2017-12-01

Acetobacter fabarum Genes Influencing *Drosophila melanogaster* Phenotypes

Kylie MaKay White
Brigham Young University

BYU ScholarsArchive Citation
White, Kylie MaKay, "*Acetobacter fabarum* Genes Influencing *Drosophila melanogaster* Phenotypes" (2017). *All Theses and Dissertations*. 6613.
https://scholarsarchive.byu.edu/etd/6613

Acetobacter fabarum Genes Influencing *Drosophila melanogaster* Phenotypes

Kylie Makay White

A thesis submitted to the faculty of
Brigham Young University
in partial fulfillment of the requirements for the degree of

Master of Science

John M. Chaston, Chair
Joel Griffitts
Laura Bridgewater

Department of Microbiology and Molecular Biology

Brigham Young University

ABSTRACT

Acetobacter fabarum Genes Influencing *Drosophila melanogaster* Phenotypes

Kylie Makay White
Department of Microbiology and Molecular Biology, BYU
Master of Science

Research in our lab has predicted hundreds of bacterial genes that influence nine different traits in the fruit fly, *Drosophila melanogaster*. As a practical alternative to creating site-directed mutants for each of the predicted genes, we created an arrayed transposon insertion library using a strain of *Acetobacter fabarum* DsW_054 isolated from fruit flies. Creation of the *Acetobacter fabarum* DsW_054 gene knock-out library was done through random transposon insertion, combinatorial mapping and Illumina sequencing. Successful mapping of transposon insertion was achieved for 6418 mutants with hits within 63% of annotated genes within *Acetobacter fabarum* DsW_054. Insertion sites were verified in 40 mutants through arbitrary PCR and sequencing. To test the utility of the library, genes were selected from MGWAS results on host colonization which show LPS pathway enrichment in the significant gene predictions. Genes upstream of Lipid-A creation show significant differences in host colonization whereas downstream genes show no effect. In addition, genes were selected from MGWAS results on *Drosophila* starvation resistance which show Methionine/Cysteine synthesis, Cobalamin synthesis, and Biotin synthesis pathway enrichment. Under our experimental conditions we could not verify influence of these pathways on host starvation resistance. However, they do appear to influence host colonization abundance. This transposon insertion mutant library will be useful for ongoing research in our lab as well as any field studying *Acetobacter* species, such as other insect microbiome and fermentation research.

Keywords: Acetobacter, Drosophila, microbiota, microbiome, lipopolysaccharide, metabolic pathways

ACKNOWLEDGEMENTS

I would first like to thank my advisor, John Chaston, for his guidance and support throughout this educational journey. I would also like to thank my committee members, Joel Griffitts and Laura Bridgewater for their support and guidance. In addition, my husband for supporting me in my goal of achieving a graduate degree.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

Host traits influenced by the gut microbiome

The gut of humans and many animals contains an immense number of microbes known as the microbiota. The abundance and composition of these bacteria have become an interest throughout the biological sciences including fields of expertise from microbiology, immunity, ecology, evolution, epigenetics, and health [1-7]. The human gut microbiota is very complex, including about 500-1000 microbial species with millions of genes constituting the microbiome [7]. In addition, the composition of the gut microbiome varies between individuals and is inconstant throughout the life of the host, changing through development as well as due to environmental factors such as disease [8]. However, studies show that there may be some constancy in functional pathways between individuals despite differing microbiota [7, 8]. The microbiome is very complex and has far reaching effects.

The complexity and variability of the gut microbiome makes it difficult to elucidate specific effects of microbes on the host. Despite these difficulties, correlations and influences of the microbiota on the host have been discovered. Of note, the microbiota has been shown to directly affect the host transcriptome regulating immune function, proliferation of cells and metabolic functions [9]. There also appears to be a correlation between the gut microbiome and metabolic disorders such as obesity and diabetes [3, 5, 10] as well as diseases including cancer [6] and Crohn's disease [11]. In addition there is a connection between the gut microbiome and the brain, including a correlation with mental health diseases such as anxiety and depression [12, 13]. These effects cannot be thoroughly studied in human subjects; model organisms provide an opportunity to further our understanding of this important part of human health and development.

Metagenome-Wide Association to predict microbial gene effects on host phenotype

Both forward and reverse genetics are useful in the discovery of genes that affect specific phenotypes. Forward genetics involves selecting a phenotype of interest and then identifying mutants that display the phenotype. Forward genetic screens involve the identification of a phenotype of interest and random mutagenesis to identify mutants with the desired phenotype. Reverse genetics involves the identification of a gene and targeted gene knock-out to identify the resulting phenotype. Genetics screens have resulted in the discovery of many gene functions in many organisms from microbes to mammals.

Next-generation and high-throughput techniques have enabled the use of reverse genetic approaches via computational prediction. For example, RNA sequencing (RNA-seq) in transcriptomics allows for the identification of genes expressed under variable environmental conditions. These studies reveal genes that are involved in cell response to any environmental condition such as infection, low nutrient availability, or other specific cell stressors [14-18]. Transposon sequencing (TnSeq) aids in the identification of genes that are essential for survival under specified conditions. This has been performed for many microbes including *Escherichia coli*, *Caulobacter crescentus*, *Rhodobacter spaeroides, Rhizobium leguminosarum* and numerous others to identify genes essential for growth under laboratory conditions [19-21]. Tn Seq has also been utilized to identify genes needed for growth in other environments such as the gut [22, 23]. High throughput sequencing experiments such as these provide deep insights into the basic functions of the cell and deepen our understanding of a myriad of cell functions.

Metagenome-wide association studies (MGWAS) are another technique for the prediction of microbial genetic effects on host phenotypes [24-29]. They are useful because they predict a large number of gene effects, even in cases where a genetic screen would be difficult and time consuming such as the gut microbiome. In humans, the identification of microbial genetic effects is of interest due to the great number of genes found in the microbiome in comparison with host genes [30-32]. The microbiome has also been linked to various diseases and metabolic phenotypes as well as immune response [1, 7, 29]. The use of 16S rRNA has been used but provides low resolution and is limiting due to insufficient information on microbiome function. Shotgun sequencing provides higher resolution but is computationally challenging in comparison with 16S rRNA data [29]. Despite these challenges, MGWA has revealed a number of microbial genetic effects including obesity, cancer and diabetes [5, 26, 29, 33]. High throughput sequencing techniques have already led to increased understanding of human gut microbiome diversity and variability [8].

Drosophila as a model organism for microbiome research

The microbiome is a complex system. *Drosophila melanogaster* (fruit fly) is a good model organism in which to study the influence of microbes on the host [34]. Fruit flies have a relatively simple composition of about 5-20 species, dominated by species in the *Acetobacteraceae* and *Lactobacillaceae* families together with less abundant but highly prevalent *Enterococceae* and *Enterobacteriaceae* [34-37]. The composition of the microbiota is easily manipulated in the lab and flies can be raised bacteria free (axenic) by sterilization of the eggs and placement on sterile food or be raised with a defined microbiota [34, 38]. The simplicity and manipulability of the *Drosophila* microbiome makes it an ideal model organism for studying the microbiome.

The microbiota of fruit flies is also transient and inconstant throughout their life cycle [39-41], determined by numerous factors, including host genetic selection, environmental sampling, and host diet effects [42, 43]. This is similar to the inconstancy observed in other animals, including humans [8, 44]. Inconstancy of the *Drosophila* microbiome due to these factors has been demonstrated through numerous studies. 16s rRNA analysis of 21 fruit fly gut microbiomes revealed differences that would not have been anticipated with the expectation of a core microbiome. No microbe was present in every fly tested and even varied between flies of the same strain [40]. In addition the abundance of bacteria in the fly gut varies greatly between individual flies and as flies age the abundance of bacteria in the gut increases on average [41, 43, 45, 46]. This variability is in part due to the need of *Drosophila* to frequently replace its gut microbiota through ingestion as flies can lose the gut microbiota by frequently moving to sterile food [43, 45]. The total bacterial load also differs based on frequency of feeding and elapsed time since feeding [45]. Therefore, *Drosophila* relies heavily on food intake to maintain the gut microbiota resulting in an inconstant composition.

Despite inconstancy of the *Drosophila* microbiota, there are host influences on the composition of the microbiome [42, 47]. Food that is inoculated with *Acetobacter* and Lactobacillus cultures and kept free of flies results in lowered levels of *Lactobacillus*, probably due to antagonistic effects by *Acetobacters*. However, inoculated food inhabited by flies maintains levels of *Lactobacillus* [47]. It has also been shown that host genetic factors influence the abundance of *Acetobacter tropicalis* in mono-associated flies [42]. Additionally, fly isolates of bacteria confer a different nutritional phenotype than non-fly isolates, perhaps due to host selection for beneficial microbial functions [48]. Specific differences have been observed in bacteria isolated from flies such as uric acid degradation and lack of flagellar motility [49]. Bacteria that release uracil cause activation of the host immune system whereas lack of uracil excretion does not have this effect as seen in resident bacterial species [50]. Together these finding suggest that flies re-inoculate their food sources with bacteria that have been selected for within the gut. This influences the balance of microbes on the food which is then consumed by the flies, reestablishing the microbiota of the fly. Through these mechanisms, both host genetic factors as well as diet and environment affect the composition of the *Drosophila* microbiome.

Due to their small size, short generation time and ease of microbiota manipulation, fruit flies are an ideal model organism for investigating complex biological influences of the microbiome. One such application is the use of meta-genome-wide association studies (MGWA) through the use of mono-associated flies. This has been performed on a number of fruit fly traits including triglyceride content, development time [24], starvation resistance, lifespan and host colonization (our lab). One published study on triglyceride content (the main fat in fruit flies) used a comparison of 42 different bacterial species and mono-associated them with *Drosophila melanogaster* and observed differences in fly fat content based on the associated microbes (see figure 1) [24]. They then performed an MGWA on the fly fat content with the associated bacterial genes (presence/absence), returning a list of bacterial genes that are predicted to affect fly fat content [24]. These genes were grouped into functional pathway using KEGG pathway mapping [51-53] and the glucose oxidation pathway was predicted to significantly affect fly fat content, probably due to competition for glucose [24]. The next step was then to create gene knock-out mutants to validate predicted effects. However, site directed mutants could not be created in the bacterial species of interest, so plasmids bearing glucose oxidation genes were utilized in a strain that does not inherently contain them to confirm the effects of predicted genes (see figure 2)[24]. Due to the success of this method, we want to predict and verify genes influencing additional fly traits. However, the rate limiting step is the creation of mutants which is time consuming (particularly when a large number are desired) and site directed mutants are not currently possible in the species of interest.

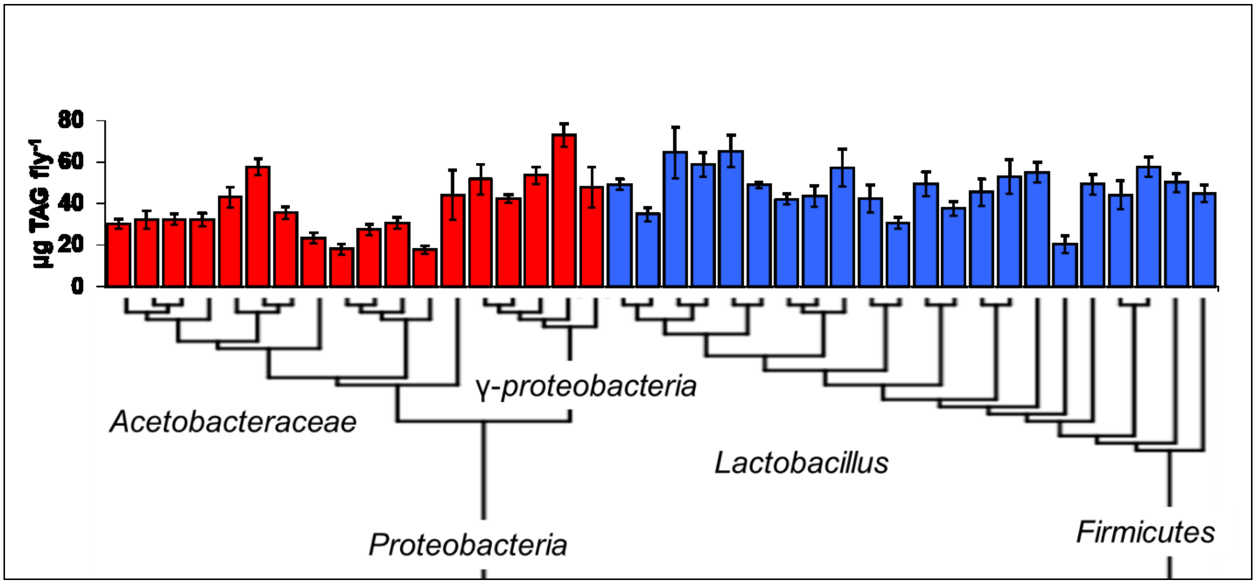


Figure 1: Bar plot representing MGWA data on triglyceride (TAG) content. Each bar represent the average TAG content for flies mono-associated with a specific bacterial species. Variation is observed even among closely related species. This allows for the prediction of genes that may be associated with fly TAG content due to bacterial genetic variation.

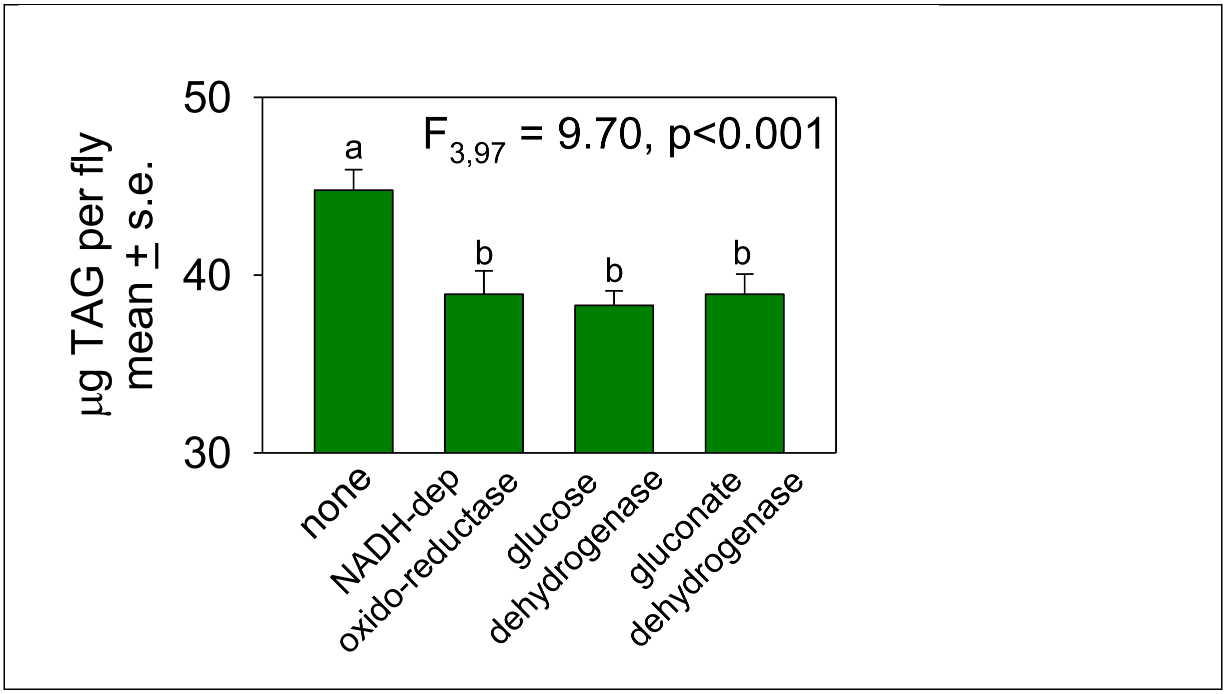


Figure 2: Bar plot of A. pasteurianus expressing glucose oxidation genes on a plasmid and associated fly TAG content. Genes were taken from *A. tropicalis*. A drop in the associated fly TAG content is observed with the addition of gens in the glucose oxidation pathway. This verifies the MGWA prediction that the presence of the glucose oxidation pathway confers a lower TAG content in the flies.

To fill this need, I created an arrayed transposon insertion library in *Acetobacter fabarum* DsW_054 and used these mutants to verify MGWA predictions for host colonization and *Drosophila* starvation resistance. The use of gene knock-out mutants that I have utilized in my research provides further evidence in validating bacterial gene effects on host phenotypes. Details are included in the research chapters. Genetic resources such as mutant libraries of *Drosophila* associated microbes will continue to prove useful in furthering our understanding of the *Drosophila* associated microbiome.

Acetobacter species in the microbiome and other disciplines

The bacterial family *Acetobacteraceae* are important members of the *Drosophila* microbiota. Species include *Acetobacter, Gluconobacter*, and *Komagataeibacter* species. In *Drosophila*, *Acetobacter* and *Gluconoacetobacter* species have been linked to faster development time and lowered triglyceride content in mono-associated *Drosophila melanogaster* [24, 46, 54]. Lowered lipid content may be due to reduction of glucose in food by *Acetobacter* species [55]. *Acetobacter* species have been linked to glucose, glycogen, triglyceride, and protein contents within the flies, although it has been shown that host genetics contribute to *Acetobacter* abundance and therefore influence these nutritional statuses [42]. Additionally, complex microbial interactions between *Acetobacter* and other gut microbes are important for influencing various phenotypes of fruit flies [46, 56]. For example, fly triglyceride content differs between flies mono-associated with either *Acetobacter* or *Lactobacillus* species, axenic flies and flies associated with both *Acetobacter* and *Lactobacillus* species [46]. *Acetobacter* species also interact with *Saccharomyces* to produce metabolites that influence *Drosophila* behavior such as where they lay their eggs [56]. *Acetobacter pomorum* has also been shown to be involved in host immune response to viral infections [57]. In addition, early exposure to *Acetobacter* species can influence *Drosophila* feeding behaviors in favor of food containing *Acetobacter* despite innate preference for *Lactobacillus* [58]. Therefore, the study of *Acetobacter* genetics will prove useful in defining the effects of the *Drosophila* microbiome on host traits.

Acetobacter species are also well-studied for their involvement in production of vinegar (acetic acid), kefir and ethanol through fermentation [59-62]. *Acetobacter* species have been compared for oxidation rates of ethanol and lactic acid to determine key starter cultures in fermentations in order to improve production [61, 63]. Recently, a study was performed on improving the production of acetic acid by *Acetobacter pasteurianus*. They overexpressed two subunits of pyrroquinoline quinone-dependent alcohol dehydrogenase (PQQ-ADH), an important factor in acetic acid fermentation, and observed an increase in acetic acid production while also decreasing residual ethanol [62, 64]. Studies have also sought to determine the genetic mechanisms of this species in both production and resistance to acetic acid [65-68]. These studies aim to identify *Acetobacter* strains and genes that can be used and manipulated to optimize production of fermentation products through higher acetic acid concentrations.

In numerous cases, genetic approaches have been used to confirm the mechanistic causes for the phenotypic effects of *Acetobacter*, although site-directed genetic analysis in *Acetobacter* species isolated from fruit flies has been a challenge [24, 54]. Expanding on the genetic tools available in *Acetobacter* will enable more detailed functional studies in the corresponding fields of study.

Lipopolysaccharide effect on microbe-host interactions

Lipopolysaccharides (LPS) are molecules on the outer membrane of gram-negative bacterial species and many genes involved in LPS synthesis are considered essential in *E.*

coli[69-71]. LPS are composed of a lipid A base protein with core oligosaccharides and O antigen components [69, 71]. Lipid A is highly conserved among gram-negative bacteria and consists of six hydrophobic chains that are contained within the outer membrane, anchoring the molecule. Core oligosaccharides link lipid A to the O antigen [69-71]. Some genes within the LPS biosynthetic pathway have been successfully removed whereas mutations in other genes are lethal to the cell [69-72]. Deletion of *rfaD* (*gmhD*) from *E. coli* results in decreased ability to form biofilms, increased cell permeability, aggregation and hydrophobicity [72]. Deletion of *msbB* in *Salmonella* causes growth defects, but these can be reversed by inactivation of additional genes within *Salmonella* [73]. Therefore, LPS is important in the viability of gram-negative bacteria but select mutations within this pathway are not lethal to the cell.

LPS is an important factor in host-microbe interactions for both pathogenic and symbiotic bacteria. Lipid A is an endotoxin and causes an innate immune response in many animals including humans through activation of Toll-like receptor complexes [69, 74]. However, formation of LPS has also been identified as an important factor in colonization of the host gut. A Tn Seq experiment in a honey bee symbiont revealed decreased representation of LPS synthesis gene knock-outs when introduced to the host. They concluded that it is important in the successful colonization of the host gut, perhaps due to cell interactions, immune system evasion, and cell envelope resilience [22, 75]. Although LPS is an important immune activator, it may also be important in successful host colonization by symbiotic bacteria.

Arrayed mutant libraries as a genetic resource

Arrayed mutant libraries allow for the high-throughput identification of thousands of knock-out mutants in a single sequencing run. Transposon insertion mutants are arrayed in 96 wells plates, combined into sequencing pools in unique presence-absence patterns, and all library members sequenced in a single sequencing run. The transposon insertion site for each bacterial mutant was then mapped to its location in a 96-well plate by decoding the unique presence-absence pattern it was inoculated to during sequencing preparation. One early successful method was previously described by Goodman et al [76, 77] where the created mutants were used to determine bacterial functions that are necessary for survival in the gut [77]. They found that necessary genes differed based on other microbes present and the availability of nutrients, specifically B12 [77]. This study proved the utility of arrayed mutant libraries.

Recently, other arrayed libraries have been created. An arrayed library of 12,000 transposon mutants was created for *Klebsiella pneumonia*e, a cause of hospital-acquired infections, and has been useful in antibiotic sensitivity screens. They were able to identify several mutants that had increased sensitivity to ss-lactams and that mutations in cpxAR (a two-component regulator) increased the microbes sensitivity to multiple antibiotic types [78]. An arrayed mutant library in another member of the *Drosophila* microbiota, *Lactobacillus plantarum*, was published recently, and aided in confirming a role for teichoic acids in *Lactobacillus – Drosophila* associations. They showed that D-anylation of teichoic acids aided in the growth of *Drosophila* under chronic nutrition by influencing peptidase expression by the host [79]. Arrayed libraries such as these can be useful when site-directed mutagenesis is not possible or when a large number of mutants are needed and site-directed mutagenesis would be impractical.

CHAPTER 1

Metagenome-wide association and mutant analysis for *Acetobacter* genetic determinants of *Drosophila* association

White, Kylie Makay; Matthews, Melinda K; Hughes R; Sommer, Andrew J; Newell, Peter D; Griffits, Joel; Chaston, John M

Foreword: *Acetobacter fabarum* DsW_054 was discovered by the Peter Newell lab and selected for creation of the mutant library. The conjugation protocol and the transposon insertion library was created and evaluated almost exclusively by Kylie Makay White. The TnSeq protocol and pipeline used in this study was from the Joel Griffitts lab. Lindy Koyle aided in the LPS mutant phenotyping data collection. Kylie Makay White performed the KEGG analysis to compare predicted essential pathways of *Acetobacter fabarum* DsW_054 and *Rhodobacter spaeroides, Rhizobium leguminosarum* and *Caulobacter crescentus*. Kylie Makay White generated all figures with guidance from John Chaston.

ABSTRACT

A metagenome wide association study of host colonization in Drosophila predicted LPS biosynthesis genes are significantly associated with host colonization. We were unable to create site-directed mutants for each of the predicted genes in *Acetobacter*, so we created an arrayed transposon insertion library using *Acetobacter fabarum* DsW_054 isolated from *Drosophila*. Creation of the *A. fabarum* DsW_054 gene knock-out library was done through random transposon insertion, combinatorial mapping and Illumina sequencing. Successful mapping of insertion location was achieved for 6418 mutants with hits within 63% of annotated genes within *A. fabarum* DsW_054. Insertion sites were verified in 40 mutants through arbitrary PCR and sequencing. To test the utility of the library, genes were selected from MGWAS results on host

colonization. Genes upstream of Lipid-A creation show significant differences in host colonization whereas downstream genes show no effect. This transposon insertion mutant library will be useful for ongoing research in our lab as well as any field studying *Acetobacter* species, such as other insect microbiome and fermentation research.

INTRODUCTION

Animal associated microbes ('microbiota') are associated with numerous host phenotypes including metabolic function, mental health and various diseases [80-85]. The taxonomic and functional complexity of the microbiota is a challenge in defining the interactions underlying these phenotypic influences. The *Drosophila melanogaster* microbiota is relatively simple, mainly comprised of yeasts, acetic acid bacteria (AABs) and lactic acid bacteria (LABs), together with less abundant but highly prevalent *Enterobacteriaceae* [34-37]. The identity and abundance of associated bacteria are apparently inconstant [40], determined by numerous factors, including host genetic selection, environmental sampling, and dietary effects [42, 43, 47, 48]. For example, flies replenish their associated microbiota through dietary replenishment, and bacterial loads can be reduced by frequent transfer of flies to sterile diets [43, 45]. There are apparently reciprocal interactions between the host and the diet since sterile fly diets inoculated with bacteria alone have a different composition than fly diets inoculated with flies and the same bacterial communities [47]. The gut microbiota also varies in composition and abundance within species as well as throughout the life of individual flies [40, 41, 43, 45, 46]. So far, little evidence has been presented for host retention of specific bacterial taxa or functions within or across generations; instead, host genotype appears to select from among sampled microbes, with no evidence for a host phylogenetic signal on the identity of associated microbes [40].

Gut microbes also influence the composition of the *Drosophila* gut microbiome but little is known about specific host colonization factors. However, recent studies have begun to characterize specific bacterial effects. The *Drosophila* gut is able to elicit an immune response to non-symbiotic bacteria by detection of bacterial uracil production through the dual oxidase-regulatory pathways, responding differently to commensal and or pathogenic microbes. [50, 86]. Recently, it was shown that D-alanylated teichoic acids on the cell walls of *L. plantarum* were sensed by the *Drosophila* enterocytes, enhancing host digestion and promoting growth and maturation of the host [79]. In addition, a study of gut associated *Acetobacter* species in comparison with free living bacteria show differences in uric acid degradation in order to better inhabit the host gut [49]. Together, these findings reveal the complexity of gut microbe-host interactions.

Acetic acid bacteria are important members of the *Drosophila* microbiota, including *Acetobacter, Gluconobacter*, and *Komagataeibacter* species. In *Drosophila*, *Acetobacter* and *Gluconoacetobacter* species have been linked to faster development time and lowered triglyceride content in mono-associated *Drosophila melanogaster* [24, 46, 54]. In addition, complex microbial interactions between *Acetobacter* and other gut microbes are important for influencing various phenotypes of fruit flies [46]. *Acetobacter* species are also well-studied for their involvement in production of vinegar (acetic acid), kefir and ethanol through fermentation [59-62]. In numerous cases, genetic approaches have been used to confirm the mechanistic causes for the phenotypic effects of *Acetobacter*, although site-directed genetic analysis in *Acetobacter* species isolated from fruit flies has been a challenge [24, 54]. Expanding on the genetic tools available in *Acetobacter* will enable more detailed functional studies in the corresponding fields of study.

Because there were no successful approaches for site-directed mutagenesis in fruit fly isolates of *Acetobacter*, and because our preliminary efforts to develop such approaches failed, we created a mapped and arrayed transposon insertion library of *Acetobacter* mutants. Arrayed mutant libraries allow for the high-throughput identification of thousands of knock-out mutants in a single sequencing run. One early successful method was previously described by Goodman et al [76, 77], where transposon insertion mutants were arrayed in 96 wells plates, combined into sequencing pools in unique presence-absence patterns, and all library members sequenced in a single sequencing run. The transposon insertion site for each bacterial mutant was then mapped to its location in a 96-well plate by decoding the unique presence-absence pattern it was inoculated to during the sequencing, and the created mutants were used to determine bacterial functions that are necessary for survival in the gut [77]. An arrayed library of 12,000 transposon mutants was created for *Klebsiella pneumonia*e, and has been useful in antibiotic sensitivity screens [78]. An arrayed mutant library in a another member of the *Drosophila* microbiota, *Lactobacillus plantarum*, was published recently, and aided in confirming a role for teichoic acids in *Lactobacillus – Drosophila* associations [79]. We provide a proof-of-concept first use of an *A. fabarum* DsW_054 mutant library by testing five LPS mutants for their ability to associate with *Drosophila*.

MATERIALS AND METHODS

Bacterial and fly growth media and conditions.

D. melanogaster Canton S flies were grown at 25°C on a yeast glucose diet containing 100 g/ liter brewer's yeast (inactive) (MP Biomedicals), 100 g/ liter glucose (Sigma), 12 g/ liter agar (Apex), and preservatives (0.04% phosphoric acid and 0.42% propionic acid (Sigma) on a 12-h-light/12-h-dark cycle.

Bacteria strains used in the study are included in table 1. Media used included lysogeny broth (LB)/agar (sigma), modified MRS broth/agar and potato dextrose broth/ agar (Sigma). The plasmid bearing *E. coli* strain was cultured with 50 µg/ml kanamycin and *Acetobacter* gene knock-out mutants were cultured with 30µg/ml chloramphenicol and 50µg/ml kanamycin. All bacterial strains were cultured at 30ºC. *A. fabarum* DsW_054 was cultured in potato dextrose broth prior to matings.

Table 1: Strain list

Strain Name	**Abbreviation**	**Preferred Medium**	**Citation**
***A. fabarum* DsW_054**		mMRS	Winans, 2017
***Escherichia coli* S17_pJG714**		LB-kan	
***A. fabarum* DsW_054 Tn5::lpxC**	lpxC	mMRS	This study
***Acetobacter* DsW_054 Tn5::lpxB**	lpxB	mMRS	This study
***A. fabarum* DsW_054 Tn5::lpxK**	lpxK	mMRS	This study
***A. fabarum* DsW_054 Tn5::gmhD_1**	gmhD_1	mMRS	This study
***A. fabarum* DsW_054 Tn5::gmhD_2**	gmhD_2	mMRS	This study

Creation of an arrayed mutant library

An arrayed transposon insertion library was created in two steps: by conjugally transferring the Tn*5* transposon vector pJG714 into *A. fabarum* DsW_054; and by arraying the exconjugants into 96-well plates. *A. fabarum* DsW_054 cells were cultured in potato medium for 24 -36 hours at 30°C and mixed with 18-24 h cultures of *E. coli* S17-pir containing the plasmid pJG714, cultured in LB-kanamycin. Two 3 mL cultures at about 0.6 OD and 500 ul E. coli culture near saturation were used for the conjugation. Prior to mixing, the cells were washed three times in potato medium and then *A. fabarum* DsW_054 were condensed to 100 µl and *E. coli* were re-suspended in 500 µl. The two strains were mixed in a 1:1 volumetric ratio and transferred to potato medium plates in 50 µl spots. After 4 hrs at 30°C the cells were collected from the plate in 1ml LB, dilution plated (1:50) onto 2X-YPG plates containing kanamycin and chloramphenicol, incubated at 30ºC for four days, and stored at 4°C for no more than 1 week before arraying in 96-well plates. Colonies were individually picked into MRS broth in 96-well plates to array the transposon insertion library. Each plate was then sealed with Parafilm and incubated with gentle shaking for 48 hours at 30ºC until most cell densities were between OD_{600} 0.5 and 1.0, and frozen in MRS-25% glycerol.

Combinatorial mapping and sequencing:

To identify the insertion site of each mutant, we used a combinatorial mapping approach, which was performed using an Eppendorf EpMotion 5075 TMX pipetting robot. A 24 bit binary barcode was assigned to each well of each 96 well plate, corresponding to the presence (1) or absence (0) of the bacteria from each well in the corresponding pooled vials as in[87]. Intermediate sets of 24 pools were created from five 96-well plates at a time in a the attached thermocycler feature held at 4ºC by pipetting 10 µl to each intermediate pool for which a '1' was assigned to that sample of the 96-well plate. The different pools were stored at -20ºC for a maximum of 2 months. Once all the intermediate pools had been created, a final set of 24 pools was created by mixing all intermediate pools from the same barcode positions (e.g. all 'Pool 1' tubes) in equal volumetric ratios.

For Illumina sequencing, each of the 24 final pools was assigned a 63 bp primer with a unique 6 bp indexing barcode that was introduced by PCR. All replicate pools were centrifuged, re-suspended, and DNA extracted. DNA was fragmented using a DNA fragmentase, optimized for an average fragment size of 1000 bp with a reaction time of exactly 12 minutes. We performed C-tailing to prepare the fragments for PCR to add on the Illumina indexing and sequencing primer and two rounds of PCR. The first round added a region homologous to the indexing primers at the C-tail end and amplifying from the transposon end. The second round added the Illumina indexing primers and the sequencing primers with the transposon end. All primer sequences and more detailed methodology are included in the supplementary materials.

Data analysis:

The Illumina sequencing data was mapped to the *A. fabarum* DsW_054 genome using the TnSeq pipeline that has been published previously [21]. A 24-bit barcode was assigned to each mapped insertion site in the genome using a threshold of 50 reads per sequencing pool. For example, if there were more than 50 reads for a particular insertion site in sequencing pool 1, a 1 was assigned at the first position in the barcode; if there were less than 50 reads in the second sequencing pool, a 0 was assigned at the second barcode position, etc. We used 50 reads as a cutoff point, but most sites had more than 200 reads for each positive indexing primer. Once the insertion site barcodes were assigned, they were matched to the barcodes from the original combinatorial mapping assignments for the well location in the 96-well plate library.

Library validation:

Arbitrary PCR was used to validate the mapped insertion sites for the arrayed library. A transposon specific primer was paired with arbitrary primers for the first round and the second round used a primer specific to the transposon and a primer specific to the tail of the initial arbitrary primers. Primer sequences are included in the supplementary data. A single colony that was suspended in 10µl H_2O and boiled for 10 minutes at 99°C served as the template. For first round arbitrary PCR we mixed 14µl H_2O, 2.5ul 10x $(NH_4)_2SO_4$ buffer, 1µl DMSO, 2µl $MgCl_2$ (25mM), 1ul dNTP (10uM), 1µl Arb1 primer (20µM), 1µl Arb6 primer (20µM), 0.5µl 133 primer (20μM), 1μl Taq polymerase, and 1μl template (boiled cell preparation). We ran the reaction using the following program: 94°C for 3:00 followed by six cycles of 94°C for 0:20, 30°C for 0:20 and 72°C for 1:00, followed by 30 cycles of 94°C for 0:20, 45°C for 0:20, 72°C for 1:00 and finished at 72°C for 5:00.

This was followed by a second round of arbitrary PCR. For each sample we mixed 31.25 μl H_2O, 5μl 10x $(NH_4)_2SO_4$ buffer, 2μl DMSO, 4μl $MgCl_2$ (25mM), 2μl DNTP (10μM), 2μl Arb2 primer (20μM), 2μl 134 primer (20μM), 1μl Taq polymerase (1 U), 1μl Template (Product from first round). We ran the solution at 94°C for 1:00 followed by 35 cycles of 94°C for 0:15, 52°C for 0:20, 72°C for 1:00, and finish at 72°C for 5:00. The product was visualized on a 1% agarose gel to verify amplification before sequencing via Sanger sequencing. The specific insertion site was verified by mapping to the *A. fabarum* DsW_054 genome using the BLAST feature in RAST [88].

Metagenome-wide-association study and KEGG pathway analysis (host colonization):

A metagenome wide association study (MGWA) was performed previously to predict bacterial effect on fly triacylglyceride content. To conduct the MGWA we used previously collected phenotype and genotype data [24]. The phenotype data were collected by measuring the bacterial load in *D. melanogaster* that were sterilized through two 2.5 minute washed in 0.6% hypochlorite solution, washed three times in sterile water and placed on sterile food in a laminar flow hood, mono-associated with each of 42 different bacterial strains. Orthologous groups (OGs) in the 42 bacterial strains were clustered using OrthoMCL, yielding 12,354 OGs. Statistically significant associations between the CFU abundances in *D. melanogaster* and the presence-absence patterns of the OGs were identified in R {MAGNAMWAR}. Data were processed using a linear mixed model with log-transformed CFU abundances as the response variable, experiment and bacterial treatment as independent random effects. Statistically significant outputs were Bonferroni-corrected, and the R MAGNAMWAR package was used to produce other visual representations of the data.

We performed a KEGG pathway analysis on data from the MGWA to identify enriched pathways from the significant results. We assigned KEGG pathway numbers to all OGs in the dataset using 'BLASTKOALA' and compared the number of OGs in different KEGG pathways between a reference dataset (all OGs) and a significant dataset (the top 324 significant OGs from the MGWA, based on a p-value less than 0.001 using the 'KEGG Mapper – Search Pathway' online tool [51-53]. Significant enrichment of KEGG pathways in the top 324 significant OGs was determined by chi-square analysis, with false-discovery-rate p-value correction. Pathways were only used in the analysis if they had 4 or greater counts in both the top and the reference set of OGs. All analyses were performed in R.

Mutant phenotyping in fruit flies

Genes were selected from enriched pathways to verify the effects predicted in the KEGG analysis. LPS mutants were selected from the *A. fabarum* DsW_054 library (Table 1). Male and female flies were placed together in a cage containing grape juice agar for 16-18 hours to allow for egg collection. Fly eggs were collected, sterilized twice for 2.5 minutes in 0.6% hypochlorite solution, rinsed three times in sterile water, and transferred to sterile food vials at a density of 30-80 eggs per vial. Eggs were then mono-associated with selected transposon insertion mutants (see Table 1) by addition of 50 μl of bacterial culture that was previously normalized to OD_{600} of 0.1 [38]. Three separate experiments containing all experimental treatments were performed, each in triplicate. At 5-7 days of age, pools of 5 female flies were lightly anesthetized on CO_2

and homogenized with 125 µl Lysing Matrix D ceramic beads (MP Biomedicals 11654034) on a FastPrep-24 homogenizer for 30-60s. The homogenate was dilution plated on mMRS plates and colony forming units (CFUs) were manually counted. Any flies bearing bacteria other than *Acetobacter* (determined by visual inspection of colony morphology) were removed from the experiment.

RESULTS

Creation of an arrayed and mapped transposon insertion library in *A. fabarum* DsW_054

To isolate transposon insertion mutants that could be used to validate the MGWA predictions in this study, and that could be used for future functional genetic studies, we constructed a mapped, arrayed transposon insertion library in an *Acetobacter* isolate from *Drosophila.* We were initially unable to obtain transposon-insertion-bearing exconjugants from matings that used as recipients two different strains of *Acetobacter* isolated from laboratory flies, *A. pomorum* DmCS_004 and *A. tropicalis* DmCS_005 {Newell, 2014}. As a follow-up, we screened 17 strains of *Acetobacter* for amenability to genetic modification. Of these, *A. fabarum* DsW_054, a strain that was isolated from wild-caught *Drosophila suzukii [49],* yielded the greatest number of exconjugants with a kanamycin-marked Tn*5* transposon. Pairwise nucleotide alignments of the *A. fabarum* DsW_054 genome with those of two *A. fabarum* strains (KR and OG2) recently added to the NCBI WGS database, indicated >98% ANI with both, allowing us to provisionally assign this isolate to the species *fabarum.*

A. fabarum DsW_054 was subjected to further optimization of a conjugation protocol to transfer a plasmid-based mini-Tn5 from donor *E. coli* cells. The final protocol was obtained after varying co-incubation ratios and times with an *E. coli* donor bearing pJG714, and selecting parameters that maximized exconjugant recovery (final protocol is described in methods). Proof-of-concept arbitrary PCR mapping confirmed that in eight randomly selected colonies, each mutant contained a single, unique transposon insertion site (data not shown).

We created a mapped and arrayed transposon insertion library in *A. fabarum* DsW_054, following the approach of Goodman, et al (2011). 8,550 mutants were created in groups no larger than 480 mutants at a time, individually transferred to 96-well plates, and the transposon insertion sites in each arrayed mutant were defined in a single Illumina sequencing run by a combinatorial mapping approach. The insertion sites for 6,418 mutants were precisely mapped, with unmapped mutants resulting from insufficient read coverage across all sequencing pools or to duplicate insertion sites in the library (possibly from sister clones). For example, a subset of transposon insertion sites were present in more than 14 sequencing pools, most likely representing duplicate insertion sites; whereas the insertion sites present in fewer than 10 sequencing pools were mostly likely not abundant enough to detect in some pools (see Figure 3). The relatively large number of insertion sites that were present in just 1 or 2 pools likely results from sequencing errors. To confirm the validity of the mappings, the insertion site was validated manually by arbitrary PCR and Sanger sequencing in 41 of 41 mutants selected from the library, suggesting a high level of accuracy in the mapping of the mutants to their 96-well plate arrayed location. Therefore, we are confident that our method is highly accurate for mapping the insertion site of library mutants.

We determined near saturation of the insertion library through analysis of hits within predicted genes. 5,559 mutants mapped within an open reading frame (ORF) called by RAST, representing insertions in 63% of the 2,579 annotated genes in the *A. fabarum* DsW_054 genome (Table S1). To assess the degree of gene saturation represented by the 5,559 ORF-mapped transposon insertion mutants, we performed a rarefaction analysis (Fig 2). The strong plateau of the curve suggested that the mutant library was well-represented by non-essential *A. fabarum* DsW_054 genes and that mapping insertion sites in more mutants was unlikely to substantially increase the gene coverage in the collection.

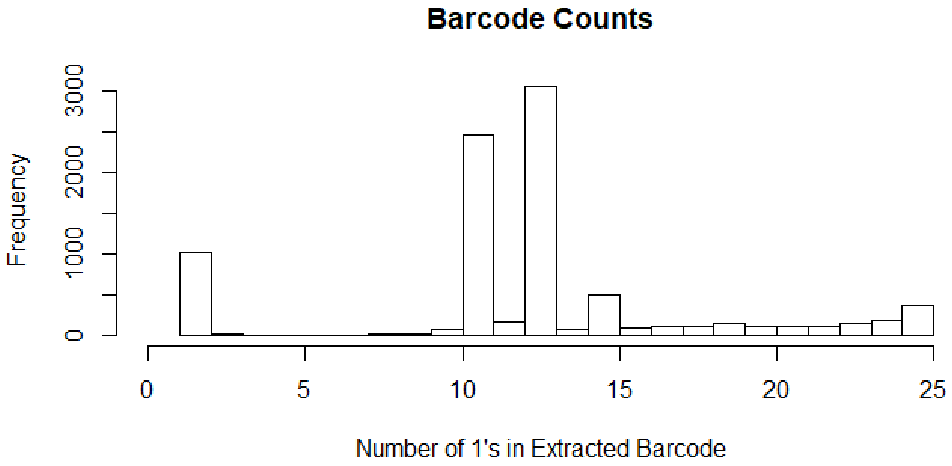


Figure 3: Histogram of "present" sequencing pools returned from Illumina sequencing run. Expected barcodes contained 10-14 "present" sequencing pools. Those containing more than 14 or less than 10 could not be mapped to the library.

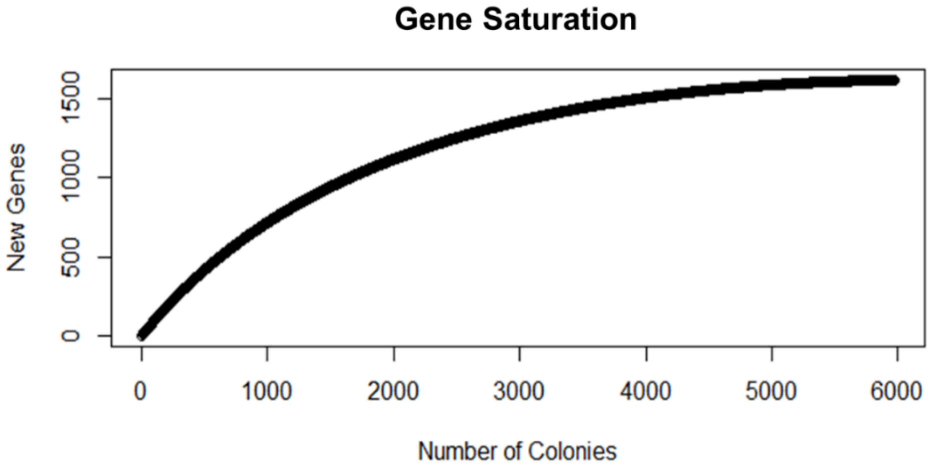


Figure 4: Rarefaction curve of *Acetobacter fabarum* DsW_054 gene saturation. A rarefaction curve showing the number of new genes with insertions as new colonies were added to the library. This shows that the addition of mutant colonies would not add a significant number of genes to the mutant library.

Prediction of essential genes in *A. fabarum* DsW_054

Because of an estimated high level of functional saturation in the transposon mutant library, we predicted that the 37% of genes lacking any insertions are essential- or are located near essential-genes for growth in mMRS. A chi-square analysis of the KEGG pathways that were under- or over-represented in the genes bearing at least 1 transposon insertion site in our library suggested that genes encoding ribosomal components or involved in aminoacyl-tRNA biosynthesis, cell cycle, and protein export were essential for growth in mMRS; whereas the ABC transporters, starch and sucrose metabolism and two-component system pathways were enriched for non-essential genes (Table 2). Together, this analysis points to key *A. fabarum* DsW_054 genes for growth and survival in laboratory culture, the first such analysis of which we are aware for any *Acetobacteraceae* strain.

Prediction of bacterial pathways that influence bacterial load in *D. melanogaster*

To predict bacterial genes that are necessary to associate with *D. melanogaster* we performed a MGWA analysis. The analysis was performed using previously published data from a survey of CFU abundances in *D. melanogaster* that were individually associated with each of 41 genome-sequenced bacterial strains[24]. An MGWA that associated bacterial CFU abundance data with OG presence-absence patterns in the 41 strains predicted 3084 bacterial genes that influence host association using a p-value cutoff of 0.05 (Table S2). Because our previous MGWA analysis had successfully identified genes by looking for enriched functions among top hits, we performed a KEGG enrichment analysis to identify pathways that were enriched in the top 324 hits from the MGWA. After correction for multiple tests, genes from just one KEGG pathway, lipopolysaccharide biosynthesis, were significantly enriched in the top MGWA hits (Table 3).

Therefore, MGWA predicted a key role for bacterial LPS biosynthesis in its ability to associate with *D. melanogaster*.

Table 2: The KEGG pathway analysis of genes containing no insertions. The KEGG pathway analysis of genes containing no insertions in our mutant library reveals a list of potential pathways that are essential for growth in our laboratory conditions. Ribosome, tRNA synthesis, cell cycle and protein export pathways were the most significant candidates for essentiality in *A. fabarum* DsW_054.

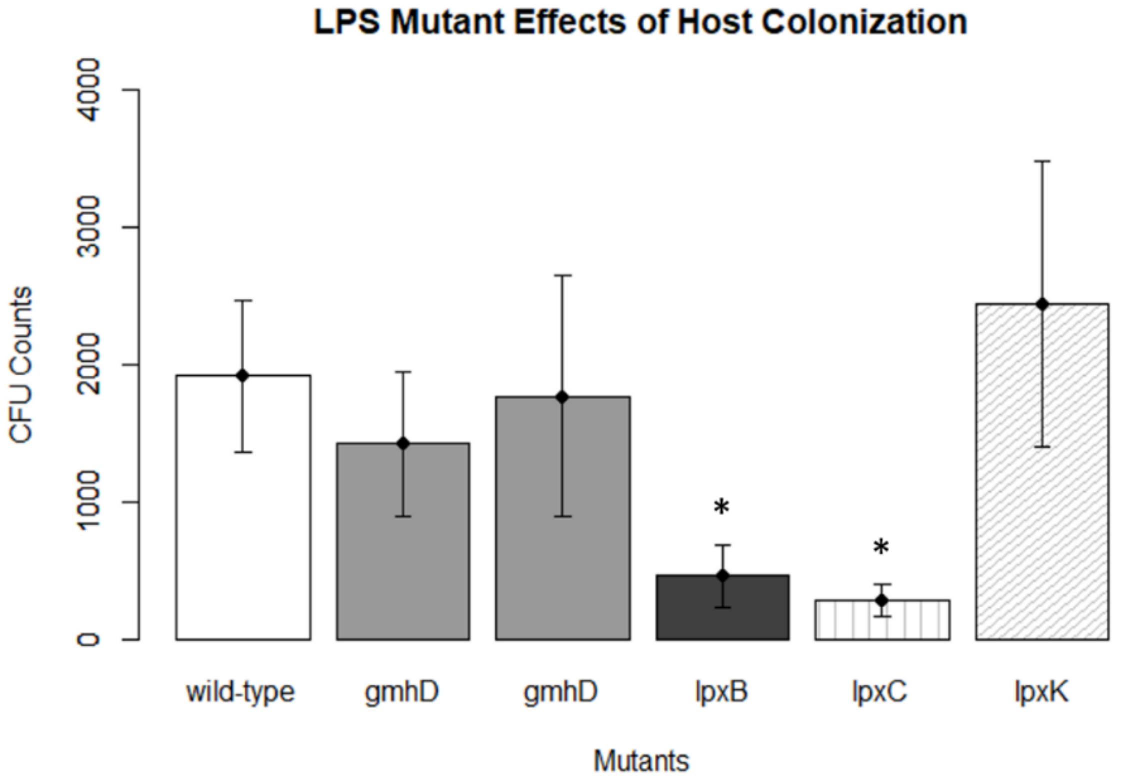
KO	**Pathway**	**top_hit**	**top_hit_adj**	**Reference**	**p-value**	**Fdr correction**	**Essentiality**
ko02010	ABC transporters	9	11	236	0.00049975	0.010594703	nonessential
ko03010	Ribosome	46	46	52	0.00049975	0.010594703	essential
ko00970	Aminoacyl-tRNA biosynthesis	21	22	24	0.00049975	0.010594703	essential
ko03060	Protein export	13	13	19	0.00049975	0.010594703	essential
ko04112	Cell cycle - Caulobacter	12	12	14	0.00049975	0.010594703	essential
ko00500	Starch and sucrose metabolism	1	1	75	0.00149925	0.026486757	nonessential
ko02020	Two-component system	13	15	170	0.002498751	0.037838224	nonessential
ko00195	Photosynthesis	7	7	7	0.003498251	0.046351824	essential
ko01120	Microbial metabolism in diverse environments	44	47	376	0.003998001	0.047087567	nonessential
ko00330	Arginine and proline metabolism	1	1	53	0.005497251	0.058270865	nonessential
ko00010	Glycolysis / Gluconeogenesis	3	3	66	0.008495752	0.081868157	nonessential
ko00240	Pyrimidine metabolism	27	28	78	0.010994503	0.087027915	essential
ko02040	Flagellar assembly	1	1	42	0.010994503	0.087027915	nonessential
ko00780	Biotin metabolism	10	11	22	0.011494253	0.087027915	essential
ko01502	Vancomycin resistance	5	5	5	0.017991004	0.127136432	essential
ko01110	Biosynthesis of secondary metabolites	102	107	419	0.019990005	0.130875739	essential
ko00052	Galactose metabolism	1	1	41	0.020989505	0.130875739	nonessential
ko00620	Pyruvate metabolism	4	4	69	0.023488256	0.138319729	nonessential
ko00550	Peptidoglycan biosynthesis	11	11	25	0.035982009	0.200741734	essential
ko01230	Biosynthesis of amino acids	47	49	176	0.037981009	0.20129935	essential
ko00250	Alanine, aspartate and glutamate metabolism	12	13	34	0.042478761	0.202681268	essential
ko00561	Glycerolipid metabolism	1	1	31	0.042478761	0.202681268	nonessential
ko00740	Riboflavin metabolism	6	6	10	0.043978011	0.202681268	essential
ko02024	Quorum sensing	12	12	112	0.047976012	0.207656172	nonessential
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	13	13	33	0.048975512	0.207656172	essential

Table 3: A KEGG pathway analysis of genes predicted to affect host colonization. A KEGG pathway analysis of genes predicted to affect host colonization revealed that the LPS synthesis pathway is significant in determining bacterial abundance in the fly gut.

KEGG #	Pathway annotation	# genes in top hits	# genes in all ASAHP groups	chisq pval	fdr-corrected pval
ko00540	Lipopolysaccharide biosynthesis	9	24	0.00049975	0.04797601
ko00270	Cysteine and methionine metabolism	7	44	0.03498251	0.88755622
ko00480	Glutathione metabolism	4	16	0.03548226	0.88755622
ko01501	beta-Lactam resistance	4	21	0.05997001	0.88755622
ko03020	RNA polymerase	2	5	0.06446777	0.88755622
ko00240	Pyrimidine metabolism	8	61	0.07246377	0.88755622
ko00450	Selenocompound metabolism	3	14	0.07796102	0.88755622

Validation of MGWA predictions by mutant analysis

Based on the MGWA predictions, we hypothesized that *A. fabarum* DsW_054 bearing lesions in LPS biosynthesis genes would show a reduced ability to associate with *D. melanogaster*. To test this hypothesis, we searched the *A. fabarum* DsW_054 transposon insertion library for all mutants corresponding to one of the KEGG LPS Biosynthesis pathway genes. Five mutants including disruptions in four genes were selected for analysis,, and were individually reared with sterile *D. melanogaster* eggs. CFU load was measured in 5-7 days old adults, revealing that, of the tested genes, *lpxB* and *lpxC* mutants that preceded synthesis ofof Lipid A disaccharide were significantly impaired in their ability to associate with the host relative to wild type *A. fabarum* DsW_054 (Figures 3 and 4). Disruption of two genes downstream of Lipid A disaccharide biosynthesis, *gmhD* and *lpxK*, including 2 distinct *gmhD* lesions, did not significantly alter the ability of *A. fabarum* DsW_054 to associate with its animal host. Taken together, these results suggest an important role for *A. fabarum* DsW_054 Lipid A in *D. melanogaster* association.



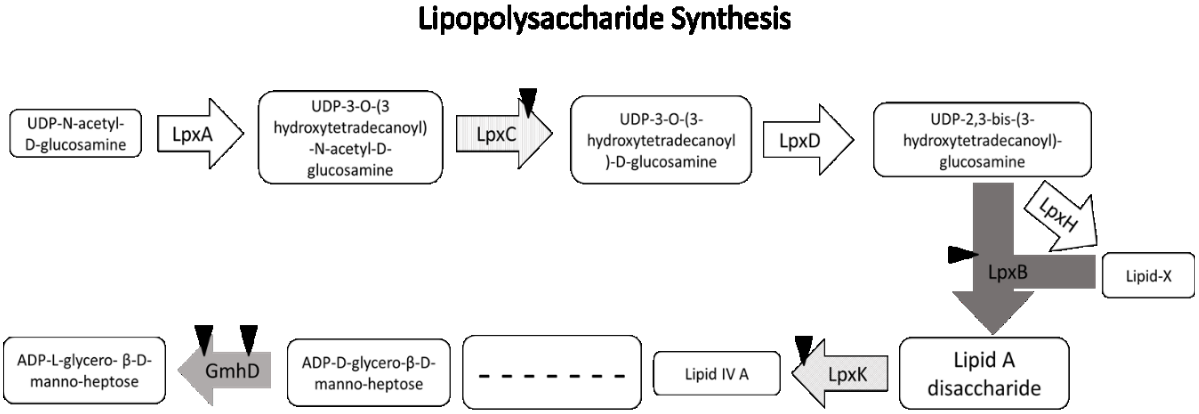


Figure 5: LPS insertion mutant effects on host colonization. Insertion mutants in *lpxB* and *lpxC* have a significant effect on bacterial abundance in the fly gut. Insertion mutants in *gmhD* and *lpxK* did not have a significant effect.

Figure 6: LPS pathway map**.** An analysis of the LPS pathway shows that genes upstream of Lipid A appear to have an affect whereas genes following Lipid A synthesis do not have an effect.

DISCUSSION

In this study we report on an MGWA analysis to predict bacterial genes that influence the association with the fruit fly *D. melanogaster,* the creation of a mapped and arrayed transposon insertion library to identity gene-specific insertions in *A. fabarum* DsW_054, and the use of the mutant library to test the MGWA-predictions. The library includes 6,418 mutants that were mapped to 1,625 genes and 859 intergenic insertions. A 100% validation rate suggested a high accuracy rate of the mapping. Furthermore, based on frequencies of gene insertions suggested near-saturating coverage of non-essential genes and allowed us to make inferences about which genes are essential for *A. fabarum* DsW_054 growth on MRS medium. The host-association tests confirmed the prediction that bacterial LPS biosynthesis genes are necessary for increased bacterial load in the fruit fly, and identified Lipid A biosynthesis genes as key players for these effects. Follow-up experiments that utilize the rich resources available for interrogating host-microbe interactions in *Drosophila* are necessary to characterize the molecular basis for these genetic interactions. The mutant library we report in this manuscript adds to those available resources.

In this study we identified two lipid A biosynthesis genes as important for maintaining abundant *A. fabarum* CFU loads in *Drosophila melanogaster.* This effect was not necessarily surprising given established relationships between bacterial LPS and animal colonization. Consistent with our current findings, the structure of Lipid A in *Francisella tularensis* is important in bacterial resistance to fruit fly anti-microbial peptides, and a lipid A mutant persisted in lower CFU loads during infection than a wild-type control strain [89]. Although the Toll and IMD immune pathways in *Drosophila* do not respond to LPS, *Drosophila* can sense LPS through neuron stimulation, allowing for pathogen protection and infection avoidance. It is hypothesized that this occurs through taste as flies eat, allowing them to avoid unwanted bacteria [90]. LPS causes an increase in serotonin production in insects that increases phagocytosis by hemocytes and improves the insect's ability to fight infection [91]. LPS is also important for bacterial persistence in other animals. For example, *E. coli* LPS mutants are hyper-susceptible to host immunity in c elegans ([92]), and LPS is important for *E. coli* colonization and persistence in sheep [93]. *Vibrio cholerae* LPS mutants had a 30 fold reduction in colonization of the mouse gut[94]. Inactivation of PA0011 (involved in lipid A biosynthesis) in *Pseudomonas aeruginosa* caused decreased virulence and increased susceptibility to antibiotics [95]. A Tn Seq experiment of *Snodgrassella alvi* colonization in honey bees also revealed that LPS is an important factor in colonization [22].Taken together, these findings suggest that LPS biosynthesis is important for host association across the animal kingdom. It has been postulated that it is important because LPS is recognized by the host innate immune system to recognize and defend against potential pathogens prior to infection [96, 97]; however, there must also be other explanations since LPS does not appear to stimulate immune activity in *Drosophila* [98, 99].

An analysis of essential genes in an *Acetobacteraceae* strain has not been determined previously. A method that samples more deeply than our study is necessary for a comprehensive reporting of essential *A. fabarum* DsW_054 genes (e.g. by TnSeq), but the saturation of non-essential genes as estimated by a rarefaction curve (Fig 2) suggests some preliminary insights can be gleaned from our work, including that ribosome, aminoacyl tRNA biosynthesis, protein export and cell cycle functions are likely essential for *A. fabarum* DsW_054 growth in MRS. As a secondary confirmation for this prediction, we detected congruence between these predictions and TnSeq analyses of the closest *A. fabarum* DsW_054 relatives for which a study had been performed : *Alphaproteobacteria Caulobacter crescentus* [19], *Rhizobium leguminosarum* [100] and

Rhodobacter sphaeroides [20]. Chi-square tests on the KEGG pathways enriched in predicted essential genes from these two studies confirmed essential roles for ribosome and Aminoacyl-tRNA biosynthesis in all three organisms, along with nonsignificant but trending enrichment for cell cycle and metabolic pathways (see Supplmentary file 2). One limitation of our analysis *A. fabarum* DsW_054 is that any gene with at least one insertion is binned as non-essential; this categorization does not take into account genes that are only partially disabled by transposon insertion (e.g. into the 3' end of a gene) that could be assigned as essential. Regardless, consistency between the essential genes detected in our study and in other conphyletic taxa lend support to these cautious interpretations.

The arrayed and mapped *A. fabarum* DsW_054 transposon insertion library we created in this study will be a resource for use in any field that studies *Acetobacter* genetics. *Acetobacter* species are studied in a diversity of research fields, including as members of insect microbiomes and in commercial production facilities (e.g. fermentation, cellulose production). We focused on *Acetobacter* as representative members of the *Drosophila* gut microbiota, and previous studies have identified species-specific influence of *Acetobacter* strains on numerous traits, including triacylglyeride and glucose content, metabolic rate, development time, fecundity, dietary choices, and egg laying preferences [24, 56, 101-103]. *Acetobacter* are also commonly associated with numerous other insect species, including honey bees (*Apis mellifera*), *Anopheles* and *Aedes* mosquitos, leafhoppers (*Scaphoideus titanus*), and mealybugs (*Saccharicoccus sacchari*) [104]. *Acetobacter* species are also important in commercial production of acetic acid or fermentation products, such as Kefir, a fermented beverage [60, 61, 63, 105-107]. *Acetobacter* species have also been used in other applications in biotechnology, including microbial fuel cell technology to produce both electricity and acetic acid [108], in the production of bacterial cellulose scaffolds to grow cartilage [109] skin tissue [110] and is a hopeful candidate for dermal medical applications [111]. As such, this mutant library has the potential to serve as a resource for numerous areas of research into the genetic basis for any of these *Acetobacter* applications, and we welcome requests for specific strains of interest.

CHAPTER 2

Influence of *Acetobacter* mutants on *Drosophila melanogaster* starvation resistance

Kylie Makay White; John Chaston; Lindy Koyle; Amber Wise; Rachel Hughes

Foreword: Mutants were selected and cultured by K. Makay White. Lindy Koyle, Rachel Hughes, Amber Wise aided in preparation of mono-associated flies and counting of perished flies. All CFUs were counted by K. Makay White.

INTRODUCTION

Effects of *Drosophila* genetics and behavior on starvation resistance have been characterized previously. The transcriptome of *Drosophila* in response to starvation conditions has been studied and genes that are associated with starvation response have been identified [112, 113]. The feeding behavior of *Drosophila* larvae, but not adults, has been shown to be changed due to starvation conditions to exhibit carnivorous traits [114]. *Drosophila* that show starvation resistance tend to have increased sleep under starvation conditions [115, 116] and tend to become obese [117]. Female *Drosophila* that have been mated show greater variability in starvation resistance compared to males and is also affected by fly genotype [118]. *Drosophila* undergo a tradeoff of starvation resistance and fecundity as ovarian lipid abundance is not affected with changes in starvation resistance [119].

MATERIALS AND METHODS

Bacterial and Fly growth media and conditions.

D. melanogaster Canton S flies were grown at 25°C on a yeast glucose diet containing 100 g/ liter brewer's yeast (inactive) (MP Biomedicals), 100 g/ liter glucose (Sigma), 12 g/ liter agar

(Apex), and preservatives (0.04% phosphoric acid and 0.42% propionic acid (Sigma) on a 12-h-light/12-h-dark cycle.

Bacteria strains used in the study are wild type *Acetobacter fabarum* DsW_054 and transposon insertion mutants of this species (see table 4). Media used included modified MRS broth/agar. *Acetobacter fabarum* gene knock-out mutants were cultured with 30µg/ml chloramphenicol and 50µg/ml kanamycin. All bacterial strains were cultured at 30ºC.

KEGG pathway analysis of MGWAS predictions

The MGWA was performed previously in the Chaston lab and details can be obtained by contacting John Chaston, BYU PWS department. We performed a KEGG pathway analysis on data from the MGWA to identify enriched pathways from the significant results. We selected the top significant gene hits that had a p-value of less than 0.001 and performed a KEGG pathway assignment to identify the number of significant genes in each pathway. The list of KO numbers associated with the significant OG hits was processed through the KEGG Mapper Pathway tool which returned a list of pathways and number of entered OGs in each pathway [51-53]. We performed the same process for all OGs included in the MGWA. Pathways were only used in the analysis if they had 4 or greater counts. We then performed a chi-square test to determine the significance of each pathway containing significant genes to determine pathway significance.

Mutant phenotyping in fruit flies

Mutants were selected from the *Acetobacter fabarum DsW_054* library from significant pathways including methionine, cobalamin, and biotin synthesis. A full list is found in supplementary table 6. Male and female flies were placed together in a cage containing grape juice agar for 16-18 hours to allow for egg collection. Fly eggs were collected and sterilized using 50% bleach solution and placed in sterile food vials with 30-80 eggs. . Eggs were then mono-associated with selected transposon insertion mutants (see table 4) by addition of 50ul 24-48 hour bacterial culture that was normalized to OD_{600} of 0.1. Axenic flies received a sterile inoculation of mMRS. More details can be found in a previous publication from the lab [38]. These mono-associated flies were grown to maturity and processed using the same method as the MGWAS. However, flies were counted at smaller intervals in order to differentiate small differences between mutant and wild type bacteria. They were counted every four hours during the day, and 8 hours over the night (7 am, 11 am, 3 pm, 7 pm and 11 pm) until there were no surviving flies.

RESULTS

KEGG pathway analysis of genes predicted to influence *Drosophila* starvation resistance

The KEGG analysis revealed that bacterial Methionine/Cysteine synthesis, Cobalamin synthesis and Biotin synthesis pathways are predicted to have a significant effect on starvation resistance in fruit flies. (see table 4). Therefore, we selected mutants from the *A. fabarum* gene knock-out library with insertions in genes within these pathways.

Mutant phenotyping in flies: Starvation Resistance

We performed a starvation resistance analysis using mutants selected from the KEGG pathway analysis. We also selected the top twelve significant genes that were predicted in the MGWAS and were present in our gene knock-out library (see table S1). Two mutants were returned as significant in our analysis, cobU/T and ATE1 with p-values of .008173 and .029136 respectively (see figure 7). However, the other mutant in the same gene for each was not significant. The significant mutant in the *ate1* gene was in the middle of the gene while the other was near the very end, perhaps conserving some functionality of the gene. Both *cobU/T* insertion mutants were near the middle of the gene. In addition, the *flgF* mutant also had a low p-value of .0515. Considering these results alone, we could not come to the conclusion that these pathways had a significant effect on starvation resistance in the flies.

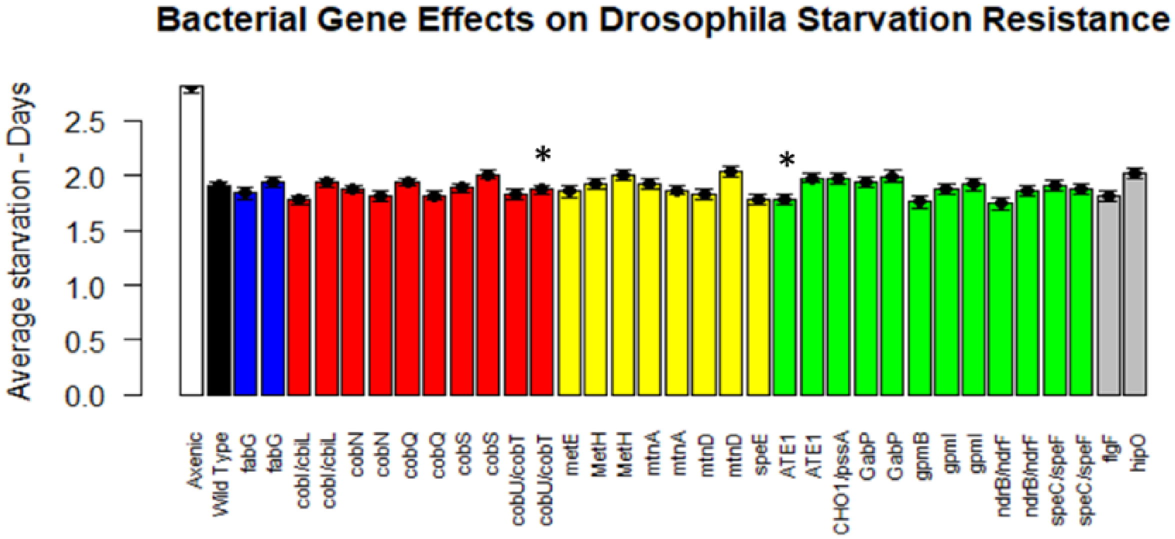


Figure 7: Average time to death under starvation conditions for each of the selected genes. Blue are genes within the Biotin synthesis pathway. Red is genes within the Cobalamin synthesis pathway. Yellow is genes within the Cysteine/methionine synthesis pathway. Green is other genes that were highly significant in the MGWAS predictions. Grey are randomly selected genes to act as controls.

Mutant phenotyping in flies: CFU abundance

In addition to measuring starvation resistance, we calculated the CFUs from fly homogenate and compared to the wild type strain, *Acetobacter fabarum* DsW_054. The results were highly varied with large margins of standard error (see Figure 8). Almost all mutants tested were significant (see table 4). Of note, two mutants, one in ATE1 and one in gpmI, did not return significant values. However, the other mutants in these genes were significant in CFU abundance. These results suggest that each of these metabolic pathways, cysteine/methionine synthesis, cobalamin synthesis, biotin synthesis pathways may be important in determining microbial abundance within the fly gut.

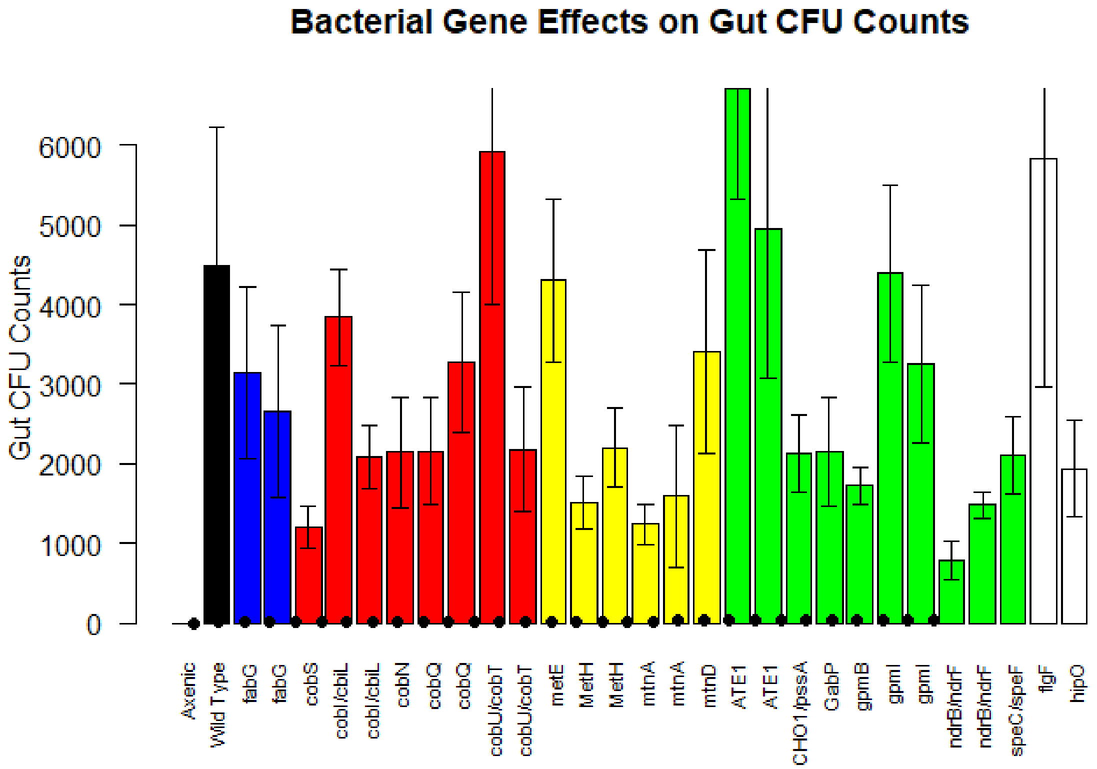


Figure 8: Average CFU counts. Blue are genes within the Biotin synthesis pathway. Red is genes within the Cobalamin synthesis pathway. Yellow is genes within the Cysteine/methionine synthesis pathway. Green is other genes that were highly significant in the MGWAS predictions. Grey are randomly selected genes to act as controls.

DISCUSSION

Considering the mutant phenotyping for starvation resistance, individual gene effects may be small so our time intervals of counting may not have been close enough to observe differences. Starvation results may be observed by counting at smaller intervals such as every 2 hours during the day and 4 hours at night. Fewer mutants should be studied at a time to make this possible.

It is interesting to note that the *flgF* transposon insertion mutant was significant in increasing the CFU count of the *Drosophila* gut. A previous study connected the absence of flagellar motility to commensal *Acetobacter* strains when compared to free living strains [49].

Table 4: Starvation resistance and CFU counts. Insertion mutants selected from the *Acetobacter* DsW_054 library with the associated p-value from the mutant phenotyping analysis (starvation, CFU analysis) and associated gene and pathway.

PlateID	Starvation p-value	CFU p-value	Gene	Pathway
33f7	0.08558636	1.02141E-14	fabG	Biotin
48g9	0.2900261	0	fabG	Biotin
14c5	0.3821282	0	cobI/cbiL	Cobalamin
79g12	0.3961088	0	cobI/cbiL	Cobalamin
36b5	0.6405019	9.67224E-08	cobN	Cobalamin
2g1	0.07580662	#N/A	cobQ	Cobalamin
81a1	0.1452245	5.6033E-12	cobQ	Cobalamin
43g7	0.7782372	0	cobS	Cobalamin
28c11	0.5479124	0	cobU/cobT	Cobalamin
43d7	0.00817322	3.0893E-08	cobU/cobT	Cobalamin
15f11	0.3236036	0.03883268	metE	Cysteine/Methionine
51a8	0.3215517	3.76419E-10	MetH	Cysteine/Methionine
67a5	0.9285515	0	MetH	Cysteine/Methionine
15g9	0.4994935	0	mtnA	Cysteine/Methionine
2c11	0.1139076	0	mtnA	Cysteine/Methionine
52c5	0.344389	0.006904666	mtnD	Cysteine/Methionine
16d12	0.02913587	8.26677E-11	ATE1	Significant from MGWA
78h7	0.7332837	0.335593	ATE1	Significant from MGWA
23c3	0.7414607	6.18772E-12	CHO1/pssA	Significant from MGWA
67h2	0.1608132	8.88148E-16	GabP	Significant from MGWA
17g2	0.224628	0.01110454	gpmB	Significant from MGWA
12h2	0.8328992	0.5814617	gpmI	Significant from MGWA
2h3	0.8920664	1.87838E-09	gpmI	Significant from MGWA
90a11	0.7121406	0	ndrB/ndrF	Significant from MGWA
93c9	0.1867904	0	ndrB/ndrF	Significant from MGWA
7b7	0.3272973	1.26404E-08	speC/speF	Significant from MGWA
22g11	0.05148672	0	flgF	Control
88h8	0.7235707	4.58357E-06	hipO	Control

SUMMARY

We created an arrayed *Acetobacter fabarum* DsW_054 transposon insertion library that provides gene knock-out mutants in 63% of predicted open reading frames. The utility of this resource has been proven in our validation of bacterial genes that affect host colonization abundance in *Drosophila*. The MGWA predicted that the Lipopolysaccharide pathway is important in determining abundance of animal associated bacteria. Our study validated this prediction with genes upstream of Lipid A formation significantly reducing the abundance of *Drosophila* associated bacteria. In addition, we performed a starvation resistance analysis using genes predicted to affect the trait in a previously performed MGWA. From our results we could not verify the effect of biotin, cobalamin or Methionine/cysteine pathways on *Drosophila* starvation resistance. However, these pathways do appear to be important in the abundance of *Drosophila* associated microbes.

The transposon insertion library yielded an important genetic resource and will serve as a resource in our lab, collaborators and other labs that may be interested in *Acetobacter* genetics. This may include labs studying *Drosophila* and other insect associated microbiomes and fermentation research. Mutants of interest can be identified in the attached library file or the file available online with the published manuscript.

BIBLIOGRAPHY

1. Cresci, G.A. and E. Bawden, *Gut Microbiome: What We Do and Don't Know.* Nutr Clin Pract, 2015. 30(6): p. 734-46.
2. Dethlefsen, L., M. McFall-Ngai, and D.A. Relman, *An ecological and evolutionary perspective on human-microbe mutualism and disease.* Nature, 2007. 449(7164): p. 811-8.
3. Gerard, P., *Gut Microbiome and Obesity. How to Prove Causality?* Ann Am Thorac Soc, 2017. 14(Supplement_5): p. S354-s356.
4. Qin, Y. and P.A. Wade, *Crosstalk between the microbiome and epigenome: messages from bugs.* J Biochem, 2017.
5. Sanmiguel, C., A. Gupta, and E.A. Mayer, *Gut Microbiome and Obesity: A Plausible Explanation for Obesity.* Curr Obes Rep, 2015. 4(2): p. 250-61.
6. Hullar, M.A. and B.C. Fu, *Diet, the gut microbiome, and epigenetics.* Cancer J, 2014. 20(3): p. 170-5.
7. Tuddenham, S. and C.L. Sears, *The intestinal microbiome and health.* Curr Opin Infect Dis, 2015. 28(5): p. 464-70.
8. Lozupone, C.A., et al., *Diversity, stability and resilience of the human gut microbiota.* Nature, 2012. 489(7415): p. 220-30.
9. Sommer, F., et al., *Site-specific programming of the host epithelial transcriptome by the gut microbiota.* Genome Biol, 2015. 16: p. 62.
10. Kostic, A.D., et al., *The dynamics of the human infant gut microbiome in development and in progression toward type 1 diabetes.* Cell Host Microbe, 2015. 17(2): p. 260-73.
11. Oyri, S.F., G. Muzes, and F. Sipos, *Dysbiotic gut microbiome: A key element of Crohn's disease.* Comp Immunol Microbiol Infect Dis, 2015. 43: p. 36-49.
12. Dash, S., et al., *The gut microbiome and diet in psychiatry: focus on depression.* Curr Opin Psychiatry, 2015. 28(1): p. 1-6.
13. Flowers, S.A. and V.L. Ellingrod, *The Microbiome in Mental Health: Potential Contribution of Gut Microbiota in Disease and Pharmacotherapy Management.* Pharmacotherapy, 2015. 35(10): p. 910-6.
14. Yin, F. and D. Qian, *Transcriptomic analysis reveals the key immune-related signalling pathways of Sebastiscus marmoratus in response to infection with the parasitic ciliate Cryptocaryon irritans.* Parasit Vectors, 2017. 10(1): p. 576.
15. Proll, M.J., et al., *Transcriptome profile of lung dendritic cells after in vitro porcine reproductive and respiratory syndrome virus (PRRSV) infection.* PLoS One, 2017. 12(11): p. e0187735.
16. Benard, E.L., et al., *Transcriptomic Approaches in the Zebrafish Model for Tuberculosis-Insights Into Host- and Pathogen-specific Determinants of the Innate Immune Response.* Adv Genet, 2016. 95: p. 217-51.
17. Slany, M., J. Oppelt, and L. Cincarova, *Formation of Staphylococcus aureus biofilm in the presence of sub-lethal concentrations of disinfectants: a transcriptomic analysis using RNA-seq.* Appl Environ Microbiol, 2017.
18. Li, Q., et al., *Genome-Wide Transcriptome Profiling of Mycobacterium smegmatis MC(2) 155 Cultivated in Minimal Media Supplemented with Cholesterol, Androstenedione or Glycerol.* Int J Mol Sci, 2016. 17(5).
19. Christen, B., et al., *The essential genome of a bacterium.* Mol Syst Biol, 2011. 7: p. 528.

20. Burger, B.T., et al., *Combining Genome-Scale Experimental and Computational Methods To Identify Essential Genes in Rhodobacter sphaeroides.* mSystems, 2017. 2(3).
21. Arnold, M.F.F., et al., *Genome-Wide Sensitivity Analysis of the Microsymbiont Sinorhizobium meliloti to Symbiotically Important, Defensin-Like Host Peptides.* MBio, 2017. 8(4).
22. Powell, J.E., et al., *Genome-wide screen identifies host colonization determinants in a bacterial gut symbiont.* Proc Natl Acad Sci U S A, 2016. 113(48): p. 13887-13892.
23. Russell, C.W., et al., *The Rhomboid Protease GlpG Promotes the Persistence of Extraintestinal Pathogenic Escherichia coli within the Gut.* Infect Immun, 2017. 85(6).
24. Chaston, J.M., P.D. Newell, and A.E. Douglas, *Metagenome-wide association of microbial determinants of host phenotype in Drosophila melanogaster.* MBio, 2014. 5(5): p. e01631-14.
25. Meijerink, M., et al., *Identification of genetic loci in Lactobacillus plantarum that modulate the immune response of dendritic cells using comparative genome hybridization.* PLoS One, 2010. 5(5): p. e10632.
26. Qin, J., et al., *A metagenome-wide association study of gut microbiota in type 2 diabetes.* Nature, 2012. 490(7418): p. 55-60.
27. Spinler, J.K., et al., *From prediction to function using evolutionary genomics: human-specific ecotypes of Lactobacillus reuteri have diverse probiotic functions.* Genome Biol Evol, 2014. 6(7): p. 1772-89.
28. van Hemert, S., et al., *Identification of Lactobacillus plantarum genes modulating the cytokine response of human peripheral blood mononuclear cells.* BMC Microbiol, 2010. 10: p. 293.
29. Wang, J. and H. Jia, *Metagenome-wide association studies: fine-mining the microbiome.* Nat Rev Microbiol, 2016. 14(8): p. 508-22.
30. *A framework for human microbiome research.* Nature, 2012. 486(7402): p. 215-21.
31. Li, J., et al., *An integrated catalog of reference genes in the human gut microbiome.* Nat Biotechnol, 2014. 32(8): p. 834-41.
32. Qin, J., et al., *A human gut microbial gene catalogue established by metagenomic sequencing.* Nature, 2010. 464(7285): p. 59-65.
33. Weir, T.L., et al., *Stool microbiome and metabolome differences between colorectal cancer patients and healthy adults.* PLoS One, 2013. 8(8): p. e70803.
34. Ma, D., et al., *Studying host-microbiota mutualism in Drosophila: Harnessing the power of gnotobiotic flies.* Biomed J, 2015. 38(4): p. 285-93.
35. Erkosar, B., et al., *Host-intestinal microbiota mutualism: "learning on the fly".* Cell Host Microbe, 2013. 13(1): p. 8-14.
36. Broderick, N.A. and B. Lemaitre, *Gut-associated microbes of Drosophila melanogaster.* Gut Microbes, 2012. 3(4): p. 307-21.
37. Wong, C.N., P. Ng, and A.E. Douglas, *Low-diversity bacterial community in the gut of the fruitfly Drosophila melanogaster.* Environ Microbiol, 2011. 13(7): p. 1889-900.
38. Koyle, M.L., et al., *Rearing the Fruit Fly Drosophila melanogaster Under Axenic and Gnotobiotic Conditions.* J Vis Exp, 2016(113).
39. Erkosar, B. and F. Leulier, *Transient adult microbiota, gut homeostasis and longevity: novel insights from the Drosophila model.* FEBS Lett, 2014. 588(22): p. 4250-7.
40. Wong, A.C., J.M. Chaston, and A.E. Douglas, *The inconstant gut microbiota of Drosophila species revealed by 16S rRNA gene analysis.* Isme j, 2013. 7(10): p. 1922-32.

41. Ren, C., et al., *Increased internal and external bacterial load during Drosophila aging without life-span trade-off.* Cell Metab, 2007. 6(2): p. 144-52.
42. Chaston, J.M., et al., *Host Genetic Control of the Microbiota Mediates the Drosophila Nutritional Phenotype.* Appl Environ Microbiol, 2015. 82(2): p. 671-9.
43. Blum, J.E., et al., *Frequent replenishment sustains the beneficial microbiome of Drosophila melanogaster.* MBio, 2013. 4(6): p. e00860-13.
44. Rogers, G.B., et al., *Functional divergence in gastrointestinal microbiota in physically-separated genetically identical mice.* Sci Rep, 2014. 4: p. 5437.
45. Broderick, N.A., N. Buchon, and B. Lemaitre, *Microbiota-induced changes in drosophila melanogaster host gene expression and gut morphology.* MBio, 2014. 5(3): p. e01117-14.
46. Newell, P.D. and A.E. Douglas, *Interspecies interactions determine the impact of the gut microbiota on nutrient allocation in Drosophila melanogaster.* Appl Environ Microbiol, 2014. 80(2): p. 788-96.
47. Wong, A.C., et al., *The Host as the Driver of the Microbiota in the Gut and External Environment of Drosophila melanogaster.* Appl Environ Microbiol, 2015. 81(18): p. 6232-40.
48. Newell, P.D., et al., *In vivo function and comparative genomic analyses of the Drosophila gut microbiota identify candidate symbiosis factors.* Front Microbiol, 2014. 5: p. 576.
49. Winans, N.J., et al., *A genomic investigation of ecological differentiation between free-living and Drosophila-associated bacteria.* Mol Ecol, 2017. 26(17): p. 4536-4550.
50. Lee, K.A., et al., *Bacterial-derived uracil as a modulator of mucosal immunity and gut-microbe homeostasis in Drosophila.* Cell, 2013. 153(4): p. 797-811.
51. Kanehisa, M., et al., *KEGG: new perspectives on genomes, pathways, diseases and drugs.* Nucleic Acids Res, 2017. 45(D1): p. D353-d361.
52. Kanehisa, M. and S. Goto, *KEGG: kyoto encyclopedia of genes and genomes.* Nucleic Acids Res, 2000. 28(1): p. 27-30.
53. Kanehisa, M., et al., *KEGG as a reference resource for gene and protein annotation.* Nucleic Acids Res, 2016. 44(D1): p. D457-62.
54. Shin, S.C., et al., *Drosophila microbiome modulates host developmental and metabolic homeostasis via insulin signaling.* Science, 2011. 334(6056): p. 670-4.
55. Huang, J.H. and A.E. Douglas, *Consumption of dietary sugar by gut bacteria determines Drosophila lipid content.* Biol Lett, 2015. 11(9): p. 20150469.
56. Fischer, C.N., et al., *Metabolite exchange between microbiome members produces compounds that influence Drosophila behavior.* Elife, 2017. 6.
57. Sansone, C.L., et al., *Microbiota-Dependent Priming of Antiviral Intestinal Immunity in Drosophila.* Cell Host Microbe, 2015. 18(5): p. 571-81.
58. Wong, A.C., et al., *Gut Microbiota Modifies Olfactory-Guided Microbial Preferences and Foraging Decisions in Drosophila.* Curr Biol, 2017. 27(15): p. 2397-2404.e4.
59. Bonatelli, M.L., et al., *Characterization of the contaminant bacterial communities in sugarcane first-generation industrial ethanol production.* FEMS Microbiol Lett, 2017. 364(17).
60. Viana, R.O., et al., *Fermentation process for production of apple-based kefir vinegar: microbiological, chemical and sensory analysis.* Braz J Microbiol, 2017. 48(3): p. 592-601.

61. Wang, L., et al., *The evaluation of kefir pure culture starter: Liquid-core capsule entrapping microorganisms isolated from kefir grains.* Food Sci Technol Int, 2016. 22(7): p. 598-608.
62. Wu, X., et al., *Improving Acetic Acid Production by Over-Expressing PQQ-ADH in Acetobacter pasteurianus.* Front Microbiol, 2017. 8: p. 1713.
63. Moens, F., T. Lefeber, and L. De Vuyst, *Oxidation of metabolites highlights the microbial interactions and role of Acetobacter pasteurianus during cocoa bean fermentation.* Appl Environ Microbiol, 2014. 80(6): p. 1848-57.
64. Yakushi, T. and K. Matsushita, *Alcohol dehydrogenase of acetic acid bacteria: structure, mode of action, and applications in biotechnology.* Appl Microbiol Biotechnol, 2010. 86(5): p. 1257-65.
65. Xia, K., et al., *New insights into the mechanisms of acetic acid resistance in Acetobacter pasteurianus using iTRAQ-dependent quantitative proteomic analysis.* Int J Food Microbiol, 2016. 238: p. 241-251.
66. Nakano, S. and M. Fukaya, *Analysis of proteins responsive to acetic acid in Acetobacter: molecular mechanisms conferring acetic acid resistance in acetic acid bacteria.* Int J Food Microbiol, 2008. 125(1): p. 54-9.
67. Nakano, S., M. Fukaya, and S. Horinouchi, *Putative ABC transporter responsible for acetic acid resistance in Acetobacter aceti.* Appl Environ Microbiol, 2006. 72(1): p. 497-505.
68. Mullins, E.A., et al., *Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile Acetobacter aceti has a distinctive electrostatic surface and inherent acid stability.* Protein Sci, 2012. 21(5): p. 686-96.
69. Emiola, A., J. George, and S.S. Andrews, *A Complete Pathway Model for Lipid A Biosynthesis in Escherichia coli.* PLoS One, 2014. 10(4): p. e0121216.
70. Raetz, C.R. and C. Whitfield, *Lipopolysaccharide endotoxins.* Annu Rev Biochem, 2002. 71: p. 635-700.
71. Whitfield, C. and M.S. Trent, *Biosynthesis and export of bacterial lipopolysaccharides.* Annu Rev Biochem, 2014. 83: p. 99-128.
72. Wang, J., et al., *Construction and characterization of an Escherichia coli mutant producing Kdo(2)-lipid A.* Mar Drugs, 2014. 12(3): p. 1495-511.
73. Karsten, V., et al., *msbB deletion confers acute sensitivity to CO2 in Salmonella enterica serovar Typhimurium that can be suppressed by a loss-of-function mutation in zwf.* BMC Microbiol, 2009. 9: p. 170.
74. Molinaro, A., et al., *Chemistry of lipid A: at the heart of innate immunity.* Chemistry, 2015. 21(2): p. 500-19.
75. Lerouge, I. and J. Vanderleyden, *O-antigen structural variation: mechanisms and possible roles in animal/plant-microbe interactions.* FEMS Microbiol Rev, 2002. 26(1): p. 17-47.
76. Goodman, A.L., *Identifying microbial fitness determinants by Insertion Sequencing (INSeq) using genome-wide transposon mutant libraries.* Nat Protoc, 2012. 6(12): p. 1969-1980.
77. Goodman, A.L., et al., *Identifying genetic determinants needed to establish a human gut symbiont in its habitat.* Cell Host Microbe, 2009. 6(3): p. 279-89.
78. Ramage, B., et al., *Comprehensive arrayed transposon mutant library of Klebsiella pneumoniae outbreak strain KPNIH1.* J Bacteriol, 2017.

79. Matos, R.C., et al., *D-Alanylation of teichoic acids contributes to Lactobacillus plantarum-mediated Drosophila growth during chronic undernutrition.* Nat Microbiol, 2017.
80. De Palma, G., et al., *Microbiota and host determinants of behavioural phenotype in maternally separated mice.* Nat Commun, 2015. 6: p. 7735.
81. Ussar, S., et al., *Interactions between Gut Microbiota, Host Genetics and Diet Modulate the Predisposition to Obesity and Metabolic Syndrome.* Cell Metab, 2015. 22(3): p. 516-530.
82. Cammarota, G., et al., *The involvement of gut microbiota in inflammatory bowel disease pathogenesis: potential for therapy.* Pharmacol Ther, 2015. 149: p. 191-212.
83. Verdu, E.F., H.J. Galipeau, and B. Jabri, *Novel players in coeliac disease pathogenesis: role of the gut microbiota.* Nat Rev Gastroenterol Hepatol, 2015. 12(9): p. 497-506.
84. Bienenstock, J., W. Kunze, and P. Forsythe, *Microbiota and the gut-brain axis.* Nutr Rev, 2015. 73 Suppl 1: p. 28-31.
85. Petra, A.I., et al., *Gut-Microbiota-Brain Axis and Its Effect on Neuropsychiatric Disorders With Suspected Immune Dysregulation.* Clin Ther, 2015. 37(5): p. 984-95.
86. Ha, E.M., et al., *Coordination of multiple dual oxidase-regulatory pathways in responses to commensal and infectious microbes in drosophila gut.* Nat Immunol, 2009. 10(9): p. 949-57.
87. Goodman, A.L., *Identifying microbial fitness determinants by Insertion Sequencing (INSeq) using genome-wide transposon mutant libraries.* Nat Protoc, 2012: p. 1969-1980.
88. Wattam, A.R., et al., *Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center.* Nucleic Acids Res, 2017. 45(D1): p. D535-d542.
89. Vonkavaara, M., et al., *Francisella is sensitive to insect antimicrobial peptides.* J Innate Immun, 2013. 5(1): p. 50-9.
90. Soldano, A., et al., *Gustatory-mediated avoidance of bacterial lipopolysaccharides via TRPA1 activation in Drosophila.* Elife, 2016. 5.
91. Qi, Y.X., et al., *Serotonin modulates insect hemocyte phagocytosis via two different serotonin receptors.* Elife, 2016. 5.
92. Kuo, C.J., et al., *Mutation of the Enterohemorrhagic Escherichia coli Core LPS Biosynthesis Enzyme RfaD Confers Hypersusceptibility to Host Intestinal Innate Immunity In vivo.* Front Cell Infect Microbiol, 2016. 6: p. 82.
93. Cornick, N.A., et al., *Use of signature-tagged mutagenesis to identify genes associated with colonization of sheep by E. coli O157:H7.* Vet Microbiol, 2017. 201: p. 177-182.
94. Nesper, J., et al., *Role of Vibrio cholerae O139 surface polysaccharides in intestinal colonization.* Infect Immun, 2002. 70(11): p. 5990-6.
95. Wang, B., et al., *Pleiotropic effects of temperature-regulated 2-OH-lauroytransferase (PA0011) on Pseudomonas aeruginosa antibiotic resistance, virulence and type III secretion system.* Microb Pathog, 2016. 91: p. 5-17.
96. Charroux, B., et al., *Bacterial detection by Drosophila peptidoglycan recognition proteins.* Microbes Infect, 2009. 11(6-7): p. 631-6.
97. Kurata, S., *Peptidoglycan recognition proteins in Drosophila immunity.* Dev Comp Immunol, 2014. 42(1): p. 36-41.
98. Kaneko, T., et al., *Monomeric and polymeric gram-negative peptidoglycan but not purified LPS stimulate the Drosophila IMD pathway.* Immunity, 2004. 20(5): p. 637-49.

99. Leulier, F., et al., *The Drosophila immune system detects bacteria through specific peptidoglycan recognition.* Nat Immunol, 2003. 4(5): p. 478-84.
100. Perry, B.J., M.S. Akter, and C.K. Yost, *The Use of Transposon Insertion Sequencing to Interrogate the Core Functional Genome of the Legume Symbiont Rhizobium leguminosarum.* Front Microbiol, 2016. 7: p. 1873.
101. Ridley, E.V., et al., *Impact of the resident microbiota on the nutritional phenotype of Drosophila melanogaster.* PLoS One, 2012. 7(5): p. e36765.
102. Morimoto, J., S.J. Simpson, and F. Ponton, *Direct and trans-generational effects of male and female gut microbiota in Drosophila melanogaster.* Biol Lett, 2017. 13(7).
103. Leitao-Goncalves, R., et al., *Commensal bacteria and essential amino acids control food choice behavior and reproduction.* PLoS Biol, 2017. 15(4): p. e2000862.
104. Crotti, E., et al., *Acetic acid bacteria, newly emerging symbionts of insects.* Appl Environ Microbiol, 2010. 76(21): p. 6963-70.
105. Cleenwerck, I., et al., *Acetobacter fabarum sp. nov., an acetic acid bacterium from a Ghanaian cocoa bean heap fermentation.* Int J Syst Evol Microbiol, 2008. 58(Pt 9): p. 2180-5.
106. Garofalo, C., et al., *Bacteria and yeast microbiota in milk kefir grains from different Italian regions.* Food Microbiol, 2015. 49: p. 123-33.
107. Gulitz, A., et al., *The microbial diversity of water kefir.* Int J Food Microbiol, 2011. 151(3): p. 284-8.
108. Tanino, T., et al., *Coproduction of acetic acid and electricity by application of microbial fuel cell technology to vinegar fermentation.* J Biosci Bioeng, 2013. 116(2): p. 219-23.
109. Yin, N., et al., *Agarose particle-templated porous bacterial cellulose and its application in cartilage growth in vitro.* Acta Biomater, 2015. 12: p. 129-38.
110. Keskin, Z., A. Sendemir Urkmez, and E.E. Hames, *Novel keratin modified bacterial cellulose nanocomposite production and characterization for skin tissue engineering.* Mater Sci Eng C Mater Biol Appl, 2017. 75: p. 1144-1153.
111. Taokaew, S., M. Phisalaphong, and B.Z. Newby, *Modification of Bacterial Cellulose with Organosilanes to Improve Attachment and Spreading of Human Fibroblasts.* Cellulose (Lond), 2015. 22(4): p. 2311-2324.
112. Moskalev, A., et al., *A comparison of the transcriptome of Drosophila melanogaster in response to entomopathogenic fungus, ionizing radiation, starvation and cold shock.* BMC Genomics, 2015. 16 Suppl 13: p. S8.
113. Thimgan, M.S., et al., *Identification of genes associated with resilience/vulnerability to sleep deprivation and starvation in Drosophila.* Sleep, 2015. 38(5): p. 801-14.
114. Ahmad, M., et al., *Starvation-Induced Dietary Behaviour in Drosophila melanogaster Larvae and Adults.* Sci Rep, 2015. 5: p. 14285.
115. Masek, P., et al., *Altered regulation of sleep and feeding contributes to starvation resistance in Drosophila melanogaster.* J Exp Biol, 2014. 217(Pt 17): p. 3122-32.
116. Slocumb, M.E., et al., *Enhanced Sleep Is an Evolutionarily Adaptive Response to Starvation Stress in Drosophila.* PLoS One, 2015. 10(7): p. e0131275.
117. Hardy, C.M., et al., *Obesity-associated cardiac dysfunction in starvation-selected Drosophila melanogaster.* Am J Physiol Regul Integr Comp Physiol, 2015. 309(6): p. R658-67.
118. Jang, T. and K.P. Lee, *The genetic basis for mating-induced sex differences in starvation resistance in Drosophila melanogaster.* J Insect Physiol, 2015. 82: p. 56-65.

119. Kalra, B. and R. Parkash, *Trade-off of ovarian lipids and total body lipids for fecundity and starvation resistance in tropical populations of Drosophila melanogaster.* J Evol Biol, 2014. 27(11): p. 2371-85.

APPENDICES

Supplementary Table 1: Primers used

Primer	Sequence
1TN	CTGACCCGGTCGAC
1OLIGOG	CAGACGTGTGCTCTTCCGATCggggggggggg
2TNA	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTnTCGAGATGTGTATAAGAGACAG
2TNB	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTnnTCGAGATGTGTATAAGAGACAG
2TNC	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTnnnTCGAGATGTGTATAAGAGACAG
2TND	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTnnnnTCGAGATGTGTATAAGAGACAG
2BAR01	CAAGCAGAAGACGGCATACGAGAT***ATCACG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR02:	CAAGCAGAAGACGGCATACGAGAT***CGATGT***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR03:	CAAGCAGAAGACGGCATACGAGAT***TTAGGC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR04:	CAAGCAGAAGACGGCATACGAGAT***GCCAAT***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR05:	CAAGCAGAAGACGGCATACGAGAT***ACAGTG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR06:	CAAGCAGAAGACGGCATACGAGAT***CAGATC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR07:	CAAGCAGAAGACGGCATACGAGAT***TGACCA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR08:	CAAGCAGAAGACGGCATACGAGAT***GATCAG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR09:	CAAGCAGAAGACGGCATACGAGAT***ACTTGA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR10:	CAAGCAGAAGACGGCATACGAGAT***CTTGTA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR11:	CAAGCAGAAGACGGCATACGAGAT***TAGCTT***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR12:	CAAGCAGAAGACGGCATACGAGAT***GGCTAC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR13:	CAAGCAGAAGACGGCATACGAGAT***AGTCAA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR14:	CAAGCAGAAGACGGCATACGAGAT***CGTACG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR15:	CAAGCAGAAGACGGCATACGAGAT***TAATCG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR16:	CAAGCAGAAGACGGCATACGAGAT***GTAGAG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR17:	CAAGCAGAAGACGGCATACGAGAT***AGTTCC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR18:	CAAGCAGAAGACGGCATACGAGAT***CAACTA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR19:	CAAGCAGAAGACGGCATACGAGAT***TACAGC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR20:	CAAGCAGAAGACGGCATACGAGAT***GAGTGG***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR21:	CAAGCAGAAGACGGCATACGAGAT***ATGTCA***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR22:	CAAGCAGAAGACGGCATACGAGAT***CACGAT***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR23:	CAAGCAGAAGACGGCATACGAGAT***TCATTC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC
2BAR24:	CAAGCAGAAGACGGCATACGAGAT***GGTAGC***GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC

Supplementary Table 2: Arrayed Transposon insertion library of *Acetobacter* DsW_054. Gene identification (in RAST) is listed in column 1 with all insertions within that gene in column 2 and associated KO numbers listed in the final column.

GeneID	Locations in Arrayed Library	KO #
peg.1	Plate99-C3,Plate37-H3,Plate49-G12,Plate31-E4	0
peg.2	Plate10-D6,Plate21-G4,Plate5-F1,Plate34-A3,Plate40-B1,Plate9-H5,Plate36-A8	K00114
peg.3	Plate26-G5,Plate41-C9,Plate86-G9,Plate28-D11,Plate94-E8	K01975
peg.4	Plate36-H6,Plate79-H6	K06890
peg.5	0	K02297
peg.6	0	K02298
peg.7	0	K02299
peg.8	0	K02300
peg.9	0	K05524
peg.10	Plate78-A5,Plate22-C5,Plate35-G2,Plate50-F11,Plate2-C1,Plate72-H4,Plate21-H2,Plate1-B3,Plate48-F11,Plate81-H8,Plate92-A8,Plate15-B5,Plate16-A7,Plate40-A1,Plate30-E7,Plate30-A4,Plate44-G2	K17675
peg.11	Plate12-C3,Plate55-E1,Plate43-A2,Plate47-D10,Plate23-G6,Plate68-D7	K01255
peg.12	Plate52-B11,Plate52-B11	0
peg.13	Plate2-C6,Plate38-A8	0
peg.14	Plate66-H7,Plate55-A1,Plate18-A6,Plate84-D3,Plate72-A7,Plate2-H1	0
peg.15	0,Plate36-D4,Plate2-A1,Plate13-H6	K13013
peg.16	Plate27-B8,Plate81-F2	0
peg.17	0	0
peg.18	0	0
peg.19	0	0
peg.20	0	K02651
peg.21	0	K02279
peg.22	Plate43-B4,Plate67-G7	K02280
peg.23	0	0
peg.24	0	K02282
peg.25	Plate89-H1	K02283
peg.26	Plate71-C5,Plate29-C12	K12510
peg.27	0	K12511
peg.28	Plate57-H4,Plate59-A12	0
peg.29	0	0
peg.30	Plate86-F11	0
peg.31	Plate89-A2,Plate51-F12	0
peg.32	0	K01465
peg.33	Plate50-B9,Plate68-G8,Plate44-G5,Plate83-A1,Plate13-A1,Plate71-E8	K00383
peg.34	0	K00528
peg.35	Plate89-D5,Plate89-D5	0
peg.36	Plate61-E4,Plate4-E12,Plate36-G7,Plate5-C4,Plate1-H9,Plate66-H1,Plate4-G8,Plate132-C10,Plate99-F11,Plate43-C3,Plate86-A1	K17675
peg.37	Plate27-D3,Plate2-E10,Plate17-E11,Plate53-A2,Plate77-F5	0
peg.38	Plate60-F7,Plate26-C8,Plate79-E5	0
peg.39	Plate27-D1,Plate56-C5,Plate49-D10,Plate87-E8,Plate11-B6,Plate3-D2,Plate81-E12,Plate51-F4,Plate34-D1,Plate34-D2,Plate59-B10,Plate10-C12,Plate84-C12,Plate46-G7	0
peg.40	Plate17-C4,Plate96-C6,Plate66-B11,Plate32-G11,Plate27-B1	K00029
peg.41	0	K02601
peg.42	0	K03073
peg.43	0	0
peg.44	0	K02113
peg.45	0	K02111
peg.46	0	K02115
peg.47	0	K02112
peg.48	Plate56-F4,Plate56-F4	K02114
peg.49	0	K09457
peg.50	Plate11-H4,Plate11-H4	K03684
peg.51	Plate64-E8,Plate61-A1,Plate81-B6,Plate67-B5,Plate66-G3,Plate83-C9,Plate67-C4	0
peg.52	Plate5-B10,Plate2-B5,Plate58-G7	0
peg.53	0	K13583
peg.54	Plate8-G2,Plate42-B3,Plate10-D2	K00767
peg.55	Plate92-H8,Plate92-H8	K03517
peg.56	Plate10-H1,Plate131-B2	0

peg.57	0	0
peg.58	0	0
peg.59	0	K09771
peg.60	0	K00569
peg.61	0	0
peg.62	Plate52-B6,Plate62-C7	0
peg.63	0	0
peg.64	0	K03704
peg.65	Plate68-H1,Plate30-A6,Plate46-F6	0
peg.66	0	K16137
peg.67	Plate29-A3,Plate29-A3	K00135
peg.68	0	K03885
peg.69	Plate68-C8,Plate81-E8,Plate48-G6,Plate99-A8,Plate3-B2	0
peg.70	0	0
peg.71	Plate79-F8,Plate79-F8	K01420
peg.72	Plate21-C7,Plate21-C7	0
peg.73	Plate26-A4,Plate96-C4,Plate66-D6,Plate58-E10,Plate3-A5,Plate27-B7,Plate66-B12,Plate6-B10,Plate79-G4,Plate29-C6,Plate36-A12	0
peg.74	0	0
peg.75	Plate21-D1,Plate14-A4,Plate14-D5,Plate99-B3,Plate100-G6	0
peg.76	Plate88-A9,Plate66-F8,Plate59-D6	K19813
peg.77	Plate31-F9,Plate42-G7,Plate93-B5	0
peg.78	Plate131-B5,Plate32-D8	0
peg.79	Plate89-E5,Plate29-H2,Plate12-F4,Plate63-G5,Plate27-C5,Plate59-E7,Plate35-B12,Plate7-E1	0
peg.80	0	0
peg.81	0	0
peg.82	Plate18-B5,Plate18-B5	K07267
peg.83	Plate2-C7,Plate45-A5,Plate17-E3	0
peg.84	0	0
peg.85	Plate37-H10,Plate84-C2	0
peg.86	0	0
peg.87	Plate94-C11,Plate94-C11	K00817
peg.88	Plate78-E12,Plate45-D6,Plate37-D3,Plate29-A7,Plate5-F5,Plate68-C3,Plate90-G9	K06016
peg.89	Plate87-B4,Plate28-A6,Plate27-C4,Plate35-B4	K12972
peg.90	Plate21-E9,Plate93-H9,Plate91-H3	0
peg.91	0	0
peg.92	Plate50-G10,Plate68-G3	0
peg.93	Plate29-B9,Plate66-F10,Plate54-G5	K02029
peg.94	Plate55-B4,Plate89-F3,Plate59-H7	K09972
peg.95	Plate31-F6,Plate31-F6	K02014
peg.96	0	0
peg.97	Plate3-E8,Plate26-G3,Plate29-H3,Plate131-E5	0
peg.98	0	0
peg.99	Plate48-G1,Plate93-F9,Plate41-F5,Plate93-C8	0
peg.100	Plate76-C9,Plate76-C9	0
peg.101	Plate7-B4,Plate59-B4	0
peg.102	Plate47-B4,Plate47-B4	K02014
peg.103	Plate95-C8,Plate84-H11,Plate10-E9	0
peg.104	Plate28-H9,Plate9-A6,Plate11-E7	0
peg.105	0	0
peg.106	Plate28-E12,Plate100-H4,Plate36-B3,Plate95-B6	0
peg.107	Plate26-C2,Plate62-H4,Plate66-F9,Plate93-G12	K01714
peg.108	0	K18118
peg.109	0	0
peg.110	Plate17-H9,Plate17-H9	K07090
peg.649	Plate72-C3,Plate72-C3	0
peg.650	Plate7-C2,Plate80-G3,Plate10-A2,Plate29-A10,Plate93-F12,Plate30-G12,Plate60-F12	K07137
peg.651	Plate88-C5,Plate76-A8,Plate45-C2,Plate18-A7,Plate2-C12,Plate29-D2	0
peg.652	Plate4-C9,Plate4-C9	0
peg.653	0,Plate35-D6,Plate47-G11	0
peg.654	Plate49-A6,Plate100-F12,Plate52-D9,Plate92-F3,Plate41-B1,Plate17-B4,Plate30-D6	0
peg.655	Plate63-F6,Plate16-D6,Plate50-G4,Plate58-D12,Plate64-G2,Plate92-E6,Plate90-A5,Plate16-B11,Plate48-C11,Plate98-D4	0
peg.656	Plate26-H1,Plate25-B7	0
peg.657	0	0

peg.658	0,Plate25-B5,Plate41-B3	0
peg.659	Plate49-G11,Plate131-D2,Plate2-G10,Plate71-D8	K11996
peg.660	Plate84-E3	0
peg.661	Plate55-F8,Plate98-D11	0
peg.662	0	0
peg.663	Plate49-H11,Plate40-A12,Plate53-E12,Plate71-C12,Plate59-D5	K00873
peg.664	Plate33-D3,Plate43-B2	0
peg.665	Plate96-C2,Plate35-C5,Plate93-G5,Plate90-F1,Plate71-H5,Plate11-B1,Plate94-H6	K01053
peg.666	Plate59-H5,Plate99-E1,Plate132-E8,Plate21-H5,Plate3-G1	0
peg.667	Plate56-E3,Plate56-E3	0
peg.668	Plate6-A9,Plate6-A9	K06207
peg.669	0	0
peg.670	0	0
peg.671	Plate45-F5,Plate11-B12,Plate21-C12,Plate6-C7	K00285
peg.672	0	K00384
peg.673	Plate97-A4,Plate82-F1,Plate14-F6,Plate41-H5,Plate68-B11	K00031
peg.674	Plate39-E1,Plate39-E1	0
peg.675	Plate86-A3,Plate7-D12	0
peg.676	0	0
peg.677	0,Plate24-B6,Plate27-D6,Plate8-A10,Plate42-H3,Plate54-H1,Plate100-D5,Plate64-H3,Plate4-C2,Plate42-D5	0
peg.678	0	K04751
peg.679	0	K01915
peg.680	0	0
peg.681	Plate13-D9,Plate54-C2,Plate95-D3,Plate34-G12,Plate59-B12,Plate42-H5,Plate14-B12	K00117
peg.682	Plate35-E3,Plate35-E3	0
peg.683	Plate98-A10,Plate42-F5,Plate93-A4,Plate8-D4,Plate87-B9	0
peg.684	0,Plate96-F11,Plate83-B5,Plate53-C1,Plate37-D1	0
peg.685	0,Plate36-F3	K03596
peg.686	0	0
peg.687	Plate52-D5,Plate21-C8,Plate58-E2	K00641
peg.688	Plate82-B3,Plate16-G2	0
peg.689	0	K11927
peg.690	Plate95-G1	0
peg.691	0	K01673
peg.692	0	0
peg.693	0	K00950
peg.694	0	K03060
peg.695	Plate11-G1,Plate63-G2	K00951
peg.696	0	K00997
peg.697	0	K03100
peg.698	0	K03685
peg.699	0	K03595
peg.700	0	K09903
peg.701	0	K02838
peg.702	Plate48-E10,Plate48-E10	K00806
peg.703	0	K00981
peg.704	0	K00099
peg.705	Plate26-H9,Plate36-H10,Plate82-D6	K11749
peg.706	0	K07277
peg.707	0	0
peg.708	0	K02536
peg.709	0	K02372
peg.710	0	K00677
peg.711	0	K09949
peg.712	Plate91-B12,Plate91-B12	K01759
peg.713	Plate63-A7,Plate24-G9,Plate79-B2	0
peg.714	Plate77-B1,Plate77-B1	K02914
peg.715	0	K03536
peg.716	0	K03217
peg.717	0	K03978
peg.718	0	K00930
peg.719	0	K00674
peg.720	0	K01439
peg.721	Plate38-B12,Plate43-G1	0

peg.722	Plate43-C6,Plate53-E7	K06173
peg.723	0	K00604
peg.724	0	K01462
peg.725	0	0
peg.726	Plate1-E12,Plate17-E8	0
peg.727	Plate22-E5,Plate35-B9	0
peg.728	Plate38-E10,Plate38-E10	0
peg.729	Plate58-E3,Plate58-E3	0
peg.730	Plate82-E7,Plate91-E3,Plate91-A5,Plate11-A5,Plate57-E11,Plate3-D7	K07140
peg.731	0	K06861
peg.732	0	K09774
peg.733	0	K11719
peg.734	0	K06041
peg.735	Plate42-B10,Plate131-A4,Plate41-B2,Plate29-G12,Plate51-C4	K03684
peg.736	Plate78-F8,Plate5-D2,Plate5-F7	K03218
peg.737	Plate72-G4,Plate34-C12,Plate61-G10,Plate62-F3,Plate12-E10,Plate67-A3,Plate32-H11,Plate32-C3,Plate83-E10,Plate5-H2,Plate23-G7,Plate28-B10	0
peg.738	Plate21-F11,Plate56-E4,Plate78-F1,Plate80-B5,Plate17-E9	0
peg.739	0	K00942
peg.740	0	K02314
peg.741	Plate42-A8,Plate18-E2,Plate87-C10,Plate131-G3,Plate40-B12,Plate40-B3,Plate43-E10	0
peg.742	Plate91-C12,Plate91-C12	0
peg.743	0	0
peg.744	Plate2-G2,Plate86-G11,Plate92-B3,Plate8-E5	K02065
peg.745	Plate35-C6,Plate35-C6	K02066
peg.746	Plate38-G10,Plate10-A11,Plate82-F12,Plate94-D1,Plate11-G10,Plate57-B9,Plate98-F11,Plate72-C5	K04485
peg.747	0,Plate68-C12,Plate8-D8,Plate28-C4,Plate43-E2,Plate100-D11	0
peg.748	0,Plate63-D5,Plate98-A3,Plate21-G6,Plate45-D8,Plate80-G2,Plate11-F10,Plate14-C9,Plate67-H2,Plate132-E3	K11735
peg.749	0	0
peg.750	Plate76-G5,Plate76-B6,Plate12-D4,Plate98-A12,Plate37-B4,Plate58-F8,Plate132-C11,Plate51-H1,Plate1-B1,Plate40-D11,Plate32-D3,Plate64-C9,Plate44-E12,Plate59-D12,Plate82-E5,Plate53-H4,Plate52-H11,Plate46-E5,Plate46-F5,Plate24-A11	K13821
peg.751	0,Plate45-B6,Plate89-F5,Plate9-B2,Plate80-G4,Plate47-C9,Plate26-F9	0
peg.752	0	0
peg.753	0	0
peg.754	Plate51-B2,Plate51-B2	0
peg.755	Plate39-B8,Plate44-C2,Plate54-B6,Plate29-D12,Plate54-B10,Plate50-F12,Plate22-A1,Plate51-A3,Plate46-H9,Plate56-E10,Plate18-G6,Plate29-H4	K01895
peg.756	Plate53-D1,Plate66-G5	0
peg.757	0	0
peg.758	0,Plate17-A3,Plate10-A3	0
peg.759	Plate30-A7,Plate30-A7	0
peg.760	0,Plate85-F7,Plate31-A5,Plate26-B1,Plate79-C1,Plate31-C10	K06968
peg.761	Plate50-F5,Plate81-C4	0
peg.762	Plate83-F1,Plate83-F1	K00798
peg.763	Plate73-G5,Plate73-G5	0
peg.764	Plate60-G12,Plate53-G1	0
peg.765	Plate1-G6,Plate50-H1,Plate61-G9	0
peg.766	0,Plate44-G10,Plate17-E12	0
peg.767	Plate11-G11,Plate18-D1,Plate88-G1	0
peg.768	0	K07566
peg.769	0	K01082
peg.770	0	K01255
peg.771	0	K02339
peg.772	Plate4-E7,Plate87-A5,Plate78-C10,Plate45-G3,Plate7-E12,Plate60-B2,Plate85-C9,Plate71-G3	0
peg.773	Plate42-B7,Plate100-A3,Plate61-D3	K04771
peg.774	Plate31-A9,Plate87-G9,Plate1-A10,Plate23-F7,Plate131-D4,Plate51-D1,Plate8-C3,Plate36-D9,Plate94-C3,Plate15-B3,Plate55-F6	K03579
peg.775	0	0
peg.776	Plate49-B2,Plate71-B8,Plate86-B7,Plate25-A10	K04083
peg.777	0	0
peg.778	Plate84-B6,Plate84-B6	K00611
peg.779	Plate18-C1,Plate15-A9,Plate8-D5	K00821
peg.780	Plate5-D12,Plate5-D12	0
peg.781	0,Plate21-F7,Plate47-A10,Plate28-B11,Plate5-G6,Plate42-E12	K03565

peg.782	Plate10-G10,Plate21-G3,Plate15-E10,Plate100-G5,Plate131-F4	0
peg.783	0	0
peg.784	0	K03116
peg.785	0	K08964
peg.786	Plate39-F3,Plate52-C5,Plate45-F2	K08967
peg.787	Plate29-A4,Plate89-H6	K09880
peg.788	0	K11753
peg.789	0	K01870
peg.790	0	K03101
peg.791	0	0
peg.792	Plate85-E9,Plate9-A4,Plate96-B2,Plate37-F6,Plate58-B6,Plate54-A1,Plate82-C2,Plate39-C11	K03572
peg.793	Plate4-H9,Plate77-C2,Plate58-D3,Plate49-A3,Plate14-C2,Plate79-A2,Plate9-C9	K00342
peg.794	Plate96-B7,Plate79-B9	K11939
peg.795	0	K02622
peg.796	0	0
peg.797	Plate50-D12,Plate50-D12	0
peg.798	Plate57-C5,Plate31-D1	0
peg.799	0	0
peg.800	0	K01738
peg.801	0	0
peg.802	0	0
peg.803	0	0
peg.804	0,Plate14-B8	K03797
peg.805	0,Plate38-C8,Plate60-F8,Plate33-F11,Plate37-H1	K12573
peg.806	0	K03168
peg.807	Plate23-G5,Plate88-H3,Plate36-E3,Plate36-F10,Plate59-D2,Plate81-F10,Plate45-F7,Plate45-G9	K04096
peg.808	Plate47-D6,Plate47-D6	K08591
peg.809	0	K01465
peg.810	0	K00609
peg.811	0	K01885
peg.812	Plate56-B10,Plate34-E3,Plate76-E6,Plate22-D7,Plate97-B5,Plate34-B9,Plate83-D6,Plate92-D7,Plate22-B7,Plate52-H9,Plate40-F5,Plate83-E12,Plate39-A7,Plate25-F3,Plate98-D5,Plate54-C12,Plate82-F7	K02238
peg.813	Plate132-B12,Plate90-H1	0
peg.814	Plate3-D9,Plate62-E6,Plate71-F12,Plate12-B12,Plate71-E4	K06916
peg.815	0	K00164
peg.816	Plate36-H5,Plate36-H5	0
peg.817	Plate12-B5,Plate12-B5	K00658
peg.818	Plate83-A8,Plate72-C11	K00382
peg.819	Plate37-H2,Plate21-H1	0
peg.820	Plate47-B12,Plate5-A8,Plate50-D3,Plate64-H2,Plate57-E12	0
peg.821	0	0
peg.822	0	K01251
peg.823	Plate66-D12,Plate10-B11	K00655
peg.824	0	0
peg.825	Plate51-D3,Plate16-H3,Plate16-H4	0
peg.826	Plate60-B8,Plate59-H8,Plate57-C2,Plate40-C1,Plate5-A3	K01069
peg.827	Plate64-A6,Plate27-D2,Plate10-B3,Plate72-G7	0
peg.828	Plate89-D10,Plate89-A7,Plate4-F12,Plate33-H10,Plate51-D12,Plate57-F12,Plate40-H11,Plate12-C12,Plate56-B12,Plate6-E4,Plate100-C4,Plate39-D11,Plate64-D1,Plate25-D9,Plate58-G4	0
peg.829	Plate46-F12,Plate66-F4	0
peg.830	Plate6-H2,Plate35-F1	0
peg.831	Plate24-C10,Plate32-A11,Plate77-H10	0
peg.832	Plate79-G7,Plate90-C3,Plate13-F11,Plate68-E10,Plate5-B4	0
peg.833	0	0
peg.834	Plate23-C3,Plate23-C3	K17103
peg.835	0	K01613
peg.836	0	K01872
peg.837	Plate49-A8,Plate49-A8	0
peg.838	0	0
peg.839	Plate56-B9,Plate56-B9	0
peg.840	0	0
peg.841	0	0
peg.842	0	K13829
peg.843	Plate41-C4,Plate41-C4	0
peg.844	Plate79-H4,Plate2-B7,Plate63-D12,Plate50-B1	K04763

peg.845	0	0
peg.846	Plate28-G9,Plate28-G9	K01962
peg.847	Plate49-E11,Plate36-D12,Plate92-F9,Plate131-G9,Plate93-H2	0
peg.848	0	K04566
peg.849	Plate5-F10,Plate76-H2,Plate83-B4,Plate80-B6,Plate83-G9,Plate49-F8,Plate11-E11,Plate85-E4	K14205
peg.850	Plate26-G6,Plate30-E6	K05595
peg.851	Plate21-A9,Plate92-H6	K07115
peg.852	0	K01409
peg.853	Plate3-B9,Plate3-B9	0
peg.854	0	K01749
peg.855	0	0
peg.856	0	K01719
peg.857	Plate22-A4,Plate22-A4	K03071
peg.858	0,Plate25-A1	0
peg.859	Plate90-C11,Plate90-C11	0
peg.860	Plate100-F4,Plate100-F4	K00571
peg.861	0,Plate66-G10	K00428
peg.862	Plate37-G5,Plate55-H1,Plate85-B5,Plate83-G8	0
peg.863	Plate76-A11,Plate37-C8,Plate78-C8	0
peg.864	0	K00228
peg.865	Plate72-H11,Plate93-B11,Plate49-C9,Plate55-B3,Plate78-E7,Plate25-B6,Plate76-H8,Plate37-G6,Plate7-B1	K00412
peg.866	Plate51-E9,Plate44-F4	K00413
peg.867	Plate50-E5,Plate68-F11,Plate58-A7,Plate31-B6,Plate10-D5	K00772
peg.868	0	0
peg.869	0	0
peg.870	Plate35-A8,Plate95-C5,Plate91-G3	0
peg.871	0	0
peg.872	0	K00606
peg.873	Plate100-E1,Plate53-E6	0
peg.874	Plate29-F5,Plate131-H6	0
peg.875	Plate43-E12,Plate82-H6	K13953
peg.876	Plate39-B6,Plate39-B6	0
peg.877	Plate50-E9,Plate52-D6,Plate50-E4,Plate95-A10,Plate8-H10,Plate7-F2,Plate9-B4,Plate37-F1,Plate81-C5,Plate60-H4,Plate72-D6,Plate76-F8	0
peg.878	0	K01586
peg.879	0	0
peg.880	0	K01755
peg.881	0	0
peg.882	Plate79-F7,Plate33-A1,Plate90-D8,Plate26-H3,Plate28-H11	0
peg.883	0	K00014
peg.884	0	K00859
peg.885	0	K02342
peg.886	0	0
peg.887	Plate50-H3,Plate50-H3	0
peg.888	0	0
peg.889	0	0
peg.890	Plate58-A4,Plate37-A7	K01783
peg.891	Plate30-A3,Plate43-F2,Plate68-F10,Plate23-D3,Plate36-B1,Plate64-D9,Plate23-D12,Plate94-E12,Plate25-B12,Plate8-E1,Plate30-A1,Plate47-E1,Plate42-G10,Plate71-F6,Plate58-G8,Plate77-B4	K03500
peg.892	0	K11175
peg.893	0	K01933
peg.894	Plate14-D12,Plate14-D12	0
peg.895	Plate33-F10,Plate33-F10	0
peg.896	Plate51-C2,Plate52-B10,Plate66-C9	K00937
peg.897	Plate62-D2,Plate85-G3	K01524
peg.898	Plate31-E8,Plate48-B9,Plate28-B3,Plate85-E8,Plate43-D4,Plate66-C3,Plate67-G3,Plate82-H5,Plate83-B11,Plate14-B7,Plate86-G12	0
peg.899	Plate3-C11,Plate35-B5,Plate48-G3,Plate77-D3,Plate22-G2	K02066
peg.900	Plate13-A7,Plate37-G1,Plate2-A12	K02065
peg.901	Plate61-D8,Plate90-B3,Plate63-G9,Plate92-F1	K02067
peg.902	Plate24-A6,Plate89-F11,Plate93-H8,Plate58-E11,Plate7-C7	0
peg.903	Plate57-H5,Plate53-H6	K08715
peg.904	Plate73-G3,Plate38-B4,Plate95-A8,Plate66-E1	0
peg.905	Plate4-G12,Plate41-B10,Plate68-H5	0
peg.906	Plate51-E12,Plate35-D11	0

peg.907	0,Plate8-A11	K02200
peg.908	0	K02200
peg.909	Plate84-A8,Plate56-E6	K02199
peg.910	Plate82-C1,Plate64-D10	K02198
peg.911	Plate62-D12,Plate62-D12	K02197
peg.912	0	K02196
peg.913	Plate91-H10,Plate40-D2,Plate87-H8,Plate90-C6,Plate82-B7,Plate67-G1	K02195
peg.914	Plate90-G11,Plate90-G11	K09780
peg.915	Plate93-H4,Plate17-E10,Plate63-F1,Plate82-F2,Plate24-F1,Plate55-A2	0
peg.916	0	0
peg.917	Plate38-C1,Plate28-B2,Plate33-H9,Plate31-A8	0
peg.918	Plate40-A10	0
peg.919	0	0
peg.920	Plate57-A11,Plate2-E11,Plate61-H4,Plate71-G1,Plate21-G10,Plate58-H11,Plate3-C10	0
peg.921	0,Plate92-C6,Plate3-A3,Plate50-C6	K00684
peg.922	Plate85-F5,Plate85-F5	0
peg.923	0	0
peg.924	Plate38-A7,Plate22-D4	0
peg.925	0,Plate60-A7	0
peg.926	Plate32-C6,Plate53-F10,Plate54-B4,Plate39-G5,Plate3-E5,Plate30-D7,Plate14-C3,Plate50-B2,Plate9-E1,Plate93-F7,Plate28-C6	0
peg.927	Plate48-G12,Plate4-G4,Plate73-A7,Plate12-B1,Plate3-B6	K00982
peg.928	0	K03564
peg.1336	0	K00666
peg.1337	0	0
peg.1338	0	K00652
peg.1339	0	0
peg.1340	0	0
peg.1341	0	0
peg.1342	0	K07091
peg.1343	0	K11720
peg.1344	Plate93-H6,Plate25-G4,Plate63-A4,Plate31-F2	0
peg.1345	0	0
peg.1346	Plate25-E4,Plate10-G6	K01091
peg.1347	0	K04042
peg.1348	0	K00820
peg.1349	Plate132-E2,Plate5-E4,Plate63-E6,Plate83-G3,Plate68-D4	0
peg.1350	Plate3-A10,Plate16-E2	K20539
peg.1351	0	0
peg.1352	0	K00432
peg.1353	0	K09810
peg.1354	0	K09808
peg.1355	0	K01881
peg.1356	0,Plate12-E6,Plate52-D2	K12574
peg.1357	0	K03525
peg.1358	0	K03524
peg.1359	Plate22-A9,Plate23-E5,Plate97-E4	K00343
peg.1360	Plate57-D9,Plate11-H8,Plate82-G4,Plate64-G3,Plate37-F8	K00341
peg.1361	0	K00340
peg.1362	Plate8-B8,Plate1-G12	K00339
peg.1363	Plate32-A1,Plate32-A1	K00338
peg.1364	Plate47-D5,Plate47-D5	K00337
peg.1365	Plate64-C7,Plate48-F1,Plate47-D3,Plate31-D2	K00336
peg.1366	0	K00335
peg.1367	Plate6-B1,Plate80-H3	K00334
peg.1368	Plate6-F3,Plate44-C6	K00333
peg.1369	0	K00332
peg.1370	0	K00331
peg.1371	Plate63-G7,Plate63-G7	K00330
peg.1372	0	K03530
peg.1373	Plate72-B3,Plate77-C10,Plate91-B3	K01338
peg.1374	0	K03544
peg.1375	0	K01358
peg.1376	Plate71-B12,Plate56-B1,Plate12-B7,Plate48-H4,Plate97-G11,Plate26-F11	K03545

peg.1377	0,Plate24-A4,Plate28-C5,Plate24-B1,Plate4-F2,Plate15-B9,Plate97-F8,Plate96-C8	0
peg.1378	Plate84-B4,Plate33-G5	0
peg.1379	Plate95-D12,Plate66-D1,Plate11-A12	0
peg.1380	0,Plate45-F8,Plate55-G12,Plate81-A6,Plate68-H6,Plate27-B2,Plate66-E12	K03215
peg.1381	0	K13628
peg.1382	0	0
peg.1383	Plate86-F7,Plate37-A8,Plate59-G11,Plate64-E10,Plate71-C9	K04488
peg.1384	0	K11717
peg.1385	0	K09015
peg.1386	0	K09013
peg.1387	0	K09014
peg.1388	Plate32-E7,Plate17-F4,Plate6-C1,Plate38-D10	0
peg.1389	Plate46-D4,Plate81-F5,Plate38-B2	0
peg.1390	0	0
peg.1391	Plate32-H10,Plate36-A9,Plate63-C12,Plate96-D11,Plate76-H9,Plate35-G8,Plate81-D5,Plate93-H5,Plate85-A2,Plate53-B11,Plate79-E1,Plate7-F12,Plate18-F11,Plate131-A10	K01595
peg.1392	0	K02355
peg.1393	0	K02902
peg.1394	Plate57-B11,Plate2-A11	0
peg.1395	Plate56-B7,Plate92-F2,Plate11-E8,Plate94-B8,Plate80-C4,Plate96-G7,Plate39-G1,Plate94-E6,Plate6-G7,Plate83-H1,Plate97-D4	K06147
peg.1396	0,Plate12-A9,Plate47-G4	0
peg.1397	0	K00990
peg.1398	Plate52-F7,Plate57-B2,Plate34-G9,Plate48-C1,Plate1-F2,Plate52-A2,Plate55-H9,Plate28-D8,Plate40-F7,Plate83-H3,Plate35-F10,Plate29-F8,Plate95-A9,Plate82-C3,Plate29-F1,Plate71-D11,Plate13-C5,Plate44-E5	K03555
peg.1399	Plate38-G7,Plate38-F4,Plate39-H5,Plate81-A7,Plate5-H9,Plate11-G5,Plate50-E1,Plate68-F8	0
peg.1400	Plate13-E4,Plate92-C12,Plate77-H11,Plate60-B11,Plate46-D8,Plate23-B4,Plate36-B11,Plate11-F12	K01299
peg.1401	Plate51-H3,Plate31-B5,Plate31-B12	0
peg.1402	0	K01733
peg.1403	Plate78-G6,Plate73-A11,Plate34-F9	0
peg.1404	Plate52-C9,Plate5-A5	K03592
peg.1405	Plate62-H6,Plate92-G6	0
peg.1406	0	0
peg.1407	0	K02301
peg.1408	Plate47-G2,Plate131-F5,Plate68-H7,Plate87-C2	K02274
peg.1409	0	0
peg.1410	0	K00570
peg.1411	Plate94-A2,Plate73-H2,Plate45-B10	K01920
peg.1412	Plate46-A6,Plate92-B10,Plate86-B12,Plate29-E8	0
peg.1413	Plate94-D8,Plate44-B8	K00721
peg.1414	0	0
peg.1415	0,Plate2-A3,Plate88-F3	K00384
peg.1416	Plate15-F12,Plate15-F12	0
peg.1417	0	0
peg.1418	Plate35-G7,Plate91-E1,Plate86-B4,Plate48-C5,Plate58-E8	K02334
peg.1419	0	K03980
peg.1420	Plate49-F10,Plate61-G6,Plate46-D5,Plate57-D1,Plate21-B4,Plate98-C6,Plate31-G9	0
peg.1421	Plate29-F11,Plate22-G7,Plate67-B9	0
peg.1422	0	K04764
peg.1423	0	K00648
peg.1424	0	K03621
peg.1425	Plate4-E4,Plate4-E4	0
peg.1426	Plate90-A1,Plate90-A1	0
peg.1427	Plate25-E12,Plate55-B8,Plate38-D4,Plate51-B10	K07638
peg.1428	0	K07659
peg.1429	Plate95-G3,Plate63-H8,Plate34-G1	0
peg.1430	Plate61-C7,Plate53-E8,Plate27-F11	K18587
peg.1431	0	K01462
peg.1432	0	K02970
peg.1433	Plate25-B3,Plate7-A10	K00052
peg.1434	Plate46-G8,Plate46-G8	K01704
peg.1435	Plate8-C6,Plate57-C7,Plate64-D3,Plate31-B1,Plate36-B9,Plate16-C2	K01703
peg.1436	0	K02884
peg.1437	Plate56-A12,Plate98-F2,Plate97-B9,Plate40-H6	K00554
peg.1438	0	K02860

peg.1439	0	K02959
peg.1440	0	K03106
peg.1441	Plate67-B11,Plate67-B11	K06006
peg.1442	0	0
peg.1443	Plate24-G3,Plate13-B3,Plate42-F12,Plate24-G10,Plate60-C5,Plate86-G3,Plate46-E1,Plate59-G10,Plate58-H7,Plate29-A9,Plate91-G7,Plate54-D11,Plate91-E12,Plate16-D9,Plate77-H2,Plate41-F2	K07289
peg.1444	0	K06179
peg.1445	Plate54-C4,Plate36-G9,Plate81-A3,Plate99-E4,Plate41-C3,Plate49-D6,Plate91-A10	K07478
peg.1446	0	0
peg.1447	0	K03179
peg.1448	Plate23-H7,Plate23-H7	0
peg.1449	Plate58-F4,Plate4-B11,Plate50-G11,Plate36-H4,Plate30-H3,Plate3-G12,Plate1-C6,Plate87-A9	K09761
peg.1450	0	K01919
peg.1451	Plate34-B10,Plate40-D7,Plate53-H1,Plate42-D4,Plate96-B1	0
peg.1452	Plate14-G6,Plate56-D7,Plate99-D5,Plate11-H6,Plate80-B2,Plate24-H11,Plate16-C7	K08169
peg.1453	0	K03977
peg.1454	0	0
peg.1455	Plate23-B5,Plate27-A5,Plate56-D12	0
peg.1456	0	0
peg.1457	Plate100-G9,Plate73-E2	0
peg.1458	0,Plate6-H11,Plate92-G7	0
peg.1459	Plate13-E6,Plate84-G12,Plate81-E5,Plate26-E10,Plate22-E12,Plate81-D3	K06980
peg.1460	Plate92-B5,Plate92-B5	K01496
peg.1461	Plate40-D6,Plate40-D6	K00748
peg.1462	Plate49-D9,Plate49-D9	0
peg.1463	Plate92-B7,Plate36-C8	K03321
peg.1464	Plate46-E3,Plate54-D9	K17247
peg.1465	Plate30-C1,Plate73-C12,Plate84-E12,Plate49-B1	0
peg.1466	Plate61-A2,Plate58-D6,Plate83-A3,Plate60-D7	K02291
peg.1467	Plate14-B6,Plate14-B6	0
peg.1468	0	K04564
peg.1469	0,Plate83-B12,Plate88-G12,Plate78-B1,Plate94-C2,Plate55-F9,Plate52-G3,Plate30-B8	K03695
peg.1470	Plate46-B1,Plate46-B1	0
peg.1471	Plate33-F9,Plate33-F9	0
peg.1472	Plate38-G6,Plate90-C9,Plate52-G8	K03665
peg.1473	0	K03666
peg.1474	0	K13599
peg.1475	Plate52-A12,Plate22-A5	K13598
peg.1476	0,Plate62-D8,Plate100-A4,Plate60-C4	K07712
peg.1477	Plate15-B10,Plate21-B12	K07708
peg.1478	0,Plate17-C6,Plate40-C9,Plate87-B5,Plate79-E10,Plate42-G1,Plate31-G10,Plate45-H10	0
peg.1479	0	K12506
peg.1480	Plate29-D1,Plate29-D1	K04752
peg.1481	0	K03185
peg.1482	0	K00640
peg.1483	0	0
peg.1484	0	K00769
peg.1485	Plate85-A1,Plate85-A1	0
peg.1486	0	0
peg.1487	Plate56-A7,Plate56-A7	0
peg.1488	Plate92-H1	0
peg.1489	Plate81-B1,Plate6-G5,Plate46-B7,Plate56-F1,Plate66-B2,Plate41-F6,Plate60-F3,Plate61-F2,Plate34-B3	K02014
peg.1490	Plate95-B4,Plate57-G6,Plate58-A6,Plate27-F2	K07165
peg.1491	0	K03088
peg.1492	Plate46-F11,Plate81-D4	0
peg.1493	0	K10679
peg.1494	0	0
peg.1495	0	0
peg.1496	Plate25-D3,Plate25-D3	0
peg.1497	0,Plate28-D7	0
peg.1498	Plate53-F1,Plate53-F1	0
peg.1499	Plate39-E7,Plate132-G10	0
peg.1500	Plate47-F8,Plate47-F8	0
peg.1501	0	K02356

peg.1502	0	K01092
peg.1503	Plate15-E7,Plate76-F2,Plate8-D3	0
peg.1504	Plate51-C7,Plate54-C10,Plate61-C8,Plate45-H9,Plate31-H10,Plate22-G12,Plate64-C12,Plate61-H2,Plate52-C7,Plate23-C4	K03722
peg.1505	Plate45-E9,Plate45-E9	K03704
peg.1506	Plate85-E2,Plate93-B9,Plate23-B6,Plate42-H2	K01061
peg.1507	0	K04078
peg.1508	0	K04077
peg.1509	Plate38-A10,Plate38-A10	0
peg.1510	0,Plate5-C5,Plate23-F3	K03320
peg.1511	0	K15034
peg.1512	0	0
peg.1513	0,Plate7-D3	0
peg.1514	Plate131-B7,Plate5-F6,Plate72-H9,Plate15-G11,Plate71-H9,Plate88-C8,Plate23-E8,Plate23-B3,Plate89-G9	K01259
peg.1515	Plate51-C9,Plate82-E2,Plate63-F7,Plate85-C3	K03733
peg.1516	Plate85-H3,Plate94-G12	K04066
peg.1517	Plate2-E2,Plate24-G1	K03210
peg.1518	Plate90-E11,Plate17-H10,Plate49-F7	K06923
peg.1519	Plate22-B5,Plate93-C4	0
peg.1520	Plate17-D1,Plate50-B10,Plate88-F9,Plate77-E6,Plate23-E1	K03574
peg.1521	Plate26-C10,Plate26-H2,Plate27-A6,Plate23-G11,Plate94-G6,Plate54-E8,Plate26-G2	K10764
peg.1522	Plate132-E5,Plate28-B9,Plate97-E7,Plate12-F11,Plate10-G3,Plate48-D11	K06195
peg.1523	0	K01495
peg.1524	0	K05520
peg.1525	0,Plate72-A10,Plate91-F10	K03638
peg.1526	Plate7-G3,Plate4-F8,Plate55-A12,Plate7-F1,Plate58-C2	K07267
peg.1527	Plate21-D7,Plate61-F1,Plate57-A6,Plate64-E11,Plate79-H1,Plate32-C11,Plate21-C3,Plate41-A3,Plate131-G6,Plate54-B2,Plate131-F10	0
peg.1528	Plate36-A10,Plate131-D3,Plate4-B4,Plate45-H1,Plate55-B1,Plate25-C6,Plate14-D3,Plate92-G11	0
peg.1529	0	0
peg.1530	Plate39-A12,Plate5-B5	0
peg.1531	0	0
peg.1532	Plate66-H9,Plate11-F6	0
peg.1533	Plate59-F2,Plate95-C7,Plate57-E7,Plate64-F7	0
peg.1534	Plate37-G3,Plate14-D1,Plate37-D11,Plate39-B4,Plate85-C4,Plate32-B3,Plate39-C8,Plate53-B5,Plate42-B11,Plate66-B7,Plate37-A2,Plate14-E12	K07789
peg.1535	0	0
peg.1536	Plate96-D1,Plate83-D12,Plate93-E6,Plate131-B1,Plate48-A6	K17218
peg.1537	0	K07003
peg.1538	Plate32-H7,Plate2-B11,Plate95-E6,Plate24-B5,Plate3-B11	0
peg.1539	0	K00794
peg.1540	0	K14652
peg.1541	0	K00793
peg.1542	0	K11752
peg.1543	Plate23-C9,Plate44-A12,Plate17-A6	K00412
peg.1544	Plate89-F12,Plate21-C5	K00413
peg.1545	Plate36-C2,Plate36-C2	K00411
peg.1546	Plate97-H10,Plate94-F8	0
peg.1547	Plate45-A4,Plate51-E8,Plate40-G6,Plate76-G1,Plate88-B3,Plate94-G1,Plate58-A11,Plate24-C12,Plate14-C1,Plate84-D5,Plate91-D10	0
peg.1548	Plate26-B2,Plate26-B2	0
peg.1549	Plate43-B12,Plate43-B12	0
peg.1550	Plate83-H2,Plate131-C4	0
peg.1551	Plate66-G4,Plate36-C6,Plate87-D3	0
peg.1552	Plate90-E3,Plate18-A4	K01476
peg.1553	0	0
peg.1554	Plate131-C2,Plate98-G1,Plate21-E9	K01534
peg.1555	0	0
peg.1556	Plate50-D2,Plate2-F8,Plate27-F6,Plate132-H10	0
peg.1557	0,Plate88-C6,Plate67-C1,Plate42-F11,Plate22-G4,Plate81-B7	0
peg.1558	Plate94-B5,Plate132-E4	0
peg.1559	0	0
peg.1560	0	0
peg.1561	Plate47-C11,Plate47-E4,Plate31-A1	0
peg.1562	0	0

peg.1563	0	0
peg.1564	0	K02888
peg.1565	0	K02899
peg.1566	0	K03979
peg.1567	Plate86-C4,Plate79-C11,Plate28-E3,Plate33-G8,Plate3-D10,Plate26-E1,Plate97-A1	K00931
peg.1568	Plate96-D2,Plate7-D9,Plate12-D10	0
peg.1569	0	0
peg.1570	Plate61-C10,Plate78-C4,Plate16-F12,Plate6-E8,Plate77-G10,Plate79-D6,Plate94-H1,Plate35-D3,Plate51-F2	K00036
peg.1571	Plate49-B10,Plate9-E12	0
peg.1572	Plate7-H3,Plate51-G4,Plate42-H4,Plate79-E12,Plate16-D11,Plate51-G3,Plate36-E6,Plate61-G7,Plate15-B4,Plate62-E4,Plate39-A3	K01066
peg.1573	0	0
peg.1574	0	0
peg.1575	Plate88-G5,Plate26-C4	K03925
peg.1576	Plate88-E4,Plate42-H9	K03438
peg.1577	0	0
peg.1578	0	K03587
peg.1579	0	K01928
peg.1580	0	K01929
peg.1581	0	K01000
peg.1582	0	K01925
peg.1583	0	K03588
peg.1584	0	K02563
peg.1585	0	K01924
peg.1586	0	K00075
peg.1587	0	K01921
peg.1588	0	K03589
peg.1589	0	K03590
peg.1590	0	K03531
peg.1591	Plate12-F8,Plate12-F8	K02535
peg.1592	0	K05807
peg.1593	Plate4-F4,Plate31-D8,Plate47-E2,Plate79-B6,Plate8-E2,Plate13-C10,Plate5-G2,Plate53-G3,Plate6-D11,Plate99-B7	K03631
peg.1594	0	K01972
peg.1595	0,Plate53-B4,Plate82-G11,Plate34-B4,Plate61-B9,Plate91-C7,Plate12-A2,Plate66-G2	K01006
peg.1596	0	K09773
peg.1597	0	0
peg.1598	Plate44-G7,Plate32-F10	0
peg.1599	0	0
peg.1600	0	K01626
peg.1601	Plate9-G3,Plate92-A10,Plate59-B8,Plate9-F7	K00763
peg.1602	Plate14-F11,Plate77-A10,Plate56-G12,Plate55-G10	0
peg.1603	0	K01885
peg.1604	Plate68-C7,Plate68-C7	0
peg.1605	Plate34-B5,Plate49-C6,Plate97-H4	0
peg.1606	Plate91-C2,Plate50-A4,Plate13-H8,Plate63-A8,Plate76-D6,Plate88-C4,Plate33-A3	K17686
peg.1607	Plate66-E9,Plate66-H3	0
peg.1608	Plate73-G7,Plate28-C7,Plate51-G5,Plate66-E6,Plate88-B6,Plate23-G12,Plate23-G10,Plate79-E9,Plate41-G8,Plate29-E7	0
peg.1609	Plate13-E3,Plate97-D12,Plate21-B6,Plate8-B7,Plate44-C5	K07233
peg.1610	Plate26-A10,Plate82-F11	0
peg.1611	Plate71-D5,Plate23-D1,Plate57-F10,Plate27-G4	K11927
peg.1612	Plate9-C8,Plate18-D10,Plate33-B7	K03781
peg.1613	Plate61-E2	0
peg.1614	0	0
peg.1615	Plate81-B4,Plate83-B3	K00053
peg.1616	Plate72-E11,Plate40-D5,Plate36-D6,Plate14-D6	K01653
peg.1617	0,Plate53-A7,Plate26-D7,Plate92-H4,Plate38-B8,Plate91-G11,Plate12-G6,Plate98-D9,Plate71-F9	K01652
peg.1618	Plate64-D5,Plate59-C10,Plate30-F11,Plate76-G10,Plate2-G5,Plate72-G1,Plate97-D10,Plate95-D10,Plate14-B11,Plate7-E4	K00791
peg.1619	0	K01079
peg.1620	0	0
peg.1621	Plate29-B6	K07807
peg.1622	Plate45-E11,Plate37-F2,Plate46-F8,Plate46-C9	0
peg.1623	0	K07276

peg.1624	0	0
peg.1625	0	K11927
peg.1626	Plate33-G1,Plate11-F2,Plate7-F10,Plate55-G4,Plate91-F3,Plate47-A8	0
peg.1627	Plate67-F7,Plate57-C9,Plate45-A2,Plate43-C1	0
peg.1628	0	K00600
peg.1629	Plate15-B8,Plate27-G7	0
peg.1630	0	K01698
peg.1631	Plate78-H7,Plate16-D12	K00685
peg.1632	0	K02621
peg.1633	Plate64-A10,Plate32-C10	K03584
peg.1634	0	K02357
peg.1635	0	K02967
peg.1636	0,Plate15-C3,Plate50-C1	0
peg.1637	Plate59-C6,Plate92-C11,Plate47-F4,Plate15-E11,Plate93-D5	K00826
peg.1638	Plate60-E6,Plate100-E3,Plate132-A8	K01665
peg.1639	0	K02337
peg.1640	0	K01918
peg.1641	Plate48-B12,Plate35-G3,Plate84-G3	0
peg.1642	Plate76-E3,Plate22-E11	K02051
peg.1643	Plate32-G4,Plate48-A4	0
peg.1644	0,Plate79-H10,Plate9-A3	K00812
peg.1645	Plate66-D7,Plate62-D1,Plate32-H8	K00812
peg.1646	Plate131-G1,Plate8-A1,Plate53-F9,Plate25-F12	K01894
peg.1647	Plate31-F11,Plate87-A8,Plate72-D4	0
peg.1648	Plate66-D8,Plate97-C7	0
peg.1649	Plate87-E3,Plate86-B6	K07213
peg.1650	Plate67-H5,Plate37-A5,Plate43-C4,Plate93-A7,Plate97-E10	0
peg.1651	Plate84-E2,Plate9-H7,Plate41-D3,Plate95-B8,Plate30-E5	0
peg.1652	0	K00940
peg.1653	Plate8-G1,Plate92-A12	K06158
peg.1654	0	0
peg.1655	Plate16-E3,Plate1-F5,Plate100-E11,Plate9-D3,Plate4-G6,Plate76-C11,Plate50-B8	K19577
peg.1656	Plate66-G7,Plate91-G12,Plate63-D11,Plate23-A1	0
peg.1657	0,Plate93-G1	K02483
peg.1658	Plate11-E2,Plate54-F6,Plate18-B11,Plate18-D12,Plate83-F11	0
peg.1659	Plate23-H4,Plate23-H4	0
peg.1660	Plate55-A6,Plate8-C9,Plate31-D3	0
peg.1661	0	K02520
peg.1662	0	K01868
peg.1663	Plate63-F11,Plate97-D6,Plate4-A7	0
peg.1664	Plate78-A10,Plate9-D9,Plate67-D11,Plate2-A6,Plate73-B3,Plate5-E6	0
peg.1665	Plate66-G12,Plate66-G12	0
peg.1666	0	K00858
peg.1667	0	0
peg.1669	0	K03469
peg.1670	0	K02204
peg.1671	0	K03527
peg.1672	0	0
peg.1673	0	0
peg.1674	Plate97-H11,Plate15-H8,Plate26-F12,Plate57-B5,Plate57-F3,Plate37-H6,Plate34-G11	K08602
peg.1675	Plate18-A2,Plate48-B5,Plate3-H11,Plate64-B4,Plate78-H1,Plate64-G10,Plate35-A5,Plate77-B9,Plate27-F12,Plate37-G9,Plate44-F12,Plate80-C2,Plate53-A8,Plate17-D5,Plate12-G4,Plate38-H8,Plate5-D7,Plate55-F11,Plate36-B7	K00265
peg.1676	Plate63-B1,Plate77-G11,Plate17-C1,Plate78-G7,Plate86-D1,Plate72-H7,Plate87-A12	K00266
peg.1677	Plate35-F5,Plate35-F5	0
peg.1678	Plate93-G2,Plate32-C9,Plate5-H10,Plate54-E9,Plate87-F7,Plate59-B1,Plate32-E1	K00329
peg.1679	Plate79-C10,Plate26-F3,Plate86-C2	K01448
peg.1680	Plate72-G3,Plate8-E6,Plate22-E3,Plate3-H8,Plate56-C2,Plate38-F2	K08300
peg.1681	0	0
peg.1682	0	K00765
peg.1683	0	K00013
peg.1684	0	K02518
peg.2028	0	0
peg.2029	Plate39-C12,Plate81-H2	K01633

peg.2030	Plate30-G3,Plate30-G3	0
peg.2031	Plate80-A4,Plate80-E1,Plate18-D8,Plate21-D8	K00102
peg.2032	0,Plate11-A2	K02073
peg.2033	Plate10-G4,Plate52-G9,Plate27-B11,Plate34-F5	K02071
peg.2034	0	K02072
peg.2035	Plate47-E3,Plate47-E3	0
peg.2036	Plate77-G5,Plate9-B10,Plate35-E7	K02014
peg.2037	Plate81-C12,Plate81-C12	0
peg.2038	Plate52-H2,Plate9-G12	K03919
peg.2039	0	0
peg.2040	Plate57-E3	K03307
peg.2041	0	0
peg.2042	Plate10-A7,Plate26-H8	0
peg.2043	Plate47-G1,Plate80-C3,Plate6-F10	K09001
peg.2044	Plate49-H4,Plate11-F7	0
peg.2045	0	K03474
peg.2046	0	K00097
peg.2047	Plate17-E2,Plate17-E2	0
peg.2048	0	K01591
peg.2049	0	K01817
peg.2176	0	0
peg.2177	Plate31-C2,Plate91-H11,Plate36-A5,Plate80-D6,Plate23-D7,Plate2-D5,Plate94-F12,Plate85-A4	K03561
peg.2178	0,Plate82-E4,Plate18-E10	K03559
peg.2179	Plate99-D4,Plate99-D4	K03832
peg.2180	0	K03711
peg.2181	0	0
peg.2182	0	K03088
peg.2183	Plate32-G2,Plate51-B4	K07165
peg.2184	Plate44-H5,Plate41-H11,Plate56-F7	K02014
peg.2185	Plate17-B10,Plate17-B10	0
peg.2186	Plate35-G9,Plate35-G9	0
peg.2187	0	0
peg.2188	0	0
peg.2189	Plate26-H4,Plate26-H4	0
peg.2190	0	K01779
peg.2191	0	0
peg.2192	0	0
peg.2193	Plate96-A4,Plate96-A4	0
peg.2194	Plate85-B1,Plate80-B10,Plate29-C7,Plate72-D9	K02083
peg.2195	0	K03424
peg.2196	Plate44-B6,Plate12-E7	K01486
peg.2197	Plate56-C1,Plate49-D4,Plate12-B8,Plate60-A1	K06901
peg.2198	Plate61-C9,Plate87-C3,Plate36-F1,Plate5-H7,Plate6-C2,Plate82-G6	K01620
peg.2199	Plate17-G11,Plate17-G11	K04046
peg.2200	Plate48-F8,Plate12-E1,Plate88-B9,Plate78-H4,Plate80-E5,Plate51-H5,Plate53-C9	0
peg.2201	0,Plate76-F4,Plate2-D2,Plate96-H1,Plate79-B12,Plate47-C10	K02014
peg.2202	Plate22-D3,Plate31-A12,Plate16-A2	K01133
peg.2203	Plate10-E7,Plate10-E7	0
peg.2204	0	K07112
peg.2205	Plate30-A8,Plate30-A8	K07112
peg.2206	Plate86-B2,Plate64-A2,Plate45-C3,Plate88-G10,Plate59-G4,Plate71-C4	K11717
peg.2207	Plate50-G7,Plate50-G7	0
peg.2208	0	K00640
peg.2209	0	0
peg.2210	Plate22-A8,Plate22-A8	0
peg.2211	0	K06045
peg.2212	Plate95-H4,Plate95-H4	0
peg.2213	Plate22-B4,Plate57-C3	0
peg.2214	Plate30-A10,Plate30-A10	0
peg.2215	Plate83-G5,Plate83-G5	K06199
peg.2216	Plate12-H6,Plate29-D10,Plate90-A4,Plate44-D7	0
peg.2217	Plate29-B1,Plate29-B1	0
peg.2218	Plate81-F4,Plate87-F1	0
peg.2219	Plate39-H11,Plate66-D9	0

peg.2220	0	0
peg.2221	0	0
peg.2222	Plate28-D2,Plate22-B1,Plate36-E5,Plate42-F4	K13069
peg.2223	0	0
peg.2224	0	K07336
peg.2225	Plate53-B12,Plate54-G12,Plate62-H3	0
peg.2226	Plate93-E2,Plate83-D1	0
peg.2227	Plate131-A3,Plate37-C4,Plate62-E9,Plate95-G4	K01093
peg.2228	0	0
peg.2229	0	0
peg.2230	0	K03088
peg.2231	Plate40-C10,Plate13-E10,Plate34-E12,Plate91-B2,Plate25-F7,Plate21-E5	0
peg.2232	Plate40-H1,Plate40-H1	K07110
peg.2233	Plate33-C10,Plate76-A10,Plate77-G9	K01720
peg.2234	Plate39-F7,Plate46-G3	K01659
peg.2235	Plate7-E3,Plate7-E3	K03417
peg.2236	Plate18-G3,Plate34-H9	K01895
peg.2237	Plate57-B4,Plate57-B4	K08178
peg.2238	Plate87-C6,Plate83-A5	0
peg.2239	0	0
peg.2240	Plate14-C7,Plate55-H10,Plate5-G7	0
peg.2241	Plate83-A11,Plate81-H9,Plate131-F7	K00661
peg.2242	Plate5-B11,Plate47-H9,Plate34-B6	0
peg.2243	0	0
peg.2244	Plate90-A7,Plate49-E5	K19689
peg.2245	Plate88-C12,Plate89-H5,Plate76-B4	0
peg.2246	0,Plate6-D4,Plate81-A9,Plate84-F3,Plate72-B9,Plate72-C6,Plate91-H1,Plate11-H9,Plate46-B6	0
peg.2247	Plate63-C7,Plate42-A5	0
peg.2248	0	K01876
peg.2249	Plate49-A12,Plate49-A12	0
peg.2250	Plate33-B3,Plate57-H3,Plate18-A8,Plate35-A10,Plate14-C10,Plate132-H11,Plate85-F3,Plate44-C7,Plate64-B11	K01620
peg.2251	0	K02897
peg.2252	0	K01056
peg.2253	0	K06942
peg.2254	Plate28-E8,Plate9-A11,Plate49-B8,Plate10-D12	K00147
peg.2255	Plate34-E7,Plate34-E7	K00969
peg.2256	Plate67-B8,Plate67-B8	K09710
peg.2257	Plate81-D9,Plate4-A6	K00783
peg.2258	0,Plate78-F9	0
peg.2259	Plate42-E5,Plate28-E10,Plate90-H9,Plate2-G12,Plate5-C1,Plate23-E2	K11738
peg.2260	0	0
peg.2261	Plate2-F12,Plate2-E3,Plate41-F9,Plate60-H5	K03719
peg.2262	0	0
peg.2263	Plate37-E12,Plate26-G11,Plate73-E12	K01575
peg.2264	Plate52-E10,Plate48-E2,Plate40-E4,Plate36-G1	K01652
peg.2265	Plate3-F12,Plate32-G8,Plate49-C7,Plate60-D2,Plate6-D3,Plate89-F8,Plate63-B10,Plate85-D12,Plate18-B8	K00104
peg.2266	Plate25-H10,Plate49-A5,Plate13-H2,Plate4-D1,Plate3-C9	K11472
peg.2267	Plate42-C8,Plate97-B1,Plate62-D9,Plate48-G7,Plate63-E4	K11473
peg.2268	Plate95-A6,Plate1-D8,Plate36-E10,Plate18-E4,Plate48-B4,Plate43-H4	K01576
peg.2269	Plate45-D4,Plate40-C12,Plate81-H5	K18928
peg.2270	Plate131-B6,Plate57-E4,Plate46-E8,Plate92-G1,Plate10-B7	K18929
peg.2271	Plate77-H8,Plate43-F5	K00782
peg.2272	0	K00790
peg.2273	0	K01494
peg.2274	Plate46-G11,Plate46-G11	0
peg.2275	Plate60-C2,Plate60-C2	K07267
peg.2276	0	0
peg.2277	0	0
peg.2278	0	0
peg.2279	Plate39-H7,Plate8-H5	0
peg.2280	0	K00720
peg.2281	0	K07323
peg.2310	0,Plate9-A8,Plate25-E10,Plate57-G3,Plate34-C3,Plate56-H6,Plate16-F4,Plate96-E6,Plate45-C10	0
peg.2311	0	K02837

peg.2312	Plate98-H3,Plate26-F8	0
peg.2313	Plate61-B10,Plate92-D3,Plate13-B5,Plate12-A1,Plate6-F8,Plate89-G6,Plate18-H1,Plate84-D1	0
peg.2314	0	K00030
peg.2315	Plate73-E1,Plate71-E1,Plate11-F1,Plate83-F2,Plate27-E10	K01262
peg.2316	Plate71-G7,Plate15-G1,Plate72-D11,Plate7-C4,Plate53-C4,Plate26-E5,Plate89-F9	K02687
peg.2317	Plate131-G5,Plate16-G6,Plate78-B11,Plate50-E3,Plate50-D11,Plate12-D7	K03657
peg.2318	Plate94-C4,Plate85-C10,Plate61-G2	K03630
peg.2319	Plate17-G8,Plate93-A5,Plate84-B5,Plate94-H5	K03630
peg.2320	0	K01589
peg.2321	0	K01588
peg.2322	Plate36-E4,Plate36-E4	0
peg.2323	0	0
peg.2324	Plate94-A3,Plate37-B2,Plate87-E1	K09987
peg.2325	Plate36-H1,Plate42-D11,Plate17-C5,Plate40-F10,Plate23-B1	K04080
peg.2326	0	K02909
peg.2327	Plate37-E3,Plate37-E3	K03282
peg.2328	Plate72-F7,Plate72-F7	0
peg.2329	0	K03074
peg.2330	0	K03072
peg.2331	0	0
peg.2332	Plate62-A9,Plate22-G8,Plate13-C3,Plate42-H11	0
peg.2333	Plate17-C8,Plate95-F11	K00525
peg.2334	Plate90-A11,Plate93-C9	K00526
peg.2335	Plate81-C1,Plate30-D1,Plate131-A6,Plate86-A2,Plate31-E9	0
peg.2336	0	K02523
peg.2337	0	K01776
peg.2338	0	K00762
peg.2339	Plate42-H1,Plate42-H1	0
peg.2340	0	0
peg.2341	Plate84-A3	K01647
peg.2342	0	0
peg.2343	Plate99-D8,Plate99-D8	K08296
peg.2344	0	K04092
peg.2345	Plate84-A4,Plate84-A4	0
peg.2346	0	0
peg.2347	0	0
peg.2348	0,Plate6-E9,Plate38-G9,Plate9-G10,Plate30-E1	K18118
peg.2349	Plate2-A5,Plate84-H11,Plate1-C10,Plate51-C8	0
peg.2350	Plate93-B10,Plate82-H7,Plate60-C9,Plate55-D11,Plate100-E2,Plate68-G7,Plate25-H1,Plate85-H1,Plate84-A5,Plate60-D3,Plate29-E4,Plate91-D8,Plate10-G1,Plate15-D12,Plate41-A4,Plate55-C5,Plate51-G9,Plate39-D10,Plate56-D5,Plate16-A8	K03529
peg.2351	Plate132-F5,Plate80-D3	0
peg.2352	0	0
peg.2353	0	K07042
peg.2354	Plate1-A7,Plate48-B3,Plate14-H10,Plate28-F2,Plate85-H7,Plate87-C12	K06217
peg.2355	Plate76-B3,Plate5-H1,Plate28-E4,Plate32-B9	K06168
peg.2356	0,Plate67-G11	K00655
peg.2357	Plate49-G3,Plate32-A10,Plate92-C1,Plate2-H9,Plate30-H11,Plate72-E7,Plate51-E2	K07278
peg.2358	Plate91-H9,Plate85-E10,Plate9-B11,Plate95-B7,Plate54-A9,Plate58-G1,Plate77-D5,Plate26-D5,Plate32-F6,Plate38-G2,Plate40-F12,Plate55-D4,Plate53-D5,Plate37-D9,Plate2-H4,Plate66-A1,Plate38-G1	K09800
peg.2359	0	0
peg.2360	Plate32-F1,Plate38-A1	K01142
peg.2361	Plate89-D9,Plate51-F10,Plate1-D6,Plate67-F1,Plate34-A8,Plate58-F3,Plate41-C5	K01273
peg.2362	Plate90-G8,Plate55-A10,Plate37-B1,Plate37-B8,Plate33-E12,Plate94-E11,Plate1-F7,Plate27-B12,Plate1-H1,Plate17-C3	K03703
peg.2363	0	K08744
peg.2364	0	0
peg.2365	0	K03636
peg.2366	0,Plate88-F8,Plate14-B9,Plate15-G7	K03635
peg.2367	0	K00833
peg.2368	0	K00652
peg.2369	0	K02170
peg.2370	0	K01935
peg.2371	0	K01356
peg.2372	Plate18-B2,Plate40-F1,Plate18-E7,Plate6-E12,Plate29-G4,Plate2-C3	K03750

peg.2373	0	0
peg.2374	Plate91-A7,Plate92-C7,Plate67-C7,Plate40-C2,Plate8-E4	K01689
peg.2375	Plate26-B6,Plate32-B4	0
peg.2376	Plate99-D3,Plate6-F5,Plate52-C4,Plate73-D7,Plate78-G8,Plate71-B6,Plate97-D1,Plate47-F1	K03153
peg.2377	0	K03154
peg.2378	Plate53-H11,Plate24-B4,Plate11-A8,Plate99-D1	K03149
peg.2379	Plate10-C8,Plate96-E4,Plate96-G11	K00788
peg.2380	0,Plate83-A4,Plate16-H9,Plate32-E5,Plate22-F7,Plate68-C4,Plate26-C11,Plate131-F6	K03655
peg.2381	0	K09159
peg.2382	Plate14-F1,Plate44-D3,Plate45-E10,Plate43-F8,Plate38-D5,Plate98-C10,Plate46-B8,Plate28-H1,Plate21-A7,Plate25-H8,Plate77-H7,Plate89-B3	K03723
peg.2383	Plate42-G4,Plate42-G4	0
peg.2384	Plate44-B2,Plate23-D5,Plate15-D9,Plate29-E9	K14347
peg.2385	Plate77-C8,Plate68-D5,Plate39-G10,Plate96-E10,Plate95-F9,Plate98-E8,Plate94-E7,Plate62-E10,Plate6-F9,Plate3-G7	0
peg.2386	0,Plate86-D2,Plate62-C2,Plate40-D3,Plate62-E2,Plate39-B3	K09883
peg.2387	Plate43-G7,Plate40-E7,Plate56-C12,Plate85-B2	K09882
peg.2388	Plate35-H2,Plate43-H3,Plate80-A5,Plate56-E9	0
peg.2389	Plate54-H4,Plate54-H4	K05527
peg.2390	0	0
peg.2391	0	K03801
peg.2392	0	K00963
peg.2393	0	K01840
peg.2394	Plate99-D6,Plate48-D9,Plate39-H8	K03639
peg.2395	Plate8-G10,Plate48-A8,Plate96-C12,Plate99-C1,Plate13-G1,Plate12-G12,Plate56-C11	0
peg.2396	Plate55-B11,Plate82-F8,Plate80-H1	0
peg.2397	Plate63-F8,Plate8-A12,Plate3-D4	0
peg.2398	0	K03676
peg.2399	0	0
peg.2400	Plate71-F2,Plate71-F2	0
peg.2401	0	K00568
peg.2402	0,Plate81-G1,Plate50-G12	K00928
peg.2403	0	K02371
peg.2404	Plate55-C11,Plate45-H8,Plate45-H8	K15539
peg.2405	0	K03526
peg.2406	0	K01892
peg.2407	0	K02835
peg.2408	Plate91-A9,Plate64-B10,Plate86-D7,Plate25-E9	0
peg.2409	0,Plate90-G10	K02493
peg.2410	0	0
peg.2411	Plate66-G8,Plate86-D3	0
peg.2412	Plate72-F3,Plate72-F3	K02067
peg.2413	0	K06153
peg.2414	Plate7-C11,Plate44-B1,Plate28-A4	K03294
peg.2415	Plate2-G6,Plate92-C2,Plate43-B9,Plate34-A9	0
peg.2416	0,Plate3-H4,Plate24-B9,Plate66-E7	0
peg.2417	Plate15-A4,Plate27-A7	K08305
peg.2418	0,Plate35-H1,Plate34-C5	K03642
peg.2419	Plate13-F3,Plate21-D9,Plate95-A3	K07258
peg.2420	0	K00943
peg.2421	0	K02341
peg.2422	0	K01874
peg.2423	0	K03424
peg.2424	Plate85-B7,Plate85-B7	K06167
peg.2425	Plate41-E8,Plate16-A3,Plate14-E8,Plate23-C2,Plate44-C3,Plate76-D12	0
peg.2426	0	K00275
peg.2427	0	K00208
peg.2428	0	K01736
peg.2429	0	K04063
peg.2430	0	K00116
peg.2431	0	K01737
peg.2432	Plate96-D4,Plate22-D12	K06920
peg.2433	Plate57-G4,Plate52-H4,Plate66-C8	0
peg.2434	0	K01012
peg.2435	Plate67-C5,Plate21-E6,Plate40-E6	K09712

peg.2436	Plate29-F2,Plate41-F8	K09958
peg.2437	Plate71-D1,Plate7-E5,Plate96-F12,Plate13-D1,Plate52-G11,Plate47-B10	0
peg.2438	Plate56-A6,Plate62-F7	0
peg.2439	Plate96-A8,Plate11-E12,Plate93-E12,Plate21-B7,Plate49-A9,Plate30-F9	K01754
peg.2440	Plate49-C10,Plate67-G2,Plate91-D3	0
peg.2441	Plate54-C5,Plate54-C5	K00390
peg.2442	Plate21-C1,Plate62-A8	K00957
peg.2443	Plate18-H4,Plate85-C6,Plate4-F3,Plate12-C2,Plate7-E2	K00955
peg.2444	Plate84-G8,Plate46-A8,Plate45-A10,Plate87-E10	K02046
peg.2445	Plate59-B11,Plate32-H3	K02047
peg.2446	Plate33-E6,Plate33-F1,Plate18-G4	K02045
peg.2447	0	0
peg.2448	Plate76-E11,Plate79-G2	K00381
peg.2449	0,Plate79-A10	0
peg.2450	Plate26-B12,Plate10-F10,Plate77-E5	K02527
peg.2451	Plate56-F6,Plate56-F6	K00912
peg.2452	Plate54-B3,Plate63-A12,Plate53-A9,Plate78-E1,Plate61-C5,Plate29-A1	K02517
peg.2453	Plate48-C9,Plate30-D4,Plate25-D7,Plate80-F11	K01092
peg.2454	Plate2-F7,Plate49-E1	0
peg.2455	Plate13-G10,Plate60-E4	K07082
peg.2456	0	K09458
peg.2457	0	K02078
peg.2458	0	K00059
peg.2459	0	K00645
peg.2460	0	0
peg.2461	Plate53-A11,Plate47-H3,Plate58-H12,Plate62-C9,Plate95-F12,Plate84-G7,Plate31-E6	0
peg.2462	Plate92-B1,Plate92-B1	K02002
peg.2463	0	0
peg.2464	0	0
peg.2465	Plate14-C6,Plate16-H6	0
peg.2466	0	K03704
peg.2467	0	K03664
peg.2468	0	K01714
peg.2469	Plate31-E7,Plate52-G4,Plate41-E1,Plate55-C9,Plate94-F7,Plate27-B6,Plate62-A6,Plate66-H11	K04518
peg.2470	0	K00979
peg.2471	Plate64-F1,Plate64-F1	0
peg.2472	0	K08738
peg.2473	0	0
peg.2474	Plate60-F4,Plate60-F4	K00058
peg.2475	Plate68-G6,Plate68-G6	K07391
peg.2476	Plate50-C7,Plate86-H10	K07391
peg.2477	Plate67-B3,Plate17-F12,Plate92-C4,Plate26-D6,Plate29-E12	K01760
peg.2478	Plate26-A6,Plate26-G10	K01011
peg.2479	Plate54-A6,Plate100-D8	0
peg.2480	0,Plate80-D11,Plate59-H3	0
peg.2481	Plate33-A5,Plate55-D7	K06131
peg.2482	Plate44-F1,Plate44-F1	0
peg.2483	0	0
peg.2484	0	K07390
peg.2485	0	0
peg.2486	0	K01952
peg.2487	0	K01952
peg.2488	Plate17-G12,Plate17-G12	0
peg.2489	0	K01952
peg.2490	0	K01923
peg.2491	0	K01756
peg.2492	0	0
peg.2493	Plate3-E6,Plate47-E10,Plate43-E9,Plate72-D5,Plate3-H12,Plate40-C7,Plate48-E6,Plate35-D12	K08309
peg.2494	Plate10-C7,Plate10-C7	K01095
peg.2495	Plate49-H7,Plate52-F1,Plate99-F2,Plate85-H8	K03743
peg.2496	Plate9-E9,Plate1-B10,Plate5-B9	0
peg.2497	0	K18588
peg.2498	0	K03644
peg.2499	Plate37-E7,Plate87-B3,Plate59-F9	K00382

peg.2500	0,Plate47-H1,Plate47-H1	K00627
peg.2501	Plate7-F7,Plate86-A8,Plate31-G8,Plate31-B7,Plate29-H8,Plate57-A3	K00162
peg.2502	Plate2-F3,Plate43-B5,Plate31-F8,Plate79-E4,Plate90-B7	K00161
peg.2503	Plate44-D10,Plate44-D10	K03637
peg.2504	0	K01609
peg.2505	0	K00766
peg.2506	0	K01658
peg.2507	0	K01657
peg.2508	0,Plate82-G5,Plate46-D3,Plate45-G8	K03770
peg.2509	0	K01803
peg.2510	0	K03075
peg.2511	0	K01937
peg.2512	0	K01627
peg.2513	0	K02470
peg.2514	Plate88-A1,Plate11-C2,Plate83-F4	K03629
peg.2515	0	K02338
peg.2516	0	K02313
peg.2517	0	K02968
peg.2518	Plate45-D10,Plate85-G1	K10563
peg.2519	0	K03183
peg.2520	0	K13038
peg.2521	0	K01520
peg.2522	Plate80-B11,Plate29-B8,Plate2-B1	K02050
peg.2523	Plate31-E10,Plate30-G1,Plate99-G1,Plate51-B5	K02049
peg.2524	Plate62-H10,Plate62-H10	K07304
peg.2525	0	K01873
peg.2526	Plate41-D8,Plate41-D8	0
peg.2527	Plate68-F12,Plate50-G9,Plate10-F5,Plate68-B5,Plate56-F11	K12340
peg.2528	Plate17-A8,Plate49-B5,Plate21-F6,Plate12-E4	K00573
peg.2529	Plate99-A11,Plate11-D9,Plate16-E5,Plate90-B2,Plate72-F4	K01462
peg.2530	0	K03322
peg.2531	Plate77-A3,Plate77-A3	0
peg.2532	Plate56-A1,Plate16-E4	K00627
peg.2533	Plate53-D6,Plate46-E7,Plate80-A7,Plate26-E2	K00162
peg.2534	0,Plate11-D11,Plate88-H11,Plate56-H4	K00161
peg.2535	Plate26-E11,Plate46-D11,Plate36-A3,Plate73-F12	0
peg.2536	Plate68-C5,Plate36-D8,Plate13-H4	K00925
peg.2537	Plate36-F11,Plate62-F1	K00625
peg.2538	Plate40-A3,Plate58-E6,Plate60-A12,Plate29-B10	0
peg.2539	0	0
peg.2540	0,Plate38-E12	0
peg.2541	Plate35-F2,Plate67-A11	0
peg.2542	Plate86-H6	0
peg.2543	Plate86-C1,Plate39-B7,Plate24-B12	K00121
peg.2544	0	0
peg.2545	0	0
peg.2546	0	0
peg.2547	Plate9-B3,Plate5-A4,Plate27-E12,Plate8-F9,Plate97-C4,Plate41-G5	0
peg.2548	Plate40-E10,Plate40-E10	0
peg.2549	Plate13-A11,Plate87-B2,Plate16-B3	K19784
peg.2550	0,Plate93-E1	K06911
peg.2551	0,Plate73-E6	0
peg.2552	0	0
peg.2553	0	0
peg.2554	Plate96-B3,Plate56-H5,Plate15-F3,Plate5-F4,Plate47-B8,Plate66-A8	K05916
peg.2555	0,Plate15-G8,Plate82-C4,Plate48-C6,Plate91-D9,Plate56-E8	0
peg.2556	Plate14-G11,Plate91-F1,Plate83-H5,Plate62-E1	0
peg.2557	Plate93-D11,Plate81-E11	0
peg.2558	Plate58-C9,Plate44-B3,Plate61-C4,Plate30-E4,Plate27-H1	0
peg.2559	Plate53-G6,Plate83-E6,Plate68-D11	K02379
peg.2560	Plate11-C3,Plate38-H10,Plate45-C9	K03752
peg.2561	Plate51-E11,Plate51-E11	K03753
peg.2562	Plate13-G5,Plate92-B9,Plate46-H4	K03750
peg.2563	Plate57-G5,Plate32-F7	K02380

peg.2564	0	K00127
peg.2565	Plate52-H5,Plate40-F2,Plate10-A8,Plate22-B3,Plate72-H1	K00124
peg.2566	Plate47-F10,Plate3-D1,Plate87-B12,Plate15-C7,Plate50-E6,Plate98-F4,Plate64-A8,Plate56-C9,Plate33-E2,Plate5-E3,Plate87-A10	K00123
peg.2567	Plate26-D1,Plate26-D1	K09758
peg.2568	Plate79-D12,Plate22-C1	0
peg.2569	Plate84-G10,Plate84-G10	0
peg.2570	0	K03406
peg.2571	0	K03406
peg.2572	Plate87-B1,Plate33-A2	0
peg.2573	Plate39-G6,Plate82-H9,Plate10-F12,Plate7-E8,Plate45-B5,Plate63-B5	K01524
peg.2574	0	K02427
peg.2575	Plate99-H9,Plate99-H9	K04085
peg.2576	0	K03602
peg.2577	0	K00795
peg.2579	Plate26-B7,Plate27-E7,Plate58-G11,Plate90-E9,Plate45-G6	0
peg.111	Plate13-B2,Plate13-B2	0
peg.112	0	0
peg.113	Plate79-C4,Plate79-C4	0
peg.114	Plate82-D4,Plate9-H1,Plate53-F12,Plate3-D11,Plate44-C10,Plate14-G10,Plate37-F10,Plate60-A9	0
peg.115	Plate68-H2,Plate38-E1,Plate84-D9,Plate32-D4,Plate43-H7,Plate4-F6	0
peg.116	Plate54-B12,Plate23-F1,Plate59-G1,Plate28-F6,Plate32-C4,Plate13-C11,Plate59-F1,Plate97-H9,Plate81-B11,Plate131-A5	K02400
peg.117	Plate131-B4,Plate50-A7	K02404
peg.118	Plate72-F5,Plate72-F5	0
peg.119	0	0
peg.120	0	0
peg.121	Plate25-G5,Plate9-A9	K03411
peg.122	Plate54-D5,Plate12-G3	K03413
peg.123	0,Plate27-A3	K03412
peg.124	0	K00575
peg.125	Plate58-D4,Plate58-D4	K03408
peg.126	Plate31-D12,Plate79-F11,Plate47-C6,Plate21-B9,Plate1-D12,Plate64-H1,Plate94-F1	K03407
peg.127	0	K03413
peg.128	Plate31-C8,Plate96-E11,Plate90-E1,Plate22-A6,Plate63-A3,Plate22-A12,Plate39-C3,Plate98-F3,Plate82-A9	K03406
peg.129	0	0
peg.130	Plate7-B5,Plate7-B5	K02419
peg.131	Plate1-H2,Plate1-H2	0
peg.132	0	K02417
peg.133	Plate26-B8,Plate9-G8,Plate23-E4	K02411
peg.134	Plate42-B6,Plate72-B5,Plate7-B9,Plate82-E8	K02410
peg.135	Plate55-H4,Plate93-A2,Plate78-E8,Plate9-D1,Plate15-E7	K02409
peg.136	0,Plate86-A5,Plate50-D10	0
peg.137	0	0
peg.138	Plate59-G8,Plate42-C9,Plate38-E6	0
peg.139	Plate56-C8,Plate56-C8	0
peg.140	0	0
peg.141	Plate4-G5,Plate85-G9,Plate5-E1,Plate77-A1,Plate32-F4	K02393
peg.142	Plate17-F11,Plate78-D4,Plate41-A6,Plate47-H7,Plate95-D6	K02386
peg.143	Plate80-C8,Plate16-H7,Plate35-C11,Plate35-G1	K02392
peg.144	Plate53-C8,Plate53-C8	0
peg.145	Plate71-A8,Plate40-F9,Plate22-G11	K02391
peg.146	Plate8-E10,Plate3-F6,Plate84-D11,Plate48-E5,Plate86-E5	K02396
peg.147	Plate67-D4,Plate17-A2,Plate66-A12,Plate33-H1,Plate46-D10,Plate60-G1,Plate58-A3	0
peg.148	Plate98-D3,Plate41-E7,Plate86-E8,Plate62-B7	0
peg.149	Plate43-F12,Plate11-F5,Plate77-A4,Plate11-E6,Plate42-D8,Plate42-C4,Plate87-G4,Plate67-F11,Plate131-B10,Plate72-C2,Plate3-A8,Plate79-H9,Plate33-E10,Plate30-F3,Plate54-A3,Plate41-G9,Plate39-A8,Plate6-E5,Plate67-A5,Plate51-A8	K00548
peg.150	Plate59-H9,Plate59-C11,Plate8-F7	0
peg.151	Plate97-C10,Plate97-C10	K03558
peg.152	Plate81-C7,Plate96-H5	K00764
peg.153	Plate131-D10,Plate72-C1,Plate50-H4,Plate12-A10	K03366
peg.154	Plate24-E4,Plate99-F10,Plate43-B11,Plate24-F8	K09857
peg.155	Plate15-C8,Plate84-D7,Plate8-G4,Plate93-A12,Plate50-C8,Plate56-H1,Plate14-F8,Plate91-G8,Plate4-D4,Plate91-B9,Plate44-F9	K06192

peg.156	Plate50-C12,Plate37-B9,Plate26-G7,Plate11-F9,Plate8-F6,Plate66-B4	K03808
peg.157	Plate13-D5,Plate85-B6	0
peg.158	0	0
peg.159	0	K00721
peg.160	0	K02109
peg.161	Plate4-H1,Plate4-H1	K02109
peg.162	0	K02110
peg.163	0	K02108
peg.164	Plate77-B6,Plate77-B6	K02116
peg.165	0	K03110
peg.166	0	K18707
peg.167	0	K01778
peg.168	Plate72-B4,Plate72-B4	K01759
peg.169	0,Plate3-H1,Plate80-H6,Plate25-F5,Plate132-B7,Plate2-A8,Plate35-A3	0
peg.170	Plate39-G8,Plate39-G8	0
peg.171	Plate46-E12,Plate22-D11,Plate56-F12,Plate97-E2,Plate66-E10,Plate90-F4,Plate24-C3,Plate49-C2	K05592
peg.172	Plate23-D4,Plate23-D4	0
peg.173	Plate73-F9,Plate4-H2,Plate7-D1,Plate99-H5,Plate80-B8,Plate86-C8,Plate47-B7	0
peg.174	0	K02996
peg.175	0	K02871
peg.176	Plate57-D4,Plate57-D4	0
peg.177	Plate93-A9,Plate8-B6,Plate79-F3,Plate67-B1,Plate46-F4	0
peg.178	Plate22-F3,Plate54-A2	0
peg.179	0	K02039
peg.180	0	K02036
peg.181	Plate6-H4,Plate15-C5,Plate28-F11	K02038
peg.182	0	K02037
peg.183	0	0
peg.184	0,Plate72-B12	K01687
peg.185	Plate96-B8,Plate17-H11,Plate49-E12,Plate61-H9,Plate97-E12,Plate5-H8,Plate53-A6,Plate49-E9	K03316
peg.186	Plate10-A9,Plate25-A9,Plate67-A7	0
peg.187	Plate95-A4,Plate43-H2	0
peg.188	Plate57-A9,Plate57-A9	0
peg.189	Plate99-A7,Plate98-G3,Plate32-G6,Plate41-B8,Plate82-E1,Plate56-E12	K00344
peg.190	Plate72-E5,Plate76-G8,Plate25-E2,Plate3-A11,Plate85-H4,Plate6-F7,Plate53-B9,Plate94-H11,Plate76-F1	0
peg.191	Plate18-H11,Plate22-D2,Plate21-A2	K04771
peg.192	Plate34-F6,Plate62-E12,Plate94-B11	0
peg.193	Plate27-H10,Plate79-G10	0
peg.194	0	K03593
peg.195	0	0
peg.196	0	0
peg.197	0	K03465
peg.198	0	0
peg.199	Plate76-E5,Plate62-G9,Plate72-G2,Plate5-D4	K09985
peg.200	Plate68-A3,Plate38-F11,Plate22-B12,Plate99-H8,Plate45-H2,Plate38-B11	K01676
peg.201	Plate78-C5,Plate78-C5	0
peg.202	Plate55-C2,Plate55-C2	0
peg.203	Plate13-G3,Plate99-C7,Plate95-G11,Plate25-E11,Plate84-F7,Plate51-A11	0
peg.204	Plate132-C6,Plate57-F4,Plate85-D6	0
peg.205	0	0
peg.206	0	K00012
peg.207	Plate34-C7,Plate17-F9	K03274
peg.208	Plate78-H5,Plate78-H5	K03272
peg.209	0	K01809
peg.210	0,Plate84-H4,Plate9-H10	K00285
peg.211	0	K01775
peg.212	Plate92-E2,Plate92-E2	0
peg.213	Plate59-E2,Plate59-E2	K02834
peg.214	0	K02519
peg.215	Plate46-F10,Plate81-C8,Plate67-B2,Plate25-B8,Plate71-A5	K07742
peg.216	0	K02600
peg.217	Plate48-A12,Plate48-A12	K09748
peg.218	Plate51-C3,Plate60-E12,Plate23-B9,Plate61-A6	0
peg.219	Plate27-C8,Plate79-A12,Plate89-A11,Plate10-C9,Plate9-F5,Plate40-E9,Plate16-B6	0

peg.220	Plate91-B10,Plate91-B10	0
peg.221	Plate16-F7,Plate26-C6	0
peg.222	Plate83-E4,Plate80-H7,Plate31-G3,Plate131-A8,Plate35-D5,Plate45-A7	K02029
peg.223	Plate84-H8,Plate57-A4	K02028
peg.224	0	K01681
peg.225	Plate82-E12,Plate50-A1	K02193
peg.226	Plate17-G9,Plate47-H9,Plate24-F7	K02194
peg.227	Plate12-F3,Plate8-H11	0
peg.228	Plate45-A8,Plate1-A3,Plate100-A1	0
peg.229	Plate7-B7,Plate37-E9,Plate95-H6,Plate62-C11	K01581
peg.230	Plate29-A1,Plate14-C11,Plate31-D4,Plate62-D5,Plate98-E9,Plate96-G3,Plate26-A7,Plate13-A2,Plate63-H9	K07058
peg.231	0,Plate5-E9,Plate7-G1	K03642
peg.232	0	K03786
peg.233	0	K02160
peg.234	0	K01961
peg.235	Plate94-G3,Plate17-F3,Plate42-E3,Plate60-E7,Plate54-D1,Plate95-F6,Plate64-A7,Plate41-B7,Plate15-C6	0
peg.236	0	0
peg.237	Plate82-G10,Plate39-F11,Plate56-C7,Plate81-B5,Plate88-H1,Plate27-F10,Plate87-E6	K03147
peg.238	0	0
peg.239	0	0
peg.240	0	K07243
peg.241	0	K07230
peg.242	Plate66-A3,Plate71-E10,Plate54-D2,Plate99-E3,Plate14-D8	0
peg.243	Plate62-G2,Plate59-D7	0
peg.244	Plate78-H6,Plate42-E10	0
peg.245	Plate23-C1,Plate82-D7,Plate25-H5,Plate9-A5,Plate56-G7	K02014
peg.246	Plate66-D3,Plate55-A3,Plate98-B8,Plate17-C11,Plate36-C4	K00135
peg.247	Plate12-F2,Plate12-F2	0
peg.248	Plate55-D12,Plate55-D12	K02231
peg.249	Plate95-D4,Plate4-C4,Plate9-E5,Plate43-D7,Plate28-C11	K00768
peg.250	Plate63-E11,Plate97-E5,Plate36-F8,Plate38-B7,Plate96-A9	K02233
peg.251	Plate21-D3,Plate21-D3	0
peg.252	Plate37-D12,Plate84-F5,Plate52-E2,Plate33-D6,Plate50-C5	K02225
peg.253	Plate9-D5,Plate100-D2,Plate68-E11,Plate80-E4,Plate16-G3,Plate44-F7,Plate2-B10,Plate68-E1	K02227
peg.254	0,Plate55-A9,Plate11-H7,Plate8-B4	K04719
peg.255	Plate2-G1,Plate81-A1,Plate54-E1	K02232
peg.256	Plate58-A1,Plate21-H8	K19221
peg.257	Plate60-F6,Plate37-C10	K02226
peg.258	Plate35-H11,Plate59-G5	K02224
peg.259	Plate36-B5,Plate76-E8,Plate98-H7,Plate81-H10,Plate30-B5,Plate48-G5,Plate14-F12	K02230
peg.260	Plate17-B2,Plate41-G11,Plate5-F9	K02234
peg.261	Plate30-D12,Plate30-D12	0
peg.262	Plate58-G6,Plate58-G6	0
peg.263	Plate11-B3,Plate56-A3	K06075
peg.264	Plate15-G3,Plate3-H2,Plate98-F7,Plate32-F9,Plate21-G8	0
peg.265	Plate100-B7,Plate39-F1	K07034
peg.266	Plate46-H6,Plate5-B6,Plate94-G9,Plate93-B4	K01692
peg.267	Plate14-E10,Plate14-E10	K09024
peg.268	0	0
peg.269	Plate37-H4,Plate95-C3	K02075
peg.270	Plate90-E5,Plate78-A9,Plate43-F10,Plate72-G8	K02074
peg.271	Plate31-G6,Plate95-G2,Plate47-G5,Plate81-F3,Plate34-A12	K02077
peg.272	Plate88-B11,Plate23-G4	K09823
peg.273	0	0
peg.274	Plate132-D3,Plate90-B1	0
peg.275	Plate9-G7,Plate9-G7	0
peg.276	Plate89-F7,Plate48-G2,Plate68-A4,Plate2-C11,Plate15-G9	K08963
peg.277	0	K03976
peg.278	Plate39-F2,Plate13-F10,Plate91-D12	0
peg.279	0	K01738
peg.280	0	0
peg.281	0	0
peg.282	Plate28-G8,Plate28-G8	0
peg.283	Plate14-H11,Plate14-H11	K02014

peg.284	Plate52-H3,Plate97-C6,Plate28-C1,Plate41-G10	0
peg.285	0	K07152
peg.286	0	K01951
peg.287	Plate93-A6,Plate9-G2	0
peg.288	Plate76-H4,Plate88-D6,Plate37-E8,Plate39-H1	0
peg.289	0,Plate86-F6,Plate26-D10,Plate35-E1,Plate86-H5	0
peg.290	Plate77-B2,Plate85-F8,Plate18-A1,Plate89-F4	K03303
peg.291	Plate26-C9,Plate26-C9	0
peg.292	0	K13292
peg.293	Plate89-E9,Plate4-G11,Plate67-E10,Plate63-G8,Plate16-E11	0
peg.294	Plate63-D2,Plate6-C6,Plate57-D7,Plate43-H5,Plate80-C1,Plate32-C12	K05810
peg.295	Plate80-G5,Plate50-A2	0
peg.296	0	0
peg.297	Plate64-E5,Plate64-E5	0
peg.298	Plate88-A12,Plate88-A12	K16074
peg.299	Plate48-C3,Plate85-E3	0
peg.300	0	0
peg.301	0	K00817
peg.302	Plate81-C10,Plate46-E2,Plate97-B2,Plate131-H1,Plate58-D1	K06867
peg.303	0	0
peg.304	0	K00615
peg.305	Plate89-C11	K13810
peg.306	0	K00033
peg.307	Plate32-C2,Plate77-E11,Plate40-H2	0
peg.308	Plate9-B8,Plate9-B8	K01057
peg.309	0	K01807
peg.310	Plate11-G4,Plate32-E9	K00851
peg.311	0	0
peg.312	Plate8-A6,Plate8-A6	0
peg.313	Plate85-E1,Plate85-E1	K02016
peg.314	Plate8-D11,Plate90-D2,Plate98-H8,Plate64-E2,Plate82-H10,Plate73-E3,Plate59-D3,Plate2-F2	K03281
peg.315	Plate53-G8,Plate86-H11,Plate23-H10,Plate64-A3,Plate37-G7	0
peg.316	Plate53-B6,Plate2-D9,Plate89-B8,Plate5-C2,Plate5-A2,Plate46-H10	K06997
peg.317	Plate25-C10,Plate11-G8,Plate132-F9,Plate78-F4,Plate22-H11	K03549
peg.318	Plate50-H7,Plate4-A3,Plate98-G4,Plate94-A6,Plate45-H11	K02495
peg.319	0	0
peg.320	Plate12-D5,Plate12-D5	K19577
peg.321	0	0
peg.322	Plate38-C2,Plate90-F10	0
peg.323	Plate59-A11,Plate58-D11,Plate21-E4	0
peg.324	Plate36-F12,Plate39-F10	0
peg.325	Plate91-F7,Plate88-F7,Plate71-D7,Plate66-C12,Plate1-H6,Plate32-D2,Plate78-A1	0
peg.326	0	0
peg.327	Plate12-C6,Plate45-E6,Plate132-F2,Plate53-C7,Plate22-D10,Plate28-B12,Plate89-F2,Plate45-E5	0
peg.328	0	0
peg.329	0	K03594
peg.330	Plate84-C10,Plate62-G8	0
peg.331	Plate95-F3,Plate95-F3	0
peg.332	0	K15549
peg.333	Plate54-B1,Plate91-H5,Plate76-C2,Plate73-B1	K15547
peg.334	Plate26-F7,Plate39-B1,Plate47-F3,Plate132-D10,Plate53-A10	0
peg.335	Plate98-B11,Plate98-B11	K01246
peg.336	0	0
peg.337	Plate23-H6,Plate25-D5,Plate87-F2	K03386
peg.338	Plate86-G8,Plate44-D6,Plate4-D9,Plate62-B3	0
peg.339	Plate25-B4,Plate25-B4	K07090
peg.340	Plate90-H2,Plate48-B10,Plate27-H11,Plate81-D11,Plate61-D11,Plate99-C12,Plate1-A11	0
peg.341	Plate91-D1,Plate9-G11	K00537
peg.342	Plate14-A11,Plate11-E5,Plate5-A6,Plate92-F10,Plate6-E6,Plate41-F1,Plate56-F3,Plate46-G5,Plate33-G6	K05358
peg.343	Plate36-E12,Plate63-F5,Plate42-E11	K01568
peg.344	Plate43-A6,Plate7-E9,Plate64-C8,Plate1-C5,Plate4-B12,Plate4-E3,Plate6-B9,Plate45-H3	K07267
peg.345	Plate98-H2,Plate98-H2	K10806
peg.346	0	0
peg.347	0	0

peg.348	Plate95-B9,Plate59-B9	K08169
peg.349	Plate93-C11,Plate53-G9,Plate36-E11	0
peg.350	0	0
peg.351	Plate15-A5,Plate42-E9,Plate28-D1,Plate83-F12,Plate25-G11,Plate2-F4,Plate11-A6	K04079
peg.352	Plate83-E7,Plate45-E1	K04765
peg.353	0	K00145
peg.354	Plate48-G9,Plate48-G9	K00059
peg.355	0	0
peg.356	Plate132-F8,Plate83-G4,Plate83-G2,Plate12-E3	K00426
peg.357	Plate93-D4,Plate93-D4	K00425
peg.358	Plate1-B4,Plate24-A2,Plate34-A4	K16012
peg.359	Plate78-D6,Plate35-C12,Plate28-D2	K16013
peg.360	Plate22-G1,Plate46-C5,Plate82-A6	K19745
peg.361	Plate21-A4,Plate13-G8,Plate1-G7,Plate72-C7,Plate82-D8	0
peg.362	0	0
peg.363	Plate97-F7,Plate2-F5	K07221
peg.364	0,Plate95-E9,Plate11-H5,Plate10-A4	K02040
peg.365	0	0
peg.366	Plate57-D8,Plate93-C10,Plate10-C11	K07636
peg.367	Plate62-B10,Plate62-B10	K07657
peg.368	0	0
peg.369	0	0
peg.370	0	K01939
peg.371	Plate34-G5,Plate88-E8,Plate64-B1,Plate14-A7,Plate12-E9,Plate59-A9	K02502
peg.372	Plate96-B11,Plate1-C4,Plate54-E10,Plate24-C6	K06915
peg.373	Plate93-G7,Plate98-C5,Plate10-H5,Plate16-G12,Plate131-F1	K07007
peg.374	0	K01695
peg.375	0	K01696
peg.376	Plate14-H2,Plate21-B3,Plate22-C4	K03284
peg.377	0	K03628
peg.378	Plate100-F8,Plate100-F8	0
peg.379	0	K03711
peg.380	0	0
peg.381	0	K03820
peg.382	0	0
peg.383	0	K09945
peg.384	Plate41-C2,Plate41-C2	0
peg.385	0	K01878
peg.386	0	K01879
peg.387	Plate80-A10,Plate80-A10	0
peg.388	Plate10-A12,Plate45-B3,Plate1-F10,Plate83-E3	0
peg.389	0	K00602
peg.390	Plate55-D6,Plate55-D6	K03439
peg.391	0	K00789
peg.392	0	K00215
peg.393	0,Plate79-C12,Plate39-C2	K03686
peg.394	0	K04043
peg.395	0	K03687
peg.396	0	K14981
peg.397	0	K14980
peg.398	Plate10-C5,Plate10-C5	0
peg.399	Plate36-G3,Plate36-G3	K06958
peg.400	0,Plate85-F4,Plate50-D7,Plate42-H7	K07735
peg.401	Plate43-G12,Plate131-H3,Plate132-A7	0
peg.402	Plate33-A7,Plate9-A2	0
peg.403	0	0
peg.404	Plate87-H2,Plate21-B5	0
peg.405	0,Plate11-B10,Plate9-E10,Plate2-D1	K03694
peg.406	0	0
peg.407	Plate82-H8,Plate95-E10,Plate13-B7	K06891
peg.408	Plate24-G5,Plate24-G5	K01286
peg.409	0	K01265
peg.410	Plate67-H3,Plate92-A11,Plate84-C11,Plate87-H11,Plate64-C3,Plate38-F6,Plate9-G6,Plate34-H1,Plate18-H7,Plate73-D3	K00681

peg.411	Plate63-G12,Plate63-G12	K01843
peg.412	Plate57-A7,Plate57-A7	K04568
peg.413	Plate30-A5,Plate18-C7	0
peg.414	Plate86-F4,Plate86-F4	0
peg.415	0,Plate32-F12,Plate71-C2	K00788
peg.416	0	K11645
peg.417	Plate48-H1,Plate48-H1	0
peg.418	Plate11-B11	0
peg.419	0	K09888
peg.420	Plate23-C12,Plate28-A10	K01934
peg.421	0	K09769
peg.422	Plate84-A10,Plate84-A10	0
peg.423	0,Plate59-F12,Plate80-F6,Plate83-D2,Plate5-H3	0
peg.424	0	K00254
peg.425	Plate38-A2,Plate31-G4,Plate40-G4,Plate23-A3,Plate3-A4	0
peg.426	0	0
peg.427	Plate23-A8,Plate56-D8,Plate28-A11,Plate67-D1	K02346
peg.428	0	0
peg.429	Plate98-E3,Plate12-G5,Plate96-C7	K07263
peg.430	Plate14-B4,Plate14-B4	0
peg.431	Plate89-E4,Plate18-D5,Plate16-F9,Plate100-H1	K03702
peg.432	Plate24-C5,Plate24-C5	0
peg.433	0	0
peg.434	Plate37-E4,Plate37-E4	0
peg.435	Plate57-G2,Plate57-G2	K00697
peg.436	0,Plate89-H8	K01087
peg.437	Plate98-B6,Plate98-B6	0
peg.438	0	0
peg.439	Plate94-C7,Plate85-A10	K02067
peg.440	Plate63-F3,Plate63-F3	0
peg.441	Plate67-D2,Plate72-A3,Plate61-D2,Plate7-F6,Plate63-B4,Plate55-G5,Plate52-G6,Plate43-A5,Plate51-G12,Plate3-B10,Plate66-C1,Plate14-H9,Plate66-A7,Plate37-D5,Plate2-G9	0
peg.442	Plate41-E3,Plate99-H11	0
peg.443	Plate3-C8,Plate37-D8,Plate42-D6,Plate32-E3,Plate9-E8,Plate93-E9,Plate59-C3	K09919
peg.444	0	K01491
peg.445	Plate43-D10,Plate30-F1,Plate45-D5	K00297
peg.446	Plate16-A4,Plate68-D2,Plate84-B8,Plate97-B7,Plate51-B11,Plate81-B2,Plate77-C1,Plate43-C7,Plate72-F12,Plate57-A5,Plate68-D8,Plate29-D4,Plate52-A8,Plate39-B11,Plate21-G12,Plate94-D11,Plate58-G12,Plate52-E8	0
peg.447	Plate43-G3,Plate34-B12,Plate93-F4,Plate28-D9	K06910
peg.448	Plate68-F9,Plate14-E4,Plate35-F8	0
peg.449	Plate95-G9,Plate39-C5,Plate96-D6,Plate78-D11,Plate15-H7,Plate30-D3	K07568
peg.450	Plate38-C11,Plate94-B1,Plate67-H10,Plate46-F2,Plate36-B10,Plate32-E8,Plate17-A12,Plate11-G9,Plate6-D9,Plate32-A4,Plate9-C2,Plate12-A5	K00773
peg.451	Plate90-B10,Plate62-A2,Plate34-A11,Plate33-B10,Plate2-F10,Plate90-G7,Plate38-H5	K18979
peg.452	Plate1-B9,Plate6-G9,Plate85-E6,Plate37-G4	0
peg.453	Plate132-D11,Plate9-H4,Plate81-C6,Plate94-A1	0
peg.454	Plate51-B12,Plate24-C2	K00077
peg.455	Plate62-E7,Plate2-A4,Plate25-D6,Plate44-D2	K05801
peg.456	0	K04754
peg.457	Plate86-H8,Plate86-H8	K07323
peg.458	0	0
peg.459	Plate33-C11,Plate33-C11	0
peg.460	0	K01507
peg.461	Plate57-G10,Plate3-G2,Plate50-C2	0
peg.462	0	K04756
peg.463	0	0
peg.464	0	K03386
peg.465	Plate10-D10,Plate67-E11,Plate85-F2,Plate18-A5	K04761
peg.466	0	K02919
peg.467	Plate4-H10,Plate1-B2,Plate8-G9,Plate30-C5	0
peg.468	0	K00220
peg.469	0	0
peg.470	Plate67-H7,Plate67-H7	0
peg.471	Plate100-B2,Plate4-C1,Plate98-E11,Plate67-E4,Plate18-B1,Plate14-C12	0

peg.472	0	0
peg.473	0	K02291
peg.474	0	0
peg.475	0	0
peg.476	0	0
peg.477	0	0
peg.478	0	0
peg.479	Plate61-A7,Plate39-A6	K06075
peg.480	0	0
peg.481	Plate35-D9,Plate39-D2	0
peg.482	Plate80-D1,Plate85-E5,Plate48-A11,Plate34-A6,Plate87-G12,Plate81-C2,Plate48-D5,Plate27-E11	K02052
peg.483	Plate52-B5,Plate25-A11	K02055
peg.484	Plate85-F6,Plate85-F6	0
peg.485	Plate90-A2,Plate90-A2	K09160
peg.486	0	K07043
peg.487	0	0
peg.488	0	0
peg.489	Plate11-C1,Plate11-C1	K07124
peg.490	Plate38-H7,Plate38-H7	0
peg.491	Plate60-B7,Plate60-B7	K06147
peg.492	Plate15-B1,Plate99-G3	K06147
peg.493	Plate24-B11,Plate60-A11,Plate49-B6,Plate15-H10	K15721
peg.494	0	K05373
peg.495	0	K16088
peg.496	0	0
peg.497	Plate45-F3,Plate27-H2	0
peg.498	Plate132-D8,Plate132-D8	0
peg.499	Plate97-B4,Plate43-E8	K02014
peg.500	0	K09474
peg.501	Plate63-D3,Plate4-D3	0
peg.502	0,Plate23-E9,Plate63-B11,Plate10-H4,Plate28-C3,Plate42-C6,Plate93-H3,Plate93-A1,Plate132-E9,Plate57-F2,Plate1-E9,Plate88-H7,Plate47-G8	K03701
peg.503	Plate64-D12,Plate48-B11,Plate89-B7	0
peg.504	Plate24-G7,Plate24-G7	0
peg.505	Plate88-E12,Plate21-A1	0
peg.506	Plate58-F12,Plate78-C12,Plate71-A10,Plate53-A4,Plate15-H11,Plate24-C11	K19661
peg.507	Plate60-C3,Plate61-G11,Plate62-E5	0
peg.508	Plate33-D5,Plate15-F5,Plate36-E1,Plate89-B2	K06281
peg.509	Plate78-H8,Plate132-C7,Plate26-G12	K04656
peg.510	Plate42-F2,Plate48-F3,Plate48-A1,Plate83-C11,Plate15-D11	K06282
peg.511	Plate96-F2,Plate49-A4,Plate22-H10	K06281
peg.512	Plate72-E12,Plate94-A5	K03620
peg.513	Plate15-A10,Plate4-B3,Plate43-E11,Plate2-D3,Plate7-H9	K03605
peg.514	Plate73-F7,Plate73-F7	K04653
peg.515	0	K03619
peg.516	Plate31-H7,Plate18-F3,Plate93-A11,Plate44-G9,Plate3-E9	K03618
peg.517	Plate23-C8,Plate56-A2	0
peg.518	Plate42-A4,Plate12-H11,Plate99-G7	0
peg.519	0	K04651
peg.520	Plate83-G12,Plate33-E8,Plate8-C4	K04652
peg.521	Plate25-B2,Plate67-E1,Plate59-F7,Plate10-E4	K19641
peg.522	Plate27-E6,Plate88-G8	K04653
peg.523	Plate36-G5,Plate36-G5	K04654
peg.524	Plate132-H8,Plate5-E5	K04655
peg.525	Plate21-D12,Plate21-D12	K07241
peg.526	0,Plate37-H7	K03092
peg.527	0	0
peg.528	Plate13-E12,Plate13-E12	0
peg.529	0	0
peg.530	0	0
peg.531	Plate60-H8,Plate51-E5,Plate22-H9,Plate58-C10,Plate59-F4,Plate132-D12,Plate41-H2,Plate67-E12	K05367
peg.532	Plate17-F2,Plate10-H10,Plate47-G12,Plate42-G5,Plate66-A11,Plate35-F11,Plate5-F12	K06894
peg.533	0,Plate81-G6,Plate96-C3,Plate50-F3	K06894
peg.534	Plate18-C2,Plate17-H1,Plate35-H6,Plate46-B12	0

peg.535	Plate95-H3,Plate15-E4,Plate24-C8,Plate31-F5,Plate50-A12,Plate62-G7,Plate11-F3	0
peg.536	Plate40-F3,Plate8-D12	K02033
peg.537	Plate5-G3,Plate85-G8,Plate100-E7,Plate1-G10,Plate78-F10	K02034
peg.538	Plate53-F2,Plate14-D11,Plate89-C4,Plate52-E9,Plate12-G10,Plate3-H6	K15738
peg.539	Plate29-G11,Plate29-G11	0
peg.540	0	K03088
peg.541	Plate29-H1,Plate4-E6	K03088
peg.542	Plate91-E10,Plate91-E10	0
peg.543	Plate53-C5,Plate1-C11,Plate81-H1,Plate3-F9,Plate5-A9,Plate62-B2	0
peg.544	Plate93-D8,Plate53-G4	K16013
peg.545	Plate61-H6,Plate7-D11,Plate92-G10,Plate32-H5,Plate9-D6,Plate86-H7,Plate12-E2	K16012
peg.546	Plate57-F8,Plate51-A7	0
peg.547	Plate11-D8,Plate100-B1,Plate16-B4,Plate3-D5,Plate91-C1,Plate3-H10	K03654
peg.548	Plate54-G2,Plate56-F10,Plate43-A3	K02444
peg.549	0	K00111
peg.550	Plate100-E5,Plate90-A6,Plate32-D12	K02440
peg.551	Plate76-F10,Plate25-C8,Plate21-D6	K00864
peg.552	Plate44-F5,Plate44-F5	0
peg.553	0	K07738
peg.554	0	K03625
peg.555	0	K00946
peg.556	0	0
peg.557	0	0
peg.558	0,Plate53-D4,Plate35-H9,Plate16-C3	K00135
peg.559	Plate61-E12,Plate61-E12	0
peg.560	0,Plate18-B9,Plate36-B2,Plate58-C7,Plate4-A8	K02302
peg.561	Plate47-C8,Plate47-C8	0
peg.562	Plate14-D4,Plate10-G11,Plate4-H11,Plate42-F10,Plate8-B1,Plate13-F6,Plate91-D7,Plate51-D10,Plate17-H8,Plate42-A9,Plate30-C9	K02229
peg.563	Plate97-G9,Plate99-C9	K06042
peg.564	Plate1-E5,Plate8-A2,Plate13-D11,Plate14-C5,Plate79-G12	K03394
peg.565	Plate51-B9,Plate42-C7	K05934
peg.566	Plate78-H3,Plate48-D3,Plate88-D1,Plate39-E6	K05895
peg.567	Plate26-E9,Plate66-H8,Plate83-F8,Plate18-G1	K00595
peg.568	Plate90-C1,Plate34-C10	K02189
peg.569	Plate18-H9,Plate18-H9	K05936
peg.570	Plate58-A8,Plate41-F7,Plate7-H1,Plate52-E5	K02188
peg.571	Plate25-C9,Plate8-C11,Plate17-C9,Plate27-C3,Plate33-C6	0
peg.572	Plate57-D11,Plate58-D9	K03735
peg.573	Plate39-D5,Plate39-D5	K03736
peg.574	Plate84-F4,Plate40-B9,Plate73-A2,Plate58-D7,Plate41-B11	K16238
peg.575	Plate64-C10,Plate83-E9,Plate12-A3	0
peg.576	Plate71-G12,Plate71-G12	0
peg.577	0,Plate85-H5,Plate12-D12,Plate80-E2	0
peg.578	Plate33-E3,Plate27-C1,Plate78-F11,Plate27-H6,Plate79-C7	K06919
peg.579	0	0
peg.580	0	0
peg.581	Plate89-G8,Plate89-G8	0
peg.582	Plate44-A3,Plate44-A3	0
peg.583	Plate23-A6,Plate23-A6	0
peg.584	0,Plate68-A1,Plate97-F12,Plate96-A6	K06287
peg.585	0	K01599
peg.586	0	0
peg.587	0	K08973
peg.588	0	K06966
peg.589	0	0
peg.590	0	0
peg.591	0	0
peg.592	0	0
peg.593	Plate86-B8,Plate86-B8	K00567
peg.594	Plate16-B8,Plate16-B8	K03650
peg.595	Plate132-A9,Plate132-A9	K03495
peg.596	Plate48-A2,Plate99-G9	K03501
peg.597	Plate78-G10,Plate78-G10	K03496

peg.598	Plate25-D1,Plate25-D1	K03497
peg.599	0	0
peg.600	Plate2-C5,Plate68-H9,Plate89-A5	0
peg.601	0	0
peg.602	Plate58-G10,Plate5-G4,Plate18-F7,Plate29-F4,Plate48-A9,Plate34-C11,Plate13-D6,Plate38-D6,Plate32-D6,Plate66-C11,Plate51-F5	0
peg.603	Plate23-H3,Plate91-G10,Plate7-B8,Plate18-B6,Plate38-E11,Plate89-G5	0
peg.604	Plate79-E2,Plate79-E2	0
peg.605	Plate80-E8,Plate49-H10	0
peg.606	Plate73-D1,Plate30-C11	0
peg.607	Plate9-E4	0
peg.608	Plate72-E3,Plate6-H1,Plate6-H8,Plate8-F8	0
peg.609	Plate94-G7,Plate94-G7	0
peg.610	0	0
peg.611	0	0
peg.612	Plate68-A12,Plate80-E11,Plate80-A12,Plate92-A3,Plate5-G9,Plate89-C10,Plate44-E10,Plate3-B5	0
peg.613	0	0
peg.614	0	K01950
peg.615	0	K01693
peg.616	0	K02501
peg.617	Plate93-E3,Plate33-E11,Plate5-C12,Plate16-D7,Plate43-E3	0
peg.618	0	K01814
peg.619	0	K02500
peg.620	Plate63-G4,Plate83-F6	K01523
peg.621	Plate10-A6,Plate10-A6	0
peg.622	Plate38-B10,Plate60-A4	0
peg.623	0	0
peg.624	0	0
peg.625	Plate73-F1,Plate47-C12,Plate14-F10	0
peg.626	Plate50-H6,Plate25-A6	K03530
peg.627	Plate4-H8,Plate18-H5,Plate78-F3	0
peg.628	Plate86-E9	0
peg.629	Plate12-B6,Plate63-F12,Plate88-D11	K00286
peg.630	0,Plate38-C4	0
peg.631	Plate86-A4,Plate86-A4	0
peg.632	0	0
peg.633	Plate27-C7,Plate6-D8,Plate1-G4,Plate8-F11,Plate79-D1,Plate91-H6,Plate39-G4	0
peg.634	0	0
peg.635	0	0
peg.636	0	0
peg.637	Plate4-E9,Plate44-B12,Plate42-C12,Plate12-D1,Plate57-H8,Plate2-G8,Plate8-F2,Plate8-G7,Plate131-B8,Plate46-D6,Plate10-B5,Plate28-C8,Plate13-H3,Plate10-B1,Plate30-G6	0
peg.638	Plate36-E7,Plate36-E7	0
peg.639	0	K00620
peg.640	Plate61-F4,Plate6-B7,Plate6-A8,Plate25-G9,Plate100-B4	K03769
peg.641	Plate41-A7,Plate62-G4	K03070
peg.642	0,Plate7-G8,Plate80-G1	0
peg.643	Plate98-D7,Plate49-E6	K01159
peg.644	Plate30-B7,Plate67-E6	K03550
peg.645	0,Plate7-B2,Plate97-F10,Plate50-B7,Plate16-G8	K03551
peg.646	Plate49-H1,Plate49-H1	K07107
peg.647	0	K03562
peg.648	0	K03560
peg.929	Plate1-A4,Plate83-E5,Plate132-E10,Plate24-F5,Plate5-D6,Plate47-A12,Plate96-G2,Plate96-C5,Plate3-C7,Plate55-E7,Plate60-G6,Plate24-D5,Plate91-C3,Plate96-G8,Plate72-G5	K12373
peg.930	Plate85-G2,Plate38-F9,Plate9-G1,Plate57-B6,Plate33-H2,Plate92-D10,Plate41-E2,Plate28-B5,Plate12-H3,Plate4-G9,Plate98-G10	0
peg.931	Plate68-E12,Plate38-B9,Plate60-A6	K07106
peg.932	Plate77-A6,Plate4-B8,Plate98-C4,Plate85-C1,Plate52-G5,Plate43-A10,Plate97-D3,Plate18-E11,Plate80-H2,Plate6-A5,Plate100-A6,Plate5-E10,Plate13-H9,Plate45-E3	0
peg.933	Plate47-A6,Plate47-A6	0
peg.934	Plate61-C2,Plate61-C2	K07305
peg.935	Plate61-A4,Plate56-H2,Plate49-D12,Plate80-G10	0
peg.936	Plate92-E3,Plate99-A1	0
peg.937	Plate7-A6,Plate94-F2,Plate47-H5,Plate50-D4,Plate131-G8,Plate76-A6	K09758

peg.938	Plate37-H11,Plate37-H11	K04047
peg.939	Plate37-D10,Plate37-D10	0
peg.940	Plate25-G6,Plate97-G3,Plate47-D4	K00057
peg.941	Plate16-E10,Plate16-E10	0
peg.942	Plate41-B9,Plate12-E11	0
peg.943	Plate43-C5,Plate66-G1,Plate92-D6,Plate80-H9	0
peg.944	Plate32-E11,Plate86-F1,Plate16-A12	K15229
peg.945	0	0
peg.946	Plate77-B12,Plate64-E6	0
peg.947	Plate67-F4,Plate67-F4	K15228
peg.948	Plate87-B8,Plate87-B8	0
peg.949	Plate29-E5,Plate29-H10,Plate68-F1,Plate14-D7,Plate29-B2,Plate12-F9,Plate49-D2,Plate77-G12	0
peg.950	0	0
peg.951	0	0
peg.952	Plate5-C3,Plate58-A2,Plate93-C12,Plate72-D8	0
peg.953	Plate61-H3,Plate61-H3	0
peg.954	Plate83-C8,Plate56-A8	K07248
peg.955	Plate95-B1,Plate47-H8,Plate41-G1,Plate96-D7,Plate71-A12	0
peg.956	Plate11-H1,Plate16-C10,Plate77-H1,Plate84-H6,Plate37-G10,Plate50-D8,Plate92-A1,Plate49-D7	K07303
peg.957	Plate4-F11,Plate86-E7,Plate42-C3	K07302
peg.958	Plate4-E8,Plate23-B10	0
peg.959	0	K02221
peg.960	0	0
peg.961	Plate56-H10,Plate32-B5,Plate34-F7,Plate60-G2	0
peg.962	0,Plate49-G9,Plate85-G10,Plate43-D1,Plate1-D2	0
peg.963	0	0
peg.964	Plate39-C10,Plate132-C8,Plate36-B12,Plate50-E7	0
peg.965	0,Plate46-B3,Plate55-A5	0
peg.966	Plate21-E10,Plate21-E10	0
peg.967	0,Plate54-F1,Plate33-B2,Plate13-E8,Plate78-G5	0
peg.968	Plate132-E12,Plate58-H3	0
peg.969	Plate51-H4,Plate28-B6,Plate4-D7,Plate79-E7,Plate26-F1,Plate39-C9,Plate25-C12,Plate44-F3,Plate16-C6	K00681
peg.970	Plate21-E2,Plate1-H8,Plate100-A2,Plate38-G4	K01487
peg.971	Plate81-H3,Plate72-A2,Plate63-B8,Plate57-E1,Plate28-G5	0
peg.972	Plate43-B6,Plate82-A7,Plate40-G1,Plate51-H10,Plate33-B4,Plate47-A9	0
peg.973	0	0
peg.974	Plate63-D8,Plate9-E7,Plate51-B3	K13485
peg.975	0	K07127
peg.976	Plate26-G1,Plate94-E5,Plate26-H11,Plate12-H9,Plate48-B2	0
peg.977	Plate59-E6,Plate78-C9,Plate41-A8,Plate62-F11,Plate28-G4,Plate31-B3,Plate41-C10,Plate63-B6,Plate90-C4	K13481
peg.978	Plate52-A5,Plate58-B1,Plate30-E3,Plate82-F6,Plate64-D3,Plate30-C8	K13482
peg.979	Plate42-A6	K07402
peg.980	Plate47-B5,Plate87-D10	0
peg.981	0	K05596
peg.982	Plate5-D9,Plate5-D9	K06895
peg.983	Plate67-G9,Plate82-C10,Plate55-D5,Plate58-B9	K01685
peg.984	Plate68-G9,Plate41-H7,Plate100-G2	0
peg.985	Plate94-D9,Plate94-D9	0
peg.986	Plate4-G2,Plate4-G2	0
peg.987	0	0
peg.988	Plate37-D4,Plate37-D4	K01715
peg.989	Plate9-H6,Plate9-H6	0
peg.990	0	0
peg.991	Plate6-F12,Plate83-E1	K02014
peg.992	Plate59-D4,Plate59-A2,Plate34-H2	K02433
peg.993	0	0
peg.994	Plate98-G8,Plate99-H6	0
peg.995	Plate54-H10,Plate5-A1,Plate52-F9	K00839
peg.996	Plate48-D12,Plate17-D11,Plate84-E5,Plate43-H6,Plate29-F10,Plate41-F11,Plate36-C3	K02083
peg.997	Plate31-G5,Plate51-C12,Plate68-H11	0
peg.998	Plate23-B8,Plate61-B6,Plate21-E12	0
peg.999	Plate71-C8,Plate21-A6,Plate54-D8,Plate5-D3	K11103
peg.1000	0	0
peg.1001	0,Plate16-G4,Plate40-D4	K06966

peg.1002	Plate28-E11,Plate47-C4,Plate14-H6,Plate60-A8,Plate36-A11,Plate21-H7,Plate81-E7	K03306
peg.1003	Plate86-E3,Plate14-A9,Plate81-F12	0
peg.1004	Plate45-E7,Plate12-C7,Plate56-G9,Plate73-B7	0
peg.1005	Plate51-G8,Plate86-E4,Plate15-G4,Plate24-H1	K07152
peg.1006	Plate84-B12,Plate72-G6,Plate71-C6,Plate59-E11,Plate3-E10,Plate47-A5,Plate54-H3,Plate94-H9,Plate94-D12	K02335
peg.1007	Plate38-C3,Plate50-B3,Plate64-G8,Plate33-B1,Plate49-C11	K00826
peg.1008	Plate87-A7,Plate66-B6,Plate52-G2,Plate84-D6,Plate39-H3,Plate98-D1,Plate31-C6,Plate32-E10,Plate32-C7,Plate83-H11,Plate50-B12,Plate63-H7	0
peg.1009	Plate47-E9,Plate34-A2,Plate62-G5,Plate85-E7,Plate84-A6	K02013
peg.1010	Plate58-C7,Plate71-C11,Plate47-H6,Plate58-F10,Plate72-D7,Plate132-B10,Plate4-E1,Plate90-D7,Plate94-D4	K02015
peg.1011	0	0
peg.1012	Plate55-E12,Plate15-F7,Plate29-E2,Plate67-H1,Plate87-C9,Plate54-E11,Plate11-C11,Plate21-E1	K06180
peg.1013	0	K03089
peg.1014	0	K07462
peg.1015	0	K11532
peg.1016	0	K00003
peg.1017	Plate11-E1,Plate86-B3,Plate100-D4,Plate2-D11,Plate85-C2,Plate35-H10	K14261
peg.1018	Plate80-A1,Plate80-A1	0
peg.1019	0,Plate8-G5	0
peg.1020	Plate87-F5,Plate18-D9	K01358
peg.1021	Plate33-G10,Plate84-D8,Plate17-B8,Plate33-H7	0
peg.1022	Plate35-D7,Plate61-A12	K06193
peg.1023	Plate79-B1,Plate12-H8	0
peg.1024	0,Plate48-F4,Plate5-F3,Plate17-H2	K06139
peg.1025	0	K06138
peg.1026	Plate91-G9,Plate16-F10,Plate73-B4	K06137
peg.1027	Plate11-D2,Plate47-B6,Plate43-G2,Plate87-D6,Plate44-F8	K06136
peg.1028	Plate45-E2,Plate13-E2,Plate22-C8,Plate72-D2	0
peg.1029	Plate9-D8,Plate87-D8,Plate4-D12,Plate62-A3	K01142
peg.1030	0	0
peg.1031	Plate52-C1,Plate46-E10,Plate55-H5,Plate63-B7,Plate54-B5	K01129
peg.1032	0	K01887
peg.1033	Plate64-A11,Plate34-E2,Plate57-E8,Plate48-H5,Plate98-E6,Plate57-H10	0
peg.1034	Plate91-G5,Plate95-G5,Plate26-B11,Plate40-F8,Plate84-F1,Plate93-F10,Plate73-B5	K05896
peg.1035	Plate81-D7,Plate6-F11	K06024
peg.1036	0	K03117
peg.1037	0	K03118
peg.1038	0	K01875
peg.1039	0,Plate51-D6	K03297
peg.1040	0,Plate82-F9,Plate53-F6,Plate88-B1,Plate98-B10,Plate11-B2,Plate2-H10,Plate91-C8	K04084
peg.1041	0	0
peg.1042	Plate83-F9,Plate89-D11,Plate85-G6,Plate44-A1,Plate59-D1	0
peg.1043	0	0
peg.1044	Plate40-B2,Plate40-B2	0
peg.1045	Plate90-D10,Plate83-D10,Plate26-C7,Plate86-B9	K01669
peg.1046	Plate16-E1,Plate16-E1	0
peg.1047	0	0
peg.1048	Plate61-F12,Plate26-A2,Plate11-C6,Plate94-A4,Plate51-A4,Plate12-D11	K07444
peg.1049	Plate18-E5,Plate18-E5	0
peg.1050	Plate80-C10,Plate45-F1,Plate53-F3,Plate28-D3,Plate86-G6,Plate31-H2,Plate21-B2,Plate71-D12,Plate57-H2	0
peg.1051	0	0
peg.1052	0	0
peg.1053	0	K06886
peg.1054	Plate48-E8,Plate48-E8	0
peg.1055	Plate9-E6,Plate72-G9	0
peg.1056	Plate89-G12,Plate39-G7	K02575
peg.1057	Plate78-D2,Plate68-E2	0
peg.1058	Plate22-C9,Plate10-B2,Plate26-B4,Plate67-B12,Plate6-G4	K00362
peg.1059	0,Plate34-D12,Plate132-C2,Plate60-C1,Plate40-A8,Plate4-E10,Plate63-E9,Plate32-A8,Plate58-F7,Plate13-F4,Plate46-C6,Plate58-F1,Plate99-E11,Plate79-B3,Plate95-H7,Plate77-E9,Plate38-H1,Plate26-F2,Plate63-H11	K00380
peg.1060	Plate1-E11,Plate11-D10,Plate3-G8	K07183
peg.1061	Plate15-C10,Plate15-C10	K02049
peg.1062	0	0
peg.1063	Plate60-G4,Plate60-G4	K09862
peg.1064	Plate71-D4,Plate87-E5,Plate3-B3,Plate99-G8,Plate86-B10,Plate71-D2,Plate89-D7	0

peg.1065	0	K06287
peg.1066	Plate33-F5,Plate131-E3,Plate66-E3,Plate64-E7,Plate93-D7	0
peg.1067	Plate81-D12,Plate81-D12	0
peg.1068	0	0
peg.1069	Plate59-E10,Plate59-E10	0
peg.1070	Plate90-G1,Plate9-C3,Plate54-F7,Plate27-A10,Plate25-A7,Plate8-E11,Plate94-H7	0
peg.1071	0	K04080
peg.1072	Plate131-A1,Plate90-F7	0
peg.1073	Plate52-H7,Plate52-H7	0
peg.1074	Plate42-A3,Plate42-A3	0
peg.1075	Plate43-C2,Plate94-A11,Plate3-E12,Plate48-H8,Plate72-E4	0
peg.1076	Plate11-C9,Plate11-C9	0
peg.1077	Plate73-D6,Plate60-F2,Plate82-A1,Plate15-H1,Plate80-D10,Plate41-C1	0
peg.1078	Plate96-C11,Plate55-F12	0
peg.1079	Plate43-G11,Plate30-B10,Plate63-C10	K03497
peg.1080	0	K07124
peg.1081	0	K09958
peg.1082	0	0
peg.1083	Plate26-C5,Plate26-C5	0
peg.1084	Plate83-C5,Plate67-A1	0
peg.1085	Plate63-A9,Plate17-D8	K00077
peg.1086	0	0
peg.1087	0	K20533
peg.1088	Plate61-D10,Plate49-H3,Plate58-B4	K20532
peg.1089	Plate62-F4,Plate73-D11	K20531
peg.1090	Plate94-E1,Plate94-E1	K07344
peg.1091	Plate28-C9,Plate28-C9	K20266
peg.1092	Plate23-E7,Plate26-D11,Plate8-D11,Plate11-F4,Plate38-A11,Plate34-D4,Plate81-A8,Plate1-E10,Plate32-H2,Plate6-C11	K20530
peg.1093	Plate59-D9,Plate59-D9	K20529
peg.1094	Plate16-D4,Plate99-G11,Plate28-D4	K20528
peg.1095	Plate17-E7,Plate45-C5	K20527
peg.1096	0	0
peg.1097	Plate7-A1,Plate59-E12,Plate25-G1,Plate37-B6,Plate34-G8,Plate40-E2,Plate21-A12	K03205
peg.1098	0	K00558
peg.1099	Plate18-F5,Plate78-C6	0
peg.1100	Plate8-B11,Plate98-D10	0
peg.1101	0	0
peg.1102	Plate77-C6,Plate79-D4,Plate51-C11,Plate35-G4	0
peg.1103	0	0
peg.1104	Plate90-A10,Plate51-F7,Plate88-E5,Plate43-G9,Plate97-E11	0
peg.1105	Plate56-H9	K00558
peg.1106	Plate97-H6,Plate97-H6	0
peg.1107	Plate72-B8,Plate86-C5,Plate3-C1	0
peg.1108	Plate41-A10,Plate41-A10	0
peg.1109	Plate54-F12,Plate132-B11	0
peg.1110	0	0
peg.1111	0	0
peg.1112	0	0
peg.1113	Plate49-E8,Plate49-E8	K00571
peg.1114	0	0
peg.1115	0	0
peg.1116	Plate17-A1,Plate37-C12,Plate99-E9,Plate53-G7	K03581
peg.1117	Plate49-D5,Plate63-C6	0
peg.1118	Plate68-G5,Plate4-G1,Plate3-E4	0
peg.1119	0	K06442
peg.1120	Plate2-C10,Plate2-C10	0
peg.1121	Plate79-F4,Plate71-F8,Plate80-H8,Plate63-E1	K06941
peg.1122	0	K01940
peg.1123	Plate8-A7,Plate1-B7	K03773
peg.1124	0	K01867
peg.1125	0	0
peg.1126	0	0
peg.1127	0,Plate7-C5,Plate91-B6	0

peg.1128	Plate80-D5,Plate35-B6,Plate2-C8,Plate60-E5,Plate2-B12	K01679
peg.1129	0	K00045
peg.1130	Plate23-A11,Plate54-E5,Plate92-D12	0
peg.1131	0	0
peg.1132	Plate91-E7,Plate91-E7	0
peg.1133	Plate88-H5,Plate88-H5	0
peg.1134	Plate8-C12,Plate52-D11,Plate93-D6,Plate57-H9,Plate56-G5,Plate39-C4,Plate5-A12	K00117
peg.1135	Plate30-A2,Plate30-A2	K01185
peg.1136	0	0
peg.1137	0	0
peg.1138	Plate28-G12,Plate3-G6	0
peg.1139	0	0
peg.1140	Plate47-B1,Plate47-B1	0
peg.1141	Plate44-G8,Plate44-G8	0
peg.1142	0	0
peg.1143	0	0
peg.1144	0	K01424
peg.1145	Plate79-D5,Plate40-B11,Plate22-H1,Plate90-B6,Plate23-D6,Plate35-D10	0
peg.1146	Plate2-E9,Plate2-E9	K03500
peg.1147	0	K00088
peg.1148	0	0
peg.1149	0	0
peg.1150	Plate10-B9,Plate89-G4,Plate52-B3,Plate21-H11	K02035
peg.1151	Plate78-G11,Plate78-G11	0
peg.1152	Plate30-G11,Plate30-G11	0
peg.1153	Plate22-C7,Plate90-E10,Plate58-D8,Plate59-E4,Plate68-A9,Plate36-E8	0
peg.1154	0	0
peg.1155	Plate3-D6,Plate89-H9,Plate97-B12	0
peg.1156	Plate58-C12,Plate58-C12	0
peg.1157	0,Plate45-B2	K02048
peg.1158	Plate36-F6,Plate89-A10,Plate12-F1,Plate78-B3	K07221
peg.1159	0	0
peg.1160	0	0
peg.1161	Plate42-G6,Plate64-F5,Plate99-E5	0
peg.1162	Plate92-H9,Plate92-H9	0
peg.1163	0	K04565
peg.1164	0	0
peg.1165	Plate35-H8	K03316
peg.1166	Plate24-B7,Plate45-A6	K06911
peg.1167	Plate35-G12,Plate30-F5,Plate13-B8,Plate24-F12,Plate71-A6,Plate98-A7	0
peg.1168	Plate56-B4,Plate16-F3,Plate1-F3,Plate45-B1	K03543
peg.1169	Plate85-G7,Plate62-E11,Plate88-E2	K03446
peg.1170	0	0
peg.1171	Plate53-F7,Plate53-F7	0
peg.1172	Plate21-A3,Plate55-E9	0
peg.1173	Plate10-F11,Plate28-F4,Plate38-F10,Plate54-E2	0
peg.1174	0	0
peg.1175	0,Plate35-D2	K07223
peg.1176	0	0
peg.1177	0	0
peg.1178	Plate96-B9,Plate44-D1	0
peg.1179	Plate28-H10,Plate28-H10	K19743
peg.1180	0	K07246
peg.1181	Plate33-B9,Plate94-E2,Plate88-H8	K01451
peg.1182	Plate4-H5,Plate4-H5	K00128
peg.1183	0	0
peg.1184	Plate87-H5,Plate28-G2,Plate80-D12	0
peg.1185	0	0
peg.1186	Plate44-C4,Plate35-E5,Plate89-H3	0
peg.1187	0	K00303
peg.1188	Plate11-G2,Plate67-G10	K01560
peg.1189	Plate3-A9,Plate95-C11,Plate31-C12,Plate94-H3	K02035
peg.1190	Plate38-B6,Plate2-B2,Plate54-D4,Plate17-E5,Plate40-D1	K02033
peg.1191	Plate98-G7,Plate30-H4	K02034

peg.1192	Plate132-H9,Plate47-D9,Plate37-F5	K02031
peg.1193	Plate1-D3,Plate1-D3	K00135
peg.1194	0	0
peg.1195	Plate29-D11,Plate37-G12	0
peg.1196	Plate1-C1,Plate46-A1	K12972
peg.1197	0	0
peg.1198	0	0
peg.1199	Plate18-B7,Plate18-B7	K08368
peg.1200	0	K07025
peg.1201	Plate43-H9,Plate23-F9,Plate93-E10	K02014
peg.1202	0	0
peg.1203	Plate48-E11,Plate89-A9	0
peg.1204	0	0
peg.1205	0	0
peg.1206	Plate98-A6,Plate36-F7	0
peg.1207	Plate33-F7,Plate64-B5,Plate57-F7	K00059
peg.1208	Plate77-D9,Plate77-D9	0
peg.1209	Plate13-E11,Plate49-C3,Plate100-F1,Plate52-C7	0
peg.1210	Plate77-A11,Plate40-A5,Plate17-B12,Plate26-A12	K00647
peg.1211	Plate15-D2,Plate32-F11,Plate50-H9,Plate31-B2,Plate13-A8,Plate21-A10,Plate48-D10,Plate16-F11	0
peg.1212	Plate52-G1,Plate52-G1	0
peg.1213	Plate11-B9,Plate88-A6,Plate34-B7,Plate3-F8	0
peg.1214	0,Plate132-H6,Plate95-C9	0
peg.1215	0	K02078
peg.1216	Plate68-G1,Plate68-G1	0
peg.1217	Plate38-G5,Plate38-G5	K03183
peg.1218	0	0
peg.1219	0	K09768
peg.1220	Plate12-E12,Plate78-E6	K01425
peg.1221	0	0
peg.1222	Plate27-C9,Plate27-C9	0
peg.1223	0	0
peg.1224	0	0
peg.1225	0	0
peg.1226	Plate15-F11,Plate15-F11	K00549
peg.1227	0	K03576
peg.1228	Plate6-G1,Plate82-A3,Plate15-B2	0
peg.1229	Plate26-B3,Plate26-B3	0
peg.1230	Plate78-E3,Plate21-G9,Plate37-C2	K01502
peg.1231	Plate13-E7,Plate58-B7	0
peg.1232	Plate100-A9,Plate100-A9	0
peg.1233	Plate27-H3,Plate15-E5	K07123
peg.1234	Plate77-C3,Plate1-H11,Plate86-H3	0
peg.1235	Plate131-C7,Plate131-C7	0
peg.1236	0	K07222
peg.1237	Plate12-F6,Plate12-F6	K01908
peg.1238	0	0
peg.1239	0	K12262
peg.1240	0	0
peg.1241	0	0
peg.1242	Plate92-D4,Plate92-D4	K15977
peg.1243	0	K03809
peg.1244	0	0
peg.1245	Plate31-F1,Plate24-G11	K06911
peg.1246	Plate62-D10,Plate90-H8	K18139
peg.1247	Plate132-A12,Plate132-A12	0
peg.1248	Plate60-A2,Plate23-E10,Plate39-D6,Plate53-B8	0
peg.1249	Plate17-G1,Plate37-F9,Plate14-F2,Plate31-E5,Plate21-E8,Plate90-F9,Plate33-C5,Plate79-F1,Plate47-F6,Plate54-H11,Plate25-G3,Plate29-G10,Plate61-E3,Plate26-E4	0
peg.1250	Plate14-A10,Plate14-A10	0
peg.1251	Plate8-C5,Plate8-C5	K18918
peg.1252	0	0
peg.1253	Plate35-A1,Plate131-B9	0
peg.1254	0	0

peg.1255	Plate27-G12,Plate27-G12	0
peg.1256	Plate21-A5,Plate21-A5	0
peg.1257	0	0
peg.1258	0	0
peg.1259	Plate57-D3,Plate57-D3	0
peg.1260	0	K02836
peg.1261	0	K05366
peg.1262	Plate13-E9,Plate39-C6,Plate46-F3	K03705
peg.1263	Plate10-F9,Plate95-B11,Plate18-F12	K00989
peg.1264	Plate22-F10,Plate56-D1	K02428
peg.1265	0	K02945
peg.1266	0	K00945
peg.1267	0	K00800
peg.1268	0	0
peg.1269	0,Plate66-E11	K01633
peg.1270	Plate60-H11,Plate131-C11,Plate8-G12,Plate53-H9	0
peg.1271	0	K06187
peg.1272	Plate50-E8,Plate58-E9	K09747
peg.1273	0	K02343
peg.1274	Plate5-G8,Plate5-G8	0
peg.1275	Plate98-E10,Plate59-G9	0
peg.1276	Plate54-C11,Plate6-D12,Plate40-H3,Plate5-E12	K01443
peg.1277	0	K03669
peg.1278	0	K03670
peg.1279	0	K02019
peg.1280	Plate15-H3,Plate22-A10,Plate71-C10,Plate77-C11,Plate16-E7	0
peg.1281	Plate8-F10,Plate81-G2,Plate42-D12,Plate6-F6	K03553
peg.1282	0	K00681
peg.1283	Plate32-E4,Plate61-D7	0
peg.1284	0	K03406
peg.1285	0	K00643
peg.1286	Plate88-B7,Plate88-B7	0
peg.1287	Plate14-F3,Plate7-E11,Plate98-B2,Plate77-D12,Plate131-C10,Plate3-E1,Plate68-B6	K00615
peg.1288	Plate1-H5,Plate51-A5,Plate1-D4,Plate76-C5,Plate35-G10	K00134
peg.1289	Plate28-B12,Plate54-G10,Plate34-B8	K00927
peg.1290	Plate32-G7,Plate64-B7,Plate2-D7	0
peg.1291	0	0
peg.1292	Plate35-A7,Plate35-A7	0
peg.1293	Plate2-A2,Plate2-A2	0
peg.1294	Plate78-E10	K00240
peg.1295	Plate93-C7,Plate34-D3,Plate78-A11	K00239
peg.1296	0	K00242
peg.1297	0	K00241
peg.1298	0	K00133
peg.1299	Plate77-A7,Plate55-E4,Plate17-F8,Plate39-H9	K00324
peg.1300	Plate54-G1,Plate54-G1	K00324
peg.1301	Plate96-A3,Plate43-D9,Plate29-D6,Plate90-E7,Plate60-B3,Plate67-A6,Plate6-C5	K00325
peg.1302	Plate58-E4,Plate58-E4	K13953
peg.1303	0	K00135
peg.1304	0	K00831
peg.1305	0	0
peg.1306	Plate67-E5,Plate51-A10,Plate6-B11,Plate131-A9,Plate40-A7	K03601
peg.1307	0	K01945
peg.1308	0,Plate39-A2,Plate97-F5	K03789
peg.1309	0	0
peg.1310	0	K09019
peg.1311	0	0
peg.1312	Plate49-E10,Plate49-E10	0
peg.1313	Plate81-G8,Plate25-A2,Plate10-B8,Plate7-H2	K09384
peg.1314	Plate54-F9,Plate82-G8,Plate24-H2	0
peg.1315	0	0
peg.1316	Plate43-F6,Plate43-G5,Plate99-D12,Plate89-D6	K03701
peg.1317	Plate43-G8,Plate43-G8	K05838
peg.1318	Plate55-C4,Plate83-A7	K07157

peg.1319	Plate29-C4,Plate29-C4	K09791
peg.1320	0	0
peg.1321	Plate4-B9,Plate58-G9	K07552
peg.1322	0,Plate35-F7,Plate44-A11,Plate16-H8	0
peg.1323	0,Plate94-B2,Plate96-H9,Plate76-E10	0
peg.1324	0	0
peg.1325	Plate34-G4,Plate34-G4	0
peg.1326	Plate27-G11,Plate27-G11	0
peg.1327	0	0
peg.1328	Plate99-E12,Plate99-E12	0
peg.1329	0	0
peg.1330	Plate58-A5,Plate58-A5	0
peg.1331	0	0
peg.1332	Plate15-F1,Plate15-F1	0
peg.1333	Plate78-A7,Plate48-E7,Plate76-E4,Plate92-G4,Plate18-A3	0
peg.1334	Plate34-F2,Plate34-F2	0
peg.1335	0	0
peg.1685	Plate25-B9,Plate25-B9	0
peg.1686	0	0
peg.1687	Plate68-A5,Plate68-A5	0
peg.1688	Plate13-H5	0
peg.1689	Plate37-H8,Plate31-A6	K02014
peg.1690	Plate8-H2,Plate77-B11,Plate15-C9,Plate95-D2,Plate66-B9	K00375
peg.1691	Plate36-D11,Plate56-C10	0
peg.1692	Plate81-F7,Plate26-E7,Plate1-A1,Plate32-B11,Plate62-B4,Plate49-H8,Plate36-F5,Plate55-F4	K11529
peg.1693	Plate88-D3,Plate21-D4,Plate29-E11,Plate1-A12,Plate31-A4,Plate57-G11,Plate33-F4,Plate17-C12	0
peg.1694	Plate99-G10,Plate44-A2,Plate96-B12	K00759
peg.1695	Plate63-A11,Plate80-C11,Plate40-D10,Plate64-A5,Plate62-C6,Plate99-C6,Plate76-C6,Plate16-B10,Plate57-C8	0
peg.1696	Plate5-D10,Plate12-C4	K07552
peg.1697	Plate5-B12,Plate46-E4,Plate13-H11	0
peg.1698	Plate4-C10,Plate33-A9,Plate91-F12,Plate59-C4	0
peg.1699	0,Plate31-H9,Plate2-E4,Plate10-E8,Plate22-F12	K02259
peg.1700	Plate9-C6,Plate47-F7	0
peg.1701	Plate43-H10,Plate35-C1,Plate29-E1,Plate90-C7,Plate34-D6,Plate28-F7,Plate31-D5	K01649
peg.1702	Plate49-A11,Plate49-A11	K03569
peg.1703	Plate51-H2,Plate16-F5	K03570
peg.1704	0	K03571
peg.1705	Plate95-A11,Plate60-G11	K05515
peg.1706	Plate38-D9,Plate24-E6	K05837
peg.1707	0	K03585
peg.1708	0	K18138
peg.1709	0	K18139
peg.1710	Plate77-B3,Plate25-F8,Plate5-C7,Plate38-E2,Plate91-B1	0
peg.1711	Plate77-B8,Plate95-A7	K03559
peg.1712	Plate50-G6,Plate63-E12	K03559
peg.1713	0	0
peg.1714	Plate2-A7,Plate61-D5,Plate60-E3,Plate78-F7	0
peg.1715	Plate58-H10,Plate14-A2	0
peg.1716	0	0
peg.1717	Plate24-B8,Plate52-B9,Plate34-H5,Plate58-C1,Plate10-G12,Plate8-G3	K02394
peg.1718	0	0
peg.1719	0,Plate60-F1,Plate72-C12,Plate55-A11	0
peg.1720	Plate27-C2,Plate27-C2	0
peg.1721	Plate77-C4,Plate77-C4	0
peg.1722	0,Plate28-H7	0
peg.1723	Plate7-B10,Plate35-A12,Plate79-C9,Plate73-B2,Plate3-A6,Plate1-D10	0
peg.1724	0,Plate13-E1,Plate8-B5,Plate41-H10,Plate44-E3,Plate36-C5,Plate6-B5,Plate51-E6,Plate2-B4,Plate81-E1	K02412
peg.1725	Plate57-A12,Plate7-G9,Plate79-C3,Plate23-D2	0
peg.1726	Plate9-H11,Plate62-E8,Plate60-B5	0
peg.1727	Plate64-G5,Plate32-G12,Plate96-C1,Plate53-E2,Plate35-C9	K02557
peg.1728	Plate66-D2,Plate66-D2	K02556
peg.1729	Plate50-D9,Plate61-G12,Plate62-H2,Plate53-D10,Plate10-E1,Plate81-E6,Plate68-G4,Plate91-A12,Plate1-B8,Plate33-F8	0
peg.1730	Plate93-E5,Plate93-E5	K02389

peg.1731	Plate44-E7,Plate58-B10	K03406
peg.1732	Plate40-G5,Plate40-G5	K06602
peg.1733	Plate50-D6,Plate93-D2,Plate95-A2,Plate31-G11,Plate85-B3	K03406
peg.1734	Plate37-D7,Plate68-F7,Plate33-G11,Plate56-A4,Plate18-D11,Plate47-G10,Plate25-H11	K02390
peg.1735	Plate29-A5,Plate60-D1,Plate8-E3,Plate45-G7	K02401
peg.1736	0,Plate61-B1,Plate38-D11,Plate95-E5,Plate43-B1,Plate64-C4,Plate23-H1,Plate46-E6	K02421
peg.1737	0,Plate62-H8,Plate26-D8,Plate59-H1	K02420
peg.1738	Plate73-A5,Plate8-E7,Plate80-A11	K02408
peg.1739	Plate84-D4,Plate54-F3,Plate52-F12,Plate97-E8,Plate48-E3,Plate81-F8,Plate45-C8,Plate41-H9,Plate63-H3	K13584
peg.1740	Plate55-D9,Plate7-A11,Plate100-C8	0
peg.1741	0	0
peg.1742	Plate51-G1,Plate40-D8,Plate45-B9,Plate86-G1,Plate98-B5,Plate90-H7,Plate12-G11,Plate64-E9,Plate40-G7,Plate94-D5,Plate38-D7	0
peg.1743	Plate83-D9,Plate48-A5,Plate81-B9,Plate85-F1	0
peg.1744	Plate25-E7,Plate25-E7	K02387
peg.1745	Plate46-F7,Plate46-F7	K02388
peg.1746	Plate68-A7,Plate31-H4,Plate131-H9,Plate82-C7,Plate94-A10,Plate3-B1	0
peg.1747	0	K02406
peg.1748	0	0
peg.1749	Plate64-D8,Plate9-D7,Plate57-H11,Plate15-A2	0
peg.1750	Plate3-G8,Plate88-D5,Plate68-D9	K02416
peg.1751	0	K02415
peg.1752	0	0
peg.1753	Plate41-E12,Plate4-A1	K01784
peg.1754	0	0
peg.1755	Plate10-A5,Plate10-A5	0
peg.1756	0	0
peg.1757	Plate52-D12,Plate52-D12	0
peg.1758	0,Plate33-E7,Plate63-C11,Plate45-F4	K01854
peg.1759	Plate85-A5,Plate85-A5	K09857
peg.1760	Plate68-H3,Plate89-B4,Plate25-D4,Plate72-B10,Plate41-E5	K06192
peg.1761	0	K02065
peg.1762	Plate98-B4,Plate62-E3,Plate33-B6,Plate89-B1,Plate8-A3	K02066
peg.1763	Plate71-B7,Plate5-F2,Plate3-H9,Plate64-C11	K03177
peg.1764	0	K02956
peg.1765	0	0
peg.1766	0	K00962
peg.1767	0	0
peg.1768	Plate92-A4,Plate92-A4	0
peg.1769	0	K02469
peg.1770	0	K00954
peg.1771	Plate24-C1,Plate24-C1	0
peg.1772	0	0
peg.1773	Plate72-A6,Plate72-A6	0
peg.1774	Plate43-D2,Plate18-G5,Plate78-C7,Plate13-F7,Plate60-C11	0
peg.1775	Plate45-C4,Plate45-C4	0
peg.1776	0	K03522
peg.1777	0	K03521
peg.1778	0	K00311
peg.1779	Plate21-G5,Plate21-G5	0
peg.1780	Plate55-C3,Plate6-G12,Plate83-H10,Plate13-E5,Plate44-C9,Plate16-D10	K02495
peg.1781	Plate50-F8,Plate31-H3	K07275
peg.1782	0	0
peg.1783	0	K01420
peg.1784	Plate29-C5,Plate85-D10,Plate131-E12,Plate36-H3	K04771
peg.1785	0	0
peg.1786	0	0
peg.1787	Plate58-A10,Plate98-D12,Plate54-D3,Plate80-B7,Plate17-G5,Plate71-A12	K07010
peg.1788	Plate43-F7,Plate4-C12,Plate39-H2,Plate46-B2,Plate62-B5,Plate59-B7	K06178
peg.1789	Plate56-B2,Plate73-H1,Plate84-G11,Plate86-F10,Plate5-E2,Plate64-B8,Plate59-C7,Plate27-D12	K08316
peg.1790	Plate54-G3,Plate54-G3	K03111
peg.1791	0	0
peg.1792	0	K06204
peg.1793	Plate98-C11,Plate98-C11	0

peg.1794	Plate14-F5,Plate80-E7,Plate78-G4	0
peg.1795	0	K01866
peg.1796	Plate27-D8,Plate43-A7	K03568
peg.1797	Plate15-F4,Plate84-E7,Plate53-B10,Plate62-B12,Plate56-D4,Plate27-H7,Plate15-H9	0
peg.1798	Plate15-E1,Plate39-G12,Plate81-D8,Plate78-C11,Plate53-C10,Plate24-A12,Plate78-A8,Plate96-H2,Plate71-E9	0
peg.1799	Plate22-D5,Plate22-D5	0
peg.1800	Plate10-A10,Plate22-F4	K03466
peg.1801	0	K06177
peg.1802	Plate13-A6,Plate131-D5,Plate8-H3,Plate58-D2,Plate53-H10	0
peg.1803	Plate63-B12,Plate17-F7,Plate48-G11,Plate88-F2	K00799
peg.1804	0	K00566
peg.1805	0	K04755
peg.1806	Plate60-A10,Plate95-B2,Plate12-F10,Plate34-E1,Plate95-H9	K04487
peg.1807	Plate90-B12,Plate33-C4,Plate18-A12,Plate8-D9,Plate66-G11,Plate66-E2,Plate12-A8,Plate82-B6	K04487
peg.1808	Plate46-F1,Plate36-D7	0
peg.1809	0	K07018
peg.1810	Plate64-F10,Plate27-C11	K02533
peg.1811	0	K01883
peg.1812	0	0
peg.1813	0	K11754
peg.1814	0	K01963
peg.1815	0,Plate84-A12	K03671
peg.1816	Plate4-C3,Plate29-B12,Plate3-F7,Plate40-H7,Plate55-D8,Plate37-G2,Plate47-E11,Plate10-G9,Plate21-B8,Plate93-F6,Plate2-H5,Plate66-E4,Plate8-E9,Plate15-B7,Plate10-E10,Plate7-F8,Plate60-E10,Plate30-F2,Plate90-H4	K16898
peg.1817	Plate47-C2,Plate1-A9,Plate61-D9,Plate97-F11,Plate73-A4,Plate97-D7,Plate24-H3,Plate4-A5,Plate96-F4,Plate67-B6,Plate7-A7,Plate41-F3,Plate7-H7,Plate31-B9,Plate38-D2	K16899
peg.1818	0	K06925
peg.1819	Plate32-D10,Plate1-E3,Plate15-D10,Plate6-A3,Plate78-C1,Plate9-B6	K13584
peg.1820	Plate29-H5,Plate98-E1,Plate30-H9	K00941
peg.1821	0	K03431
peg.1822	0	K00796
peg.1823	0	K03798
peg.1824	0	K04075
peg.1825	0	0
peg.1826	0	K03640
peg.1827	0	K03641
peg.1828	0	0
peg.1829	Plate18-G7,Plate49-G2,Plate30-D5	0
peg.1830	Plate76-G7,Plate85-B8,Plate44-H4,Plate55-D10,Plate71-G6,Plate44-E1,Plate60-H1,Plate131-F12,Plate27-F7,Plate87-G8	K07250
peg.1831	0	0
peg.1832	Plate85-D7,Plate85-D7	0
peg.1833	Plate31-C5,Plate97-C12	0
peg.1834	0	K07447
peg.1835	0	K02435
peg.1836	0	K02433
peg.1837	0	K02434
peg.1838	Plate35-F9,Plate35-F9	0
peg.1839	Plate22-B10,Plate29-C2,Plate36-H9,Plate68-B7,Plate90-C12	K06147
peg.1840	0,Plate13-G11	K10773
peg.1841	0	K01772
peg.1842	Plate10-E6,Plate12-A7,Plate61-B12,Plate63-C9,Plate71-B4,Plate26-C1,Plate22-A3,Plate42-E2,Plate11-A1	K03575
peg.1843	0,Plate78-H10	0
peg.1844	0,Plate56-G3	0
peg.1845	Plate50-F10,Plate71-F10,Plate43-F3	0
peg.1846	Plate39-D9,Plate16-A10,Plate13-G7,Plate83-D11,Plate2-F1,Plate50-F4,Plate47-C3,Plate85-G12,Plate41-G7,Plate46-C11,Plate81-F11,Plate87-E9,Plate85-A11,Plate48-C10	0
peg.1847	Plate47-A11,Plate47-A11	0
peg.1848	0	K01869
peg.1849	0	K03643
peg.1850	0	K02340
peg.1851	Plate58-G2,Plate58-G2	0
peg.1852	Plate7-C10,Plate83-B10,Plate54-A12	K01584
peg.1853	Plate89-D12,Plate76-E12,Plate35-A2	K07085

peg.1854	0	0
peg.1855	Plate79-E8,Plate12-G7,Plate13-B11,Plate3-G3,Plate47-G3	0
peg.1856	0	K07126
peg.1857	Plate86-C11,Plate98-A5	K16090
peg.1858	0,Plate53-C6,Plate53-C6	K03561
peg.1859	0	K03559
peg.1860	Plate53-D8,Plate54-D6	K03832
peg.1861	Plate7-D4,Plate18-H2,Plate85-B10	K04564
peg.1862	Plate7-E10,Plate93-F11	K00459
peg.1863	0	0
peg.1864	Plate97-E9,Plate35-A9,Plate4-F1,Plate30-H7,Plate44-C8,Plate6-F4	K03761
peg.1865	0,Plate97-H8,Plate48-G8,Plate3-B4,Plate12-F7	K09760
peg.1866	Plate1-H3,Plate80-F2	0
peg.1867	Plate34-C9,Plate59-A6,Plate24-C7,Plate87-D9	0
peg.1868	Plate81-G7,Plate25-D11,Plate51-C5,Plate43-G4,Plate88-D2,Plate25-H2,Plate49-C1,Plate33-A8,Plate90-D12,Plate33-C8,Plate35-B8,Plate16-D5,Plate81-G10,Plate131-E9,Plate86-C6,Plate14-B5,Plate90-G2,Plate7-F3,Plate6-H6,Plate61-A8,Plate88-B5,Plate62-C1,Plate46-G4,Plate3-A1,Plate56-E2	0
peg.1869	Plate92-D8,Plate42-G8,Plate27-E9,Plate14-E9,Plate77-H9,Plate58-H8,Plate51-D4	0
peg.1870	Plate1-A8,Plate7-F11,Plate98-G5,Plate23-A5,Plate49-E2,Plate2-C4	0
peg.1871	0	K02867
peg.1872	0	K02863
peg.1873	0	K02864
peg.1874	0	K02935
peg.1875	0	K03043
peg.1876	0	K03046
peg.1877	0	0
peg.1878	0	K02358
peg.1879	0	K02906
peg.1880	0	K02926
peg.1881	0	K02892
peg.1882	0	K02886
peg.1883	0	K02965
peg.1884	0	0
peg.1885	0	K02982
peg.1886	0	K02878
peg.1887	0	K02904
peg.1888	0	K02961
peg.1889	0	K02874
peg.1890	0	K02895
peg.1891	0	K02931
peg.1892	0	K02954
peg.1893	0	K02994
peg.1894	0	K02933
peg.1895	0	K02881
peg.1896	0	K02988
peg.1897	0	K02907
peg.1898	0	K02876
peg.1899	0	0
peg.1900	0	K03076
peg.1901	0	K00939
peg.1902	0	K02952
peg.1903	0	0
peg.1904	0	K02948
peg.1905	0	0
peg.1906	0	K03040
peg.1907	0	K02879
peg.1908	0,Plate31-D6,Plate40-C3,Plate88-A11	K02051
peg.1909	Plate1-F12,Plate45-B8,Plate77-C9,Plate13-F12	K02050
peg.1910	Plate30-A12,Plate11-A10,Plate52-G7,Plate24-C9	K02049
peg.1911	Plate72-D3,Plate72-D3	0
peg.1912	Plate31-H1,Plate31-H1	0
peg.1913	Plate5-B8,Plate72-A9,Plate97-A5	0
peg.1914	Plate15-G12,Plate36-A7,Plate55-B6,Plate61-E6,Plate79-B4,Plate36-G10,Plate4-C6,Plate37-E11,Plate60-B10,Plate50-F9,Plate63-H10	K07789

peg.1915	Plate86-G7,Plate62-B1,Plate1-G11,Plate48-B8,Plate50-E12,Plate68-G12,Plate86-A12,Plate54-E4,Plate87-F3,Plate17-H5,Plate57-A8,Plate48-G11	K07788
peg.1916	Plate76-G9,Plate27-D5,Plate54-C7,Plate7-F5,Plate24-G8	K07799
peg.1917	Plate3-G10,Plate32-D7,Plate68-G10,Plate40-H8,Plate28-B4	0
peg.1918	0	0
peg.1919	Plate13-G9,Plate99-F7,Plate94-E3	K03470
peg.1920	0	K13581
peg.1921	0	0
peg.1922	Plate31-A2,Plate9-D2,Plate24-F9,Plate89-D3,Plate81-A11,Plate2-C2,Plate38-C5,Plate49-D3,Plate62-A1,Plate64-A12,Plate22-B8	0
peg.1923	Plate51-A2,Plate82-B12,Plate26-B9,Plate22-H7,Plate7-H8,Plate97-G8,Plate50-C4,Plate52-D7,Plate21-D11,Plate18-D2,Plate46-H5,Plate49-F11,Plate27-D11,Plate46-A9,Plate59-E9	0
peg.1924	Plate61-F11,Plate26-A11,Plate47-E5	0
peg.1925	Plate93-A8,Plate1-E2,Plate62-C10,Plate49-F4	K03924
peg.1926	Plate64-C2,Plate56-B8,Plate36-H8,Plate48-B6,Plate9-E3,Plate27-F8	K09986
peg.1927	0	K00970
peg.1928	0,Plate8-H6,Plate35-H5	K11085
peg.1929	Plate67-C8,Plate99-B12,Plate88-A3,Plate38-A6	K03543
peg.1930	Plate17-E6,Plate83-C1,Plate33-H3,Plate25-A12,Plate5-C8	K03446
peg.1931	Plate2-G11,Plate56-C3	K08311
peg.1932	Plate132-G9,Plate25-G7	K09798
peg.1933	Plate40-C8,Plate12-H5	K03797
peg.1934	Plate5-B3,Plate61-G4,Plate64-B12	0
peg.1935	Plate12-H2,Plate2-H3,Plate18-G9,Plate51-F3,Plate55-F3	K15633
peg.1936	0	0
peg.1937	Plate67-F9,Plate24-B10,Plate85-H10,Plate31-D10,Plate73-H5,Plate99-C2,Plate79-A1	K01754
peg.1938	Plate73-A10,Plate73-A10	K03624
peg.1939	0	K01955
peg.1940	0	K01956
peg.1941	Plate62-C8,Plate62-C8	K09117
peg.1942	0	K02316
peg.1943	0	K03086
peg.1944	Plate3-F2,Plate96-A12	0
peg.1945	0	K02990
peg.1946	0	K02963
peg.1947	0	K02939
peg.1948	Plate16-C1,Plate63-A10	K00574
peg.1949	0,Plate28-F1	K02528
peg.1950	0	K03771
peg.1951	0	K04744
peg.1952	0	K11720
peg.1953	0	K07091
peg.1954	Plate91-G2,Plate27-G1,Plate7-F9,Plate30-F8	0
peg.1955	0	0
peg.1956	Plate88-E11,Plate88-E11	0
peg.1957	Plate44-B5,Plate71-E7,Plate67-B4,Plate82-D11,Plate1-F1,Plate92-A9,Plate77-D11,Plate29-E3,Plate96-B10	K06147
peg.1958	Plate35-D8,Plate73-D8,Plate1-G8	0
peg.1959	0	K03608
peg.1960	0,Plate13-C9,Plate59-F10	K03609
peg.1961	Plate25-G10,Plate86-B5,Plate7-G10,Plate50-H11,Plate15-E6	K03610
peg.1962	0	0
peg.1963	0	K00799
peg.1964	0,Plate90-G5,Plate85-C8,Plate73-E5,Plate40-B6,Plate23-B12,Plate9-D11,Plate83-H7	K07007
peg.1965	Plate34-D11,Plate34-D11	K07056
peg.1966	Plate80-F1,Plate10-D8,Plate89-C7,Plate33-E4,Plate8-C1	0
peg.1967	Plate31-C1,Plate4-G10,Plate38-H3,Plate67-C3,Plate16-B7,Plate50-H5,Plate27-C7	0
peg.1968	0	K07736
peg.1969	Plate12-H1,Plate25-E1,Plate47-B2	K08994
peg.1970	Plate55-B9,Plate25-C4	0
peg.1971	0,Plate66-C5,Plate71-E3	K01070
peg.1972	Plate27-D4,Plate27-D7,Plate51-C10	0
peg.1973	Plate11-H10,Plate5-G11,Plate62-F9	K09811
peg.1974	Plate51-E4,Plate2-H11,Plate131-E4	K09812
peg.1975	Plate55-F7,Plate5-A10	0
peg.1976	Plate29-D5,Plate29-D5	0

peg.1977	Plate91-C10,Plate63-B2,Plate36-G8,Plate22-F6,Plate54-D12	0
peg.1978	Plate28-A7,Plate9-A1,Plate73-C3	0
peg.1979	0	K01419
peg.1980	Plate61-E5,Plate76-B12,Plate11-H2	K03667
peg.1981	0	K02426
peg.1982	Plate85-B12,Plate10-D9,Plate92-C5,Plate99-G5,Plate34-A7,Plate49-B4	0
peg.1983	Plate13-D4,Plate94-A9,Plate21-B1	K07302
peg.1984	Plate22-C3,Plate6-C3,Plate45-F11,Plate48-D6,Plate82-C9,Plate17-F10,Plate35-F12,Plate13-G4,Plate5-E7	0
peg.1985	0	K02916
peg.1986	0	K02887
peg.1987	0	K01889
peg.1988	0	K01890
peg.1989	Plate7-A8,Plate52-B4,Plate27-C10,Plate35-B3,Plate67-E3	K02040
peg.1990	Plate67-A8,Plate88-D10,Plate9-C7,Plate24-H5	K02035
peg.1991	0	0
peg.1992	Plate64-E12,Plate84-H2	0
peg.1993	Plate8-D2,Plate8-H1	K03316
peg.1994	Plate82-A10,Plate60-D10,Plate90-B9	0
peg.1995	0	K02986
peg.1996	Plate80-E6,Plate131-A11,Plate66-H2,Plate3-E3,Plate40-G3	0
peg.1997	Plate32-B1,Plate39-F4,Plate97-B8,Plate1-C12,Plate64-C5,Plate63-C2,Plate16-D3,Plate41-F4	K07789
peg.1998	0	0
peg.1999	Plate54-G11,Plate54-G11	0
peg.2000	0	0
peg.2001	Plate84-B1,Plate39-F12,Plate72-A5	K03699
peg.2002	0	0
peg.2003	Plate73-B9,Plate24-F2,Plate59-A8,Plate12-D8,Plate56-D9,Plate30-C6,Plate81-F1,Plate8-D10,Plate14-H1	0
peg.2004	0	K02334
peg.2005	Plate4-A4,Plate4-A4	0
peg.2006	Plate37-C11,Plate13-D10,Plate14-G12,Plate87-A1,Plate6-G8	0
peg.2007	0	K00919
peg.2008	Plate90-F6,Plate29-H7,Plate97-G2,Plate23-E12,Plate46-C7,Plate26-H5,Plate53-B3,Plate45-F9,Plate54-D7	0
peg.2009	Plate27-B3,Plate5-F8	0
peg.2010	Plate61-C12,Plate31-A11	0
peg.2011	Plate14-H7,Plate64-D4,Plate42-E1	0
peg.2012	Plate36-A1,Plate36-A1	0
peg.2013	0,Plate99-B1,Plate100-E9,Plate29-A6,Plate41-G4,Plate28-G7	0
peg.2014	Plate44-D9,Plate56-G1	0
peg.2015	0	K00948
peg.2016	Plate17-G2,Plate17-G2	K15634
peg.2017	0	0
peg.2018	0,Plate71-A10	0
peg.2019	Plate28-A2,Plate28-A2	0
peg.2020	Plate55-B10,Plate73-A12	0
peg.2021	Plate32-H4,Plate44-G11,Plate83-B6,Plate27-A1	K08159
peg.2022	Plate55-F2,Plate13-A9	0
peg.2023	Plate58-A9,Plate26-E8	0
peg.2024	Plate5-B2,Plate50-E2	0
peg.2025	Plate33-D2,Plate88-F11	0
peg.2026	Plate35-B7,Plate79-F2,Plate15-C12	0
peg.2027	Plate92-H5,Plate40-H4,Plate64-G11,Plate11-B5	K03316
peg.2050	Plate54-B7,Plate63-D6	K02014
peg.2051	Plate13-G2,Plate4-B2,Plate29-H11	K00274
peg.2052	Plate45-G11,Plate15-C4	0
peg.2053	0	0
peg.2054	0	0
peg.2055	Plate50-G5,Plate50-G5	0
peg.2056	0	K06878
peg.2057	Plate33-B11,Plate33-B11	0
peg.2058	0	0
peg.2059	Plate53-A5,Plate36-D2	0
peg.2060	Plate66-C4,Plate66-C4	K03863
peg.2061	0	K03862
peg.2062	0	0

peg.2063	0	K01779
peg.2064	Plate51-G11,Plate63-E10	K01779
peg.2065	Plate85-D11,Plate34-F11,Plate73-A9,Plate46-H3,Plate59-C12,Plate92-C8	0
peg.2066	0	0
peg.2067	Plate46-H8,Plate46-H8	0
peg.2068	0,Plate9-G9,Plate62-G10	K02014
peg.2069	Plate95-G7,Plate83-F10,Plate53-D12	K08191
peg.2070	Plate41-H3,Plate84-F11	K19265
peg.2071	Plate13-B4,Plate7-H5,Plate32-C1	0
peg.2072	Plate97-F3,Plate22-G3,Plate132-A11,Plate89-A3,Plate86-A11,Plate35-B1,Plate24-H8,Plate98-G11,Plate42-F8,Plate23-A2,Plate38-C12,Plate54-F4,Plate49-D11,Plate1-H10,Plate98-G2	0
peg.2073	0	K01611
peg.2074	Plate10-E3,Plate10-E3	K00797
peg.2075	0	0
peg.2076	Plate98-C3,Plate98-C3	K00605
peg.2077	Plate83-B9,Plate46-A4,Plate1-F11	K02437
peg.2078	Plate16-F1,Plate53-F8,Plate96-D9,Plate44-B10,Plate9-F11,Plate4-B6,Plate46-D9,Plate38-G11,Plate77-D8,Plate85-G5,Plate64-F6	K00281
peg.2079	0	0
peg.2080	Plate87-C1,Plate56-G4,Plate32-H9,Plate76-A4,Plate30-H2	0
peg.2081	Plate95-E2,Plate95-E2	0
peg.2082	Plate73-G4,Plate73-G4	0
peg.2083	Plate83-B8,Plate81-C11	0
peg.2084	0	0
peg.2085	Plate84-G9,Plate53-B7,Plate53-H8,Plate33-H8,Plate27-B4,Plate40-A4	K16264
peg.2086	Plate21-F4,Plate91-B5,Plate61-A11,Plate24-E11,Plate10-C1,Plate77-H6,Plate32-H6,Plate62-C10,Plate45-E8,Plate67-E8	0
peg.2087	Plate39-F8,Plate98-B7,Plate37-A12,Plate12-G2,Plate86-C3,Plate3-B12,Plate38-A12	0
peg.2088	Plate33-E5,Plate47-F5,Plate14-A3,Plate8-B3	0
peg.2089	Plate5-D1,Plate35-E12	0
peg.2090	Plate96-H3,Plate96-H3	K03885
peg.2091	0,Plate132-B9,Plate91-C6,Plate98-F1,Plate57-F6	K00627
peg.2092	Plate53-H7,Plate99-C10,Plate87-G5,Plate90-G12,Plate22-E10,Plate51-F9,Plate31-B4,Plate11-G7,Plate55-G9,Plate55-C10	0
peg.2093	0	0
peg.2094	Plate18-E3,Plate99-A12,Plate78-F2,Plate37-B10,Plate39-A10,Plate28-F9,Plate51-H11,Plate7-B12	K07386
peg.2095	0	0
peg.2096	0	K10806
peg.2097	Plate9-E2,Plate62-B6,Plate30-D8	0
peg.2098	0	0
peg.2099	Plate11-G12,Plate57-C11	0
peg.2100	Plate29-B11,Plate97-C5,Plate66-G6,Plate42-D2,Plate28-D6,Plate18-G2,Plate78-H2	K16066
peg.2101	Plate90-H3,Plate17-D12	K13771
peg.2102	Plate48-E9,Plate48-E9	0
peg.2103	Plate27-D9,Plate56-F8,Plate60-C7,Plate41-C8,Plate91-H2,Plate68-A11	K01433
peg.2104	Plate35-E11,Plate93-G3,Plate6-G6,Plate72-F2,Plate97-C11	K03811
peg.2105	Plate39-G3,Plate33-C1,Plate59-B6,Plate25-E6,Plate7-C8,Plate86-F9	0
peg.2106	Plate82-F3,Plate7-D8,Plate38-E8,Plate59-H6	K02014
peg.2107	Plate49-G1,Plate96-H8	0
peg.2108	Plate59-C5,Plate59-C5	0
peg.2109	Plate60-A3,Plate48-C2,Plate99-B8	0
peg.2110	Plate72-E6,Plate72-E6	0
peg.2111	Plate41-H4,Plate41-H4	0
peg.2112	Plate68-F2	0
peg.2113	Plate55-C6,Plate8-D6,Plate131-D1,Plate43-F1,Plate66-B8,Plate24-F4,Plate24-H6,Plate14-G3	0
peg.2114	0	0
peg.2115	0	0
peg.2116	0	K07448
peg.2117	0	0
peg.2118	0	0
peg.2119	Plate59-B2,Plate59-B2	0
peg.2120	0	0
peg.2121	0	0
peg.2122	0	0
peg.2123	Plate14-G9,Plate14-G9	0

peg.2124	0	0
peg.2125	Plate27-F5,Plate23-F12,Plate48-B7	0
peg.2126	Plate79-E3,Plate79-E3	K00558
peg.2127	0	0
peg.2128	Plate58-B8,Plate11-C8,Plate97-G1,Plate26-E3,Plate63-B9,Plate39-E9	0
peg.2129	Plate18-E6,Plate9-C1	0
peg.2130	0	0
peg.2131	Plate25-E12,Plate59-D10	0
peg.2132	Plate90-C8,Plate23-E3	0
peg.2133	0	K06223
peg.2134	0,Plate52-H8,Plate14-G4	0
peg.2135	Plate50-A11,Plate50-A11	0
peg.2136	Plate10-G8,Plate10-G8	0
peg.2137	Plate71-A11,Plate35-E9	K03406
peg.2138	0	0
peg.2139	Plate132-G3,Plate132-G3	0
peg.2140	0,Plate27-E8	0
peg.2141	0	0
peg.2142	0	0
peg.2143	0	K00824
peg.2144	0	0
peg.2145	0	0
peg.2146	Plate22-A2,Plate22-A2	0
peg.2147	Plate58-E7,Plate73-G8	0
peg.2148	Plate28-H4,Plate28-H4	0
peg.2149	Plate72-A12,Plate13-H10,Plate29-H6	K02051
peg.2150	Plate95-H1,Plate95-H1	K02050
peg.2151	Plate3-C4,Plate3-C4	K02049
peg.2152	0	K07722
peg.2153	Plate6-D1,Plate6-D1	K09967
peg.2154	0	K09967
peg.2155	Plate22-A11,Plate6-A6,Plate13-C4,Plate49-E3,Plate17-B6,Plate80-C5,Plate56-A10,Plate26-A3,Plate8-C7,Plate83-C10	K01941
peg.2156	Plate53-C11,Plate68-D1,Plate88-A10	K01457
peg.2157	0	0
peg.2158	Plate28-A5,Plate28-A5	0
peg.2159	Plate44-A4,Plate22-G9,Plate81-C9,Plate22-B9	0
peg.2160	Plate81-F9,Plate81-F9	K07146
peg.2161	0	0
peg.2162	Plate23-A9,Plate23-A9	0
peg.2163	Plate57-E10,Plate2-G7	0
peg.2164	Plate23-E6,Plate23-E6	0
peg.2165	0	0
peg.2166	Plate93-B8,Plate77-D7	K07141
peg.2167	Plate55-G1,Plate99-F3,Plate22-D8,Plate132-G11,Plate96-F7,Plate82-E9,Plate88-A4,Plate56-G11,Plate98-H10,Plate17-A9	K07402
peg.2168	0,Plate77-F9,Plate44-A8	0
peg.2169	Plate59-E8,Plate11-D7,Plate45-A9	0
peg.2170	0	0
peg.2171	Plate45-G10,Plate73-G12,Plate33-D9,Plate76-D5	K09005
peg.2172	Plate73-H6,Plate39-H10,Plate33-G9,Plate6-A12,Plate97-F6	K08679
peg.2173	Plate95-C12,Plate72-A4,Plate79-A7,Plate91-E8,Plate85-C7	0
peg.2174	0	0
peg.2175	0	0
peg.2282	Plate2-E1,Plate2-E1	0
peg.2283	Plate96-F5,Plate96-F5	K03119
peg.2284	Plate37-F4,Plate37-F4	0
peg.2285	Plate99-H7,Plate99-H7	0
peg.2286	0	0
peg.2287	Plate87-H6,Plate52-H1,Plate24-D1	0
peg.2288	0	0
peg.2289	Plate61-H7,Plate22-E8,Plate78-G2,Plate10-G5	0
peg.2290	Plate86-D9,Plate86-D9	0
peg.2291	0	0
peg.2292	0	0

peg.2293	0	0
peg.2294	0	0
peg.2295	0	0
peg.2296	Plate60-B1,Plate60-B1	0
peg.2297	0	0
peg.2298	0	0
peg.2299	Plate6-B12,Plate6-B12	0
peg.2300	Plate86-F12,Plate14-F4	0
peg.2301	0	K00355
peg.2302	Plate17-D6,Plate25-B11,Plate52-B8	0
peg.2303	0	K01155
peg.2304	0,Plate78-B10	K01155
peg.2305	Plate91-B11,Plate13-D7	0
peg.2306	0	0
peg.2307	Plate34-H3,Plate33-A11,Plate49-D1	0
peg.2308	Plate15-A7	0
peg.2309	Plate33-A6,Plate87-A3,Plate62-A7,Plate63-E7,Plate57-E6	0
peg.2578	0	0
peg.2579	0	0

Supplementary Table 3: MGWA results – CFU analysis. Top 324 hits from the MGWA (p-value less than 0.001) used for the KEGG enrichment analysis.

OG	pval1	corrected_pval1	mean_OGContain	mean_OGLack	KEGG
ASAHP03698	5.69E-08	0.00029348	8.921595687	11.75045372	K01521
ASAHP01854	1.61E-06	0.008278976	10.00468644	12.07778233	#N/A
ASAHP05347	1.76E-06	0.009086672	8.577006564	11.61871491	K06197
ASAHP01858	1.77E-06	0.009119216	9.997101768	12.07364032	#N/A
ASAHP02096	3.79E-06	0.019562497	9.880578744	11.95747985	K01093
ASAHP01712	3.84E-06	0.019822123	10.02506509	12.05479005	#N/A
ASAHP03164	4.08E-06	0.02104721	9.462494511	11.78984541	K08304
ASAHP00567	4.69E-06	0.02418186	10.32608515	12.33653143	K00045
ASAHP01726	5.64E-06	0.029092981	10.03965126	12.04495741	K04751
ASAHP01229	5.66E-06	0.029188388	12.21597501	10.29486072	K16899
ASAHP01233	5.66E-06	0.029188388	12.21597501	10.29486072	K07177
ASAHP01107	5.77E-06	0.029749903	12.15842759	10.23980232	#N/A
ASAHP03047	6.88E-06	0.035455171	9.612547921	11.82034621	K00851
ASAHP01653	7.65E-06	0.039462926	12.32052272	10.39569703	K03048
ASAHP01002	8.03E-06	0.041402427	10.12069054	12.08688231	#N/A
ASAHP01414	8.03E-06	0.041402427	10.12069054	12.08688231	K09015
ASAHP01491	8.03E-06	0.041402427	10.12069054	12.08688231	K07391
ASAHP01562	8.03E-06	0.041402427	10.12069054	12.08688231	K08281
ASAHP01565	8.03E-06	0.041402427	10.12069054	12.08688231	K03274
ASAHP01741	8.03E-06	0.041402427	10.12069054	12.08688231	K00769
ASAHP01567	8.03E-06	0.041402427	10.12069054	12.08688231	K02040
ASAHP01617	8.03E-06	0.041402427	10.12069054	12.08688231	K03060
ASAHP00101	8.03E-06	0.041402427	12.08688231	10.12069054	#N/A
ASAHP00900	8.03E-06	0.041402427	12.08688231	10.12069054	#N/A
ASAHP00948	8.03E-06	0.041402427	12.08688231	10.12069054	K01274
ASAHP01223	8.54E-06	0.044007759	12.20233248	10.30800326	#N/A
ASAHP01026	9.54E-06	0.049206677	12.13540571	10.18905113	K06967
ASAHP01113	9.54E-06	0.049206677	12.13540571	10.18905113	K00243
ASAHP01659	1.06E-05	0.054774348	12.24974849	10.36120179	#N/A
ASAHP00864	1.36E-05	0.069895515	10.2588936	12.18021663	K01524
ASAHP01585	1.73E-05	0.089044835	10.08541649	12.01410673	K06167
ASAHP01713	1.73E-05	0.089044835	10.08541649	12.01410673	K08997
ASAHP01714	1.73E-05	0.089044835	10.08541649	12.01410673	K03669
ASAHP01742	1.73E-05	0.089044835	10.08541649	12.01410673	K04092
ASAHP01749	1.73E-05	0.089044835	10.08541649	12.01410673	K03179
ASAHP01916	1.73E-05	0.089044835	10.08541649	12.01410673	#N/A
ASAHP01095	1.88E-05	0.096696258	12.16192842	10.2571737	K04487
ASAHP01483	1.94E-05	0.099917871	10.2083432	12.10947176	K08311
ASAHP01500	2.02E-05	0.104243696	12.28253827	10.42522049	#N/A
ASAHP00721	2.18E-05	0.112560475	12.22683252	10.39017709	K03502
ASAHP01409	2.31E-05	0.11915987	12.29081508	10.40087318	#N/A
ASAHP02926	2.99E-05	0.154108322	12.89656992	10.70588006	#N/A
ASAHP01725	3.12E-05	0.16085811	10.11178339	11.99633262	K01255
ASAHP01791	3.21E-05	0.165261768	12.25877887	10.46073062	K03652
ASAHP01748	3.23E-05	0.166426074	9.893113668	11.87013396	K03559
ASAHP06178	3.87E-05	0.199644711	8.534377019	11.55124135	K09020
ASAHP01513	4.54E-05	0.234050232	12.31163814	10.49719443	K06885
ASAHP03487	5.30E-05	0.273473803	9.506271151	11.70696985	#N/A
ASAHP01582	5.91E-05	0.30461874	10.26954475	12.07540803	K03777
ASAHP01081	6.44E-05	0.331959472	12.12402152	10.30735338	K03529
ASAHP00852	6.94E-05	0.357773249	12.06742991	10.26842172	K02825
ASAHP05146	7.13E-05	0.367593018	8.922574682	11.56919753	K05523
ASAHP01177	7.41E-05	0.381845452	10.30361653	12.01191702	K03688
ASAHP01559	8.34E-05	0.429869175	10.21641082	12.01408097	K00799
ASAHP01576	9.14E-05	0.471032519	10.10089451	11.93017501	K04084
ASAHP02038	9.14E-05	0.471032519	10.10089451	11.93017501	K09880
ASAHP05923	0.00011549	0.595468154	13.90874286	10.93627766	#N/A
ASAHP02789	0.000117505	0.605853426	9.777942798	11.76823098	#N/A
ASAHP01698	0.000121451	0.626202657	10.16542335	11.98453666	K12144
ASAHP01502	0.000128121	0.660589514	12.14466132	10.3911036	#N/A

ASAHP00977	0.000136812	0.705403194	12.05154098	10.2558347	#N/A
ASAHP00783	0.000136812	0.705403282	10.2558347	12.05154098	K13771
ASAHP01485	0.000136812	0.705403282	10.2558347	12.05154098	K06168
ASAHP01493	0.000136812	0.705403282	10.2558347	12.05154098	K01599
ASAHP01199	0.000136812	0.705403282	10.2558347	12.05154098	K01175
ASAHP01318	0.000136812	0.705403282	10.2558347	12.05154098	K02446
ASAHP01307	0.000136812	0.705403282	10.2558347	12.05154098	K00833
ASAHP01444	0.000136812	0.705403282	10.2558347	12.05154098	K01843
ASAHP00596	0.000145911	0.752318804	10.17569761	11.95324759	K02014
ASAHP02130	0.000152773	0.787698528	12.32599185	10.55125643	K03811
ASAHP01643	0.000159715	0.823489715	12.21200486	10.47179522	#N/A
ASAHP01899	0.000161275	0.83153176	10.18865292	11.95238814	K07034
ASAHP06025	0.000169913	0.8760708	14.2059687	10.96054461	K08196
ASAHP01330	0.000177789	0.916681336	10.32277611	12.09090373	K03149
ASAHP01785	0.000177822	0.916849095	12.25478248	10.51283896	#N/A
ASAHP01037	0.000183252	0.944849881	10.24749917	11.99043631	K00426
ASAHP01579	0.000183252	0.944849881	10.24749917	11.99043631	K09791
ASAHP01580	0.000183252	0.944849881	10.24749917	11.99043631	K05838
ASAHP01608	0.000183252	0.944849881	10.24749917	11.99043631	K13584
ASAHP01622	0.000183252	0.944849881	10.24749917	11.99043631	#N/A
ASAHP01266	0.000183252	0.944849881	10.24749917	11.99043631	K03641
ASAHP01420	0.000183252	0.944849881	10.24749917	11.99043631	K01494
ASAHP01489	0.000183252	0.944849881	10.24749917	11.99043631	K15777
ASAHP01715	0.000183252	0.944849881	10.24749917	11.99043631	K06192
ASAHP02006	0.000193699	0.998712423	9.720554608	11.71651889	K16135
ASAHP00677	0.000195173	1	10.24189375	11.9865089	K18139
ASAHP01421	0.000195173	1	10.24189375	11.9865089	K03568
ASAHP00984	0.000195173	1	10.24189375	11.9865089	K03185
ASAHP01408	0.000195173	1	10.24189375	11.9865089	K05788
ASAHP01575	0.000195173	1	10.24189375	11.9865089	K00652
ASAHP01626	0.000195173	1	10.24189375	11.9865089	K03071
ASAHP01658	0.000199252	1	12.18526168	10.50877427	K01442
ASAHP03537	0.000203045	1	9.597416943	11.67520899	#N/A
ASAHP01850	0.000203336	1	10.11887683	11.89633017	K15034
ASAHP01730	0.000208421	1	10.13161692	11.91912318	K16055
ASAHP01866	0.000208421	1	10.13161692	11.91912318	K03500
ASAHP01882	0.000208421	1	10.13161692	11.91912318	K01087
ASAHP01896	0.000208421	1	10.13161692	11.91912318	#N/A
ASAHP01920	0.000208421	1	10.13161692	11.91912318	K09019
ASAHP02007	0.000219276	1	9.831119982	11.73504708	K02510
ASAHP03025	0.000240914	1	9.831064584	11.74891397	K02670
ASAHP07814	0.000245255	1	8.307563034	11.47390788	K07154
ASAHP01751	0.000249955	1	10.21934433	11.92382502	K03733
ASAHP01760	0.000249955	1	10.21934433	11.92382502	K02913
ASAHP01761	0.000249955	1	10.21934433	11.92382502	K03089
ASAHP01752	0.000249955	1	10.21934433	11.92382502	K03675
ASAHP01609	0.000261519	1	10.23168505	11.9778698	K03284
ASAHP01737	0.000261519	1	10.23168505	11.9778698	K00797
ASAHP01664	0.000262694	1	12.1769086	10.49134436	#N/A
ASAHP01506	0.00026747	1	12.24465873	10.53565771	K07024
ASAHP03545	0.000268752	1	9.615818332	11.69133343	#N/A
ASAHP02020	0.000272077	1	10.1561792	11.88904501	K09712
ASAHP07862	0.000276047	1	8.343588974	11.48003965	#N/A
ASAHP01075	0.000277111	1	10.45006116	12.12781606	K06189
ASAHP01167	0.00028587	1	10.36439479	12.06081837	K01760
ASAHP04078	0.000290297	1	9.453409839	11.62558227	#N/A
ASAHP01400	0.000302951	1	10.15468037	11.88256403	#N/A
ASAHP02958	0.000315825	1	12.51679813	10.69959548	K02042
ASAHP06268	0.000316852	1	8.367493815	11.47803606	#N/A
ASAHP02090	0.00031773	1	12.45017405	10.64558092	#N/A
ASAHP01784	0.000332809	1	12.16876877	10.49780949	#N/A
ASAHP00700	0.000335937	1	10.62255364	12.34345053	K09812
ASAHP00828	0.000344716	1	10.21527279	11.91896391	#N/A
ASAHP01085	0.00036185	1	10.3229711	12.00406736	K01653

ASAHP01516	0.000374164	1	12.09775789	10.39087212	K02342
ASAHP01852	0.000374959	1	10.1574782	11.87359461	K13628
ASAHP00748	0.000399507	1	10.28180042	11.95648566	K00285
ASAHP02332	0.000400704	1	12.3355149	10.61984703	K03328
ASAHP01597	0.000412297	1	10.18905012	11.86208843	#N/A
ASAHP01601	0.000412297	1	10.18905012	11.86208843	K00652
ASAHP01897	0.000412297	1	10.18905012	11.86208843	K02843
ASAHP01332	0.000415167	1	12.03956603	10.46480444	K02244
ASAHP03284	0.000433379	1	12.94062756	10.84660285	#N/A
ASAHP01892	0.000434016	1	10.18311583	11.87281396	#N/A
ASAHP03065	0.00045596	1	9.910712158	11.73320571	#N/A
ASAHP00931	0.00045881	1	11.9956818	10.34264183	K06023
ASAHP00946	0.00045881	1	11.9956818	10.34264183	K03589
ASAHP00983	0.00045881	1	11.9956818	10.34264183	K00655
ASAHP00986	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP00988	0.00045881	1	11.9956818	10.34264183	K07816
ASAHP00996	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP00998	0.00045881	1	11.9956818	10.34264183	K02990
ASAHP01008	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01009	0.00045881	1	11.9956818	10.34264183	K05985
ASAHP01015	0.00045881	1	11.9956818	10.34264183	K01992
ASAHP01016	0.00045881	1	11.9956818	10.34264183	K16511
ASAHP01017	0.00045881	1	11.9956818	10.34264183	K09772
ASAHP01018	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01019	0.00045881	1	11.9956818	10.34264183	K04074
ASAHP01020	0.00045881	1	11.9956818	10.34264183	K09787
ASAHP01021	0.00045881	1	11.9956818	10.34264183	K07742
ASAHP01022	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01023	0.00045881	1	11.9956818	10.34264183	K03700
ASAHP01024	0.00045881	1	11.9956818	10.34264183	K02086
ASAHP01030	0.00045881	1	11.9956818	10.34264183	K09762
ASAHP01031	0.00045881	1	11.9956818	10.34264183	K02240
ASAHP01120	0.00045881	1	11.9956818	10.34264183	K01641
ASAHP01127	0.00045881	1	11.9956818	10.34264183	K01823
ASAHP01123	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01126	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01129	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01137	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP01236	0.00045881	1	11.9956818	10.34264183	#N/A
ASAHP00262	0.00045881	1	10.34264183	11.9956818	K18138
ASAHP00925	0.00045881	1	10.34264183	11.9956818	K02426
ASAHP00962	0.00045881	1	10.34264183	11.9956818	K03773
ASAHP00978	0.00045881	1	10.34264183	11.9956818	K03585
ASAHP01080	0.00045881	1	10.34264183	11.9956818	K03562
ASAHP01170	0.00045881	1	10.34264183	11.9956818	K07277
ASAHP01178	0.00045881	1	10.34264183	11.9956818	K04764
ASAHP01185	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01205	0.00045881	1	10.34264183	11.9956818	K08300
ASAHP01214	0.00045881	1	10.34264183	11.9956818	K00979
ASAHP01302	0.00045881	1	10.34264183	11.9956818	K03474
ASAHP01303	0.00045881	1	10.34264183	11.9956818	K07460
ASAHP01312	0.00045881	1	10.34264183	11.9956818	K01159
ASAHP01313	0.00045881	1	10.34264183	11.9956818	K01507
ASAHP01315	0.00045881	1	10.34264183	11.9956818	K03771
ASAHP01320	0.00045881	1	10.34264183	11.9956818	K03592
ASAHP01321	0.00045881	1	10.34264183	11.9956818	K02066
ASAHP00773	0.00045881	1	10.34264183	11.9956818	K09024
ASAHP01174	0.00045881	1	10.34264183	11.9956818	K14347
ASAHP01187	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01204	0.00045881	1	10.34264183	11.9956818	K16074
ASAHP01285	0.00045881	1	10.34264183	11.9956818	K04754
ASAHP01289	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01306	0.00045881	1	10.34264183	11.9956818	K03919
ASAHP01323	0.00045881	1	10.34264183	11.9956818	#N/A

ASAHP01331	0.00045881	1	10.34264183	11.9956818	K02065
ASAHP01334	0.00045881	1	10.34264183	11.9956818	K00990
ASAHP01335	0.00045881	1	10.34264183	11.9956818	K01082
ASAHP01412	0.00045881	1	10.34264183	11.9956818	K02533
ASAHP01413	0.00045881	1	10.34264183	11.9956818	K02621
ASAHP01422	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01424	0.00045881	1	10.34264183	11.9956818	K01920
ASAHP01432	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01437	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01439	0.00045881	1	10.34264183	11.9956818	K07278
ASAHP01441	0.00045881	1	10.34264183	11.9956818	K06287
ASAHP01442	0.00045881	1	10.34264183	11.9956818	K15738
ASAHP01443	0.00045881	1	10.34264183	11.9956818	K02067
ASAHP01451	0.00045881	1	10.34264183	11.9956818	K06179
ASAHP01452	0.00045881	1	10.34264183	11.9956818	K00568
ASAHP01454	0.00045881	1	10.34264183	11.9956818	K03820
ASAHP01456	0.00045881	1	10.34264183	11.9956818	K04046
ASAHP01457	0.00045881	1	10.34264183	11.9956818	K03980
ASAHP01458	0.00045881	1	10.34264183	11.9956818	K05807
ASAHP01466	0.00045881	1	10.34264183	11.9956818	K00164
ASAHP01467	0.00045881	1	10.34264183	11.9956818	K02622
ASAHP01468	0.00045881	1	10.34264183	11.9956818	K06195
ASAHP01469	0.00045881	1	10.34264183	11.9956818	K00684
ASAHP01471	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01474	0.00045881	1	10.34264183	11.9956818	K06891
ASAHP01476	0.00045881	1	10.34264183	11.9956818	K07323
ASAHP01477	0.00045881	1	10.34264183	11.9956818	K01011
ASAHP01480	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01484	0.00045881	1	10.34264183	11.9956818	K03801
ASAHP01487	0.00045881	1	10.34264183	11.9956818	K09160
ASAHP00866	0.00045881	1	10.34264183	11.9956818	K01070
ASAHP01158	0.00045881	1	10.34264183	11.9956818	#N/A
ASAHP01265	0.00045881	1	10.34264183	11.9956818	K02535
ASAHP01418	0.00045881	1	10.34264183	11.9956818	K00748
ASAHP01447	0.00045881	1	10.34264183	11.9956818	K00677
ASAHP01448	0.00045881	1	10.34264183	11.9956818	K02536
ASAHP01462	0.00045881	1	10.34264183	11.9956818	K00912
ASAHP01464	0.00045881	1	10.34264183	11.9956818	K00275
ASAHP01481	0.00045881	1	10.34264183	11.9956818	K02990
ASAHP01163	0.00045881	1	10.34264183	11.9956818	K07799
ASAHP01169	0.00045881	1	10.34264183	11.9956818	K00116
ASAHP01403	0.00045881	1	10.34264183	11.9956818	K03808
ASAHP01423	0.00045881	1	10.34264183	11.9956818	K07638
ASAHP01430	0.00045881	1	10.34264183	11.9956818	K08994
ASAHP01560	0.00045881	1	10.34264183	11.9956818	K00798
ASAHP01569	0.00045881	1	10.34264183	11.9956818	K07390
ASAHP01620	0.00045881	1	10.34264183	11.9956818	K03608
ASAHP01621	0.00045881	1	10.34264183	11.9956818	K03610
ASAHP01628	0.00045881	1	10.34264183	11.9956818	K07115
ASAHP01630	0.00045881	1	10.34264183	11.9956818	K02427
ASAHP02649	0.000476989	1	10.00161962	11.82622765	#N/A
ASAHP01011	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01014	0.000477468	1	12.04150743	10.39392553	K03565
ASAHP01076	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01116	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01117	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01118	0.000477468	1	12.04150743	10.39392553	K14540
ASAHP01119	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01121	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01130	0.000477468	1	12.04150743	10.39392553	K06286
ASAHP01133	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01238	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP01356	0.000477468	1	12.04150743	10.39392553	#N/A
ASAHP02329	0.000481514	1	12.48541658	10.70604997	#N/A

ASAHP05030	0.000490902	1	9.158443277	11.54266826	#N/A
ASAHP01801	0.00050123	1	12.14593362	10.5159465	#N/A
ASAHP01843	0.000515173	1	12.19864083	10.58956711	#N/A
ASAHP03528	0.000533086	1	9.566072409	11.62109092	K15125
ASAHP04066	0.000535034	1	9.140452382	11.55268599	K07458
ASAHP01498	0.000566936	1	12.13665479	10.49183651	#N/A
ASAHP01068	0.000572555	1	10.40363372	12.03225431	K06041
ASAHP01328	0.000572555	1	10.40363372	12.03225431	K00957
ASAHP00618	0.000574429	1	10.7101012	12.44492443	K07106
ASAHP01545	0.000601848	1	12.12391485	10.54851073	K01779
ASAHP01970	0.000614762	1	10.10113052	11.84045237	K01126
ASAHP02097	0.000614762	1	10.10113052	11.84045237	K04565
ASAHP00958	0.000616387	1	12.02843334	10.40764261	K00687
ASAHP01125	0.000616387	1	12.02843334	10.40764261	K03816
ASAHP03157	0.000625842	1	12.57004501	10.75292108	#N/A
ASAHP04794	0.000634506	1	8.46796682	11.46096463	#N/A
ASAHP05690	0.000634506	1	8.46796682	11.46096463	#N/A
ASAHP05245	0.000634506	1	8.46796682	11.46096463	K00688
ASAHP03109	0.000654776	1	9.905724135	11.72839292	K01169
ASAHP02018	0.000676385	1	10.06520571	11.80277748	K01194
ASAHP01507	0.000682976	1	12.12573321	10.50089343	K07040
ASAHP01968	0.000693369	1	10.07947184	11.77578379	#N/A
ASAHP01047	0.000701039	1	10.08968244	11.81830447	#N/A
ASAHP01104	0.000701901	1	12.06486152	10.44889657	K07456
ASAHP00523	0.000706035	1	10.84201731	12.93076813	K01443
ASAHP01029	0.000709828	1	12.01558575	10.40350366	K06881
ASAHP01109	0.000709828	1	12.01558575	10.40350366	K01926
ASAHP01132	0.000709828	1	12.01558575	10.40350366	#N/A
ASAHP01219	0.000709828	1	12.01558575	10.40350366	K02221
ASAHP01203	0.000725991	1	12.06921891	10.46149059	K02902
ASAHP01228	0.000725991	1	12.06921891	10.46149059	K03698
ASAHP01235	0.000725991	1	12.06921891	10.46149059	K07030
ASAHP01362	0.000725991	1	12.06921891	10.46149059	K11144
ASAHP00682	0.000748779	1	12.06421023	10.45788361	K03657
ASAHP01226	0.000748779	1	12.06421023	10.45788361	#N/A
ASAHP01347	0.000757516	1	12.01471627	10.41328328	#N/A
ASAHP01001	0.000757516	1	10.41328328	12.01471627	K01079
ASAHP02115	0.000769884	1	12.23536541	10.61543368	#N/A
ASAHP01242	0.000772623	1	12.12304415	10.48716357	#N/A
ASAHP01587	0.000776823	1	10.32673257	11.94537278	#N/A
ASAHP08154	0.000785338	1	14.04792776	10.99310135	#N/A
ASAHP08496	0.000785338	1	14.04792776	10.99310135	#N/A
ASAHP01007	0.000808087	1	11.92419337	10.32472309	K16786
ASAHP00471	0.000808087	1	10.32472309	11.92419337	K00117
ASAHP01300	0.000808087	1	10.32472309	11.92419337	K03670
ASAHP01450	0.000808087	1	10.32472309	11.92419337	K03594
ASAHP01453	0.000808087	1	10.32472309	11.92419337	K00528
ASAHP01581	0.000808087	1	10.32472309	11.92419337	#N/A
ASAHP01164	0.000808087	1	10.32472309	11.92419337	K16011
ASAHP01211	0.000808087	1	10.32472309	11.92419337	K01673
ASAHP01479	0.000808087	1	10.32472309	11.92419337	K02902
ASAHP01482	0.000808087	1	10.32472309	11.92419337	K00548
ASAHP01731	0.000808087	1	10.32472309	11.92419337	#N/A
ASAHP00782	0.000867206	1	10.47095452	12.05907526	K07659
ASAHP04809	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06133	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06146	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06707	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06708	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06709	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP06732	0.00089044	1	8.9686063	11.50083974	#N/A
ASAHP04810	0.000910466	1	8.47319684	11.44342315	#N/A
ASAHP07435	0.000910466	1	8.47319684	11.44342315	#N/A
ASAHP02759	0.000941094	1	9.828301847	11.66957225	K01690

ASAHP04640	0.000957687	1	9.442114713	11.55929956	K03299
ASAHP01631	0.000958905	1	10.1679128	11.81849098	K12262
ASAHP01723	0.000958905	1	10.1679128	11.81849098	K06911
ASAHP01611	0.000959615	1	12.15682176	10.55333171	K03733
ASAHP02067	0.000968612	1	10.26162433	11.82550756	K02226
ASAHP01874	0.000970618	1	10.25511368	11.89240332	K08964
ASAHP02136	0.000979117	1	12.20434622	10.614118	#N/A
ASAHP04525	0.000980617	1	9.476195774	11.55974273	#N/A

Supplementary Table 4: KEGG enrichment analysis – CFU counts. Chi-square analysis comparing top hits, by pathway, from the MGWA to all OGs in the MGWA for each pathway.

KEGG #	Pathway annotation	# genes in top hits	# genes in all ASAHP groups	chisq pval	fdr-corrected pval
ko00540	Lipopolysaccharide biosynthesis	9	24	0.0005	0.04798
ko00270	Cysteine and methionine metabolism	7	44	0.03498	0.88756
ko00480	Glutathione metabolism	4	16	0.03548	0.88756
ko01501	beta-Lactam resistance	4	21	0.05997	0.88756
ko03020	RNA polymerase	2	5	0.06447	0.88756
ko00240	Pyrimidine metabolism	8	61	0.07246	0.88756
ko00450	Selenocompound metabolism	3	14	0.07796	0.88756
ko00965	Betalain biosynthesis	1	1	0.10645	0.88756
ko05020	Prion diseases	1	1	0.10845	0.88756
ko00121	Secondary bile acid biosynthesis	1	1	0.12444	0.88756
ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	3	18	0.12694	0.88756
ko01503	Cationic antimicrobial peptide	3	19	0.13493	0.88756
ko00750	Vitamin B6 metabolism	2	10	0.14943	0.88756
ko04112	Cell cycle - Caulobacter	2	10	0.15692	0.88756
ko00120	Primary bile acid biosynthesis	1	2	0.16592	0.88756
ko01100	Metabolic pathways	66	843	0.16992	0.88756
ko01054	Nonribosomal peptide structures	1	2	0.17041	0.88756
ko00780	Biotin metabolism	2	11	0.17841	0.88756
ko00310	Lysine degradation	2	13	0.2089	0.88756
ko00785	Lipoic acid metabolism	1	3	0.21439	0.88756
ko04213	Longevity regulating pathway - multiple species	1	3	0.21789	0.88756
ko01524	Platinum drug resistance	1	3	0.21889	0.88756
ko04217	Necroptosis	1	3	0.22039	0.88756
ko04931	Insulin resistance	1	3	0.22189	0.88756
ko05204	Chemical carcinogenesis	1	3	0.24138	0.90302
ko05014	Amyotrophic lateral sclerosis	1	4	0.25337	0.90302
ko05152	Tuberculosis	1	4	0.26887	0.90302
ko04910	Insulin signaling pathway	1	4	0.28286	0.90302
ko00920	Sulfur metabolism	4	34	0.28986	0.90302
ko00980	Metabolism of xenobiotics by cytochrome P450	1	5	0.30285	0.90302
ko00982	Drug metabolism - cytochrome P450	1	5	0.30635	0.90302
ko05418	Fluid shear stress and atherosclerosis	1	5	0.30735	0.90302
ko01230	Biosynthesis of amino acids	5	125	0.34683	0.90302
ko00072	Synthesis and degradation of ketone bodies	1	6	0.35782	0.90302
ko00010	Glycolysis / Gluconeogenesis	1	42	0.36132	0.90302
ko04922	Glucagon signaling pathway	1	6	0.36882	0.90302
ko00260	Glycine, serine and threonine metabolism	1	45	0.37131	0.90302
ko00500	Starch and sucrose metabolism	5	46	0.37881	0.90302
ko00230	Purine metabolism	8	86	0.37931	0.90302
ko03420	Nucleotide excision repair	1	7	0.38131	0.90302
ko05133	Pertussis	1	7	0.3918	0.90302
ko05016	Huntington's disease	1	7	0.3968	0.90302
ko05132	Salmonella infection	1	7	0.4063	0.90302
ko03430	Mismatch repair	3	22	0.41579	0.90302
ko00190	Oxidative phosphorylation	2	61	0.42329	0.90302
ko02010	ABC transporters	8	165	0.51174	1
ko00330	Arginine and proline metabolism	1	36	0.52824	1
ko01120	Microbial metabolism in diverse environments	16	297	0.52924	1
ko00860	Porphyrin and chlorophyll metabolism	4	45	0.54123	1
ko00030	Pentose phosphate pathway	4	39	0.54473	1
ko03070	Bacterial secretion system	1	35	0.56372	1
ko00900	Terpenoid backbone biosynthesis	2	18	0.62269	1
ko00730	Thiamine metabolism	2	18	0.62419	1
ko04122	Sulfur relay system	2	15	0.64068	1
ko02024	Quorum sensing	3	71	0.64368	1
ko03018	RNA degradation	2	16	0.64518	1
ko00564	Glycerophospholipid metabolism	3	32	0.72014	1

ko00250	Alanine, aspartate and glutamate metabolism	1	28	0.72014	1
ko01210	2-Oxocarboxylic acid metabolism	1	26	0.72364	1
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	1	26	0.73563	1
ko02020	Two-component system	8	148	0.74013	1
ko00360	Phenylalanine metabolism	1	29	0.74263	1
ko00680	Methane metabolism	3	36	0.74313	1
ko02026	Biofilm formation - Escherichia coli	3	37	0.74913	1
ko01110	Biosynthesis of secondary metabolites	21	321	1	1
ko01130	Biosynthesis of antibiotics	14	218	1	1
ko01200	Carbon metabolism	7	115	1	1
ko00051	Fructose and mannose metabolism	3	44	1	1
ko00520	Amino sugar and nucleotide sugar metabolism	3	52	1	1
ko00620	Pyruvate metabolism	3	50	1	1
ko03010	Ribosome	3	46	1	1
ko00020	Citrate cycle	2	27	1	1
ko00650	Butanoate metabolism	2	34	1	1
ko03440	Homologous recombination	2	25	1	1
ko00261	Monobactam biosynthesis	1	10	1	1
ko00280	Valine, leucine and isoleucine degradation	1	20	1	1
ko00290	Valine, leucine and isoleucine biosynthesis	1	15	1	1
ko00350	Tyrosine metabolism	1	24	1	1
ko00380	Tryptophan metabolism	1	13	1	1
ko00410	beta-Alanine metabolism	1	17	1	1
ko00440	Phosphonate and phosphinate metabolism	1	11	1	1
ko00550	Peptidoglycan biosynthesis	1	20	1	1
ko00561	Glycerolipid metabolism	1	17	1	1
ko00562	Inositol phosphate metabolism	1	11	1	1
ko00660	C5-Branched dibasic acid metabolism	1	9	1	1
ko00670	One carbon pool by folate	1	14	1	1
ko00710	Carbon fixation in photosynthetic organisms	1	18	1	1
ko00740	Riboflavin metabolism	1	10	1	1
ko00760	Nicotinate and nicotinamide metabolism	1	22	1	1
ko00770	Pantothenate and CoA biosynthesis	1	21	1	1
ko00910	Nitrogen metabolism	1	24	1	1
ko02025	Biofilm formation - Pseudomonas aeruginosa	1	17	1	1
ko03030	DNA replication	1	17	1	1
ko03060	Protein export	1	15	1	1
ko03410	Base excision repair	1	13	1	1
ko04146	Peroxisome	1	11	1	1

Supplementary Table 5: MGWA results – Starvation analysis. Top 432 hits (p-value less than 1e-05) used for the KEGG enrichment analysis.

COG	p-val	corrected_p-val	mean_COGContain	mean_COGLack	Function	KO#
stl01267	2.22E-16	1.30E-12	2.516237386	1.873977143	Phosphoglycerate mutase family 5	K15634
stl01281	2.22E-16	1.30E-12	1.873977143	2.516237386	peptide transporter	0
stl01295	2.22E-16	1.30E-12	1.873977143	2.516237386	SboR	0
stl01296	2.22E-16	1.30E-12	1.873977143	2.516237386	major facilitator superfamily MFS_1	0
stl00984	6.88E-15	4.03E-11	1.898543017	2.532277457	Coenzyme PQQ synthesis protein E	K06139
stl01035	6.88E-15	4.03E-11	1.898543017	2.532277457	transporter	0
stl01934	2.35E-14	1.38E-10	1.811609705	2.4630224	hypothetical protein APT_0065	0
stl01397	2.35E-14	1.38E-10	1.811609705	2.4630224	beta-lactamase domain protein	0
stl00864	5.57E-14	3.26E-10	1.894341689	2.535028445	fused response regulator of ato operon, in two-component system with AtoS: response regulator/sigma54 interaction protein	K13599
stl00825	1.65E-13	9.68E-10	2.466603587	1.805049655	Ribonucleoside-diphosphate reductase subunit beta	K00526
stl01207	3.57E-13	2.09E-09	1.916531087	2.553787309	phosphoglyceromutase	K15633
stl00808	3.89E-13	2.28E-09	1.874984917	2.480780191	aminotransferase	K00822
stl00688	5.12E-13	3.00E-09	1.912033807	2.552440233	amino acid ABC transporter	K11735
stl01186	5.90E-13	3.46E-09	1.908776028	2.511438544	CDP-diacylglycerol--serine O-phosphatidyltransferase	K17103
stl01310	6.01E-13	3.52E-09	1.836409198	2.49287378	serine palmitoyltransferase	K00652
stl01878	1.26E-12	7.37E-09	1.854538926	2.47253175	membrane protein	0
stl00556	1.26E-12	7.37E-09	1.854538926	2.47253175	Quino(hemo)protein alcohol dehydrogenase PQQ-dependent (EC 1.1.99.8)	K17760
stl01376	1.26E-12	7.37E-09	1.854538926	2.47253175	alpha/beta hydrolase	K07018
stl01387	1.26E-12	7.37E-09	1.854538926	2.47253175	surface antigen gene	0
stl01461	1.26E-12	7.37E-09	1.854538926	2.47253175	arginyl-tRNA-protein transferase	K00685
stl01463	1.26E-12	7.37E-09	1.854538926	2.47253175	Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)	K01581
stl01466	1.26E-12	7.37E-09	1.854538926	2.47253175	FIG00695166: hypothetical protein	0
stl01470	1.26E-12	7.37E-09	1.854538926	2.47253175	2-dehydro-3-deoxyphosphoheptonate aldolase	K01626
stl01474	1.26E-12	7.37E-09	1.854538926	2.47253175	biopolymer transporter ExbD	K03560
stl01475	1.26E-12	7.37E-09	1.854538926	2.47253175	ATPase AAA	K06923
stl01477	1.26E-12	7.37E-09	1.854538926	2.47253175	DNA-directed DNA polymerase	K02341
stl01480	1.26E-12	7.37E-09	1.854538926	2.47253175	hypothetical protein AaceN1_07727	0
stl01485	1.26E-12	7.37E-09	1.854538926	2.47253175	Homoserine O-acetyltransferase (EC 2.3.1.31)	K00641
stl01486	1.26E-12	7.37E-09	1.854538926	2.47253175	Homoserine O-acetyltransferase (EC 2.3.1.31)	0
stl01487	1.26E-12	7.37E-09	1.854538926	2.47253175	Homoserine kinase (EC 2.7.1.39)	K02204
stl01488	1.26E-12	7.37E-09	1.854538926	2.47253175	hypothetical protein	K09919
stl01510	1.26E-12	7.37E-09	1.854538926	2.47253175	Protein of unknown function DUF55	0
stl01512	1.26E-12	7.37E-09	1.854538926	2.47253175	hypothetical protein	0
stl01518	1.26E-12	7.37E-09	1.854538926	2.47253175	hypothetical protein APS_1252	K08973
stl00820	1.26E-12	7.37E-09	2.47253175	1.854538926	peptidase T	K01258
stl00927	1.26E-12	7.37E-09	2.47253175	1.854538926	asparaginyl tRNA synthetase	K01893
stl01089	1.26E-12	7.37E-09	2.47253175	1.854538926	DNA polymerase III Rad3-related DNA helicase	K03722
stl00920	1.26E-12	7.37E-09	1.854538926	2.47253175	6-phosphogluconolactonase	K01057
stl01250	1.26E-12	7.37E-09	1.854538926	2.47253175	1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655
stl01369	1.26E-12	7.37E-09	1.854538926	2.47253175	ferredoxin	K05524
stl01062	1.26E-12	7.37E-09	1.854538926	2.47253175	DSBA oxidoreductase	K03446
stl01456	1.26E-12	7.37E-09	1.854538926	2.47253175	alcohol dehydrogenase cytochrome c subunit	0
stl01462	1.26E-12	7.37E-09	1.854538926	2.47253175	csbD-like family protein	0
stl01125	1.26E-12	7.37E-09	2.47253175	1.854538926	flavodoxin	0
stl01240	1.26E-12	7.37E-09	2.47253175	1.854538926	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	K01243
stl01242	1.26E-12	7.37E-09	2.47253175	1.854538926	hypothetical protein BSU34760	0
stl00091	1.26E-12	7.37E-09	1.854538926	2.47253175	transporter	0
stl00610	1.26E-12	7.37E-09	1.854538926	2.47253175	putative Na(+)/H(+) antiporter	K03316

stl01441	1.26E-12	7.37E-09	1.854538926	2.47253175	secretion system type I outer membrane efflux pump lipoprotein NodT	0
stl01608	1.26E-12	7.37E-09	1.854538926	2.47253175	hypothetical protein	0
stl01699	1.26E-12	7.37E-09	1.854538926	2.47253175	membrane protein	K09857
stl01712	1.26E-12	7.37E-09	1.854538926	2.47253175	NAD(FAD)-utilizing dehydrogenases	K07007
stl01159	1.26E-12	7.37E-09	2.47253175	1.854538926	acylphosphatase	K01512
stl01395	1.26E-12	7.37E-09	1.854538926	2.47253175	Transcriptional regulator AsnC family	0
stl01389	3.26E-12	1.91E-08	1.881643308	2.471255622	polysaccharide biosynthesis protein	K13013
stl00973	3.49E-12	2.05E-08	1.926425522	2.544138699	3-dehydroquinate dehydratase II (EC 4.2.1.10)	K03786
stl01200	3.49E-12	2.05E-08	1.926425522	2.544138699	acireductone dioxygenase	K08967
stl01224	3.49E-12	2.05E-08	1.926425522	2.544138699	methylthioribose-1-phosphate isomerase	K08963
stl01346	3.55E-12	2.08E-08	1.839848363	2.475537712	major facilitator superfamily transporter	0
stl01545	3.71E-12	2.17E-08	2.517590416	1.907909327	glutaredoxin	K06191
stl01236	3.71E-12	2.17E-08	2.517590416	1.907909327	phosphoglyceromutase	K01834
stl00596	3.75E-12	2.20E-08	2.448040033	1.842978239	Multidrug-efflux transporter major facilitator superfamily (MFS) (TC 2.A.1)	K08161
stl01956	5.40E-12	3.16E-08	1.811720143	2.445770101	ABC transporter permease protein	K02066
stl01165	5.40E-12	3.16E-08	1.811720143	2.445770101	Chloride channel protein	0
stl01689	7.03E-12	4.11E-08	1.850891806	2.467220893	putative periplasmic ligand-binding sensor protein	K09945
stl00911	1.04E-11	6.07E-08	1.91568938	2.546479832	molecular chaperone DnaK	0
stl01180	1.33E-11	7.81E-08	1.882711728	2.484003583	Multicopper oxidase	0
stl01183	1.33E-11	7.81E-08	1.882711728	2.484003583	copper resistance protein CopB	K07233
stl01390	1.33E-11	7.81E-08	1.882711728	2.484003583	exodeoxyribonuclease III	K01142
stl01233	1.33E-11	7.81E-08	1.882711728	2.484003583	microsomal dipeptidase(EC:3.4.13.19)	0
stl01354	1.33E-11	7.81E-08	1.882711728	2.484003583	oxidoreductase	0
stl01372	1.33E-11	7.81E-08	1.882711728	2.484003583	Coenzyme PQQ synthesis protein C	K06137
stl01373	1.33E-11	7.81E-08	1.882711728	2.484003583	coenzyme Pyrrolo-quinoline quinone synthesis protein B PqqB	K06136
stl01040	1.61E-11	9.40E-08	1.922548143	2.547066503	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	K03526
stl01308	1.65E-11	9.68E-08	1.877169983	2.48359286	NAD(FAD)-utilizing dehydrogenase sll0175 homolog	K07137
stl01361	1.65E-11	9.68E-08	1.877169983	2.48359286	MarR family transcriptional regulator	0
stl01469	1.65E-11	9.68E-08	1.877169983	2.48359286	lysophospholipase	0
stl01504	1.81E-11	1.06E-07	1.84844743	2.456723619	50S ribosomal protein L21	K09958
stl00010	4.46E-11	2.61E-07	1.942086869	2.568587507	nodulation protein	K07789
stl01011	4.46E-11	2.61E-07	1.942086869	2.568587507	heat shock protein 90	K04079
stl01784	4.46E-11	2.61E-07	2.568587507	1.942086869	mevalonate kinase	K00869
stl01785	4.46E-11	2.61E-07	2.568587507	1.942086869	acyl-ACP thioesterase	K01071
stl02196	4.46E-11	2.61E-07	2.568587507	1.942086869	phosphomevalonate kinase	K00938
stl00666	4.46E-11	2.61E-07	1.942086869	2.568587507	malonyl-ACP O-methyltransferase, SAM-dependent	K01935,K02169
stl00733	4.46E-11	2.61E-07	1.942086869	2.568587507	hypothetical protein BSU33850	K05595
stl00737	4.46E-11	2.61E-07	1.942086869	2.568587507	cytochrome o ubiquinol oxidase subunit I	K02298
stl00804	4.46E-11	2.61E-07	1.942086869	2.568587507	flavohemo(Hemoglobin-like protein) (Flavohemoglobin) (Nitricoxide dioxygenase) (NO oxygenase) (NOD)	K05916
stl00860	4.46E-11	2.61E-07	1.942086869	2.568587507	gamma-glutamyltranspeptidase	K00681
stl00894	4.46E-11	2.61E-07	1.942086869	2.568587507	protoheme IX farnesyltransferase	K02301
stl00909	4.46E-11	2.61E-07	1.942086869	2.568587507	phosphoadenosine phosphosulfate reductase	K00390
stl00924	4.46E-11	2.61E-07	1.942086869	2.568587507	thiamine biosynthesis protein ThiC	K03147
stl00936	4.46E-11	2.61E-07	1.942086869	2.568587507	Predicted transcriptional regulator of cysteine synthase, Rrf2 family	0
stl00968	4.46E-11	2.61E-07	1.942086869	2.568587507	Cysteine synthase (EC 2.5.1.47)	K01738
stl01001	4.46E-11	2.61E-07	1.942086869	2.568587507	RNA-binding protein Hfq	K03666
stl01008	4.46E-11	2.61E-07	1.942086869	2.568587507	periplasmic folding chaperone	K03770
stl01018	4.46E-11	2.61E-07	1.942086869	2.568587507	biotin synthase	K01012
stl01029	4.46E-11	2.61E-07	1.942086869	2.568587507	2-oxoglutarate dehydrogenase E1 component	K00164
stl01033	4.46E-11	2.61E-07	1.942086869	2.568587507	iron-sulfur cluster insertion protein	0

stl01045	4.46E-11	2.61E-07	1.942086869	2.568587507	Cytosol aminopeptidase PepA (EC 3.4.11.1)	K01255
stl01046	4.46E-11	2.61E-07	1.942086869	2.568587507	uroporphyrinogen decarboxylase	K01599
stl00736	4.46E-11	2.61E-07	1.942086869	2.568587507	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	K01433
stl00875	4.46E-11	2.61E-07	1.942086869	2.568587507	Glycine dehydrogenase	K00281
stl00887	4.46E-11	2.61E-07	1.942086869	2.568587507	glycine cleavage system T protein	K00605
stl00940	4.46E-11	2.61E-07	1.942086869	2.568587507	thiamine-monophosphate kinase	K00946
stl00942	4.46E-11	2.61E-07	1.942086869	2.568587507	outer membrane biogenesis protein BamB	0
stl00953	4.46E-11	2.61E-07	1.942086869	2.568587507	1-deoxy-D-xylulose 5-phosphate reductoisomerase	K00099
stl00957	4.46E-11	2.61E-07	1.942086869	2.568587507	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	K03527
stl00967	4.46E-11	2.61E-07	1.942086869	2.568587507	thioredoxin peroxidase	K03564
stl00972	4.46E-11	2.61E-07	1.942086869	2.568587507	citrate synthase	K01647
stl00975	4.46E-11	2.61E-07	1.942086869	2.568587507	hypothetical protein GeurL1_08726	K05810
stl00801	4.46E-11	2.61E-07	1.942086869	2.568587507	Twin-arginine translocation protein TatC	K03118
stl00861	4.46E-11	2.61E-07	1.942086869	2.568587507	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	K02299
stl01106	4.46E-11	2.61E-07	1.942086869	2.568587507	Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)	K02300
stl01107	4.46E-11	2.61E-07	1.942086869	2.568587507	cytochrome O ubiquinol oxidase subunit II	K02297
stl00879	4.46E-11	2.61E-07	1.942086869	2.568587507	lipoprotein ABC superfamily ATP binding cassette transporter, permease protein	K09808
stl00880	4.46E-11	2.61E-07	1.942086869	2.568587507	Lon protease ATP-dependent Lon	K01338
stl00898	4.46E-11	2.61E-07	1.942086869	2.568587507	7-cyano-7-deazaguanine reductase	0
stl00928	4.46E-11	2.61E-07	2.568587507	1.942086869	hypothetical protein LmalK3_02657	K15634
stl01258	4.46E-11	2.61E-07	2.568587507	1.942086869	acetyltransferase	0
stl01531	4.46E-11	2.61E-07	2.568587507	1.942086869	integral membrane protein	0
stl01824	4.46E-11	2.61E-07	2.568587507	1.942086869	glutamine amidotransferase	K07009
stl02036	4.46E-11	2.61E-07	2.568587507	1.942086869	bleomycin hydrolase	K01372
stl02039	4.46E-11	2.61E-07	2.568587507	1.942086869	diphosphomevalonate decarboxylase	K01597
stl02043	4.46E-11	2.61E-07	2.568587507	1.942086869	FIG00743560: hypothetical protein	0
stl02045	4.46E-11	2.61E-07	2.568587507	1.942086869	UDP-N-acetylmuramyl tripeptide synthase	K01928
stl00950	4.46E-11	2.61E-07	1.942086869	2.568587507	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	K00833
stl00988	4.46E-11	2.61E-07	1.942086869	2.568587507	SirA family protein	0
stl01420	4.46E-11	2.61E-07	2.568587507	1.942086869	CopY family transcriptional repressor	0
stl00616	4.70E-11	2.75E-07	1.944385865	2.573999132	EtfB protein	K03521
stl00709	4.99E-11	2.92E-07	2.550866586	1.945952819	Protein tyrosine phosphatase	K01104
stl00779	5.03E-11	2.95E-07	1.878045396	2.48665442	Iron-uptake factor PiuC	K07336
stl01384	5.03E-11	2.95E-07	1.878045396	2.48665442	glycosyltransferase	K00721
stl02003	7.97E-11	4.66E-07	1.853790367	2.452615425	hypothetical protein Gobo1_03285	0
stl02470	1.16E-10	6.79E-07	2.592034205	1.955994967	Guanylate kinase	K00942
stl02471	1.16E-10	6.79E-07	2.592034205	1.955994967	hypothetical protein OG1RF_12095	0
stl02588	1.16E-10	6.79E-07	2.592034205	1.955994967	TPR repeat-containing protein	0
stl00813	1.16E-10	6.79E-07	1.955994967	2.592034205	acetolactate synthase 3 regulatory subunit	K01653
stl02384	1.21E-10	7.10E-07	1.839110429	2.446164185	pantothenate kinase	K03525
stl01498	1.43E-10	8.37E-07	1.858950078	2.441191798	hypothetical protein Gobo1_01170	K07090
stl02462	1.58E-10	9.28E-07	2.575288177	1.949060341	nitroreductase	K07078
stl02524	1.80E-10	1.05E-06	1.75332411	2.409693534	Sel1 domain-containing protein	K07126
stl00866	2.01E-10	1.18E-06	1.937549307	2.548435251	putative electron transfer flavoprotein, NAD/FAD-binding domain and ETFP adenine nucleotide-binding domain-like protein	K03522
stl02167	2.03E-10	1.19E-06	1.809008402	2.428498042	glycerate dehydrogenase	K00050
stl01695	2.22E-10	1.30E-06	1.889329826	2.459803474	Cobalamin biosynthesis protein BluB @ 56-dimethylbenzimidazole synthase flavin destructase family	K04719
stl01529	2.49E-10	1.46E-06	2.499906477	1.903234527	cobalt transporter ATP-binding subunit	K16786
stl00868	2.49E-10	1.46E-06	1.903234527	2.499906477	Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)	0

stl00084	2.49E-10	1.46E-06	1.903234527	2.499906477	Glucose dehydrogenase PQQ-dependent (EC 1.1.5.2)	K00117
stl00571	2.49E-10	1.46E-06	1.903234527	2.499906477	oxidoreductase	K00059
stl01004	2.49E-10	1.46E-06	1.903234527	2.499906477	Glucans biosynthesis protein G precursor	K03670
stl01009	2.49E-10	1.46E-06	1.903234527	2.499906477	two component transcriptional regulator	K14981
stl01080	2.49E-10	1.46E-06	1.903234527	2.499906477	glutaredoxin 3	K03676
stl01193	2.49E-10	1.46E-06	1.903234527	2.499906477	UPF0061 family protein	0
stl01194	2.49E-10	1.46E-06	1.903234527	2.499906477	glucosyltransferase	K03669
stl01204	2.49E-10	1.46E-06	1.903234527	2.499906477	hypothetical protein GXY_02346	0
stl01235	2.49E-10	1.46E-06	2.499906477	1.903234527	hypothetical protein HMPREF9456_00546	K19225
stl00989	2.67E-10	1.56E-06	1.88975756	2.478202051	hypothetical protein HMPREF9456_01549	0
stl01222	2.67E-10	1.56E-06	1.88975756	2.478202051	S-adenosyl-L-homocysteine hydrolase NAD binding domain protein	K01251
stl01012	2.67E-10	1.56E-06	1.88975756	2.478202051	oxidoreductase	K17218
stl01377	2.67E-10	1.56E-06	1.88975756	2.478202051	DSBA oxidoreductase	K03543
stl01156	2.67E-10	1.56E-06	2.478202051	1.88975756	oxidoreductase, NAD-dependent	0
stl01311	2.67E-10	1.56E-06	1.88975756	2.478202051	alkylhydroperoxidase	0
stl01362	2.67E-10	1.56E-06	1.88975756	2.478202051	glutathione S-transferase	K00799
stl01394	2.67E-10	1.56E-06	1.88975756	2.478202051	1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655
stl01459	2.67E-10	1.56E-06	1.88975756	2.478202051	ferric iron siderophore receptor	K02014
stl01497	2.67E-10	1.56E-06	1.88975756	2.478202051	FIG00687483: hypothetical protein	0
stl01505	2.67E-10	1.56E-06	1.88975756	2.478202051	endoribonuclease L-PSP	0
stl01317	2.76E-10	1.62E-06	2.465818979	1.893776206	Uridine kinase	K00876
stl00907	2.78E-10	1.63E-06	1.885708481	2.482514951	cobalamin synthesis protein CobW	0
stl02239	3.52E-10	2.06E-06	1.76724537	2.411567044	phosphoglycerate mutase	K02226
stl02114	4.61E-10	2.70E-06	1.861812563	2.433951714	peptidase S9	0
stl00908	4.61E-10	2.70E-06	1.861812563	2.433951714	hypothetical protein HMPREF9456_01651	0
stl00851	4.89E-10	2.86E-06	1.939860697	2.547656147	pleiotropic regulatory protein DnrJ/EryC1/StrS	0
stl00961	6.34E-10	3.71E-06	1.956442639	2.508899177	transcriptional regulator MoxR	K03924
stl01508	7.95E-10	4.66E-06	1.894722097	2.464838739	ubiquinol-cytochrome c reductase cytochrome b subunit	K00412
stl00862	9.02E-10	5.28E-06	2.470999453	1.892932278	flavoprotein NrdI	K03647
stl01318	9.02E-10	5.28E-06	2.470999453	1.892932278	homoserine kinase	K00872
stl00793	1.13E-09	6.61E-06	1.914106084	2.490940593	transcriptional regulator LysR	0
stl00922	1.13E-09	6.61E-06	1.914106084	2.490940593	multidrug resistance transporter HlyD/EmrA/FusE	0
stl02198	1.20E-09	7.03E-06	2.566485016	1.949164966	hypothetical protein LmalK3_04889	0
stl02469	1.20E-09	7.03E-06	2.566485016	1.949164966	HAD superfamily hydrolase	K06950
stl02465	1.32E-09	7.74E-06	2.574524043	1.959167546	FIG00742925: hypothetical protein	0
stl02466	1.32E-09	7.74E-06	2.574524043	1.959167546	multitransmembrane protein	0
stl00029	1.32E-09	7.75E-06	1.836820346	2.452087959	transposase	0
stl01168	1.58E-09	9.23E-06	2.512607517	1.918547919	mannose-6-phosphate isomerase family protein	K01809
stl01197	1.60E-09	9.34E-06	1.896830599	2.449279672	cation/copper resistance transporter ATPase CopZ	K17686
stl01655	1.60E-09	9.34E-06	1.896830599	2.449279672	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1B	K01611
stl01657	1.60E-09	9.34E-06	1.896830599	2.449279672	oxidoreductase	0
stl01665	1.60E-09	9.34E-06	1.896830599	2.449279672	phosphatase	0
stl01371	1.60E-09	9.34E-06	1.896830599	2.449279672	tRNA 2-methylthioadenosine synthase	K18707
stl01383	1.60E-09	9.34E-06	1.896830599	2.449279672	Mitochondrial processing peptidase-like protein (EC 3.4.24.64)	0
stl01464	1.60E-09	9.34E-06	1.896830599	2.449279672	iron transporter	0
stl01468	1.60E-09	9.34E-06	1.896830599	2.449279672	CarD-like transcriptional regulator	K07736
stl01507	1.60E-09	9.34E-06	1.896830599	2.449279672	membrane protein	0
stl01714	1.64E-09	9.59E-06	1.854232739	2.449186474	histidinol-phosphate phosphatase	0
stl01126	1.73E-09	1.01E-05	1.91850617	2.520320892	chromosome partitioning protein ParA	K03593
stl01577	1.79E-09	1.05E-05	2.566539398	1.968938866	formate--tetrahydrofolate ligase	K01938
stl01842	1.79E-09	1.05E-05	2.566539398	1.968938866	Glycosyltransferase LafB responsible for the formation of Gal-Glc-DAG	K13678

stl02108	1.79E-09	1.05E-05	2.566539398	1.968938866	metallo-beta-lactamase superfamily hydrolase	K12574
stl02197	1.79E-09	1.05E-05	2.566539398	1.968938866	integral membrane protein	0
stl02112	1.80E-09	1.05E-05	1.830325336	2.423349738	hypothetical protein	0
stl02287	1.80E-09	1.05E-05	1.830325336	2.423349738	Acyl carrier protein	0
stl02363	2.08E-09	1.22E-05	1.816222536	2.418360642	hypothetical protein GXY_13883	0
stl00955	2.32E-09	1.36E-05	1.902179849	2.494032053	bacterioferritin	K03594
stl01357	2.71E-09	1.59E-05	2.489867645	1.909667275	HAD family haloacid dehalogenase hydrolase	0
stl00916	3.16E-09	1.85E-05	1.909833798	2.493761201	Electron-transferring-flavoprotein dehydrogenase	K00311
stl01028	3.16E-09	1.85E-05	1.909833798	2.493761201	Cytochrome c551 peroxidase (EC 1.11.1.5)	K00428
stl01146	3.16E-09	1.85E-05	1.909833798	2.493761201	Heme exporter protein C	K02195
stl01190	3.16E-09	1.85E-05	1.909833798	2.493761201	ribonuclease D	K03684
stl01214	3.16E-09	1.85E-05	1.909833798	2.493761201	cytochrome c assembly protein	K02198
stl01215	3.16E-09	1.85E-05	1.909833798	2.493761201	Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase	K02199
stl01216	3.16E-09	1.85E-05	1.909833798	2.493761201	cytochrome c-type biogenesis protein CycL	K02200
stl01221	3.16E-09	1.85E-05	1.909833798	2.493761201	heme exporter protein B	K02194
stl02038	3.29E-09	1.92E-05	2.591804954	1.981219322	MerR family transcriptional regulator	0
stl02190	3.29E-09	1.92E-05	2.591804954	1.981219322	integral membrane protein	0
stl02319	3.29E-09	1.92E-05	2.591804954	1.981219322	hypothetical protein	0
stl02549	3.29E-09	1.92E-05	2.591804954	1.981219322	Duplicated ATPase component YkoD of energizing module of thiamin-regulated ECF transporter for HydroxyMethylPyrimidine	K16786,K16787
stl02265	3.41E-09	2.00E-05	1.859255533	2.437520956	2-oxo-4-hydroxy-4-carboxy--5-ureidoimidazoline (OHCU) decarboxylase	K16838
stl01860	4.01E-09	2.35E-05	1.833364349	2.421618619	hypothetical protein AaceN1_04751	0
stl02062	4.77E-09	2.79E-05	1.823989823	2.387958027	FIG01225103: hypothetical protein	0
stl02042	4.94E-09	2.89E-05	2.575033557	1.967865811	hypothetical protein LverK3_00435	0
stl02046	4.94E-09	2.89E-05	2.575033557	1.967865811	hypothetical protein LfruK3_05858	0
stl02199	4.94E-09	2.89E-05	2.575033557	1.967865811	hypothetical protein SMU_1853	0
stl02464	4.94E-09	2.89E-05	2.575033557	1.967865811	hypothetical protein LGAS_0724	0
stl00852	4.94E-09	2.89E-05	1.967865811	2.575033557	7-cyano-7-deazaguanine synthase	K06920
stl01528	5.00E-09	2.93E-05	2.490221288	1.944726065	Acetyltransferase (EC 2.3.1.-)	0
stl02374	5.63E-09	3.30E-05	1.811160657	2.414388383	mechanosensitive ion channel protein MscS	0
stl00819	5.63E-09	3.30E-05	2.414388383	1.811160657	Pantothenate kinase (EC 2.7.1.33)	K00867
stl01447	5.63E-09	3.30E-05	1.811160657	2.414388383	two component hybrid sensor histidine kinase and regulator	0
stl01687	5.82E-09	3.40E-05	1.834145335	2.409270163	murein transglycosylase	0
stl02095	5.82E-09	3.40E-05	1.834145335	2.409270163	hypothetical protein ATPR_1334	0
stl02135	5.82E-09	3.40E-05	1.834145335	2.409270163	hypothetical protein AaceN1_12513	0
stl02150	5.82E-09	3.40E-05	1.834145335	2.409270163	hypothetical protein	0
stl02154	5.82E-09	3.40E-05	1.834145335	2.409270163	outer membrane protein	0
stl01976	5.82E-09	3.40E-05	1.834145335	2.409270163	Peroxiredoxin	K03386
stl02283	5.82E-09	3.40E-05	1.834145335	2.409270163	protein tyrosine phosphatase	0
stl00905	5.82E-09	3.40E-05	1.834145335	2.409270163	porin O/P polyphosphate-selective	K07221
stl01378	5.82E-09	3.40E-05	1.834145335	2.409270163	glycosyltransferase	0
stl01366	7.22E-09	4.23E-05	1.921607537	2.459515036	cobalamin biosynthesis protein CobS	K09882
stl01500	7.40E-09	4.33E-05	2.4754727	1.898964115	GMP reductase	K00364
stl00983	8.48E-09	4.96E-05	1.891378977	2.488312192	transcriptional regulator LysR	K03576
stl02453	8.58E-09	5.02E-05	2.6013382	1.980123724	hypothetical protein LGAS_1227	0
stl00389	8.69E-09	5.08E-05	1.931767816	2.50862589	anaerobic multidrug efflux transporter, ArcA-regulated	K18138
stl00633	8.69E-09	5.08E-05	1.931767816	2.50862589	secretion system type I outer membrane efflux pump lipoprotein NodT	K18139
stl00764	8.69E-09	5.08E-05	1.931767816	2.50862589	hypothetical protein	0
stl00772	8.69E-09	5.08E-05	1.931767816	2.50862589	carbonic anhydrase	K01673
stl00815	8.69E-09	5.08E-05	1.931767816	2.50862589	hypothetical protein HMPREF9456_02792	K02426
stl00826	8.69E-09	5.08E-05	1.931767816	2.50862589	Peptidyl-prolyl cis-trans isomerase(EC:5.2.1.8)	K03773

stl00838	8.69E-09	5.08E-05	1.931767816	2.50862589	RND family efflux transporter MFP subunit	K03585
stl00886	8.69E-09	5.08E-05	1.931767816	2.50862589	Cell division and transport-associated protein TolQ	K03562
stl00915	8.69E-09	5.08E-05	1.931767816	2.50862589	translocation protein TolB	K03641
stl00921	8.69E-09	5.08E-05	1.931767816	2.50862589	inorganic pyrophosphatase	K01507
stl00923	8.69E-09	5.08E-05	1.931767816	2.50862589	methionine synthase	K00548
stl00930	8.69E-09	5.08E-05	1.931767816	2.50862589	rare lipoprotein A	K03642
stl00933	8.69E-09	5.08E-05	1.931767816	2.50862589	hypothetical protein GfraN1_01570	K07277
stl00941	8.69E-09	5.08E-05	1.931767816	2.50862589	integration host factor DNA-binding subunit alpha	K04764
stl00952	8.69E-09	5.08E-05	1.931767816	2.50862589	peptidoglycan-associated lipoprotein	0
stl00966	8.69E-09	5.08E-05	1.931767816	2.50862589	Ribonuclease E (EC 3.1.26.12)	K08300
stl00974	8.69E-09	5.08E-05	1.931767816	2.50862589	3-deoxy-D-manno-octulosonate cytidylyltransferase	K00979
stl01002	8.69E-09	5.08E-05	1.931767816	2.50862589	deoxycytidine triphosphate deaminase	K01494
stl01003	8.69E-09	5.08E-05	1.931767816	2.50862589	protease TldD	K03568
stl01005	8.69E-09	5.08E-05	1.931767816	2.50862589	4-hydroxythreonine-4-phosphate dehydrogenase	K00097
stl01006	8.69E-09	5.08E-05	1.931767816	2.50862589	pyridoxal phosphate biosynthetic protein PdxJ	K03474
stl01010	8.69E-09	5.08E-05	1.931767816	2.50862589	Holliday junction resolvase	K01159
stl01014	8.69E-09	5.08E-05	1.931767816	2.50862589	peptidyl-prolyl cis-trans isomerase	K03771
stl01020	8.69E-09	5.08E-05	1.931767816	2.50862589	zinc-dependent microcin-processing U62/TldD	K03592
stl01022	8.69E-09	5.08E-05	1.931767816	2.50862589	ABC transporter permease protein	K02066
stl01027	8.69E-09	5.08E-05	1.931767816	2.50862589	pyridoxine 5'-phosphate oxidase	K00275
stl01044	8.69E-09	5.08E-05	1.931767816	2.50862589	competence protein comM	K07391
stl00632	8.69E-09	5.08E-05	1.931767816	2.50862589	Ferrichrome-iron receptor	K16090
stl01206	8.69E-09	5.08E-05	1.931767816	2.50862589	4-hydroxybenzoyl-CoA thioesterase family active site	K07107
stl00744	8.69E-09	5.08E-05	1.931767816	2.50862589	multidrug resistance transporter HlyD/EmrA/FusE	0
stl00810	8.69E-09	5.08E-05	1.931767816	2.50862589	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	K03185
stl00849	8.69E-09	5.08E-05	1.931767816	2.50862589	Putative translation initiation inhibitor	0
stl00965	8.69E-09	5.08E-05	1.931767816	2.50862589	magnesium/cobalt transporter CorA	K16074
stl00993	8.69E-09	5.08E-05	1.931767816	2.50862589	bacteriocin/colicin V production	K03558
stl00998	8.69E-09	5.08E-05	1.931767816	2.50862589	lipoprotein	K04754
stl01015	8.69E-09	5.08E-05	1.931767816	2.50862589	lipopolysaccharide ABC transporter permease	K11720
stl01017	8.69E-09	5.08E-05	1.931767816	2.50862589	ferredoxin--NADP(+) reductase	K00528
stl01031	8.69E-09	5.08E-05	1.931767816	2.50862589	4-hydroxybenzoate octaprenyltransferase	K03179
stl01037	8.69E-09	5.08E-05	1.931767816	2.50862589	ABC transporter ATP-binding protein	K02065
stl01042	8.69E-09	5.08E-05	1.931767816	2.50862589	3'(2'),5'-bisphosphate nucleotidase	K01082
stl01078	8.69E-09	5.08E-05	1.931767816	2.50862589	tRNA mC32,mU32 2'-O-methyltransferase, SAM-dependent	K02533
stl01079	8.69E-09	5.08E-05	1.931767816	2.50862589	DNA topoisomerase IV subunit A	K02621
stl01084	8.69E-09	5.08E-05	1.931767816	2.50862589	transcriptional regulator	K07735
stl01092	8.69E-09	5.08E-05	1.931767816	2.50862589	glutathione synthetase	K01920
stl01093	8.69E-09	5.08E-05	1.931767816	2.50862589	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)	K03500
stl01096	8.69E-09	5.08E-05	1.931767816	2.50862589	Glutaredoxin	K07390
stl01097	8.69E-09	5.08E-05	1.931767816	2.50862589	transcriptional regulator BolA	K05527
stl01098	8.69E-09	5.08E-05	1.931767816	2.50862589	Zinc uptake regulation protein ZUR	K09823
stl01099	8.69E-09	5.08E-05	1.931767816	2.50862589	8-amino-7-oxononanoate synthase	K00652
stl01100	8.69E-09	5.08E-05	1.931767816	2.50862589	Preprotein translocase subunit SecG (TC 3.A.5.1.1)	K03075
stl01101	8.69E-09	5.08E-05	1.931767816	2.50862589	outer membrane protein	K07278
stl01102	8.69E-09	5.08E-05	1.931767816	2.50862589	FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster	K09791
stl01103	8.69E-09	5.08E-05	1.931767816	2.50862589	thioredoxin	K05838
stl01108	8.69E-09	5.08E-05	1.931767816	2.50862589	septum formation inhibitor nucleotide-binding protein	K06287
stl01109	8.69E-09	5.08E-05	1.931767816	2.50862589	ABC transporter, ATP-binding protein	K15738
stl01110	8.69E-09	5.08E-05	1.931767816	2.50862589	hypothetical protein Swit_2554	K02067
stl01116	8.69E-09	5.08E-05	1.931767816	2.50862589	ribosomal RNA large subunit 23S rRNA pseudouridine synthase C	K06179

stl01117	8.69E-09	5.08E-05	1.931767816	2.50862589	3-demethylubiquinone-9 3-methyltransferase	K00568
stl01119	8.69E-09	5.08E-05	1.931767816	2.50862589	Proposed peptidoglycan lipid II flippase MurJ	K03980
stl01121	8.69E-09	5.08E-05	1.931767816	2.50862589	coproporphyrinogen III oxidase	K00228
stl01122	8.69E-09	5.08E-05	1.931767816	2.50862589	ABC transporter ATP-binding protein	K06158
stl01127	8.69E-09	5.08E-05	1.931767816	2.50862589	DNA topoisomerase IV subunit B	K02622
stl01128	8.69E-09	5.08E-05	1.931767816	2.50862589	protein associated with Co2+ and Mg2+ efflux	K06195
stl01129	8.69E-09	5.08E-05	1.931767816	2.50862589	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)	K00684
stl01131	8.69E-09	5.08E-05	1.931767816	2.50862589	Protein-export membrane protein SecF (TC 3.A.5.1.1)	K03074
stl01132	8.69E-09	5.08E-05	1.931767816	2.50862589	cyclase	K18588
stl01133	8.69E-09	5.08E-05	1.931767816	2.50862589	Clp protease adaptor protein ClpS	K06891
stl01134	8.69E-09	5.08E-05	1.931767816	2.50862589	toluene transporter auxiliary component Ttg2D	K07323
stl01135	8.69E-09	5.08E-05	1.931767816	2.50862589	3-mercaptopyruvate sulfurtransferase	K01011
stl01137	8.69E-09	5.08E-05	1.931767816	2.50862589	phage integrase family protein	K03733
stl01138	8.69E-09	5.08E-05	1.931767816	2.50862589	ferredoxin	K04755
stl01139	8.69E-09	5.08E-05	1.931767816	2.50862589	DNA-directed RNA polymerase subunit omega	K03060
stl01144	8.69E-09	5.08E-05	1.931767816	2.50862589	oxidoreductase	0
stl01145	8.69E-09	5.08E-05	1.931767816	2.50862589	conserved protein of unknown function; putative YcgN protein	K09160
stl01147	8.69E-09	5.08E-05	1.931767816	2.50862589	protein translocase subunit SecB	K03071
stl01150	8.69E-09	5.08E-05	1.931767816	2.50862589	50S ribosomal protein L33	K02913
stl01153	8.69E-09	5.08E-05	1.931767816	2.50862589	RNA polymerase, sigma 32 (sigma H) factor	K03089
stl00844	8.69E-09	5.08E-05	1.931767816	2.50862589	glyoxalase I	K01759
stl00882	8.69E-09	5.08E-05	1.931767816	2.50862589	Short chain dehydrogenase	K16066
stl00913	8.69E-09	5.08E-05	1.931767816	2.50862589	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	K16363
stl01085	8.69E-09	5.08E-05	1.931767816	2.50862589	Lipid-A-disaccharide synthase (EC 2.4.1.182)	K00748
stl01113	8.69E-09	5.08E-05	1.931767816	2.50862589	acyl-	K00677
stl01114	8.69E-09	5.08E-05	1.931767816	2.50862589	UDP-3-O-	K02536
stl01124	8.69E-09	5.08E-05	1.931767816	2.50862589	Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)	K00912
stl00925	8.69E-09	5.08E-05	1.931767816	2.50862589	multidrug efflux pump acriflavin resistance protein, partial	K07799
stl00931	8.69E-09	5.08E-05	1.931767816	2.50862589	malate:quinone oxidoreductase	K00116
stl01090	8.69E-09	5.08E-05	1.931767816	2.50862589	integral membrane sensor signal transduction histidine kinase	K07638
stl01091	8.69E-09	5.08E-05	1.931767816	2.50862589	chemotaxis protein CheY	K07659
stl01095	8.69E-09	5.08E-05	1.931767816	2.50862589	hypothetical protein GLX_06690	K08994
stl01195	8.69E-09	5.08E-05	1.931767816	2.50862589	paraquat-inducible protein B	K06192
stl01223	8.69E-09	5.08E-05	1.931767816	2.50862589	FIG00688012: hypothetical protein	K07275
stl01225	8.69E-09	5.08E-05	1.931767816	2.50862589	cell division topological specificity factor MinE	K03608
stl01226	8.69E-09	5.08E-05	1.931767816	2.50862589	cell division inhibitor	K03610
stl01229	8.69E-09	5.08E-05	1.931767816	2.50862589	Protein involved in catabolism of external DNA	K07115
stl01136	8.69E-09	5.08E-05	1.931767816	2.50862589	LSU ribosomal protein L28p	K02902
stl01230	8.69E-09	5.08E-05	1.931767816	2.50862589	ribosomal RNA large subunit methyltransferase E	K02427
stl01544	8.69E-09	5.08E-05	2.50862589	1.931767816	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	K15986
stl01732	8.69E-09	5.08E-05	2.50862589	1.931767816	Cell surface hydrolase, membrane-bound	K06889
stl02012	8.69E-09	5.08E-05	2.50862589	1.931767816	deoxyadenosine kinase / deoxyguanosine kinase	0
stl01766	8.69E-09	5.08E-05	2.50862589	1.931767816	dCMP deaminase	K01493
stl02013	8.69E-09	5.08E-05	2.50862589	1.931767816	ribonuclease III	K11145
stl02015	8.69E-09	5.08E-05	2.50862589	1.931767816	Transmembrane component of general energizing module of ECF transporters	K16785
stl02027	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein SMU_541	0
stl02030	8.69E-09	5.08E-05	2.50862589	1.931767816	HAD family hydrolase	K07015
stl02017	8.69E-09	5.08E-05	2.50862589	1.931767816	protein SprT-like	K03095

stl02019	8.69E-09	5.08E-05	2.50862589	1.931767816	bioY protein	K03523
stl02020	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein SMU_1141c	0
stl02026	8.69E-09	5.08E-05	2.50862589	1.931767816	peptidase propeptide and YPEB domain-containing protein	0
stl02162	8.69E-09	5.08E-05	2.50862589	1.931767816	cell division protein ()	K02221
stl00971	8.69E-09	5.08E-05	2.50862589	1.931767816	Transcriptional regulator ArsR family	0
stl01157	8.69E-09	5.08E-05	2.50862589	1.931767816	MOP superfamily multidrug/oligosaccharidyl-lipid/polysaccharide flippase transporter	0
stl01257	8.69E-09	5.08E-05	2.50862589	1.931767816	rotamase family protein	K07533
stl01418	8.69E-09	5.08E-05	2.50862589	1.931767816	Sortase A LPXTG specific	K07284
stl01429	8.69E-09	5.08E-05	2.50862589	1.931767816	penicillin-binding enzyme for formation of rod-shaped peptidoglycan cell wall	K00687
stl01534	8.69E-09	5.08E-05	2.50862589	1.931767816	Cell division protein FtsQ	K03589
stl01579	8.69E-09	5.08E-05	2.50862589	1.931767816	1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655
stl01583	8.69E-09	5.08E-05	2.50862589	1.931767816	phosphoribosyltransferase	K02242
stl01653	8.69E-09	5.08E-05	2.50862589	1.931767816	GTP pyrophosphokinase yjbM	K07816
stl01690	8.69E-09	5.08E-05	2.50862589	1.931767816	O-methyltransferase	0
stl01693	8.69E-09	5.08E-05	2.50862589	1.931767816	LSU ribosomal protein L28p	K02902
stl01728	8.69E-09	5.08E-05	2.50862589	1.931767816	hydroxymethylglutaryl-CoA synthase	K01641
stl01731	8.69E-09	5.08E-05	2.50862589	1.931767816	Tetratricopeptide repeat (TPR) family protein	0
stl01733	8.69E-09	5.08E-05	2.50862589	1.931767816	ribonuclease M5	K05985
stl01734	8.69E-09	5.08E-05	2.50862589	1.931767816	pur operon repressor	K09685
stl01735	8.69E-09	5.08E-05	2.50862589	1.931767816	RNA-binding S4 domain-containing protein	0
stl01736	8.69E-09	5.08E-05	2.50862589	1.931767816	cobalt transporter ATP-binding subunit	K16787
stl01738	8.69E-09	5.08E-05	2.50862589	1.931767816	redox-sensing transcriptional repressor Rex	K01926
stl01740	8.69E-09	5.08E-05	2.50862589	1.931767816	metal-dependent phosphohydrolase, HD family	K03698
stl01741	8.69E-09	5.08E-05	2.50862589	1.931767816	ABC superfamily ATP binding cassette transporter, membrane protein	K01992
stl01742	8.69E-09	5.08E-05	2.50862589	1.931767816	adaptor protein	K16511
stl01744	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein EF2923	0
stl01745	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein OG1RF_10732	K09772
stl01746	8.69E-09	5.08E-05	2.50862589	1.931767816	cell division protein, RNA-binding S4 domain-containing protein	0
stl01747	8.69E-09	5.08E-05	2.50862589	1.931767816	cell division initiation protein	K04074
stl01748	8.69E-09	5.08E-05	2.50862589	1.931767816	DNA-directed RNA polymerase subunit omega	K03060
stl01749	8.69E-09	5.08E-05	2.50862589	1.931767816	thiamin pyrophosphokinase	K00949
stl01750	8.69E-09	5.08E-05	2.50862589	1.931767816	FIG001802: Putative alkaline-shock protein	0
stl01751	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein SMU_229	K07030
stl01752	8.69E-09	5.08E-05	2.50862589	1.931767816	DNA-binding protein	K09787
stl01753	8.69E-09	5.08E-05	2.50862589	1.931767816	GTPase	K14540
stl01754	8.69E-09	5.08E-05	2.50862589	1.931767816	COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination	K07742
stl01755	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein LGG_01636	K09976
stl01756	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein LfruK3_00940	0
stl01757	8.69E-09	5.08E-05	2.50862589	1.931767816	cell cycle protein GpsB	0
stl01758	8.69E-09	5.08E-05	2.50862589	1.931767816	Holliday junction-specific endonuclease	K03700
stl01759	8.69E-09	5.08E-05	2.50862589	1.931767816	DNA replication protein DnaD	K02086
stl01760	8.69E-09	5.08E-05	2.50862589	1.931767816	Isopentenyl-diphosphate delta-isomerase FMN-dependent (EC 5.3.3.2)	K01823
stl01761	8.69E-09	5.08E-05	2.50862589	1.931767816	Substrate-specific component RibU of riboflavin ECF transporter	0
stl01763	8.69E-09	5.08E-05	2.50862589	1.931767816	Alkaline shock protein	0
stl01764	8.69E-09	5.08E-05	2.50862589	1.931767816	ATP-dependent RNA helicase YqfR	K18692
stl01765	8.69E-09	5.08E-05	2.50862589	1.931767816	recombination protein O	K03584
stl01767	8.69E-09	5.08E-05	2.50862589	1.931767816	protein of hypothetical function UPF0473, YrzB	0

stl01768	8.69E-09	5.08E-05	2.50862589	1.931767816	rod shape-determining protein MreD	K03571
stl01770	8.69E-09	5.08E-05	2.50862589	1.931767816	Helicase loader DnaI	K11144
stl01771	8.69E-09	5.08E-05	2.50862589	1.931767816	replication initiation and membrane attachment protein DnaB	K03346
stl01772	8.69E-09	5.08E-05	2.50862589	1.931767816	septation ring formation regulator EzrA	K06286
stl01773	8.69E-09	5.08E-05	2.50862589	1.931767816	methyl-accepting chemotaxis family protein	0
stl01774	8.69E-09	5.08E-05	2.50862589	1.931767816	Phenylalanyl-tRNA synthetase domain protein (Bsu YtpR)	K06878
stl01775	8.69E-09	5.08E-05	2.50862589	1.931767816	thioredoxin	0
stl01776	8.69E-09	5.08E-05	2.50862589	1.931767816	transcriptional regulator	0
stl01777	8.69E-09	5.08E-05	2.50862589	1.931767816	Sec family type I general secretory protein SecG	K03075
stl01778	8.69E-09	5.08E-05	2.50862589	1.931767816	FIG001886: Cytoplasmic hypothetical protein	K09762
stl01779	8.69E-09	5.08E-05	2.50862589	1.931767816	ComF operon protein 1	K02240
stl01780	8.69E-09	5.08E-05	2.50862589	1.931767816	DNA-directed RNA polymerase subunit delta	K03048
stl01782	8.69E-09	5.08E-05	2.50862589	1.931767816	Hypothetical protein possible functionally linked with Alanyl-tRNA synthetase	0
stl01337	8.69E-09	5.08E-05	2.50862589	1.931767816	glucose uptake protein GlcU	K05340
stl01411	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein HMPREF9456_01278	K03437
stl01535	8.69E-09	5.08E-05	2.50862589	1.931767816	phosphodiesterase	K18682
stl01537	8.69E-09	5.08E-05	2.50862589	1.931767816	hypothetical protein LmalK3_04439	0
stl01539	8.69E-09	5.08E-05	2.50862589	1.931767816	phosphoesterase, DHH family protein	K06881
stl01542	8.69E-09	5.08E-05	2.50862589	1.931767816	phosphohydrolase	K06885
stl01493	8.69E-09	5.08E-05	2.50862589	1.931767816	HPr kinase/phosphorylase	K06023
stl01149	9.21E-09	5.39E-05	1.912947765	2.485966522	DnaJ-class molecular chaperone CbpA	0
stl01566	9.96E-09	5.83E-05	1.867622022	2.460360891	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	K00549
stl01994	9.96E-09	5.83E-05	1.867622022	2.460360891	hypothetical protein HMPREF9086_2277	0
stl00994	1.00E-08	5.88E-05	1.870209463	2.423754272	cobyric acid synthase	K02232
stl01253	1.00E-08	5.88E-05	1.870209463	2.423754272	cobalamin synthesis protein CobW	K02234
stl01254	1.00E-08	5.88E-05	1.870209463	2.423754272	Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-) / Cobalt-precorrin-6y C15-methyltransferase	K00595
stl01333	1.00E-08	5.88E-05	1.870209463	2.423754272	precorrin-2 C(20)-methyltransferase	K03394
stl01334	1.00E-08	5.88E-05	1.870209463	2.423754272	Cobalt-precorrin-3b C17-methyltransferase	K13541
stl01335	1.00E-08	5.88E-05	1.870209463	2.423754272	Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	0
stl01336	1.00E-08	5.88E-05	1.870209463	2.423754272	Cobyrinic acid AC-diamide synthase	K02224
stl01516	1.00E-08	5.88E-05	1.870209463	2.423754272	cobalamin(vitamin B12) biosynthesis protein CobD/CbiB	K02227
stl01437	1.00E-08	5.88E-05	1.870209463	2.423754272	Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	K06042
stl01438	1.00E-08	5.88E-05	1.870209463	2.423754272	precorrin-6A reductase	K05895
stl01479	1.12E-08	6.54E-05	1.895707809	2.46328876	lipopolysaccharide biogenesis periplasmic protein	K07290
stl02655	1.44E-08	8.43E-05	1.748925989	2.388020953	sugar transporter	K08178
stl01232	1.47E-08	8.60E-05	1.919327015	2.465798951	Ribonucleotide reductase of class Ia (aerobic) beta subunit (EC 1.17.4.1)	K00526
stl00895	1.51E-08	8.83E-05	1.983014441	2.578483073	Thiazole biosynthesis protein ThiG	K03149
stl02289	1.65E-08	9.65E-05	1.829451262	2.405387639	hypothetical protein	0
stl02261	1.69E-08	9.89E-05	1.827100519	2.412765901	transcriptional regulator	0

Supplementary Table 6: KEGG Enrichment – starvation resistance.

kegg	pathway	starve	reference	pval
ko00860	Porphyrin and chlorophyll metabolism	14	42	0.001999
ko00900	Terpenoid backbone biosynthesis	8	17	0.003998001
ko00780	Biotin metabolism	6	10	0.003998001
ko02020	Two-component system	7	157	0.014492754
ko01120	Microbial metabolism in diverse environments	20	291	0.018990505
ko00270	Cysteine and methionine metabolism	11	43	0.031484258
ko00480	Glutathione metabolism	5	13	0.032983508
ko00051	Fructose and mannose metabolism	1	47	0.053973013
ko00520	Amino sugar and nucleotide sugar metabolism	1	49	0.054972514
ko02010	ABC transporters	12	176	0.067966017
ko03020	RNA polymerase	2	2	0.070964518
ko00260	Glycine, serine and threonine metabolism	10	46	0.077961019
ko01524	Platinum drug resistance	2	3	0.097451274
ko00640	Propanoate metabolism	1	38	0.12043978
ko03060	Protein export	4	14	0.12193903
ko00750	Vitamin B6 metabolism	3	9	0.122438781
ko00720	Carbon fixation pathways in prokaryotes	1	33	0.171414293
ko05418	Fluid shear stress and atherosclerosis	2	5	0.176911544
ko04612	Antigen processing and presentation	1	1	0.190904548
ko00232	Caffeine metabolism	1	1	0.193403298
ko04151	PI3K-Akt signaling pathway	1	1	0.194902549
ko04915	Estrogen signaling pathway	1	1	0.2003998
ko04914	Progesterone-mediated oocyte maturation	1	1	0.203898051
ko04657	IL-17 signaling pathway	1	1	0.204397801
ko05215	Prostate cancer	1	1	0.204897551
ko04659	Th17 cell differentiation	1	1	0.209895052
ko02024	Quorum sensing	6	87	0.230884558
ko00670	One carbon pool by folate	4	15	0.244877561
ko00540	Lipopolysaccharide biosynthesis	6	29	0.258370815
ko03018	RNA degradation	4	16	0.261869065
ko00510	N-Glycan biosynthesis	1	2	0.27836082
ko00730	Thiamine metabolism	4	16	0.284357821
ko05204	Chemical carcinogenesis	1	2	0.287356322
ko00333	Prodigiosin biosynthesis	1	2	0.290354823
ko04141	Protein processing in endoplasmic reticulum	1	2	0.297851074
ko02026	Biofilm formation - Escherichia coli	2	38	0.304847576
ko04217	Necroptosis	1	3	0.349325337
ko04621	NOD-like receptor signaling pathway	1	3	0.349825087
ko00790	Folate biosynthesis	1	23	0.353823088
ko00620	Pyruvate metabolism	3	49	0.356821589
ko05200	Pathways in cancer	1	3	0.35832084
ko04260	Cardiac muscle contraction	1	3	0.35982009
ko05111	Biofilm formation - Vibrio cholerae	1	27	0.369315342
ko04214	Apoptosis - fly	1	3	0.375312344
ko00980	Metabolism of xenobiotics by cytochrome P450	1	3	0.377811094
ko04016	MAPK signaling pathway - plant	1	3	0.381309345
ko01100	Metabolic pathways	103	792	0.39830085
ko00650	Butanoate metabolism	2	33	0.413293353
ko00061	Fatty acid biosynthesis	3	14	0.418790605
ko00330	Arginine and proline metabolism	2	35	0.427786107
ko00030	Pentose phosphate pathway	2	35	0.43828086
ko00920	Sulfur metabolism	6	34	0.43928036
ko00010	Glycolysis / Gluconeogenesis	3	40	0.476261869
ko01501	beta-Lactam resistance	4	20	0.490254873
ko00910	Nitrogen metabolism	1	22	0.504247876
ko03030	DNA replication	1	18	0.52123938
ko03430	Mismatch repair	1	22	0.526236882
ko01210	2-Oxocarboxylic acid metabolism	2	27	0.589705147
ko00680	Methane metabolism	3	39	0.608195902
ko01200	Carbon metabolism	11	110	0.632183908
ko04112	Cell cycle - Caulobacter	2	11	0.644677661
ko01130	Biosynthesis of antibiotics	26	200	0.661169415
ko03070	Bacterial secretion system	4	44	0.675162419
ko00190	Oxidative phosphorylation	8	58	0.676161919
ko00240	Pyrimidine metabolism	8	54	0.683658171

ko00410	beta-Alanine metabolism	1	17	0.706146927
ko00290	Valine, leucine and isoleucine biosynthesis	1	16	0.712143928
ko04122	Sulfur relay system	1	15	0.712143928
ko00380	Tryptophan metabolism	1	14	0.714642679
ko00561	Glycerolipid metabolism	1	15	0.71914043
ko00300	Lysine biosynthesis	1	16	0.725137431
ko00970	Aminoacyl-tRNA biosynthesis	1	15	0.727136432
ko00770	Pantothenate and CoA biosynthesis	3	20	0.730134933
ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	3	20	0.731134433
ko03010	Ribosome	2	23	0.75912044
ko01230	Biosynthesis of amino acids	13	120	0.771114443
ko00564	Glycerophospholipid metabolism	2	25	0.777611194
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	2	23	0.780609695
ko01110	Biosynthesis of secondary metabolites	37	296	0.792603698
ko00230	Purine metabolism	8	77	0.854572714
ko00630	Glyoxylate and dicarboxylate metabolism	5	40	1
ko00020	Citrate cycle	3	27	1
ko01503	Cationic antimicrobial peptide	3	27	1
ko03440	Homologous recombination	3	23	1
ko00280	Valine, leucine and isoleucine degradation	2	20	1
ko00450	Selenocompound metabolism	2	14	1
ko00550	Peptidoglycan biosynthesis	2	19	1
ko01212	Fatty acid metabolism	2	20	1
ko04932	Non-alcoholic fatty liver disease	1	4	1
ko00072	Synthesis and degradation of ketone bodies	1	6	1
ko00310	Lysine degradation	1	13	1
ko00430	Taurine and hypotaurine metabolism	1	7	1
ko00460	Cyanoamino acid metabolism	1	6	1
ko00627	Aminobenzoate degradation	1	11	1
ko00660	C5-Branched dibasic acid metabolism	1	11	1
ko00740	Riboflavin metabolism	1	10	1
ko00982	Drug metabolism - cytochrome P450	1	4	1
ko00983	Drug metabolism - other enzymes	1	9	1
ko01040	Biosynthesis of unsaturated fatty acids	1	5	1
ko03410	Base excision repair	1	13	1
ko04146	Peroxisome	1	7	1
ko04626	Plant-pathogen interaction	1	7	1
ko04922	Glucagon signaling pathway	1	6	1
ko05010	Alzheimer's disease	1	4	1
ko05012	Parkinson's disease	1	4	1
ko05016	Huntington's disease	1	6	1
ko05132	Salmonella infection	1	6	1
ko05230	Central carbon metabolism in cancer	1	6	1

Supplementary protocol 1: Library preparation for Illumina sequencing

DNA was prepared for sequencing using the TnSeq protocol from the Joel Griffitts lab.

- Genomic DNA extraction using the MoBio kit (Cat# 122550-50). Centrifuge 1.0-1.5 ml of overnight culture for two minutes. Remove supernatant and freeze pellet at -80C for at least 30 minutes. Suspend pellet in 300 ul of MicroBead solution and transfer to bead tube. Add 50 ul MD1; vortex for 10 minutes using bead beating adapter at full speed. Centrifuge for 3 minutes and move the supernatant to a new tube. Add 100 ul MD2 and vortex for 5 second. Place on ice for 5 minutes before centrifuging for 3 minutes at full speed. Move supernatant (about 350 ul) to a new tube and add 900 ul MD3. Mix using pipettor and then put through the spin filter 610 ul at a time, discarding flow through. Wash the spin filter with 300 ul MD4, discarding flow through. Wash spin filter with 500 ul PE from a Qiagen kit, discard flowthrough. Centrifuge for 1 minute at full speed and then move filter to a new tube. Add 55 ul warm 2.5 mm Tris (pH 8.0). Wait 2 minutes before centrifuging for 1 minute at full speed. The sample can be checked by running 2 ul on a gel and should be a bright high molecular-weight band. Check that the sample is at least 150ng/ul on nanodrop and normalize all samples to the lowest concentration.
- Fragementase digestions: Mix 16 ul of genomic DNA extract with 2 ul 10X fragemntase v2 buffer. Pre-vortex Fragmentase before adding 2 ul to the mixture and mixing immediately. Incubate at 37C for exactly 12 minutes (time will vary, optimize time for each batch of Fragmentase). Add 10 ul 0.25 M EDTA to stop the reaction and keep on ice until clean up.
- Qiagen (27106) clean up: Add 300 ul PB to sample and place in column. Centrifuge for 30 seconds and discard the flowthrough. Add 650 u PE, centrifuge for 30 seconds and discard the flowthrough. Centrifuge for 1 minute. Move filter to a new tube, add 50 ul warm 2.5 mM Tris (pH 8.0), wait two minutes and centrifuge for 1 minute at full speed. Check 4 ul on a gel for a smear from about 500-3000 bp.
- C tailing (TdT is NEB M0315S, ddCTP is Affimetrix 77112 0.5UM): Each reaction includes 30 ul cleaned up fragmented DNA, 4 ul 10 TdT buffer, 4 ul 2.5 mM CoC12, 2.1 ul 9.5 mM dCTP/0.5mMddCTP mix (make mix with 34 ul water, 4 ul 100 mM dCTP 2 ul 10mMddCTP), 0.6 ul TdT enzyme. Incubate for 30 minutes at 37C.
- Qiagen clean up: Same as above
- First round PCR: Each reaction includes 17.8 ul water, 8.0 ul 5X Q5 buffer, 1.2 ul 10mM dNTPs, 0.5 ul Q5 polymerase, 2.5 ul 10mM 1 TN, 5.0 ul 10uM 1OLIGOG, 5 ul template DNA from cleaned up TdT reaction. *(Q5 is NEB M0491S)*
- Qiagen clean up: Same as above but use 200 ul PB instead of 300 ul.
- Second round PCR: 22.0 ul water, 8.0 5X Q5 buffer, 0.5 ul Q5 polymerase, 3.0 ul 10 mM 2TNX, 3.0 ul 10 uM 2BARX, 2.5 ul cleaned up product from first round.
- Qiagen clean up: Same as above but elute in T5E0.5.
- Gel: Check 4 ul on a gel. Should have 150-700 bp with a strong peak around 400 bp.