51]
GMPP; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
gmd, GMDS; GDPmannose 4,6-dehydratase [EC:4.2.1.47]
TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
fucI; L-fucose isomerase [EC:5.3.1.25]
TSTA3, fcl; GDP-L-fucose synthase [EC:1.1.1.271]
FUK; fucokinase [EC:2.7.1.52]
E3.1.3.70; mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]
pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
galk; galactokinase [EC:2.7.1.6]
pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
lacZ; beta-galactosidase [EC:3.2.1.23]
dgoA; 2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]
galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]
E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]
agaA; N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]
ebgC; evolved beta-galactosidase subunit beta
bgaB, lacA; beta-galactosidase [EC:3.2.1.23]
pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
tdh; threonine 3-dehydrogenase [EC:1.1.1.103]
AOC3, AOC2, tynA; primary-amine oxidase [EC:1.4.3.21]
DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
GATM; glycine amidinotransferase [EC:2.1.4.1]
trpA; tryptophan synthase alpha chain [EC:4.2.1.20]
trpB; tryptophan synthase beta chain [EC:4.2.1.20]
E4.3.1.17, sdaA; L-serine dehydratase [EC:4.3.1.17]
dsdA; D-serine dehydratase [EC:4.3.1.18]
E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]
K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]
metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
E1.1.1.1, adh; alcohol dehydrogenase [EC:1.1.1.1]
GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
aldB; aldehyde dehydrogenase [EC:1.2.1.-]
PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
PK, pyk; pyruvate kinase [EC:2.7.1.40]

ppgK; polyphosphate glucokinase [EC:2.7.1.63]
 PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
 agp; glucose-1-phosphatase [EC:3.1.3.10]
 E3.2.1.86A, celf; 6-phospho-beta-glucosidase [EC:3.2.1.86]
 E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
 ENO, eno; enolase [EC:4.2.1.11]
 E5.1.3.3, galM; aldose 1-epimerase [EC:5.1.3.3]
 E5.1.3.15; glucose-6-phosphate 1-epimerase [EC:5.1.3.15]
 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
 PTS-Asc-EIIC, ascF; PTS system, arbutin-, cellobiose-, and salicin-specific IIC component
 eutG; alcohol dehydrogenase
 adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]
 pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
 hisD; histidinol dehydrogenase [EC:1.1.1.23]
 hisG; ATP phosphoribosyltransferase [EC:2.4.2.17]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 hutG; formiminoglutamase [EC:3.5.3.8]
 hisI; phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
 E4.2.1.19, hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]
 hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.16]
 hisF; cyclase [EC:4.1.3.-]
 hisH; glutamine amidotransferase [EC:2.4.2.-]
 E3.1.3.15B; histidinol-phosphatase (PHP family) [EC:3.1.3.15]
 lpxB; lipid-A-disaccharide synthase [EC:2.4.1.182]
 kdsA; 2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:2.5.1.55]
 htrB; lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]
 kdtA, waaA; 3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12 2.4.99.13 2.4.99.14 2.4.99.15]
 lpxD; UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.191]
 gmhA, lpcA; D-sedoheptulose 7-phosphate isomerase [EC:5.3.1.28]
 gmhC, hldE, waaE, rfaE; D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate adenosyltransferase [EC:2.7.1.12]
 gmhB; D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.82 3.1.3.83]
 gmhD, rfaD; ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]
 E5.3.1.13; arabinose-5-phosphate isomerase [EC:5.3.1.13]
 eptB; phosphoethanolamine transferase
 porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
 hyaB, hybC; hydrogenase large subunit [EC:1.12.99.6]
 hyaA, hybO; hydrogenase small subunit [EC:1.12.99.6]
 nfnB, nfsB; nitroreductase / dihydropteridine reductase [EC:1.-.-.- 1.5.1.34]
 dsrA; sulfite reductase alpha subunit [EC:1.8.99.3 1.8.99.1]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 nuoA; NADH-quinone oxidoreductase subunit A [EC:1.6.5.3]
 nuoB; NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]
 nuoC; NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]
 nuoD; NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]
 nuoH; NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]
 nuoI; NADH-quinone oxidoreductase subunit I [EC:1.6.5.3]
 nuoJ; NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]
 nuoK; NADH-quinone oxidoreductase subunit K [EC:1.6.5.3]

nuoL; NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]
nuoM; NADH-quinone oxidoreductase subunit M [EC:1.6.5.3]
nuoN; NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]
cydB; cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]
ppk; polyphosphate kinase [EC:2.7.4.1]
ATPF0B, atpF; F-type H⁺-transporting ATPase subunit b [EC:3.6.3.14]
ATPF0C, atpE; F-type H⁺-transporting ATPase subunit c [EC:3.6.3.14]
ATPF1A, atpA; F-type H⁺-transporting ATPase subunit alpha [EC:3.6.3.14]
ATPF1B, atpD; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
ATPF1D, atpH; F-type H⁺-transporting ATPase subunit delta [EC:3.6.3.14]
ATPF1E, atpC; F-type H⁺-transporting ATPase subunit epsilon [EC:3.6.3.14]
ATPF1G, atpG; F-type H⁺-transporting ATPase subunit gamma [EC:3.6.3.14]
cyoD; cytochrome o ubiquinol oxidase operon protein cyoD
cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]
ppaC; manganese-dependent inorganic pyrophosphatase [EC:3.6.1.1]
ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
panE, apbA; 2-dehydropantoate 2-reductase [EC:1.1.1.169]
E2.7.7.3A, coaD, kdtB; pantetheine-phosphate adenyltransferase [EC:2.7.7.3]
acpS; holo-[acyl-carrier protein] synthase [EC:2.7.8.7]
PPCDC, coaC; phosphopantothenoylcysteine decarboxylase [EC:4.1.1.36]
E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
panC; pantoate--beta-alanine ligase [EC:6.3.2.1]
PPCS, coaB; phosphopantothenate-cysteine ligase [EC:6.3.2.5]
acpH; acyl carrier protein phosphodiesterase [EC:3.1.4.14]
AOC3, AOC2, tyrA; primary-amine oxidase [EC:1.4.3.21]
dadA; D-amino-acid dehydrogenase [EC:1.4.99.1]
hcaD; ferredoxin--NAD⁺ reductase [EC:1.18.1.3]
hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
mhpD; 2-keto-4-pentenoate hydratase [EC:4.2.1.80]
paaE; ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE
mhpA; 3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.127]
mhpB; 2,3-dihydroxyphenylpropionate 1,2-dioxygenase [EC:1.13.11.16]
mhpC; 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase [EC:3.7.1.-]
enr; 2-enoate reductase [EC:1.3.1.31]
hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]
E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]
trpE; anthranilate synthase component I [EC:4.1.3.27]
trpG; anthranilate synthase component II [EC:4.1.3.27]
trpA; tryptophan synthase alpha chain [EC:4.2.1.20]
trpB; tryptophan synthase beta chain [EC:4.2.1.20]
aroB; 3-dehydroquinate synthase [EC:4.2.3.4]
trpF; phosphoribosylanthranilate isomerase [EC:5.3.1.24]
aroD; 3-dehydroquinate dehydratase I [EC:4.2.1.10]
tyrA1; chorismate mutase [EC:5.4.99.5]
K06001, trpB; tryptophan synthase beta chain [EC:4.2.1.20]
K11646; 3-dehydroquinate synthase II [EC:1.4.1.24]

trpGD; anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27 2.4.2.18]
 pheA; chorismate mutase / prephenate dehydratase [EC:5.4.99.5 4.2.1.51]
 secA; preprotein translocase subunit SecA
 secD; preprotein translocase subunit SecD
 secF; preprotein translocase subunit SecF
 lspA; signal peptidase II [EC:3.4.23.36]
 ftsY; fused signal recognition particle receptor
 tatA; sec-independent protein translocase protein Tata
 yajC; preprotein translocase subunit YajC
 secM; secretion monitor
 guaB; IMP dehydrogenase [EC:1.1.1.205]
 E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
 nrdD; ribonucleoside-triphosphate reductase [EC:1.17.4.2]
 purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
 purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]
 E2.6.1.-B; aminotransferase [EC:2.6.1.-]
 PK, pyk; pyruvate kinase [EC:2.7.1.40]
 PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
 sat, met3; sulfate adenylyltransferase [EC:2.7.7.4]
 pnp, PNPT1; polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]
 E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]
 allA; ureidoglycolate hydrolase [EC:3.5.3.19]
 nudF; ADP-ribose pyrophosphatase [EC:3.6.1.13]
 ppx-gppA; exopolyphosphatase / guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase [EC:3.6.1.11 3.6.1.40]
 purE; 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]
 purK; 5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]
 purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]
 purC; phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]
 E6.3.4.4, purA; adenylosuccinate synthase [EC:6.3.4.4]
 purD; phosphoribosylamine--glycine ligase [EC:6.3.4.13]
 guaA, GMPS; GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
 DPO1, polA; DNA polymerase I [EC:2.7.7.7]
 DPO3D1, hoiA; DNA polymerase III subunit delta [EC:2.7.7.7]
 rdgB; dITP/XTP pyrophosphatase [EC:3.6.1.19]
 rpoB; DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
 rpoC; DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]
 E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]
 nudE; ADP-ribose diphosphatase [EC:3.6.1.-]
 yjjG; 5'-nucleotidase [EC:3.1.3.5]
 xdhA; xanthine dehydrogenase small subunit [EC:1.17.1.4]
 yagT; xanthine dehydrogenase YagT iron-sulfur-binding subunit
 pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
 E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
 aldB; aldehyde dehydrogenase [EC:1.2.1.-]
 poxB; pyruvate dehydrogenase (quinone) [EC:1.2.5.1]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]

DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
 E2.3.1.54, pfID; formate C-acetyltransferase [EC:2.3.1.54]
 PK, pyk; pyruvate kinase [EC:2.7.1.40]
 ppdK; pyruvate, orthophosphate dikinase [EC:2.7.9.1]
 E4.1.1.3B, oadB; oxaloacetate decarboxylase, beta subunit [EC:4.1.1.3]
 ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
 E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
 adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]
 RP-L1, MRPL1, rplA; large subunit ribosomal protein L1
 RP-L11, MRPL11, rplK; large subunit ribosomal protein L11
 RP-L14, MRPL14, rplN; large subunit ribosomal protein L14
 RP-L16, MRPL16, rplP; large subunit ribosomal protein L16
 RP-L2, MRPL2, rplB; large subunit ribosomal protein L2
 RP-L20, MRPL20, rplT; large subunit ribosomal protein L20
 RP-L22, MRPL22, rplV; large subunit ribosomal protein L22
 RP-L23, MRPL23, rplW; large subunit ribosomal protein L23
 RP-L24, MRPL24, rplX; large subunit ribosomal protein L24
 RP-L25, rplY; large subunit ribosomal protein L25
 RP-L29, rpmC; large subunit ribosomal protein L29
 RP-L34, MRPL34, rpmH; large subunit ribosomal protein L34
 RP-L35, MRPL35, rpml; large subunit ribosomal protein L35
 RP-L4, MRPL4, rplD; large subunit ribosomal protein L4
 RP-L5, MRPL5, rplE; large subunit ribosomal protein L5
 RP-L7, MRPL12, rplL; large subunit ribosomal protein L7/L12
 RP-S1, rpsA; small subunit ribosomal protein S1
 RP-S17, MRPS17, rpsQ; small subunit ribosomal protein S17
 RP-S19, rpsS; small subunit ribosomal protein S19
 RP-S3, rpsC; small subunit ribosomal protein S3
 RP-S4, rpsD; small subunit ribosomal protein S4
 pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
 ppk; polyphosphate kinase [EC:2.7.4.1]
 pnp, PNPT1; polynucleotide nucleotidyltransferase [EC:2.7.7.8]
 pcnB; poly(A) polymerase [EC:2.7.7.19]
 ENO, eno; enolase [EC:4.2.1.11]
 rho; transcription termination factor Rho
 rhIB; ATP-dependent RNA helicase RhIB [EC:3.6.4.13]
 groEL, HSPD1; chaperonin GroEL
 deaD; ATP-dependent RNA helicase DeaD [EC:3.6.4.13]
 rne; ribonuclease E [EC:3.1.26.12]
 rhIE; ATP-dependent RNA helicase RhIE [EC:3.6.4.13]
 rnr, vacB; ribonuclease R [EC:3.1.-.-]
 UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
 E2.4.1.5; dextransucrase [EC:2.4.1.5]
 otsA; trehalose 6-phosphate synthase [EC:2.4.1.15]
 glgB; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
 UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]

E3.2.1.1, amyA, malS; alpha-amylase [EC:3.2.1.1]
 E3.2.1.4; endoglucanase [EC:3.2.1.4]
 xynB; xylan 1,4-beta-xylosidase [EC:3.2.1.37]
 E3.2.1.1A; alpha-amylase [EC:3.2.1.1]
 E5.1.3.6; UDP-glucuronate 4-epimerase [EC:5.1.3.6]
 pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
 glgE; starch synthase (maltosyl-transferring) [EC:2.4.99.16]
 ssuE; FMN reductase [EC:1.5.1.38]
 cysJ; sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]
 asrC; anaerobic sulfite reductase subunit C
 cysE; serine O-acetyltransferase [EC:2.3.1.30]
 sat, met3; sulfate adenylyltransferase [EC:2.7.7.4]
 cysK; cysteine synthase A [EC:2.5.1.47]
 cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]
 cysU; sulfate transport system permease protein
 cysW; sulfate transport system permease protein
 cysP, sbp; sulfate transport system substrate-binding protein
 tauD; taurine dioxygenase [EC:1.14.11.17]
 phsA, psrA; thiosulfate reductase / polysulfide reductase chain A
 dsrA; sulfite reductase alpha subunit [EC:1.8.99.3 1.8.99.1]
 thiE; thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]
 thiM; hydroxyethylthiazole kinase [EC:2.7.1.50]
 thiD; hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [EC:2.7.1.49 2.7.4.7]
 thiC; thiamine biosynthesis protein ThiC
 thiG; thiamine biosynthesis ThiG
 thiH; thiamine biosynthesis ThiH
 thiK; thiamine kinase [EC:2.7.1.89]
 cydB; cytochrome d ubiquinol oxidase subunit II [EC:1.10.3.-]
 E2.4.1.5; dextransucrase [EC:2.4.1.5]
 E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]
 ampC; beta-lactamase class C [EC:3.5.2.6]
 kdpA; K+-transporting ATPase ATPase A chain [EC:3.6.3.12]
 kdpB; K+-transporting ATPase ATPase B chain [EC:3.6.3.12]
 kdpC; K+-transporting ATPase ATPase C chain [EC:3.6.3.12]
 citE; citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.6 4.1.3.34]
 glnA; glutamine synthetase [EC:6.3.1.2]
 flhC; flagellar transcriptional activator FlhC
 flhD; flagellar transcriptional activator FlhD
 nifA; Nif-specific regulatory protein
 cheY; two-component system, chemotaxis family, response regulator CheY
 aer; aerotaxis receptor
 tsr; methyl-accepting chemotaxis protein I, serine sensor receptor
 phoQ; two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]
 envZ; two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ [EC:2.7.13.3]
 rstB; two-component system, OmpR family, sensor histidine kinase RstB [EC:2.7.13.3]
 cpxA; two-component system, OmpR family, sensor histidine kinase CpxA [EC:2.7.13.3]
 kdpD; two-component system, OmpR family, sensor histidine kinase KdpD [EC:2.7.13.3]
 torS; two-component system, OmpR family, sensor histidine kinase TorS [EC:2.7.13.3]

phoP; two-component system, OmpR family, response regulator PhoP
 baeR; two-component system, OmpR family, response regulator BaeR
 narQ; two-component system, NarL family, nitrate/nitrite sensor histidine kinase NarQ [EC:2.7.13.3]
 uhpB; two-component system, NarL family, sensor histidine kinase UhpB [EC:2.7.13.3]
 rcsD; two-component system, NarL family, sensor histidine kinase RcsD [EC:2.7.13.3]
 rcsC; two-component system, NarL family, capsular synthesis sensor histidine kinase RcsC [EC:2.7.13.3]
 barA; two-component system, NarL family, sensor histidine kinase BarA [EC:2.7.13.3]
 evgS, bvgS; two-component system, NarL family, sensor histidine kinase EvgS [EC:2.7.13.3]
 narP; two-component system, NarL family, nitrate/nitrite response regulator NarP
 rcsB; two-component system, NarL family, capsular synthesis response regulator RcsB
 uvrY; two-component system, NarL family, invasion response regulator UvrY
 evgA, bvgA; two-component system, NarL family, response regulator EvgA
 nreC; two-component system, NarL family, response regulator NreC
 arcA; two-component system, OmpR family, aerobic respiration control protein ArcA
 uhpT; MFS transporter, OPA family, hexose phosphate transport protein UhpT
 tctC; putative tricarboxylic transport membrane protein
 arnB, pmrH; UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [EC:2.6.1.87]
 torA; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]
 pgtA; two-component system, NtrC family, phosphoglycerate transport system response regulator PgtA
 vanX; D-alanyl-D-alanine dipeptidase [EC:3.4.13.22]
 pucA; light-harvesting protein B-800-850 alpha chain
 pgtP; MFS transporter, OPA family, phosphoglycerate transporter protein
 menB; naphthoate synthase [EC:4.1.3.36]
 menE; O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]
 menC; O-succinylbenzoate synthase [EC:4.2.1.113]
 menD; 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase [EC:2.2.1.9]
 menF; menaquinone-specific isochorismate synthase [EC:5.4.4.2]
 ubiA; 4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]
 ubiC; chorismate--pyruvate lyase [EC:4.1.3.40]
 menH; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [EC:4.2.99.20]
 leuB; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]
 ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]
 avtA; valine--pyruvate aminotransferase [EC:2.6.1.66]
 leuA; 2-isopropylmalate synthase [EC:2.3.3.13]
 E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
 E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]
 leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
 E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]
 alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
 pdxH, PNPO; pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]
 epd; D-erythrose 4-phosphate dehydrogenase [EC:1.2.1.72]
 pdxJ; pyridoxine 5-phosphate synthase [EC:2.6.99.2]
 pdxS, pdx1; pyridoxal 5'-phosphate synthase pdxS subunit [EC:4.3.3.6]
 pdxT, pdx2; 5'-phosphate synthase pdxT subunit [EC:4.3.3.6]
 E1.1.1.1, adh; alcohol dehydrogenase [EC:1.1.1.1]
 UGDH, ugd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]
 E1.1.1.30, bdh; 3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]

gpsA; glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]
 guaB; IMP dehydrogenase [EC:1.1.1.205]
 dxr; 1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]
 E1.1.1.-
 glcD; glycolate oxidase [EC:1.1.3.15]
 GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
 mmsA, iolA, ALDH6A1; malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.2.1]
 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
 porD; pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
 K00184; prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit
 K00185; prokaryotic molybdopterin-containing oxidoreductase family, membrane subunit
 cdhD, acsD; acetyl-CoA decarbonylase/synthase complex subunit delta [EC:2.1.1.245]
 fabI; enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]
 CPOX, hemF; coproporphyrinogen III oxidase [EC:1.3.3.3]
 sdhB; succinate dehydrogenase iron-sulfur subunit [EC:1.3.99.1]
 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
 gltB; glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]
 AOC3, AOC2, tyrA; primary-amine oxidase [EC:1.4.3.21]
 nadB; L-aspartate oxidase [EC:1.4.3.16]
 LYS1; saccharopine dehydrogenase (NAD+, L-lysine forming) [EC:1.5.1.7]
 LYS9; saccharopine dehydrogenase (NADP+, L-glutamate forming) [EC:1.5.1.10]
 metF, MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]
 ssuE; FMN reductase [EC:1.5.1.38]
 fixC; electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
 sthA, udhA; NAD(P) transhydrogenase [EC:1.6.1.1]
 pntA; NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]
 pntB; NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]
 E1.6.-.-; NADH oxidase [EC:1.6.-.-]
 nosZ; nitrous-oxide reductase [EC:1.7.2.4]
 DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
 E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]
 hpaD, hpcB; 3,4-dihydroxyphenylacetate 2,3-dioxygenase [EC:1.13.11.15]
 merA; mercuric reductase [EC:1.16.1.1]
 E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
 nrdD; ribonucleoside-triphosphate reductase [EC:1.17.4.2]
 hcaD; ferredoxin--NAD+ reductase [EC:1.18.1.3]
 E1.12.7.2L; ferredoxin hydrogenase large subunit [EC:1.12.7.2]
 ARSC1, arsC; arsenate reductase [EC:1.20.4.1]
 DNMT1, dcm; DNA (cytosine-5)-methyltransferase 1 [EC:2.1.1.37]
 rsmC; 16S rRNA (guanine1207-N2)-methyltransferase [EC:2.1.1.172]
 mnmA, trmU, TRMU; tRNA-specific 2-thiouridylase [EC:2.8.1.-]
 E2.1.1.72; site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.72]
 purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
 gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]
 pyrB, PYR2; aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]
 plsB; glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]

cysE; serine O-acetyltransferase [EC:2.3.1.30]
 fabD; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]
 E2.3.1.54, pflD; formate C-acetyltransferase [EC:2.3.1.54]
 DLST, sucB; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
 FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]
 MGAT3; beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [EC:2.4.1.144]
 pyrE; orotate phosphoribosyltransferase [EC:2.4.2.10]
 ykgG; hypothetical protein
 ispA; farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]
 GST, gst; glutathione S-transferase [EC:2.5.1.18]
 FDFT1; farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]
 hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]
 pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11]
 E2.7.1.29, DAK1, DAK2; dihydroxyacetone kinase [EC:2.7.1.29]
 PK, pyk; pyruvate kinase [EC:2.7.1.40]
 E2.7.3.-
 PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
 sat, met3; sulfate adenylyltransferase [EC:2.7.7.4]
 pnp, PNPT1; polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]
 UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
 PCYT1; choline-phosphate cytidyltransferase [EC:2.7.7.15]
 E2.7.7.24, rfbA, rffH; glucose-1-phosphate thymidyltransferase [EC:2.7.7.24]
 E2.7.7.41, CDS1, CDS2, cdsA; phosphatidate cytidyltransferase [EC:2.7.7.41]
 rph; ribonuclease PH [EC:2.7.7.56]
 ppdK; pyruvate,orthophosphate dikinase [EC:2.7.9.1]
 gctA; glutaconate CoA-transferase, subunit A [EC:2.8.3.12]
 gctB; glutaconate CoA-transferase, subunit B [EC:2.8.3.12]
 E3.1.3.1, phoA, phoB; alkaline phosphatase [EC:3.1.3.1]
 E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]
 E3.1.3.48; protein-tyrosine phosphatase [EC:3.1.3.48]
 ARSA; arylsulfatase A [EC:3.1.6.8]
 E3.1.11.1, sbcB; exodeoxyribonuclease I [EC:3.1.11.1]
 E3.1.11.2, xthA; exodeoxyribonuclease III [EC:3.1.11.2]
 xni; protein Xni
 hsdR; type I restriction enzyme, R subunit [EC:3.1.21.3]
 hsdS; type I restriction enzyme, S subunit [EC:3.1.21.3]
 rna; ribonuclease I (enterobacter ribonuclease) [EC:3.1.27.6]
 E3.2.1.1, amyA, malS; alpha-amylase [EC:3.2.1.1]
 NEU1; sialidase-1 [EC:3.2.1.18]
 lacZ; beta-galactosidase [EC:3.2.1.23]
 hya; hyaluronoglucosaminidase [EC:3.2.1.35]
 pepT; tripeptide aminopeptidase [EC:3.4.11.4]
 E3.4.11.-; aminopeptidase [EC:3.4.11.-]
 ptrB; oligopeptidase B [EC:3.4.21.83]
 E3.4.21.-
 prlC; oligopeptidase A [EC:3.4.24.70]
 yhgE; putative membrane protein
 E3.5.1.11; penicillin amidase [EC:3.5.1.11]

E3.5.1.28A, cwIA, xlyA, xlyB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
 URA4, pyrC; dihydroorotase [EC:3.5.2.3]
 ampC; beta-lactamase class C [EC:3.5.2.6]
 E3.5.3.1, rocF, arg; arginase [EC:3.5.3.1]
 comEB; dCMP deaminase [EC:3.5.4.12]
 ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]
 copB; Cu²⁺-exporting ATPase [EC:3.6.3.4]
 E4.1.1.17, ODC1, speC, speF; ornithine decarboxylase [EC:4.1.1.17]
 lysA; diaminopimelate decarboxylase [EC:4.1.1.20]
 pyrF; orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]
 ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
 E4.1.1.32, pckA, PEPCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
 pcaC; 4-carboxymuconolactone decarboxylase [EC:4.1.1.44]
 E4.1.2.22; fructose-6-phosphate phosphoketolase [EC:4.1.2.22]
 tnaA; tryptophanase [EC:4.1.99.1]
 ENO, eno; enolase [EC:4.2.1.11]
 hemB, ALAD; porphobilinogen synthase [EC:4.2.1.24]
 fabA; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
 cysK; cysteine synthase A [EC:2.5.1.47]
 E2.5.1.49, metY; O-acetylhomoserine (thiol)-lyase [EC:2.5.1.49]
 E4.3.1.17, sdaA; L-serine dehydratase [EC:4.3.1.17]
 csdA; cysteine sulfinatase desulfinate [EC:4.4.1.-]
 alr; alanine racemase [EC:5.1.1.1]
 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
 MUT; methylmalonyl-CoA mutase [EC:5.4.99.2]
 IARS, ileS; isoleucyl-tRNA synthetase [EC:6.1.1.5]
 AARS, alaS; alanyl-tRNA synthetase [EC:6.1.1.7]
 VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]
 SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]
 RARS, argS; arginyl-tRNA synthetase [EC:6.1.1.19]
 FARSB, pheT; phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
 gluQ; glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]
 sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
 sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
 glnA; glutamine synthetase [EC:6.3.1.2]
 panC; pantoate--beta-alanine ligase [EC:6.3.2.1]
 ddl; D-alanine-D-alanine ligase [EC:6.3.2.4]
 murD; UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]
 E6.3.2.-
 fhs; formate--tetrahydrofolate ligase [EC:6.3.4.3]
 guaA, GMPS; GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
 carB, CPA2; carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]
 PCCB, pccB; propionyl-CoA carboxylase beta chain [EC:6.4.1.3]
 E6.5.1.2, ligA, ligB; DNA ligase (NAD⁺) [EC:6.5.1.2]
 ABC-2.A; ABC-2 type transport system ATP-binding protein
 ABC-2.P; ABC-2 type transport system permease protein
 proW; glycine betaine/proline transport system permease protein
 cbiM; cobalt/nickel transport system permease protein

TC.FEV.OM; iron complex outermembrane receptor protein
 ABC.MR.TX; HlyD family secretion protein
 ABC.PA.S; polar amino acid transport system substrate-binding protein
 ABC.PE.A; peptide/nickel transport system ATP-binding protein
 ABC.PE.A1; peptide/nickel transport system ATP-binding protein
 phoU; phosphate transport system protein
 cysA; sulfate transport system ATP-binding protein [EC:3.6.3.25]
 cysU; sulfate transport system permease protein
 cysW; sulfate transport system permease protein
 cysP, sbp; sulfate transport system substrate-binding protein
 ABC.ZM.S; zinc/manganese transport system substrate-binding protein
 ATPFOB, atpF; F-type H⁺-transporting ATPase subunit b [EC:3.6.3.14]
 ATPFOC, atpE; F-type H⁺-transporting ATPase subunit c [EC:3.6.3.14]
 ATPF1A, atpA; F-type H⁺-transporting ATPase subunit alpha [EC:3.6.3.14]
 ATPF1B, atpD; F-type H⁺-transporting ATPase subunit beta [EC:3.6.3.14]
 ATPF1D, atpH; F-type H⁺-transporting ATPase subunit delta [EC:3.6.3.14]
 ATPF1E, atpC; F-type H⁺-transporting ATPase subunit epsilon [EC:3.6.3.14]
 ATPF1G, atpG; F-type H⁺-transporting ATPase subunit gamma [EC:3.6.3.14]
 yggC; hypothetical protein
 bfd; bacterioferritin-associated ferredoxin
 ftnB; ferritin-like protein 2
 crtB; phytoene synthase [EC:2.5.1.32]
 cyoE; protoheme IX farnesyltransferase [EC:2.5.1.-]
 dnaT; DNA replication protein DnaT
 dpo; DNA polymerase bacteriophage-type [EC:2.7.7.7]
 DPO1, polA; DNA polymerase I [EC:2.7.7.7]
 DPO2, polB; DNA polymerase II [EC:2.7.7.7]
 DPO3D1, holA; DNA polymerase III subunit delta [EC:2.7.7.7]
 DPO4, dinB; DNA polymerase IV [EC:2.7.7.7]
 tsf, TSFM; elongation factor Ts
 entF; enterobactin synthetase component F [EC:2.7.7.-]
 sufE; cysteine desulfuration protein SufE
 fucU; L-fucose mutarotase [EC:5.1.3.-]
 gatA, QRSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A [EC:6.3.5.6 6.3.5.7]
 gatB, PET112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC:6.3.5.6 6.3.5.7]
 gspD; general secretion pathway protein D
 gutM; glucitol operon activator protein
 gyrA; DNA gyrase subunit A [EC:5.99.1.3]
 gyrB; DNA gyrase subunit B [EC:5.99.1.3]
 K02477; two-component system, LytT family, response regulator
 K02478; two-component system, LytT family, sensor kinase [EC:2.7.13.3]
 K02482; two-component system, NtrC family, sensor kinase [EC:2.7.13.3]
 rssB, hnr; two-component system, unclassified family, response regulator
 hemK, prmC; release factor glutamine methyltransferase [EC:2.1.1.-]
 hpaX; MFS transporter, ACS family, 4-hydroxyphenylacetate permease
 infB, MTIF2; translation initiation factor IF-2
 infC, MTIF3; translation initiation factor IF-3
 ksgA; 16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase [EC:2.1.1.182]

menF; menaquinone-specific isochorismate synthase [EC:5.4.4.2]
mhpD; 2-keto-4-pentenoate hydratase [EC:4.2.1.80]
mpl; UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [EC:6.3.2.-]
mtlR1, mtlR; mannitol operon repressor
nagC; N-acetylglucosamine repressor
napC; cytochrome c-type protein NapC
napF; ferredoxin-type protein NapF
nirC; nitrite transporter NirC
nusA; N utilization substance protein A
nusG; transcriptional antiterminator NusG
paaY; phenylacetic acid degradation protein
parC; topoisomerase IV subunit A [EC:5.99.1.-]
pilB; type IV pilus assembly protein PilB
pilC; type IV pilus assembly protein PilC
pilD, pppA; leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-]
pilN; type IV pilus assembly protein PilN
pilT; twitching motility protein PilT
PTS-Asc-EIIC, ascF; PTS system, arbutin-, cellobiose-, and salicin-specific IIC component
PTS-Nag-EIIC, nagE; PTS system, N-acetylglucosamine-specific IIC component
rffA, wecE; dTDP-4-amino-4,6-dideoxygalactose transaminase [EC:2.6.1.59]
PTS-Ntr-EIIA, ptsN; PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]
pyrR; pyrimidine operon attenuation protein / uracil phosphoribosyltransferase [EC:2.4.2.9]
rbfA; ribosome-binding factor A
prfA, MTRF1, MRF1; peptide chain release factor 1
prfB; peptide chain release factor 2
rhaR; AraC family transcriptional regulator, L-rhamnose operon transcriptional activator RhaR
rpoB; DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
rpoC; DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]
secA; preprotein translocase subunit SecA
secD; preprotein translocase subunit SecD
secF; preprotein translocase subunit SecF
APOD; apolipoprotein D and lipocalin family protein
ftsY; fused signal recognition particle receptor
tatA; sec-independent protein translocase protein Tata
tauD; taurine dioxygenase [EC:1.14.11.17]
thiJ; 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis
thiS; sulfur carrier protein
topB; DNA topoisomerase III [EC:5.99.1.2]
yajC; preprotein translocase subunit YajC
trmL, cspR; tRNA (cytidine/uridine-2'-O-)-methyltransferase [EC:2.1.1.207]
rlmB; 23S rRNA (guanosine2251-2'-O)-methyltransferase [EC:2.1.1.185]
TC.CIC; chloride channel protein, CIC family
mscL; large conductance mechanosensitive channel
corA; magnesium transporter
MFS.SET; MFS transporter, SET family, sugar efflux transporter
TC.AAA; ATP:ADP antiporter, AAA family
TC.LCTP; lactate transporter, LctP family
TC.AGCS; alanine or glycine:cation symporter, AGCS family

TC.CPA1; monovalent cation:H⁺ antiporter, CPA1 family
yahN; amino acid exporter
dapdh; diaminopimelate dehydrogenase [EC:1.4.1.16]
E1.11.1.15, PRDX, ahpC; peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
cheY; two-component system, chemotaxis family, response regulator CheY
hsdM; type I restriction enzyme M protein [EC:2.1.1.72]
fruR1, fruR; LacI family transcriptional regulator, fructose operon transcriptional repressor
fruR2, fruR; DeoR family transcriptional regulator, fructose operon transcriptional repressor
MFS.CP; MFS transporter, CP family, cyanate transporter
TC.KEF; monovalent cation:H⁺ antiporter-2, CPA2 family
focB; formate transporter
aaeB; p-hydroxybenzoic acid efflux pump subunit AaeB
rnhB; ribonuclease HII [EC:3.1.26.4]
rnhC; ribonuclease HIII [EC:3.1.26.4]
ulaR; DeoR family transcriptional regulator, ulaG and ulaABCDEF operon transcriptional repressor
yidP; GntR family transcriptional regulator, glv operon transcriptional regulator
treR1, treR; LacI family transcriptional regulator, trehalose operon repressor
licT, bglG; beta-glucoside operon transcriptional antiterminator
yydK; GntR family transcriptional regulator, transcriptional regulator of bglA
licR; lichenan operon transcriptional antiterminator
ydhQ; GntR family transcriptional regulator
rsmB, sun; 16S rRNA (cytosine967-C5)-methyltransferase [EC:2.1.1.176]
zipA; cell division protein ZipA
clpX, CLPX; ATP-dependent Clp protease ATP-binding subunit ClpX
tig; trigger factor
sbcD; exonuclease SbcD
kup; KUP system potassium uptake protein
ruvA; holliday junction DNA helicase RuvA [EC:3.6.4.12]
mutS; DNA mismatch repair protein MutS
exbD; biopolymer transport protein ExbD
gcvA; LysR family transcriptional regulator, glycine cleavage system transcriptional activator
mutT, NUDT15, MTH2; 8-oxo-dGTP diphosphatase [EC:3.6.1.55]
hrpA; ATP-dependent helicase HrpA [EC:3.6.4.13]
hrpB; ATP-dependent helicase HrpB [EC:3.6.4.13]
recC; exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]
lepA; GTP-binding protein LepA
rseA; sigma-E factor negative regulatory protein RseA
rseB; sigma-E factor negative regulatory protein RseB
sspB; stringent starvation protein B
fadR; GntR family transcriptional regulator, negative regulator for fad regulon and positive regulator of fabA
hyaD, hybD; hydrogenase maturation protease [EC:3.4.23.-]
rlpA; rare lipoprotein A
nrdI; protein involved in ribonucleotide reduction
mnme, trmE, MSS1; tRNA modification GTPase [EC:3.6.-.-]
icc; lcc protein
hflX; GTP-binding protein HflX
mdoH; membrane glycosyltransferase [EC:2.4.1.-]
mdoG; periplasmic glucans biosynthesis protein

grxB; glutaredoxin 2
rnt; ribonuclease T [EC:3.1.13.-]
rnd; ribonuclease D [EC:3.1.13.5]
yigP; hypothetical protein
clpC; ATP-dependent Clp protease ATP-binding subunit ClpC
cbf; CMP-binding protein
uvrA; excinuclease ABC subunit A
cspA; cold shock protein (beta-ribbon, CspA family)
mfd; transcription-repair coupling factor (superfamily II helicase) [EC:3.6.4.-]
lhr; ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.4.-]
aor; aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
smg; Smg protein
sanA; SanA protein
PPIB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]
fkIB; FKBP-type peptidyl-prolyl cis-trans isomerase FkIB [EC:5.2.1.8]
aer; aerotaxis receptor
katE, CAT, catB, srpA; catalase [EC:1.11.1.6]
aphA; acid phosphatase (class B) [EC:3.1.3.2]
lipB; lipoyl(octanoyl) transferase [EC:2.3.1.181]
ampD; AmpD protein
pqiA; paraquat-inducible protein A
wcaF; putative colanic acid biosynthesis acetyltransferase WcaF [EC:2.3.1.-]
Int; apolipoprotein N-acyltransferase [EC:2.3.1.-]
yiaC; putative acetyltransferase [EC:2.3.1.-]
tyrP; tyrosine-specific transport protein
tdcC; threonine transporter
tpa; taurine-pyruvate aminotransferase [EC:2.6.1.77]
arsR; ArsR family transcriptional regulator
iucA; N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]
iucC; aerobactin synthase [EC:6.3.2.39]
iucB; acetyl CoA:N6-hydroxylysine acetyl transferase [EC:2.3.1.102]
lat; L-lysine 6-transaminase [EC:2.6.1.36]
mdaB; modulator of drug activity B
moxR; MoxR-like ATPase [EC:3.6.3.-]
obg; GTP-binding protein
dsbC; thiol:disulfide interchange protein DsbC [EC:5.3.4.1]
eutT; ethanolamine utilization cobalamin adenosyltransferase [EC:2.5.1.17]
osmB; osmotically inducible lipoprotein OsmB
priC; primosomal replication protein N"
adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]
groEL, HSPD1; chaperonin GroEL
htpG, HSP90A; molecular chaperone HtpG
ibpB; molecular chaperone IbpB
hslO; molecular chaperone Hsp33
hypA, hybF; hydrogenase nickel incorporation protein HypA/HybF
hypB; hydrogenase nickel incorporation protein HypB
hypC; hydrogenase expression/formation protein HypC

hypD; hydrogenase expression/formation protein HypD
 hypE; hydrogenase expression/formation protein HypE
 hypF; hydrogenase maturation protein HypF
 hhoB, degS; serine protease DegS [EC:3.4.21.-]
 lptD, imp, ostA; LPS-assembly protein
 rsbW; serine/threonine-protein kinase RsbW [EC:2.7.11.1]
 greB; transcription elongation factor GreB
 acuB; acetoin utilization protein AcuB
 irp1, HMWP1; yersiniabactin nonribosomal peptide/polyketide synthase
 fre, ubiB; aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3 1.5.1.41]
 cytR; LacI family transcriptional regulator, repressor for deo operon, udp, cdd, tsx, nupC, and nupG
 mrdA; penicillin-binding protein 2
 tsx; nucleoside-specific channel-forming protein
 draG; ADP-ribosylglycohydrolase [EC:3.2.-.-]
 bolA; BolA protein
 dusA; tRNA-dihydrouridine synthase A [EC:1.-.-.-]
 dusC; tRNA-dihydrouridine synthase C [EC:1.-.-.-]
 mnhB, mrpB; multicomponent Na⁺:H⁺ antiporter subunit B
 marC; multiple antibiotic resistance protein
 iciA; LysR family transcriptional regulator, chromosome initiation inhibitor
 mhpA; 3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.127]
 mhpB; 2,3-dihydroxyphenylpropionate 1,2-dioxygenase [EC:1.13.11.16]
 mhpC; 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase [EC:3.7.1.-]
 malM; maltose operon periplasmic protein
 wzzB; chain length determinant protein (polysaccharide antigen chain regulator)
 ybaO; Lrp/AsnC family transcriptional regulator
 nlpl; lipoprotein Nlpl
 rob; right origin-binding protein
 yhbH; putative sigma-54 modulation protein
 raiA; ribosome-associated inhibitor A
 argE1, lysK; LysW-gamma-L-lysine carboxypeptidase
 rhtC; threonine efflux protein
 ybbN; putative thioredoxin
 rimK; ribosomal protein S6 modification protein
 E4.6.1.1A, cyaA; adenylate cyclase, class 1 [EC:4.6.1.1]
 tsr; methyl-accepting chemotaxis protein I, serine sensor receptor
 dhaM; PTS hybrid protein
 aas; acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase / long-chain-fatty-acid--[acyl-carrier-protein] ligase [EC:2.3.1.41]
 E2.4.1.58
 cho; excinuclease Cho [EC:3.1.25.-]
 E3.2.1.40; alpha-L-rhamnosidase [EC:3.2.1.40]
 sufA; Fe-S cluster assembly protein SufA
 shc, sqhC; squalene-hopene/tetraprenyl-beta-curcumen cyclase [EC:5.4.99.17 4.2.1.129]
 ABC.VB12.P, btuC; vitamin B12 transport system permease protein
 ABC.VB12.A, btuD; vitamin B12 transport system ATP-binding protein [EC:3.6.3.33]
 slyB; outer membrane lipoprotein SlyB
 cls; cardiolipin synthase [EC:2.7.8.-]
 rnk; regulator of nucleoside diphosphate kinase

uspB; universal stress protein B
gntR; LacI family transcriptional regulator, gluconate utilization system Gnt-I transcriptional repressor
ABCF3; ATP-binding cassette, subfamily F, member 3
yojI; putative ATP-binding cassette transporter
phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]
rluE; 23S rRNA pseudouridine2457 synthase [EC:5.4.99.20]
rsuA; 16S rRNA pseudouridine516 synthase [EC:5.4.99.19]
bamE, smpA; outer membrane protein assembly factor BamE
apaG; ApaG protein
cysZ; CysZ protein
mioC; MioC protein
jag; spoIIJ-associated protein
tlyA; 23S rRNA (cytidine1920-2'-O)/16S rRNA (cytidine1409-2'-O)-methyltransferase [EC:2.1.1.226 2.1.1.227]
ABC.VB12.S1, btuF; vitamin B12 transport system substrate-binding protein
K06864; uncharacterized protein
K06867
K06898
K06916
K06918
K06940
rlmN; 23S rRNA (adenine2503-C2)-methyltransferase [EC:2.1.1.192]
tmcA; tRNA(Met) cytidine acetyltransferase [EC:2.3.1.193]
K06966
K06973
K06997
K07005
K07016
K07032
K07037
K07051
K07054
K07071
K07080
K07084
K07098
fxsA; UPF0716 protein FxsA
yfbK; Ca-activated chloride channel homolog
K07121
K07136
K07137
K07138
K07140
isdG, isdI; heme oxygenase (staphylobilin-producing) [EC:1.14.99.48]
K07146; UPF0176 protein
K07164
fecR; transmembrane sensor
prkA; serine protein kinase
FLOT; flotillin

K07219; putative molybdopterin biosynthesis protein
oprO_P; phosphate-selective porin OprO and OprP
efeO; iron uptake system component EfeO
yqjH; ferric-chelate reductase (NADPH) [EC:1.16.1.9]
tusD, dsrE; tRNA 2-thiouridine synthesizing protein D [EC:2.8.1.-]
tusC, dsrF; tRNA 2-thiouridine synthesizing protein C
TC.HME; heavy-metal exporter, HME family
FTR, efeU; high-affinity iron transporter
spsF; spore coat polysaccharide biosynthesis protein SpsF
mepA; penicillin-insensitive murein endopeptidase [EC:3.4.24.-]
pqqL; zinc protease [EC:3.4.24.-]
oprB; porin
ytfB; hypothetical protein
ompW; outer membrane protein
K07276; hypothetical protein
SAM50, TOB55, bamA; outer membrane protein insertion porin family
ydiY; putative salt-induced outer membrane protein
slp; outer membrane lipoprotein
bamC; outer membrane protein assembly factor BamC
ynfE; Tat-targeted selenate reductase subunit YnfE [EC:1.97.1.9]
ynfG; Tat-targeted selenate reductase subunit YnfG
K07340; hypothetical protein
fimE; type 1 fimbriae regulatory protein FimE
K07396; putative protein-disulfide isomerase
nfuA; Fe/S biogenesis protein NfuA
nfeD; membrane-bound serine protease (ClpP class)
ycaJ; putative ATPase
yrdD; putative DNA topoisomerase
insB; insertion element IS1 protein InsB
K07492; putative transposase
tsaC, rimN, SUA5; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]
evgS, bvgS; two-component system, NarL family, sensor histidine kinase EvgS [EC:2.7.13.3]
evgA, bvgA; two-component system, NarL family, response regulator EvgA
algH; putative transcriptional regulator
ELP3, KAT9; elongator complex protein 3 [EC:2.3.1.48]
E3.1.3.23; sugar-phosphatase [EC:3.1.3.23]
torZ; trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]
sotB; MFS transporter, DHA1 family, L-arabinose/isopropyl-beta-D-thiogalactopyranoside export protein
mdtG; MFS transporter, DHA1 family, multidrug resistance protein
mdtH; MFS transporter, DHA1 family, multidrug resistance protein
UMF2; MFS transporter, UMF2 family, putative MFS family transporter protein
lplT; MFS transporter, LPLT family, lysophospholipid transporter
caiF; transcriptional activator CaiF
E2.7.11.1; non-specific serine/threonine protein kinase [EC:2.7.11.1]
sixA; phosphohistidine phosphatase [EC:3.1.3.-]
caiB; crotonobetainyl-CoA:carnitine CoA-transferase [EC:2.8.3.-]
rng, cafA; ribonuclease G [EC:3.1.26.-]
K08303; putative protease [EC:3.4.-.-]

PTS-EI.PTSI, ptsI; phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]
PTS-EI.PTSP, ptsP; phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]
vanX; D-alanyl-D-alanine dipeptidase [EC:3.4.13.22]
yjjG; 5'-nucleotidase [EC:3.1.3.5]
mtnE, mtnV; aminotransferase [EC:2.6.1.-]
yjdF; putative membrane protein
ydiU; hypothetical protein
K08999; hypothetical protein
K09002; hypothetical protein
sufD; Fe-S cluster assembly protein SufD
K09117; hypothetical protein
K09121; hypothetical protein
K09123; hypothetical protein
K09125; hypothetical protein
K09131; hypothetical protein
K09158; hypothetical protein
aidB; putative acyl-CoA dehydrogenase
fabF; 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]
iap; alkaline phosphatase isozyme conversion protein [EC:3.4.11.-]
K09700; hypothetical protein
K09706; hypothetical protein
K09747; hypothetical protein
rsmE; 16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]
K09769; hypothetical protein
K09778; hypothetical protein
K09781; hypothetical protein
K09786; hypothetical protein
K09806; hypothetical protein
ABC.MN.P; manganese/iron transport system permease protein
ABC.MN.A; manganese/iron transport system ATP-binding protein
perR; Fur family transcriptional regulator, peroxide stress response regulator
K09893; hypothetical protein
K09894; hypothetical protein
K09902; hypothetical protein
K09907; hypothetical protein
K09908; hypothetical protein
K09909; hypothetical protein
K09912; hypothetical protein
K09914; putative lipoprotein
K09920; hypothetical protein
K09921; hypothetical protein
K09928; hypothetical protein
K09940; hypothetical protein
K09949; hypothetical protein
K09952; hypothetical protein
K09954; hypothetical protein
aapM, bztC; general L-amino acid transport system permease protein
K09974; hypothetical protein

K09992; hypothetical protein
gluB; glutamate transport system substrate-binding protein
gluC; glutamate transport system permease protein
gluD; glutamate transport system permease protein
gluA; glutamate transport system ATP-binding protein [EC:3.6.3.-]
ABC.CYST.A; cystine transport system ATP-binding protein [EC:3.6.3.-]
hisQ; histidine transport system permease protein
malF; maltose/maltodextrin transport system permease protein
ABC.GGU.S, chvE; putative multiple sugar transport system substrate-binding protein
kch, trkA, mthK, pch; voltage-gated potassium channel
hda; DnaA-homolog protein
SMUG1; single-strand selective monofunctional uracil DNA glycosylase [EC:3.2.2.-]
yciA; acyl-CoA thioesterase YciA [EC:3.1.2.-]
E2.7.13.3; histidine kinase
E2.3.1.164; isopenicillin-N N-acyltransferase [EC:2.3.1.164]
K10907; aminotransferase [EC:2.6.1.-]
acfD; accessory colonization factor AcfD
allR; lclR family transcriptional regulator, negative regulator of allantoin and glyoxylate utilization operons
E3.5.1.28D, amiD; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
msbA; ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]
ttdT; L-tartrate/succinate antiporter
PTS-Mur-EIIC, murP; PTS system, N-acetylmuramic acid-specific IIC component
PTS-Fru2-EIIA; PTS system, fructose-specific IIA-like component [EC:2.7.1.69]
yncG; GST-like protein
leuE; leucine efflux protein
fwdE, fmdE; formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]
mmcD; methylmalonyl-CoA decarboxylase [EC:4.1.1.41]
bchC; 3-hydroxyethyl bacteriochlorophyllide a dehydrogenase [EC:1.-.-.-]
glcF; glycolate oxidase iron-sulfur subunit
glcC; GntR family transcriptional regulator, glc operon transcriptional activator
sitC; manganese/iron transport system permease protein
sitD; manganese/iron transport system permease protein
sitB; manganese/iron transport system ATP-binding protein
lptC; lipopolysaccharide export system protein LptC
pheP; phenylalanine-specific permease
aroP; aromatic amino acid transport protein AroP
cycA; D-serine/D-alanine/glycine transporter
nfrA; bacteriophage N4 adsorption protein A
tqsA; AI-2 transport protein TqsA
kefB; glutathione-regulated potassium-efflux system protein KefB
kefG; glutathione-regulated potassium-efflux system ancillary protein KefG
rseP; regulator of sigma E protease [EC:3.4.24.-]
frsA; esterase FrsA [EC:3.1.-.-]
ribD; diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase [E
impl, vasC; type VI secretion system protein Impl
vasJ; type VI secretion system protein VasJ
ppkA; serine/threonine-protein kinase PpkA [EC:2.7.11.1]
cueR; MerR family transcriptional regulator, copper efflux regulator

sgrR; SgrR family transcriptional regulator
 uspG; universal stress protein G
 cof; HMP-PP phosphatase [EC:3.6.1.-]
 hspQ; heat shock protein HspQ
 tadA; tRNA(adenine34) deaminase [EC:3.5.4.33]
 traH; conjugative transfer pilus assembly protein TraH
 ebgC; evolved beta-galactosidase subunit beta
 hyfC; hydrogenase-4 component C [EC:1.-.-.-]
 hyfI; hydrogenase-4 component I [EC:1.-.-.-]
 hyfR; hydrogenase-4 transcriptional activator
 bssS; biofilm regulator BssS
 dotC, tral; defect in organelle trafficking protein DotC
 icmE, dotG; intracellular multiplication protein IcmE
 icmG, dotF; intracellular multiplication protein IcmG
 icmP, trbA; intracellular multiplication protein IcmP
 norV; anaerobic nitric oxide reductase flavorubredoxin
 msrAB; peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11 1.8.4.12]
 hofM; pilus assembly protein HofM
 ispDF; 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:2.7.7.65]
 papC; outer membrane usher protein PapC
 metL; bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
 wecF, rffT; TDP-Fuc4NAc transferase [EC:2.4.1.-]
 flu; antigen 43
 ygeR; lipoprotein YgeR
 lpxP; palmitoleoyl transferase [EC:2.3.1.-]
 wbpY; alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]
 ttuB; MFS transporter, ACS family, tartrate transporter
 E2.7.7.65; diguanylate cyclase [EC:2.7.7.65]
 ipgD, sopB; phosphatidylinositol-4,5-bisphosphate 4-phosphatase [EC:3.1.3.78]
 fhuF; ferric iron reductase protein FhuF
 secM; secretion monitor
 raxB, cvaB; ATP-binding cassette, subfamily B, bacterial RaxB
 VCP, CDC48; transitional endoplasmic reticulum ATPase
 mpa; proteasome-associated ATPase
 cobA-hemD; uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75]
 pafA; proteasome accessory factor A [EC:6.3.2.-]
 soxS; AraC family transcriptional regulator, transcriptional activator of the superoxide response regulon
 mqsA; HTH-type transcriptional regulator / antitoxin for MqsR toxin
 wcaE; putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]
 nlpC; probable lipoprotein NlpC
 inlA; internalin A
 yeeJ; adhesin/invasin
 nsrR; Rrf2 family transcriptional regulator, nitric oxide-sensitive transcriptional repressor
 GGPS; geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10 2.5.1.29]
 yejA; microcin C transport system substrate-binding protein
 yejB; microcin C transport system permease protein
 yejE; microcin C transport system permease protein
 rbbA; ribosome-dependent ATPase

gmr; cyclic di-GMP phosphodiesterase Gmr [EC:3.1.4.52]
mpaA; protein MpaA
uspE; universal stress protein E
uspF; universal stress protein F
feaR; AraC family transcriptional regulator, positive regulator of tynA and feaB
uspC; universal stress protein C
clfB; clumping factor B
SLC10A7, P7; solute carrier family 10 (sodium/bile acid cotransporter), member 7
actP; cation/acetate symporter
rimO; ribosomal protein S12 methylthiotransferase [EC:2.-.-.-]
SLC13A2_3_5; solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5
ICP; inhibitor of cysteine peptidase
ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II [EC:4.1.99.12 3.5.4.25]
yibL; ribosome-associated protein
mngB; mannosylglycerate hydrolase [EC:3.2.1.170]
mdtO; multidrug resistance protein MdtO
erpA; iron-sulfur cluster insertion protein
hipB; HTH-type transcriptional regulator, antitoxin HipB
pmm-pgm; phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
murR; RpiR family transcriptional regulator, murPQ operon repressor
K15977; putative oxidoreductase
nmpC, ompD; outer membrane porin protein LC
uidB, gusB; glucuronide carrier protein
erfK; L,D-transpeptidase
efeB; deferriochelatase/peroxidase EfeB [EC:1.11.1.-]
wzx; O-antigen flippase
bioM; biotin transport system ATP-binding protein [EC:3.6.3.-]
aksD; methanogen homoaconitase large subunit [EC:4.2.1.114]
uxaA2; altronate dehydratase large subunit [EC:4.2.1.7]

Supplementary Table 7

Sheet1

Sheet2

Annotation of the 207 and 200 genes in *A. muciniphila* and *B. wadsworthia*, respectively, that were regulated by exposure to metformin in the *in vitro* gut simulator.

Annotation in *A. muciniphila*. Rows with light green background indicate genes involved in multiple KEGG

Annotation in *B. wadsworthia*.

Genbank (N=207)	GeneID	baseMean	log2FoldChange	pvalue	padj	start
YP_001876859.1	6275288	3017.277774	-0.463434476	0.011054084	0.082253465	292855
YP_001876992.1	6274901	45811.30516	-0.78527763	0.000542933	0.012391142	443237
YP_001877321.1	6273895	1283.461854	-0.518109564	0.007070951	0.062927012	827881
YP_001878602.1	6275760	1401.547991	0.537581928	0.010892675	0.081984764	2443943
YP_001878604.1	6275754	854.1045306	0.787545203	0.002316117	0.031512559	2445725
YP_001877309.1	6273920	13085.81231	-0.48631566	0.005088793	0.052945894	816498
YP_001877783.1	6273777	1018.908448	-0.816907641	0.000435977	0.010644225	1412210
YP_001877275.1	6273981	334.1255663	-0.893353942	0.000871332	0.016012132	772777
YP_001877141.1	6274859	4000.188637	-0.402769051	0.012955186	0.091201929	614418
YP_001876657.1	6275193	3593.84774	-0.441193007	0.00690065	0.062193752	37306
YP_001877676.1	6274041	493.1624905	0.819463699	0.005292832	0.054270701	1275836
YP_001877855.1	6275401	448.2941449	-0.626773428	0.012741252	0.090672661	1499232
YP_001878021.1	6275767	11001.75575	-0.717647263	0.0000737	0.003159302	1695420
YP_001877179.1	6275519	2096.936483	0.609764911	0.00084032	0.015854031	660401
YP_001878258.1	6275794	2710.503002	0.511815091	0.00633584	0.059372278	2004200
YP_001878231.1	6273817	2052.379635	-0.526203126	0.005149699	0.053188494	1963498
YP_001876838.1	6275319	8502.10252	-0.5725936	0.000727331	0.014702474	263935
YP_001876825.1	6275340	959.7628113	-0.679694075	0.000757619	0.014886231	250061
YP_001877003.1	6274857	5922.814434	-0.540956303	0.00192346	0.027547438	461021
YP_001877176.1	6275370	823.8360332	0.631035525	0.005552886	0.055333332	656259
YP_001877811.1	6273851	1558.478176	0.596023247	0.001752581	0.025832316	1440958
YP_001878158.1	6273642	2532.537851	-0.754146212	0.0000554	0.002611291	1869588
YP_001878159.1	6273641	2872.189831	-0.828681595	0.00000106	0.000114983	1869947
YP_001876923.1	6275099	309.9156859	-0.819056362	0.003009505	0.036397	357961
YP_001876857.1	6275290	2480.944391	-0.702522031	0.0000894	0.003721205	291556
YP_001877346.1	6273797	1227.190078	-0.560025183	0.004625822	0.049875022	858403
YP_001878494.1	6275696	852.1231169	0.66643555	0.00201031	0.028164238	2306040
YP_001876723.1	6274974	1438.912364	-0.704783106	0.001676649	0.024973252	123193
YP_001876847.1	6275307	748.4659391	0.695372759	0.002896907	0.035730109	279869
YP_001876968.1	6274960	3704.688966	0.437999813	0.01362113	0.094019021	410440
YP_001877178.1	6275557	3796.066217	-0.75825493	0.0000491	0.002468565	657464
YP_001877210.1	6274710	1132.865759	0.747903672	0.000937865	0.016798464	701509
YP_001877271.1	6273985	1197.399653	-0.498394941	0.01132214	0.083441815	767420
YP_001877326.1	6273885	4793.741509	0.446505213	0.009572849	0.075253231	834204
YP_001877476.1	6274306	709.958742	-3.454821219	1.71E-51	1.21E-48	1027307
YP_001877675.1	6274042	527.7647284	1.022898862	0.0000237	0.001458118	1274628
YP_001878455.1	6275480	1093.342262	-0.714920697	0.000378574	0.01010721	2262706
YP_001877413.1	6274380	1768.272326	-0.490976613	0.006752697	0.061250428	935258
YP_001878587.1	6274118	4646.281472	0.572937449	0.002718451	0.034654122	2422591
YP_001877414.1	6274378	14960.95111	-0.648975446	0.000257463	0.007751275	937083
YP_001877423.1	6274368	1538.176311	0.678129925	0.00049595	0.011504414	951679
YP_001878022.1	6275714	5066.219969	-0.680766776	0.0000294	0.001734211	1696613
YP_001876694.1	6275071	1497.970598	-0.566279017	0.003280725	0.038961007	91155
YP_001876747.1	6274910	2177.290277	-0.498660562	0.00474917	0.050526884	149378
YP_001876765.1	6274801	3251.202891	-0.701682213	0.0000391	0.002128385	172287
YP_001876845.1	6275312	2975.372844	0.660334242	0.000101919	0.004120432	277742
YP_001876913.1	6275131	8103.819793	-0.480566133	0.004259719	0.04746065	347442

YP_001876929.1	6275084	6841.085438	-0.520352163	0.001612867	0.024679143	361097
YP_001877025.1	6274822	2786.955294	-0.651730555	0.000114023	0.004360606	486810
YP_001877160.1	6275124	2622.745801	-0.604185357	0.000423684	0.010644225	638613
YP_001877165.1	6275201	1613.077751	-0.655048182	0.000558752	0.012498592	647272
YP_001877270.1	6273987	1175.957853	-0.636484232	0.001091831	0.018840749	765313
YP_001877307.1	6273924	1685.903047	-0.503209182	0.008678349	0.071372657	813515
YP_001877342.1	6273807	1207.604969	-0.68524241	0.003482215	0.04072177	855308
YP_001877384.1	6274416	3843.738867	-0.589062595	0.003514325	0.040760404	902506
YP_001877387.1	6274413	5836.64399	-0.598479024	0.000778503	0.014886231	906706
YP_001877392.1	6274407	1920.095218	-0.89407086	0.000000441	0.000052	914942
YP_001877430.1	6274361	2994.017589	-0.733210768	0.00023698	0.007289703	961035
YP_001877438.1	6274353	13454.58774	-0.5104765	0.006049855	0.058235002	969353
YP_001877458.1	6274325	7817.929609	0.977789021	0.00000705	0.000525164	1004673
YP_001877473.1	6274309	770.3987215	-1.997326822	2.16E-20	7.66E-18	1024464
YP_001877474.1	6274308	4903.692321	-2.554396561	1.69E-52	2.39E-49	1026282
YP_001877479.1	6274303	4285.583647	0.539290772	0.00534348	0.054395861	1034186
YP_001877481.1	6274301	10138.11211	-0.481578868	0.006952525	0.0622647	1035676
YP_001877488.1	6274294	1723.540188	0.46167712	0.012751844	0.090672661	1043596
YP_001877519.1	6274261	4345.935193	-0.715088837	0.000143271	0.004944604	1081425
YP_001877527.1	6274253	2345.899274	-0.551886198	0.001310243	0.021738062	1090786
YP_001877572.1	6274204	909.0461847	0.539406797	0.01258858	0.090420508	1144360
YP_001877598.1	6274139	1630.167869	0.62807608	0.000959986	0.016979753	1181611
YP_001877647.1	6274073	10576.66162	-0.676005501	0.000039	0.002128385	1238246
YP_001877648.1	6274072	9340.092164	-0.444025976	0.005690826	0.056245637	1242515
YP_001877655.1	6274063	22103.09462	-0.608052474	0.001371096	0.022300013	1249991
YP_001877689.1	6274022	341.2563872	0.992530115	0.001458764	0.023192707	1293097
YP_001877690.1	6274021	495.76849	1.016492203	0.000709297	0.014702474	1293567
YP_001877790.1	6273825	8845.031971	-0.677191256	0.001292176	0.021738062	1418697
YP_001877816.1	6273750	20222.16953	-0.571467657	0.002383072	0.031811768	1445495
YP_001877824.1	6273760	2525.03526	-0.612402884	0.002767589	0.034965527	1457240
YP_001877850.1	6274716	524.1629752	-0.626592049	0.012243857	0.088846446	1493533
YP_001877888.1	6274884	8800.159609	-0.443945088	0.008126722	0.07011775	1544185
YP_001878011.1	6275750	471.4748137	-0.667234999	0.007355499	0.064646155	1682982
YP_001878012.1	6275718	35905.36205	-0.56007343	0.010424969	0.080170277	1683318
YP_001878146.1	6273666	502.3474463	0.816318882	0.002115521	0.029347671	1857064
YP_001878193.1	6275651	9610.498816	-0.722364337	0.000139141	0.004922115	1915359
YP_001878283.1	6275609	16838.84445	-2.056415948	2.19E-30	1.03E-27	2043845
YP_001878302.1	6274287	971.4700417	-0.568413294	0.013576188	0.094019021	2068761
YP_001878411.1	6275713	3500.75931	-0.78483641	0.00000389	0.000344418	2198164
YP_001878426.1	6275790	1535.753215	-0.678794933	0.000657754	0.013891381	2217835
YP_001878428.1	6273744	6558.7002	0.492218023	0.00200831	0.028164238	2222637
YP_001878590.1	6275724	3980.055615	0.608734135	0.000349137	0.009500561	2425874
YP_001878660.1	6274146	15819.44364	-0.929845556	0.00000794	0.00056196	2515550
YP_001878661.1	6274138	1340.89492	0.614891111	0.001430427	0.023000614	2518313
YP_001878662.1	6274122	4853.246878	0.573717664	0.001496456	0.023527612	2521055
YP_001878718.1	6274775	5692.070378	-0.408625347	0.013143558	0.092069974	2594717
YP_001877388.1	6274412	4417.397164	-0.598835625	0.000218115	0.006858521	908842
YP_001877834.1	6275772	1213.897899	-0.50980799	0.01050523	0.080350817	1475565

YP_001877798.1	6273835	560.6542977	-0.773686663	0.00238003	0.031811768	1427912
YP_001877386.1	6274414	652.4017154	0.680205587	0.002600053	0.033446132	905682
YP_001878545.1	6275107	4317.828763	-0.457381709	0.008961653	0.072024318	2368957
YP_001878288.1	6274585	4756.994847	-0.539348202	0.002985657	0.036397	2053033
YP_001877813.1	6273747	4704.952864	0.432799803	0.010373987	0.080170277	1443246
YP_001877595.1	6274148	5707.824718	-0.464205105	0.005922764	0.057402127	1178454
YP_001877267.1	6274140	441.7190964	-1.100820509	0.0000109	0.00073645	762902
YP_001878393.1	6275728	518.4442386	-0.610323999	0.014029961	0.096370847	2181989
YP_001877027.1	6274826	302.0101073	-0.929659482	0.00075684	0.014886231	488696
YP_001877272.1	6273984	851.9013765	-0.533065438	0.010692711	0.08134509	768948
YP_001878164.1	6273679	2678.60947	0.453444752	0.009243296	0.073068515	1878236
YP_001878447.1	6273724	554.0813846	-0.609996282	0.009103466	0.072367438	2251566
YP_001878541.1	6275132	3623.907399	-0.623996162	0.000134234	0.004870298	2365259
YP_001876658.1	6275189	2562.573115	-0.438389524	0.011096317	0.082253465	38259
YP_001876665.1	6275166	5008.166136	-0.516873808	0.001186868	0.020233951	51964
YP_001876673.1	6275149	434.9955508	0.831478873	0.002594052	0.033446132	62461
YP_001876676.1	6275137	328.8788329	0.937827942	0.001927347	0.027547438	64665
YP_001876762.1	6274869	1048.227826	0.931630055	0.000148431	0.00500072	169490
YP_001876766.1	6274800	1415.4067	-0.997615485	0.000000184	0.0000261	173694
YP_001876787.1	6275558	4756.287794	-0.743622932	0.0000696	0.003159302	200707
YP_001876831.1	6275331	1843.503829	-0.873352052	0.00000122	0.000123715	255650
YP_001876839.1	6275318	4339.374881	0.743347017	0.00000441	0.000366779	265829
YP_001876853.1	6275297	2348.760827	0.542654077	0.00250545	0.032826038	287811
YP_001876954.1	6275008	2883.249014	0.475771399	0.006410025	0.059672271	391336
YP_001876955.1	6275002	1386.90983	0.505656797	0.007884774	0.068447575	394158
YP_001876969.1	6274962	368.1806256	0.825549472	0.004312666	0.04767518	413055
YP_001877024.1	6274821	6447.644776	-0.610843165	0.004536017	0.049755535	486135
YP_001877029.1	6274828	646.476151	0.817456797	0.00043221	0.010644225	490756
YP_001877054.1	6275768	30731.59208	-0.814522433	0.000112378	0.004360606	519248
YP_001877069.1	6274760	477.8250822	0.801986539	0.008421051	0.070500284	535775
YP_001877140.1	6274823	17416.69401	-0.676712632	0.001622021	0.024679143	613855
YP_001877155.1	6275043	1690.726183	-0.452935853	0.01295355	0.091201929	631559
YP_001877162.1	6275128	5369.304257	-0.474581584	0.004928533	0.05192558	641820
YP_001877163.1	6275155	18030.19471	-0.538412136	0.008233742	0.070500284	642890
YP_001877169.1	6275278	3145.261244	0.742595638	0.000194558	0.006256807	649937
YP_001877208.1	6275681	5969.307107	-0.599621256	0.002410162	0.031872701	699073
YP_001877232.1	6274718	1196.447406	0.699179262	0.000565307	0.012498592	720918
YP_001877245.1	6274195	1025.934101	-0.55823594	0.005518244	0.055333332	735567
YP_001877276.1	6273980	776.8037591	-0.56775957	0.00899018	0.072024318	773602
YP_001877277.1	6273979	536.8055812	-0.686562916	0.004238913	0.04746065	774741
YP_001877305.1	6273928	117087.0011	-0.817183474	0.009693617	0.075365209	809148
YP_001877308.1	6273922	1583.614988	-0.512625823	0.005543766	0.055333332	814991
YP_001877318.1	6273901	3903.502151	-0.654052086	0.000722254	0.014702474	824865
YP_001877327.1	6273882	1774.288244	0.478601879	0.008410656	0.070500284	836235
YP_001877335.1	6273862	2582.486763	-0.936991815	0.0000000304	0.00000539	845810
YP_001877348.1	6273793	2185.825572	-0.586502614	0.006485897	0.059983953	860791
YP_001877352.1	6273783	8155.634799	0.443426971	0.007210816	0.063770656	865444
YP_001877383.1	6274417	2063.864204	-0.770000169	0.000344354	0.009500561	902001

YP_001877439.1	6274352	546.7656753	-0.72851958	0.004954031	0.05192558	973336
YP_001877470.1	6274313	539.053562	-0.871036087	0.000330395	0.009350179	1020760
YP_001877471.1	6274312	303.3004361	-0.9651465	0.000643967	0.013806257	1022488
YP_001877472.1	6274311	509.6665849	-0.837168166	0.000473291	0.011161771	1022954
YP_001877480.1	6274302	7055.718613	-0.440162661	0.006531953	0.060017617	1034862
YP_001877496.1	6274285	4373.07199	-1.080352532	2.77E-11	7.83E-09	1052357
YP_001877497.1	6274284	2696.887919	-1.091226777	0.000000003	0.000000606	1052721
YP_001877507.1	6274274	732.429613	-0.676985658	0.003859751	0.044402823	1066280
YP_001877518.1	6274262	2707.384337	-0.423382888	0.011805275	0.086105482	1080489
YP_001877522.1	6274258	512.8097587	-1.285809734	0.00000617	0.00048531	1085664
YP_001877578.1	6274192	1984.344354	-0.489575854	0.008370738	0.070500284	1151124
YP_001877593.1	6274152	28510.80923	0.708172896	0.000915164	0.016602012	1171299
YP_001877607.1	6274128	4094.326269	-0.521937867	0.001906894	0.027547438	1190851
YP_001877624.1	6274100	1897.460222	0.50577123	0.004652652	0.049875022	1209881
YP_001877632.1	6274092	730.3115748	-0.608633682	0.008472599	0.070500284	1217203
YP_001877635.1	6274089	1418.956893	-0.652857264	0.003304114	0.038961007	1220845
YP_001877672.1	6274045	1983.323127	0.719617453	0.0000506	0.002468565	1272008
YP_001877680.1	6274035	800.1609166	0.604531324	0.009687887	0.075365209	1281418
YP_001877712.1	6273996	1660.019202	-0.719727382	0.0000732	0.003159302	1320336
YP_001877750.1	6273894	20720.20766	0.542079257	0.003120883	0.037424149	1365798
YP_001877782.1	6273780	4820.118162	-0.527455432	0.001640561	0.024695679	1411344
YP_001877794.1	6273829	2320.075915	-0.568040801	0.008519822	0.070500284	1425003
YP_001877819.1	6273753	14523.11934	-1.349869335	2.23E-10	0.0000000527	1450497
YP_001877852.1	6275402	4279.838795	0.574124243	0.00042199	0.010644225	1495432
YP_001877873.1	6275566	898.5871249	0.564506987	0.008342735	0.070500284	1527967
YP_001877879.1	6275148	688.6998021	0.624032668	0.010846866	0.081984764	1534131
YP_001877882.1	6275520	2707.541979	0.843823286	0.00000264	0.000249489	1537129
YP_001877914.1	6275508	7754.606508	-0.515913948	0.008726127	0.071372657	1587603
YP_001877915.1	6275501	3178.515329	-0.566820774	0.006690793	0.061080466	1588598
YP_001877922.1	6274749	5037.059652	0.506141892	0.001579447	0.024559528	1596195
YP_001878010.1	6275679	26209.03744	-1.146685788	0.000000128	0.0000201	1680958
YP_001878016.1	6275648	19777.94119	-0.454841832	0.0089874	0.072024318	1689282
YP_001878029.1	6274504	1889.580321	-0.495748636	0.006251276	0.059307749	1712457
YP_001878070.1	6275658	2173.319014	-0.483935108	0.006287041	0.059307749	1759300
YP_001878100.1	6274565	344.3438005	1.153364378	0.0000434	0.002274172	1787041
YP_001878140.1	6273672	2511.982746	-0.462083519	0.012553875	0.090420508	1849236
YP_001878153.1	6273654	719.9904054	0.589997198	0.007498018	0.065491951	1864099
YP_001878189.1	6275593	434.8756028	-0.767581506	0.00219208	0.030114494	1910534
YP_001878200.1	6274430	2258.717359	-0.751990943	0.000278813	0.008219168	1923432
YP_001878204.1	6274451	673.7298318	-0.650005543	0.004649734	0.049875022	1926953
YP_001878246.1	6274641	378.6427164	1.021228036	0.000446953	0.010719294	1987924
YP_001878269.1	6274598	1128.97559	0.528786883	0.011102765	0.082253465	2023579
YP_001878312.1	6274528	507.3785001	-0.846522221	0.0004363	0.010644225	2081594
YP_001878349.1	6274612	1292.666143	0.895575069	0.000130005	0.004840981	2131594
YP_001878387.1	6274670	3798.769154	0.480273622	0.004154161	0.047404333	2175508
YP_001878465.1	6275795	3396.181297	0.435647243	0.013376395	0.093239407	2273148
YP_001878471.1	6275511	836.5901694	0.599460853	0.011417111	0.083705761	2280722
YP_001878497.1	6274496	1331.449698	-0.541376726	0.004203375	0.04746065	2308203

YP_001878613.1	6275625	1042.651632	-0.668201931	0.00077727	0.014886231	2455475
YP_001878640.1	6274770	1589.751925	0.549386773	0.005723938	0.056245637	2492611
YP_001878646.1	6275081	17742.60124	-0.628785654	0.001089415	0.018840749	2500653
YP_001878647.1	6274850	10197.42699	-0.77038431	0.0000182	0.001172128	2501280
YP_001878667.1	6274016	873.3333145	-0.789969761	0.00017857	0.005876187	2526716
YP_001878694.1	6273696	1333.217045	0.834584039	0.000294949	0.008517394	2558514
YP_001878701.1	6275497	436.9665539	0.759468174	0.002870195	0.035730109	2571045
YP_001878717.1	6273698	2607.19251	-0.578190745	0.000867138	0.016012132	2593123
YP_001878724.1	6274669	1147.366571	-0.477058875	0.014117344	0.096502619	2600936
YP_001878725.1	6274700	1094.435678	1.084534735	0.000000419	0.000052	2601525
YP_001878730.1	6275444	1066.071914	-0.59220244	0.00290386	0.035730109	2607696
YP_001878737.1	6275483	733.6781193	0.702192058	0.001321183	0.021738062	2615083
YP_001878741.1	6273736	28378.99174	0.732741904	0.000595313	0.012959495	2620771
YP_001878756.1	6274764	1627.629671	0.53937478	0.009009402	0.072024318	2645075
YP_001877830.1	6275575	1178.197337	0.535809722	0.00622489	0.059307749	1471661
YP_001878101.1	6275664	1653.656714	0.526462179	0.00581217	0.056718762	1788187
YP_001876657.1	6275193					
YP_001876723.1	6274974					
YP_001876723.1	6274974					
YP_001876723.1	6274974					
YP_001876723.1	6274974					
YP_001876723.1	6274974					
YP_001876825.1	6275340					
YP_001876825.1	6275340					
YP_001876825.1	6275340					
YP_001876825.1	6275340					
YP_001876913.1	6275131					
YP_001876992.1	6274901					
YP_001876992.1	6274901					
YP_001876992.1	6274901					
YP_001877178.1	6275557					
YP_001877178.1	6275557					
YP_001877271.1	6273985					
YP_001877272.1	6273984					
YP_001877277.1	6273979					
YP_001877348.1	6273793					
YP_001877414.1	6274378					
YP_001877414.1	6274378					
YP_001877414.1	6274378					
YP_001877414.1	6274378					
YP_001877414.1	6274378					
YP_001877423.1	6274368					
YP_001877423.1	6274368					
YP_001877423.1	6274368					
YP_001877423.1	6274368					
YP_001877423.1	6274368					
YP_001877430.1	6274361					
YP_001877430.1	6274361					

[illegible]

YP_001878288.1	6274585
YP_001878312.1	6274528
YP_001878312.1	6274528
YP_001878312.1	6274528
YP_001878312.1	6274528
YP_001878411.1	6275713
YP_001878455.1	6275480
YP_001878455.1	6275480
YP_001878465.1	6275795
YP_001878660.1	6274146
YP_001878660.1	6274146
YP_001878660.1	6274146
YP_001878737.1	6275483

end	strand	KO	KEGG pathway (N=56)	Overlapped KEGG pathway ID (N=22)
294519	+	K00688	ko00500	3
444637	-	K01580	ko00650	7
828954	+	NA	NA	NA
2445049	+	K01775	ko00473	NA
2447011	+	K01740	ko00270	NA
816815	-	K03671	NA	NA
1412719	+	K03098	NA	NA
773577	+	NA	NA	NA
615197	+	NA	NA	NA
38232	-	K01784	ko00052	15
1277251	+	K01251	ko00270	NA
1500299	-	K01711	ko00520	8
1696445	+	K00134	ko00010	14
661639	+	K03500	NA	NA
2006137	+	K01585	ko00330	6
1965198	-	K00600	ko01200	4
265701	-	K00156	ko00620	17
250483	+	K05606	ko01200	4
461275	-	K02956	ko03010	NA
656528	-	K02954	ko03010	NA
1441413	-	K02939	ko03010	NA
1869797	+	K02916	ko03010	NA
1870330	+	K02887	ko03010	NA
358230	-	K02965	ko03010	NA
292593	-	K00060	ko00260	NA
859473	+	K03979	NA	NA
2306474	-	K00380	ko00920	NA
124152	+	K00845	ko00010	14
280642	-	K00941	ko00730	NA
412878	-	K03798	NA	NA
658756	+	K01940	ko00220	12
702405	+	K00946	ko00730	NA
768925	+	K01928	ko00300	NA
836183	-	K03628	ko03018	NA
1029403	-	K00527	ko00230	NA
1275812	+	K00789	ko01230	9
2264379	-	K01938	ko01200	4
936739	-	K04567	ko00970	NA
2424054	-	K01667	ko00380	NA
940661	+	K03737	ko00010	14
952161	-	K01653	ko00290	22
1697824	+	K00927	ko00010	14
91850	+	K00991	ko00900	NA
150958	+	NA	NA	NA
173468	-	K01866	ko00970	NA
279124	-	K14445	NA	NA
350402	+	K01190	ko00052	15

363244	-	K02355	NA	NA
487847	+	K02536	ko00540	20
640160	+	K08301	NA	NA
647730	-	K03559	NA	NA
767412	+	K03587	ko00550	NA
814885	-	K01893	ko00970	NA
856180	-	NA	NA	NA
903042	-	NA	NA	NA
908637	-	K12308	ko00052	15
915841	+	NA	NA	NA
962135	+	K02338	ko00230	NA
973147	+	K01190	ko00052	15
1005962	-	K01689	ko00010	14
1026203	-	K14445	NA	NA
1027034	-	K04069	NA	NA
1034734	-	NA	NA	NA
1036824	-	K01179	ko00500	3
1044162	+	K02356	NA	NA
1082552	-	K12267	NA	NA
1091124	-	NA	NA	NA
1145004	+	K02428	ko00230	NA
1182426	+	K07051	NA	NA
1242442	-	K03046	ko00230	NA
1246453	-	K03043	ko00230	NA
1251175	-	K02358	NA	NA
1293504	+	NA	NA	NA
1295663	-	NA	NA	NA
1419977	-	K01689	ko00010	14
1447321	-	K01596	ko00010	14
1458352	-	K01735	ko00400	5
1494264	-	K01447	NA	NA
1545018	+	K03773	NA	NA
1683272	+	K04078	NA	NA
1684970	+	K04077	ko03018	NA
1857846	+	NA	NA	NA
1916003	-	K04564	ko04068	NA
2045851	+	K16092	NA	NA
2069255	-	K02217	NA	NA
2199642	-	K01176	ko00500	3
2218533	-	K06911	NA	NA
2223452	-	K01628	ko00051	NA
2428393	-	K01890	ko00970	NA
2517805	+	K03781	ko01200	4
2520964	-	NA	NA	NA
2521630	-	NA	NA	NA
2595913	+	K06282	ko00633	NA
910647	+	K03778	ko00620	17
1477763	-	K02343	ko00230	NA

1428970	-	K00971	ko00520	8
906335	+	NA	NA	NA
2370060	+	NA	NA	NA
2054421	+	K00382	ko00010	14
1443986	+	K03474	ko00750	18
1180412	-	K00239	ko00020	21
763357	+	K03925	NA	NA
2182795	-	NA	NA	NA
489484	-	K02049	NA	NA
770321	+	K01929	ko00300	NA
1881109	-	NA	NA	NA
2252543	-	K02031	NA	NA
2366440	+	K01787	ko00520	8
39353	-	NA	NA	NA
53448	+	NA	NA	NA
63240	-	NA	NA	NA
66170	+	NA	NA	NA
170860	-	NA	NA	NA
173915	+	NA	NA	NA
201033	+	NA	NA	NA
257146	+	NA	NA	NA
266431	-	NA	NA	NA
288308	+	NA	NA	NA
394161	-	K02004	NA	NA
394904	-	K02003	NA	NA
413852	-	NA	NA	NA
486770	+	K06142	NA	NA
491415	+	NA	NA	NA
520132	-	NA	NA	NA
536407	-	NA	NA	NA
614403	+	NA	NA	NA
632338	+	NA	NA	NA
642842	-	NA	NA	NA
646123	-	NA	NA	NA
650608	-	NA	NA	NA
700455	-	NA	NA	NA
721724	-	NA	NA	NA
737087	+	NA	NA	NA
774744	+	K03588	ko04112	NA
775865	+	K02563	ko00550	NA
812282	+	NA	NA	NA
816271	-	NA	NA	NA
825284	-	NA	NA	NA
836990	-	NA	NA	NA
847114	-	NA	NA	NA
861816	+	K01921	ko00473	NA
871260	-	NA	NA	NA
902486	-	K08999	NA	NA

974019	-	NA	NA	NA
1022373	-	K07085	NA	NA
1022967	-	K03413	ko02020	1
1024396	-	NA	NA	NA
1035437	+	NA	NA	NA
1052686	+	NA	NA	NA
1052909	+	NA	NA	NA
1066723	+	NA	NA	NA
1081052	+	NA	NA	NA
1086779	-	NA	NA	NA
1152998	+	NA	NA	NA
1177088	-	NA	NA	NA
1190979	-	NA	NA	NA
1210585	-	K08680	ko00130	11
1217976	-	K04083	NA	NA
1221495	-	NA	NA	NA
1272652	-	NA	NA	NA
1282308	+	NA	NA	NA
1320995	-	NA	NA	NA
1371773	+	NA	NA	NA
1412213	+	K07071	NA	NA
1425227	-	NA	NA	NA
1450940	+	NA	NA	NA
1496679	-	NA	NA	NA
1528656	-	NA	NA	NA
1534982	-	NA	NA	NA
1538814	-	NA	NA	NA
1588562	-	K01785	ko00010	14
1589077	-	K06077	NA	NA
1596515	-	NA	NA	NA
1682886	+	K04043	ko03018	NA
1690496	+	NA	NA	NA
1713290	+	NA	NA	NA
1759884	-	NA	NA	NA
1788090	-	NA	NA	NA
1849646	-	NA	NA	NA
1864479	+	K00330	ko00190	2
1911043	-	NA	NA	NA
1925207	-	K03770	NA	NA
1927837	-	NA	NA	NA
1988982	-	NA	NA	NA
2024574	-	NA	NA	NA
2082775	-	K01903	ko00020	21
2132610	+	K07271	NA	NA
2177031	+	NA	NA	NA
2275544	+	K01187	ko00052	15
2283049	+	NA	NA	NA
2308895	+	NA	NA	NA

2456950	+	NA	NA	NA
2494401	+	K03281	NA	NA
2500997	-	NA	NA	NA
2501651	-	NA	NA	NA
2527498	+	K01991	NA	NA
2560115	+	K02551	ko00130	11
2571692	+	NA	NA	NA
2594607	+	K07267	NA	NA
2601337	-	K09940	NA	NA
2602256	+	NA	NA	NA
2608184	+	NA	NA	NA
2616732	-	K12373	ko00520	8
2626509	+	NA	NA	NA
2646688	-	NA	NA	NA
1472377	+	NA	NA	NA
1788876	-	K05810	NA	NA

K01784	ko00520	8
K00845	ko00052	15
K00845	ko00500	3
K00845	ko00520	8
K00845	ko01200	4
K00845	ko00521	NA
K05606	ko00280	NA
K05606	ko00630	NA
K05606	ko00640	NA
K05606	ko00720	NA
K01190	ko00511	NA
K01580	ko00250	NA
K01580	ko00410	NA
K01580	ko00430	NA
K01940	ko01230	9
K01940	ko00250	NA
K01928	ko00550	NA
K01929	ko00550	NA
K02563	ko04112	NA
K01921	ko00550	NA
K03737	ko00020	21
K03737	ko00620	17
K03737	ko00650	7
K03737	ko01200	4
K03737	ko00720	NA
K01653	ko00650	7
K01653	ko00660	19
K01653	ko00770	16
K01653	ko01210	13
K01653	ko01230	9
K02338	ko00240	NA
K02338	ko03030	NA

K02338	ko03430	NA
K01190	ko00511	NA
K01689	ko01200	4
K01689	ko01230	9
K01689	ko00680	NA
K01689	ko03018	NA
K03413	ko02030	NA
K00527	ko00240	NA
K00239	ko00190	2
K00239	ko00650	7
K00239	ko01200	4
K00239	ko00720	NA
K03046	ko03020	NA
K03046	ko00240	NA
K03043	ko00240	NA
K03043	ko03020	NA
K00789	ko00270	NA
K01689	ko01200	4
K01689	ko01230	9
K01689	ko00680	NA
K01689	ko03018	NA
K00971	ko00051	NA
K01596	ko00020	21
K01596	ko00620	17
K01596	ko04068	NA
K01735	ko01230	9
K02343	ko00240	NA
K02343	ko03030	NA
K02343	ko03430	NA
K01711	ko00051	NA
K01785	ko00052	15
K00134	ko01200	4
K00134	ko01230	9
K00134	ko00710	NA
K00927	ko01200	4
K00927	ko01230	9
K00927	ko00710	NA
K00600	ko01230	9
K00600	ko00260	NA
K00600	ko00630	NA
K00600	ko00670	NA
K00600	ko00680	NA
K00382	ko00020	21
K00382	ko00620	17
K00382	ko01200	4
K00382	ko00260	NA
K00382	ko00280	NA
K00382	ko00630	NA

K00382	ko00640	NA
K01903	ko00660	19
K01903	ko01200	4
K01903	ko00640	NA
K01903	ko00720	NA
K01176	ko04973	NA
K01938	ko00670	NA
K01938	ko00720	NA
K01187	ko00500	3
K03781	ko00380	NA
K03781	ko00630	NA
K03781	ko04068	NA
K12373	ko00511	NA

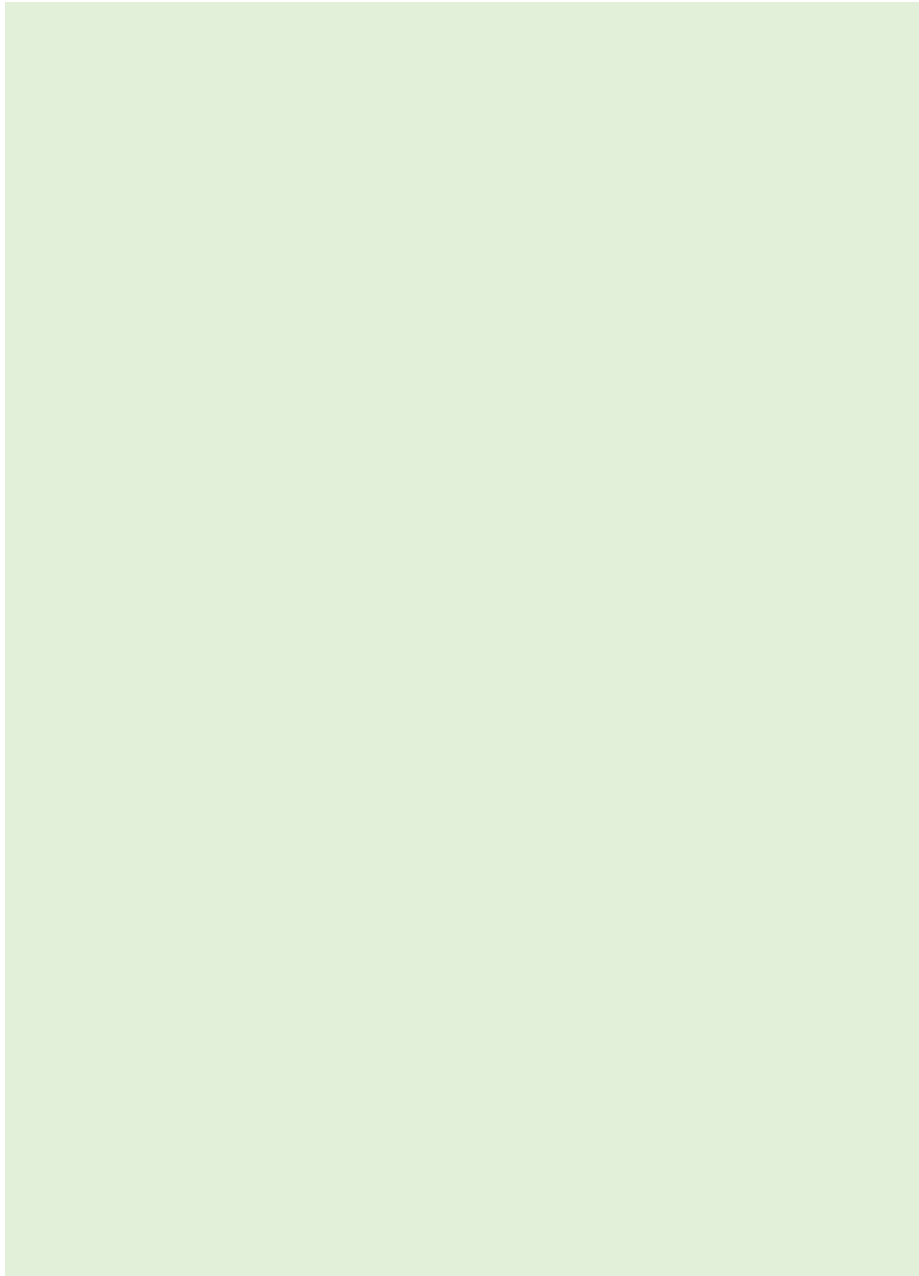
Annotation	Binding
product=alpha-glucan phosphorylase	Vitamin B6
product=glutamate decarboxylase	Vitamin B6
product=alanine--glyoxylate transaminase	Vitamin B6
product=alanine racemase	Vitamin B6
product=O-acetylhomoserine O-acetylserine sulfhydrylase	Vitamin B6
product=thioredoxin	Thioredoxin
product=lipocalin family protein	Small molecules
product=Peptidoglycan-binding LysM	Peptidoglycan
product=UBA THIF-type NAD FAD binding protein	NAD;FAD
product=NAD-dependent epimerase dehydratase	NAD
product=S-adenosyl-L-homocysteine hydrolase	NAD
product=GDP-mannose 4-epimerase	NAD
product=glyceraldehyde-3-phosphate dehydrogenase	NAD
product=sun protein	Methionine
product=arginine decarboxylase	Metal;Vitamin B6
product=Glycine hydroxymethyltransferase	Metal;Vitamin B6
product=thiamine pyrophosphate TPP binding domain	Metal;Vitamin B6
product=methylmalonyl-CoA epimerase	Metal;Vitamin B12
product=30S ribosomal protein S15	Metal;rRNA
product=30S ribosomal protein S14	Metal;rRNA
product=50S ribosomal protein L9	Metal;rRNA
product=50S ribosomal protein L35	Metal;rRNA
product=50S ribosomal protein L20	Metal;rRNA
product=30S ribosomal protein S19	Metal;rRNA
product=L-threonine 3-dehydrogenase	Metal;NAD
product=GTP-binding protein Obg CgtA	Metal;GTP
product=flavodoxin nitric oxide synthase	Metal;FMN
product=ROK family protein (glucokinase)	Metal;ATP
product=phosphomethylpyrimidine kinase	Metal;ATP
product=ATP-dependent metalloprotease FtsH	Metal;ATP
product=argininosuccinate synthase	Metal;ATP
product=thiamine-monophosphate kinase	Metal;ATP
product=UDP-N-acetylmuramyl tripeptide synthetase	Metal;ATP
product=transcription termination factor Rho	Metal;ATP
product=anaerobic ribonucleoside triphosphate reductase	Metal;ATP
product=Methionine adenosyltransferase	Metal;ATP
product=Formate--tetrahydrofolate ligase	Metal;ATP
product=lysyl-tRNA synthetase	Metal;ATP
product=tryptophanase	Metal; Vitamin B6
product=pyruvate flavodoxin ferredoxin oxidoreductase	Metal; Vitamin B1
product=acetolactate synthase small subunit	Metal; Vitamin B1
product=phosphoglycerate kinase	Metal; ATP
product=2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Metal
product=sulfatase	Metal
product=tyrosyl-tRNA synthetase	Metal
product=anion transporter	Metal
product=glycoside hydrolase family 2	Metal

product=translation elongation factor G	Metal
product=UDP-3-O-3-hydroxymyristoyl glucosamine N-acetyltransferase	Metal
product=ribonuclease Rne Rng family (ribonuclease G)	Metal
product=biopolymer transport protein ExbD TolR	Metal
product=peptidoglycan glycosyltransferase	Metal
product=asparaginyl-tRNA synthetase	Metal
product=glucan endo-1,3-beta-D-glucosidase	Metal
product=ferripyochelin binding protein fbp	Metal
product=beta-galactosidase	Metal
product=short-chain dehydrogenase reductase SDR	Metal
product=DNA polymerase III subunit beta	Metal
product=glycoside hydrolase family 2	Metal
product=Phosphopyruvate hydratase	Metal
product=anion transporter	Metal
product=anaerobic ribonucleoside-triphosphate reductase	Metal
product=rubrerythrin	Metal
product=peptidase M42 family protein	Metal
product=elongation factor P	Metal
product=methionine-R-sulfoxide reductase	Metal
product=cupin	Metal
product=Ham1 family protein	Metal
product=TatD-related deoxyribonuclease	Metal
product=DNA-directed RNA polymerase subunit beta'	Metal
product=DNA-directed RNA polymerase subunit beta	Metal
product=elongation factor Tu	Metal
product=iron dependent repressor	Metal
product=heavy metal translocating P-type ATPase	Metal
product=Phosphopyruvate hydratase	Metal
product=phosphoenolpyruvate carboxykinase	Metal
product=3-dehydroquinate synthase	Metal
product=N-acetylmuramoyl-L-alanine amidase family 2	Metal
product=FKBP-type peptidylprolyl isomerase	Metal
product=chaperonin Cpn10	Metal
product=chaperonin GroEL	Metal
product=G-D-S-L family lipolytic protein	Metal
product=Superoxide dismutase	Metal
product=TonB-dependent receptor	Metal
product=ferroxidase	Metal
product=alpha-amylase	Metal
product=Pirin domain-containing protein	Metal
product=class II aldolase adducin family protein	Metal
product=phenylalanyl-tRNA synthetase subunit beta	Metal
product=hydroperoxidase II (catalase)	Metal
product=cytochrome c assembly protein	Metal
product=rubrerythrin	Metal
product=hydrogenase NiFe small subunit HydA	Metal
product=D-lactate dehydrogenase	Metal
product=DNA polymerase III subunits gamma and tau	Metal

product=mannose-1-phosphate guanylyltransferase	GTP
product=nitroreductase	FMN
product=NADH:flavin oxidoreductase	FMN
product=dihydrolipoamide dehydrogenase	FAD;NAD
product=pyridoxine 5-phosphate synthase	FAD;FMN
product=succinate dehydrogenase flavoprotein subunit	FAD
product=MraZ protein	DNA
product=peptidase S24 and S26 domain-containing pro	DNA
product=ABC transporter	ATP
product=UDP-N-acetylmuramoylalanyl-D-glutamyl-26-d	ATP
product=ATP-dependent nuclease subunit B-like protei	ATP
product=oligopeptide dipeptide ABC transporter ATPas	ATP
product=N-acylglucosamine 2-epimerase	ATP
product=hypothetical protein	-
product=amino acid permease	-
product=hypothetical protein	-
product=MATE efflux family protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=succinate CoA transferase	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=ABC transporter	-
product=hypothetical protein	-
product=outer membrane chaperone Skp	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=3D domain-containing protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=cell cycle protein	-
product=UDP-N-acetylglucosamine-N-acetylmuramyl- p-	
product=outer membrane autotransporter barrel doma-	
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=amino acid permease	-
product=hypothetical protein	-
product=YD repeat protein	-
product=hypothetical protein	-

product=hypothetical protein	-
product=YidE YbjL duplication	-
product=response regulator receiver protein	-
product=cyclic nucleotide-binding protein	-
product=mucin-associated surface protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=ErfK YbiS YcfS YnhG family protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=YD repeat protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=disulfide bond chaperone	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=YD repeat protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=aldose 1-epimerase	-
product=17 kDa surface antigen	-
product=hypothetical protein	-
product=chaperone protein DnaK	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=OsmC family protein	-
product=NADH-ubiquinone plastoquinone oxidoreductase	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=dihydrouridine synthase DuS	-
product=hypothetical protein	-
product=succinyl-CoA synthetase beta subunit	-
product=LPS biosynthesis protein-like protein	-
product=hypothetical protein	-
product=Alpha-glucosidase	-
product=hypothetical protein	-
product=hypothetical protein	-

product=alkyl sulfatase-like protein	-
product=chloride channel protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=polysaccharide export protein	-
product=2-succinyl-6-hydroxy-24-cyclohexadiene-1-carl-	-
product=ErfK YbiS YcfS YnhG family protein	-
product=Carbohydrate-selective porin OprB	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=beta-N-acetylhexosaminidase	-
product=YD repeat protein	-
product=hypothetical protein	-
product=hypothetical protein	-
product=hypothetical protein	-



Supporting evidence for binding abilities

<http://www.ebi.ac.uk/interpro/entry/IPR011833>

https://en.wikipedia.org/wiki/Glutamate_decarboxylase

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.6.1.44>

<https://www.ebi.ac.uk/interpro/entry/IPR000821>

<http://www.uniprot.org/uniprot/A0A166YGG1>

<http://www.ebi.ac.uk/interpro/entry/IPR002345>

<https://www.ebi.ac.uk/interpro/entry/IPR015878>

<http://www.brenda-enzymes.org/enzyme.php?ecno=4.2.1.47>

<http://www.ebi.ac.uk/interpro/entry/IPR006424>

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.1.1.176>

<http://www.brenda-enzymes.org/enzyme.php?ecno=4.1.1.19>

<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>

https://en.wikipedia.org/wiki/Pyruvate_dehydrogenase

<http://www.uniprot.org/uniprot/Q96PE7>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/>; <http://rnajournal.cshlp.org/content/10/9/1366.long>

<https://www.ncbi.nlm.nih.gov/pubmed/2007567>

<https://www.ebi.ac.uk/interpro/entry/IPR014100>

<http://www.uniprot.org/uniprot/A0A101H7M1>

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.7.1.2>

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.7.4.7>

<http://www.uniprot.org/uniprot/POAAI3>

<http://www.brenda-enzymes.org/enzyme.php?ecno=6.3.4.5>

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.7.4.16>

<http://www.uniprot.org/uniprot/Q9CEN1>

<https://www.ncbi.nlm.nih.gov/pubmed/12578379>

<http://www.uniprot.org/uniprot/P28903>

<http://www.brenda-enzymes.org/enzyme.php?ecno=2.5.1.6>

<http://www.brenda-enzymes.info/enzyme.php?ecno=6.3.4.3#PDB>

<https://www.ebi.ac.uk/interpro/entry/IPR018149>

<https://en.wikipedia.org/wiki/Tryptophanase>

<https://www.ebi.ac.uk/interpro/entry/IPR004789>

https://en.wikipedia.org/wiki/Phosphoglycerate_kinase

<http://www.uniprot.org/uniprot/P69834>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2144072/>

<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>

http://www.genome.jp/dbget-bin/www_bget?ko:K14445

https://www.cazypedia.org/index.php/Glycoside_Hydrolase_Family_2

<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<http://www.brenda-enzymes.org/enzyme.php?ecno=2.3.1.191>
<http://www.uniprot.org/uniprot/POA9J0>
<https://www.ebi.ac.uk/interpro/entry/IPR003400>
<http://www.brenda-enzymes.org/enzyme.php?ecno=2.4.1.129>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<http://www.brenda-enzymes.org/enzyme.php?ecno=3.2.1.39>

<http://www.uniprot.org/uniprot/P00722>
<http://www.rcsb.org/pdb/explore.do?structureId=3PK0>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
https://www.cazypedia.org/index.php/Glycoside_Hydrolase_Family_2
<https://en.wikipedia.org/wiki/Enolase>

<https://www.ebi.ac.uk/interpro/entry/IPR012838>
<https://www.ebi.ac.uk/interpro/entry/IPR003251>
<http://merops.sanger.ac.uk/cgi-bin/famsum?family=m42>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<http://www.uniprot.org/uniprot/Q9NZV6>
<http://www.intechopen.com/books/on-biomimetics/modeling-the-metal-binding-site-in-cupin-proteins>
<http://www.cathacyc.org/ECOLI/NEW-IMAGE?type=ENZYME&object=CPLX0-7826>
<https://www.ebi.ac.uk/interpro/entry/IPR001130>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<https://www.ncbi.nlm.nih.gov/pubmed/6268521>

<https://en.wikipedia.org/wiki/Enolase>
https://en.wikipedia.org/wiki/Phosphoenolpyruvate_carboxylase
<http://www.sciencedirect.com/science/article/pii/S0031942280851090>
<http://www.uniprot.org/uniprot/Q81WA9>
<https://ecocyc.org/gene?orgid=ECOLI&id=EG11663>
<https://www.ncbi.nlm.nih.gov/pubmed/11477217>
<http://www.nature.com/nature/journal/v388/n6644/full/388741a0.html>
<http://www.uniprot.org/uniprot/A3DDK4>
https://en.wikipedia.org/wiki/Superoxide_dismutase
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3108441/>

<https://en.wikipedia.org/wiki/Alpha-amylase>
<http://www.uniprot.org/uniprot/I9W879>
<http://www.uniprot.org/uniprot/Q10WS4>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>
<https://www.ebi.ac.uk/interpro/entry/IPR002226>
<https://www.ebi.ac.uk/interpro/entry/IPR002541>
<https://en.wikipedia.org/wiki/Rubryerythrin>

<https://www.ncbi.nlm.nih.gov/pubmed/7074089>
<http://biologydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27>

<http://www.uniprot.org/uniprot/Q01410>
<http://www.ebi.ac.uk/interpro/entry/IPR000415>
<https://www.ebi.ac.uk/interpro/entry/IPR001155>
https://en.wikipedia.org/wiki/Dihydrolipoamide_dehydrogenase
<http://www.brenda-enzymes.org/enzyme.php?ecno=1.4.3.5>

<http://www.uniprot.org/uniprot/P22186>
<http://www.uniprot.org/uniprot/L2ENA7>
<http://www.uniprot.org/uniprot/K0DJQ3>
<http://www.uniprot.org/uniprot/A0A178U0X2>
<http://www.uniprot.org/uniprot/A0A163EZ29>
<http://www.uniprot.org/uniprot/Q07ZZ1>
<http://www.brenda-enzymes.org/enzyme.php?ecno=5.1.3.8>

Gene

gi|319434547|ref|NZ_GL622724.1|:c673617-672475
gi|319434549|ref|NZ_GL622726.1|:c199413-198031
gi|319434547|ref|NZ_GL622724.1|:c674108-673626
gi|319434549|ref|NZ_GL622726.1|:153514-155058
gi|319434549|ref|NZ_GL622726.1|:153016-153420
gi|319434549|ref|NZ_GL622726.1|:47254-47913
gi|319434547|ref|NZ_GL622724.1|:c45910-45038
gi|319434552|ref|NZ_GL622729.1|:80325-80888
gi|319434552|ref|NZ_GL622729.1|:80888-82561
gi|319434549|ref|NZ_GL622726.1|:694457-695188
gi|319434549|ref|NZ_GL622726.1|:c129638-127227
gi|319434548|ref|NZ_GL622725.1|:c168910-168224
gi|319434549|ref|NZ_GL622726.1|:c643162-642158
gi|319434552|ref|NZ_GL622729.1|:4380-5561
gi|319434547|ref|NZ_GL622724.1|:c1081211-1080723
gi|319434548|ref|NZ_GL622725.1|:c178999-176399
gi|319434548|ref|NZ_GL622725.1|:734449-734925
gi|319434549|ref|NZ_GL622726.1|:245900-246655
gi|319434549|ref|NZ_GL622726.1|:464685-466352
gi|319434547|ref|NZ_GL622724.1|:c43798-42746
gi|319434554|ref|NZ_GL622731.1|:c36318-34249
gi|319434550|ref|NZ_GL622727.1|:c155320-155018
gi|319434549|ref|NZ_GL622726.1|:22827-23627
gi|319434547|ref|NZ_GL622724.1|:517196-521227
gi|319434548|ref|NZ_GL622725.1|:17434-18822
gi|319434550|ref|NZ_GL622727.1|:c10029-7699
gi|319434548|ref|NZ_GL622725.1|:c77648-76110
gi|319434551|ref|NZ_GL622728.1|:c100764-99832
gi|319434551|ref|NZ_GL622728.1|:175267-175818
gi|319434549|ref|NZ_GL622726.1|:64460-66181
gi|319434548|ref|NZ_GL622725.1|:438986-440197
gi|319434547|ref|NZ_GL622724.1|:c26725-25826
gi|319434547|ref|NZ_GL622724.1|:c989965-988946
gi|319434549|ref|NZ_GL622726.1|:72010-73191
gi|319434549|ref|NZ_GL622726.1|:660286-661401
gi|319434547|ref|NZ_GL622724.1|:723204-724274
gi|319434549|ref|NZ_GL622726.1|:c652625-652242
gi|319434549|ref|NZ_GL622726.1|:c383458-381908
gi|319434550|ref|NZ_GL622727.1|:c14567-13236
gi|319434548|ref|NZ_GL622725.1|:c24288-23614
gi|319434549|ref|NZ_GL622726.1|:c294193-292922
gi|319434549|ref|NZ_GL622726.1|:672040-673314
gi|319434549|ref|NZ_GL622726.1|:c445824-441439
gi|319434547|ref|NZ_GL622724.1|:1178441-1179370
gi|319434550|ref|NZ_GL622727.1|:459993-461768
gi|319434549|ref|NZ_GL622726.1|:745055-747472
gi|319434552|ref|NZ_GL622729.1|:c141210-139993

Genbank

Dbxref=Genbank:ZP_07943205.1
Dbxref=Genbank:ZP_07944814.1
Dbxref=Genbank:ZP_07943206.1
Dbxref=Genbank:ZP_07944781.1
Dbxref=Genbank:ZP_07944780.1
Dbxref=Genbank:ZP_07944692.1
Dbxref=Genbank:ZP_07942681.1
Dbxref=Genbank:ZP_07945979.1
Dbxref=Genbank:ZP_07945980.1
Dbxref=Genbank:ZP_07945204.1
Dbxref=Genbank:ZP_07944756.1
Dbxref=Genbank:ZP_07943770.1
Dbxref=Genbank:ZP_07945158.1
Dbxref=Genbank:ZP_07945923.1
Dbxref=Genbank:ZP_07943523.1
Dbxref=Genbank:ZP_07943778.1
Dbxref=Genbank:ZP_07944248.1
Dbxref=Genbank:ZP_07944856.1
Dbxref=Genbank:ZP_07945014.1
Dbxref=Genbank:ZP_07942679.1
Dbxref=Genbank:ZP_07946164.1
Dbxref=Genbank:ZP_07945389.1
Dbxref=Genbank:ZP_07944656.1
Dbxref=Genbank:ZP_07943092.1
Dbxref=Genbank:ZP_07943647.1
Dbxref=Genbank:ZP_07945281.1
Dbxref=Genbank:ZP_07943704.1
Dbxref=Genbank:ZP_07945791.1
Dbxref=Genbank:ZP_07945849.1
Dbxref=Genbank:ZP_07944710.1
Dbxref=Genbank:ZP_07943981.1
Dbxref=Genbank:ZP_07942667.1
Dbxref=Genbank:ZP_07943448.1
Dbxref=Genbank:ZP_07944715.1
Dbxref=Genbank:ZP_07945174.1
Dbxref=Genbank:ZP_07943235.1
Dbxref=Genbank:ZP_07945168.1
Dbxref=Genbank:ZP_07944955.1
Dbxref=Genbank:ZP_07945284.1
Dbxref=Genbank:ZP_07943655.1
Dbxref=Genbank:ZP_07944891.1
Dbxref=Genbank:ZP_07945184.1
Dbxref=Genbank:ZP_07945001.1
Dbxref=Genbank:ZP_07943609.1
Dbxref=Genbank:ZP_07945655.1
Dbxref=Genbank:ZP_07945243.1
Dbxref=Genbank:ZP_07946021.1

gi|319434549|ref|NZ_GL622726.1|:c130411-129632
gi|319434548|ref|NZ_GL622725.1|:c42673-42233
gi|319434549|ref|NZ_GL622726.1|:c131052-130405
gi|319434547|ref|NZ_GL622724.1|:c178790-177219
gi|319434547|ref|NZ_GL622724.1|:792677-793264
gi|319434548|ref|NZ_GL622725.1|:c53829-53638
gi|319434549|ref|NZ_GL622726.1|:c326541-324958
gi|319434549|ref|NZ_GL622726.1|:457720-458643
gi|319434548|ref|NZ_GL622725.1|:c1069913-1068717
gi|319434548|ref|NZ_GL622725.1|:c725517-724516
gi|319434547|ref|NZ_GL622724.1|:c736495-736037
gi|319434547|ref|NZ_GL622724.1|:977935-981108
gi|319434548|ref|NZ_GL622725.1|:c1068661-1068188
gi|319434548|ref|NZ_GL622725.1|:c112657-111575
gi|319434554|ref|NZ_GL622731.1|:45781-46887
gi|319434547|ref|NZ_GL622724.1|:976727-977923
gi|319434549|ref|NZ_GL622726.1|:770349-771239
gi|319434549|ref|NZ_GL622726.1|:c244996-244352
gi|319434547|ref|NZ_GL622724.1|:1156900-1158159
gi|319434547|ref|NZ_GL622724.1|:c807340-806414
gi|319434548|ref|NZ_GL622725.1|:c387927-386779
gi|319434549|ref|NZ_GL622726.1|:c743433-741664
gi|319434547|ref|NZ_GL622724.1|:695698-697683
gi|319434547|ref|NZ_GL622724.1|:c797774-796386
gi|319434549|ref|NZ_GL622726.1|:720513-724958
gi|319434550|ref|NZ_GL622727.1|:c154741-154226
gi|319434549|ref|NZ_GL622726.1|:c391418-390474
gi|319434547|ref|NZ_GL622724.1|:1156157-1156783
gi|319434547|ref|NZ_GL622724.1|:981105-982523
gi|319434550|ref|NZ_GL622727.1|:166062-167105
gi|319434549|ref|NZ_GL622726.1|:51248-52300
gi|319434551|ref|NZ_GL622728.1|:8820-10121
gi|319434548|ref|NZ_GL622725.1|:93724-94410
gi|319434548|ref|NZ_GL622725.1|:258208-259746
gi|319434549|ref|NZ_GL622726.1|:c6153-5572
gi|319434551|ref|NZ_GL622728.1|:c76071-74125
gi|319434548|ref|NZ_GL622725.1|:c87310-84548
gi|319434548|ref|NZ_GL622725.1|:1496-2050
gi|319434549|ref|NZ_GL622726.1|:c634553-632841
gi|319434549|ref|NZ_GL622726.1|:c595391-594942
gi|319434549|ref|NZ_GL622726.1|:125449-125898
gi|319434548|ref|NZ_GL622725.1|:c51496-50753
gi|319434547|ref|NZ_GL622724.1|:350115-351659
gi|319434550|ref|NZ_GL622727.1|:172633-173208
gi|319434555|ref|NZ_GL622732.1|:c18125-17808
gi|319434548|ref|NZ_GL622725.1|:1091783-1092538
gi|319434549|ref|NZ_GL622726.1|:134062-135513
gi|319434549|ref|NZ_GL622726.1|:579174-579632

Dbxref=Genbank:ZP_07944757.1
Dbxref=Genbank:ZP_07943669.1
Dbxref=Genbank:ZP_07944758.1
Dbxref=Genbank:ZP_07942775.1
Dbxref=Genbank:ZP_07943282.1
Dbxref=Genbank:ZP_07943681.1
Dbxref=Genbank:ZP_07944918.1
Dbxref=Genbank:ZP_07945010.1
Dbxref=Genbank:ZP_07944551.1
Dbxref=Genbank:ZP_07944238.1
Dbxref=Genbank:ZP_07943241.1
Dbxref=Genbank:ZP_07943439.1
Dbxref=Genbank:ZP_07944550.1
Dbxref=Genbank:ZP_07943724.1
Dbxref=Genbank:ZP_07946176.1
Dbxref=Genbank:ZP_07943438.1
Dbxref=Genbank:ZP_07945266.1
Dbxref=Genbank:ZP_07944854.1
Dbxref=Genbank:ZP_07943591.1
Dbxref=Genbank:ZP_07943294.1
Dbxref=Genbank:ZP_07943946.1
Dbxref=Genbank:ZP_07945241.1
Dbxref=Genbank:ZP_07943222.1
Dbxref=Genbank:ZP_07943286.1
Dbxref=Genbank:ZP_07945225.1
Dbxref=Genbank:ZP_07945387.1
Dbxref=Genbank:ZP_07944961.1
Dbxref=Genbank:ZP_07943590.1
Dbxref=Genbank:ZP_07943440.1
Dbxref=Genbank:ZP_07945402.1
Dbxref=Genbank:ZP_07944697.1
Dbxref=Genbank:ZP_07945714.1
Dbxref=Genbank:ZP_07943714.1
Dbxref=Genbank:ZP_07943844.1
Dbxref=Genbank:ZP_07944642.1
Dbxref=Genbank:ZP_07945771.1
Dbxref=Genbank:ZP_07943710.1
Dbxref=Genbank:ZP_07943633.1
Dbxref=Genbank:ZP_07945150.1
Dbxref=Genbank:ZP_07945121.1
Dbxref=Genbank:ZP_07944753.1
Dbxref=Genbank:ZP_07943678.1
Dbxref=Genbank:ZP_07942945.1
Dbxref=Genbank:ZP_07945408.1
Dbxref=Genbank:ZP_07946229.1
Dbxref=Genbank:ZP_07944565.1
Dbxref=Genbank:ZP_07944761.1
Dbxref=Genbank:ZP_07945107.1

gi|319434549|ref|NZ_GL622726.1|:c440293-439262
gi|319434549|ref|NZ_GL622726.1|:c37709-37428
gi|319434549|ref|NZ_GL622726.1|:615259-615483
gi|319434549|ref|NZ_GL622726.1|:90447-90965
gi|319434549|ref|NZ_GL622726.1|:c439249-437585
gi|319434548|ref|NZ_GL622725.1|:c327307-323738
gi|319434549|ref|NZ_GL622726.1|:c324038-323268
gi|319434549|ref|NZ_GL622726.1|:c26735-26352
gi|319434550|ref|NZ_GL622727.1|:212553-213944
gi|319434555|ref|NZ_GL622732.1|:c24695-23409
gi|319434547|ref|NZ_GL622724.1|:1162948-1163952
gi|319434547|ref|NZ_GL622724.1|:956557-957474
gi|319434550|ref|NZ_GL622727.1|:210370-211659
gi|319434549|ref|NZ_GL622726.1|:c35827-35561
gi|319434549|ref|NZ_GL622726.1|:188469-189110
gi|319434549|ref|NZ_GL622726.1|:132727-134043
gi|319434549|ref|NZ_GL622726.1|:296465-297034
gi|319434548|ref|NZ_GL622725.1|:c50632-50399
gi|319434550|ref|NZ_GL622727.1|:c315574-315017
gi|319434547|ref|NZ_GL622724.1|:1200734-1201693
gi|319434549|ref|NZ_GL622726.1|:c472159-471407
gi|319434549|ref|NZ_GL622726.1|:579784-580359
gi|319434548|ref|NZ_GL622725.1|:661376-662143
gi|319434548|ref|NZ_GL622725.1|:604368-605372
gi|319434549|ref|NZ_GL622726.1|:c28821-28432
gi|319434547|ref|NZ_GL622724.1|:c926999-925476
gi|319434548|ref|NZ_GL622725.1|:744061-744909
gi|319434548|ref|NZ_GL622725.1|:c766757-766080
gi|319434555|ref|NZ_GL622732.1|:c1378-119
gi|319434551|ref|NZ_GL622728.1|:1831-2868
gi|319434548|ref|NZ_GL622725.1|:612248-613939
gi|319434550|ref|NZ_GL622727.1|:428438-428980
gi|319434548|ref|NZ_GL622725.1|:1095522-1096601
gi|319434548|ref|NZ_GL622725.1|:605509-606597
gi|319434547|ref|NZ_GL622724.1|:390532-391974
gi|319434547|ref|NZ_GL622724.1|:1119511-1120257
gi|319434547|ref|NZ_GL622724.1|:c821643-821350
gi|319434554|ref|NZ_GL622731.1|:c76463-75699
gi|319434548|ref|NZ_GL622725.1|:c67605-67114
gi|319434547|ref|NZ_GL622724.1|:c577521-576985
gi|319434550|ref|NZ_GL622727.1|:c30430-29885
gi|319434547|ref|NZ_GL622724.1|:612586-614787
gi|319434549|ref|NZ_GL622726.1|:639416-640399
gi|319434548|ref|NZ_GL622725.1|:192433-193176
gi|319434549|ref|NZ_GL622726.1|:273715-274485
gi|319434548|ref|NZ_GL622725.1|:927683-928189
gi|319434555|ref|NZ_GL622732.1|:c21847-20933
gi|319434547|ref|NZ_GL622724.1|:c745373-744447

Dbxref=Genbank:ZP_07944999.1
Dbxref=Genbank:ZP_07944682.1
Dbxref=Genbank:ZP_07945137.1
Dbxref=Genbank:ZP_07944729.1
Dbxref=Genbank:ZP_07944998.1
Dbxref=Genbank:ZP_07943899.1
Dbxref=Genbank:ZP_07944916.1
Dbxref=Genbank:ZP_07944659.1
Dbxref=Genbank:ZP_07945441.1
Dbxref=Genbank:ZP_07946235.1
Dbxref=Genbank:ZP_07943596.1
Dbxref=Genbank:ZP_07943419.1
Dbxref=Genbank:ZP_07945438.1
Dbxref=Genbank:ZP_07944677.1
Dbxref=Genbank:ZP_07944807.1
Dbxref=Genbank:ZP_07944760.1
Dbxref=Genbank:ZP_07944894.1
Dbxref=Genbank:ZP_07943677.1
Dbxref=Genbank:ZP_07945519.1
Dbxref=Genbank:ZP_07943630.1
Dbxref=Genbank:ZP_07945019.1
Dbxref=Genbank:ZP_07945108.1
Dbxref=Genbank:ZP_07944169.1
Dbxref=Genbank:ZP_07944112.1
Dbxref=Genbank:ZP_07944662.1
Dbxref=Genbank:ZP_07943396.1
Dbxref=Genbank:ZP_07944262.1
Dbxref=Genbank:ZP_07944281.1
Dbxref=Genbank:ZP_07946213.1
Dbxref=Genbank:ZP_07945709.1
Dbxref=Genbank:ZP_07944123.1
Dbxref=Genbank:ZP_07945622.1
Dbxref=Genbank:ZP_07944570.1
Dbxref=Genbank:ZP_07944113.1
Dbxref=Genbank:ZP_07942976.1
Dbxref=Genbank:ZP_07943555.1
Dbxref=Genbank:ZP_07943308.1
Dbxref=Genbank:ZP_07946201.1
Dbxref=Genbank:ZP_07943693.1
Dbxref=Genbank:ZP_07943133.1
Dbxref=Genbank:ZP_07945295.1
Dbxref=Genbank:ZP_07943162.1
Dbxref=Genbank:ZP_07945156.1
Dbxref=Genbank:ZP_07943793.1
Dbxref=Genbank:ZP_07944877.1
Dbxref=Genbank:ZP_07944434.1
Dbxref=Genbank:ZP_07946232.1
Dbxref=Genbank:ZP_07943244.1

gi|319434549|ref|NZ_GL622726.1|:c755534-755226
gi|319434547|ref|NZ_GL622724.1|:c848294-847593
gi|319434550|ref|NZ_GL622727.1|:211677-211820
gi|319434549|ref|NZ_GL622726.1|:c371616-371428
gi|319434550|ref|NZ_GL622727.1|:c31682-30675
gi|319434551|ref|NZ_GL622728.1|:49280-49723
gi|319434548|ref|NZ_GL622725.1|:622029-622403
gi|319434549|ref|NZ_GL622726.1|:c38838-38551
gi|319434549|ref|NZ_GL622726.1|:c27768-26725
gi|319434547|ref|NZ_GL622724.1|:c1035189-1034932
gi|319434548|ref|NZ_GL622725.1|:c609337-608909
gi|319434554|ref|NZ_GL622731.1|:9531-10952
gi|319434549|ref|NZ_GL622726.1|:c292684-292301
gi|319434547|ref|NZ_GL622724.1|:c1143567-1142779
gi|319434550|ref|NZ_GL622727.1|:503558-504640
gi|319434549|ref|NZ_GL622726.1|:c36017-35832
gi|319434551|ref|NZ_GL622728.1|:17113-17562
gi|319434549|ref|NZ_GL622726.1|:c29417-29304
gi|319434548|ref|NZ_GL622725.1|:928200-928610
gi|319434547|ref|NZ_GL622724.1|:878594-879136
gi|319434548|ref|NZ_GL622725.1|:c934445-933417
gi|319434548|ref|NZ_GL622725.1|:c652024-651488
gi|319434548|ref|NZ_GL622725.1|:748267-749886
gi|319434549|ref|NZ_GL622726.1|:644941-645819
gi|319434550|ref|NZ_GL622727.1|:184616-184993
gi|319434550|ref|NZ_GL622727.1|:c99682-99098
gi|319434550|ref|NZ_GL622727.1|:429143-429640
gi|319434548|ref|NZ_GL622725.1|:740174-741892
gi|319434547|ref|NZ_GL622724.1|:1164057-1164629
gi|319434547|ref|NZ_GL622724.1|:249747-250253
gi|319434548|ref|NZ_GL622725.1|:c785603-784782
gi|319434549|ref|NZ_GL622726.1|:c29286-28918
gi|319434549|ref|NZ_GL622726.1|:c704467-703496
gi|319434547|ref|NZ_GL622724.1|:1121118-1121483
gi|319434554|ref|NZ_GL622731.1|:7787-9235
gi|319434554|ref|NZ_GL622731.1|:c87747-87478
gi|319434548|ref|NZ_GL622725.1|:664015-665838
gi|319434548|ref|NZ_GL622725.1|:c183026-182550
gi|319434549|ref|NZ_GL622726.1|:c35550-35182
gi|319434548|ref|NZ_GL622725.1|:612015-612248
gi|319434548|ref|NZ_GL622725.1|:c563314-560876
gi|319434547|ref|NZ_GL622724.1|:244396-246078
gi|319434547|ref|NZ_GL622724.1|:248661-249695
gi|319434548|ref|NZ_GL622725.1|:672998-673300
gi|319434549|ref|NZ_GL622726.1|:295051-296115
gi|319434549|ref|NZ_GL622726.1|:615499-615762
gi|319434548|ref|NZ_GL622725.1|:99723-100127
gi|319434547|ref|NZ_GL622724.1|:247482-248513

Dbxref=Genbank:ZP_07945252.1
Dbxref=Genbank:ZP_07943331.1
Dbxref=Genbank:ZP_07945439.1
Dbxref=Genbank:ZP_07944949.1
Dbxref=Genbank:ZP_07945296.1
Dbxref=Genbank:ZP_07945749.1
Dbxref=Genbank:ZP_07944131.1
Dbxref=Genbank:ZP_07944684.1
Dbxref=Genbank:ZP_07944660.1
Dbxref=Genbank:ZP_07943487.1
Dbxref=Genbank:ZP_07944117.1
Dbxref=Genbank:ZP_07946143.1
Dbxref=Genbank:ZP_07944890.1
Dbxref=Genbank:ZP_07943577.1
Dbxref=Genbank:ZP_07945689.1
Dbxref=Genbank:ZP_07944678.1
Dbxref=Genbank:ZP_07945722.1
Dbxref=Genbank:ZP_07944664.1
Dbxref=Genbank:ZP_07944435.1
Dbxref=Genbank:ZP_07943357.1
Dbxref=Genbank:ZP_07944440.1
Dbxref=Genbank:ZP_07944159.1
Dbxref=Genbank:ZP_07944267.1
Dbxref=Genbank:ZP_07945161.1
Dbxref=Genbank:ZP_07945418.1
Dbxref=Genbank:ZP_07945348.1
Dbxref=Genbank:ZP_07945623.1
Dbxref=Genbank:ZP_07944259.1
Dbxref=Genbank:ZP_07943597.1
Dbxref=Genbank:ZP_07942857.1
Dbxref=Genbank:ZP_07944297.1
Dbxref=Genbank:ZP_07944663.1
Dbxref=Genbank:ZP_07945212.1
Dbxref=Genbank:ZP_07943557.1
Dbxref=Genbank:ZP_07946142.1
Dbxref=Genbank:ZP_07946209.1
Dbxref=Genbank:ZP_07944171.1
Dbxref=Genbank:ZP_07943783.1
Dbxref=Genbank:ZP_07944676.1
Dbxref=Genbank:ZP_07944122.1
Dbxref=Genbank:ZP_07944083.1
Dbxref=Genbank:ZP_07942853.1
Dbxref=Genbank:ZP_07942856.1
Dbxref=Genbank:ZP_07944179.1
Dbxref=Genbank:ZP_07944893.1
Dbxref=Genbank:ZP_07945138.1
Dbxref=Genbank:ZP_07943718.1
Dbxref=Genbank:ZP_07942855.1

gi 319434555 ref NZ_GL622732.1 :c24996-24697	Dbxref=Genbank:ZP_07946236.1
gi 319434548 ref NZ_GL622725.1 :1073329-1074429	Dbxref=Genbank:ZP_07944556.1
gi 319434548 ref NZ_GL622725.1 :749995-750561	Dbxref=Genbank:ZP_07944268.1
gi 319434548 ref NZ_GL622725.1 :c65896-65069	Dbxref=Genbank:ZP_07943691.1
gi 319434548 ref NZ_GL622725.1 :1071459-1072544	Dbxref=Genbank:ZP_07944553.1
gi 319434547 ref NZ_GL622724.1 :1151886-1153328	Dbxref=Genbank:ZP_07943586.1
gi 319434548 ref NZ_GL622725.1 :1072766-1073341	Dbxref=Genbank:ZP_07944555.1
gi 319434547 ref NZ_GL622724.1 :c171378-170779	Dbxref=Genbank:ZP_07942769.1
gi 319434547 ref NZ_GL622724.1 :c172593-171460	Dbxref=Genbank:ZP_07942770.1

baseMean	log2FoldChange	pvalue	padj	Start	End	Strand
466.8564282	3.04680426	1.18E-24	2.15E-21	672475	673617	-
195.8997013	2.581940241	4.15E-13	2.53E-10	198031	199413	-
154.6254288	2.421841692	1.42E-10	3.25E-08	673626	674108	-
186.0574428	1.720601135	1.48E-06	0.000117369	153514	155058	+
160.341329	1.532366509	1.33E-05	0.000604244	153016	153420	+
489.1436227	1.511824377	8.04E-08	8.84E-06	47254	47913	+
821.3162221	1.423503359	2.12E-09	3.87E-07	45038	45910	-
930.9561331	1.227996165	6.86E-09	1.14E-06	80325	80888	+
212.8819895	1.13819764	0.000555245	0.013014094	80888	82561	+
153.226975	1.125638947	0.001701121	0.029062146	694457	695188	+
1995.052906	1.106882187	8.22E-08	8.84E-06	127227	129638	-
134.9458963	1.100950615	0.002288133	0.035148806	168224	168910	-
468.8026128	1.040176938	8.37E-05	0.003000077	642158	643162	-
154.2665691	1.031270464	0.003017559	0.042431524	4380	5561	+
281.9447461	1.018623998	0.000505713	0.01283949	1080723	1081211	-
494.011249	1.008648408	6.03E-05	0.0022953	176399	178999	-
215.69094	0.996447142	0.001611674	0.027793779	734449	734925	+
363.9110274	0.99291366	0.000398885	0.010759183	245900	246655	+
2509.993611	0.972440054	1.79E-06	0.000136569	464685	466352	+
287.5440307	0.957371812	0.001093827	0.021733872	42746	43798	-
1137.259845	0.941399328	4.93E-06	0.000281532	34249	36318	-
2806.15836	0.89802298	1.34E-06	0.000111204	155018	155320	-
559.7830901	0.888946753	0.000179717	0.00608376	22827	23627	+
342.2547367	0.884272778	0.002451817	0.037034823	517196	521227	+
1367.304419	0.881972755	1.27E-05	0.000603768	17434	18822	+
660.6786198	0.879651345	0.00031468	0.009250061	7699	10029	-
230.9715954	0.870180414	0.004866037	0.05930077	76110	77648	-
288.983045	0.869758177	0.004125839	0.052741494	99832	100764	-
258.6056846	0.869215816	0.00465533	0.057866058	175267	175818	+
411.63976	0.854288769	0.001029586	0.020682238	64460	66181	+
213.3032756	0.847586969	0.00712694	0.074262989	438986	440197	+
464.7705997	0.835041915	0.001112613	0.021748584	25826	26725	-
212.5094981	0.831250652	0.010571809	0.097560419	988946	989965	-
789.3771486	0.825425245	0.00023059	0.007527123	72010	73191	+
362.1074476	0.822238012	0.002578864	0.038326526	660286	661401	+
347.7032712	0.817523083	0.003587793	0.04696235	723204	724274	+
572.2500383	0.780428109	0.001142158	0.021748584	652242	652625	-
964.3256063	0.775251556	0.000300547	0.009250061	381908	383458	-
448.7521756	0.771873787	0.003268287	0.044346224	13236	14567	-
964.9254547	0.763081112	0.000315839	0.009250061	23614	24288	-
393.6319035	0.753172544	0.008680236	0.085308989	292922	294193	-
1528.317841	0.751130436	0.000357578	0.010056202	672040	673314	+
2110.735265	0.750940971	8.17E-05	0.002987074	441439	445824	-
541.9810509	0.733971095	0.002884879	0.041524086	1178441	1179370	+
658.8283033	0.728582669	0.001521876	0.026749904	459993	461768	+
1090.015063	0.703297942	0.00154243	0.026852965	745055	747472	+
657.3595839	0.696303369	0.001985853	0.032411964	139993	141210	-

471.5035142	0.695237194	0.005405063	0.063779218	129632	130411 -
2582.289495	0.694096276	0.000168639	0.005816471	42233	42673 -
648.5889145	0.689772415	0.002938939	0.041971723	130405	131052 -
588.4881402	0.675664345	0.003540484	0.046898584	177219	178790 -
505.4164267	0.675070609	0.009259153	0.088792667	792677	793264 +
633.2942386	0.670350893	0.003299281	0.044346224	53638	53829 -
1661.788842	0.662951248	0.000926722	0.019454043	324958	326541 -
2100.158566	0.654658624	0.000541234	0.013014094	457720	458643 +
1159.915646	0.646527139	0.001942443	0.03227987	1068717	1069913 -
1018.786232	0.645208387	0.003445751	0.045976882	724516	725517 -
4080.805177	0.628018704	0.000306489	0.009250061	736037	736495 -
1786.575443	0.621555308	0.001510776	0.026749904	977935	981108 +
747.3206596	0.619874885	0.006664814	0.072090415	1068188	1068661 -
846.8232062	0.606705917	0.00755979	0.076349704	111575	112657 -
608.467207	0.602824524	0.010245164	0.096339893	45781	46887 +
885.1029202	0.596989524	0.005411989	0.063779218	976727	977923 +
2106.246965	0.588450604	0.002212104	0.034268872	770349	771239 +
1022.028824	0.571854369	0.005512646	0.063779218	244352	244996 -
1431.52183	0.567676056	0.004268374	0.054184635	1156900	1158159 +
2583.564974	0.565056313	0.009277571	0.088792667	806414	807340 -
831.6055344	0.555677705	0.009385157	0.089354515	386779	387927 -
1153.764207	0.545679484	0.007197212	0.074262989	741664	743433 -
1208.237023	0.54407022	0.007038568	0.074262989	695698	697683 +
1011.884185	0.539900376	0.010448521	0.097448449	796386	797774 -
1690.844761	0.537994636	0.005566957	0.0640025	720513	724958 +
5163.204531	0.530993298	0.001340981	0.024760738	154226	154741 -
1876.642917	0.515854861	0.007765891	0.078000263	390474	391418 -
1990.044858	0.512037129	0.007231298	0.074262989	1156157	1156783 +
1854.49524	0.492601806	0.010620636	0.097560419	981105	982523 +
3361.351533	0.48977336	0.006156399	0.068574629	166062	167105 +
2683.302275	0.485961035	0.007312838	0.074680822	51248	52300 +
5758.991808	0.476480495	0.007110261	0.074262989	8820	10121 +
2349.806796	0.473483798	0.010196663	0.096339893	93724	94410 +
6255.99896	0.419849016	0.010276958	0.096339893	258208	259746 +
6603.097107	-0.451285116	0.006334027	0.069750606	5572	6153 -
3676.084971	-0.468473294	0.006189723	0.068574629	74125	76071 -
20081.57069	-0.474642753	0.004624642	0.057866058	84548	87310 -
3998.125145	-0.479640922	0.005463052	0.063779218	1496	2050 +
18868.97499	-0.480020737	0.002777389	0.040616543	632841	634553 -
1680.538385	-0.490411744	0.010754481	0.098295958	594942	595391 -
3550.460955	-0.502987306	0.004684998	0.057866058	125449	125898 +
2208.121764	-0.50817906	0.006059298	0.06795336	50753	51496 -
2646.571177	-0.508839085	0.009110889	0.088120133	350115	351659 +
1959.784465	-0.510595748	0.008616175	0.085137121	172633	173208 +
2993.889085	-0.51915634	0.006920342	0.073978861	17808	18125 -
4842.138295	-0.526190527	0.00215541	0.033942259	1091783	1092538 +
40657.61411	-0.539871494	0.00412024	0.052741494	134062	135513 +
2527.492103	-0.555554072	0.004769038	0.058508738	579174	579632 +

3459.703632	-0.560225877	0.001270062	0.02393477	439262	440293 -
2584.088048	-0.561936482	0.002971334	0.04210542	37428	37709 -
1469.41031	-0.563754495	0.005186419	0.062373508	615259	615483 +
3729.920227	-0.569997563	0.001141952	0.021748584	90447	90965 +
4773.029661	-0.572657301	0.002172453	0.033942259	437585	439249 -
4470.819794	-0.576190888	0.001132679	0.021748584	323738	327307 -
957.8016999	-0.576823078	0.005036075	0.060966524	323268	324038 -
4475.360649	-0.577061155	0.000531501	0.012954457	26352	26735 -
7902.37103	-0.577773804	0.000273113	0.008607768	212553	213944 +
1126.322007	-0.577868675	0.008821887	0.085778778	23409	24695 -
22611.70052	-0.585291548	0.000428554	0.011353588	1162948	1163952 +
676.9380524	-0.586729679	0.008074202	0.080215446	956557	957474 +
4815.804898	-0.586828211	0.002010549	0.032524641	210370	211659 +
2539.120419	-0.593409309	0.002384865	0.03632945	35561	35827 -
1678.660026	-0.594629891	0.002164472	0.033942259	188469	189110 +
37185.40671	-0.601941086	0.000811361	0.017554455	132727	134043 +
1558.246075	-0.602178538	0.003112	0.043264335	296465	297034 +
3327.538093	-0.604199603	0.000502228	0.01283949	50399	50632 -
799.0106881	-0.606089915	0.005644899	0.064467931	315017	315574 -
690.7163211	-0.611301941	0.008807757	0.085778778	1200734	1201693 +
2839.265145	-0.613615101	0.000562425	0.013014094	471407	472159 -
3515.216055	-0.613863248	0.000516546	0.012855148	579784	580359 +
2001.317803	-0.624663852	0.006833196	0.073476953	661376	662143 +
2618.429484	-0.635354801	0.000997328	0.02025684	604368	605372 +
2276.764185	-0.635804317	0.00096831	0.019888431	28432	28821 -
2433.290737	-0.63683819	0.000754213	0.016813425	925476	926999 -
1039.749617	-0.638420736	0.00459309	0.057866058	744061	744909 +
1669.206586	-0.640908933	0.007231105	0.074262989	766080	766757 -
7694.718584	-0.644922487	0.0002299	0.007527123	119	1378 -
1422.186208	-0.645352376	0.001790984	0.030314059	1831	2868 +
2466.983097	-0.648998851	0.000400232	0.010759183	612248	613939 +
518.8392514	-0.653326489	0.006405985	0.070120601	428438	428980 +
85791.54026	-0.660796442	0.002861073	0.041508269	1095522	1096601 +
512.4347056	-0.671254351	0.005795533	0.065396511	605509	606597 +
518.0586311	-0.676902659	0.007354828	0.07469236	390532	391974 +
1511.813936	-0.677256346	0.000936519	0.019454043	1119511	1120257 +
625.4544139	-0.678878169	0.002471689	0.037034823	821350	821643 -
582.804976	-0.67928617	0.00328353	0.044346224	75699	76463 -
408.6815706	-0.682439243	0.008067259	0.080215446	67114	67605 -
1631.832579	-0.69163686	0.000802746	0.017554455	576985	577521 -
1549.472875	-0.705171495	0.000816263	0.017554455	29885	30430 -
662.838396	-0.707107097	0.001449966	0.02598567	612586	614787 +
2282.027278	-0.711147072	0.000111151	0.003907399	639416	640399 +
3425.916001	-0.718513057	0.000505032	0.01283949	192433	193176 +
602.2507358	-0.721645845	0.001424493	0.025781916	273715	274485 +
735.4206219	-0.721728669	0.00083942	0.017842559	927683	928189 +
1728.566407	-0.722276752	0.000384909	0.010660821	20933	21847 -
441.2163118	-0.734901001	0.003596679	0.04696235	744447	745373 -

303.9189511	-0.744799774	0.006990988	0.074262989	755226	755534 -
1075.558327	-0.749790478	0.000674244	0.015216264	847593	848294 -
452.3035051	-0.760082864	0.00196873	0.032411964	211677	211820 +
7450.728496	-0.769190948	3.00E-06	0.000182847	371428	371616 -
9085.357617	-0.780602388	4.22E-06	0.00024907	30675	31682 -
361.3650193	-0.78077571	0.003189724	0.043840718	49280	49723 +
369.6919796	-0.781005084	0.00312412	0.043264335	622029	622403 +
2199.584421	-0.794024567	6.28E-05	0.00234449	38551	38838 -
10858.90203	-0.794598846	1.94E-06	0.000141493	26725	27768 -
377.6857444	-0.795359299	0.002643493	0.038970202	1034932	1035189 -
833.7620672	-0.802803468	0.001332189	0.024760738	608909	609337 -
9870.258395	-0.807798059	3.88E-07	3.57E-05	9531	10952 +
3436.512505	-0.812269653	1.14E-05	0.000562357	292301	292684 -
186.1902194	-0.817824637	0.010511295	0.097536279	1142779	1143567 -
2392.42626	-0.828504493	1.07E-05	0.000551783	503558	504640 +
1316.655398	-0.831907545	2.61E-05	0.001058249	35832	36017 -
338.5623471	-0.832820833	0.001864698	0.031272181	17113	17562 +
587.2897299	-0.833809914	0.000250796	0.008043065	29304	29417 -
364.8947056	-0.836223606	0.001413942	0.025781916	928200	928610 +
1500.086899	-0.853537165	5.78E-05	0.002246882	878594	879136 +
193.8854073	-0.85988753	0.006575453	0.071547189	933417	934445 -
412.5556268	-0.872953091	0.000520394	0.012855148	651488	652024 -
963.1107327	-0.883915538	2.14E-05	0.000907809	748267	749886 +
241.3160375	-0.909395329	0.00210429	0.033742479	644941	645819 +
411.7820512	-0.91679761	0.000322029	0.009250061	184616	184993 +
790.999974	-0.923386466	1.50E-05	0.00065256	99098	99682 -
162.3350426	-0.933676031	0.005483918	0.063779218	429143	429640 +
2927.358323	-0.933984998	2.74E-06	0.000176571	740174	741892 +
894.3336436	-0.943879173	1.36E-05	0.000604244	1164057	1164629 +
2029.441934	-0.946888984	4.21E-07	3.67E-05	249747	250253 +
194.3282436	-0.955247711	0.00364664	0.047277001	784782	785603 -
3871.469486	-0.970274428	3.65E-08	4.76E-06	28918	29286 -
127.9761236	-0.983373597	0.005436646	0.063779218	703496	704467 -
960.1284585	-0.987517612	1.09E-05	0.000551783	1121118	1121483 +
345.2656361	-0.988448901	0.000556672	0.013014094	7787	9235 +
1333.910052	-0.992621185	2.56E-05	0.001058249	87478	87747 -
933.4838109	-0.996342117	2.15E-06	0.000145624	664015	665838 +
264.9436167	-1.02190879	0.000574967	0.013137998	182550	183026 -
2243.376116	-1.023324177	5.90E-08	7.19E-06	35182	35550 -
742.2637375	-1.033176704	6.66E-06	0.000358268	612015	612248 +
136.6525973	-1.051615528	0.005677974	0.064467931	560876	563314 -
2025.869616	-1.06179552	5.21E-06	0.000288847	244396	246078 +
7552.918805	-1.088226419	6.46E-11	1.69E-08	248661	249695 +
1819.309798	-1.088790034	1.05E-08	1.61E-06	672998	673300 +
317.5562862	-1.09023081	0.000323853	0.009250061	295051	296115 +
804.6451556	-1.096822238	3.91E-07	3.57E-05	615499	615762 +
1062.235893	-1.161988743	1.58E-08	2.22E-06	99723	100127 +
7388.054389	-1.173627775	1.41E-12	6.43E-10	247482	248513 +

523.7137699	-1.206010817	2.88E-07	2.93E-05	24697	24996 -
364.5201604	-1.236554808	2.80E-06	0.000176571	1073329	1074429 +
179.7178611	-1.340847879	5.11E-05	0.002031447	749995	750561 +
228.0428737	-1.398224783	1.29E-05	0.000603768	65069	65896 -
619.2056968	-1.558304733	6.06E-11	1.69E-08	1071459	1072544 +
151.0013251	-1.736709987	2.01E-06	0.000141493	1151886	1153328 +
365.9244025	-1.809555752	2.43E-11	8.89E-09	1072766	1073341 +
285.9209258	-1.859401466	4.18E-10	8.49E-08	170779	171378 -
253.2702098	-2.276526251	8.84E-14	8.08E-11	171460	172593 -

Annotation	KO	Cofactor	
product=major facilitator superfamily transporter			
product=MatE protein			
product=MarR family protein			
product=molybdopterin oxidoreductase	K00123	Metal	
product=molybdopterin oxidoreductase Fe4S4 domain-containing		Metal	
product=heme exporter protein A	K02193	Metal	
product=cobalt chelatase	K02190	Metal	
product=peroxiredoxin	K03386		
product=thioredoxin-disulfide reductase	K00384	Metal/FAD	http://www
product=hypothetical protein			
product=tetratricopeptide			
product=phosphate transport system regulatory protein	K02039		
product=methionyl-tRNA formyltransferase	K00604		
product=hypothetical protein			
product=hypothetical protein			
product=radical SAM superfamily protein		Metal	https://en.
product=hypothetical protein			
product=multi-copper polyphenol oxidoreductase laccase	K05810	Metal	
product=hypothetical protein			
product=hypothetical protein			
product=DNA mismatch repair protein MutL	K03572	Metal	https://ww
product=ribosomal protein S6	K02990		
product=pyrroline-5-carboxylate reductase	K00286	NAD	
product=SNF2 family domain-containing protein		DNA	
product=aspartate ammonia-lyase	K01744	Metal	http://patl
product=hypothetical protein			
product=hypothetical protein			
product=DNA polymerase III subunit delta	K02341	Metal	http://biol
product= Energy-coupling factor transport system	K16929	Metal	
product=YcaO-like family protein			
product=beta-ketoacyl synthase domain-containing prote	K09458		
product=xylose isomerase-like TIM barrel protein			
product=peptide/nickel transport system ATP-binding prc	K02031	Metal	Metallic ca
product=iron-containing alcohol dehydrogenase	K13954	Metal	
product=hypothetical protein			
product=hypothetical protein			
product=hypothetical protein			
product=bacterial dnaA helix-turn-helix domain-containin	K02313		
product=SWIM zinc finger protein		Metal	
product=peptidase family M50		Metal	https://ww
product=MltA specific insert domain-containing protein	K08304		
product=glutamate-1-semialdehyde-2%2C1-aminomutase	K01845	Pyridoxal 5'-phosphate	
product=BadF BadG BcrA BcrD ATPase			
product=homoserine O-succinyltransferase	K00651		
product=formate-tetrahydrofolate ligase	K01938		
product=homocysteine S-methyltransferase	K00548	Metal	http://www
product=peptidase family M20 M25 M40	K01295	Metal	https://ww

product=hisF cyclase	K02500	Metal	https://www
product=transcription antitermination factor NusB	K03625		
product=glutamine amidotransferase	K02501	Metal	http://cpln
product=bacterial extracellular solute-binding protein%2C	K02035		
product=hypothetical protein	K00782		
product=ribosomal protein L32	K02911	Metal;rRNA	https://www
product=hypothetical protein	K07121		
product=hypothetical protein			
product=serine threonine sodium symporter		Metal	
product=ATPase			
product=flavodoxin		FMN	
product=multidrug efflux pump	K18138		
product=hypothetical protein			
product=hypothetical protein			
product=obg family GTPase CgtA	K03979	GTP	
product=efflux transporter	K03585		
product=4- cytidine 5%-diphospho -2-C-methyl-D-eryth	K00919	ATP	
product=phosphoesterase	K07096	Metal	https://en
product=uracil-xanthine permease	K02824		
product=hypothetical protein			
product=iron-containing alcohol dehydrogenase		Metal	
product=tetratricopeptide			
product=stage II sporulation protein E	K07315		
product=sigma-54 interaction domain-containing protein		ATP	
product=hypothetical protein	K09800		
product=ribosomal protein L9	K02939	Metal;rRNA	https://www
product=dihydroorotate dehydrogenase	K17828	FMN	
product=uracil phosphoribosyltransferase	K00761	GTP	
product=NodT family efflux transporter	K18139		
product=MreB Mrl family cell shape determining protein	K03569		
product=aspartate-semialdehyde dehydrogenase	K00133		
product=tRNA guanine-N1 -methyltransferase	K00554		
product=hypothetical protein			
product=signal recognition particle protein	K03106		
product=hypothetical protein			
product=hypothetical protein			
product=amidohydrolase	K07047	Metal	http://www
product=hypothetical protein			
product=ribosomal protein S1	K02945		
product=hypothetical protein			
product=universal stress family protein			
product=3-oxoacyl- acyl-carrier-protein reductase	K00059	NAD	
product=bacterial extracellular solute-binding protein%2C	K13889		
product=ATP synthase	K02109	ATP	
product=thioredoxin	K03671		
product=ABC transporter	K02049		
product=sulfite reductase	K11181	Metal	http://www
product=ferric uptake regulator family protein		Metal	

product=nitrate reductase gamma subunit		Metal	https://bsi
product=ribosomal protein S19	K02965		
product=hypothetical protein			
product=ribosomal protein L10	K02864	Metal;rRNA	https://ww
product=hypothetical protein			
product=phosphoenolpyruvate synthase	K01007	Metal	https://ww
product=glucose-1-phosphate cytidyltransferase	K00978	Metal	http://www
product=ribosomal protein L17	K02879	Metal;rRNA	https://ww
product=cysteine-rich domain-containing protein			
product=glycine sarcosine betaine reductase component	K10670		
product=bacterial extracellular solute-binding protein%2C family 7			
product=hypothetical protein			
product=polysulphide reductase			
product=30S ribosomal protein S17	K02961		
product=hypothetical protein			
product=sulfite reductase	K11180	Metal	http://www
product=heterodisulfide reductase subunit C	K03390	Metal	http://www
product=acyl carrier protein	K02078		
product=translation elongation factor P	K02356	Oligonucleotide	
product=integral membrane protein TerC family protein	K05794		
product=bacterial extracellular solute-binding protein%2C	K02030		
product=rubrerythrin		Metal	https://ww
product=hypothetical protein	K07164		
product=fructose-1-6-bisphosphatase	K03841	Metal	https://en
product=30S ribosomal protein S11	K02948		
product=aldehyde dehydrogenase	K00140	NAD	
product=NifU-like N terminal domain-containing protein	K13819	Metal	http://www
product=adenylate kinase	K00939	Metal	https://ww
product=receptor family ligand binding region	K01999		
product=tRNA synthetase class II core domain-containing	K01889	ATP	
product=acetolactate synthase	K01652	Metal	http://www
product=USH1C-binding protein 1			
product=hypothetical protein			
product=glycoprotease	K01409	Metal	http://www
product=hypothetical protein			
product=hypothetical protein			
product=bacterial DNA-binding protein	K04764	DNA	
product=3-deoxy-D-manno-octulosonate cytidyltransfer	K00979	CTP	
product=hypothetical protein			
product=bacterioferritin	K03594	Metal	
product=tripartite ATP-independent periplasmic transporter			
product=GGDEF domain-containing protein			
product=glyceraldehyde-3-phosphate dehydrogenase	K00134	NAD	
product=bacterial extracellular solute-binding protein%2C	K02030		
product=cytidyltransferase	K00979		
product=HIT domain-containing protein	K19710		
product=thioredoxin-disulfide reductase	K00384	FAD/NADPH	
product=GGDEF domain-containing protein			

product=stress responsive A B Barrel domain-containing protein			
product=ATP synthase subunit A	K02108	ATP	
product=hmc operon protein 4			
product=4Fe-4S binding domain-containing protein		Metal	
product=bacterial extracellular solute-binding protein%2C family 7			
product=MarR family protein			
product=bacterial OB fold protein		Oligonucleotide	
product=ribosomal protein L23	K02892	Metal;rRNA	https://www
product=DNA-directed RNA polymerase	K03040	Metal	http://biol
product=hypothetical protein			
product=ACT domain-containing protein			
product=carbon starvation protein CstA			
product=desulfoferrodoxin	K05919	Metal	
product=glycosyl transferase family 2			
product=NMT1 THI5 like protein			
product=ribosomal L29 protein	K02904		
product=universal stress family protein			
product=ribosomal protein L36	K02919	Metal;rRNA	https://www
product=hypothetical protein			
product=outer membrane protein	K06142		
product=Holliday junction DNA helicase RuvB	K03551	ATP	
product=sigma 54 modulation protein S30EA ribosomal p	K05808	DNA	
product=metallo-beta-lactamase superfamily protein	K07576	Metal	
product=prepilin-type N-terminal cleavage methylation domain-containing protein			
product=glycine cleavage system H protein	K02437	NAD	
product=hypothetical protein			
product=type III secretion low calcium response chaperone LcrH S		Metal	
product=amidohydrolase	K07047	Metal	http://www
product=tripartite ATP-independent periplasmic transporter			
product=tripartite ATP-independent periplasmic transporter			
product=HD domain-containing protein			
product=30S ribosomal protein S13	K02952		
product=hypothetical protein			
product=hypothetical protein			
product=hypothetical protein			
product=ribosomal protein S15	K02956		
product=AMP-binding enzyme	K01897	AMP	
product=hypothetical protein			
product=ribosomal protein L14	K02874		
product=hypothetical protein			
product=DmsA YnfE family anaerobic dimethyl sulfoxide r	K07306	Metal	http://www
product=amidohydrolase	K07047	Metal	http://www
product=bacterial extracellular solute-binding protein%2C family 7			
product=bacterial DNA-binding protein	K04764	DNA	
product=hypothetical protein			
product=hypothetical protein	K09888		
product=transcriptional regulator			
product=bacterial extracellular solute-binding protein%2C family 7			

product=transcription factor HES-4		
product=sugar kinase	ATP	
product=RsmD family RNA methyltransferase	K08316 Nucleic acid	
product=phosphate binding protein	K02040 Phosphate	
product=hypothetical protein	K07112	
product=hypothetical protein		
product=hypothetical protein		
product=selenium metabolism protein YedF		
product=2-hydroxyglutaryl-CoA dehydratase	Metal	https://www

www.brenda-enzymes.org/all_enzymes.php?ecno=1.8.1.9&table=Metals_Ions

en.wikipedia.org/wiki/Radical_SAM

www.ncbi.nlm.nih.gov/pubmed/22749142

www.yeastgenome.org/ECOLI/NEW-IMAGE?type=ENZYME&object=ASPARTASE-CPLX

www.biomedcentral.com/articles/10.1186/1745-6150-4-27

tion, iron-siderophore and vitamin B12 transport system

www.ebi.ac.uk/interpro/entry/IPR008915

www.uniprot.org/uniprot/Q93088

www.ebi.ac.uk/interpro/entry/IPR008915

www.ncbi.nlm.nih.gov/pmc/articles/PMC4871644/

n.biocuckoo.org/show.php?entry=fAkxZjtWMcm2RtgDI2L&id=80738

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>

.wikipedia.org/wiki/PDE1

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>

w.els.net/WileyCDA/ElsArticle/refId-a0020546.html

w.uniprot.org/uniprot/O23813

jbcyc.org/BSUB/NEW-IMAGE?type=POLYPEPTIDE&object=BSU37250-MONOMER

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>

www.ncbi.nlm.nih.gov/pmc/articles/PMC94928/

www.uniprot.org/uniprot/P26396

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>

www.uniprot.org/uniprot/O23813

www.uniprot.org/uniprot/Q58154

www.ebi.ac.uk/interpro/entry/IPR003251

[.wikipedia.org/wiki/Fructose_1,6-bisphosphatase](http://en.wikipedia.org/wiki/Fructose_1,6-bisphosphatase)

www.uniprot.org/uniprot/Q09JH0

www.ncbi.nlm.nih.gov/pubmed/9862211

www.brenda-enzymes.org/all_enzymes.php?ecno=2.2.1.6&table=Metals_Ions

www.uniprot.org/uniprot/A0A160P937

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>
ogydirect.biomedcentral.com/articles/10.1186/1745-6150-4-27

www.ncbi.nlm.nih.gov/pmc/articles/PMC2757297/; <http://rnajournal.cshlp.org/content/10/9/1366.long>

www.uniprot.org/uniprot/D5DCM7

w.uniprot.org/uniprot/S1PAT1
w.uniprot.org/uniprot/D5DCM7

www.ncbi.nlm.nih.gov/pubmed/11106419