

Supplementary data

Age-associated microbiome shows the giant panda lives on hemicelluloses, not on celluloses

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Supplemental Methods

16S rRNA gene and ITS sequencing data processing

To characterize the taxonomic profile of the panda gut microbiome, we sequenced the V3 region of the 16S rRNA gene using universal primers targeting most bacteria (F: 5'-ACTCCTACGGGAGGCAGCAG-3', R: 5'-TTACCGCGGCTGCTGGCAC-3') (Chen et al 2014) with a 6-bp barcode unique to each sample for the reverse primer. For the fungal analyses, we sequenced ITS-1 region using universal primer (F: 5'-GCTGCGTTCTTCATCGATGC-3', R: 5'-GGAAGTAAAAGTCGTAACAAGG-3') (Bellemain et al 2010) with a 6-bp barcode unique to each sample for the paired primer. The PCR conditions were 94°C for 4 min, followed by 30 cycles of 94°C for 30s, 54°C for 30s and 72°C for 30s and then 72°C for 5 min. The single amplifications were performed in 25 µL reactions with 50 ng template DNA. Normalized equimolar concentrations of PCR products were then pooled and sequenced using the Illumina MiSeq PE-250 platform. Barcodes and sequencing primers were trimmed before assembly.

Paired-end sequence reads were assembled using FLASH (Magoc and Salzberg 2011) (<http://ccb.jhu.edu/software/FLASH/>) and quality filtering was done with QIIME (Caporaso et al 2010) with the default settings. These trimmed sequences were then chimera filtered, singletons discarded, and assigned to operational taxonomic units (OTUs, cutoff 97% sequence identity for 16S rRNA and ITS) using UPARSE (Edgar 2013) pipeline (<http://drive5.com/uparse/>). Representative sequences for each OTU

were chosen for classification using the RDP-classifier (version 2.2, (Wang et al 2007)) with an 80% confidence level against the Greengenes 13.5 database and UNITE database for 16S rRNA and ITS sequences, respectively. Alpha- and Beta-diversity analyses were performed using observed OTUs and Unifrac distances respectively, as implemented in QIIME.

Shotgun metagenome sequencing and data processing

Based on the bacterial diversity and Unifrac distances of 332 samples from giant pandas, 57 samples were selected for shotgun metagenome sequencing (Supplementary Table S1). Our samples included different seasons and bamboo stem/leaves or shoots as diet. Metagenome DNA libraries were generated using NEBNext® Ultra™ DNA Library Prep Kit for Illumina (NEB, USA) following the manufacturer's instruction (Illumina HiSeq2500) and index codes were added to attribute sequences to each sample. One paired-end library with an insert size of 300 bp for each sample was built and sequenced with 125bp read length from each end. After sequencing, adaptor contamination, low quality reads, giant panda host reads, and the reads of food contamination were removed from the raw sequencing reads by the SoapAligner module in the SOAP package (Li et al 2009). On average, 5.2Gbp clean data per sample were generated (Supplementary Table S3). The proportion of high-quality clean data of all raw data from each sample was 80.1% on average.

The clean data were assembled into contigs for each sample by SOAPdenovo2 (Luo et al 2012). We tried different *K-mer* values (45, 55, 65, 75, and 85) to obtain optimal

assembly results and used N50 lengths to determine the best assembly result. The K-mer (55) was used in our study. Scaffigs (using information from special type of spanning reads to assemble contigs together into larger sequences) derived from assembled scaffolds longer than 500 nt were maintained and clustered into a non-redundant data set by CD-HIT (Fu et al 2012) using a sequence identity cut-off of 0.95 (Karlsson et al 2013).

Then, a pan-metagenome was constructed and used to analyze metagenome development from birth to juvenile of giant pandas.

Pan-metagenome construction

The pan-metagenome was constructed in the following steps (Supplemental Fig. S2):

(1) Blastall was used to align assembled contigs (parameters: -e 1e-5) of all samples.

Contigs were clustered by identity \geq 95% and coverage \geq 95% and only the longest

sequence in one cluster was kept for the following analysis; (2) if two alignment

sequences had both un-aligned end parts shorter than 30bp, a GC content difference of

less than 10%, and an alignment length \geq 100bp, a connection will be established

between the sequences. If no bifurcation occurred in the alignment of one connection

of two sequences, the two sequences will be combined to one sequence and all those

sequences were merged in a file named "chain.fasta"; otherwise, the remaining

sequences were written to a file named "unchain.fasta". All unmapped reads to

assemble the results of reads, were named "unmap.fasta". Finally, "chain.fasta",

“unchain.fasta” and “unmap.fasta” were merged, and the above steps were repeated to obtain the non-redundant genome sets (pan-metagenome).

Taxonomy annotation and abundance analysis

The Micro_NT taxonomy database composed of microbial reference genomes was extracted from the National Center for Biological Information (NCBI) NT database (Version: 2014-10-19). The non-redundant scaffigs set of the pan-metagenome was aligned to reference genomes by BLAST using an e-value cut-off of 10^{-5} . Then, we determined the taxonomic level of each scaffig by the lowest common ancestor (LCA)-based algorithm implemented in MEGAN4 (Qin et al. 2010; Huson et al. 2011). The abundance of annotated microbes can be assessed by mapping of all high-quality sequencing reads from individual samples onto the non-redundant scaffigs set of the pan-metagenome (Le Chatelier et al. 2013) by using Bowtie (Langmead and Salzberg 2012).

Metagenome linking group (MLG) construction

STEP1: SOAP2 (SOAPaligner) was used to map all the reads of each sample to the pan-metagenome. If one contig of the pan-metagenome had no mapping reads in more than 51 samples, the contig will be filtered for next steps. Then, Qin’s method (Qin et al 2012) was used here to evaluate the abundance of contigs. The abundance value of each contig of the pan-metagenome in each sample was obtained by the following formula (1).

$$a_i = \frac{x_i / L_i}{\sum_j x_j / L_j} \quad (1)$$

a_i : The relative abundance of contig i in sample S .

L_i : The length of contig i .

x_i : The times which gene i can be detected in sample S (the number of mapped reads). In our sequence-based profiling analysis, only two types of alignments could be accepted: 1). an entire of a paired-end read can be mapped onto a contig with the correct insert-size; 2). one end of the paired-end read can be mapped onto the end of a contig, only if the other end of read was mapped outside the contig region. In both cases, the mapped read was counted as one copy.

The abundance value of each contig of the pan-metagenome in all samples (57 samples) was combined in abundance vector.

STEP2: The triple codon frequency (TCF) of each contig of the pan-metagenome was obtained using a 3bp window size starting with the first base pair of the contig and moving 1 bp every time. Moreover, the TCF of the reverse complementary sequence

of the same contig was obtained following the same protocol. The two TCFs were combined to obtain the final TCF vector for the contig.

STEP3: Based on abundance and TCF vectors of each contig of the pan-metagenome, the Pearson correlation coefficients (PCC) of abundance (abundance -PCC) and TCF (TCF-PCC) were calculated between two contigs (X and Y) following formula (2), respectively. Then the two contigs with TCF-PCC>0.9 and abundance-PCC>0.9 were selected to establish a single connection.

$$PCC(X,Y) = \frac{N \sum XY - \sum X \sum Y}{\sqrt{N \sum X^2 - (\sum X)^2} \sqrt{N \sum Y^2 - (\sum Y)^2}} \quad (2)$$

N: number of samples (57);

X: contig X vector (abundance or TCF for each sample);

Y: contig Y vector (abundance or TCF for each sample);

PCC(X,Y): the Pearson correlation coefficients between contig X and contig Y

(for abundance or TCF).

STEP4: According to the single connection, all the related sequences were clustered into one class in which every two sequence must have abundance-PCC>0.9 and TCF-PCC>0.9.

STEP5: abundance and TCF were re-calculated with weighting the total sequence length in one class from STEP4 for each contig of the pan-metagenome with the following formula (3). Then STEP3-5 was repeated until no more sequences could be merged into one class obtained from STEP4. Then all contigs in one class were one MLG.

$$V(G,i) = \frac{\sum_{j \in G} V(j,i) * L(j)}{\sum_{j \in G} L(j)} \quad (3)$$

$V(G,i)$: the value (abundance or TCF) of the new class G in sample i;

j: the original contigs or classes beyond to class G;

$V(j,i)$: the value (abundance or TCF) of contig (or class) j in sample i;

$L(j)$: the total number of sequence base within contig (or class) j.

MLG taxonomy annotation

The taxonomy annotation of each MLG was performed on reference genomes derived from the NCBI NT database (Version: 2014-10-19). Genome sequences <1 Mbp were filtered in the database and reference genomes covering more than 1% of the MLG were kept for subsequent analysis. Finally, the reference genome with highest MLG coverage was used for the taxonomy information of the MLG (Supplemental Table S5).

Gene prediction and function annotation

Gene prediction was performed by MetaGeneMark (Zhu et al. 2010) and a non-redundant predicted gene catalogue was constructed with CD-HIT using a sequence identity cut-off of 0.95. BLASTP was used to search the protein sequences of the predicted unique genes set against the following databases: KEGG (Kyoto Encyclopedia of Genes and Genomes, Kanehisa et al. 2016), eggNOG (evolutionary genealogy of genes: Non-supervised Orthologous Groups, Jensen et al. 2008) and CAZy (Carbohydrate-Active Enzymes Database, Lombard et al. 2014), respectively, with a filter for E-values $>1 \times 10^{-5}$. Genes were annotated as a function of the CAZy, eggNOG or KEGG homologs with the lowest E-value.

Estimating the abundance of genes/KEGG orthologous groups

The abundance of each predicted gene from a sample was estimated according to the method of the contig coverage in sequence assembly. If $R = \{r\}$ is the set of

assembled reads overlapping the locus of predicted gene g in a contig, abundance of

g was calculated by the following formula (4) (Arumugam et al. 2011).

$$abundance(g) = \sum \frac{base_overlap(g,r)}{base_length(g)} \quad (4)$$

Predicted proteins were also aligned to proteins from KEGG database (blastp e-value < 1e-5). Each protein was assigned to the KEGG orthologous group (KO) containing the best hit result. From these alignments between the set of predicted proteins $G = \{g\}$ from a sample and the set of KO reference proteins $K = \{k\}$, the abundance of each KO reference protein k in the sample was calculated as the sum abundance of all the related proteins abundance (g).

Significant differences of KO copy numbers of each MLG between groups

The significant difference of KO copy numbers of each MLG between groups was obtained by the following method: First, the average abundance of single copy genes of the MLG in a sample was calculated and the copy number of one gene in the MLG was equal to the gene abundance divided by the average abundance of the single copy genes with the MLG sequences. The single copy gene of each MLG is defined as the gene in the contig contained in the MLG, with only one copy, and the clustering information of the genes refer to the results of CD-HIT previously mentioned. The copy number of KO is the sum of the copies of the genes it contained. Second, T-test was used to analyze the difference of gene/KO copy numbers among groups with

Benjamin & Hochberg correction and P -values < 0.001 were recognized as significant differences.

Function enrichment analysis among groups

The significant difference of KO abundance among groups was obtained following the method:

First: Calculate OR-score for each function item (KO) on the following formula (5):

$$OR(k, G) = \frac{\sum_{s \in G} A_{sk} / \sum_{s \in G} \sum_{i \neq k} A_{si}}{\sum_{s \notin G} A_{sk} / \sum_{s \notin G} \sum_{i \neq k} A_{si}} \quad (5)$$

k: each KO;

s: each sample;

A_{si} : abundance of KO i in sample s;

G: the checking group G;

OR(k,G): OR-score of KO k in checking group G.

Second: calculate chi-square and p-value (R packages, pchisq function)

Third: According to OR-score and p-values:

enriched: OR-score > 2 and p-value < 0.05

depleted: OR-score < 0.5 and p-value < 0.05

The same method also was used to analyze the significant difference of EC or eggNOG or CAZy function catalogs abundance among groups.

Supplemental Figure Legends:

Supplemental Figure S1. The pipeline in this study.

Supplemental Figure S2. The pipeline for the construction of the pan-metagenome.

Supplemental Figure S3. Relative abundances of the phyla present in samples for group S1 (green bar), S2 (blue bar), S3 (pink bar), and S4 (red bar) with increasing age from left to right for each group. Colors correspond to different phyla (see insert). The meanings of S1-4 are shown in the text and in supplemental_ Table_ S1.

Supplemental Figure S4. Taxonomic profile of panda gut bacterial phylotypes. (A) Relative taxa abundance plots for individuals from the four groups, summarized at the family level. Individuals are represented along the horizontal axis, and relative taxa frequency is denoted by the vertical axis. The rare and unclassified taxa are summarized as “Others”. (B) Relationships between relative abundances of dominant bacterial groups and increased ages of pandas. Linear regressions were used to test Spearman correlation between each taxon’s relative abundance and ages.

Supplemental Figure S5. Alpha diversity of the giant panda gut microbiota from birth to juvenile. Analyses were performed on 16S rRNA V3 region data, with a rarefaction depth of 6,044 reads per sample. The number of observed OTUs was

obtained for OTUs sharing $\geq 97\%$ nucleotide sequence identity between all samples. A and B: The number of observed OTUs; C and D: Shannon diversity indices. The lines and squares inside boxes represent the median and mean, respectively. The meanings of S1-4 are shown in the text and in Table S1.

Supplemental Figure S6. Phylogenetic tree of *Clostridiales*-related lineages and OTUs in giant pandas. The prefix 'OTU' highlighted with red or blue text represents the OTUs present in giant pandas and the red text denotes the OTUs whose relative abundance reliably discriminated S1 and S3/4 samples. Muscle (Version: 3.8.31, parameter: -maxiters 16) was used for multiple sequences alignment and Treebest software (Version: treebest-1.9.2, parameter -b 1000) was used for constructing phylogenetic tree through NJ method. (Separate file)

Supplemental Figure S7. Taxonomic profile of the fungal phlotypes of the giant panda. A: Relative abundances of the phyla present in samples for group S1 (green bar), S2 (blue bar), S3 (pink bar), and S4 (red bar) with increasing age from left to right for each group. Colors correspond to phyla (see insert). The rare and unclassified taxa were summarized as "Others". B: The top 5 fungal classes in different groups. Individuals were represented along the horizontal axis, and relative taxa frequency was denoted by the vertical axis. The rare and unclassified taxa were summarized as "Others". The meanings of S1-4 are shown in the text and in Supplemental_ Table_ S1.

Supplemental Figure S8. Alpha diversity of the giant panda gut microbiota based on ITS-1. Analyses were performed on ITS-1 data, with a rarefaction depth of 8783 reads per sample. The number of observed OTUs was obtained for sharing $\geq 97\%$ nucleotide sequence identity for all samples. In panel B, the lines and squares inside boxes represented the median and mean, respectively. The meanings of S1-4 are shown in the text and in Supplemental_ Table_ S1.

Supplemental Figure S9. PCA plot based on relative abundance at phylum (A), class (B), order (C), family (D), genus (E), or species (F) level of the fungal phylotypes of the giant panda.

Supplemental Figure S10. Principal coordinates analysis (PCoA) using unweighted (A) and weighted (B) UniFrac distances of ITS-1 data. The percentage of variation explained by the plotted principal coordinates was indicated on the axes. Each point corresponded to a community colored by age and diet (see the text and Supplemental_ Table_ S1).

Supplemental Figure S11. Metagenome linking group (MLG) assembly statistical result and phylogeny identification estimate. (A) Relation between MLG contig number and genome size at phylum level. (B) Homology relationship between MLG

and the nearest species at NT database, estimated by whole genome alignment coverage. (C) and (D) respectively represented the estimate ahead as (A) and (B) for four microbial classes (*Streptococcaceae*, *Enterobacteriaceae*, *Clostridiaceae*, *Lactobacillaceae*), which have high relative abundance according to the 16S rRNA data.

Supplemental Figure S12. Panda metagenome gene catalog annotation statistical result. (A) Non-redundant gene numbers for each group. The average unique gene number was 61190, 108150, 138911, and 181941 for S1, S2, S3 and S4, respectively. The unique gene number difference between any two groups was significant (P -value ≤ 0.0259321) except between S2 and S3 (P -value= 0.3675733) with Wilcoxon rank-sum test. (B) CAZy database annotation. (C) KEGG database annotation result. (D) eggNOG database annotation result.

Supplemental Figure S13. Principal component analysis on gene relative abundance of all genes (A), KEGG (B), eggNOG (C), and CAZy (D) database among the four groups. Samples at each group were clustered into a closer region. Cross marked for outliers.

Supplemental Figure S14. Gut unique genes classified giant pandas from different groups. To estimate the minimal number of top ranking age-discriminatory genes

required for prediction, the performance of the predictive model was evaluated with a 5-fold cross-validation approach and measured as cross-validation error following the random forest model of R package. The model was trained using relative abundance of the genes in the S1-S4 samples. (A): Distribution of 5 trials of 5-fold cross-validation error in random forest classification of giant pandas as the number of unique genes increases. The model was trained using relative abundance of the unique genes (681,167 genes) in 57 samples. The black line indicates the average of the five trials (grey lines) and the pink line marks the number of unique genes in the optimal set. (B): Box-and-whisker plot for the probability of different groups of giant pandas in the unique genes set. (C): Box-and-whisker plot for the probability of different groups of giant pandas in the genes training set according to the model in A.

Supplemental Figure S15: The giant panda fecal microbiome starch metabolism pathway based on the 1000 genes obtained from random forest shown in Fig 3. Blue indicates $SCC > 0.4$, red indicates $-0.4 < SCC < 0.4$, and grey indicates no ECs in giant pandas.

Supplemental Figure S16. The starch metabolism pathway for all genes present in the gut microbiomes of giant pandas. Blue: at least one KO existed in giant panda metagenome; Green: at least one KO had significant difference between one group and another group with $P < 0.05$ (T-test); Red: at least one KO had a positive age-

related change (SCC>0.5) and higher abundance in group S3\4 than group 1. See Supplementary Table S11 for details.

Supplemental Figure S17.UPGMA-clustering dendrogram of CAZyme abundances.

Dietary compositions, taxonomy (at family level), and CAZy functional level1 are indicated by tip label colors.

Supplemental Figure S18. The carbohydrate-active enzymes (CAZy) functional compositions of giant pandas' and other mammals' microbiomes. Principal component analysis ordinations of predicted metagenomic potential function showed giant panda microbiomes were distinct from those of herbivores and carnivores but showed similarity to those of *Ursidae* when considering pathways involved in carbohydrate metabolism.

Supplemental Figure S19. Partial alignment of amylase gene sequences of tigers and giant pandas. Three heterozygosity sites existed in an intron of amylase of the giant panda and no heterozygosity sites in that of tigers with our PCR primers.

Supplemental Table Legends

Supplemental Table S1: samples used in this study.

Supplemental Table S2: the OOB classification error rates of the 51 OTUs (Figure 1D).

Supplemental Table S3: the statistics of sequence and assembly information.

Supplemental Table S4: Pan-metagenome assembly index of giant panda gut microbiome.

Supplemental Table S5: The assembly and taxonomy information of MLGs.

Supplemental Table S6: The CheckM estimate for MLGs > 500 Kpb.

Supplemental Table S7 (Microsoft Excel format): the statistics of KO copy number variation in MLG with significant difference among groups. (Separate file)

Supplemental Table S8 (Microsoft Excel format): the annotation results of 1000 genes obtained from random forest. (Separate file)

Supplemental Table S9: The OOB classification error rates of the 1000 genes (Figure 3 and Supplementary Table S8).

Supplemental Table S10 (Microsoft Excel format): The statistics of enrichment analysis and T_test of KEGG, CAZy, and eggNOG databases. (Separate file).

Supplemental Table S11 (Microsoft Excel format): The comparison of abundance of all ECs and KOs involving in starch pathway among groups. (Separate file)

Supplemental Table S12: The CAZy annotation of microbiome of S3/4 giant pandas and other mammals.

Supplemental Table S13.The qPCR primers for *TP53* and amylase genes.

Supplemental Table S14. Amylase copy numbers in individuals quantified using real time PCR. Mean estimates of each individual from three replicates are reported.

Supplemental Table S15. Amylase copy numbers found in whole genome data in *Carnivora* from NCBI.

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Figure S1

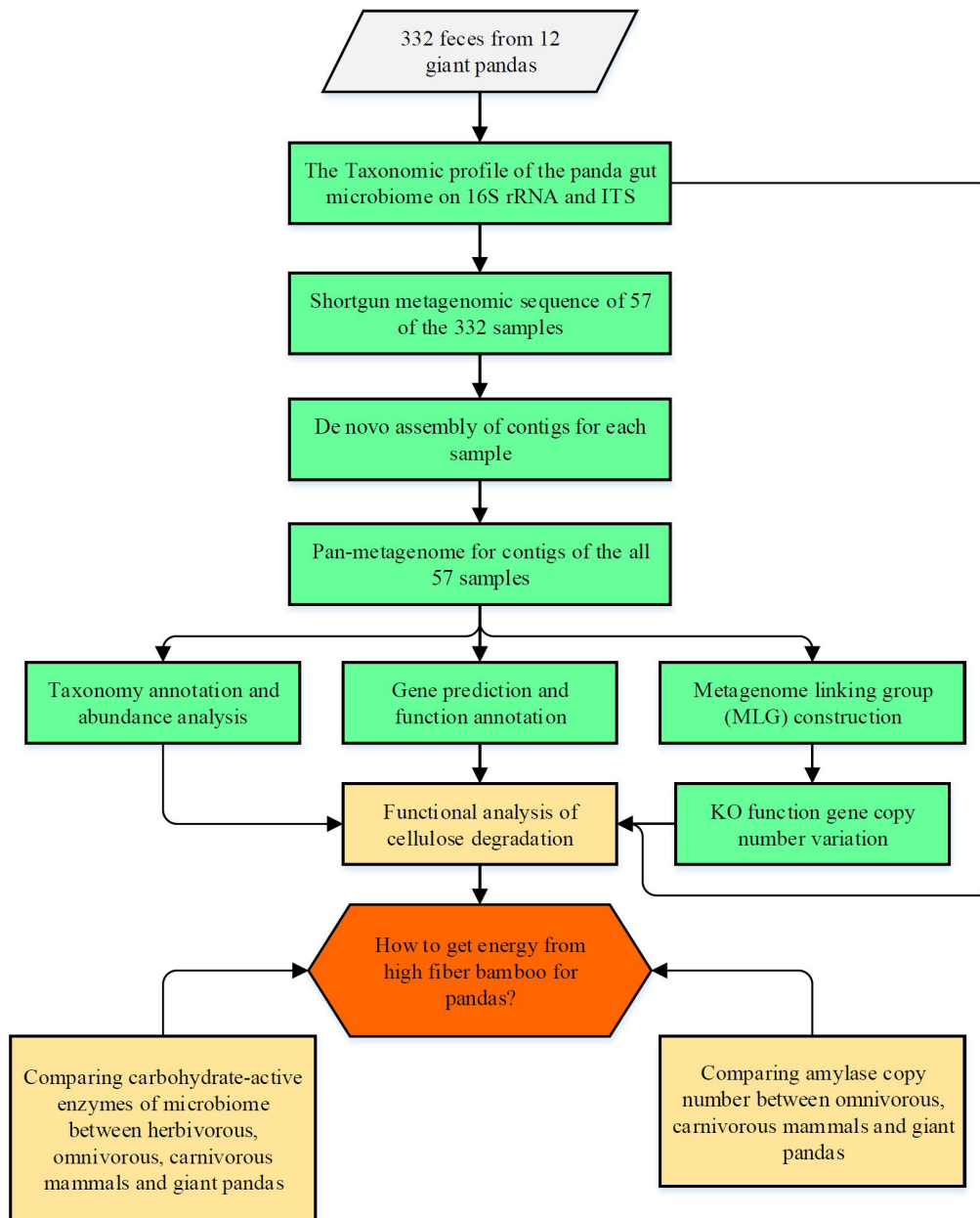


Figure S2

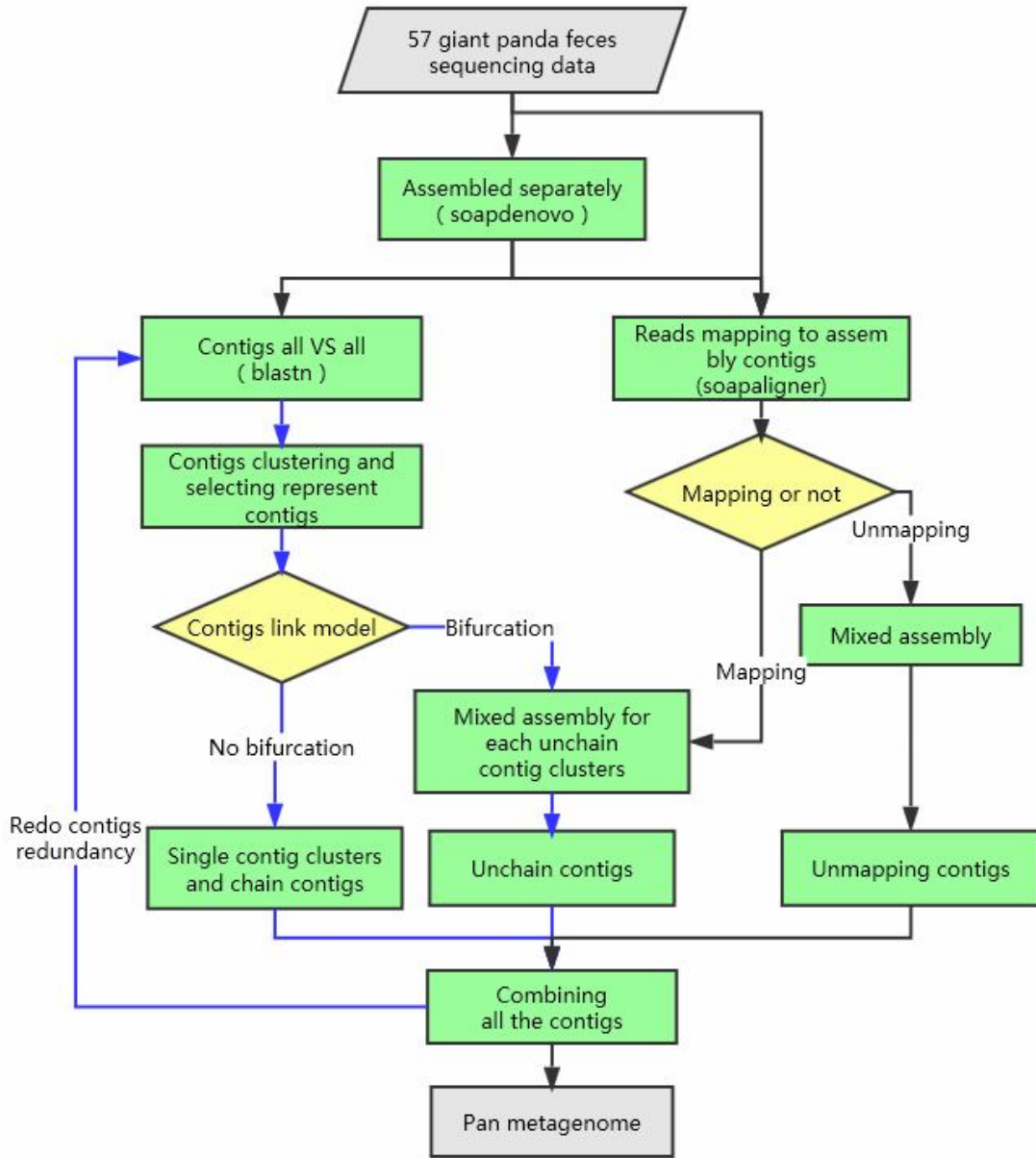


Figure S3

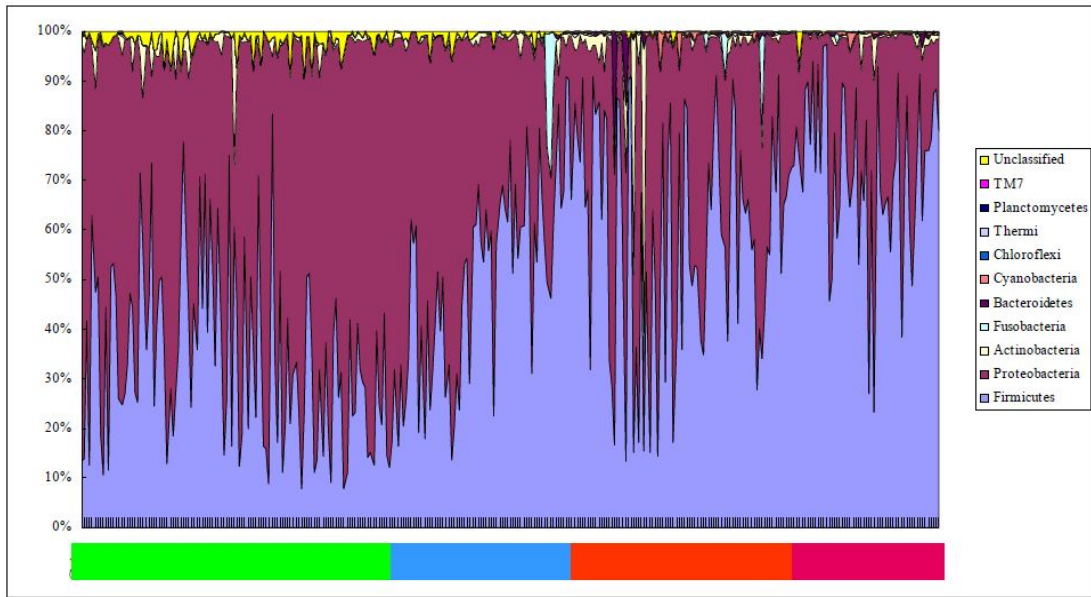
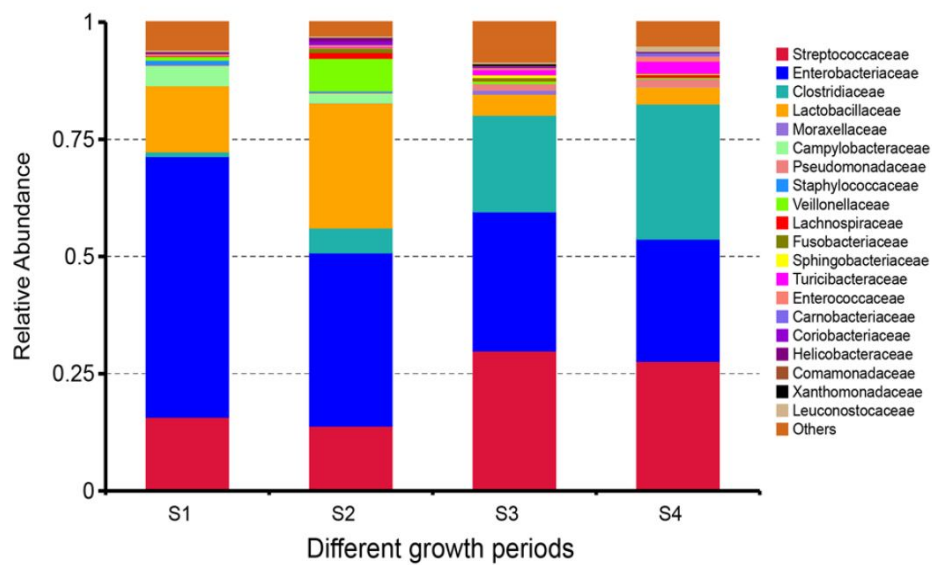
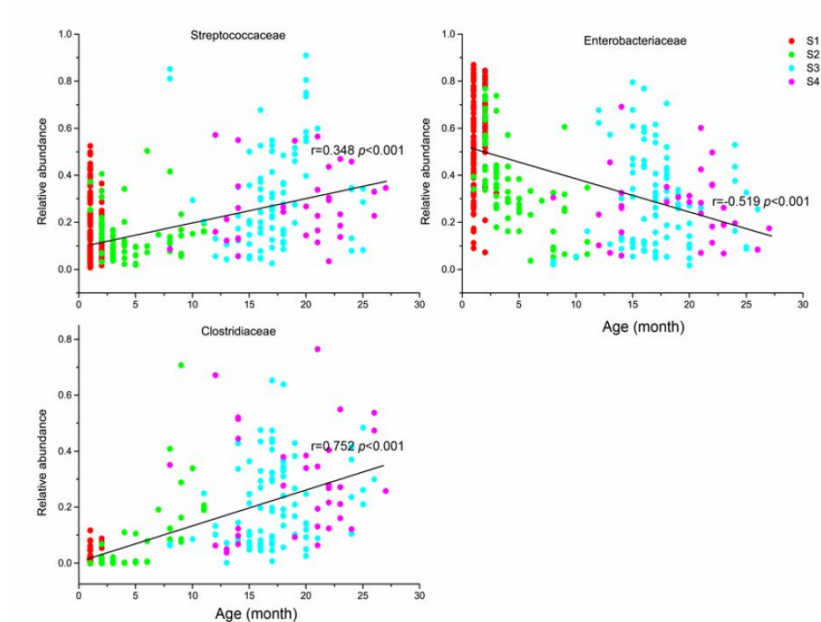


Figure S4



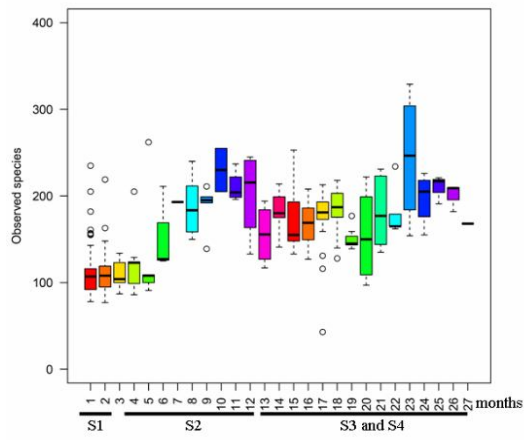
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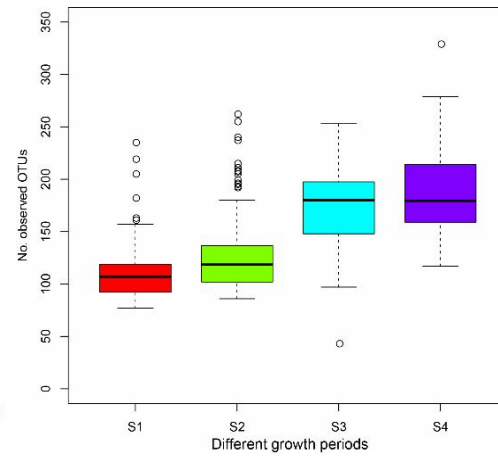
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Figure S5

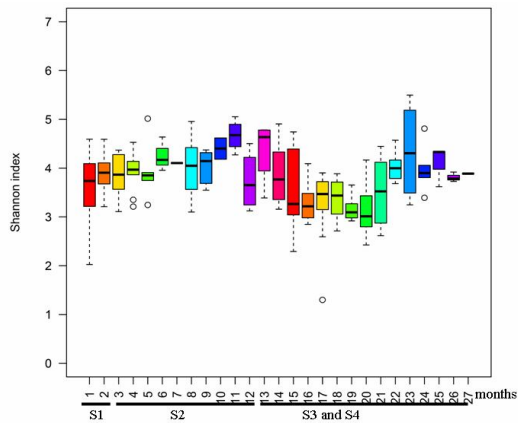
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B



C



D

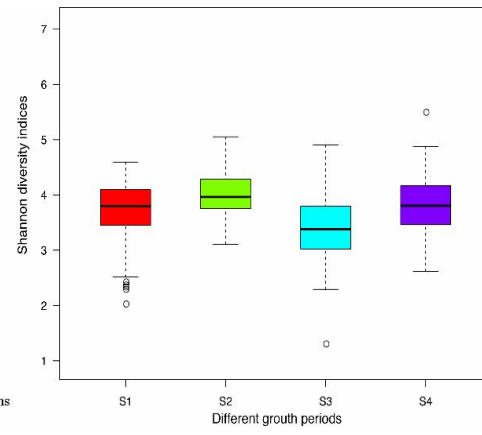
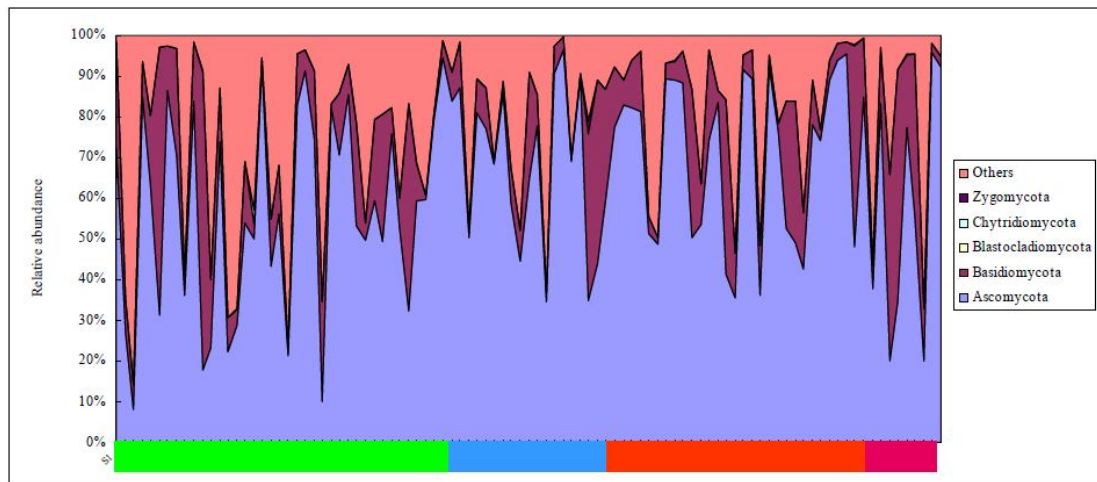


Figure S7

A



B

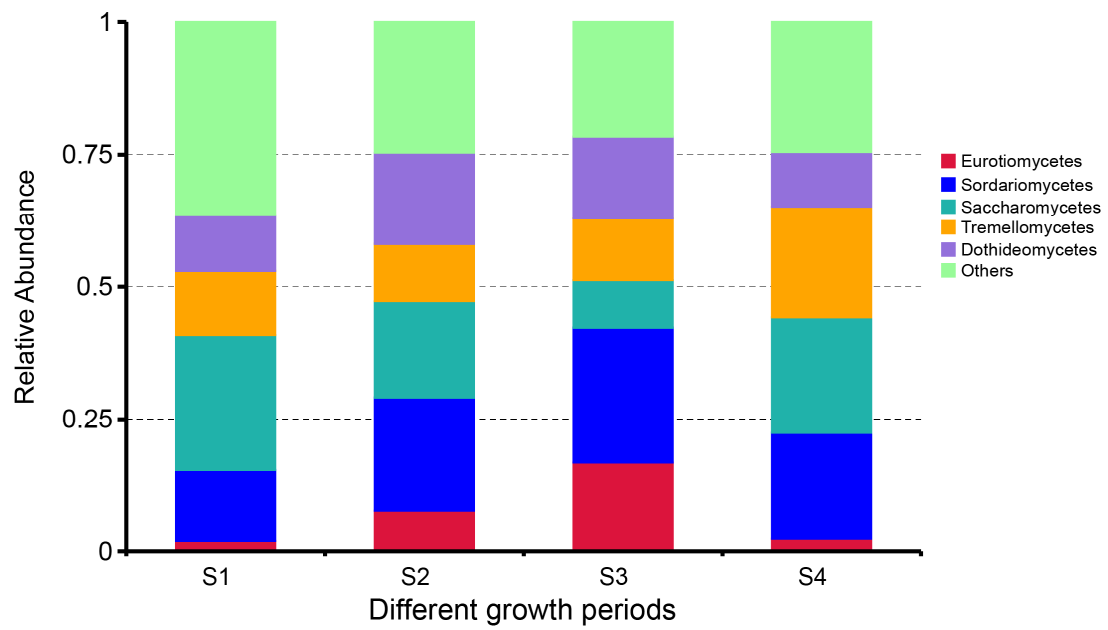
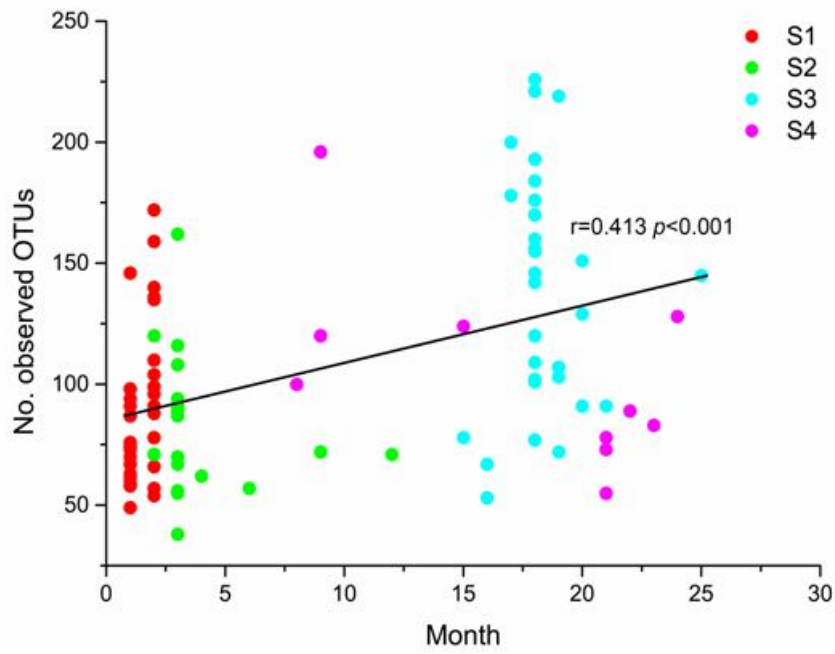


Figure S8

A



B

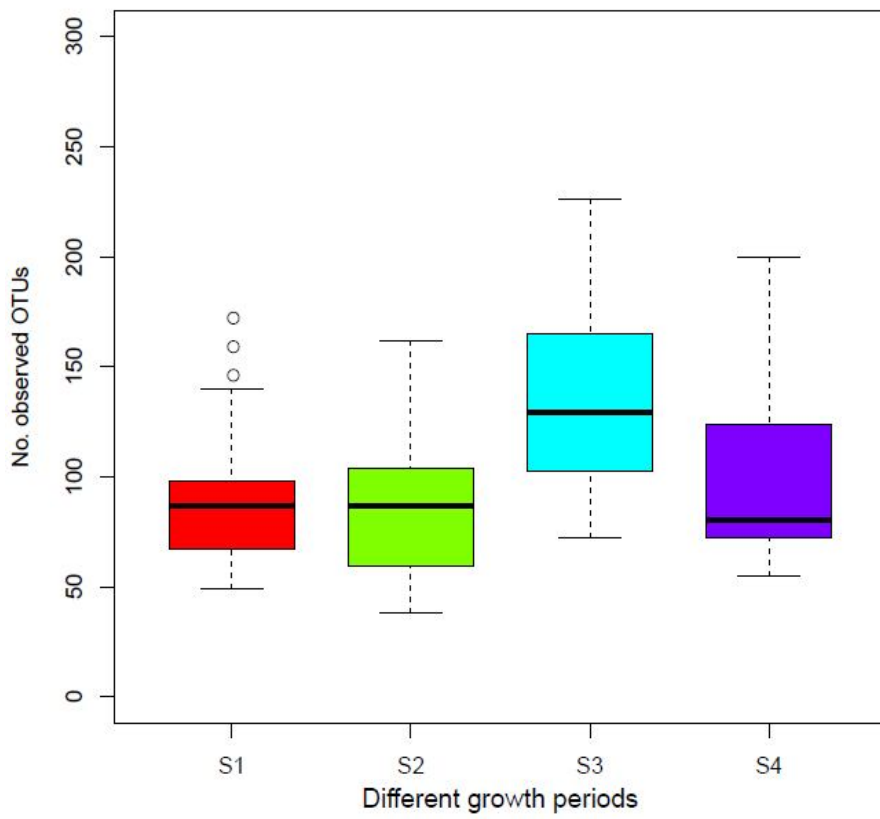


Figure S9

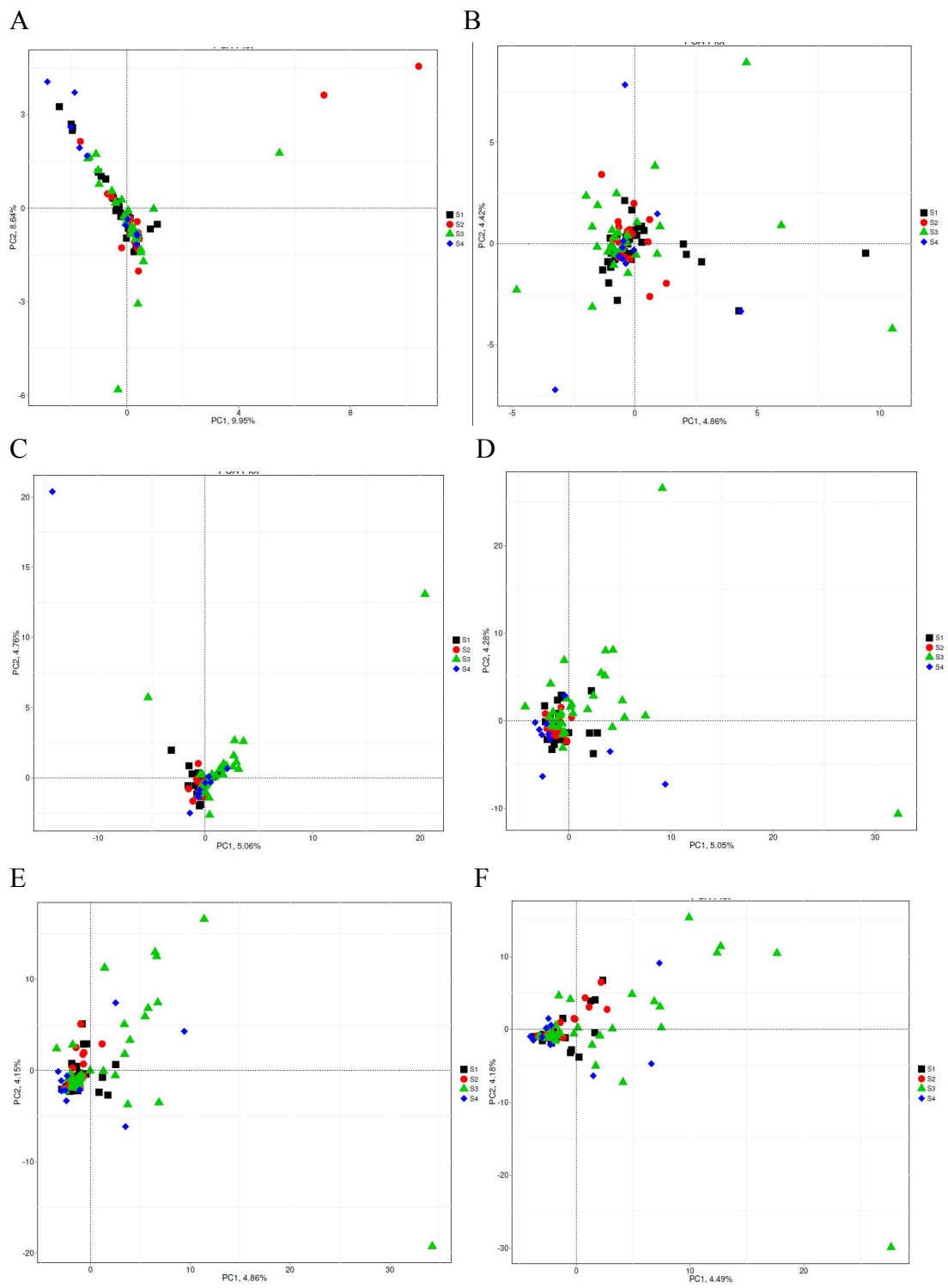
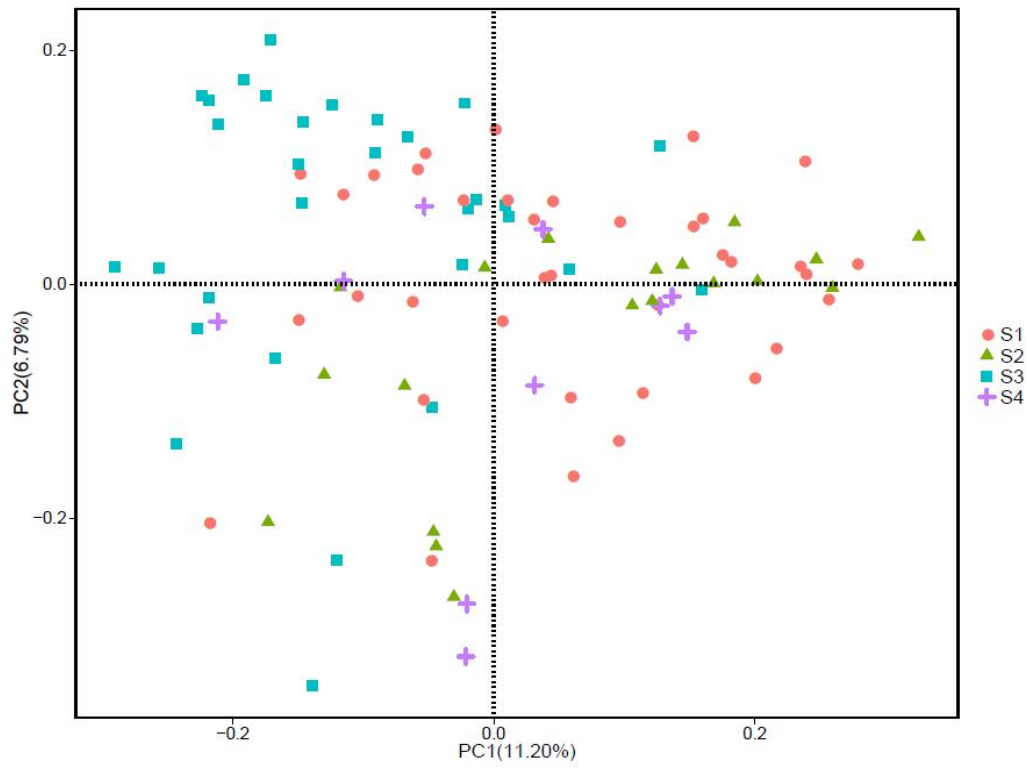


Figure S10

A



B

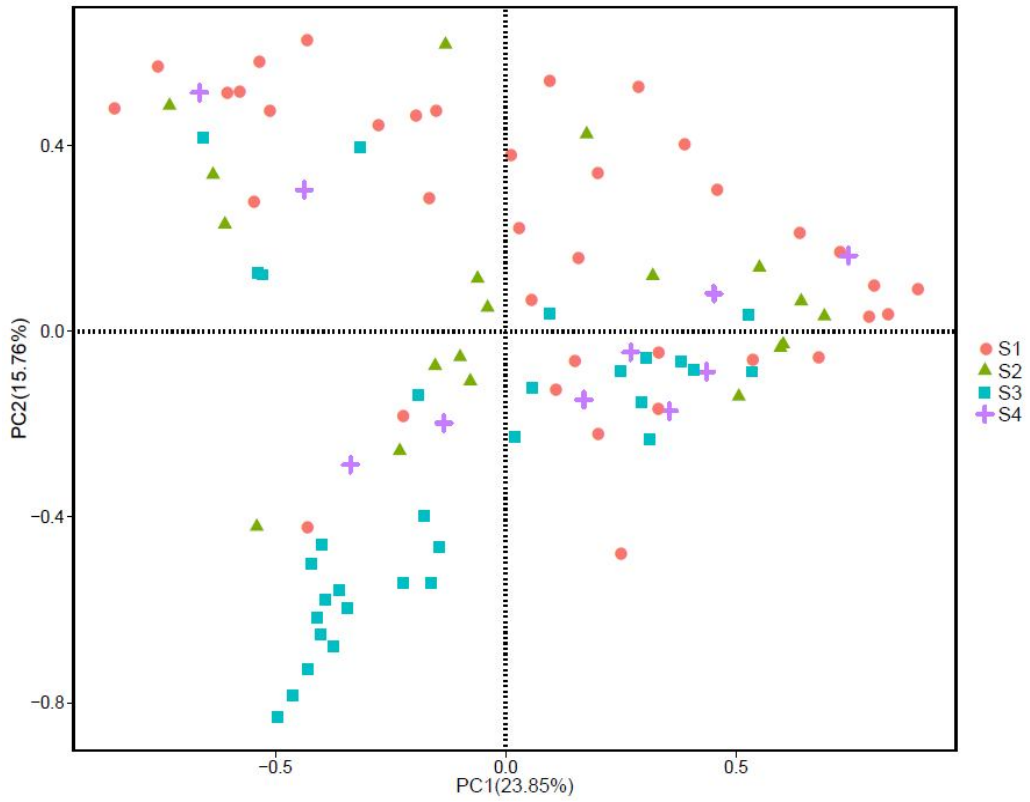


Figure S11

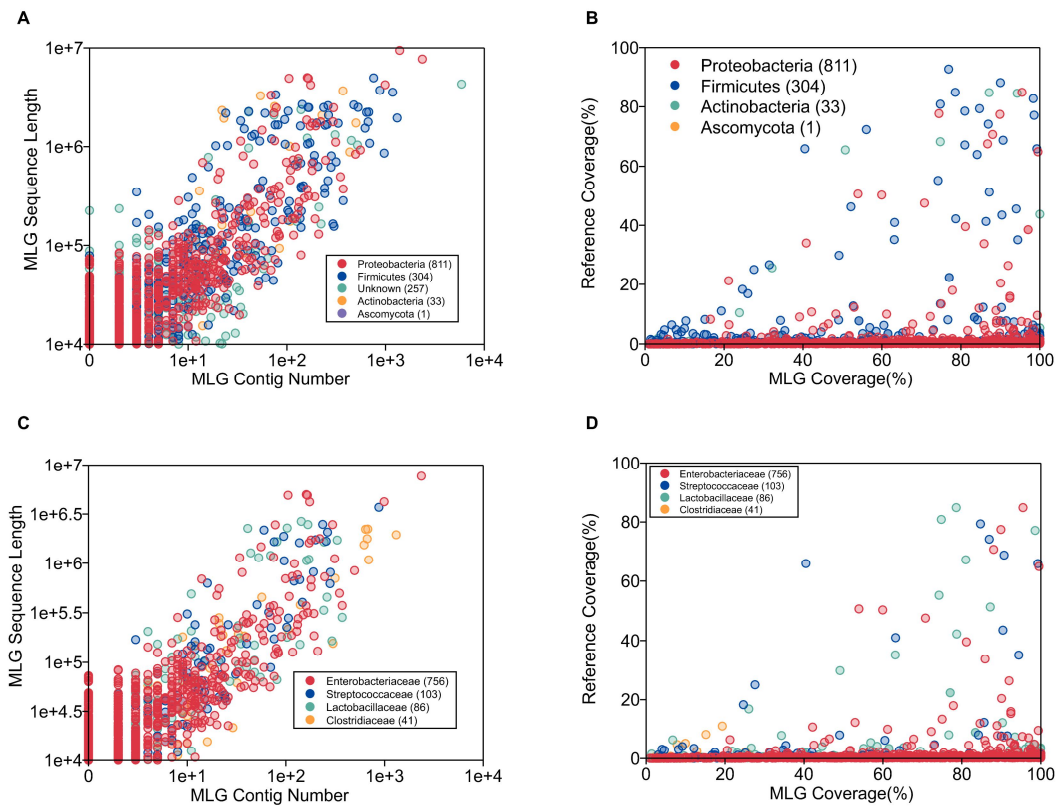


Figure S12

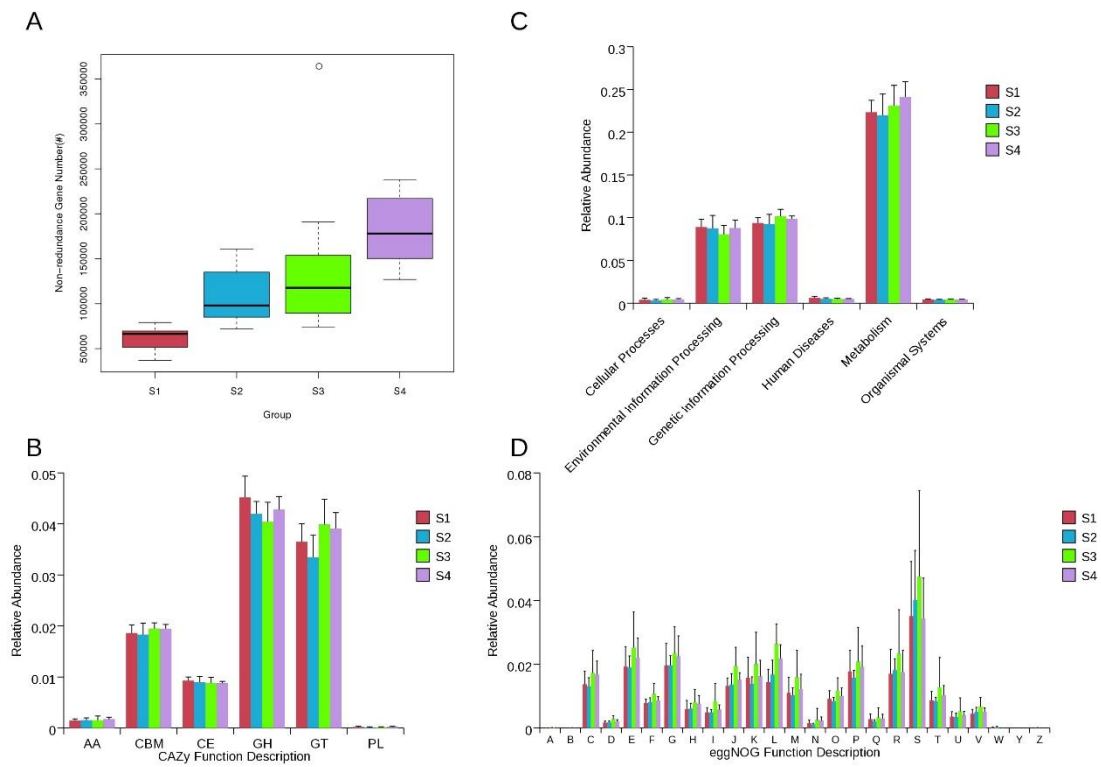


Figure S13

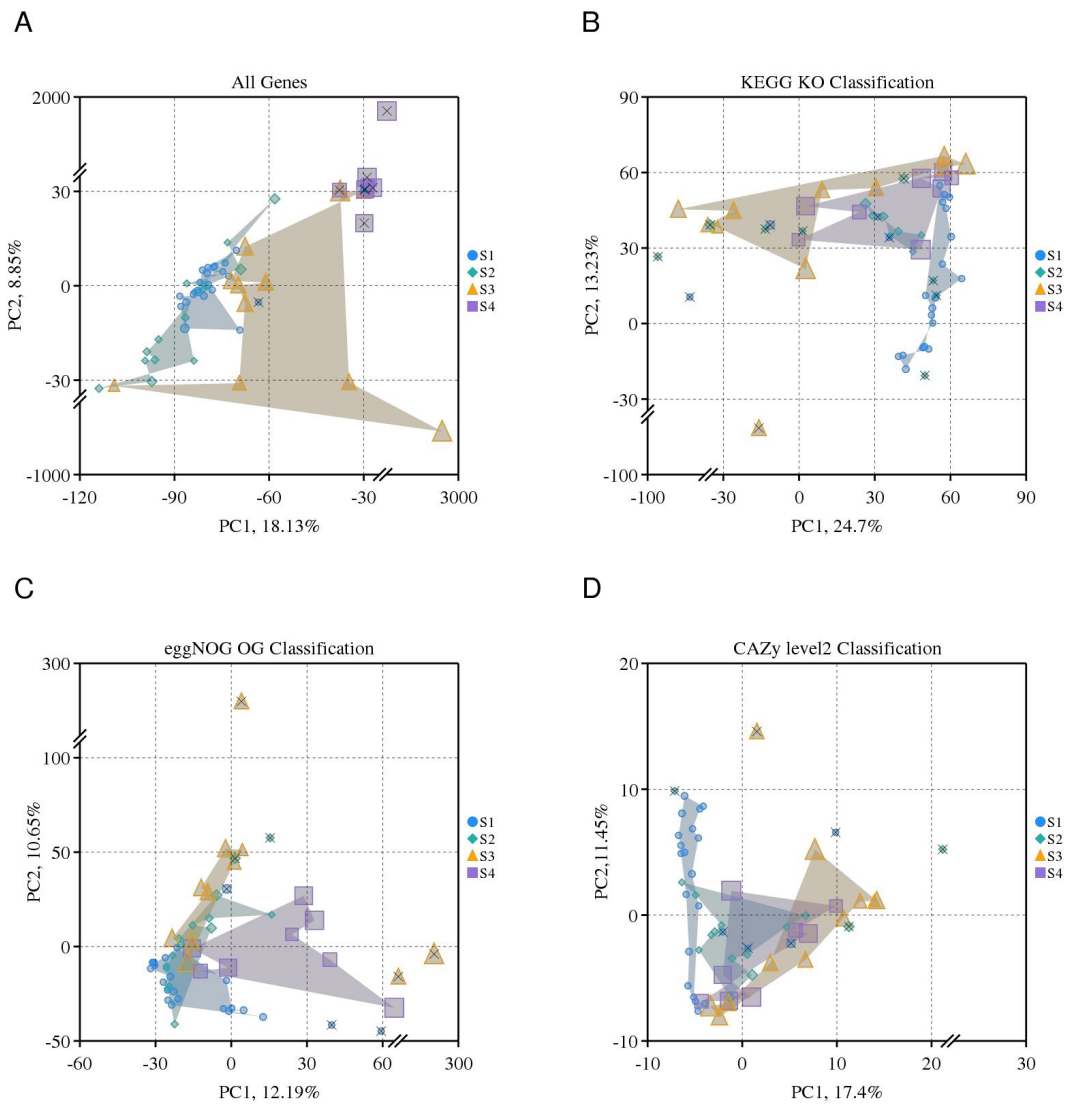
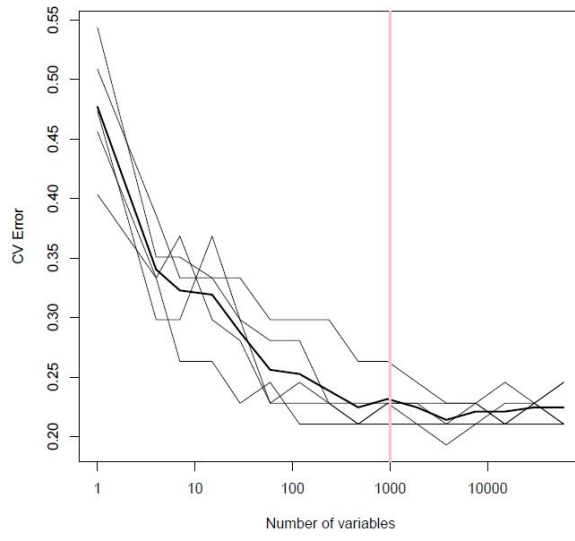
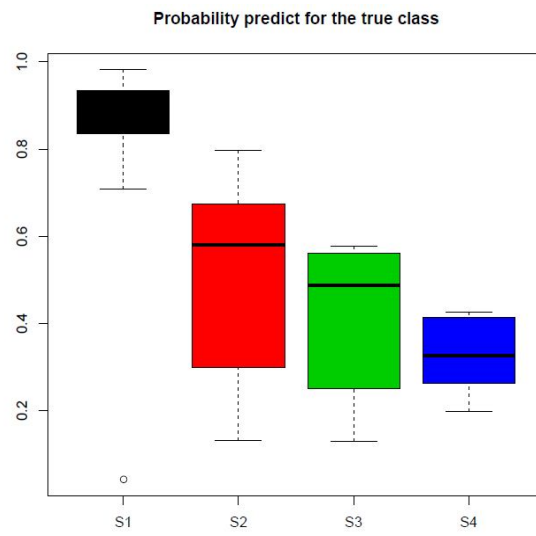


Figure S14

A



B



C

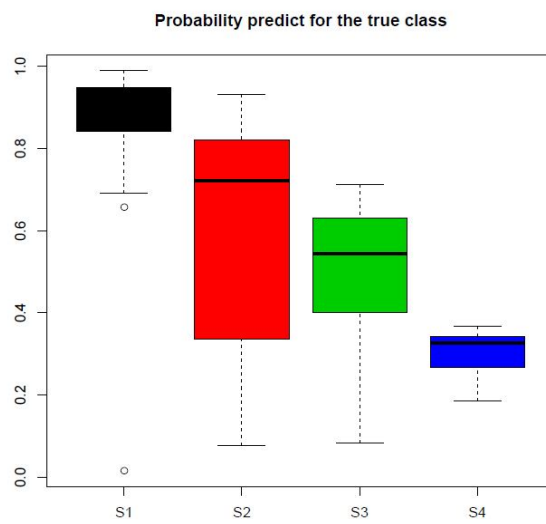


Figure S17

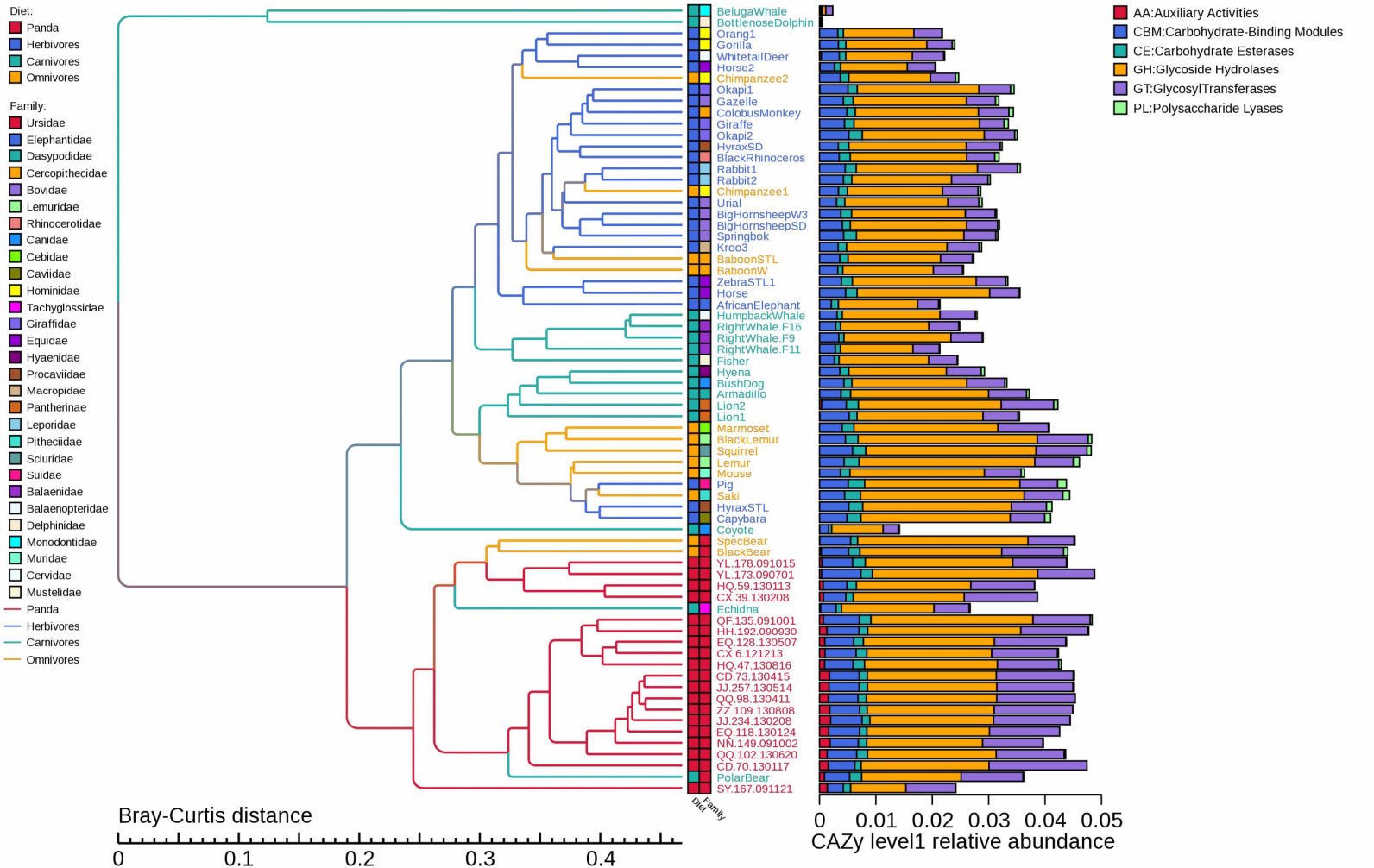


Figure S18

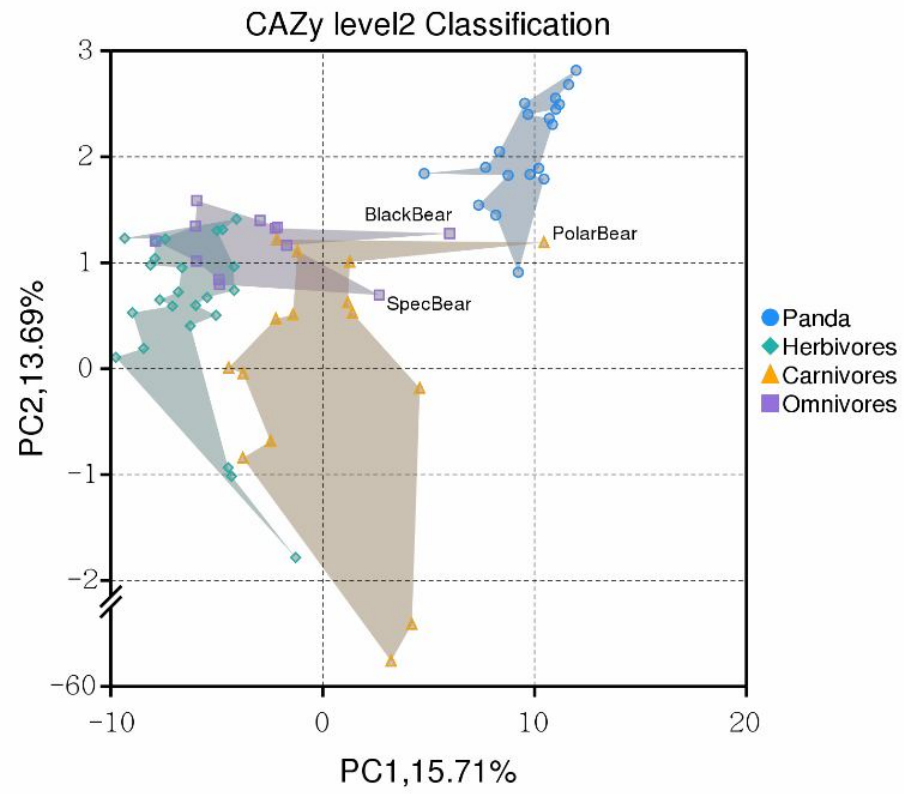
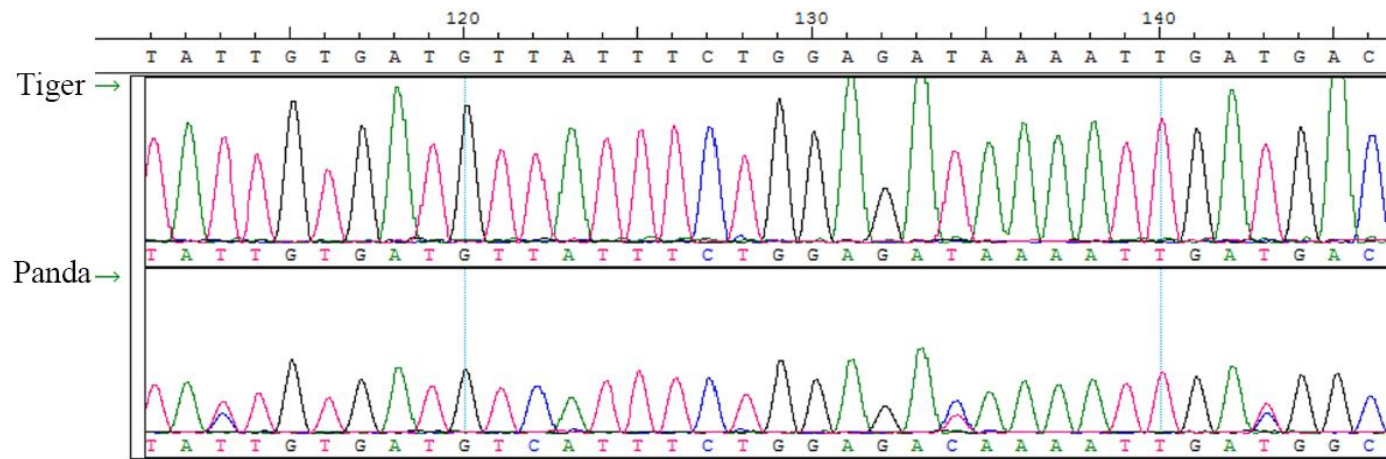


Figure S19



Supplemental Table S1: samples used in this study.

Sample_ID	Panda_ID	Group_ID	Sex	Studbook	Birth_date	Sampling_date (yy/mon/day)	Shortgun_ sequencing	ITS_ sequencing	16S_ Tags_number	ITS_ Tags_number
CX.1.121026	Chengxiao	S3	Male	825	2011/8/15	121026			7,148	0
CX.10.121107	Chengxiao	S3	Male	825	2011/8/15	121107		Yes	8,520	41,018
CX.11.121129	Chengxiao	S3	Male	825	2011/8/15	121129		Yes	8,743	30,470
CX.12.121114	Chengxiao	S3	Male	825	2011/8/15	121114			8,737	0
CX.13.121112	Chengxiao	S3	Male	825	2011/8/15	121112			8,895	0
CX.15.121121	Chengxiao	S3	Male	825	2011/8/15	121121			8,138	0
CX.16.121207	Chengxiao	S3	Male	825	2011/8/15	121207			8,383	0
CX.17.121211	Chengxiao	S3	Male	825	2011/8/15	121211			8,019	0
CX.18.121202	Chengxiao	S3	Male	825	2011/8/15	121202			6,364	0
CX.19.121223	Chengxiao	S3	Male	825	2011/8/15	121223			6,467	0
CX.20.121225	Chengxiao	S3	Male	825	2011/8/15	121225			7,450	0
CX.22.121030	Chengxiao	S3	Male	825	2011/8/15	121030		Yes	8,010	22,267
CX.25.130129	Chengxiao	S3	Male	825	2011/8/15	130129		Yes	8,339	56,723
CX.27.130117	Chengxiao	S3	Male	825	2011/8/15	130117		Yes	6,056	33,263
CX.29.130108	Chengxiao	S3	Male	825	2011/8/15	130108		Yes	8,116	56,395
CX.3.121209	Chengxiao	S3	Male	825	2011/8/15	121209			7,931	0
CX.31.130113	Chengxiao	S3	Male	825	2011/8/15	130113		Yes	8,268	46,587
CX.33.130202	Chengxiao	S3	Male	825	2011/8/15	130202		Yes	8,258	55,439
CX.34.130125	Chengxiao	S3	Male	825	2011/8/15	130125		Yes	8,249	49,510
CX.35.120827	Chengxiao	S4	Male	825	2011/8/15	120827			6,881	0
CX.36.130108	Chengxiao	S3	Male	825	2011/8/15	130108		Yes	7,973	58,643
CX.38.130202	Chengxiao	S3	Male	825	2011/8/15	130202		Yes	6,044	34,670
CX.39.130208	Chengxiao	S3	Male	825	2011/8/15	130208	Yes	Yes	8,091	47,237
CX.4.121221	Chengxiao	S3	Male	825	2011/8/15	121221		Yes	7,846	58,591
CX.40.130401	Chengxiao	S3	Male	825	2011/8/15	130401		Yes	6,295	34,307
CX.41.130402	Chengxiao	S3	Male	825	2011/8/15	130402			8,136	0

CX.42.130403	Chengxiao	S3	Male	825	2011/8/15	130403			7,725	0
CX.5.121203	Chengxiao	S3	Male	825	2011/8/15	121203			8,048	0
CX.6.121213	Chengxiao	S3	Male	825	2011/8/15	121213	Yes		8,128	0
CX.7.121208	Chengxiao	S3	Male	825	2011/8/15	121208			8,247	0
CX.8.121209	Chengxiao	S3	Male	825	2011/8/15	121209			8,541	0
CX.9.121215	Chengxiao	S3	Male	825	2011/8/15	121215			8,504	0
CX.m1.110816	Chengxiao	S1	Male	825	2011/8/15	110816	Yes	Yes	6,582	51,757
CX.m11.110903	Chengxiao	S1	Male	825	2011/8/15	110903			8,118	0
CX.m12.110905	Chengxiao	S1	Male	825	2011/8/15	110905			8,275	0
CX.m13.110907	Chengxiao	S1	Male	825	2011/8/15	110907		Yes	8,206	50,289
CX.m14.110909	Chengxiao	S1	Male	825	2011/8/15	110909			8,358	0
CX.m15.110911	Chengxiao	S1	Male	825	2011/8/15	110911			8,343	0
CX.m16.110913	Chengxiao	S1	Male	825	2011/8/15	110913			8,274	0
CX.m17.110915	Chengxiao	S1	Male	825	2011/8/15	110915		Yes	8,506	8,783
CX.m18.110917	Chengxiao	S1	Male	825	2011/8/15	110917	Yes		8,316	0
CX.m19.110919	Chengxiao	S1	Male	825	2011/8/15	110919		Yes	8,076	44,005
CX.m22.110929	Chengxiao	S1	Male	825	2011/8/15	110929		Yes	7,781	57,488
CX.m29.111025	Chengxiao	S2	Male	825	2011/8/15	111025		Yes	8,501	57,527
CX.m30.111031	Chengxiao	S2	Male	825	2011/8/15	111031		Yes	8,578	21,881
CX.m31.111101	Chengxiao	S2	Male	825	2011/8/15	111101	Yes	Yes	8,441	11,992
CX.m6.110826	Chengxiao	S1	Male	825	2011/8/15	110826		Yes	8,116	62,653
HQ.43.130202	Heqi	S3	Female	821	2011/8/12	130202		Yes	8,366	28,984
HQ.44.130819	Heqi	S3	Female	821	2011/8/12	130819		Yes	7,993	0
HQ.45.130815	Heqi	S3	Female	821	2011/8/12	130815			6,819	0
HQ.46.130828	Heqi	S3	Female	821	2011/8/12	130828		Yes	7,672	0
HQ.47.130816	Heqi	S3	Female	821	2011/8/12	130816	Yes	Yes	8,080	35,782
HQ.48.130903	Heqi	S3	Female	821	2011/8/12	130903		Yes	7,816	0
HQ.50.130129	Heqi	S4	Female	821	2011/8/12	130129			8,179	0
HQ.51.130108	Heqi	S3	Female	821	2011/8/12	130108			7,458	11,614

HQ.52.130111	Heqi	S3	Female	821	2011/8/12	130111			8,062	0
HQ.53.130121	Heqi	S3	Female	821	2011/8/12	130121			8,095	28,252
HQ.56.130130	Heqi	S3	Female	821	2011/8/12	130130			7,833	0
HQ.58.130129	Heqi	S4	Female	821	2011/8/12	130129			7,922	0
HQ.59.130113	Heqi	S3	Female	821	2011/8/12	130113	Yes		8,141	34,820
HQ.m125.110819	Heqi	S1	Female	821	2011/8/12	110819	Yes		8,432	0
HQ.m126.110822	Heqi	S1	Female	821	2011/8/12	110822			8,479	0
HQ.m127.110824	Heqi	S1	Female	821	2011/8/12	110824			7,191	0
HQ.m128.110826	Heqi	S1	Female	821	2011/8/12	110826			8,496	0
HQ.m129.110828	Heqi	S1	Female	821	2011/8/12	110828			8,362	0
HQ.m130.110831	Heqi	S1	Female	821	2011/8/12	110831			8,280	0
HQ.m32.110901	Heqi	S1	Female	821	2011/8/12	110901		Yes	8,817	35,686
HQ.m33.110903	Heqi	S1	Female	821	2011/8/12	110903		Yes	8,500	41,251
HQ.m34.110907	Heqi	S1	Female	821	2011/8/12	110907	Yes		8,647	0
HQ.m37.110912	Heqi	S1	Female	821	2011/8/12	110912		Yes	8,461	16,054
HQ.m38.110915	Heqi	S1	Female	821	2011/8/12	110915		Yes	8,663	23,051
HQ.m39.110917	Heqi	S1	Female	821	2011/8/12	110917			8,471	0
HQ.m40.110919	Heqi	S1	Female	821	2011/8/12	110919		Yes	8,453	18,071
HQ.m41.110921	Heqi	S1	Female	821	2011/8/12	110921		Yes	8,604	47,594
HQ.m42.110923	Heqi	S1	Female	821	2011/8/12	110923			8,324	0
HQ.m43.110926	Heqi	S1	Female	821	2011/8/12	110926		Yes	8,363	22,522
HQ.m44.110928	Heqi	S1	Female	821	2011/8/12	110928		Yes	8,624	50,310
HQ.m45.110930	Heqi	S1	Female	821	2011/8/12	110930		Yes	8,481	55,005
HQ.m46.111002	Heqi	S1	Female	821	2011/8/12	111002		Yes	8,636	56,724
HQ.m47.111005	Heqi	S1	Female	821	2011/8/12	111005			8,736	0
HQ.m48.111008	Heqi	S1	Female	821	2011/8/12	111008			8,897	0
HQ.m49.111012	Heqi	S1	Female	821	2011/8/12	111012			8,733	0
HQ.m50.111015	Heqi	S2	Female	821	2011/8/12	111015			8,645	0
HQ.m52.111023	Heqi	S2	Female	821	2011/8/12	111023			8,510	0

HQ.m53.111027	Heqi	S2	Female	821	2011/8/12	111027		Yes	8,277	55,964
HQ.m54.111030	Heqi	S2	Female	821	2011/8/12	111030		Yes	8,304	51,099
HQ.m55.111101	Heqi	S2	Female	821	2011/8/12	111101	Yes	Yes	8,355	44,064
HQ.m56.111104	Heqi	S2	Female	821	2011/8/12	111104		Yes	8,392	50,450
CD.66.130207	Chengda	S3	Female	824	2011/8/15	130207		Yes	8,272	54,322
CD.68.130109	Chengda	S3	Female	824	2011/8/15	130109		Yes	8,120	61,572
CD.70.130117	Chengda	S3	Female	824	2011/8/15	130117	Yes	Yes	8,217	30,489
CD.71.130104	Chengda	S3	Female	824	2011/8/15	130104		Yes	8,327	39,348
CD.73.130415	Chengda	S4	Female	824	2011/8/15	130415	Yes	Yes	7,287	21,174
CD.m120.111012	Chengda	S1	Female	824	2011/8/15	111012			8,480	0
CD.m121.111017	Chengda	S2	Female	824	2011/8/15	111017	Yes	Yes	8,476	58,248
CD.m122.111023	Chengda	S2	Female	824	2011/8/15	111023			8,475	0
CD.m189.111102	Chengda	S2	Female	824	2011/8/15	111102		Yes	8,682	58,351
CD.m65.110830	Chengda	S1	Female	824	2011/8/15	110830			7,723	0
CD.m66.110902	Chengda	S1	Female	824	2011/8/15	110902			8,732	0
CD.m67.110904	Chengda	S1	Female	824	2011/8/15	110904			8,513	0
CD.m69.110908	Chengda	S1	Female	824	2011/8/15	110908			7,422	0
CD.m70.110910	Chengda	S1	Female	824	2011/8/15	110910			8,715	0
CD.m71.110912	Chengda	S1	Female	824	2011/8/15	110912	Yes	Yes	8,180	18,388
CD.m72.110915	Chengda	S1	Female	824	2011/8/15	110915		Yes	8,503	55,155
CD.m73.110918	Chengda	S1	Female	824	2011/8/15	110918			8,825	0
CD.m74.110924	Chengda	S1	Female	824	2011/8/15	110924		Yes	8,576	17,547
CD.m75.110927	Chengda	S1	Female	824	2011/8/15	110927		Yes	8,894	13,686
CD.m76.110930	Chengda	S1	Female	824	2011/8/15	110930		Yes	8,791	11,538
CD.m77.111002	Chengda	S1	Female	824	2011/8/15	111002	Yes	Yes	8,643	23,412
CD.m78.111005	Chengda	S1	Female	824	2011/8/15	111005			8,325	0
CD.m79.111008	Chengda	S1	Female	824	2011/8/15	111008			8,210	0
QQ.101.130916	Qiaoqiao	S4	Male	815	2011/8/4	130916			7,896	0

QQ.102.130620	Qiaoqiao	S4	Male	815	2011/8/4	130620	Yes		8,059	0
QQ.103.130424	Qiaoqiao	S4	Male	815	2011/8/4	130424			8,094	0
QQ.83.130314	Qiaoqiao	S3	Male	815	2011/8/4	130314			6,835	0
QQ.85.130322	Qiaoqiao	S3	Male	815	2011/8/4	130322			7,969	0
QQ.86.130108	Qiaoqiao	S3	Male	815	2011/8/4	130108			7,874	0
QQ.87.130409	Qiaoqiao	S3	Male	815	2011/8/4	130409			6,984	0
QQ.92.130119	Qiaoqiao	S3	Male	815	2011/8/4	130119			8,054	0
QQ.97.130418	Qiaoqiao	S4	Male	815	2011/8/4	130418			7,784	0
QQ.98.130411	Qiaoqiao	S4	Male	815	2011/8/4	130411	Yes		8,047	0
QQ.m135.110817	Qiaoqiao	S1	Male	815	2011/8/4	110817	Yes		7,913	0
QQ.m137.110823	Qiaoqiao	S1	Male	815	2011/8/4	110823			8,126	0
QQ.m139.110829	Qiaoqiao	S1	Male	815	2011/8/4	110829			8,699	0
QQ.m140.110901	Qiaoqiao	S1	Male	815	2011/8/4	110901			8,337	0
QQ.m142.110907	Qiaoqiao	S1	Male	815	2011/8/4	110907			7,119	0
QQ.m144.110913	Qiaoqiao	S1	Male	815	2011/8/4	110913			8,595	0
QQ.m146.110922	Qiaoqiao	S1	Male	815	2011/8/4	110922			8,630	0
QQ.m148.110930	Qiaoqiao	S1	Male	815	2011/8/4	110930			8,547	0
QQ.m150.111008	Qiaoqiao	S2	Male	815	2011/8/4	111008			8,261	0
QQ.m151.111015	Qiaoqiao	S2	Male	815	2011/8/4	111015			8,627	0
QQ.m152.111015	Qiaoqiao	S2	Male	815	2011/8/4	111015	Yes		8,564	0
EQ.118.130124	Erqiao	S3	Female	823	2011/8/23	130124	Yes		7,596	0
EQ.124.130313	Erqiao	S3	Female	823	2011/8/23	130313			7,775	0
EQ.125.130315	Erqiao	S4	Female	823	2011/8/23	130315			7,797	0
EQ.126.130105	Erqiao	S3	Female	823	2011/8/23	130105			7,874	0
EQ.128.130507	Erqiao	S4	Female	823	2011/8/23	130507	Yes		8,339	0
EQ.m108.110828	Erqiao	S1	Female	823	2011/8/23	110828			8,335	0
EQ.m114.110825	Erqiao	S1	Female	823	2011/8/23	110825	Yes		7,265	0
EQ.m118.110830	Erqiao	S1	Female	823	2011/8/23	110830			8,306	0

EQ.m154.110902	Erqiao	S1	Female	823	2011/8/23	110902			8,602	0
EQ.m155.110909	Erqiao	S1	Female	823	2011/8/23	110909			8,537	0
EQ.m156.110915	Erqiao	S1	Female	823	2011/8/23	110915			8,713	0
EQ.m157.110920	Erqiao	S1	Female	823	2011/8/23	110920			8,774	0
EQ.m158.110925	Erqiao	S1	Female	823	2011/8/23	110925			8,773	0
EQ.m159.110929	Erqiao	S1	Female	823	2011/8/23	110929			8,717	0
EQ.m160.111002	Erqiao	S1	Female	823	2011/8/23	111002			8,621	0
EQ.m161.111006	Erqiao	S1	Female	823	2011/8/23	111006			8,726	0
EQ.m162.111011	Erqiao	S1	Female	823	2011/8/23	111011			8,810	0
EQ.m163.111017	Erqiao	S1	Female	823	2011/8/23	111017			8,074	0
EQ.m164.111020	Erqiao	S1	Female	823	2011/8/23	111020	Yes		7,949	0
EQ.m165.111024	Erqiao	S2	Female	823	2011/8/23	111024			8,605	0
EQ.m166.111031	Erqiao	S2	Female	823	2011/8/23	111031			8,755	0
EQ.m168.111104	Erqiao	S2	Female	823	2011/8/23	111104	Yes		8,427	0
QF.129.090428	Qifu	S2	Female	709	2008/9/26	90428		Yes	7,799	25,084
QF.131.090529	Qifu	S2	Female	709	2008/9/26	90529	Yes		8,587	0
QF.132.090610	Qifu	S4	Female	709	2008/9/26	90610		Yes	8,574	9,870
QF.133.090620	Qifu	S2	Female	709	2008/9/26	90620		Yes	8,776	10,415
QF.134.090930	Qifu	S4	Female	709	2008/9/26	90930			7,819	0
QF.135.091001	Qifu	S4	Female	709	2008/9/26	91001	Yes		8,877	0
QF.138.091013	Qifu	S4	Female	709	2008/9/26	91013			8,412	0
QF.140.091021	Qifu	S3	Female	709	2008/9/26	91021			7,935	0
QF.141.091025	Qifu	S3	Female	709	2008/9/26	91025			6,778	0
QF.m322.080927	Qifu	S1	Female	709	2008/9/26	80927	Yes		8,202	0
QF.m323.080928	Qifu	S1	Female	709	2008/9/26	80928			9,117	0
QF.m324.081005	Qifu	S1	Female	709	2008/9/26	81005			8,138	0
QF.m325.081015	Qifu	S1	Female	709	2008/9/26	81015			8,944	0
QF.m326.081022	Qifu	S1	Female	709	2008/9/26	81022			8,907	0

QF.m327.081029	Qifu	S1	Female	709	2008/9/26	81029			8,800	0
QF.m328.081106	Qifu	S1	Female	709	2008/9/26	81106		Yes	8,624	19,137
QF.m329.081113	Qifu	S1	Female	709	2008/9/26	81113			8,803	0
QF.m330.081207	Qifu	S2	Female	709	2008/9/26	81207	Yes	Yes	8,632	33,341
QF.m333.090121	Qifu	S2	Female	709	2008/9/26	90121	Yes		7,656	0
NN.144.090425	Nini	S2	Female	725	2008/8/23	90425	Yes		7,576	0
NN.145.090428	Nini	S2	Female	725	2008/8/23	90428			7,401	0
NN.146.090501	Nini	S2	Female	725	2008/8/23	90501			7,684	0
NN.148.090713	Nini	S2	Female	725	2008/8/23	90713			7,695	0
NN.149.091002	Nini	S4	Female	725	2008/8/23	91002	Yes		7,177	0
NN.154.091025	Nini	S3	Female	725	2008/8/23	91025			7,646	0
NN.156.091104	Nini	S3	Female	725	2008/8/23	91104			8,051	0
NN.m219.080824	Nini	S1	Female	725	2008/8/23	80824			7,861	0
NN.m221.080829	Nini	S1	Female	725	2008/8/23	80829	Yes		9,058	0
NN.m223.080904	Nini	S1	Female	725	2008/8/23	80904			7,681	0
NN.m224.080915	Nini	S1	Female	725	2008/8/23	80915			7,511	0
NN.m226.080925	Nini	S1	Female	725	2008/8/23	80925			8,497	0
NN.m227.080930	Nini	S1	Female	725	2008/8/23	80930			8,632	0
NN.m228.081004	Nini	S1	Female	725	2008/8/23	81004	Yes		8,735	0
NN.m230.081017	Nini	S1	Female	725	2008/8/23	81017			8,708	0
NN.m231.081023	Nini	S1	Female	725	2008/8/23	81023			8,892	0
NN.m232.081030	Nini	S2	Female	725	2008/8/23	81030			8,670	0
NN.m233.081102	Nini	S2	Female	725	2008/8/23	81102			8,669	0
NN.m234.081109	Nini	S2	Female	725	2008/8/23	81109			8,327	0
NN.m236.081124	Nini	S2	Female	725	2008/8/23	81124			8,328	0
NN.m237.081201	Nini	S2	Female	725	2008/8/23	81201			8,454	0
NN.m238.081204	Nini	S2	Female	725	2008/8/23	81204	Yes		8,334	0
NN.m239.081225	Nini	S2	Female	725	2008/8/23	81225			8,330	0

NN.m241.090111	Nini	S2	Female	725	2008/8/23	90111			7,316	0
SY.159.090502	Suyun	S2	Male	718	2008/8/5	90502		Yes	7,980	19,993
SY.163.090706	Suyun	S2	Male	718	2008/8/5	90706		Yes	7,152	10,598
SY.165.091104	Suyun	S3	Male	718	2008/8/5	91104			8,030	0
SY.166.091106	Suyun	S3	Male	718	2008/8/5	91106			7,357	0
SY.167.091121	Suyun	S3	Male	718	2008/8/5	91121	Yes		8,268	0
SY.168.091027	Suyun	S3	Male	718	2008/8/5	91027			8,037	0
SY.170.091018	Suyun	S3	Male	718	2008/8/5	91018			8,199	0
SY.171.091009	Suyun	S3	Male	718	2008/8/5	91009			8,237	0
SY.m190.080809	Suyun	S1	Male	718	2008/8/5	80809		Yes	8,712	52,635
SY.m193.080817	Suyun	S1	Male	718	2008/8/5	80817		Yes	7,560	19,390
SY.m195.080824	Suyun	S1	Male	718	2008/8/5	80824	Yes	Yes	8,620	0
SY.m197.080904	Suyun	S1	Male	718	2008/8/5	80904			8,771	0
SY.m198.080910	Suyun	S1	Male	718	2008/8/5	80910			8,815	0
SY.m199.080917	Suyun	S1	Male	718	2008/8/5	80917			9,022	0
SY.m201.080929	Suyun	S1	Male	718	2008/8/5	80929			9,040	0
SY.m202.081003	Suyun	S1	Male	718	2008/8/5	81003	Yes		8,985	0
SY.m204.081018	Suyun	S2	Male	718	2008/8/5	81018			8,831	0
SY.m205.081025	Suyun	S2	Male	718	2008/8/5	81025			8,938	0
SY.m207.081103	Suyun	S2	Male	718	2008/8/5	81103			8,317	0
SY.m209.081113	Suyun	S2	Male	718	2008/8/5	81113			8,644	0
SY.m210.081125	Suyun	S2	Male	718	2008/8/5	81125	Yes		8,573	0
SY.m211.081205	Suyun	S2	Male	718	2008/8/5	81205			8,740	0
SY.m212.081215	Suyun	S2	Male	718	2008/8/5	81215			8,486	0
SY.m213.081222	Suyun	S2	Male	718	2008/8/5	81222			8,518	0
SY.m214.090102	Suyun	S2	Male	718	2008/8/5	90102			8,955	0
SY.m215.090120	Suyun	S2	Male	718	2008/8/5	90120			8,769	0
SY.m216.090120	Suyun	S2	Male	718	2008/8/5	90120		Yes	8,738	59,573
SY.m217.090126	Suyun	S2	Male	718	2008/8/5	90126			8,855	0

SY.m218.081229	Suyun	S2	Male	718	2008/8/5	81229			8,743	0
YL.172.090417	Yalin	S2	Male	726	2008/8/24	90417			7,434	0
YL.173.090701	Yalin	S3	Male	726	2008/8/24	90701	Yes		7,766	0
YL.174.090710	Yalin	S3	Male	726	2008/8/24	90710			7,567	0
YL.175.090831	Yalin	S3	Male	726	2008/8/24	90831			8,196	0
YL.176.090903	Yalin	S3	Male	726	2008/8/24	90903			8,225	0
YL.177.091008	Yalin	S3	Male	726	2008/8/24	91008			7,581	0
YL.178.091015	Yalin	S3	Male	726	2008/8/24	91015	Yes		7,856	0
YL.180.091023	Yalin	S3	Male	726	2008/8/24	91023			7,866	0
YL.182.091101	Yalin	S3	Male	726	2008/8/24	91101			8,159	0
YL.183.091104	Yalin	S3	Male	726	2008/8/24	91104			7,393	0
YL.m247.080904	Yalin	S1	Male	726	2008/8/24	80904			7,239	0
YL.m248.080906	Yalin	S1	Male	726	2008/8/24	80906			8,660	0
YL.m249.080909	Yalin	S1	Male	726	2008/8/24	80909			8,326	0
YL.m250.080912	Yalin	S1	Male	726	2008/8/24	80912			8,586	0
YL.m251.080916	Yalin	S1	Male	726	2008/8/24	80916			8,304	0
YL.m252.080919	Yalin	S1	Male	726	2008/8/24	80919	Yes		8,762	0
YL.m253.080924	Yalin	S1	Male	726	2008/8/24	80924			8,584	0
YL.m255.081001	Yalin	S1	Male	726	2008/8/24	81001			8,609	0
YL.m256.081008	Yalin	S1	Male	726	2008/8/24	81008			8,536	0
YL.m257.081014	Yalin	S1	Male	726	2008/8/24	81014			8,803	0
YL.m258.081022	Yalin	S1	Male	726	2008/8/24	81022			8,779	0
YL.m260.081105	Yalin	S1	Male	726	2008/8/24	81105			8,597	0
YL.m261.081113	Yalin	S2	Male	726	2008/8/24	81113			8,338	0
YL.m262.081122	Yalin	S2	Male	726	2008/8/24	81122			8,185	0
YL.m263.081213	Yalin	S2	Male	726	2008/8/24	81213			8,418	0
YL.m264.081212	Yalin	S2	Male	726	2008/8/24	81212	Yes		8,526	0
YL.m265.090109	Yalin	S2	Male	726	2008/8/24	90109	Yes		8,555	0

JJ.104.130515	Junjun	S4	Female	813	2011/8/1	130515		Yes	7,626	18,428
JJ.14.121127	Junjun	S3	Female	813	2011/8/1	121127			8,464	0
JJ.226.121029	Junjun	S3	Female	813	2011/8/1	121029		Yes	8,698	53,051
JJ.227.130101	Junjun	S3	Female	813	2011/8/1	130101		Yes	8,061	50,139
JJ.228.130108	Junjun	S3	Female	813	2011/8/1	130108			8,113	0
JJ.229.130113	Junjun	S3	Female	813	2011/8/1	130113			8,817	0
JJ.230.130116	Junjun	S3	Female	813	2011/8/1	130116		Yes	7,889	56,783
JJ.231.130129	Junjun	S3	Female	813	2011/8/1	130129		Yes	8,853	60,248
JJ.232.130204	Junjun	S3	Female	813	2011/8/1	130204			8,787	0
JJ.233.130206	Junjun	S3	Female	813	2011/8/1	130206			8,117	0
JJ.234.130208	Junjun	S3	Female	813	2011/8/1	130208	Yes	Yes	8,553	54,660
JJ.235.130214	Junjun	S3	Female	813	2011/8/1	130214			8,778	0
JJ.236.130217	Junjun	S3	Female	813	2011/8/1	130217			8,562	0
JJ.250.130315	Junjun	S3	Female	813	2011/8/1	130315		Yes	8,653	18,442
JJ.251.130321	Junjun	S3	Female	813	2011/8/1	130321		Yes	8,784	34,745
JJ.252.130328	Junjun	S3	Female	813	2011/8/1	130328			8,821	0
JJ.253.130417	Junjun	S4	Female	813	2011/8/1	130417		Yes	8,663	9,173
JJ.254.130423	Junjun	S4	Female	813	2011/8/1	130423			8,348	0
JJ.255.130501	Junjun	S4	Female	813	2011/8/1	130501			8,518	0
JJ.256.130510	Junjun	S4	Female	813	2011/8/1	130510			8,494	0
JJ.257.130514	Junjun	S4	Female	813	2011/8/1	130514	Yes		8,214	0
JJ.258.130524	Junjun	S4	Female	813	2011/8/1	130524			8,215	0
JJ.259.130605	Junjun	S4	Female	813	2011/8/1	130605		Yes	7,534	52,180
JJ.260.130618	Junjun	S4	Female	813	2011/8/1	130618			7,518	0
JJ.261.130624	Junjun	S4	Female	813	2011/8/1	130624		Yes	8,068	20,639
JJ.263.130710	Junjun	S3	Female	813	2011/8/1	130710			8,049	0
JJ.264.130918	Junjun	S3	Female	813	2011/8/1	130918			7,936	0
JJ.265.130922	Junjun	S4	Female	813	2011/8/1	130922		Yes	8,082	0
JJ.m100.110929	Junjun	S1	Female	813	2011/8/1	110929	Yes	Yes	8,389	0

JJ.m102.111008	Junjun	S2	Female	813	2011/8/1	111008		Yes	8,285	0
JJ.m104.111025	Junjun	S2	Female	813	2011/8/1	111025		Yes	8,287	0
JJ.m83.110808	Junjun	S1	Female	813	2011/8/1	110808			8,344	0
JJ.m88.110820	Junjun	S1	Female	813	2011/8/1	110820	Yes	Yes	8,208	19,716
JJ.m92.110901	Junjun	S1	Female	813	2011/8/1	110901		Yes	8,392	0
JJ.m94.110908	Junjun	S1	Female	813	2011/8/1	110908		Yes	8,530	0
JJ.m96.110915	Junjun	S1	Female	813	2011/8/1	110915	Yes	Yes	8,471	0
ZZ.105.130403	Zhenzhen	S3	Female	814	2011/8/4	130403		Yes	6,699	60,577
ZZ.106.130918	Zhenzhen	S4	Female	814	2011/8/4	130918			7,776	0
ZZ.107.130327	Zhenzhen	S3	Female	814	2011/8/4	130327		Yes	7,958	0
ZZ.109.130808	Zhenzhen	S3	Female	814	2011/8/4	130808	Yes	Yes	8,113	0
ZZ.112.130109	Zhenzhen	S3	Female	814	2011/8/4	130109		Yes	7,997	59,667
ZZ.115.130410	Zhenzhen	S4	Female	814	2011/8/4	130410		Yes	8,010	25,987
ZZ.m173.110815	Zhenzhen	S1	Female	814	2011/8/4	110815	Yes	Yes	8,858	0
ZZ.m175.110820	Zhenzhen	S1	Female	814	2011/8/4	110820		Yes	8,759	0
ZZ.m177.110826	Zhenzhen	S1	Female	814	2011/8/4	110826		Yes	8,825	16,642
ZZ.m179.110902	Zhenzhen	S1	Female	814	2011/8/4	110902		Yes	8,745	0
ZZ.m181.110915	Zhenzhen	S1	Female	814	2011/8/4	110915		Yes	8,701	0
ZZ.m183.110928	Zhenzhen	S1	Female	814	2011/8/4	110928	Yes	Yes	8,864	0
ZZ.m187.111013	Zhenzhen	S2	Female	814	2011/8/4	111013			8,703	0
ZZ.m188.111015	Zhenzhen	S2	Female	814	2011/8/4	111015	Yes	Yes	8,837	0
HH.184.090203	Huanhuan	S2	Female	723	2008/8/10	90203			7,616	0
HH.185.090502	Huanhuan	S2	Female	723	2008/8/10	90502			8,092	0
HH.186.090510	Huanhuan	S2	Female	723	2008/8/10	90510	Yes		7,765	0
HH.187.090530	Huanhuan	S2	Female	723	2008/8/10	90530			8,124	0
HH.188.090613	Huanhuan	S2	Female	723	2008/8/10	90613			6,960	0
HH.190.090715	Huanhuan	S2	Female	723	2008/8/10	90715			7,331	0
HH.192.090930	Huanhuan	S4	Female	723	2008/8/10	90930	Yes		8,547	0

HH.193.091001	Huanhuan	S4	Female	723	2008/8/10	91001			8,702	0
HH.195.091007	Huanhuan	S4	Female	723	2008/8/10	91007			8,594	0
HH.196.091011	Huanhuan	S4	Female	723	2008/8/10	91011			8,111	0
HH.197.091013	Huanhuan	S4	Female	723	2008/8/10	91013			8,296	0
HH.202.091106	Huanhuan	S3	Female	723	2008/8/10	91106			8,679	0
HH.m272.080901	Huanhuan	S1	Female	723	2008/8/10	80901			8,169	0
HH.m273.080908	Huanhuan	S1	Female	723	2008/8/10	80908			8,481	0
HH.m274.080918	Huanhuan	S1	Female	723	2008/8/10	80918			8,861	0
HH.m275.080925	Huanhuan	S1	Female	723	2008/8/10	80925	Yes		9,287	0
HH.m276.081001	Huanhuan	S1	Female	723	2008/8/10	81001			9,006	0
HH.m277.081006	Huanhuan	S1	Female	723	2008/8/10	81006			8,985	0
HH.m278.081017	Huanhuan	S2	Female	723	2008/8/10	81017	Yes		8,963	0
HH.m280.081222	Huanhuan	S2	Female	723	2008/8/10	81222			8,800	0
HH.m281.081225	Huanhuan	S2	Female	723	2008/8/10	81225	Yes		8,463	0
HH.m313.081222	Huanhuan	S2	Female	723	2008/8/10	81222			8,408	0
YD.m314.080809	Yuanda	S1	Male	627	2008/8/6	80809			8,531	0
YD.m318.080827	Yuanda	S1	Male	627	2008/8/6	80827			8,498	0
YD.m319.080831	Yuanda	S1	Male	627	2008/8/6	80831			8,704	0
YD.m320.080907	Yuanda	S1	Male	627	2008/8/6	80907			9,002	0
YD.m321.080914	Yuanda	S1	Male	627	2008/8/6	80914			8,866	0
YX.m244.080811	Yuanxiao	S1	Male	628	2008/8/6	80811			7,086	0
YX.m245.080813	Yuanxiao	S1	Male	628	2008/8/6	80813			8,273	0

Supplemental Table S2: the OOB classification error rates of the 51 OTUs (Figure 1D).

Class	S1	S2	S3	S4	Class error (%)
S1	92.12	1.3	6.37	0.21	7.88
S2	59.17	19.27	20.22	1.33	80.73
S3	15.57	6.49	73.59	4.35	26.41
S4	4.19	2.52	84.83	8.46	91.54

Note: OOB estimate of error rate: 51.64%.

Supplemental Table S3: the statistics of sequence and assembly information.

SampleID	Different growth stages	RawData (Mb)	CleanData (Mb)	NonHostData (Mb)	Percentage(%)	Scaffigs number	Scaffigs length(bp)	N50 (bp)	N90 (bp)	Max (bp)	Min (bp)	Average len.(bp)
CD.m71.110914	S1	8,238	8,025	6,849	0.83	11,980	20,091,270	2,604	650	118,118	500	1,677
CD.m77.111001	S1	5,327	5,161	2,875	0.54	8,719	11,630,855	1,629	615	60,251	500	1,334
CX.m1.110827	S1	8,021	7,709	7,462	0.93	1,115	12,496,895	42,416	5,553	444,346	500	11,208
CX.m18.110917	S1	5,594	5,457	3,962	0.71	3,863	11,534,228	11,955	873	362,695	500	2,986
EQ.m114.110825	S1	5,435	5,278	4,792	0.88	5,497	8,416,600	2,047	630	88,255	500	1,531
EQ.m164.111020	S1	5,470	5,331	4,644	0.85	8,551	17,076,260	3,677	709	109,140	500	1,997
HH.m275.080925	S1	8,207	7,481	3,769	0.46	3,787	13,280,253	16,833	948	352,612	500	3,507
HQ.m125.110820	S1	5,337	5,083	4,984	0.93	2,728	4,042,069	1,963	629	35,778	500	1,482
HQ.m34.110906	S1	8,875	8,647	7,963	0.9	2,512	8,046,807	10,200	1,031	119,068	500	3,203
JJ.m100.110929	S1	7,126	6,938	4,440	0.62	7,850	15,592,888	3,753	681	361,161	500	1,986
JJ.m88.110820	S1	5,318	5,166	4,774	0.9	5,838	13,027,436	4,529	760	92,297	500	2,231
JJ.m95.110911	S1	9,283	8,937	8,401	0.91	10,683	23,091,526	4,047	770	106,466	500	2,162
NN.m221.080829	S1	5,502	5,037	2,814	0.51	9,029	16,973,370	3,062	715	58,498	500	1,880
NN.m228.081002	S1	7,711	7,380	5,201	0.67	10,089	16,502,604	2,211	676	118,590	500	1,636
QF.m322.080927	S1	5,377	5,223	5,142	0.96	3,061	10,565,891	7,272	1,278	89,278	500	3,452
QQ.m135.110814	S1	5,233	5,075	5,026	0.96	2,120	11,316,574	16,696	1,970	182,235	500	5,338
SY.m195.080827	S1	5,250	5,081	5,037	0.96	9,146	21,633,075	10,253	710	350,225	500	2,365
SY.m202.081002	S1	5,178	4,909	1,734	0.33	7,452	21,754,413	10,993	843	157,532	500	2,919

YL.m252.080918	S1	5,815	5,607	5,516	0.95	6,314	17,616,432	7,500	926	168,315	500	2,790
ZZ.m173.110828	S1	5,289	5,111	5,034	0.95	6,734	18,539,887	9,719	872	464,334	500	2,753
ZZ.m183.110929	S1	8,364	8,042	4,526	0.54	9,520	11,667,812	1,394	582	107,597	500	1,226
YL.m265.090109	S2	6,133	5,415	5,159	0.84	15,405	34,589,820	4,023	802	336,922	500	2,245
HH.m278.081017	S2	6,448	6,137	2,854	0.44	8,577	25,501,463	8,511	937	168,735	500	2,973
CD.m121.111017	S2	7,466	7,252	5,942	0.8	11,811	16,879,825	1,809	644	107,932	500	1,429
CX.m31.111104	S2	8,238	7,646	5,584	0.68	7,215	15,117,784	4,331	720	286,459	500	2,095
EQ.m168.111104	S2	5,325	5,091	2,060	0.39	10,698	22,641,356	5,857	685	405,373	500	2,116
HH.186.090510	S2	5,127	4,921	4,888	0.95	18,838	31,308,385	2,303	683	127,204	500	1,662
HH.m281.081225	S2	8,079	6,628	3,150	0.39	16,414	27,415,793	2,637	644	99,768	500	1,670
HQ.m55.111105	S2	7,165	6,793	2,639	0.37	16,574	16,828,013	1,027	565	41,689	500	1,015
NN.144.090425	S2	7,978	7,723	7,702	0.97	19,535	37,270,516	3,200	699	163,330	500	1,908
NN.m238.081204	S2	6,017	5,737	3,084	0.51	10,357	27,805,781	8,606	788	447,565	500	2,685
QF.131.090529	S2	5,729	5,434	5,406	0.94	11,323	16,658,383	1,918	638	34,000	500	1,471
QF.m330.081218	S2	7,785	7,544	4,284	0.55	14,026	37,804,432	9,057	807	376,305	500	2,695
QF.m333.090121	S2	5,285	4,964	4,152	0.79	19,516	43,231,063	4,876	743	260,603	500	2,215
QQ.m152.111015	S2	8,107	7,776	6,740	0.83	7,456	12,000,636	2,318	655	72,810	500	1,610
SY.m210.081125	S2	5,271	5,006	1,462	0.28	9,345	18,174,450	3,933	679	224,117	500	1,945
YL.m264.081212	S2	5,245	5,113	4,548	0.87	10,858	24,206,897	4,964	731	118,631	500	2,229
ZZ.m188.111015	S2	5,286	5,085	4,269	0.81	7,100	9,308,276	1,570	609	60,234	500	1,311
CD.70.130117	S3	8,228	7,405	7,350	0.89	10,749	13,298,705	1,433	592	31,247	500	1,237

CX.39.130208	S3	5,409	5,238	5,193	0.96	4,651	5,031,505	1,173	567	46,880	500	1,082
CX.6.121213	S3	8,305	8,084	7,701	0.93	17,203	38,703,543	5,472	713	224,108	500	2,250
EQ.118.130124	S3	8,387	8,090	8,054	0.96	10,685	19,902,231	3,099	685	225,695	500	1,863
HQ.47.130816	S3	10,080	9,831	9,707	0.96	89,866	111,531,867	1,408	596	57,354	500	1,241
HQ.59.130113	S3	5,429	5,146	5,126	0.94	8,581	10,185,427	1,352	598	28,249	500	1,187
JJ.234.130208	S3	5,454	5,166	5,137	0.94	9,723	13,496,943	1,742	622	44,646	500	1,388
SY.167.091121	S3	7,997	7,479	7,456	0.93	14,486	39,389,888	7,601	826	247,727	500	2,719
YL.173.090701	S3	5,717	5,537	5,465	0.96	22,247	50,961,106	4,607	797	285,447	500	2,291
YL.178.091015	S3	7,840	7,639	7,370	0.94	28,460	49,192,912	2,596	683	65,014	500	1,728
ZZ.109.130808	S3	5,729	5,501	5,473	0.96	7,918	8,097,084	1,061	562	18,710	500	1,023
CD.73.130415	S4	5,517	5,258	5,232	0.95	19,634	28,185,900	1,826	656	46,149	500	1,436
EQ.128.130507	S4	5,735	5,536	5,461	0.95	28,508	36,433,156	1,493	607	101,676	500	1,278
HH.192.090930	S4	5,363	5,059	4,864	0.91	27,008	36,590,744	1,643	626	82,842	500	1,355
JJ.257.130514	S4	5,800	5,671	5,645	0.97	25,772	32,832,019	1,502	614	29,932	500	1,274
NN.149.091002	S4	8,075	7,771	7,701	0.95	10,089	14,297,087	1,879	628	24,766	500	1,417
QF.135.091001	S4	7,672	7,486	7,365	0.96	27,540	43,347,118	2,117	672	133,505	500	1,574
QQ.102.130620	S4	5,542	5,275	5,261	0.95	56,796	74,542,470	1,598	620	42,303	500	1,312
QQ.98.130411	S4	5,303	5,034	5,010	0.94	20,406	29,134,722	1,805	631	57,842	500	1,428

Supplemental Table S4: Pan-metagenome assembly index of giant panda gut microbiome.

#Level	ContigNum	Total Length(bp)	N50_Length(bp)	N90_Length(bp)	Max_Length(bp)	Min_Length(bp)	GC%
ContigLen>= 300bp	461,872	551,924,865	2,679	403	464,334	300	47.57
ContigLen>= 500bp	222,746	460,864,873	4,579	694	464,334	500	47.54
ContigLen>= 1,000bp	89,948	370,293,669	8,046	1,425	464,334	1,000	47.32
ContigLen>= 10,000bp	5,909	168,292,670	36,151	12,610	464,334	10,000	47.84
ContigLen>= 100,000bp	224	37,592,733	173,600	113,285	464,334	100,171	50.69

Supplemental Table S5: The assembly and taxonomy information of MLG.

#ML Gname	ContigNum	TotalSize	MaxLen	AlignLen	Coverage	RefID	RefSize	RefAlignLen	RefCoverage	RefTaxID	RefTaxonomy
MLG1	1389	943816	166021	3852785	40.82	gi 647802220 gb C P008696.1	7122173	2422461	34.01	325	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas chlororaphis
MLG2	2359	7707564	38498	4156157	53.92	gi 662712225 gb C P008823.1	4852980	2458544	50.66	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG3	161	4995154	395672	4769492	95.48	gi 150953431 gb C P000647.1	5315120	4510735	84.87	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG4	757	4965613	164164	2783016	56.05	gi 378937014 gb C P003351.1	2955294	2137445	72.33	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG5	105	4914501	257487	4326869	88.04	gi 394343076 gb C P003683.1	6097032	4310576	70.7	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG6	165	4910119	309921	4413079	89.88	gi 334732565 gb C P002824.1	5280350	4089534	77.45	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG7	5889	4294619	4191	0	0	0	-	0	0	0	Unknow
MLG8	990	4226704	61888	2991179	70.77	gi 480474683 gb C P004142.1	5398151	2567363	47.56	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG9	174	4215722	316083	2526899	59.94	gi 440045023 gb C P003938.1	4762179	2395751	50.31	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG10	875	3711220	49059	1502041	40.47	gi 527122546 gb C P003025.1	1975541	1301701	65.89	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG11	370	3662098	158535	1857300	50.72	gi 291516109 emb FP929034.1	2384987	1562084	65.5	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium longum
MLG12	1180	3543762	29932	366318	10.34	gi 326539903 gb C P002582.1	4714237	364459	7.73	51	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Cellulosilyticum;s__Cellulosilyticum lentocellum
MLG13	77	3341033	464334	2568988	76.89	gi 327533853 gb C P002621.1	2739625	2540901	92.75	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
MLG14	69	3302369	247727	546532	16.55	gi 160361034 gb C P000884.1	6767514	558234	8.25	1012	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__Delftia acidovorans
MLG15	54	3265280	260603	3077809	94.26	gi 410821238 gb C P003493.1	3656170	3091264	84.55	929	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__Propionibacterium acidipropionici
MLG16	143	2667936	85047	2629138	98.55	gi 308044682 gb C P002222.1	3254376	2510258	77.13	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG17	477	2634625	34725	129293	4.91	gi 378937014 gb C P003351.1	2955294	139273	4.71	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG18	261	2593772	84012	2181618	84.11	gi 478439721 gb C P004856.1	3427276	2191613	63.95	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG19	75	2541211	123797	82362	3.24	gi 116608677 gb C P000454.1	4698945	84038	1.79	949	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__Arthrobacter sp. FB24
MLG20	526	2495233	38991	2453919	98.34	gi 392334715 gb C P003504.1	2827741	2339950	82.75	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus hirae
MLG21	236	2486742	106241	2106421	84.71	gi 334281572 dbj AP012054.1	2100077	1666627	79.36	368	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus pasteurianus
MLG22	164	2483450	85036	2011321	80.99	gi 323463200 gb C P002478.1	2572216	2020067	78.53	154	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus pseudintermedius
MLG23	167	2476783	405373	1852417	74.79	gi 41584196 gb AE 017198.1	1992676	1611278	80.86	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG24	297	2474294	36116	2462420	99.52	gi 455418716 gb C P004345.1	3799539	2465410	64.89	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganelia;s__Morganelia morgani

MLG 25	78	24599 81	32645 1	19960 81	81.14	gii619734722 gb C P007557.1	50990 34	20194 70	39.6	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 26	139	23646 50	65419	0	0	0	-	0	0	0	Unknow
MLG 27	22	23212 19	37630 5	20228 72	87.15	gii585129876 gb C P006713.1	23590 09	20000 65	84.78	895	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium breve
MLG 28	103	22844 01	32768 2	17947 84	78.57	gii300213939 gb C P002034.1	18281 69	15515 77	84.87	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 29	41	22641 25	32950 7	31845	1.41	gii183225820 dbj AP008937.1	20986 85	31847	1.52	414	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus fermentum
MLG 30	41	22341 42	35695 2	0	0	0	-	0	0	0	Unknow
MLG 31	675	22299 13	24181	33804 8	15.16	gii406718232 emb FR745875.1	37815 09	31013 5	8.2	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 32	642	22183 98	34647	17452 9	7.87	gii188497817 gb C P001078.1	36596 44	17453 5	4.77	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 33	74	21904 32	14437 9	46349 3	21.16	gii313004821 emb FN995097.1	22206 06	47123 9	21.22	1167	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__Neisseria lactamica
MLG 34	24	21770 05	33615 8	11349 98	52.14	gii341821300 emb HE576794.1	24747 18	11460 98	46.31	651	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;s__Megasphaera elsdenii
MLG 35	60	21763 88	13313 9	60051 4	27.59	gii325177128 emb FR824043.1	23564 44	58975 9	25.03	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 36	74	20808 48	13849 6	0	0	0	-	0	0	0	Unknow
MLG 37	264	20744 92	10343 4	18812 93	90.69	gii281374316 gb C P001834.1	25981 44	17864 20	68.76	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 38	227	20721 84	20639 9	66629 8	32.15	gii320459527 dbj AP010890.1	24003 12	61442 3	25.6	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium longum
MLG 39	1311	19486 64	17520	19428 8	9.97	gii187720473 gb C P001056.1	38003 27	19710 9	5.19	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 40	23	19370 14	18019 8	14484 09	74.78	gii408465077 gb C P003325.1	21673 04	14795 36	68.27	889	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium asteroides
MLG 41	95	18788 11	93943	46331 4	24.66	gii325177128 emb FR824043.1	23564 44	43130 0	18.3	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 42	159	18606 68	17309 7	13849 96	74.44	gii523830301 gb C P006006.1	17023 98	13230 10	77.71	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteriaceae;g__Campylobacter;s__Campylobacter jejuni
MLG 43	34	18246 63	26134 4	16424 42	90.01	gii169803215 gb D Q489736.1	17962 84	15842 29	88.19	818	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__Leuconostoc citreum
MLG 44	294	17834 00	32625	10393 6	5.83	gii333741867 gb C P002735.1	66858 42	10398 2	1.56	1019	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__Delftia sp. Cs1-4
MLG 45	220	17821 03	54725	15302 10	85.87	gii612150118 gb C P007546.1	45619 05	15409 77	33.78	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 46	666	17776 92	13032	34322 7	19.31	gii47118322 dbj B A000016.3	30314 30	33506 1	11.05	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 47	501	17339 73	41676	41440 4	23.9	gii323272819 dbj AP012052.1	39820 34	41641 1	10.46	956	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Microbacterium;s__Microbacterium testaceum
MLG 48	200	17326 15	94762	15060 83	86.93	gii343179174 dbj AP009332.1	19501 35	14459 57	74.15	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 49	180	17249 37	12997 7	15862 36	91.96	gii349736152 gb C P003034.1	53135 31	14021 65	26.39	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 50	331	17214 85	45335	11628 9	6.76	gii690347849 gb C P007646.1	18362 97	11706 1	6.37	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 51	256	16769 20	72810	16641 15	99.24	gii124491690 emb AM406671.1	25294 78	16665 26	65.88	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis

MLG 52	81	16586 52	18807 7	12309 22	74.21	gii526120653 gb C P006603.1	21454 45	11852 23	55.24	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 53	76	16567 41	13482 7	66927	4.04	gii353737348 gb C P002644.1	21830 59	68848	3.15	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 54	244	16441 77	63272	13316 31	80.99	gii158967071 gb C P000033.3	19935 60	13390 44	67.17	212	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus acidophilus
MLG 55	196	16207 17	54659	14059 17	86.75	gii301154649 emb FQ312002.1	20868 75	14097 31	67.55	419	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__Haemophilus parainfluenzae
MLG 56	137	16182 95	62106	10227 54	63.2	gii288730948 emb FN597254.1	23509 11	96407 7	41.01	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 57	172	16117 26	40558	34267 0	21.26	gii523439782 gb C P006252.1	52386 12	33699 1	6.43	274	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia liquefaciens
MLG 58	620	15386 17	31884	45232	2.94	gii549807177 gb C P006721.1	51078 14	56892	1.11	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 59	37	15143 18	15634 8	47651 1	31.47	gii169803215 gb D Q489736.1	17962 84	47878 8	26.65	818	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__Leuconostoc citreum
MLG 60	56	14700 60	13571 2	62003 3	42.18	gii612156087 gb C P004887.1	59144 07	63383 2	10.72	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoea
MLG 61	47	13312 43	20925 8	23093	1.73	gii269093698 gb C P001820.1	21321 42	23635	1.11	91	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;s__Veillonella parvula
MLG 62	308	13190 85	51865	0	0	0	-	0	0	0	Unknow
MLG 63	44	12752 84	15468 6	11119 12	87.19	gii526120653 gb C P006603.1	21454 45	11005 18	51.3	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 64	161	12220 23	54815	0	0	0	-	0	0	0	Unknow
MLG 65	70	11991 91	11939 5	75705 5	63.13	gii78609255 emb C R936503.1	18846 61	66306 2	35.18	364	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus sakei
MLG 66	450	11573 63	16441	0	0	0	-	0	0	0	Unknow
MLG 67	75	11482 90	63927	89377 2	77.84	gii619734722 gb C P007557.1	50990 34	91679 1	17.98	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 68	53	11412 36	73997	29691 1	26.02	gii557470476 gb C P006854.1	17891 38	30148 4	16.85	401	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__Pediococcus pentosaceus
MLG 69	34	11395 19	17417 6	10262 67	90.06	gii619734722 gb C P007557.1	50990 34	10402 95	20.4	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 70	312	11117 66	24229	58852 2	52.94	gii440045023 gb C P003938.1	47621 79	58474 8	12.28	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 71	171	10944 24	13119 3	53756 9	49.12	gii557470476 gb C P006854.1	17891 38	53385 7	29.84	401	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__Pediococcus pentosaceus
MLG 72	690	10835 51	16792	25570	2.36	gii549807177 gb C P006721.1	51078 14	27042	0.53	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 73	162	10652 30	57986	83827 7	78.69	gii41584196 gb AE 017198.1	19926 76	84167 6	42.24	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 74	96	10590 69	73012	95725 9	90.39	gii338744031 emb FR873482.1	22105 74	96220 1	43.53	375	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus salivarius
MLG 75	519	10402 89	22426	0	0	0	-	0	0	0	Unknow
MLG 76	25	10279 33	22410 8	88763 5	86.35	gii269093698 gb C P001820.1	21321 42	88169 6	41.35	91	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;s__Veillonella la parvula
MLG 77	19	10216 75	19898 5	96062 2	94.02	gii269093698 gb C P001820.1	21321 42	97212 5	45.59	91	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;s__Veillonella la parvula
MLG 78	106	10108 80	43102	28095	2.78	gii328454937 gb C P002628.1	21156 81	28103	1.33	882	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Coriobacteriales;f__Coriobacteriaceae;g__Coriobacterium;s__Coriobacterium glomerans

MLG 79	122	990698	58821	743052	75	gii480474683 gb C P004142.1	5398151	723616	13.4	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella a;s__Raoultella omithinolytica
MLG 80	41	970244	143047	0	0	0	-	0	0	0	Unknown
MLG 81	555	926357	4758	362396	39.12	gii334728683 gb C P000245.1	4070193	368042	9.04	812	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Ramlibacter;s__Ramlibacter tatauiniensis
MLG 82	434	884702	7869	884699	100	gii514422290 gb C P004053.1	1938606	849248	43.81	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
MLG 83	969	861841	16038	133800	15.52	gii115249003 emb AM180355.1	4290252	132707	3.09	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 84	496	841665	10934	514907	61.18	gii662712225 gb C P008823.1	4852980	484168	9.98	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 85	190	816487	69447	37730	4.62	gii372283141 emb HE613569.1	2130034	60337	2.83	372	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus macedonicus
MLG 86	282	809037	25306	74388	9.19	gii343179174 dbj AP009332.1	1950135	79121	4.06	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 87	36	806618	206601	745316	92.4	gii640850664 gb C P007731.1	5241638	801960	15.3	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella a;s__Klebsiella pneumoniae
MLG 88	16	782047	385024	0	0	0	-	0	0	0	Unknown
MLG 89	131	761333	46096	644005	84.59	gii480474683 gb C P004142.1	5398151	646110	11.97	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella a;s__Raoultella omithinolytica
MLG 90	116	735698	19583	679882	92.41	gii325663854 gb C P002246.1	4552107	727182	15.97	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 91	247	730785	16340	339336	46.43	gii662712225 gb C P008823.1	4852980	326287	6.72	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 92	129	715791	17408	0	0	0	-	0	0	0	Unknown
MLG 93	186	705157	10709	105936	15.02	gii291548560 emb FP929055.1	3341681	105930	3.17	163	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__[Ruminococcus] torques
MLG 94	315	704704	14689	90563	12.85	gii188497817 gb C P001078.1	3659644	88779	2.43	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 95	99	697660	23404	143478	20.57	gii523439782 gb C P006252.1	5238612	145131	2.77	274	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia liquefaciens
MLG 96	14	693032	218601	616130	88.9	gii672600155 gb C P009114.1	5297511	593324	11.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella a;s__Klebsiella pneumoniae
MLG 97	138	683941	26935	645617	94.4	gii116100249 gb C P000419.1	1856368	651881	35.12	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 98	180	679117	17773	490647	72.25	gii157320013 gb C P000826.1	5448853	501063	9.2	282	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia proteamaculans
MLG 99	46	670827	135310	171856	25.62	gii160361034 gb C P000884.1	6767514	178916	2.64	1012	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__Delftia acidovorans
MLG 100	121	661486	35191	54382	8.22	gii116100249 gb C P000419.1	1856368	57754	3.11	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 101	206	632622	21690	333648	52.74	gii388532432 gb C P003583.1	2698137	343002	12.71	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG 102	16	629008	150319	76299	12.13	gii556048476 gb C P006246.1	2240234	77406	3.46	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 103	280	622524	15423	19487	3.13	gii334279325 dbj AP012053.1	2362241	29310	1.24	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 104	109	582462	21755	189732	32.57	gii674993598 dbj AP014630.1	464848	189908	4.09	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 105	180	576136	18494	260410	45.2	gii682108593 gb C P008897.1	4633407	260641	5.63	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae

MLG 106	21	552938	134516	235092	42.52	gii582030173 gb C P006659.1	5435369	247899	4.56	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
MLG 107	349	498391	11526	337785	67.78	gii662712225 gb C P008823.1	4852980	322721	6.65	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 109	20	473884	89243	412270	89.03	gii660550561 gb C P008700.1	5365144	417422	7.78	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
MLG 110	108	463069	24058	451530	99.36	gii689262542 gb C P009451.1	4876443	466690	9.57	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 111	261	454445	4837	155701	34.3	gii41584196 gb AE O17198.1	1992676	157027	7.88	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 112	57	453928	65464	25085	6.22	gii188497817 gb C P001078.1	3659644	25100	0.69	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 113	147	403446	11990	342592	85.62	gii692326398 gb C P009472.1	2398044	294711	12.29	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 114	83	400144	52350	190728	48.33	gii156617157 gb C P000057.2	1914490	191740	10.02	164	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__Haemophilus influenzae
MLG 115	139	394653	6956	285675	74.81	gii269093698 gb C P001820.1	2132142	286655	13.44	91	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;s__Veillonella parvula
MLG 116	51	381889	33354	186860	49.03	gii124491690 emb AM406671.1	2529478	202812	8.02	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 117	140	381110	18974	17596	4.62	gii47118322 dbj B A000016.3	3031430	15541	0.51	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 118	241	380830	8542	11192	2.94	gii295089810 emb FP929037.1	3769775	11235	0.3	843	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;s__Clostridium)saccharolyticum
MLG 119	54	380342	24563	122827	32.76	gii291482100 emb FN665653.1	4047729	122878	3.04	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 120	372	374935	5504	356541	95.32	gii571260215 emb HFS71988.1	4940199	371846	7.53	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 121	75	374030	12663	338159	90.63	gii400173048 gb C P003737.1	4726582	343586	7.27	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 122	52	373117	29509	109536	29.45	gii674993598 dbj AP014630.1	4648418	104985	2.26	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 123	160	371929	9600	352272	96.9	gii169752989 gb C P000946.1	4746218	337101	7.1	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 124	69	363556	28409	306853	85.82	gii619734722 gb C P007557.1	5099034	314763	6.17	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 125	13	357543	65880	20596	6.13	gii283133067 dbj AP011540.1	2264603	20762	0.92	792	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Rothia;s__Rothia mucilaginos
MLG 127	242	335888	8144	289222	90.27	gii472232670 dbj AP012167.1	2395134	292554	12.21	400	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus brevis
MLG 128	86	327280	30243	213879	67.23	gii345091121 gb C P003026.1	4812833	207430	4.31	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 129	67	320395	14652	110177	35.4	gii692326398 gb C P009472.1	2398044	106776	4.45	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 130	166	318115	7483	284348	92.34	gii294489418 gb C P001969.1	5108383	281906	5.52	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 131	192	311216	34447	3013	1	gii309700213 emb FN649414.1	5153435	3014	0.06	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 132	10	307940	116684	12435	4.12	gii527122546 gb C P003025.1	1975547	14033	0.71	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 133	40	302709	33268	217151	72.91	gii440045023 gb C P003938.1	4762179	208882	4.39	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 134	150	302067	11458	97161	32.77	gii304557459 gb C P002154.1	3684607	98604	2.68	294	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Edwardsiella;s__Edwardsiella tarda

MLG 135	69	297815	10147	249471	86.12	gii170517292 gb C P000970.1	5068389	238537	4.71	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 136	40	296530	23332	69120	24.27	gii291482254 emb FN668944.1	4178227	69030	1.65	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 137	19	289662	84104	0	0	0	-	0	0	0	Unknow
MLG 138	372	284760	18062	75162	26.65	gii526120653 gb C P006603.1	2145445	76598	3.57	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 139	8	284233	145963	184847	66.11	gii612150118 gb C P007546.1	4561905	191512	4.2	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 140	21	282022	165878	69652	25.2	gii47118322 dbj B A00016.3	3031430	67682	2.23	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 141	106	279586	16395	47799	17.42	gii325177128 emb FR824043.1	2356444	48773	2.07	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 142	133	276387	15322	106568	39.24	gii295054830 gb C P001918.1	531454	107794	2.03	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 143	46	274369	28030	251090	93.37	gii597512677 emb FO834906.1	5438894	265100	4.87	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 144	82	271583	18409	211848	81.72	gii440045023 gb C P003938.1	4762179	215074	4.52	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 145	19	268921	129286	17125	6.73	gii281177210 dbj A P009378.1	4717338	17124	0.36	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 146	37	259228	21534	15082	6.05	gii443901024 emb FO203355.1	5419609	15083	0.28	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 147	42	254524	47249	88514	35.78	gii392322800 gb C P003678.1	4968248	90359	1.82	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 148	40	249455	12788	243258	98.42	gii170517292 gb C P000970.1	5068389	246120	4.86	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 149	60	247401	21580	126754	51.72	gii682108593 gb C P008897.1	4633407	128585	2.78	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 150	21	247152	106940	32264	13.39	gii549807177 gb C P006721.1	5107814	33867	0.66	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 151	211	245063	18773	0	0	0	-	0	0	0	Unknow
MLG 152	131	240868	14085	6770	2.82	gii597512677 emb FO834906.1	5438894	6764	0.12	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 153	26	240511	28491	197888	84.19	gii334279325 dbj A P012053.1	2362241	190552	8.07	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 154	12	240186	175538	9781	4.32	gii527122546 gb C P003025.1	1975547	9901	0.5	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 155	33	235053	49078	48817	21.78	gii41584196 gb AE 017198.1	1992676	49600	2.49	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 156	102	226607	28294	7408	3.32	gii527122546 gb C P003025.1	1975547	7448	0.38	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 158	71	224141	20180	134291	60.49	gii338744031 emb FR873482.1	2210574	137812	6.23	375	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus salivarius
MLG 159	140	223453	12165	215561	98.24	gii478439721 gb C P004856.1	3427276	215854	6.3	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG 160	32	223130	147747	111450	51.61	gii392322800 gb C P003678.1	4968248	121483	2.45	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 161	54	222017	16909	198367	93.13	gii281177210 dbj A P009378.1	4717338	199398	4.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 162	43	219422	18200	3563	1.71	gii320455049 dbj A P010888.1	2385164	4625	0.19	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium longum

MLG 163	105	215947	19960	12865	6.24	gii188497817 gb C P001078.1	3659644	12571	0.34	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 164	22	213011	32134	115886	56.69	gii619734722 gb C P007557.1	5099034	122935	2.41	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 165	11	208456	47336	152285	76.69	gii329666391 gb C P002464.1	1966342	158813	8.08	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 166	129	206294	11832	189468	97.45	gii26111730 gb AE 014075.1	5231428	177720	3.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 168	19	204416	49969	169773	89.81	gii157065147 gb C P000802.1	4643538	168406	3.63	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 169	30	198579	34422	126542	67.32	gii68342549 gb CP 000076.1	7074893	128623	1.82	463	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas protegens
MLG 170	33	194416	33081	6638	3.54	gii110681940 gb C P000312.1	2897393	8329	0.29	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 171	58	190222	21516	109780	58.98	gii689262542 gb C P009451.1	4876443	110874	2.27	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 172	23	189040	29289	2568	1.38	gii549807177 gb C P006721.1	5107814	4954	0.1	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 173	114	187975	11399	36046	19.51	gii569535620 gb C P007025.1	4701875	36980	0.79	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 174	136	187254	9744	18270	99.16	gii478439721 gb C P004856.1	3427276	183549	5.36	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG 175	120	186143	12197	162206	89.02	gii150839411 gb C P000746.1	2319663	162083	6.99	1216	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Actinobacillus;s__Actinobacillus succinogenes
MLG 176	193	185772	10846	18058	9.98	gii253778933 emb FM162591.1	5064808	18043	0.36	306	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Photorhabdus;s__Photorhabdus asymbiotica
MLG 177	38	184722	27198	8846	4.92	gii451782877 gb C P004121.1	6530257	10475	0.16	35	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharoperbutylacetonicum
MLG 178	22	184249	24343	167316	93.38	gii325663854 gb C P002246.1	4552107	199683	4.39	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 179	90	182210	6812	153954	87.02	gii480474683 gb C P004142.1	5398151	157703	2.92	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG 180	9	180920	49432	45941	26.16	gii188497817 gb C P001078.1	3659644	45073	1.23	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 181	103	179730	21734	16804	9.62	gii41584196 gb AE 017198.1	1992676	17095	0.86	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 182	40	179185	14214	22670	13.07	gii686507741 gb C P006693.1	4574846	25724	0.56	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 183	34	176918	17381	77202	44.59	gii329666391 gb C P002464.1	1966342	79156	4.03	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 184	108	175604	9624	58433	33.85	gii118764602 dbj AP009256.1	2089645	59052	2.83	893	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium adolescentis
MLG 185	126	174631	18846	0	0	0	-	0	0	0	Unknown
MLG 186	8	173462	49469	39072	23.14	gii526120653 gb C P006603.1	2145445	39964	1.86	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 187	76	173139	20203	41957	25.13	gii325177128 emb FR824043.1	2356444	44015	1.87	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 188	41	172605	21143	0	0	0	-	0	0	0	Unknown
MLG 189	41	171047	8455	0	0	0	-	0	0	0	Unknown
MLG 191	30	168884	23999	52579	32.64	gii122087364 emb AM286415.1	4615899	58407	1.27	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica

MLG 192	60	16697 2	21064	15661 6	97.3	gii443901024[emb] FO203355.1]	54196 09	16523 1	3.05	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 193	293	16517 9	3699	89989	56.91	gii512154926[gb]C P006011.1]	19477 06	10632 2	5.46	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 194	222	16484 6	5026	0	0	0	-	0	0	0	Unknow
MLG 195	12	16226 3	54719	14200 9	91.51	gii343179174[dbj] AP009332.1]	19501 35	15080 5	7.73	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 196	28	16110 8	18720	93963	60.7	gii349736152[gb]C P003034.1]	53135 31	94377	1.78	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 197	22	16095 4	33623	17087	11.05	gii301318648[gb]C P002106.1]	20518 96	17864	0.87	885	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Coriobacteriales;f__Coriobacteriaceae;g__Olsenella;s__Olsenella uli
MLG 198	7	15811 2	55387	13654 6	89.06	gii402539130[gb]C P003785.1]	53867 05	14046 0	2.61	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 199	300	15607 2	1422	8388	5.51	gii28204652[gb]AE 015927.1]	27992 51	8207	0.29	43	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium tetani
MLG 200	40	15517 8	31235	13512 0	89.96	gii339277069[emb] FR875178.1]	19299 05	14850 3	7.69	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 201	13	15480 6	41574	0	0	0	-	0	0	0	Unknow
MLG 202	35	15462 3	13167	14455 3	98.23	gii342240345[emb] AL935263.2]	33082 73	16452 8	4.97	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 203	5	15332 4	55741	13530 4	93.44	gii512154926[gb]C P006011.1]	19477 06	14336 5	7.36	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 204	139	15210 6	10087	38919	27.62	gii308044682[gb]C P002222.1]	32543 76	39875	1.23	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 205	48	15019 7	13657	82051	58.53	gii526120653[gb]C P006603.1]	21454 45	89918	4.19	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 206	12	14830 1	42354	5195	3.75	gii187720473[gb]C P001056.1]	38003 27	5302	0.14	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 207	11	14716 2	32555	42639	31.4	gii334281572[dbj] AP012054.1]	21000 77	41307	1.97	368	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus pasteurianus
MLG 208	14	14480 3	10117 0	13091 8	96.81	gii307551844[gb]C P001671.1]	51313 97	13143 3	2.56	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 209	28	14090 4	31718	12278 2	91.59	gii222031834[emb] CU651637.1]	47731 08	77303	1.62	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 210	17	14019 5	21534	97591	73.05	gii334281572[dbj] AP012054.1]	21000 77	99103	4.72	368	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus pasteurianus
MLG 211	80	13851 9	8508	52180	39.42	gii315059226[gb]C P002185.1]	49009 68	53530	1.09	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 212	12	13578 8	51751	23004	17.4	gii288730948[emb] FN597254.1]	23509 11	26742	1.14	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 213	16	13522 5	36500	22074	16.72	gii527122546[gb]C P003025.1]	19755 47	22896	1.16	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 214	5	13405 7	40618	0	0	0	-	0	0	0	Unknow
MLG 215	10	13359 4	48642	0	0	0	-	0	0	0	Unknow
MLG 216	10	13238 0	49331	23553	18.22	gii326539903[gb]C P002582.1]	47142 37	23537	0.5	51	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Cellulosilyticum;s__Cellulosilyticum lentocellum
MLG 217	25	13221 0	25601	2172	1.71	gii329124738[gb]C P002410.1]	27731 57	2299	0.08	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 218	10	13205 8	82716	45674	36.1	gii365906294[gb]C P003218.1]	59741 09	46521	0.78	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca

MLG 220	14	131629	28709	9373	7.54	gii529202214 gb C P006620.1	2994661	13734	0.46	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG 221	210	129935	1480	116163	94.18	gii569535620 gb C P007025.1	4701875	113390	2.41	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 222	83	129295	22060	31477	25.86	gii582030173 gb C P006659.1	5435369	45230	0.83	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 223	117	126936	5379	91705	75.41	gii440045023 gb C P003938.1	4762179	92916	1.95	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 224	22	126520	26953	76821	64.1	gii514423830 gb C P006250.1	5328010	76972	1.44	278	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia plymuthica
MLG 225	5	125488	62462	86974	72.72	gii480474683 gb C P004142.1	5398151	87971	1.63	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 226	84	124302	4054	116681	98.26	gii573966439 gb C P006027.1	5585613	106125	1.9	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 227	26	123335	20511	90216	77.86	gii619734722 gb C P007557.1	5099034	91026	1.79	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 228	9	121725	33831	20070	17.53	gii552063405 gb C P006766.1	2589250	23716	0.92	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 229	8	121608	98257	97995	86.28	gii170517292 gb C P000970.1	5068389	96916	1.91	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 230	39	119850	10385	99784	87.93	gii170517292 gb C P000970.1	5068389	69240	1.37	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 231	77	119609	8051	73633	64.92	gii660567586 gb C P008788.1	6152190	81409	1.32	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella oxytoca
MLG 232	11	118745	33368	110354	98.53	gii612150118 gb C P007546.1	4561905	113967	2.5	9	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 233	10	115869	45008	55683	50.47	gii392334715 gb C P003504.1	2827741	55532	1.96	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus hirae
MLG 234	20	114467	20104	64019	58.81	gii480474683 gb C P004142.1	5398151	64182	1.19	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 235	12	113572	25560	59806	55.12	gii690347849 gb C P007646.1	1836297	63321	3.45	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 236	7	113484	36448	104825	97.04	gii472232670 dbj AP012167.1	2395134	106658	4.45	400	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus brevis
MLG 237	4	113426	50515	5355	4.99	gii229359445 emb AM181176.4	6722539	5356	0.08	317	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas fluorescens
MLG 238	17	111999	41936	67019	62.72	gii480474683 gb C P004142.1	5398151	70408	1.3	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 239	33	110331	13923	42725	40.71	gii674993598 dbj AP014630.1	4648418	41719	0.9	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 240	20	108855	15503	14941	14.32	gii674993598 dbj AP014630.1	4648418	15389	0.33	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 241	12	108502	41852	103166	100	gii219620149 gb C P001213.1	1933695	103329	5.34	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
MLG 242	22	108027	12034	0	0	0	-	0	0	0	Unknow
MLG 243	8	107228	36138	85213	82.78	gii480474683 gb C P004142.1	5398151	86180	1.6	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 244	20	106858	19578	27727	27.24	gii291548560 emb FP929055.1	3341681	27723	0.83	163	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__Blautia [Ruminococcus] torques
MLG 245	48	104939	9372	66408	65.26	gii526120653 gb C P006603.1	2145445	80254	3.74	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 246	22	104360	9772	42287	42	gii372283141 emb HE613569.1	2130034	44604	2.09	372	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus macedonicus

MLG 247	48	103166	14452	57556	57.18	gii528171613 gb C P006631.1	4915960	44170	0.9	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 248	7	103148	21021	65865	65.58	gii480474683 gb C P004142.1	5398151	62901	1.17	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 249	15	102935	28721	12855	12.82	gii372283141 emb HE613569.1	2130034	14179	0.67	372	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus macedonicus
MLG 250	31	101777	9982	68452	68.52	gii295054830 gb C P001918.1	5314581	66861	1.26	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 251	10	101754	22460	35917	36.02	gii282947233 emb FN543502.1	5346659	71568	1.34	266	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter rodentium
MLG 252	15	100676	57842	23915	24.26	gii692332123 gb C P009531.1	1926135	23851	1.24	233	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus sp. wkB8
MLG 253	6	100656	35650	16229	16.59	gii307551844 gb C P001671.1	5131397	16231	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 254	21	100427	12202	95913	99.94	gii448273020 gb C P004082.1	3203964	103497	3.23	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 255	36	100298	11422	4603	4.86	gii603129120 gb C P007332.1	4807994	4609	0.1	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 256	54	99906	14324	6895	7.28	gii160426828 gb C P000885.1	4847594	6896	0.14	110	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;s__Lachnoclostridium phytofermentans
MLG 257	9	99727	32207	91619	97.49	gii150953431 gb C P000647.1	5315120	93405	1.76	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 258	40	98561	9450	16565	17.66	gii150953431 gb C P000647.1	5315120	17576	0.33	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 259	13	97839	27476	19482	20.8	gii334279325 dbj AP012053.1	2362241	19528	0.83	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 260	10	95970	44147	0	0	0	-	0	0	0	Unknow
MLG 261	8	94766	31085	31274	33.62	gii394343076 gb C P003683.1	6097032	31969	0.52	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella oxytoca
MLG 262	33	94697	7739	36680	39.59	gii526120653 gb C P006603.1	2145445	49719	2.32	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 263	9	93975	47364	2344	2.54	gii662712225 gb C P008823.1	4852980	2346	0.05	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 264	9	93820	19620	0	0	0	-	0	0	0	Unknow
MLG 265	10	93671	28914	82414	92.38	gii257751862 dbj AP010953.1	5697240	81813	1.44	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 266	84	93446	4223	11361	12.75	gii219620149 gb C P001213.1	1933695	11631	0.6	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
MLG 268	11	93020	17334	3872	4.36	gii326539903 gb C P002582.1	4714237	3880	0.08	51	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Cellulosilyticum;s__Cellulosilyticum lentocellum
MLG 269	8	92660	35695	79092	89.18	gii26111730 gb AE 014075.1	5231428	79118	1.51	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 270	14	92240	15813	33919	38.34	gii343179174 dbj AP009332.1	1950135	33952	1.74	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 271	14	91552	15218	0	0	0	-	0	0	0	Unknow
MLG 272	14	89213	17599	54851	63.11	gii582030173 gb C P006659.1	5435369	60113	1.11	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 273	40	89102	9395	35213	40.59	gii690347849 gb C P007646.1	1836297	35207	1.92	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 274	48	88834	13188	0	0	0	-	0	0	0	Unknow

MLG 275	60	88710	7967	12810	14.99	gii660567586 gb C P008788.1	61521 90	12910	0.21	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 276	9	88692	40390	54326	64.19	gii343179174 dbj AP009332.1	19501 35	53542	2.75	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 277	70	88458	4410	6387	7.56	gii527122546 gb C P003025.1	19755 47	6620	0.34	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 278	24	87922	7255	42340	50.37	gii400173048 gb C P003737.1	47265 82	44601	0.94	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 279	8	86914	30152	6769	8.1	gii160361034 gb C P000884.1	67675 14	7703	0.11	1012	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__Delftia acidovorans
MLG 280	17	86750	36545	8620	10.33	gii549807177 gb C P006721.1	51078 14	10578	0.21	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 281	5	85925	43455	58327	70.72	gii349736152 gb C P003034.1	53135 31	63267	1.19	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 282	6	85449	31819	47247	57.4	gii148530277 gb C P000705.1	19996 18	50168	2.51	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 283	43	84631	8616	0	0	0	-	0	0	0	Unknow
MLG 284	8	84507	57907	32494	40.03	gii660567586 gb C P008788.1	61521 90	43493	0.71	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 285	19	84057	19841	27574	34.02	gii569535620 gb C P007025.1	47018 75	27624	0.59	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 287	36	83548	8017	3836	4.78	gii333109300 gb C P002743.1	23274 92	3833	0.16	895	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium breve
MLG 288	19	83485	28807	0	0	0	-	0	0	0	Unknow
MLG 289	7	82478	19302	0	0	0	-	0	0	0	Unknow
MLG 290	7	82307	29316	18619	23.37	gii571260215 emb HF571988.1	49401 99	18623	0.38	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 291	22	81897	6455	44551	55.96	gii671341910 gb C P007443.1	22032 22	45850	2.08	893	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium adolescentis
MLG 292	12	81182	20444	37111	46.8	gii480474683 gb C P004142.1	53981 51	37783	0.7	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 293	7	81052	35144	54925	69.63	gii343776783 gb C P002986.1	45444 77	55150	1.21	444	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;s__Stenotrophomonas maltophilia
MLG 294	5	80536	29033	11590	14.78	gii194405610 gb C P001120.1	48887 68	10909	0.22	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 295	9	80235	25136	28395	36.43	gii334279325 dbj AP012053.1	23622 41	26829	1.14	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 296	9	79901	36671	20525	26.34	gii145316543 gb C P000653.1	45187 12	20576	0.46	272	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. 638
MLG 297	139	79762	1321	4118	5.37	gii325205106 gb C P002423.1	22504 49	4118	0.18	522	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__Neisseria meningitidis
MLG 298	19	79663	9356	0	0	0	-	0	0	0	Unknow
MLG 299	33	79614	10021	18667	24.68	gii595583568 gb C P007265.1	47586 29	18978	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 300	32	79300	6743	27029	35.76	gii170517292 gb C P000970.1	50683 89	21487	0.42	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 301	48	78886	4595	70617	93.98	gii116098028 gb C P000416.1	22912 20	71541	3.12	400	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus brevis
MLG 303	9	78415	24006	8772	11.73	gii308746527 gb C P002272.1	48140 49	14421	0.3	8	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter lignolyticus

MLG 304	9	77948	24148	8812	11.81	gii343179174 dbj AP009332.1	1950135	8831	0.45	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 305	10	77912	18025	13345	17.9	gii288730948 emb FN597254.1	2350911	13554	0.58	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus galloyticus
MLG 306	5	76734	30576	14497	19.5	gii334281572 dbj AP012054.1	2100077	15230	0.73	368	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus pasteurianus
MLG 307	5	75713	29830	24032	32.5	gii662712225 gb C P008823.1	4852980	24022	0.49	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 308	5	75651	27775	60389	81.77	gii392322800 gb C P003678.1	4968248	64483	1.3	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 309	31	75580	10302	9287	12.58	gii374681091 gb C P003295.1	1988420	9284	0.47	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius
MLG 310	19	75143	6893	51994	70.5	gii682108593 gb C P008897.1	4633407	54190	1.17	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 311	39	75094	6134	14605	19.86	gii603299224 gb C P007421.1	4760449	14868	0.31	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 312	4	74767	31727	56888	78.11	gii157320013 gb C P000826.1	5448853	57612	1.06	282	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia proteamaculans
MLG 313	44	74605	9803	41433	56.95	gii440050501 gb C P003942.1	4858216	41692	0.86	16	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia marcescens
MLG 314	16	74542	20208	24706	34.33	gii647802220 gb C P008696.1	7122173	26459	0.37	325	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas chlororaphis
MLG 315	22	74359	17682	25276	35.33	gii527122546 gb C P003025.1	1975547	23831	1.21	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 316	23	73941	14161	46562	65.5	gii647802220 gb C P008696.1	7122173	43744	0.61	325	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas chlororaphis
MLG 317	9	73855	26093	5871	8.31	gii673531252 emb LK931336.1	4763704	5873	0.12	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter koseri
MLG 318	12	73819	29348	10343	14.68	gii612150118 gb C P007546.1	4561905	10339	0.23	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 319	64	73751	4350	0	0	0	-	0	0	0	Unknow
MLG 320	6	73557	47262	989	1.41	gii401794054 gb C P003747.1	5083176	1569	0.03	104	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__Bacillus cereus
MLG 322	23	72831	6578	56742	82.06	gii443419838 gb C P004009.1	4798435	57538	1.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 323	8	72757	24945	45203	65.44	gii660567586 gb C P008788.1	6152190	47673	0.77	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 324	76	71964	4766	61324	89.27	gii455418716 gb C P004345.1	3799539	68146	1.79	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__Morganella morganii
MLG 325	23	71538	17240	59349	87.16	gii339759707 gb C P002910.1	5259571	59415	1.13	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 326	42	71083	7634	50680	75.27	gii145316543 gb C P000653.1	4518712	53244	1.18	272	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. 638
MLG 327	7	70624	22962	15082	22.68	gii480474683 gb C P004142.1	5398151	15368	0.28	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG 328	5	70454	34121	0	0	0	-	0	0	0	Unknow
MLG 329	11	70381	26829	53685	81.81	gii440045023 gb C P003938.1	4762179	56646	1.19	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 330	55	70276	8639	63007	96.12	gii526120653 gb C P006603.1	2145445	71476	3.33	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 331	24	70086	14501	15675	24.02	gii619734722 gb C P007557.1	5099034	15676	0.31	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii

MLG 332	10	69143	20149	2368	3.64	gii374681091 gb C P003295.1	19884 20	2880	0.14	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius
MLG 333	12	69075	53342	33696	51.83	gii448273020 gb C P004082.1	32039 64	31192	0.97	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 335	18	68697	8354	21448	33.05	gii619734722 gb C P007557.1	50990 34	22257	0.44	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 336	6	68094	21564	64583	99.94	gii500236135 gb C P005958.1	20646 20	75685	3.67	414	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus fermentum
MLG 337	21	67335	14127	63644	98.78	gii569535620 gb C P007025.1	47018 75	64913	1.38	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 338	9	66508	14974	25255	39.29	gii326539903 gb C P002582.1	47142 37	28329	0.6	51	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Cellulosilyticum;s__Cellulosilyticum lentocellum
MLG 339	81	66472	4337	44660	69.48	gii148530277 gb C P000705.1	19996 18	48616	2.43	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 340	10	65619	14313	14832	23.1	gii218430358 emb C U928163.2	52020 90	14814	0.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 341	12	65551	31705	7600	11.84	gii187427012 gb C P001063.1	46159 97	8099	0.18	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella boydii
MLG 343	14	65253	12689	14846	23.27	gii116100249 gb C P000419.1	18563 68	20775	1.12	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 344	4	65128	35773	62017	97.96	gii374269796 emb HE616528.1	49885 04	78353	1.57	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 345	9	65009	36210	1767	2.81	gii329124738 gb C P002410.1	27731 57	1767	0.06	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 346	16	64988	16437	0	0	0	-	0	0	0	Unknow
MLG 347	13	64888	11154	15643	24.99	gii564116047 gb C P006731.1	43775 44	16922	0.39	271	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cronobacter;s__Cronobacter sakazakii
MLG 348	15	64625	7524	60582	96.98	gii349736152 gb C P003034.1	53135 31	51622	0.97	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 349	10	64430	16082	51384	82.41	gii392322800 gb C P003678.1	49682 48	54669	1.1	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 350	49	64283	5850	29463	47.3	gii110341805 gb C P000247.1	49389 20	32175	0.65	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 351	8	64281	22034	47755	76.82	gii595583568 gb C P007265.1	47586 29	60849	1.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 352	11	64208	16965	36187	58.63	gii365906294 gb C P003218.1	59741 09	35894	0.6	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella oxytoca
MLG 353	8	64165	13849	24445	39.61	gii582035815 gb C P004081.1	29610 43	28298	0.96	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
MLG 354	7	64054	35908	11780	19.12	gii218368405 emb C U928164.2	51320 68	11779	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 355	27	63809	22189	26498	43.65	gii329127738 gb C P002652.1	25063 01	29441	1.17	395	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus buchneri
MLG 356	13	63309	10167	17133	28.28	gii392322800 gb C P003678.1	49682 48	18071	0.36	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 357	59	62951	4846	22584	37.74	gii560171871 emb HG326223.1	51138 02	22911	0.45	16	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia marcescens
MLG 358	4	62877	33066	2550	4.32	gii451782877 gb C P004121.1	65302 57	2602	0.04	35	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharoperbutylacetonicum
MLG 359	4	62596	21029	54289	92.24	gii41584196 gb AE 017198.1	19926 76	55513	2.79	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 361	9	62466	14720	58223	99.5	gii308044682 gb C P002222.1	32543 76	58289	1.79	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum

MLG 362	4	62353	41278	1717	2.95	gi 647802220 gb C_P008696.1	7122173	1717	0.02	325	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadales;g__Pseudomonas;s__Pseudomonas chlororaphis
MLG 363	12	62284	11205	44465	76.45	gi 325663854 gb C_P002246.1	4552107	49217	1.08	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 364	3	62168	23151	3487	6	gi 595583568 gb C_P007265.1	4758629	3487	0.07	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 365	32	61725	8705	1223	2.11	gi 187720473 gb C_P001056.1	3800327	1223	0.03	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 366	18	61719	27334	4887	8.45	gi 218354981 emb CU928158.2	4588711	4925	0.11	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 367	18	61611	11780	1793	3.1	gi 189427298 gb C_P000605.1	2375792	2668	0.11	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium longum
MLG 368	14	60707	12971	3060	5.31	gi 122087364 emb AM286415.1	4615899	3039	0.07	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 369	12	60584	17782	1990	3.48	gi 549807177 gb C_P006721.1	5107814	3245	0.06	24	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium saccharobutylicum
MLG 370	16	59839	7989	55481	97.63	gi 312944605 gb C_P001855.1	4747819	55697	1.17	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 371	44	59039	6819	8562	15.1	gi 348600280 dbj AP012046.1	2562720	8568	0.33	209	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Tetragenococcus;s__Tetragenococcus halophilus
MLG 372	10	58857	25103	44751	79.65	gi 443419838 gb C_P004009.1	4798435	44744	0.93	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 375	15	58517	13961	7427	13.34	gi 334279325 dbj AP012053.1	2362241	7428	0.31	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 376	7	58513	11712	27501	49.39	gi 571260215 emb HF571988.1	4940199	27539	0.56	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 377	7	58295	32622	54837	98.6	gi 689262542 gb C_P009451.1	4876437	57329	1.18	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 378	15	58165	9535	26134	47.31	gi 121504137 gb C_P000538.1	1616554	28170	1.74	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteriaceae;g__Campylobacter;s__Campylobacter jejuni
MLG 379	10	58163	25353	6327	11.47	gi 157081501 gb C_P000822.1	4720462	6326	0.13	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter koseri
MLG 380	58	57973	7214	0	0	0	-	0	0	0	Unknow
MLG 381	4	57849	29656	2401	4.36	gi 187720473 gb C_P001056.1	3800327	2401	0.06	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 382	5	57759	33580	1862	3.4	gi 187720473 gb C_P001056.1	3800327	1862	0.05	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 383	18	57586	10702	19654	36.54	gi 695936535 gb C_P009578.1	4874804	19654	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 384	38	57252	10545	24482	45.83	gi 206564770 gb C_P000964.1	5641239	24718	0.44	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 385	5	56830	16522	52298	98.46	gi 218354981 emb CU928158.2	4588711	26587	0.58	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 386	12	56690	39897	8108	15.34	gi 283101593 gb C_P001750.1	2636367	8116	0.31	909	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium dentium
MLG 387	7	56188	25203	48854	92.61	gi 110341805 gb C_P000247.1	4938920	59949	1.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 388	69	56101	3629	49314	93.71	gi 582030173 gb C_P006659.1	5435369	52085	0.96	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 389	8	55865	23183	22516	43.05	gi 689257448 gb C_P009450.1	5489680	23470	0.43	11	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pluralibacter;s__Pluralibacter gergoviae
MLG 390	4	55694	33520	2398	4.59	gi 291482099 emb FN665652.1	4159517	1629	0.04	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile

MLG 391	35	55681	8397	17679	33.86	gii215263233 emb FM180568.1	4965553	17690	0.36	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 392	12	55616	11292	14824	28.47	gii334279325 dbj AP012053.1	2362241	14763	0.62	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 393	21	55240	10449	50683	97.51	gii334732565 gb C P002824.1	5280350	53712	1.02	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 394	20	55176	7239	11486	22.23	gii619734722 gb C P007557.1	5099034	11487	0.23	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 395	3	55138	30780	5619	10.96	gii400173048 gb C P003737.1	4726582	5618	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 396	47	55114	5813	40575	79.42	gii573932891 gb C P006262.1	5402276	41061	0.76	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 397	29	54767	7387	44950	88.26	gii29350190 gb AE 016830.1	3218031	49926	1.55	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
MLG 398	5	53783	23410	0	0	0	-	0	0	0	Unknow
MLG 399	12	53419	7726	3647	7.19	gii499527875 emb FO203501.1	5270770	2542	0.05	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 400	5	53117	21508	0	0	0	-	0	0	0	Unknow
MLG 401	9	52844	20464	5172	10.33	gii675818151 emb LK999983.1	1893946	5172	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 402	5	52751	29430	24157	49.27	gii662712225 gb C P008823.1	4852980	26054	0.54	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 404	3	52624	28568	23108	47.48	gii47232670 dbj AP012167.1	2395134	23812	0.99	400	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus brevis
MLG 405	10	52302	31579	16033	33.02	gii695172424 gb C P008929.1	5317001	18388	0.35	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 406	22	52237	22087	1248	2.59	gii485080253 gb C P002099.1	4791958	1243	0.03	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 407	13	52209	11412	46818	97.57	gii125496804 gb C P000387.1	2388435	47016	1.97	409	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus sanguinis
MLG 409	7	52063	24820	42809	89.84	gii269093698 gb C P001820.1	2132142	52515	2.46	91	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;s__Veillonella parvula
MLG 410	9	51976	10326	43173	91.18	gii218354981 emb CU928158.2	4588711	39947	0.87	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 411	4	51678	16255	34481	72.93	gii440045023 gb C P003938.1	4762179	35545	0.75	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 412	5	51286	21454	46678	99.59	gii334732565 gb C P002824.1	5280350	53162	1.01	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 413	5	51087	22876	46738	99.86	gii365906294 gb C P003218.1	5974109	54834	0.92	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 414	23	50930	5606	3280	7.02	gii295107714 emb FP929054.1	3757491	3434	0.09	721	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__[Ruminococcus] obeum
MLG 415	14	50780	10097	39189	84.05	gii145316543 gb C P000653.1	4518712	36355	0.8	272	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. 638
MLG 416	10	50752	11205	22677	48.7	gii397335222 gb C P003726.1	2987450	25202	0.84	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
MLG 418	4	50200	18313	36603	78.91	gii662712225 gb C P008823.1	4852980	35904	0.74	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 419	15	50085	9105	6043	13.14	gii372283141 emb HE613569.1	2130034	6733	0.32	372	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus macedonicus
MLG 420	23	49033	6292	45768	99.59	gii170517292 gb C P000970.1	5068389	45299	0.89	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

MLG 421	8	48894	17127	39344	86.06	gii571260215 emb HF571988.1	4940199	40502	0.82	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 422	13	48673	14325	0	0	0	-	0	0	0	Unknow
MLG 424	6	48554	14282	31042	70.1	gii253992019 gb C_P000094.2	6438405	30655	0.48	317	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas fluorescens
MLG 425	12	48109	20830	29967	67.91	gii689262542 gb C_P009451.1	4876443	33754	0.69	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 426	17	47982	5510	13271	30.21	gii145316543 gb C_P000653.1	4518712	13269	0.29	272	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. 638
MLG 427	14	47672	10658	0	0	0	-	0	0	0	Unknow
MLG 428	7	47649	20576	34235	78.4	gii150953431 gb C_P000647.1	5315120	34247	0.64	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 430	10	47350	8298	8972	20.62	gii664693170 gb C_P005998.1	4944397	8973	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 431	13	47278	8176	38628	88.81	gii440045023 gb C_P003938.1	4762179	38799	0.81	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 432	6	46869	35351	6535	15.12	gii291482100 emb FN665653.1	4047729	6977	0.17	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 433	61	46802	2039	607	1.41	gii392334715 gb C_P003504.1	2827741	1381	0.05	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococaceae;g__Enterococcus;s__Enterococcus hirae
MLG 434	7	46726	23800	6032	14.04	gii667688329 gb C_P007588.1	1355853	6032	0.44	457	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__Weissella ceti
MLG 435	10	46624	10450	17629	41.07	gii323272819 dbj AP012052.1	3982034	17802	0.45	956	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Microbacterium;s__Microbacterium testaceum
MLG 436	9	46564	8458	5249	12.25	gii478439721 gb C_P004856.1	3427276	5247	0.15	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG 437	20	46395	5574	4491	10.49	gii322506180 gb C_P001921.1	3940614	4491	0.11	552	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter baumannii
MLG 438	24	46387	7597	1254	2.94	gii343181122 dbj AP009333.1	1963964	1248	0.06	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 440	8	45980	22727	17930	42.11	gii281374316 gb C_P001834.1	2598144	18077	0.7	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococaceae;g__Lactococcus;s__Lactococcus lactis
MLG 441	7	45957	13483	18637	44.12	gii206564770 gb C_P000964.1	5641239	18683	0.33	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 442	13	45717	6483	14627	34.8	gii387159426 gb C_P003041.1	5962570	14614	0.25	317	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas fluorescens
MLG 443	11	45625	7396	7878	18.77	gii282947233 emb FN543502.1	5346659	7922	0.15	266	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter rodentium
MLG 444	23	45472	7666	498	1.19	gii300213939 gb C_P002034.1	1828169	498	0.03	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 446	21	44282	8880	21099	50.57	gii527122546 gb C_P003025.1	1975547	21100	1.07	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 447	26	44130	5658	11897	28.55	gii619734722 gb C_P007557.1	5099034	11898	0.23	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 448	4	43926	16159	25563	61.74	gii392322800 gb C_P003678.1	4968248	26024	0.52	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 449	73	43894	5789	4260	10.33	gii558607752 dbj AP013036.1	3022186	4261	0.14	153	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococaceae;g__Enterococcus;s__Enterococcus mundtii
MLG 450	3	43669	22574	5573	13.63	gii692326398 gb C_P009472.1	2398091	6029	0.25	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococaceae;g__Lactococcus;s__Lactococcus lactis
MLG 451	6	43634	12356	26199	64.21	gii222031834 emb CU651637.1	4773108	13651	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

MLG 452	8	43508	17821	10963	26.89	gii295095013 emb FP929040.1	4908759	11763	0.24	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 453	11	43496	11473	20642	50.98	gii619734722 gb C P007557.1	5099034	20800	0.41	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 454	52	43234	3873	37002	91.43	gii392334715 gb C P003504.1	2827741	38241	1.35	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus hirae
MLG 455	4	43053	25151	880	2.18	gii10681940 gb C P000312.1	2897393	880	0.03	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 457	24	42957	5004	18947	47.11	gii334279325 db j AP012053.1	2362241	19036	0.81	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 458	25	42926	3925	19079	47.65	gii445187230 gb C P004063.1	2635572	19815	0.75	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG 459	15	42849	7969	33590	83.9	gii440045023 gb C P003938.1	4762179	34998	0.73	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 460	6	42806	16507	28655	72.38	gii569535620 gb C P007025.1	4701875	24260	0.52	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 463	12	42669	11021	0	0	0	-	0	0	0	Unknow
MLG 464	8	42607	8252	8138	20.82	gii122087364 emb AM286415.1	4615899	8139	0.18	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 465	18	42579	19944	37825	97.05	gii571260215 emb HF571988.1	4940199	41487	0.84	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 466	11	42239	9461	0	0	0	-	0	0	0	Unknow
MLG 467	5	42037	13389	3964	10.23	gii291482099 emb FN665652.1	4159517	3807	0.09	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 468	4	41977	23216	21600	56.2	gii552063405 gb C P006766.1	2589250	34323	1.33	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 469	13	41929	6109	15129	39.4	gii662706586 gb C P008841.1	5865090	16428	0.28	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 470	7	41752	24827	33838	88.85	gii307625127 gb C P002167.1	4993013	26169	0.52	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 471	15	41723	12953	31175	81.87	gii116100249 gb C P000419.1	1856368	31160	1.68	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 472	6	41678	21447	0	0	0	-	0	0	0	Unknow
MLG 473	12	41402	22731	31727	84.06	gii619734722 gb C P007557.1	5099034	32960	0.65	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 474	16	41236	6205	18715	49.73	gii218363708 emb CU928161.2	5032268	29470	0.59	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 477	20	40874	14577	37143	99.96	gii400173048 gb C P003737.1	4726582	37141	0.79	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 478	5	40801	14942	5323	14.34	gii158967071 gb C P000033.3	1993560	6344	0.32	212	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus acidophilus
MLG 479	25	40770	6152	20347	55.06	gii206564770 gb C P000964.1	5641239	21876	0.39	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 480	6	40487	10115	21922	59.6	gii326405597 gb C P002365.1	2399458	22798	0.95	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 481	25	40469	4214	1006	2.75	gii527122546 gb C P003025.1	1975547	2656	0.13	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 482	19	40423	13898	18485	50.7	gii571260215 emb HF571988.1	4940199	18483	0.37	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 483	12	40285	24472	12363	34.12	gii554510692 gb C P006784.1	5129938	11129	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

MLG 484	9	40219	13292	35995	99.77	gii124491690 emb AM406671.1	2529478	37013	1.46	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 486	9	40043	11659	12757	35.74	gii660567586 gb C P008788.1	6152190	12822	0.21	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 487	7	40035	10687	33843	95.09	gii254044096 gb C P001617.1	3197759	34621	1.08	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 488	4	39590	24731	18424	52.27	gii512154926 gb C P006011.1	1947706	16934	0.87	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 489	7	39304	14716	3855	10.94	gii188497817 gb C P001078.1	3659644	3996	0.11	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 490	7	39231	12762	1064	3.03	gii480474683 gb C P004142.1	5398151	1058	0.02	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG 491	3	39164	13280	2192	6.25	gii312944605 gb C P001855.1	4747819	2193	0.05	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 492	12	39091	6446	7161	20.61	gii674993598 dbj AP014630.1	4648418	7296	0.16	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 493	7	38973	12069	34683	100	gii569535620 gb C P007025.1	4701875	35604	0.76	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 494	5	38771	23072	22888	66.26	gii339759707 gb C P002910.1	5259571	24341	0.46	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 495	51	38751	3445	15077	43.67	gii672605233 gb C P006704.1	6062703	15609	0.26	1008	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Comamonas;s__Comamonas testosteroni
MLG 496	12	38435	9745	27876	80.89	gii554510692 gb C P006784.1	5129938	18787	0.37	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 498	5	38399	11512	18842	54.89	gii353737348 gb C P002644.1	2183059	22642	1.04	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 499	5	38085	12728	29675	87.12	gii110341805 gb C P000247.1	4938920	30419	0.62	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 500	7	38079	11590	20511	60.69	gii667688329 gb C P007588.1	1355853	18012	1.33	457	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__Weissella ceti
MLG 501	7	38038	9212	33728	99.95	gii455418716 gb C P004345.1	3799539	34176	0.9	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganelle;s__Morganelle morgani
MLG 502	11	37744	14808	3335	9.91	gii47118322 dbj B A000016.3	3031430	3335	0.11	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 503	3	37634	13333	15156	45.06	gii682108593 gb C P008897.1	4633407	16480	0.36	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 504	5	37357	10084	32845	98.36	gii169887498 gb C P000948.1	4686137	33749	0.72	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 505	12	37271	8750	18484	55.84	gii218359353 emb CU928160.2	4700560	18487	0.39	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 506	4	37158	17721	0	0	0	-	0	0	0	Unknow
MLG 507	31	37115	6473	0	0	0	-	0	0	0	Unknow
MLG 508	10	36952	6272	20475	63.97	gii122087364 emb AM286415.1	4615899	21999	0.48	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 509	23	36784	7458	28357	88.77	gii394343076 gb C P003683.1	6097032	28425	0.47	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 511	11	36541	20478	2251	7.16	gii188497817 gb C P001078.1	3659644	2311	0.06	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 512	9	36459	7664	23758	75.81	gii674993598 dbj AP014630.1	4648418	23664	0.51	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 513	3	36239	21221	6980	22.4	gii374681091 gb C P003295.1	1988420	6978	0.35	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius

MLG 514	8	36079	18317	14546	46.74	gii49529273[emb]C R543861.1	3598621	14547	0.4	410	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter sp. ADP1
MLG 515	5	35715	12497	0	0	0	-	0	0	0	Unknow
MLG 516	14	35698	5394	7804	25.22	gii696593549[gb]C P009565.1	4726694	7800	0.17	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 517	12	35592	6162	9844	31.88	gii569535620[gb]C P007025.1	4701875	10125	0.22	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 519	7	35246	23374	26120	86.74	gii612150118[gb]C P007546.1	4561905	29129	0.64	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 520	17	35238	11302	3649	12.35	gii295092884[emb]FP929039.1	3123007	3658	0.12	1281	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coprococcus;s__Coprococcus sp. ART55/1
MLG 521	6	35143	13088	0	0	0	-	0	0	0	Unknow
MLG 522	10	35060	14219	10606	36.55	gii365906294[gb]C P003218.1	5974109	11271	0.19	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 525	8	34748	5899	24506	85.99	gii308746527[gb]C P002272.1	4814049	26190	0.54	8	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter lignolyticus
MLG 526	4	34683	11777	8098	28.96	gii257751862[dbj]AP010953.1	5697240	8629	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 527	5	34542	15391	27671	100	gii209157093[gb]C P001164.1	5572075	27681	0.5	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 528	8	34527	9232	13700	49.8	gii218354981[emb]CU928158.2	4588711	14478	0.32	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 529	7	34460	15378	7575	27.73	gii122087364[emb]AM286415.1	4615899	7557	0.16	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 531	13	34359	6585	8104	29.84	gii329666391[gb]C P002464.1	1966342	9889	0.5	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 532	5	34326	21301	8206	30.34	gii569535620[gb]C P007025.1	4701875	8196	0.17	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 533	8	34063	12714	750	2.78	gii329666391[gb]C P002464.1	1966342	702	0.04	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 534	5	33799	11415	1545	5.77	gii426265132[gb]C P003880.1	6183388	1600	0.03	336	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas sp. UW4
MLG 535	13	33745	5432	26595	99.39	gii290760697[gb]C P001846.1	5386352	26808	0.5	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 536	16	33645	6088	6503	24.49	gii527122546[gb]C P003025.1	1975547	6178	0.31	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 537	5	33633	10967	17770	67.12	gii392334715[gb]C P003504.1	2827741	23073	0.82	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus hirae
MLG 538	8	33393	8058	24792	93.87	gii689262542[gb]C P009451.1	4876443	22359	0.46	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 540	4	33101	18484	1436	5.52	gii157081501[gb]C P000822.1	4720462	1436	0.03	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter koseri
MLG 543	5	32448	16075	9100	35.49	gii612150118[gb]C P007546.1	4561905	10156	0.22	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 544	9	32263	11251	264	1.03	gii187720473[gb]C P001056.1	3800327	264	0.01	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 545	7	32007	9013	23080	90.18	gii394343076[gb]C P003683.1	6097032	21942	0.36	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 547	5	31945	8337	24656	97.22	gii115511419[gb]C P000468.1	5082025	24655	0.49	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 549	5	31870	13848	8801	34.81	gii600567586[gb]C P008788.1	6152190	9350	0.15	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca

MLG 550	25	31458	2561	0	0	0	-	0	0	0	Unknown
MLG 551	11	31338	6910	22611	91.78	gii325663854 gb C P002246.1	4552107	26342	0.58	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 552	6	31167	12499	672	2.73	gii343179174 dbj AP009332.1	1950135	672	0.03	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 554	7	31121	7466	8676	35.74	gii619734722 gb C P007557.1	5099034	9038	0.18	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 555	9	31041	5570	14097	58.18	gii526120653 gb C P006603.1	2145445	15443	0.72	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 556	5	30946	12783	15413	63.77	gii660550561 gb C P008700.1	5365144	15813	0.29	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 557	7	30875	8239	10704	44.39	gii115511419 gb C P000468.1	5082025	12497	0.25	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 558	5	30457	9141	5074	21.24	gii32263428 gb AE 017125.1	1799146	5067	0.28	645	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Helicobacteriaceae;g__Helicobacter;s__Helicobacter hepaticus
MLG 562	9	30112	15944	10901	46.18	gii619734722 gb C P007557.1	5099034	10890	0.21	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter er;s__Citrobacter freundii
MLG 564	4	29553	11685	8333	35.51	gii334279325 dbj AP012053.1	2362241	14193	0.6	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 565	14	29025	5947	22737	97.6	gii209910450 dbj AP009240.1	4887515	23022	0.47	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 566	24	29017	2436	11078	47.85	gii291482100 emb FN665653.1	4047729	11649	0.29	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 567	19	28852	7386	20082	86.98	gii480474683 gb C P004142.1	5398151	20085	0.37	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 569	3	28560	13897	10300	44.93	gii118764602 dbj AP009256.1	2089645	10302	0.49	893	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium adolescentis
MLG 570	13	28498	5787	0	0	0	-	0	0	0	Unknown
MLG 573	5	27960	11940	542	2.44	gii338853710 gb C P002899.1	1422478	542	0.04	403	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__Weissella korensis
MLG 575	3	27671	15609	5993	27.83	gii378937014 gb C P003351.1	2955294	10337	0.35	165	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
MLG 577	6	27512	13059	620832	97.03	gii121504137 gb C P000538.1	1616554	623243	38.55	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteriaceae;g__Campylobacter;s__Campylobacter jejuni
MLG 578	7	27313	5459	377361	77.04	gii690347849 gb C P007646.1	1836297	409956	22.33	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 579	5	27288	9093	189339	54.17	gii341821300 emb HE576794.1	2474718	191199	7.73	651	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;s__Megasphaera elsdenii
MLG 580	21	27157	6278	0	0	0	-	0	0	0	Unknown
MLG 581	5	27050	9964	171509	83.42	gii329666391 gb C P002464.1	1966342	175286	8.91	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 582	6	26982	14331	59136	34.72	gii527122546 gb C P003025.1	1975547	58491	2.96	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 583	3	26797	11640	44831	31.35	gii332341332 gb C P002729.1	5186416	44488	0.86	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 584	5	26758	8080	0	0	0	-	0	0	0	Unknown
MLG 587	8	26555	8778	0	0	0	-	0	0	0	Unknown
MLG 588	25	26473	4469	0	0	0	-	0	0	0	Unknown

MLG 589	6	26411	7231	0	0	0	-	0	0	0	Unknown
MLG 590	4	26408	13915	64494	69.32	gii440045023 gb C P003938.1	4762179	65299	1.37	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 591	4	26020	12387	5396	6.44	gii662712225 gb C P008823.1	4852980	5894	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 592	15	25880	5361	55560	67.46	gii569550235 gb C P003999.1	5307003	34691	0.65	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 593	11	25833	5055	0	0	0	-	0	0	0	Unknown
MLG 595	12	25642	3736	18397	23.84	gii383101383 gb C P002291.1	4935294	27974	0.57	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 596	10	25621	12064	0	0	0	-	0	0	0	Unknown
MLG 597	6	25593	7296	45167	61.51	gii116094265 gb C P000413.1	1894360	64978	3.43	384	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus gasseri
MLG 598	4	25485	11916	0	0	0	-	0	0	0	Unknown
MLG 599	4	25360	14167	64152	95.44	gii356601232 gb C P002797.2	4971461	33807	0.68	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 600	4	25317	9517	44000	66.59	gii695172424 gb C P008929.1	5317001	36670	0.69	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 601	4	25280	8801	3002	4.65	gii169752989 gb C P000946.1	4746218	5141	0.11	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 602	17	25042	5061	30870	49.36	gii365906294 gb C P003218.1	5974109	31062	0.52	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 603	6	24635	6260	1488	2.4	gii603129120 gb C P007332.1	4807994	1488	0.03	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 604	13	24585	8348	42396	72.11	gii582030173 gb C P006659.1	5435369	44612	0.82	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 606	5	24382	7209	18078	31.49	gii339759707 gb C P002910.1	5259571	18992	0.36	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 609	6	24275	8175	3502	6.36	gii675820319 emb LM996882.1	1086344	3491	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 610	5	24229	9882	0	0	0	-	0	0	0	Unknown
MLG 611	14	24171	8749	22115	41.03	gii660577155 gb C P008797.1	5396164	24904	0.46	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 612	3	24113	10704	0	0	0	-	0	0	0	Unknown
MLG 614	19	23889	10139	0	0	0	-	0	0	0	Unknown
MLG 616	5	23805	8927	19489	37.95	gii341821300 emb HE576794.1	2474718	19496	0.79	651	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;s__Megasphaera elsdenii
MLG 617	5	23723	11197	50667	99.5	gii569535620 gb C P007025.1	4701875	53428	1.14	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 618	6	23637	11255	849	1.68	gii121504137 gb C P000538.1	1616554	857	0.05	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteraceae;g__Campylobacter;s__Campylobacter jejuni
MLG 619	5	23606	7663	0	0	0	-	0	0	0	Unknown
MLG 621	10	23493	6953	32360	66.78	gii640845263 gb C P007727.1	5395263	52965	0.98	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
MLG 622	9	23469	6852	27322	57.16	gii251817111 emb FM252032.1	2146229	30349	1.41	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis

MLG 624	8	23297	7889	10410	22.53	gi 282947233 emb FN543502.1	5346659	10394	0.19	266	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter rodentium
MLG 625	20	23152	10141	20225	43.99	gi 156530483 gb C P000783.1	4368373	20223	0.46	271	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cronobacter;s__Cronobacter sakazakii
MLG 627	4	23087	7763	0	0	0	-	0	0	0	Unknow
MLG 628	6	23071	6865	0	0	0	-	0	0	0	Unknow
MLG 629	5	22924	9205	11652	26.04	gi 284919779 emb FN554766.1	5241977	17357	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 630	8	22884	4306	23033	51.49	gi 597512677 emb FO834906.1	5438894	25138	0.46	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 632	26	22678	2599	5728	13.04	gi 595607150 gb C P007394.1	5090442	6137	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 633	9	22318	3695	0	0	0	-	0	0	0	Unknow
MLG 636	10	22197	4418	17866	41.84	gi 281374316 gb C P001834.1	2598144	20109	0.77	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 638	14	21751	4336	1448	3.51	gi 569535620 gb C P007025.1	4701875	1448	0.03	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 643	11	21531	4751	32399	81.39	gi 170517292 gb C P000970.1	5068389	35008	0.69	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 645	12	21254	4729	0	0	0	-	0	0	0	Unknow
MLG 108	127	639830	15850	620832	97.03	gi 121504137 gb C P000538.1	1616554	623243	38.55	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteraceae;g__Campylobacter;s__Campylobacter jejuni
MLG 126	11	489826	176856	377361	77.04	gi 690347849 gb C P007646.1	1836297	409956	22.33	192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus salivarius
MLG 157	3	349534	255034	189339	54.17	gi 341821300 emb HE576794.1	2474718	191199	7.73	651	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;s__Megasphaera elsdenii
MLG 167	2	236553	224182	0	0	0	-	0	0	0	Unknow
MLG 190	4	205603	80041	171509	83.42	gi 329666391 gb C P002464.1	1966342	175286	8.91	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 219	3	170347	68574	59136	34.72	gi 527122546 gb C P003025.1	1975547	58491	2.96	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 267	4	143020	55932	44831	31.35	gi 332341332 gb C P002729.1	5186416	44488	0.86	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 286	4	135485	59457	0	0	0	-	0	0	0	Unknow
MLG 585	16	131826	40354	0	0	0	-	0	0	0	Unknow
MLG 586	3	118269	106067	0	0	0	-	0	0	0	Unknow
MLG 302	3	106676	71264	0	0	0	-	0	0	0	Unknow
MLG 321	2	100268	96525	0	0	0	-	0	0	0	Unknow
MLG 334	4	99838	47975	0	0	0	-	0	0	0	Unknow
MLG 342	18	93044	12419	64494	69.32	gi 440045023 gb C P003938.1	4762179	65299	1.37	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 360	2	83764	77679	5396	6.44	gi 662712225 gb C P008823.1	4852980	5894	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae

MLG 373	2	82364	78819	55560	67.46	gii569550235 gb C P003999.1	5307003	34691	0.65	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 374	5	80581	46682	0	0	0	-	0	0	0	Unknow
MLG 594	2	78099	39448	0	0	0	-	0	0	0	Unknow
MLG 403	3	77176	41828	18397	23.84	gii383101383 gb C P002291.1	4935294	27974	0.57	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 408	4	74369	26898	0	0	0	-	0	0	0	Unknow
MLG 417	3	73436	67087	45167	61.51	gii116094265 gb C P000413.1	1894360	64978	3.43	384	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus gasserii
MLG 423	5	68926	27767	0	0	0	-	0	0	0	Unknow
MLG 429	2	67215	33856	64152	95.44	gii356601232 gb C P002797.2	4971461	33807	0.68	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 439	3	66072	35463	44000	66.59	gii695172424 gb C P008929.1	5317001	36670	0.69	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 445	2	64529	61426	3002	4.65	gii169752989 gb C P000946.1	4746218	5141	0.11	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 456	3	62544	38821	30870	49.36	gii365906294 gb C P003218.1	5974109	31062	0.52	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 461	2	61896	59655	1488	2.4	gii603129120 gb C P007332.1	4807994	1488	0.03	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 462	2	58793	35078	42396	72.11	gii582030173 gb C P006659.1	5435369	44612	0.82	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 605	2	58620	34688	0	0	0	-	0	0	0	Unknow
MLG 475	3	57415	31061	18078	31.49	gii339759707 gb C P002910.1	5259571	18992	0.36	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 607	3	56264	42056	12767	22.69	gii365906294 gb C P003218.1	5974109	12864	0.22	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 608	2	55962	41016	0	0	0	-	0	0	0	Unknow
MLG 476	3	55055	32945	3502	6.36	gii675820319 emb LM996882.1	1086344	3491	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 485	2	54538	48232	0	0	0	-	0	0	0	Unknow
MLG 497	3	53898	45217	22115	41.03	gii660577155 gb C P008797.1	5396164	24904	0.46	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 510	2	53850	29984	0	0	0	-	0	0	0	Unknow
MLG 613	12	52698	8150	48733	92.48	gii122087364 emb AM286415.1	4615899	65400	1.42	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 518	2	52095	40224	0	0	0	-	0	0	0	Unknow
MLG 615	2	51620	50977	0	0	0	-	0	0	0	Unknow
MLG 523	7	51348	13059	19489	37.95	gii341821300 emb HE576794.1	2474718	19496	0.79	651	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;s__Megasphaera elsdenii
MLG 524	3	50922	29231	50667	99.5	gii569535620 gb C P007025.1	4701875	53428	1.14	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 530	17	50565	15406	849	1.68	gii121504137 gb C P000538.1	1616554	857	0.05	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteraceae;g__Campylobacter;s__Campylobacter jejuni

MLG 539	5	50292	16569	0	0	0	-	0	0	0	Unknown
MLG 620	3	48655	41474	48353	99.38	gii526120653 gb C P006603.1	21454 45	55793	2.6	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 541	2	48460	37279	32360	66.78	gii640845263 gb C P007727.1	53952 63	52965	0.98	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 542	2	47800	26010	27322	57.16	gii251817111 emb FM252032.1	21462 29	30349	1.41	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 623	15	47744	16154	5005	10.48	gii408667903 gb C P003871.2	16352 52	5277	0.32	98	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Campylobacteraceae;g__Campylobacter;s__Campylobacter jejuni
MLG 546	5	46214	18029	10410	22.53	gii282947233 emb FN543502.1	53466 59	10394	0.19	266	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter rodentium
MLG 548	2	45973	35762	20225	43.99	gii156530483 gb C P000783.1	43683 73	20223	0.46	271	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cronobacter;s__Cronobacter sakazakii
MLG 626	2	45775	28398	45775	100	gii110341805 gb C P000247.1	49389 20	48381	0.98	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 553	2	45351	38956	0	0	0	-	0	0	0	Unknown
MLG 559	3	45189	31048	0	0	0	-	0	0	0	Unknown
MLG 560	2	44741	23285	11652	26.04	gii284919779 emb FN54766.1	52419 77	17357	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 561	2	44733	25195	23033	51.49	gii597512677 emb FO834906.1	54388 94	25138	0.46	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 631	3	44203	28349	28357	64.15	gii674133359 gb C P009208.1	53748 34	28399	0.53	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 563	4	43925	18920	5728	13.04	gii595607150 gb C P007394.1	50904 42	6137	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 568	2	43754	42067	0	0	0	-	0	0	0	Unknown
MLG 634	2	42988	42303	685	1.59	gii526125113 gb C P006608.1	46835 51	685	0.01	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
MLG 635	3	42744	39109	22741	53.2	gii660567586 gb C P008788.1	61521 90	23396	0.38	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella oxytoca
MLG 571	6	42700	29991	17866	41.84	gii281374316 gb C P001834.1	25981 44	20109	0.77	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 637	6	41970	33468	23022	54.85	gii675819096 emb LM995659.1	12361 24	23019	1.86	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 572	2	41204	38043	1448	3.51	gii569535620 gb C P007025.1	47018 75	1448	0.03	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 639	10	41161	7205	14758	35.85	gii537637238 gb C P003909.1	22336 40	16493	0.74	1170	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__Neisseria gonorrhoeae
MLG 640	5	41138	17839	0	0	0	-	0	0	0	Unknown
MLG 641	3	40793	36371	14692	36.02	gii443419838 gb C P004009.1	47984 35	24705	0.51	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 642	7	40054	20129	24269	60.59	gii666899293 gb C P008921.1	22923 60	42898	1.87	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 574	2	39806	30738	32399	81.39	gii170517292 gb C P000970.1	50683 89	35008	0.69	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 644	2	39505	25311	23199	58.72	gii407051884 gb C P003289.1	52730 97	29111	0.55	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 576	2	39376	34303	0	0	0	-	0	0	0	Unknown

MLG 646	5	38589	12678	0	0	0	-	0	0	0	Unknow
MLG 647	2	38573	29271	0	0	0	-	0	0	0	Unknow
MLG 648	3	38408	26397	23344	60.78	gii601101465 gb C P007505.1	48644 10	23336	0.48	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 649	2	37616	28444	19761	52.53	gii657146798 gb C P006692.1	43945 00	21096	0.48	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
MLG 650	5	37290	14064	0	0	0	-	0	0	0	Unknow
MLG 651	3	37207	19854	0	0	0	-	0	0	0	Unknow
MLG 652	2	37142	26645	17639	47.49	gii290760697 gb C P001846.1	53863 52	17624	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 653	2	36939	19873	12462	33.74	gii480474683 gb C P004142.1	53981 51	12548	0.23	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 654	2	36660	29599	0	0	0	-	0	0	0	Unknow
MLG 655	3	36461	18814	0	0	0	-	0	0	0	Unknow
MLG 656	5	36434	23181	7458	20.47	gii339759707 gb C P002910.1	52595 71	7669	0.15	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 657	2	35493	33315	35493	100	gii334732565 gb C P002824.1	52803 50	35656	0.68	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 658	2	35448	19562	0	0	0	-	0	0	0	Unknow
MLG 659	2	35366	22247	33527	94.8	gii595597955 gb C P007392.1	50545 09	33728	0.67	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 660	2	35124	19554	0	0	0	-	0	0	0	Unknow
MLG 661	2	35016	33743	20011	57.15	gii595620023 gb C P006918.1	52933 01	20029	0.38	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 662	12	34962	17071	23034	65.88	gii291482100 emb FN665653.1	40477 29	24213	0.6	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile
MLG 663	2	34603	29495	29495	85.24	gii392334715 gb C P003504.1	28277 41	30007	1.06	108	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus hirae
MLG 664	3	34423	20560	0	0	0	-	0	0	0	Unknow
MLG 665	33	34304	3403	0	0	0	-	0	0	0	Unknow
MLG 666	2	34004	31927	32087	94.36	gii315059226 gb C P002185.1	49009 68	30561	0.62	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 667	2	33652	27162	23030	68.44	gii315059226 gb C P002185.1	49009 68	23021	0.47	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 668	2	33384	31333	17840	53.44	gii115511419 gb C P000468.1	50820 25	17860	0.35	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 669	8	33324	8027	0	0	0	-	0	0	0	Unknow
MLG 670	2	33252	18982	29848	89.76	gii443419838 gb C P004009.1	47984 35	37024	0.77	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 671	2	33109	26915	0	0	0	-	0	0	0	Unknow
MLG 672	4	33015	23420	31665	95.91	gii284919779 emb FN554766.1	52419 77	31665	0.6	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

MLG 673	3	32780	12866	30729	93.74	gii215263233 emb FM180568.1	4965553	31024	0.62	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 674	5	32020	8380	31717	99.05	gii295089810 emb FP929037.1	3769775	31713	0.84	843	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;s__Clostridium)saccharolyticum
MLG 675	3	32000	20895	5042	15.76	gii671341910 gb C P007443.1	2203222	5341	0.24	893	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium adolescentis
MLG 676	2	31874	23454	29736	93.29	gii365906294 gb C P003218.1	5974109	29937	0.5	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 677	4	31548	15201	27738	87.92	gii527122546 gb C P003025.1	1975547	27730	1.4	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 678	3	31463	20927	342	1.09	gii589630713 gb C P001220.2	5373644	342	0.01	1008	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Comamonas;s__Comamonas testosteroni
MLG 679	2	31155	28291	20403	65.49	gii345283481 gb C P003032.1	2066652	20350	0.98	370	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus ruminis
MLG 680	2	30951	22962	24677	79.73	gii323128316 gb C P002487.1	4878013	24842	0.51	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 681	2	30929	23597	0	0	0	-	0	0	0	Unknow
MLG 682	2	30544	20300	30048	98.38	gii218368405 emb C U928164.2	5132068	30482	0.59	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 683	2	30437	22016	3076	10.11	gii573019581 gb C P006569.1	4709528	3079	0.07	302	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Sodalis;s__Sodalis sp. HS1
MLG 684	2	30417	29648	18557	61.01	gii374681091 gb C P003295.1	1988420	18736	0.94	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius
MLG 685	3	30416	24766	923	3.03	gii455418716 gb C P004345.1	3799539	919	0.02	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganelle;s__Morganelle morganii
MLG 686	5	30404	28155	383	1.26	gii326539903 gb C P002582.1	4714237	383	0.01	51	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Cellulosilyticum;s__Cellulosilyticum lentocellum
MLG 687	2	30398	22520	7314	24.06	gii571260215 emb HF571988.1	4940199	8376	0.17	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 688	5	30313	16252	30306	99.98	gii402539130 gb C P003785.1	5386705	29907	0.56	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 689	3	29794	11637	0	0	0	-	0	0	0	Unknow
MLG 690	5	29672	11339	24072	81.13	gii218430358 emb C U928163.2	5202090	16631	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 691	2	29397	24502	24784	84.31	gii374269796 emb HE616528.1	4988504	22486	0.45	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 692	2	29141	16069	29118	99.92	gii170517292 gb C P000970.1	5068389	23555	0.46	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 693	12	28983	5869	8577	29.59	gii526120653 gb C P006603.1	2145445	10156	0.47	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 694	2	28764	23722	28623	99.51	gii218368405 emb C U928164.2	5132068	29893	0.58	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 695	4	28688	11661	12233	42.64	gii194405610 gb C P001120.1	4888768	12243	0.25	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 696	10	28451	18337	7209	25.34	gii584454940 emb HG917868.1	2917864	7215	0.25	36	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium sp. M2/40
MLG 697	8	28400	6580	0	0	0	-	0	0	0	Unknow
MLG 698	3	28284	13557	11810	41.76	gii612156087 gb C P004887.1	5914407	11967	0.2	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 699	2	28072	20303	25192	89.74	gii295095013 emb FP929040.1	4908759	25186	0.51	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae

MLG 700	15	27995	5435	0	0	0	-	0	0	0	Unknown
MLG 701	2	27733	25699	19805	71.41	gii315059226 gb C P002185.1	49009 68	19807	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 702	2	27724	19292	0	0	0	-	0	0	0	Unknown
MLG 703	2	27672	21437	2561	9.25	gii84778498 dbj A P008232.1	41711 46	2705	0.06	304	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Sodalis;s__Sodalis glossinidius
MLG 704	2	27543	14945	0	0	0	-	0	0	0	Unknown
MLG 705	2	27391	26360	0	0	0	-	0	0	0	Unknown
MLG 706	6	27148	8214	15711	57.87	gii170517292 gb C P000970.1	50683 89	15711	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 707	2	27077	25915	19460	71.87	gii409033099 gb C P001600.2	38123 01	20014	0.52	297	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Edwardsiella;s__Edwardsiella ictaluri
MLG 708	2	26938	19571	18613	69.1	gii595583568 gb C P007265.1	47586 29	13633	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 709	2	26664	25082	26664	100	gii157076741 gb C P000800.1	49796 19	26658	0.54	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 710	3	26632	17056	14963	56.18	gii526125113 gb C P006608.1	46835 51	15086	0.32	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
MLG 711	3	26272	12467	22056	83.95	gii605511148 gb C P007530.1	46943 75	16108	0.34	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 712	2	26188	25634	26089	99.62	gii394343076 gb C P003683.1	60970 32	29840	0.49	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 713	3	26043	13788	18734	71.93	gii612150118 gb C P007546.1	45619 05	18730	0.41	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 714	3	25859	12771	0	0	0	-	0	0	0	Unknown
MLG 715	4	25646	18480	12340	48.12	gii116094265 gb C P000413.1	18943 60	13374	0.71	384	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus gasseri
MLG 716	3	24404	14150	12865	52.72	gii512154926 gb C P006011.1	19477 06	13649	0.7	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 717	2	24379	24075	243	1	gii526120653 gb C P006603.1	21454 45	245	0.01	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 718	4	24310	10571	14332	58.96	gii288730948 emb FN597254.1	23509 11	11469	0.49	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 719	2	24276	14775	14775	60.86	gii549815675 gb C P006648.1	51668 57	14769	0.29	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 720	2	24177	20808	24177	100	gii569535620 gb C P007025.1	47018 75	24173	0.51	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 721	12	23972	7227	18250	76.13	gii682108593 gb C P008897.1	46334 07	17849	0.39	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 722	4	23928	7200	3846	16.07	gii365906294 gb C P003218.1	59741 09	3887	0.07	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 723	2	23822	21542	22772	95.59	gii281177210 dbj AP009378.1	47173 38	22764	0.48	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 724	3	23503	10250	0	0	0	-	0	0	0	Unknown
MLG 725	4	23502	10779	10461	44.51	gii284919779 emb FN554766.1	52419 77	14873	0.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 726	3	23451	18080	10123	43.17	gii557470476 gb C P006854.1	17891 38	11245	0.63	401	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__Pediococcus pentosaceus

MLG 727	34	23402	1203	0	0	0	-	0	0	0	Unknown
MLG 728	2	23140	22770	0	0	0	-	0	0	0	Unknown
MLG 729	2	23131	14371	7768	33.58	gii619734722 gb C P007557.1	50990 34	10282	0.2	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 730	8	22925	7962	2610	11.38	gii110681940 gb C P000312.1	28973 93	2610	0.09	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 731	2	22914	16971	16843	73.51	gii662712225 gb C P008823.1	48529 80	16985	0.35	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 732	2	22902	17923	11329	49.47	gii26111730 gb AE 014075.1	52314 28	15366	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 733	2	22739	14185	0	0	0	-	0	0	0	Unknown
MLG 734	5	22672	10293	3352	14.78	gii511525997 gb C P005991.1	50390 27	3349	0.07	268	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. R4-368
MLG 735	2	22487	14192	8295	36.89	gii218430358 emb CU928163.2	52020 90	8295	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 736	2	22303	18090	5527	24.78	gii682100560 gb C P008943.1	48065 94	5536	0.12	308	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia pseudotuberculosis
MLG 737	5	22301	7223	20140	90.31	gii170517292 gb C P000970.1	50683 89	14442	0.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 738	2	22297	18959	19717	88.43	gii557470476 gb C P006854.1	17891 38	19899	1.11	401	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__Pediococcus pentosaceus
MLG 739	2	22279	21777	12077	54.21	gii288730948 emb FN597254.1	23509 11	12070	0.51	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 740	2	22048	11805	11375	51.59	gii334732565 gb C P002824.1	52803 50	13613	0.26	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 741	2	21845	20365	0	0	0	-	0	0	0	Unknown
MLG 742	2	21756	16651	0	0	0	-	0	0	0	Unknown
MLG 743	3	21677	15111	1659	7.65	gii619734722 gb C P007557.1	50990 34	1658	0.03	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 744	29	21661	3893	1034	4.77	gii110681940 gb C P000312.1	28973 93	1037	0.04	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 745	2	21553	19885	19488	90.42	gii309700213 emb FN649414.1	51534 35	19494	0.38	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 746	3	21547	12098	21547	100	gii569535620 gb C P007025.1	47018 75	21614	0.46	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 747	2	21533	14963	0	0	0	-	0	0	0	Unknown
MLG 748	51	21503	761	20525	95.45	gii681102165 emb FO904942.1	40871 60	554	0.01	851	k__Eukaryota;p__Ascomycota;c__Sordariomycetes;o__Sordariales;f__Lasiosphaeriaceae;g__Podospora;s__Podospora anserina
MLG 749	4	21461	8905	20772	96.79	gii364515570 gb C P003200.1	53339 42	18582	0.35	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 750	3	21402	8932	21254	99.31	gii281177210 dbj AP009378.1	47173 38	10000	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 751	2	21356	20535	15016	70.31	gii229368777 gb C P001485.1	31495 84	15001	0.48	435	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Vibrio;s__Vibrio cholerae
MLG 752	7	21260	6211	19566	92.03	gii338741860 emb FR873481.1	22171 84	21659	0.98	375	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus salivarius
MLG 753	2	21173	14161	18595	87.82	gii295054830 gb C P001918.1	53145 81	17564	0.33	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae

MLG 754	5	21166	8640	297	1.4	gii361055534 gb C P003137.1	1829111	297	0.02	176	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__Pediococcus clausenii
MLG 755	2	21128	13971	0	0	0	-	0	0	0	Unknow
MLG 756	2	21047	18650	9904	47.06	gii514423830 gb C P006250.1	5328010	9898	0.19	278	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia plymuthica
MLG 757	3	20930	8545	0	0	0	-	0	0	0	Unknow
MLG 758	2	20900	14032	0	0	0	-	0	0	0	Unknow
MLG 759	2	20808	14280	5932	28.51	gii394343076 gb C P003683.1	6097032	6252	0.1	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 760	2	20802	17485	20801	100	gii406775301 gb C P003297.1	5253138	24712	0.47	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 761	3	20702	18183	0	0	0	-	0	0	0	Unknow
MLG 762	2	20494	12075	20301	99.06	gii612150118 gb C P007546.1	4561905	19812	0.43	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 763	2	20489	14226	18687	91.21	gii619734722 gb C P007557.1	5099034	19408	0.38	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 764	4	20432	11343	18641	91.23	gii478439721 gb C P004856.1	3427276	18604	0.54	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG 765	7	20409	3675	13313	65.23	gii573926912 gb C P007044.1	5485588	13724	0.25	290	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__Serratia fonticola
MLG 766	3	20249	11616	5552	27.42	gii639440343 gb C P007215.2	4902024	5551	0.11	269	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Kosakonia;s__Kosakonia sacchari
MLG 767	5	20236	12027	0	0	0	-	0	0	0	Unknow
MLG 768	23	20204	1926	0	0	0	-	0	0	0	Unknow
MLG 769	2	20108	11956	20108	100	gii110341805 gb C P000247.1	4938920	20854	0.42	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 770	36	20089	1181	0	0	0	-	0	0	0	Unknow
MLG 771	3	20089	13128	0	0	0	-	0	0	0	Unknow
MLG 772	2	20086	17556	19406	96.61	gii569535620 gb C P007025.1	4701875	26493	0.56	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 773	7	20004	4354	888	4.44	gii374269796 emb HE616528.1	4988504	882	0.02	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 774	3	19854	12328	12283	61.87	gii365906294 gb C P003218.1	5974109	12439	0.21	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 775	2	19763	10573	16979	85.91	gii209157093 gb C P001164.1	5572075	23168	0.42	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 776	3	19706	7227	0	0	0	-	0	0	0	Unknow
MLG 777	33	19623	2780	1196	6.09	gii335332259 emb FR871757.1	1755458	94	0.01	669	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacteriales;f__Helicobacteriaceae;g__Helicobacter;s__Helicobacter bizzozeronii
MLG 778	2	19588	12479	5209	26.59	gii605546632 gb C P007534.1	4737447	5208	0.11	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 779	3	19585	11484	9137	46.65	gii160863331 gb C P000880.1	4600800	11066	0.24	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 780	4	19580	11252	0	0	0	-	0	0	0	Unknow

MLG 781	2	19577	11482	18532	94.66	gii569535620 gb C P007025.1	47018 75	22035	0.47	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 782	2	19535	17368	13653	69.89	gii526120653 gb C P006603.1	21454 45	15372	0.72	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 783	5	19517	6313	2376	12.17	gii283101593 gb C P001750.1	26363 67	2376	0.09	909	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium dentium
MLG 784	2	19470	15085	19194	98.58	gii440045023 gb C P003938.1	47621 79	21152	0.44	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 785	2	19443	12619	17710	91.09	gii157076741 gb C P000800.1	49796 19	17703	0.36	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 786	2	19165	9854	17068	89.06	gii110341805 gb C P000247.1	49389 20	17068	0.35	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 787	2	19134	15332	8315	43.46	gii206564770 gb C P000964.1	56412 39	8316	0.15	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 788	3	19052	9696	0	0	0	-	0	0	0	Unknow
MLG 789	3	18896	9167	4857	25.7	gii513034319 gb C P006033.1	30446 78	4862	0.16	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 790	2	18892	14649	7099	37.58	gii157065147 gb C P000802.1	46435 38	7118	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 791	2	18840	15266	18840	100	gii26111730 gb AE 014075.1	52314 28	18839	0.36	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 792	3	18749	13223	1076	5.74	gii288730948 emb FN597254.1	23509 11	1072	0.05	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 793	3	18714	15059	614	3.28	gii684200017 gb C P008920.1	42859 51	614	0.01	327	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Providencia;s__Providencia stuartii
MLG 794	2	18655	16757	18655	100	gii290760697 gb C P001846.1	53863 52	18650	0.35	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 795	5	18622	13213	17283	92.81	gii291516109 emb FP929034.1	23849 87	17482	0.73	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium longum
MLG 796	10	18597	4709	17174	92.35	gii209157093 gb C P001164.1	55720 75	19076	0.34	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 797	2	18544	12616	17508	94.41	gii209157093 gb C P001164.1	55720 75	14402	0.26	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 798	17	18533	2332	0	0	0	-	0	0	0	Unknow
MLG 799	3	18519	12639	14350	77.49	gii345091121 gb C P003026.1	48128 33	14520	0.3	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 800	2	18447	14775	13838	75.01	gii526120653 gb C P006603.1	21454 45	16649	0.78	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 801	2	18373	10265	8701	47.36	gii660577155 gb C P008797.1	53961 64	9417	0.17	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 802	3	18328	8636	8636	47.12	gii307551844 gb C P001671.1	51313 97	8636	0.17	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 803	2	18287	9570	0	0	0	-	0	0	0	Unknow
MLG 804	2	18264	9418	0	0	0	-	0	0	0	Unknow
MLG 805	2	18149	15290	13517	74.48	gii601101465 gb C P007505.1	48644 10	15428	0.32	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 806	7	18107	8649	1280	7.07	gii674133359 gb C P009208.1	53748 34	1281	0.02	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 807	8	17989	5953	3796	21.1	gii597812552 gb C P007446.1	25279 78	4672	0.18	1175	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Snodgrassella;s__Snodgrassella alvi

MLG 808	3	17956	13142	0	0	0	-	0	0	0	Unknown
MLG 809	2	17939	9887	15296	85.27	gii218430358 emb CU928163.2	5202090	15610	0.3	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 810	9	17925	4822	0	0	0	-	0	0	0	Unknown
MLG 811	4	17915	6764	17438	97.34	gii301154649 emb FQ312002.1	2086875	17431	0.84	419	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__Haemophilus parainfluenzae
MLG 812	5	17889	7771	2848	15.92	gii116100249 gb C P000419.1	1856368	2848	0.15	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
MLG 813	3	17833	8646	12237	68.62	gii682108593 gb C P008897.1	4633407	10490	0.23	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 814	3	17737	8305	0	0	0	-	0	0	0	Unknown
MLG 815	4	17596	7008	12261	69.68	gii308746527 gb C P002272.1	4814049	12367	0.26	8	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter lignolyticus
MLG 816	5	17552	7987	16507	94.05	gii124491690 emb AM406671.1	2529478	16460	0.65	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 817	3	17427	10440	17427	100	gii170517292 gb C P000970.1	5068389	17745	0.35	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 818	3	17313	12250	17313	100	gii480474683 gb C P004142.1	5398151	17785	0.33	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a_s__Raoultella omithinolytica
MLG 819	5	17310	6522	13003	75.12	gii440045023 gb C P003938.1	4762179	14978	0.31	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 820	6	17270	12862	3558	20.6	gii392322800 gb C P003678.1	4968248	6176	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 821	2	17260	8817	0	0	0	-	0	0	0	Unknown
MLG 822	3	17150	15648	16082	93.77	gii148530277 gb C P000705.1	1999618	16027	0.8	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 823	2	16997	14040	9225	54.27	gii295107714 emb FP929054.1	3757491	9546	0.25	721	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__[Ruminococcus] obeum
MLG 824	2	16965	8620	12038	70.96	gii334732565 gb C P002824.1	5280350	19734	0.37	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 825	3	16941	12283	16689	98.51	gii110613622 gb C P000266.1	4574284	16704	0.37	261	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella flexneri
MLG 826	2	16876	9231	16876	100	gii157076741 gb C P000800.1	4979619	16876	0.34	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 827	2	16843	9561	6309	37.46	gii394343076 gb C P003683.1	6097032	6307	0.1	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a_s__Klebsiella oxytoca
MLG 828	3	16679	7054	16679	100	gii569535620 gb C P007025.1	4701875	16690	0.35	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 829	3	16609	15465	13170	79.29	gii374672113 dbj AP012281.1	2421471	13172	0.54	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 830	3	16450	11325	11245	68.36	gii288730948 emb FN597254.1	2350911	9710	0.41	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 831	4	16333	5569	13055	79.93	gii400173048 gb C P003737.1	4726582	13040	0.28	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 832	2	16306	8688	0	0	0	-	0	0	0	Unknown
MLG 833	2	16302	10164	0	0	0	-	0	0	0	Unknown
MLG 834	7	16277	7030	4060	24.94	gii13400022 gb AE 005176.1	2365589	6708	0.28	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis

MLG 835	4	16238	6191	12987	79.98	gii455418716 gb C P004345.1	37995 39	12987	0.34	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganel la;s__Morganella morganii
MLG 836	2	16155	8226	0	0	0	-	0	0	0	Unknow
MLG 837	2	16115	14541	15569	96.61	gii353735273 gb C P002641.1	21776 56	14234	0.65	34	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus suis
MLG 838	4	16111	5274	2361	14.65	gii218425442 emb CU928162.2	52095 48	2352	0.05	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 839	7	16063	4098	2489	15.5	gii343179174 dbj AP009332.1	19501 35	2975	0.15	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 840	2	15932	10476	3714	23.31	gii110341805 gb C P000247.1	49389 20	3713	0.08	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 841	3	15896	7148	6448	40.56	gii570286338 gb C P006580.1	53699 29	6449	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enteroba cter;s__Enterobacter cloacae
MLG 842	2	15850	12014	3377	21.31	gii365906294 gb C P003218.1	59741 09	3386	0.06	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiell a;s__Klebsiella oxytoca
MLG 843	3	15800	9562	15752	99.7	gii602773583 gb C P007273.1	50521 73	18725	0.37	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmone lla;s__Salmonella enterica
MLG 844	2	15798	14319	4385	27.76	gii47118301 dbj B A000007.2	54984 50	8162	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 845	3	15724	6685	3020	19.21	gii384478111 gb C P003488.1	44021 09	3018	0.07	327	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Providen cia;s__Providencia stuartii
MLG 846	2	15703	8124	8124	51.74	gii311772326 gb C P002286.1	22659 43	8123	0.36	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium; s__Bifidobacterium longum
MLG 847	6	15657	7099	2971	18.98	gii124491690 emb AM406671.1	25294 78	5836	0.23	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 848	2	15656	13881	0	0	0	-	0	0	0	Unknow
MLG 849	6	15641	11871	15577	99.59	gii334732565 gb C P002824.1	52803 50	17986	0.34	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enteroba cter;s__Enterobacter aerogenes
MLG 850	16	15575	2468	8847	56.8	gii187720473 gb C P001056.1	38003 27	8848	0.23	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 851	2	15514	12639	5767	37.17	gii320459527 dbj AP010890.1	24003 12	7818	0.33	890	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium; s__Bifidobacterium longum
MLG 852	3	15513	6308	13467	86.81	gii675819096 emb LM995659.1	12361 24	13483	1.09	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 853	2	15510	13137	2373	15.3	gii110341805 gb C P000247.1	49389 20	2479	0.05	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 854	5	15451	5053	812	5.26	gii218354981 emb CU928158.2	45887 11	811	0.02	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia fergusonii
MLG 855	2	15330	10893	13670	89.17	gii169752989 gb C P000946.1	47462 18	10141	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 856	14	15314	2486	15314	100	gii219620149 gb C P001213.1	19336 95	15482	0.8	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium; s__Bifidobacterium animalis
MLG 857	3	15265	11859	7933	51.97	gii526120653 gb C P006603.1	21454 45	7937	0.37	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 858	2	15203	14443	0	0	0	-	0	0	0	Unknow
MLG 859	2	15181	13309	14987	98.72	gii480474683 gb C P004142.1	53981 51	14968	0.28	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultell a;s__Raoultella omithinolytica
MLG 860	2	15175	12898	13273	87.47	gii170517292 gb C P000970.1	50683 89	13267	0.26	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escheric hia;s__Escherichia coli
MLG 861	3	15165	8738	0	0	0	-	0	0	0	Unknow

MLG 862	2	15164	8041	15164	100	gii569535620 gb C P007025.1	4701875	15164	0.32	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 863	10	15148	4031	1499	9.9	gii110673209 gb C P000246.1	3256683	1491	0.05	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 864	5	15101	10945	8042	53.25	gii188497817 gb C P001078.1	3659644	7073	0.19	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 865	2	15101	9630	15101	100	gii664693170 gb C P005998.1	4944397	15101	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 866	2	15025	14352	13917	92.63	gii660550561 gb C P008700.1	5365144	13981	0.26	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 867	10	15003	3536	4114	27.42	gii218354981 emb CU928158.2	4588711	4226	0.09	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 868	3	15001	8143	9543	63.62	gii569535620 gb C P007025.1	4701875	9561	0.2	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 869	2	15001	9882	14745	98.29	gii569535620 gb C P007025.1	4701875	14910	0.32	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 870	2	14980	10389	4591	30.65	gii480474683 gb C P004142.1	5398151	4596	0.09	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a__Raoultella omithinolytica
MLG 871	2	14978	11330	0	0	0	-	0	0	0	Unknow
MLG 872	6	14971	11846	0	0	0	-	0	0	0	Unknow
MLG 873	10	14951	2343	13567	90.74	gii150839411 gb C P000746.1	2319663	13674	0.59	1216	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Actinobacillus;s__Actinobacillus succinogenes
MLG 874	4	14902	5942	0	0	0	-	0	0	0	Unknow
MLG 875	4	14853	5335	11441	77.03	gii660567586 gb C P008788.1	6152190	8865	0.14	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella oxytoca
MLG 876	4	14841	5597	0	0	0	-	0	0	0	Unknow
MLG 877	2	14826	13629	1185	7.99	gii499053647 gb C P005942.1	3033566	1185	0.04	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 878	7	14795	8126	14062	95.05	gii149901357 gb C P000721.1	6000632	14610	0.24	37	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium beijerinckii
MLG 879	2	14794	12607	11577	78.25	gii595597955 gb C P007392.1	5054509	11566	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 880	3	14773	6512	14773	100	gii218430358 emb CU928163.2	5202090	14752	0.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 881	8	14764	3296	11340	76.81	gii440045023 gb C P003938.1	4762179	12521	0.26	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 882	2	14752	7948	7056	47.83	gii384478111 gb C P003488.1	4402109	3526	0.08	327	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Providencia;s__Providencia stuartii
MLG 883	2	14706	11096	4718	32.08	gii619734722 gb C P007557.1	5099034	4717	0.09	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 884	4	14705	8041	14705	100	gii170517292 gb C P000970.1	5068389	14704	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 885	3	14702	6798	11979	81.48	gii595583568 gb C P007265.1	4758629	9815	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 886	4	14668	11454	4208	28.69	gii222031834 emb CU651637.1	4773108	4208	0.09	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 887	4	14652	6150	5414	36.95	gii660550561 gb C P008700.1	5365144	5576	0.1	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 888	2	14600	8547	6241	42.75	gii295054830 gb C P001918.1	5314581	6247	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae

MLG 889	8	14584	3969	402	2.76	gi 670938612 gb C P006630.1	2833899	402	0.01	135	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus aureus
MLG 890	7	14527	3542	7347	50.57	gi 295095013 emb FP929040.1	4908759	7369	0.15	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 891	3	14464	8185	11538	79.77	gi 443901024 emb F0203355.1	5419609	12048	0.22	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 892	2	14460	10033	6809	47.09	gi 170517292 gb C P000970.1	5068389	6806	0.13	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 893	2	14409	10177	5292	36.73	gi 675819096 emb LM995659.1	1236124	5292	0.43	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 894	2	14407	12111	0	0	0	-	0	0	0	Unknow
MLG 895	2	14392	8258	10387	72.17	gi 523811606 gb C P006053.1	4730612	7029	0.15	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 896	2	14365	7575	8707	60.61	gi 662712225 gb C P008823.1	4852980	8701	0.18	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 897	2	14346	11529	13938	97.16	gi 308044682 gb C P002222.1	3254376	13939	0.43	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 898	2	14325	8013	0	0	0	-	0	0	0	Unknow
MLG 899	8	14306	3178	14306	100	gi 110673209 gb C P000246.1	3256683	14306	0.44	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens
MLG 900	2	14265	13620	4314	30.24	gi 116094265 gb C P000413.1	1894360	4314	0.23	384	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus gasseri
MLG 901	4	14259	7204	14200	99.59	gi 169752989 gb C P000946.1	4746218	14528	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 902	2	14243	13700	9763	68.55	gi 667708115 gb C P006798.1	5348284	9763	0.18	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 903	2	14226	9624	13892	97.65	gi 169887498 gb C P000948.1	4686137	13897	0.3	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 904	2	14224	13374	13374	94.02	gi 569550235 gb C P003999.1	5307003	13374	0.25	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 905	4	14207	6483	0	0	0	-	0	0	0	Unknow
MLG 906	2	14205	12601	0	0	0	-	0	0	0	Unknow
MLG 907	2	14201	8479	13810	97.25	gi 222031834 emb CU651637.1	4773108	13807	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 908	2	14143	11512	6737	47.63	gi 169752989 gb C P000946.1	4746218	5709	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 909	4	14102	4184	0	0	0	-	0	0	0	Unknow
MLG 910	2	14073	10168	12022	85.43	gi 612156087 gb C P004887.1	5914407	9510	0.16	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 911	5	14037	6890	4861	34.63	gi 526120653 gb C P006603.1	2145445	4879	0.23	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 912	3	14025	6663	12897	91.96	gi 619734722 gb C P007557.1	5099034	12883	0.25	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 913	2	14003	10107	13542	96.71	gi 400173048 gb C P003737.1	4726582	12129	0.26	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 914	3	13938	8653	3508	25.17	gi 281599365 gb C P001383.1	4650856	8710	0.19	261	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella flexneri
MLG 915	2	13924	7696	6665	47.87	gi 291482250 emb FN668375.1	4308325	12011	0.28	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium difficile

MLG 916	3	13871	10753	11952	86.17	gii329127738 gb C P002652.1	2506301	11463	0.46	395	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus buchneri
MLG 917	2	13868	11223	0	0	0	-	0	0	0	Unknow
MLG 918	2	13845	12159	13845	100	gii115511419 gb C P000468.1	5082025	13472	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 919	3	13841	6381	2792	20.17	gii302195072 gb C P002109.1	4662871	2792	0.06	843	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;s__[Clostridium] saccharolyticum
MLG 920	2	13833	12642	6772	48.96	gii682108593 gb C P008897.1	4633407	7508	0.16	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 921	2	13815	7481	8411	60.88	gii394343076 gb C P003683.1	6097032	5749	0.09	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 922	3	13798	8347	3400	24.64	gii601101465 gb C P007505.1	4864410	5539	0.11	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 923	2	13796	10442	8212	59.52	gii602773583 gb C P007273.1	5052173	8909	0.18	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 924	3	13733	5765	10721	78.07	gii334279325 dbj AP012053.1	2362241	13694	0.58	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 925	2	13716	12471	7129	51.98	gii549815675 gb C P006648.1	5166857	7822	0.15	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 926	3	13694	6248	11108	81.12	gii218354981 emb CU928158.2	4588711	11108	0.24	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 927	3	13629	4992	0	0	0	-	0	0	0	Unknow
MLG 928	2	13610	7738	0	0	0	-	0	0	0	Unknow
MLG 929	2	13605	11976	13137	96.56	gii110341805 gb C P000247.1	4938920	11848	0.24	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 930	2	13536	8290	2804	20.72	gii267983018 gb C P001135.1	3760463	2803	0.07	294	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Edwardsiella;s__Edwardsiella tarda
MLG 931	2	13493	7463	6633	49.16	gii374681091 gb C P003295.1	1988420	6633	0.33	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius
MLG 932	4	13473	9161	13472	99.99	gii374269796 emb HE616528.1	4988504	14873	0.3	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 933	3	13419	7155	9975	74.33	gii619734722 gb C P007557.1	5099034	9972	0.2	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 934	2	13384	10770	3875	28.95	gii183225820 dbj AP008937.1	2098685	3875	0.18	414	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus fermentum
MLG 935	5	13336	3729	13254	99.39	gii122087364 emb AM286415.1	4615899	24461	0.53	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 936	2	13258	8232	0	0	0	-	0	0	0	Unknow
MLG 937	2	13238	11262	13238	100	gii455418716 gb C P004345.1	3799539	13484	0.35	301	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganelia;s__Morganelia morganii
MLG 938	2	13169	10960	8211	62.35	gii219620149 gb C P001213.1	1933695	8204	0.42	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
MLG 939	2	13148	7897	0	0	0	-	0	0	0	Unknow
MLG 940	3	13128	4886	0	0	0	-	0	0	0	Unknow
MLG 941	2	13115	8160	0	0	0	-	0	0	0	Unknow
MLG 942	3	13099	9454	0	0	0	-	0	0	0	Unknow

MLG 943	5	13083	3754	2723	20.81	gii291548560 emb FP929055.1	3341681	2738	0.08	163	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__[Ruminococcus]torques
MLG 944	2	13083	9914	0	0	0	-	0	0	0	Unknow
MLG 945	2	13065	9441	8494	65.01	gii365906294 gb C P003218.1	5974109	8734	0.15	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 946	4	13044	7526	13044	100	gii219620149 gb C P001213.1	1933695	13136	0.68	898	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
MLG 947	2	13021	10566	7931	60.91	gii386922183 gb C P001560.1	4158725	7979	0.19	273	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shimwellia;s__Shimwellia blattae
MLG 948	3	13018	11030	11009	84.57	gii440045023 gb C P003938.1	4762179	11266	0.24	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 949	2	12997	8680	4250	32.7	gii602758695 gb C P007270.1	4942215	4931	0.1	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 950	2	12972	9378	9378	72.29	gii218430358 emb C U928163.2	5202090	9378	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 951	2	12968	8081	11194	86.32	gii573966439 gb C P006027.1	5585613	11197	0.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 952	2	12967	7906	8643	66.65	gii602773583 gb C P007273.1	5052173	8300	0.16	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 953	2	12949	12349	12349	95.37	gii284919779 emb FN554766.1	5241977	13475	0.26	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 954	3	12945	5275	12941	99.97	gii569535620 gb C P007025.1	4701875	14882	0.32	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 955	30	12907	916	0	0	0	-	0	0	0	Unknow
MLG 956	6	12863	4260	9758	75.86	gii301154649 emb FQ312002.1	2086875	9758	0.47	419	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__Haemophilus parainfluenzae
MLG 957	2	12855	6900	0	0	0	-	0	0	0	Unknow
MLG 958	2	12768	10451	10989	86.07	gii526125113 gb C P006608.1	4683551	11168	0.24	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
MLG 959	3	12734	7500	12734	100	gii569535620 gb C P007025.1	4701875	12733	0.27	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 960	2	12706	9176	9176	72.22	gii150953431 gb C P000647.1	5315120	9176	0.17	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 961	2	12655	6872	12655	100	gii281177210 dbj AP009378.1	4717338	12655	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 962	2	12648	11490	5538	43.79	gii697784296 gb C P009610.1	1850897	5537	0.3	164	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__Haemophilus influenzae
MLG 963	2	12639	6344	4289	33.93	gii145562801 gb C P000681.1	4659220	4289	0.09	836	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__Shewanella putrefaciens
MLG 964	2	12623	11299	4814	38.14	gii218354981 emb C U928158.2	4588711	4907	0.11	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
MLG 965	8	12608	2481	0	0	0	-	0	0	0	Unknow
MLG 966	2	12586	8957	8957	71.17	gii309700213 emb FN649414.1	5153435	8958	0.17	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 967	11	12513	4974	9340	74.64	gii329666391 gb C P002464.1	1966342	1916	0.1	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 968	2	12479	10215	0	0	0	-	0	0	0	Unknow
MLG 969	6	12452	3336	0	0	0	-	0	0	0	Unknow

MLG 970	2	12442	11773	10727	86.22	gii169147133 embl CU459141.1	3936291	14903	0.38	552	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter baumannii
MLG 971	2	12390	9148	11396	91.98	gii170517292 gb CP000970.1	5068389	11396	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 972	10	12379	2724	0	0	0	-	0	0	0	Unknow
MLG 973	2	12232	8427	2003	16.38	gii662712225 gb CP008823.1	4852980	4006	0.08	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 974	8	12187	2448	12167	99.84	gii125496804 gb CP000387.1	2388435	12160	0.51	409	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus sanguinis
MLG 975	2	12171	8314	9906	81.39	gii169752989 gb CP000946.1	4746218	14501	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 976	2	12171	9214	0	0	0	-	0	0	0	Unknow
MLG 977	2	12151	8244	7867	64.74	gii257762509 dbj AP010960.1	5371077	8176	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 978	2	12119	9327	10276	84.79	gii41584196 gb AE017198.1	1992676	11219	0.56	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 979	2	12090	7371	0	0	0	-	0	0	0	Unknow
MLG 980	2	12084	11432	11266	93.23	gii295054830 gb CP001918.1	5314581	11275	0.21	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 981	24	12064	668	0	0	0	-	0	0	0	Unknow
MLG 982	3	12040	4754	8426	69.98	gii443901024 embl FO203355.1	5419609	9084	0.17	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
MLG 983	7	12027	3618	0	0	0	-	0	0	0	Unknow
MLG 984	2	12012	8860	8860	73.76	gii640850664 gb CP007731.1	5241638	28291	0.54	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 985	2	12002	6330	10381	86.49	gii157081501 gb CP000822.1	4720462	10998	0.23	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter koseri
MLG 986	3	11951	5456	5152	43.11	gii527122546 gb CP003025.1	1975547	5166	0.26	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
MLG 987	4	11909	6618	1421	11.93	gii537631739 gb CP003859.1	1991156	1421	0.07	374	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus constellatus
MLG 988	4	11893	7507	10652	89.57	gii667688329 gb CP007588.1	1355853	10648	0.79	457	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__Weissella ceti
MLG 989	2	11893	9278	11306	95.06	gii569535620 gb CP007025.1	4701875	11905	0.25	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 990	2	11886	7560	2804	23.59	gii288887617 gb CP001891.1	5458505	2801	0.05	10	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella varicola
MLG 991	12	11799	1682	0	0	0	-	0	0	0	Unknow
MLG 992	2	11784	7073	7073	60.02	gii206564770 gb CP000964.1	5641239	11193	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella pneumoniae
MLG 993	2	11767	10060	10060	85.49	gii218363708 embl CU928161.2	5032268	10060	0.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 994	2	11740	8826	8826	75.18	gii284919779 embl FN554766.1	5241977	11486	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 995	7	11728	4462	11407	97.26	gii29350190 gb AE016830.1	3218031	11886	0.37	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
MLG 996	2	11523	8590	11523	100	gii110341805 gb CP000247.1	4938920	11522	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

MLG 997	2	11493	8571	4612	40.13	gi 169752989 gb C P000946.1	47462 18	4861	0.1	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 998	3	11476	5546	5546	48.33	gi 660567586 gb C P008788.1	61521 90	5589	0.09	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 999	2	11448	8131	0	0	0	-	0	0	0	Unknow
MLG 1000	2	11430	9985	10161	88.9	gi 81244029 gb CP 000036.1	45198 23	10237	0.23	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella boydii
MLG 1001	2	11428	10989	437	3.82	gi 262396937 emb FN298497.1	17559 93	431	0.02	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
MLG 1002	7	11427	3586	0	0	0	-	0	0	0	Unknow
MLG 1003	2	11425	9301	9454	82.75	gi 110341805 gb C P000247.1	49389 20	8135	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1004	5	11414	6340	6340	55.55	gi 334281572 dbj AP012054.1	21000 77	6340	0.3	368	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus pasteurianus
MLG 1005	7	11407	3089	0	0	0	-	0	0	0	Unknow
MLG 1006	2	11391	8511	2475	21.73	gi 595583568 gb C P007265.1	47586 29	2480	0.05	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1007	3	11331	4758	10050	88.69	gi 400173048 gb C P003737.1	47265 82	12643	0.27	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 1008	2	11317	8266	9109	80.49	gi 294489418 gb C P001969.1	51083 83	6940	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1009	2	11302	5955	10072	89.12	gi 157081501 gb C P000822.1	47204 62	10154	0.22	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter koseri
MLG 1010	3	11296	5670	10488	92.85	gi 209157093 gb C P001164.1	55720 75	8072	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1011	8	11273	5903	2464	21.86	gi 188497817 gb C P001078.1	36596 44	2555	0.07	20	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium botulinum
MLG 1012	2	11239	10163	9783	87.05	gi 374672113 dbj AP012281.1	24214 71	9788	0.4	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 1013	2	11233	10901	10624	94.58	gi 124491690 emb AM406671.1	25294 78	10850	0.43	88	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus lactis
MLG 1014	2	11224	6090	0	0	0	-	0	0	0	Unknow
MLG 1015	2	11216	9077	9479	84.51	gi 410816915 gb C P003917.1	46438 44	7559	0.16	437	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Alteromonadaceae;g__Alteromonas;s__Alteromonas macleodii
MLG 1016	2	11213	6680	0	0	0	-	0	0	0	Unknow
MLG 1017	2	11164	7376	6862	61.47	gi 281599365 gb C P001383.1	46508 56	8781	0.19	261	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella flexneri
MLG 1018	2	11158	9529	6054	54.26	gi 209157093 gb C P001164.1	55720 75	6053	0.11	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1019	3	11136	9423	1358	12.19	gi 343179174 dbj AP009332.1	19501 35	1359	0.07	365	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus garvieae
MLG 1020	2	11129	5971	11129	100	gi 218430358 emb CU928163.2	52020 90	11130	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1021	3	11099	10359	189	1.7	gi 569535620 gb C P007025.1	47018 75	189	0	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 1022	2	11031	9282	0	0	0	-	0	0	0	Unknow
MLG 1023	3	11005	5555	0	0	0	-	0	0	0	Unknow

MLG 1024	2	10991	5737	0	0	0	-	0	0	0	Unknown
MLG 1025	2	10942	6834	10924	99.84	gii281177210 dbj AP009378.1	4717338	10931	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1026	2	10924	8849	5209	47.68	gii451908558 gb C P004027.1	4634161	5459	0.12	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
MLG 1027	2	10921	5688	0	0	0	-	0	0	0	Unknown
MLG 1028	3	10903	5647	2463	22.59	gii150953431 gb C P000647.1	5315120	2462	0.05	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
MLG 1029	5	10889	5160	9118	83.74	gii662706586 gb C P008841.1	5865090	12327	0.21	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 1030	7	10869	4091	0	0	0	-	0	0	0	Unknown
MLG 1031	3	10865	9048	0	0	0	-	0	0	0	Unknown
MLG 1032	2	10849	6297	0	0	0	-	0	0	0	Unknown
MLG 1033	3	10848	5717	10848	100	gii157065147 gb C P000802.1	4643538	10847	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1034	3	10840	6996	9249	85.32	gii526125113 gb C P006608.1	4683551	7947	0.17	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
MLG 1035	4	10829	5645	0	0	0	-	0	0	0	Unknown
MLG 1036	3	10800	4976	0	0	0	-	0	0	0	Unknown
MLG 1037	4	10793	7550	4720	43.73	gii295054830 gb C P001918.1	5314581	4720	0.09	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 1038	12	10779	1622	10779	100	gii689262542 gb C P009451.1	4876443	10887	0.22	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 1039	2	10768	6337	0	0	0	-	0	0	0	Unknown
MLG 1040	2	10761	8233	7060	65.61	gii325177128 emb FR824043.1	2356444	6763	0.29	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
MLG 1041	3	10757	4861	10697	99.44	gii478439721 gb C P004856.1	3427276	10712	0.31	363	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus casseliflavus
MLG 1042	2	10750	7811	10567	98.3	gii374269796 emb HE616528.1	4988504	15387	0.31	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 1043	15	10749	1440	0	0	0	-	0	0	0	Unknown
MLG 1044	2	10747	8110	10747	100	gii209157093 gb C P001164.1	5572075	10747	0.19	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1045	2	10739	5556	0	0	0	-	0	0	0	Unknown
MLG 1046	2	10738	5700	10552	98.27	gii571260215 emb HF571988.1	4940199	11213	0.23	296	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__Yersinia enterocolitica
MLG 1047	7	10730	2932	10730	100	gii689262542 gb C P009451.1	4876443	10730	0.22	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 1048	2	10723	7623	7422	69.22	gii365906294 gb C P003218.1	5974109	6583	0.11	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 1049	2	10723	9892	6687	62.36	gii169887498 gb C P000948.1	4686137	6687	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1050	5	10701	2988	10698	99.97	gii110673209 gb C P000246.1	3256683	9205	0.28	21	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Clostridium perfringens

MLG 1051	4	10672	6827	0	0	0	-	0	0	0	Unknown
MLG 1052	2	10660	7392	10660	100	gii209157093 gb C P001164.1	5572075	10641	0.19	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1053	2	10653	7622	10653	100	gii569535620 gb C P007025.1	4701875	10875	0.23	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
MLG 1054	2	10586	7500	10342	97.7	gii342240345 emb AL935263.2	3308273	10859	0.33	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus plantarum
MLG 1055	5	10533	3535	4151	39.41	gii209157093 gb C P001164.1	5572075	4171	0.07	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1056	3	10533	4221	0	0	0	-	0	0	0	Unknown
MLG 1057	3	10531	8685	3678	34.93	gii291520697 emb FP929038.1	3522704	3684	0.1	109	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coprococcus;s__Coprococcus catus
MLG 1058	2	10498	5759	6892	65.65	gii218368405 emb CU928164.2	5132068	7294	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1059	3	10472	8128	269	2.57	gii674993598 dbj AP014630.1	4648418	269	0.01	206	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter guillouiae
MLG 1060	2	10451	7211	0	0	0	-	0	0	0	Unknown
MLG 1061	5	10442	3031	2350	22.51	gii394343076 gb C P003683.1	6097032	2501	0.04	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 1062	3	10442	4700	1876	17.97	gii674114364 gb C P007573.1	2036353	1932	0.09	366	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus anginosus
MLG 1063	2	10435	5546	10435	100	gii480474683 gb C P004142.1	5398151	9949	0.18	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG 1064	5	10422	7799	0	0	0	-	0	0	0	Unknown
MLG 1065	2	10411	7494	2928	28.12	gii394343076 gb C P003683.1	6097032	2932	0.05	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
MLG 1066	2	10404	8963	0	0	0	-	0	0	0	Unknown
MLG 1067	2	10383	8572	7148	68.84	gii526120653 gb C P006603.1	2145445	9784	0.46	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
MLG 1068	3	10374	8535	10374	100	gii288887617 gb C P001891.1	5458505	11064	0.2	10	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella variicola
MLG 1069	2	10372	7287	10288	99.19	gii689262542 gb C P009451.1	4876443	12660	0.26	19	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cedecea;s__Cedecea neteri
MLG 1070	4	10361	3781	4898	47.27	gii328454937 gb C P002628.1	2115681	4899	0.23	882	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Coriobacteriales;f__Coriobacteriaceae;g__Coriobacterium;s__Coriobacterium glomerans
MLG 1071	2	10339	9673	0	0	0	-	0	0	0	Unknown
MLG 1072	2	10315	9640	0	0	0	-	0	0	0	Unknown
MLG 1073	3	10302	8741	886	8.6	gii209157093 gb C P001164.1	5572075	886	0.02	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1074	4	10248	4208	10146	99	gii374269796 emb HE616528.1	4988504	12863	0.26	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
MLG 1075	21	10239	884	0	0	0	-	0	0	0	Unknown
MLG 1076	3	10218	7386	0	0	0	-	0	0	0	Unknown
MLG 1077	2	10213	9129	9041	88.52	gii160863331 gb C P000880.1	4600800	11723	0.25	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica

MLG 1078	2	10186	9186	9917	97.36	gii115511419 gb C P000468.1	50820 25	9922	0.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1079	2	10149	5879	2736	26.96	gii619734722 gb C P007557.1	50990 34	2806	0.06	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 1080	2	10146	5799	0	0	0	-	0	0	0	Unknow
MLG 1081	2	10144	9735	10079	99.36	gii345091121 gb C P003026.1	48128 33	11088	0.23	9	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter asburiae
MLG 1082	4	10144	3608	9919	97.78	gii116098028 gb C P000416.1	22912 20	9917	0.43	400	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus brevis
MLG 1083	2	10136	6109	3250	32.06	gii332341332 gb C P002729.1	51864 16	4123	0.08	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1084	2	10109	7866	10109	100	gii480474683 gb C P004142.1	53981 51	10729	0.2	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;s__Raoultella omithinolytica
MLG 1085	2	10094	5568	2428	24.05	gii383101383 gb C P002291.1	49352 94	2419	0.05	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1086	2	10093	9341	10042	99.49	gii115511419 gb C P000468.1	50820 25	10043	0.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1087	2	10073	7825	8772	87.08	gii682108593 gb C P008897.1	46334 073	7593	0.16	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 1088	22	10071	666	0	0	0	-	0	0	0	Unknow
MLG 1089	3	10071	4571	6664	66.17	gii619734722 gb C P007557.1	50990 34	6656	0.13	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
MLG 1090	5	10066	2582	6949	69.03	gii440045023 gb C P003938.1	47621 79	6932	0.15	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
MLG 1091	2	10064	6179	5804	57.67	gii215263233 emb FM180568.1	49655 53	5806	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
MLG 1092	2	10042	5180	4979	49.58	gii295054830 gb C P001918.1	53145 81	5906	0.11	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 1093	2	10041	5852	5852	58.28	gii295054830 gb C P001918.1	53145 81	5894	0.11	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
MLG 1094	2	10027	5890	4335	43.23	gii169147133 emb CU459141.1	39362 91	2397	0.06	552	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter baumannii
MLG 1095	2	10022	5502	0	0	0	-	0	0	0	Unknow
MLG 1096	8	10016	2721	0	0	0	-	0	0	0	Unknow
UC-34432	1	16247	16247	16247	100	gii115511419 gb C P000468.1	50820 25	16256	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-35103	1	11517	11517	5571	48.37	gii664682453 gb C P008801.1	47185 45	5571	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-36980	1	23235	23235	12736	54.81	gii672600155 gb C P009114.1	52975 11	13023	0.25	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-36984	1	35378	35378	0	0	0	-	0	0	0	Unknow
UC-37049	1	11165	11165	9107	81.57	gii573019581 gb C P006569.1	47095 28	9104	0.19	302	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Sodalis;s__Sodalis sp. H51
UC-39752	1	11882	11882	6493	54.65	gii400173048 gb C P003737.1	47265 82	6540	0.14	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-39843	1	28926	28926	0	0	0	-	0	0	0	Unknow
UC-47653	1	24907	24907	24709	99.21	gii573932891 gb C P006262.1	54022 76	24709	0.46	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

UC-48875	1	10189	10189	7061	69.3	gii605537200 gb C P007533.1	4603849	7062	0.15	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-56717	1	11299	11299	6656	58.91	gii564743501 gb C P005995.1	4783867	6655	0.14	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-56733	1	18303	18303	6809	37.2	gii113886955 gb C P000444.1	4792610	6821	0.14	524	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__Shewanella sp. MR-7
UC-56734	1	18689	18689	16384	87.67	gii400173048 gb C P003737.1	4726582	16377	0.35	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-56761	1	16221	16221	16221	100	gii170517292 gb C P000970.1	5068389	16221	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-56885	1	10902	10902	10902	100	gii312910970 dbj AP011957.1	4954814	11494	0.23	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-56886	1	15498	15498	15498	100	gii312910970 dbj AP011957.1	4954814	16290	0.33	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-57257	1	31572	31572	29966	94.91	gii222031834 emb C0651637.1	4773108	29968	0.63	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-57296	1	22174	22174	14586	65.78	gii640850664 gb C P007731.1	5241638	15349	0.29	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-58618	1	27056	27056	23986	88.65	gii218350208 emb CU928145.2	5154862	29484	0.57	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-59666	1	225695	225695	0	0	0	-	0	0	0	Unknow
UC-62958	1	16095	16095	10669	66.29	gii449096568 gb C P004091.1	4344092	10668	0.25	271	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Cronobacter;s__Cronobacter sakazakii
UC-63712	1	47374	47374	0	0	0	-	0	0	0	Unknow
UC-63857	1	10355	10355	10355	100	gii169887498 gb C P000948.1	4686137	11415	0.24	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-65875	1	15853	15853	15853	100	gii169752989 gb C P000946.1	4746218	15853	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-65877	1	16304	16304	8598	52.74	gii549815675 gb C P006648.1	5166857	8593	0.17	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C33	1	26642	26642	25106	94.23	gii317160986 gb C P002439.1	2617381	50872	1.94	154	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus pseudintermedius
C43	1	10883	10883	10406	95.62	gii110341805 gb C P000247.1	4938920	10406	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C69	1	46459	46459	36050	77.6	gii595607150 gb C P007394.1	5090442	36053	0.71	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C99	1	11726	11726	3851	32.84	gii619734722 gb C P007557.1	5099034	5228	0.1	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
C189	1	24482	24482	8041	32.84	gii110341805 gb C P000247.1	4938920	9056	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C290	1	16247	16247	0	0	0	-	0	0	0	Unknow
C520	1	13010	13010	9788	75.23	gii374681091 gb C P003295.1	1988420	9774	0.49	228	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus infantarius
C538	1	65424	65424	57464	87.83	gii597512677 emb FO834906.1	5438894	58310	1.07	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C752	1	12708	12708	9359	73.65	gii294489418 gb C P001969.1	5108383	9360	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1096	1	15207	15207	14820	97.46	gii110341805 gb C P000247.1	4938920	15137	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1203	1	12501	12501	0	0	0	-	0	0	0	Unknow
C1227	1	23833	23833	16626	69.76	gii674299053 gb C P009072.1	5130767	23821	0.46	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

C1231	1	34428	34428	28134	81.72	gii597512677 emb FO834906.1	5438894	28135	0.52	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1303	1	15533	15533	15533	100	gii218359353 emb CU928160.2	4700560	15533	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1305	1	11346	11346	8817	77.71	gii253322479 gb C P001665.1	4570938	9115	0.2	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1367	1	26574	26574	23891	89.9	gii257757386 dbj AP010958.1	5449314	23892	0.44	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1689	1	10889	10889	3483	31.99	gii595583568 gb C P007265.1	4758629	3476	0.07	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1718	1	11476	11476	6982	60.84	gii30407157 emb A L513382.1	4809037	7005	0.15	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
C1803	1	12338	12338	8744	70.87	gii384478111 gb C P003488.1	4402109	8742	0.2	327	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Providencia;s__Providencia stuartii
C1807	1	15745	15745	15745	100	gii110341805 gb C P000247.1	4938920	15735	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1831	1	32680	32680	23767	72.73	gii110341805 gb C P000247.1	4938920	23749	0.48	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1849	1	17022	17022	17022	100	gii257757386 dbj AP010958.1	5449314	92927	1.71	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1872	1	11885	11885	6295	52.97	gii601101465 gb C P007505.1	4864410	6289	0.13	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
C1876	1	11005	11005	11005	100	gii660550561 gb C P008700.1	5365144	11318	0.21	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1899	1	10029	10029	7536	75.14	gii672600155 gb C P009114.1	5297511	7614	0.14	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1943	1	11555	11555	6381	55.22	gii257751862 dbj AP010953.1	5697240	6767	0.12	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2354	1	28350	28350	28350	100	gii257757386 dbj AP010958.1	5449314	28349	0.52	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2389	1	10373	10373	10319	99.48	gii257751862 dbj AP010953.1	5697240	57732	1.01	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2402	1	21041	21041	0	0	0	-	0	0	0	Unknow
C2541	1	13568	13568	13568	100	gii157065147 gb C P000802.1	4643538	13568	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2591	1	16136	16136	0	0	0	-	0	0	0	Unknow
C2628	1	13693	13693	0	0	0	-	0	0	0	Unknow
C2731	1	11936	11936	4547	38.09	gii619734722 gb C P007557.1	5099034	4618	0.09	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
C2986	1	18642	18642	17247	92.52	gii115511419 gb C P000468.1	5082025	20536	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C3173	1	14011	14011	0	0	0	-	0	0	0	Unknow
C3334	1	21333	21333	10797	50.61	gii597512677 emb FO834906.1	5438894	10938	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C3483	1	47206	47206	14265	30.22	gii595583568 gb C P007265.1	4758629	17161	0.36	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C3497	1	13530	13530	0	0	0	-	0	0	0	Unknow
C3560	1	38530	38530	22312	57.91	gii336447599 gb C P002844.1	2264399	23386	1.03	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
C3729	1	23173	23173	16914	72.99	gii530342600 gb C P006656.1	5273813	31471	0.6	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae

C3783	1	10204	10204	9950	97.51	gii26111730 gb AE014075.1	5231428	9954	0.19	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C4076	1	10567	10567	9610	90.94	gii257751862 dbj AP010953.1	5697240	10197	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C4078	1	21724	21724	21724	100	gii150953431 gb C000647.1	5315120	22088	0.42	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C4287	1	46187	46187	0	0	0	-	0	0	0	Unknow
C4328	1	10455	10455	10144	97.03	gii480474683 gb C004142.1	5398151	10133	0.19	14	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Raoultella;a;s__Raoultella omithinolytica
C4331	1	11770	11770	6611	56.17	gii339759707 gb C002910.1	5259571	6606	0.13	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
C4612	1	18305	18305	9807	53.58	gii511525997 gb C005991.1	5039027	10414	0.21	268	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sp. R4-368
C4638	1	14789	14789	14789	100	gii383101383 gb C002291.1	4935294	15406	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C5321	1	10541	10541	5202	49.35	gii662712225 gb C008823.1	4852980	5213	0.11	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
C5427	1	33144	33144	24467	73.82	gii308746527 gb C002272.1	4814049	24791	0.51	8	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter lignolyticus
C5468	1	10397	10397	10397	100	gii288887617 gb C001891.1	5458505	11071	0.2	10	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella variicola
UC-77341	1	12323	12323	3737	30.33	gii595597955 gb C007392.1	5054509	3940	0.08	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-77728	1	10402	10402	8487	81.59	gii290760697 gb C001846.1	5386352	8487	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-79091	1	39285	39285	0	0	0	-	0	0	0	Unknow
UC-79120	1	10285	10285	7788	75.72	gii309700213 emb FN649414.1	5153435	7786	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-79233	1	11344	11344	5113	45.07	gii675819096 emb LM995659.1	1236124	8408	0.68	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-79296	1	20745	20745	20150	97.13	gii315059226 gb C002185.1	4900968	20446	0.42	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-79329	1	15205	15205	5746	37.79	gii339511397 emb FR877557.1	4460105	6102	0.14	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
UC-79391	1	12570	12570	10830	86.16	gii170517292 gb C000970.1	5068389	10833	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-79651	1	18910	18910	10327	54.61	gii329666391 gb C002464.1	1966342	10273	0.52	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
UC-82762	1	10230	10230	7735	75.61	gii281177210 dbj AP009378.1	4717338	7734	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-83160	1	10024	10024	7888	78.69	gii218430358 emb CU928163.2	5202090	7885	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-83207	1	10719	10719	7831	73.06	gii619734722 gb C007557.1	5099034	7831	0.15	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
UC-83982	1	23692	23692	0	0	0	-	0	0	0	Unknow
UC-90958	1	38677	38677	0	0	0	-	0	0	0	Unknow
UC-93396	1	47805	47805	39463	82.55	gii332341332 gb C002729.1	5186416	40837	0.79	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-93470	1	41575	41575	41575	100	gii222031834 emb CU651637.1	4773108	43986	0.92	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-	1	24659	24659	14958	60.66	gii640850664 gb C	52416	15318	0.29	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella

93731						P007731.1]	38				a;s_Klebsiella pneumoniae
UC-93755	1	28603	28603	18494	64.66	gii523815970 gb C P006055.1]	4977480	18484	0.37	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-94079	1	87855	87855	0	0	0	-	0	0	0	Unknow
UC-108246	1	13020	13020	0	0	0	-	0	0	0	Unknow
C6040	1	12829	12829	5314	41.42	gii619734722 gb C P007557.1]	5099034	7803	0.15	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
C6065	1	12971	12971	11809	91.04	gii301795385 emb FP929140.1]	4587455	11806	0.26	516	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Unclassified;f__Unclassified;g__Unclassified;s__gamma proteobacterium HdN1
C6285	1	10341	10341	9562	92.47	gii110341805 gb C P000247.1]	4938920	9560	0.19	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C6511	1	12349	12349	8954	72.51	gii440045023 gb C P003938.1]	4762179	9041	0.19	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57
C681-4	1	12734	12734	12734	100	gii218430358 emb CU928163.2]	5202090	12734	0.24	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1540-7	1	17304	17304	9315	53.83	gii695172424 gb C P008929.1]	5317001	10558	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C1269-3	1	15089	15089	15089	100	gii26111730 gb AE 014075.1]	5231428	16514	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C360-10	1	63521	63521	41448	65.25	gii695172424 gb C P008929.1]	5317001	41450	0.78	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C181-7	1	43336	43336	21043	48.56	gii660577155 gb C P008797.1]	5396164	22490	0.42	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C3038-1	1	17603	17603	10642	60.46	gii307551844 gb C P001671.1]	5131397	10837	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C539-9	1	14189	14189	14189	100	gii312910970 dbj AP011957.1]	4954814	17377	0.35	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
C537-2	1	19893	19893	19893	100	gii170517292 gb C P000970.1]	5068389	20218	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C537-5	1	11304	11304	11304	100	gii170517292 gb C P000970.1]	5068389	11304	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C400-3	1	12292	12292	12292	100	gii569550235 gb C P003999.1]	5307003	12292	0.23	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C3470-2	1	23673	23673	23673	100	gii157065147 gb C P000802.1]	4643538	27149	0.58	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1737-1	1	16082	16082	12162	75.62	gii218354981 emb CU928158.2]	4588711	12163	0.27	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
C539-10	1	13485	13485	5720	42.42	gii312910970 dbj AP011957.1]	4954814	7873	0.16	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
C999-3	1	22349	22349	22349	100	gii218363708 emb CU928161.2]	5032268	24691	0.49	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C558-1	1	14724	14724	4802	32.61	gii549815675 gb C P006648.1]	5166857	5038	0.1	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
C3470-3	1	21895	21895	8083	36.92	gii660567586 gb C P008788.1]	6152190	8092	0.13	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
C539-8	1	14299	14299	7788	54.47	gii326698716 gb C P001875.2]	4703373	7984	0.17	305	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea ananatis
C746-1	1	16021	16021	15591	97.32	gii288730948 emb FN597254.1]	2350911	15656	0.67	373	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus gallolyticus
C2355-3	1	11130	11130	8791	78.98	gii440045023 gb C P003938.1]	4762179	8803	0.18	3	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Unclassified;s__Enterobacteriaceae bacterium strain FGI 57

C666-4	1	24857	24857	12409	49.92	gii402539130 gb C P003785.1	53867 05	12409	0.23	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C666-3	1	25951	25951	20579	79.3	gii597512677 emb FO834906.1	54388 94	20585	0.38	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1677-3	1	16062	16062	0	0	0	-	0	0	0	Unknow
C1304-4	1	13952	13952	7742	55.49	gii295054830 gb C P001918.1	53145 81	9521	0.18	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
C924-3	1	13125	13125	0	0	0	-	0	0	0	Unknow
C1078-4	1	10867	10867	9173	84.41	gii257751862 dbj AP010953.1	56972 40	9109	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C534-3	1	33347	33347	23436	70.28	gii605520020 gb C P007531.1	47061 01	23430	0.5	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
C1415-6	1	16572	16572	11637	70.22	gii595620023 gb C P006918.1	52933 01	17081	0.32	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1719-2	1	21755	21755	19729	90.69	gii349736152 gb C P003034.1	53135 31	19809	0.37	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1054-1	1	19622	19622	19622	100	gii222031834 emb CU651637.1	47731 08	23650	0.5	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C960-6	1	14183	14183	14183	100	gii170517292 gb C P000970.1	50683 89	16295	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2488-3	1	13501	13501	10198	75.54	gii326698716 gb C P001875.2	47033 73	10199	0.22	305	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea ananatis
C496-1	1	38873	38873	0	0	0	-	0	0	0	Unknow
C3760-3	1	13352	13352	0	0	0	-	0	0	0	Unknow
C1415-8	1	23691	23691	10662	45	gii150953431 gb C P000647.1	53151 20	10638	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella pneumoniae
C1056-4	1	10349	10349	10349	100	gii157076741 gb C P000800.1	49796 19	10349	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C2868-3	1	21162	21162	19891	93.99	gii675819050 emb LM995613.1	10000 52	19887	1.99	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1269-4	1	10199	10199	9906	97.13	gii307551844 gb C P001671.1	51313 97	11980	0.23	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
C1724-4	1	11483	11483	11183	97.39	gii569535620 gb C P007025.1	47018 75	11284	0.24	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
C583-6	1	10816	10816	10745	99.34	gii569535620 gb C P007025.1	47018 75	15726	0.33	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii
C1153-3	1	21734	21734	20640	94.97	gii218350208 emb CU928145.2	51548 62	20665	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-138722	1	19928	19928	10198	51.17	gii326698716 gb C P001875.2	47033 73	10199	0.22	305	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea ananatis
UC-140840	1	12714	12714	0	0	0	-	0	0	0	Unknow
UC-150128	1	19039	19039	16433	86.31	gii400173048 gb C P003737.1	47265 82	16428	0.35	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-151954	1	48984	48984	0	0	0	-	0	0	0	Unknow
C539-19	1	13061	13061	13006	99.58	gii383101383 gb C P002291.1	49352 94	19712	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

CS22-5	1	20852	20852	15647	75.04	gii595597955 gb C P007392.1	5054509	22810	0.45	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
CS27-3	1	12272	12272	3730	30.39	gii73854091 gb CP000038.1	4825265	3764	0.08	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella sonnei
UC-242	1	11228	11228	6294	56.06	gii215263233 emb FM1180568.1	4965553	6294	0.13	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-362	1	15369	15369	11195	72.84	gii218350208 emb CU928145.2	5154862	11463	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-418	1	19879	19879	8268	41.59	gii691220640 gb C P009454.1	4327607	8253	0.19	277	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea rwandensis
UC-424	1	19982	19982	11910	59.6	gii660567586 gb C P008788.1	6152190	11891	0.19	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
UC-525	1	17967	17967	17967	100	gii257757386 dbj AP010958.1	5449314	17967	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-536	1	11293	11293	6767	59.92	gii170517292 gb C P000970.1	5068389	7769	0.15	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-765	1	17151	17151	11531	67.23	gii339759707 gb C P002910.1	5259571	11867	0.23	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-824	1	14012	14012	14012	100	gii26111730 gb AE014075.1	5231428	16064	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-827	1	20429	20429	20429	100	gii309700213 emb FN649414.1	5153435	20452	0.4	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-970	1	26419	26419	19506	73.83	gii394343076 gb C P003683.1	6097032	23145	0.38	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca
UC-1019	1	12727	12727	11543	90.7	gii218354981 emb CU928158.2	4588711	11541	0.25	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
UC-1229	1	13353	13353	5098	38.18	gii527122546 gb C P003025.1	1975547	6064	0.31	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus lutetiensis
UC-1250	1	31608	31608	16778	53.08	gii569550235 gb C P003999.1	5307003	18258	0.34	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-1256	1	16699	16699	7280	43.6	gii284919779 emb FN554766.1	5241977	7280	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-1394	1	10014	10014	8124	81.13	gii110613622 gb C P000266.1	4574284	6278	0.14	261	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella flexneri
UC-1491	1	10984	10984	10984	100	gii365747213 gb C P002886.1	4734438	11127	0.24	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-1578	1	72584	72584	0	0	0	-	0	0	0	Unknow
UC-1683	1	45156	45156	35241	78.04	gii554510692 gb C P006784.1	5129938	35295	0.69	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-1700	1	36482	36482	36482	100	gii209157093 gb C P001164.1	5572075	36475	0.65	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-1845	1	11555	11555	9519	82.38	gii402539130 gb C P003785.1	5386705	9519	0.18	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-1872	1	12490	12490	11749	94.07	gii573966439 gb C P006027.1	5585613	11753	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-2573	1	14138	14138	10308	72.91	gii310757913 gb C P002287.1	7013095	12471	0.18	462	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Achromobacter;s__Achromobacter xylosoxidans
UC-2731	1	78557	78557	78553	99.99	gii582035815 gb C P004081.1	2961043	83081	2.81	72	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecalis
UC-2845	1	16383	16383	16383	100	gii209910450 dbj AP009240.1	4887515	16383	0.34	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-2941	1	19960	19960	16843	84.38	gii523815970 gb C P006055.1	4977480	17288	0.35	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica

UC-3101	1	11728	11728	0	0	0	-	0	0	0	Unknown
UC-176707	1	15577	15577	0	0	0	-	0	0	0	Unknown
UC-177731	1	20042	20042	20005	99.82	gi 406775301 gb CP003297.1	5253138	25727	0.49	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-177811	1	12184	12184	12184	100	gi 595597955 gb CP007392.1	5054509	12184	0.24	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-186777	1	13762	13762	0	0	0	-	0	0	0	Unknown
UC-187176	1	13433	13433	0	0	0	-	0	0	0	Unknown
UC-187526	1	44646	44646	15250	34.16	gi 662712225 gb CP008823.1	4852980	15274	0.31	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-201392	1	11330	11330	6268	55.32	gi 206564770 gb CP000964.1	5641239	6254	0.11	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-201428	1	12559	12559	8131	64.74	gi 675820478 emb LM997040.1	1374643	8135	0.59	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-201457	1	18687	18687	18687	100	gi 26111730 gb AE014075.1	5231428	21473	0.41	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-201528	1	12658	12658	12658	100	gi 26111730 gb AE014075.1	5231428	12658	0.24	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-201640	1	16846	16846	6016	35.71	gi 523806722 gb CP006048.1	4859931	24500	0.5	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-201691	1	19384	19384	0	0	0	-	0	0	0	Unknown
UC-202265	1	11600	11600	7863	67.78	gi 355418401 gb CP002211.1	5038386	7863	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-202793	1	10078	10078	10078	100	gi 334732565 gb CP002824.1	5280350	10078	0.19	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
UC-202834	1	13209	13209	13209	100	gi 443901024 emb F0203355.1	5419609	13209	0.24	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
UC-202961	1	10623	10623	5267	49.58	gi 334732565 gb CP002824.1	5280350	5345	0.1	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
UC-212127	1	10872	10872	0	0	0	-	0	0	0	Unknown
UC-212461	1	14879	14879	14865	99.91	gi 383101383 gb CP002291.1	4935294	24986	0.51	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli

UC-21288	1	23732	23732	11754	49.53	gii660567586 gb C P008788.1	6152190	12459	0.2	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella oxytoca
UC-213590	1	11560	11560	6725	58.17	gii640850664 gb C P007731.1	5241638	6825	0.13	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
UC-213693	1	11057	11057	10702	96.79	gii364515570 gb C P003200.1	5333942	10914	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
UC-215113	1	10648	10648	7920	74.38	gii595597955 gb C P007392.1	5054509	8209	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;a;s__Escherichia coli
UC-215119	1	18296	18296	18296	100	gii339759707 gb C P002910.1	5259571	18559	0.35	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
UC-215123	1	21625	21625	0	0	0	-	0	0	0	Unknown
UC-3784	1	39440	39440	34312	87	gii157076741 gb C P000800.1	4979619	34278	0.69	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;a;s__Escherichia coli
UC-3817	1	72883	72883	41349	56.73	gii660567586 gb C P008788.1	6152190	45220	0.74	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella oxytoca
UC-3865	1	22923	22923	18056	78.77	gii364515570 gb C P003200.1	5333942	18925	0.35	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
UC-4008	1	13846	13846	0	0	0	-	0	0	0	Unknown
UC-4054	1	16308	16308	8568	52.54	gii564743501 gb C P005995.1	4783867	8570	0.18	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;a;s__Salmonella enterica
UC-4146	1	16250	16250	9369	57.66	gii443901024 emb F0203355.1	5419609	9505	0.18	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;a;s__Enterobacter aerogenes
UC-4380	1	16362	16362	10057	61.47	gii573966439 gb C P006027.1	5585613	8793	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;a;s__Escherichia coli
UC-4423	1	12610	12610	12610	100	gii554510692 gb C P006784.1	5129938	13025	0.25	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;a;s__Escherichia coli
UC-4481	1	19781	19781	19633	99.25	gii187427012 gb C P001063.1	4615997	48100	1.04	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;a;s__Shigella boydii
UC-4681	1	19559	19559	0	0	0	-	0	0	0	Unknown
UC-4948	1	15385	15385	9928	64.53	gii365747213 gb C P002886.1	4734438	14794	0.31	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;a;s__Enterobacter cloacae
UC-5340	1	15418	15418	0	0	0	-	0	0	0	Unknown
UC-5358	1	10181	10181	10118	99.38	gii206564770 gb C P000964.1	5641239	10202	0.18	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella pneumoniae
UC-5370	1	12738	12738	10040	78.82	gii157081501 gb C P000822.1	4720462	12297	0.26	6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;a;s__Citrobacter koseri
UC-5427	1	13386	13386	10091	75.38	gii308746527 gb C P002272.1	4814049	10090	0.21	8	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;a;s__Enterobacter lignolyticus
UC-5808	1	13729	13729	13729	100	gii218430358 emb CU928163.2	5202090	13729	0.26	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;a;s__Escherichia coli
UC-6256	1	11680	11680	6642	56.87	gii585129876 gb C P006713.1	2359009	6643	0.28	895	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;a;s__Bifidobacterium breve
UC-6479	1	13261	13261	12312	92.84	gii187427012 gb C P001063.1	4615997	23728	0.51	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;a;s__Shigella boydii
UC-6503	1	18792	18792	17379	92.48	gii394343076 gb C P003683.1	6097032	18426	0.3	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a;s__Klebsiella oxytoca

UC-7012	1	10535	10535	10535	100	gii110341805 gb C P000247.1	4938920	10558	0.21	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-7325	1	10484	10484	10484	100	gii573966439 gb C P006027.1	5585613	18286	0.33	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-7527	1	16168	16168	16168	100	gii218350208 emb CU928145.2	5154862	16168	0.31	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-7531	1	10039	10039	6145	61.21	gii383101383 gb C P002291.1	4935294	6172	0.13	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-7730	1	36384	36384	0	0	0	-	0	0	0	Unknow
UC-7893	1	16131	16131	0	0	0	-	0	0	0	Unknow
UC-217427	1	11668	11668	0	0	0	-	0	0	0	Unknow
UC-217628	1	12593	12593	8117	64.46	gii215263233 emb FM180568.1	4965553	8121	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-217652	1	19479	19479	0	0	0	-	0	0	0	Unknow
UC-224107	1	11349	11349	11349	100	gii309700213 emb FN649414.1	5153435	11349	0.22	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-225189	1	25498	25498	0	0	0	-	0	0	0	Unknow
UC-226407	1	17816	17816	17306	97.14	gii386922183 gb C P001560.1	4158725	17309	0.42	273	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shimwellia;s__Shimwellia blattae
UC-226418	1	12528	12528	0	0	0	-	0	0	0	Unknow
UC-226440	1	13735	13735	0	0	0	-	0	0	0	Unknow
UC-227493	1	11759	11759	6355	54.04	gii339277069 emb FR875178.1	1929905	6353	0.33	379	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus thermophilus
UC-227495	1	12478	12478	5736	45.97	gii696593549 gb C P009565.1	4726694	5732	0.12	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-227496	1	13636	13636	5182	38	gii662712225 gb C P008823.1	4852980	5187	0.11	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter cloacae
UC-227530	1	23818	23818	7771	32.63	gii582030173 gb C P006659.1	5435369	8609	0.16	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-227536	1	12276	12276	10150	82.68	gii339759707 gb C P002910.1	5259571	10137	0.19	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-227662	1	11620	11620	4519	38.89	gii559161187 gb C P006811.1	1887251	3896	0.21	193	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus johnsonii
UC-22768	1	13485	13485	13485	100	gii365906294 gb C P003218.1	5974109	13678	0.23	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca

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UC-227685	1	10797	10797	10795	99.98	gii569535620 gb C P007025.1	4701875	13276	0.28	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii	
UC-227755	1	18886	18886	0	0	0	-	0	0	0	Unknow	
UC-227763	1	11215	11215	0	0	0	-	0	0	0	Unknow	
UC-227780	1	11136	11136	11136	100	gii569535620 gb C P007025.1	4701875	12135	0.26	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii	
UC-227905	1	13024	13024	13024	100	gii569535620 gb C P007025.1	4701875	13025	0.28	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii	
UC-228815	1	10916	10916	10916	100	gii569535620 gb C P007025.1	4701875	11404	0.24	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii	
UC-229010	1	13453	13453	13449	99.97	gii569535620 gb C P007025.1	4701875	14837	0.32	264	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia albertii	
UC-229103	1	19213	19213	8185	42.6	gii573932891 gb C P006262.1	5402276	8462	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-230105	1	13033	13033	8480	65.07	gii332341332 gb C P002729.1	5186416	8474	0.16	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-230116	1	21369	21369	20932	97.95	gii333109300 gb C P002743.1	2327492	21235	0.91	895	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium breve	
UC-233196	1	10670	10670	0	0	0	-	0	0	0	Unknow	
UC-236879	1	16879	16879	0	0	0	-	0	0	0	Unknow	
UC-240648	1	13039	13039	11419	87.58	gii333109300 gb C P002743.1	2327492	13155	0.57	895	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium breve	
UC-8354	1	23037	23037	13343	57.92	gii110341805 gb C P000247.1	4938920	13341	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-8356	1	22525	22525	7973	35.4	gii674133359 gb C P009208.1	5374834	12780	0.24	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae	
UC-9375	1	10886	10886	0	0	0	-	0	0	0	Unknow	
UC-9468	1	28270	28270	28270	100	gii170517292 gb C P000970.1	5068389	30807	0.61	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-9476	1	17755	17755	14562	82.02	gii257757386 dbj AP010958.1	5449314	14554	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-9481	1	15319	15319	15319	100	gii115511419 gb C P000468.1	5082025	16351	0.32	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	
UC-9490	1	10749	10749	8940	83.17	gii218350208 emb CU928145.2	5154862	8913	0.17	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli	

UC-10414	1	18921	18921	18921	100	gii307551844 gb C P001671.1	5131397	19872	0.39	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-10421	1	10038	10038	3139	31.27	gii187427012 gb C P001063.1	4615997	100710	2.18	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella boydii
UC-10682	1	11646	11646	10002	85.88	gii218350208 emb CU928145.2	5154862	15120	0.29	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-10915	1	42999	42999	0	0	0	-	0	0	0	Unknow
UC-11344	1	68479	68479	35513	51.86	gii526125113 gb C P006608.1	4683551	35505	0.76	13	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella bongori
UC-11421	1	10329	10329	10329	100	gii257751862 dbj AP010953.1	5697240	10329	0.18	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-11669	1	13717	13717	6522	47.55	gii605537200 gb C P007533.1	4603849	8041	0.17	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-11863	1	12034	12034	5606	46.58	gii523815970 gb C P006055.1	4977480	6599	0.13	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella enterica
UC-11864	1	10066	10066	8443	83.88	gii187427012 gb C P001063.1	4615997	8439	0.18	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella boydii
UC-12182	1	14752	14752	0	0	0	-	0	0	0	Unknow
UC-12289	1	15880	15880	0	0	0	-	0	0	0	Unknow
UC-12430	1	29018	29018	21910	75.5	gii674299053 gb C P009072.1	5130767	25851	0.5	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
UC-281134	1	58549	58549	0	0	0	-	0	0	0	Unknow
UC-281383	1	13053	13053	12898	98.81	gii218354981 emb CU928158.2	4588711	12898	0.28	2	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia fergusonii
UC-284586	1	12788	12788	8819	68.96	gii575870901 emb HG530068.1	7586152	14282	0.19	352	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas aeruginosa
UC-295887	1	12391	12391	7794	62.9	gii619734722 gb C P007557.1	5099034	9438	0.19	267	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__Citrobacter freundii
UC-297627	1	22952	22952	0	0	0	-	0	0	0	Unknow
UC-298927	1	12584	12584	8720	69.29	gii667708115 gb C P006798.1	5348284	8703	0.16	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-300068	1	11959	11959	0	0	0	-	0	0	0	Unknow
UC-300082	1	10692	10692	4448	41.6	gii291558333 emb FP929061.1	3114788	4547	0.15	33	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Unclassified;g__Unclassified;s__butyrate-producing bacterium SSC/2
UC-303369	1	36840	36840	0	0	0	-	0	0	0	Unknow
UC-12997	1	37642	37642	30582	81.24	gii187427012 gb C P001063.1	4615997	33080	0.72	263	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella boydii
UC-13142	1	12970	12970	0	0	0	-	0	0	0	Unknow

UC-13448	1	11894	11894	4258	35.8	gii73854091 gb CP000038.1	4825265	4288	0.09	262	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Shigella;s__Shigella_sonnei
UC-15672	1	48875	48875	21052	43.07	gii660577155 gb CP008797.1	5396164	22844	0.42	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_pneumoniae
UC-15719	1	14536	14536	14536	100	gii674133359 gb CP009208.1	5374834	14536	0.27	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_pneumoniae
UC-15931	1	14488	14488	0	0	0	-	0	0	0	Unknow
UC-16995	1	45265	45265	0	0	0	-	0	0	0	Unknow
UC-320067	1	20647	20647	17718	85.81	gii115249003 emb AM180355.1	4290252	17734	0.41	22	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium;s__Peptoclostridium_difficile
UC-325828	1	41458	41458	0	0	0	-	0	0	0	Unknow
UC-325917	1	13473	13473	7182	53.31	gii309700213 emb FN649414.1	5153435	7223	0.14	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia_coli
UC-325997	1	22048	22048	17549	79.59	gii549815675 gb CP006648.1	5166857	17548	0.34	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_pneumoniae
UC-326106	1	10738	10738	4228	39.37	gii523806722 gb CP006048.1	4859931	10604	0.22	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella_enterica
UC-326245	1	22248	22248	11583	52.06	gii660567586 gb CP008788.1	6152190	11561	0.19	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_oxytoca
UC-327575	1	10386	10386	6816	65.63	gii523815970 gb CP006055.1	4977480	7082	0.14	5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__Salmonella_enterica
UC-327576	1	11113	11113	6387	57.47	gii570286338 gb CP006580.1	5369929	6387	0.12	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter_cloacae
UC-330826	1	14468	14468	12648	87.42	gii595583568 gb CP007265.1	4758629	12644	0.27	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia_coli
UC-17274	1	15173	15173	15173	100	gii254044096 gb CP001617.1	3197759	15174	0.47	385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum
UC-17674	1	13418	13418	0	0	0	-	0	0	0	Unknow
UC-17818	1	15395	15395	10282	66.79	gii350278064 gb CP003058.1	2487765	10540	0.42	606	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Acidaminococcaceae;g__Acidaminococcus;s__Acidaminococcus_intestini
UC-18493	1	14348	14348	14348	100	gii218350208 emb CU928145.2	5154862	14348	0.28	1	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia_coli
UC-18562	1	11844	11844	6929	58.5	gii392322800 gb CP003678.1	4968248	6958	0.14	4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter_cloacae
UC-18567	1	16915	16915	0	0	0	-	0	0	0	Unknow
UC-20182	1	21022	21022	10565	50.26	gii365906294 gb CP003218.1	5974109	11112	0.19	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_oxytoca
UC-20395	1	12135	12135	10607	87.41	gii667708115 gb CP006798.1	5348284	10552	0.2	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;a__Klebsiella_pneumoniae
UC-21146	1	19413	19413	14972	77.12	gii527122546 gb CP003025.1	1975547	15084	0.76	207	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_lutetiensis

UC-21511	1	13587	13587	10245	75.4	gii512154926 gb C P006011.1	19477 06	10216	0.52	367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus reuteri
UC-22863	1	70800	70800	49612	70.07	gii443901024 emb FO203355.1	54196 09	51432	0.95	15	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter aerogenes
UC-23254	1	12103	12103	11938	98.64	gii364515570 gb C P003200.1	53339 42	17890	0.34	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-23492	1	11216	11216	0	0	0	-	0	0	0	Unknow
UC-23584	1	24707	24707	24101	97.55	gii582030173 gb C P006659.1	54353 69	25288	0.47	7	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella pneumoniae
UC-23585	1	13290	13290	0	0	0	-	0	0	0	Unknow
UC-24295	1	16058	16058	0	0	0	-	0	0	0	Unknow
UC-24626	1	11138	11138	10402	93.39	gii365906294 gb C P003218.1	59741 09	10404	0.17	12	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella oxytoca

Supplemental Table S6 The CheckM estimate for MLG > 500 Kpb.

MLGid	ContigNum	TotalSize	Marker lineage	# genomes	# markers	# marker sets	0	1	2	3	4	5+	Completeness	Contamination	Strain heterogeneity
MLG27	22	2321219	f__Bifidobacteriaceae (UID1462)	65	476	217	0	472	4	0	0	0	100	1.61	100
MLG43	34	1824663	f__Leuconostocaceae (UID486)	29	443	178	2	426	15	0	0	0	99.33	5.81	86.67
MLG35	60	2176388	o__Lactobacillales (UID544)	293	475	267	5	465	5	0	0	0	98.75	1.25	60
MLG29	41	2264125	o__Lactobacillales (UID355)	490	336	184	3	268	65	0	0	0	98.64	21.94	100
MLG4	757	4965613	k__Bacteria (UID203)	5449	104	58	1	28	57	16	2	0	98.28	113.89	31.62
MLG28	103	2284401	o__Lactobacillales (UID374)	471	350	191	7	275	67	1	0	0	97.82	22.91	98.57
MLG33	74	2190432	c__Betaproteobacteria (UID3888)	323	387	234	9	378	0	0	0	0	97.41	0	0
MLG22	164	2483450	c__Bacilli (UID285)	586	319	176	5	314	0	0	0	0	97.16	0	0
MLG15	54	3265280	o__Actinomycetales (UID1530)	622	258	152	9	249	0	0	0	0	96.71	0	0
MLG36	74	2080848	o__Lactobacillales (UID374)	471	350	191	46	302	2	0	0	0	96.45	0.63	50
MLG59	37	1514318	f__Leuconostocaceae (UID486)	29	443	178	30	413	0	0	0	0	96.3	0	0
MLG56	137	1618295	o__Lactobacillales (UID544)	293	475	267	35	402	36	2	0	0	95.92	8.43	88.1
MLG40	23	1937014	f__Bifidobacteriaceae (UID1458)	77	464	220	19	438	5	2	0	0	95.52	2.35	0
MLG30	41	2234142	p__Actinobacteria (UID2112)	31	211	124	13	197	1	0	0	0	95.26	0.81	100
MLG13	77	3341033	o__Lactobacillales (UID544)	293	475	267	22	421	29	3	0	0	95.04	7.2	18.42
MLG42	159	1860668	g__Campylobacter (UID3076)	40	926	174	42	825	56	3	0	0	93.62	6.34	86.15
MLG3	161	4995154	f__Enterobacteriaceae (UID5121)	138	1162	336	118	968	76	0	0	0	93.02	6.77	82.89
MLG20	526	2495233	o__Lactobacillales (UID544)	293	475	267	68	384	19	4	0	0	92.31	6.72	100
MLG23	167	2476783	g__Lactobacillus (UID380)	58	449	129	69	342	38	0	0	0	90.27	10.17	81.58
MLG21	236	2486742	o__Lactobacillales (UID544)	293	475	267	83	303	82	7	0	0	89.77	22.88	98.06
MLG12	1180	3543762	o__Clostridiales (UID1212)	172	263	149	28	128	88	19	0	0	89.32	51.95	3.45
MLG10	875	3711220	o__Lactobacillales (UID544)	293	475	267	83	218	128	39	6	1	89.26	56.92	24.05
MLG16	143	2667936	o__Lactobacillales (UID462)	85	367	162	70	278	17	2	0	0	88.82	6.48	82.61
MLG11	370	3662098	k__Bacteria (UID203)	5449	104	58	14	39	37	14	0	0	88.56	82.29	30.38
MLG48	200	1732615	o__Lactobacillales (UID543)	294	469	262	63	397	9	0	0	0	87.12	2.54	77.78
MLG41	95	1878811	o__Lactobacillales (UID544)	293	475	267	93	334	48	0	0	0	86.59	10.86	89.58

MLG50	331	1721485	o__Lactobacillales (UID374)	471	350	191	78	262	9	0	1	0	86.5	3.58	20
MLG55	196	1620717	f__Pasteurellaceae (UID4932)	83	767	440	118	645	4	0	0	0	84.92	0.91	50
MLG37	264	2074492	o__Lactobacillales (UID543)	294	471	264	70	380	21	0	0	0	83.08	4.31	85.71
MLG34	24	2177005	o__Selenomonadales (UID1024)	64	334	167	46	287	1	0	0	0	82.63	0.6	0
MLG51	256	1676920	o__Lactobacillales (UID543)	294	472	265	79	389	4	0	0	0	82.45	1.26	50
MLG46	666	1777692	o__Clostridiales (UID1375)	50	332	124	72	245	14	1	0	0	82.3	7.34	88.24
MLG18	261	2593772	o__Lactobacillales (UID544)	293	473	265	104	356	13	0	0	0	82.28	2.91	0
MLG14	69	3302369	f__Comamonadaceae (UID4119)	39	693	323	128	554	11	0	0	0	80.14	1.05	0
MLG54	244	1644177	g__Lactobacillus (UID377)	91	430	154	112	318	0	0	0	0	77.82	0	0
MLG31	675	2229913	k__Bacteria (UID203)	5449	104	58	52	37	12	3	0	0	76.02	23.43	61.9
MLG19	75	2541211	f__Micrococcaceae (UID1623)	39	457	218	88	364	5	0	0	0	74.33	1.15	0
MLG38	227	2072184	f__Bifidobacteriaceae (UID1460)	70	502	225	131	254	108	9	0	0	74.32	28.23	31.11
MLG63	44	1275284	k__Bacteria (UID203)	5449	104	58	51	51	2	0	0	0	74.14	3.45	100
MLG26	139	2364650	k__Bacteria (UID203)	5449	103	57	56	47	0	0	0	0	71.93	0	0
MLG17	477	2634625	k__Bacteria (UID203)	5449	104	58	56	48	0	0	0	0	68.97	0	0
MLG61	47	1331243	o__Selenomonadales (UID1024)	64	334	167	124	210	0	0	0	0	68.26	0	0
MLG68	53	1141236	o__Lactobacillales (UID462)	85	367	162	142	224	1	0	0	0	67.16	0.12	100
MLG32	642	2218398	k__Bacteria (UID203)	5449	104	58	60	42	2	0	0	0	65.86	3.45	50
MLG52	81	1658652	k__Bacteria (UID203)	5449	104	58	58	42	4	0	0	0	65.52	5.17	75
MLG65	70	1199191	o__Lactobacillales (UID355)	490	336	184	131	136	63	6	0	0	64.34	23.43	29.63
MLG47	501	1733973	o__Actinomycetales (UID1593)	69	400	198	145	248	7	0	0	0	62.29	2.01	42.86
MLG44	294	1783400	f__Comamonadaceae (UID4119)	39	693	323	263	424	6	0	0	0	61.42	0.83	50
MLG53	76	1656741	o__Lactobacillales (UID544)	293	474	267	210	255	7	2	0	0	58.55	2.91	30.77
MLG5	105	4914501	k__Bacteria (UID203)	5449	102	57	62	40	0	0	0	0	56.3	0	0
MLG74	96	1059069	g__Streptococcus (UID684)	26	668	229	314	348	6	0	0	0	56.16	0.5	66.67
MLG9	174	4215722	k__Bacteria (UID203)	5449	104	58	69	35	0	0	0	0	55.17	0	0
MLG77	19	1021675	o__Selenomonadales (UID1024)	64	334	167	141	193	0	0	0	0	52.69	0	0
MLG39	1311	1948664	k__Bacteria (UID203)	5449	104	58	68	31	5	0	0	0	52.59	7.76	100
MLG1	1389	9438116	k__Bacteria (UID203)	5449	103	57	68	20	14	1	0	0	52.11	25.44	70.59

MLG64	161	1222023	k__Bacteria (UID203)	5449	104	58	69	35	0	0	0	0	51.72	0	0
MLG6	165	4910119	k__Bacteria (UID203)	5449	104	58	72	30	2	0	0	0	50	3.45	50
MLG24	297	2474294	k__Bacteria (UID203)	5449	103	57	69	34	0	0	0	0	50	0	0
MLG78	106	1010880	p__Actinobacteria (UID2112)	31	211	124	120	91	0	0	0	0	47.98	0	0
MLG108	127	639830	k__Bacteria (UID203)	5449	104	58	68	36	0	0	0	0	43.73	0	0
MLG58	620	1538617	c__Bacilli (UID285)	586	325	181	171	121	20	13	0	0	41.26	13.86	22.03
MLG97	138	683941	k__Bacteria (UID203)	5449	104	58	74	28	2	0	0	0	40.63	3.45	100
MLG66	450	1157363	k__Bacteria (UID203)	5449	104	58	77	26	1	0	0	0	40.52	1.72	100
MLG102	16	629008	o__Lactobacillales (UID544)	293	475	267	300	175	0	0	0	0	39.77	0	0
MLG101	206	632622	k__Bacteria (UID203)	5449	104	58	79	24	1	0	0	0	36.55	1.72	100
MLG76	25	1027933	k__Bacteria (UID203)	5449	103	58	80	23	0	0	0	0	36.21	0	0
MLG81	555	926357	o__Burkholderiales (UID4000)	193	427	214	241	172	14	0	0	0	35.46	3.68	14.29
MLG75	519	1040289	k__Bacteria (UID203)	5449	104	58	81	23	0	0	0	0	33.62	0	0
MLG69	34	1139519	k__Bacteria (UID203)	5449	104	58	81	23	0	0	0	0	33.1	0	0
MLG62	308	1319085	c__Bacilli (UID285)	586	325	181	216	103	6	0	0	0	32.8	2.58	33.33
MLG80	41	970244	o__Selenomonadales (UID1024)	64	334	167	211	123	0	0	0	0	31.14	0	0
MLG92	129	715791	k__Bacteria (UID203)	5449	104	58	84	20	0	0	0	0	30.17	0	0
MLG49	180	1724937	k__Bacteria (UID203)	5449	104	58	88	15	1	0	0	0	27.59	1.72	100
MLG94	315	704704	k__Bacteria (UID203)	5449	104	58	81	23	0	0	0	0	27.35	0	0
MLG106	21	552938	k__Bacteria (UID203)	5449	104	58	85	19	0	0	0	0	25.86	0	0
MLG82	434	884702	k__Bacteria (UID203)	5449	104	58	77	26	1	0	0	0	25.63	0.34	0
MLG2	2359	7707564	root (UID1)	5656	56	24	50	4	1	1	0	0	25	12.5	25
MLG73	162	1065230	k__Bacteria (UID203)	5449	104	58	90	14	0	0	0	0	22.41	0	0
MLG90	116	735698	k__Bacteria (UID203)	5449	104	58	89	15	0	0	0	0	20.69	0	0
MLG93	186	705157	k__Bacteria (UID203)	5449	104	58	92	12	0	0	0	0	19.83	0	0
MLG57	172	1611726	k__Bacteria (UID203)	5449	104	58	89	13	2	0	0	0	18.97	1.72	100
MLG8	990	4226704	root (UID1)	5656	56	24	52	3	1	0	0	0	16.67	4.17	100
MLG25	78	2459981	root (UID1)	5656	56	24	52	4	0	0	0	0	16.67	0	0
MLG83	969	861841	k__Bacteria (UID203)	5449	103	58	93	9	1	0	0	0	15.52	1.72	100

MLG71	171	1094424	k__Bacteria (UID203)	5449	104	58	92	11	1	0	0	0	14.81	1.72	0
MLG104	109	582462	k__Bacteria (UID203)	5449	104	58	95	9	0	0	0	0	13.79	0	0
MLG100	121	661486	k__Bacteria (UID203)	5449	104	58	93	11	0	0	0	0	13.79	0	0
MLG60	56	1470060	k__Bacteria (UID203)	5449	104	58	97	7	0	0	0	0	12.07	0	0
MLG95	99	697660	k__Bacteria (UID203)	5449	104	58	99	5	0	0	0	0	8.62	0	0
MLG99	46	670827	root (UID1)	5656	56	24	54	2	0	0	0	0	8.33	0	0
MLG98	180	679117	root (UID1)	5656	56	24	54	2	0	0	0	0	8.33	0	0
MLG85	190	816487	k__Bacteria (UID1453)	901	171	117	144	27	0	0	0	0	7.78	0	0
MLG79	122	990698	k__Bacteria (UID203)	5449	104	58	99	5	0	0	0	0	7.76	0	0
MLG45	220	1782103	k__Bacteria (UID203)	5449	104	58	99	5	0	0	0	0	6.03	0	0
MLG72	690	1083551	k__Bacteria (UID203)	5449	103	57	96	7	0	0	0	0	5.9	0	0
MLG88	16	782047	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
MLG87	36	806618	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
MLG70	312	1111766	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
MLG67	75	1148290	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
MLG105	180	576136	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
MLG103	280	622524	k__Bacteria (UID203)	5449	104	58	103	1	0	0	0	0	0.86	0	0
MLG96	14	693032	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
MLG91	247	730785	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
MLG89	131	761333	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
MLG86	282	809037	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
MLG84	496	841665	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
MLG7	5889	4294619	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0

Supplemental Table S9: the OOB classification error rates of the 1000 genes (Figure 3 and Supplementary Table S8).

Class	S1	S2	S3	S4	Class error (%)
S1	86.07	10.21	1.74	1.98	13.93
S2	36.53	32.16	15.79	15.53	67.84
S3	13.44	7.45	39.32	39.79	60.68
S4	3.9	7.79	43.03	45.28	54.72

Note: OOB estimate of error rate: 49.29%.

Supplemental Table S12: the CAZy annotation of microbiome of S3/4 giant pandas and other mammals.

		GH2 3	CB M50	GH2 8	CB M48	GH2 6	GH1 3	GH4	GH5 1	GH3 5	GH1 02	GH2 4	GH9	AA6	GH3 7	AA1	GH5	GH3 0	AA3	CB M5	GH8	CB M34	GH8 0	GH4 7	GH6 3	GH1 9	GH1	GH8	GH3 8	GH3 1
Armadillo	carnivore	0.00 100 9	0.00 055 7	0.00 0418	0.00 1148	3.48 E-05	0.00 2471	0.00 0209	0.00 087	0.00 1496	0	6.96 E-05	0.00 0104	0	0	3.48 E-05	0.00 0452	0.00 0139	0	3.48 E-05	0	0.00 0418	0	0	0	0	0.00 0905	3.48 E-05	0.00 0418	0.00 1462
BelugaWhale	carnivore	4.80 E-05	3.34 E-05	3.55 E-05	5.43 E-05	4.18 E-06	1.04 E-05	8.35 E-06	5.85 E-05	8.35 E-06	1.67 E-05	0	0	6.26 E-06	4.18 E-06	2.71 E-05	1.04 E-05	1.67 E-05	1.04 E-05	1.04 E-05	0	0	0	1.88 E-05	4.18 E-06	6.26 E-06	0	8.35 E-05	1.88 E-05	2.09 E-05
BottlenoseDolphin	carnivore	9.87 E-07	4.93 E-06	0	6.91 E-06	0	5.92 E-06	0	4.93 E-06	1.18 E-05	0	0	0	2.96 E-06	0	0	0	6.91 E-06	0	1.97 E-06	0	9.87 E-07	0	5.92 E-06	0	0	3.95 E-06	4.93 E-06	0	2.07 E-05
BushDog	carnivore	0.00 052 6	0.00 068 1	0.00 0541	0.00 116	9.28 E-05	0.00 2181	0.00 0186	0.00 0696	0.00 0975	1.55 E-05	1.55 E-05	3.09 E-05	0	0	0.00 0449	9.28 E-05	0	0	0	1.55 E-05	0.00 034	0	0	0.00 0325	0	0.00 0588	0.00 017	0.00 0387	0.00 0387
Coyote	carnivore	0.00 042 8	0.00 036 9	0.00 0164	0.00 0253	6.57 E-05	0.00 0642	9.50 E-05	0.00 0275	0.00 0269	9.96 E-06	4.25 E-05	0.00 0149	1.99 E-06	1.99 E-06	1.33 E-06	0.00 0103	0.00 0104	6.64 E-07	1.46 E-05	1.99 E-06	0.00 01	0	8.63 E-06	9.56 E-05	8.63 E-06	0.00 0284	5.45 E-05	9.16 E-05	0.00 0212
Echidna	carnivore	0.00 107 3	0.00 114 9	0.00 023	0.00 0536	0.00 0138	0.00 2206	0.00 0169	0.00 1777	0.00 0444	7.66 E-05	1.53 E-05	3.06 E-05	0	0	7.66 E-05	0.00 023	0.00 0337	3.06 E-05	9.19 E-05	7.66 E-05	0.00 0306	0	3.06 E-05	0	0.00 2697	0.00 0444	0.00 0245	0.00 0598	
Fisher	carnivore	0.00 056 4	0.00 053 8	0.00 0253	0.00 0708	0.00 0177	0.00 153	0.00 0409	0.00 0464	0.00 0756	4.05 E-06	0.00 0221	5.03 E-05	0	3.24 E-06	7.30 E-06	0.00 0447	4.13 E-05	1.62 E-06	7.62 E-05	4.86 E-06	0.00 0202	0	1.30 E-05	0.00 0186	1.86 E-05	0.00 1179	0.00 0169	0.00 0558	0.00 0486
HumpbackWhale	carnivore	0.00 034 4	0.00 070 4	0.00 0256	0.00 0524	0.00 0194	0.00 1322	6.20 E-05	0.00 0562	0.00 0865	7.87 E-06	4.03 E-05	4.13 E-05	0	0	5.90 E-06	0.00 0346	0.00 0137	0	0.00 0103	0	0.00 0116	1.97 E-06	4.62 E-05	0.00 0126	1.48 E-05	0.00 0107	7.18 E-05	0.00 0256	0.00 049
Hyena	carnivore	0.00 046 2	0.00 105 2	0.00 0511	0.00 0891	0.00 0117	0.00 1651	0.00 0278	0.00 0862	0.00 0818	0	5.84 E-05	4.38 E-05	0	0	4.38 E-05	0.00 038	7.30 E-05	0	2.92 E-05	4.38 E-05	0.00 0161	0	0	0.00 0146	0	0.00 019	8.76 E-05	0.00 0248	0.00 0394
Lion1	carnivore	0.00 063 2	0.00 062 3	0.00 0351	0.00 1194	0.00 014	0.00 1897	0.00 0211	0.00 0983	0.00 0702	0	0.00 0211	0	0	0	7.02 E-05	0.00 0211	7.02 E-05	0	0	0	0.00 0351	0	7.02 E-05	0	0	0.00 1897	0.00 0702	0.00 0562	0.00 0843
Lion2	carnivore	0.00 1	0.00 144	0.00 0547	0.00 0867	0.00 0147	0.00 2133	0.00 0533	0.00 1346	0.00 152	9.33 E-05	0.00 028	0.00 0253	4.00 E-05	0.00 0187	0.00 0213	0.00 0387	0.00 02	0.00 012	6.67 E-05	0.00 0133	6.67 E-05	2.67 E-05	0.00 0307	4.00 E-05	0.00 12	0.00 0253	0.00 0427	0.00 0827	
PolarBear	carnivore	0.00 141 9	0.00 191 6	0.00 0479	0.00 0798	0.00 016	0.00 2359	0.00 1011	0.00 2164	0.00 1454	0.00 0266	0.00 0319	0.00 0692	0.00 0142	0.00 0372	0.00 0266	0.00 0426	0.00 0514	0.00 0319	0.00 0922	0.00 0443	0.00 0408	0.00 0266	5.32 E-05	0.00 0568	0.00 0213	0.00 1153	0.00 0195	0.00 0674	0.00 0709
RightWhaleF11	carnivore	0.00 028 1	0.00 069 1	0.00 0268	0.00 0565	0.00 0186	0.00 1139	0.00 017	0.00 0498	0.00 0755	0	8.78 E-05	2.35 E-05	0	0	0.00 0426	8.23 E-05	0.00 0129	0	0.00 0173	0	0.00 0173	0	1.63 E-05	0.00 0112	2.44 E-05	0.00 0139	7.33 E-05	0.00 0296	0.00 0307
RightWhaleF16	carnivore	0.00 031 1	0.00 069 7	0.00 0267	0.00 0486	0.00 0115	0.00 1322	5.19 E-05	0.00 0579	0.00 0789	6.49 E-06	1.25 E-05	7.53 E-05	0	0	8.65 E-07	0.00 0355	0.00 0141	0	8.91 E-05	8.65 E-07	0.00 0106	0	3.98 E-05	0.00 013	1.90 E-05	8.22 E-05	6.32 E-05	0.00 0225	0.00 0414
RightWhaleF9	carnivore	0.00 036 4	0.00 125 8	0.00 0326	0.00 0459	0.00 0109	0.00 1445	0.00 0141	0.00 055	0.00 0799	8.17 E-06	1.63 E-05	6.44 E-05	2.04 E-06	0	2.04 E-06	0.00 0343	0.00 0157	0	0.00 0108	0	8.58 E-05	0	5.42 E-05	0.00 012	1.74 E-05	9.20 E-05	7.56 E-05	0.00 0276	0.00 0455
Gorilla	herbivore	0.00 032 1	0.00 096 3	0.00 0201	0.00 0562	8.02 E-05	0.00 1203	0	0.00 0562	0.00 0762	0	0	4.01 E-05	0	0	0.00 0481	4.01 E-05	0	4.01 E-05	4.01 E-05	0.00 012	0	0	4.01 E-05	4.01 E-05	0.00 0281	0.00 012	8.02 E-05	0.00 0361	
AfricanElephant	herbivore	0.00 019 2	0.00 041 9	0.00 0206	0.00 0199	7.81 E-05	0.00 0724	0.00 0121	0.00 0369	0.00 0405	7.10 E-06	2.84 E-05	7.81 E-05	0	0	0.00 0206	0.00 0121	0	0	7.81 E-05	3.55 E-05	0	0	2.84 E-05	7.10 E-06	6.39 E-05	1.42 E-05	8.52 E-05	0.00 0412	
BigHornsheepSD	herbivore	0.00 050 4	0.00 118 2	0.00 0263	0.00 0898	0.00 0197	0.00 0372	0.00 0504	0.00 1182	0	8.76 E-05	4.38 E-05	0	0	0	0.00 0394	4.38 E-05	0	2.19 E-05	2.19 E-05	0.00 0131	0	0	0	0	0.00 0175	8.76 E-05	0.00 0306	0.00 0547	
BigHornsheepW3	herbivore	0.00 032 8	0.00 125 3	0.00 0308	0.00 0675	0.00 0116	0.00 1966	0.00 0463	0.00 0655	0.00 1118	1.93 E-05	1.93 E-05	0.00 0116	0	0	0.00 0405	0.00 0116	1.93 E-05	1.93 E-05	1.93 E-05	0.00 0212	0	0	0	1.93 E-05	0.00 0173	0.00 0703	0.00 0559	0.00 0578	
BlackRhinoceros	herbivore	0.00 040 2	0.00 067 7	0.00 0254	0.00 0434	0.00 0106	0.00 128	0.00 0106	0.00 0529	0.00 0931	1.06 E-05	3.17 E-05	0.00 0169	0	1.06 E-05	0	0.00 0338	0.00 0148	0	1.06 E-05	5.29 E-05	0.00 0106	0	0	1.06 E-05	0.00 0212	7.40 E-05	0.00 0106	0.00 0677	
Capybara	herbivore	0.00 050 3	0.00 084 7	0.00 027	0.00 0577	0.00 0102	0.00 187	0.00 0121	0.00 0698	0.00 094	0	8.38 E-05	5.58 E-05	0	0	1.86 E-05	0.00 0456	0.00 0177	0	2.79 E-05	5.58 E-05	0.00 0121	0	0	1.86 E-05	0.00 0707	1.86 E-05	0.00 0112	0.00 0996	
ColobusMonkey	herbivore	0.00 053 2	0.00 102	0.00 0163	0.00 0592	0.00 0163	0.00 1449	0.00 0163	0.00 0621	0.00 0828	1.48 E-05	0.00 0118	4.44 E-05	0	1.48 E-05	0	0.00 0503	0.00 0148	0	1.48 E-05	5.92 E-05	0.00 0177	0	0	4.44 E-05	0.00 0148	0.00 0118	0.00 0311	0.00 0799	
Gazelle	herbivore	0.00 038 1	0.00 083 5	0.00 0234	0.00 0659	7.32 E-05	0.00 1743	0.00 0146	0.00 0615	0.00 0806	5.86 E-05	0	1.46 E-05	0	1.46 E-05	0	0.00 0264	8.79 E-05	1.46 E-05	5.86 E-05	1.46 E-05	0.00 0234	0	0	8.79 E-05	0	0.00 0132	4.39 E-05	0.00 0249	0.00 0659

Giraffe	herbivore	0.00 027 9	0.00 072 7	0.00 0279	0.00 0596	3.73 E-05	0.00 1491	0.00 0317	0.00 0503	0.00 0969	1.86 E-05	9.32 E-05	5.59 E-05	0	0	0	0.00 0279	7.45 E-05	1.86 E-05	0	5.59 E-05	0.00 0242	0	0	7.45 E-05	0	0.00 0149	1.86 E-05	0.00 0186	0.00 0689
Horse	herbivore	0.00 031 4	0.00 071 9	0.00 0213	0.00 0344	0.00 0121	0.00 1144	0.00 0202	0.00 0739	0.00 0749	3.04 E-05	2.02 E-05	4.05 E-05	0	0	0	0.00 0243	0.00 0213	0	2.02 E-05	0.00 0142	0.00 0162	0	1.01 E-05	0.00 0101	0	8.10 E-05	0.00 0111	0.00 0223	0.00 085
Horse2	herbivore	0.00 023 8	0.00 075 9	0.00 0239	0.00 0412	0.00 0132	0.00 0972	0.00 0171	0.00 0592	0.00 064	2.95 E-05	3.48 E-05	2.41 E-05	1.43 E-05	9.83 E-06	1.07 E-05	0.00 0339	0.00 0119	3.31 E-05	2.77 E-05	3.13 E-05	0.00 0122	1.79 E-06	8.04 E-06	3.84 E-05	1.16 E-05	0.00 0207	5.27 E-05	0.00 0155	0.00 041
HyraxSD	herbivore	0.00 054 6	0.00 104 4	0.00 019	0.00 0403	7.12 E-05	0.00 1329	4.75 E-05	0.00 0664	0.00 0854	2.37 E-05	7.12 E-05	0.00 0261	0	0	0	0.00 019	0.00 0142	0	2.37 E-05	9.49 E-05	9.49 E-05	0	0	2.37 E-05	0.00 0214	9.49 E-05	0.00 0261	0.00 0664	
HyraxSTL	herbivore	0.00 051 4	0.00 107 4	0.00 0242	0.00 0605	0.00 0136	0.00 177	0.00 0166	0.00 0756	0.00 0666	3.03 E-05	0.00 0121	0.00 0136	0	0	1.51 E-05	0.00 0197	0.00 0197	0	1.51 E-05	7.56 E-05	0.00 0166	0	1.51 E-05	6.05 E-05	0	0.00 0348	6.05 E-05	0.00 0242	0.00 1225
Kroo3	herbivore	0.00 027 2	0.00 108 8	0.00 0363	0.00 0408	0.00 0136	0.00 1723	0.00 0227	0.00 0499	0.00 059	4.54 E-05	9.07 E-05	9.07 E-05	0	0	0	0.00 0408	0.00 0136	0	0	0	0.00 0136	0	0	9.07 E-05	0	4.54 E-05	0	0.00 0181	0.00 0317
Okapi1	herbivore	0.00 033 5	0.00 091 5	0.00 0366	0.00 0762	9.15 E-05	0.00 192	0.00 0152	0.00 0671	0.00 1006	3.05 E-05	6.10 E-05	0	0	0	0.00 0366	9.15 E-05	3.05 E-05	0	0	0.00 0335	0	0	0	0	3.05 E-05	0.00 0305	0.00 0152	0.00 0335	0.00 0671
Okapi2	herbivore	0.00 039 8	0.00 123 8	0.00 0354	0.00 0619	4.42 E-05	0.00 2034	0.00 0265	0.00 0442	0.00 1105	0	0.00 0177	0.00 0133	0	0	0	0.00 0265	8.84 E-05	0	0	0.00 0177	0.00 031	0	4.42 E-05	4.42 E-05	0	0.00 0177	4.42 E-05	0.00 0133	0.00 0663
Orang1	herbivore	0.00 041 1	0.00 071 9	0.00 0308	0.00 0616	3.42 E-05	0.00 1266	0.00 0137	0.00 0684	0.00 089	0	0	0.00 0103	0	0	0	0.00 024	0.00 0103	0	3.42 E-05	3.42 E-05	0.00 0103	0	0	3.42 E-05	0	0.00 0376	0.00 0103	0.00 0103	0.00 0308
Pig	herbivore	0.00 054 1	0.00 138 6	0.00 022	0.00 0355	0.00 0169	0.00 1927	5.07 E-05	0.00 0828	0.00 0727	3.38 E-05	8.45 E-05	5.07 E-05	0	3.38 E-05	0	0.00 0338	0.00 0135	0	1.69 E-05	8.45 E-05	0.00 0237	0	0	0.00 0101	0.00 0152	0.00 0169	0.00 0135	0.00 0135	0.00 1217
Rabbit1	herbivore	0.00 030 4	0.00 083 9	0.00 0289	0.00 1216	0.00 026	0.00 2127	0.00 0145	0.00 0651	0.00 1244	1.45 E-05	4.34 E-05	0.00 013	0	0	0	0.00 0463	8.68 E-05	0	1.45 E-05	7.24 E-05	0.00 0333	0	1.45 E-05	2.89 E-05	0	0.00 026	0.00 0116	0.00 0174	0.00 0724
Rabbit2	herbivore	0.00 034 1	0.00 085 1	0.00 0345	0.00 0949	0.00 0227	0.00 1717	0.00 0117	0.00 0527	0.00 1072	1.38 E-05	9.20 E-05	5.58 E-05	2.17 E-06	1.45 E-06	2.90 E-06	0.00 0425	5.73 E-05	0	1.01 E-05	8.99 E-05	0.00 0228	0	2.17 E-05	2.83 E-05	2.90 E-06	0.00 0303	0.00 012	6.67 E-05	0.00 0607
Springbok	herbivore	0.00 059 3	0.00 141 3	0.00 0266	0.00 0633	0.00 0102	0.00 2044	0.00 0266	0.00 096	0.00 0695	0	2.04 E-05	8.17 E-05	0	2.04 E-05	0	0.00 0204	0.00 0123	0	0.00 0123	4.09 E-05	0.00 0184	0	0	4.09 E-05	2.04 E-05	0.00 0163	0.00 0123	0.00 049	
Urial	herbivore	0.00 021 9	0.00 066 6	0.00 0406	0.00 0656	0.00 0188	0.00 2094	0.00 0281	0.00 0344	0.00 075	0	6.25 E-05	0	0	0	0	0.00 0375	9.38 E-05	0	3.13 E-05	0	0.00 0156	0	3.13 E-05	3.13 E-05	3.13 E-05	0.00 0438	6.25 E-05	0.00 025	0.00 0844
Whitetail Deer	herbivore	0.00 039 5	0.00 081 9	0.00 0296	0.00 0706	0.00 0105	0.00 1459	0.00 0185	0.00 065	0.00 0699	6.02 E-05	4.20 E-05	0.00 0123	2.38 E-05	1.27 E-05	9.59 E-05	0.00 03	0.00 0125	0.00 0128	1.51 E-05	4.75 E-05	0.00 0141	5.55 E-06	3.64 E-05	3.17 E-05	6.50 E-05	0.00 0357	0.00 0104	0.00 0178	0.00 0348
ZebraSTL1	herbivore	0.00 023 4	0.00 066 2	0.00 0389	0.00 035	3.89 E-05	0.00 1051	0.00 0117	0.00 0428	0.00 0973	0	0	7.78 E-05	0	0	0	0.00 0272	0.00 0195	0	0	0.00 0234	7.78 E-05	0	0	0	3.89 E-05	0.00 0311	0.00 0195	0.00 0117	0.00 0467
BaboonSTL	omnivore	0.00 044 4	0.00 143 4	0.00 0344	0.00 0555	5.74 E-05	0.00 1606	0.00 0153	0.00 065	0.00 0918	0	7.65 E-05	3.82 E-05	0	0	0	0.00 0306	0.00 0153	0	1.91 E-05	1.91 E-05	0.00 0134	0	0	5.74 E-05	3.82 E-05	0.00 0115	5.74 E-05	0.00 021	0.00 0287
BaboonW	omnivore	0.00 041 4	0.00 060 5	0.00 0382	0.00 0955	9.55 E-05	0.00 1877	0.00 0127	0.00 0445	0.00 1082	0	3.18 E-05	0	0	3.18 E-05	0	0.00 0414	0.00 0191	0	6.36 E-05	0	0.00 0255	0	0	3.18 E-05	3.18 E-05	0.00 0159	0.00 0159	0.00 0318	0.00 0605
BlackBear	omnivore	0.00 114 7	0.00 119 9	0.00 0595	0.00 1829	0.00 0145	0.00 2323	0.00 0508	0.00 4399	0.00 1248	8.71 E-05	0.00 0116	0.00 0319	2.90 E-05	0.00 0189	8.71 E-05	0.00 0116	0.00 0131	0.00 0145	5.81 E-05	5.81 E-05	8.71 E-05	7.26 E-05	1.45 E-05	0.00 0102	1.45 E-05	0.00 4384	0.00 0189	0.00 0276	0.00 0392
BlackLemur	omnivore	0.00 064 7	0.00 056 6	0.00 062	0.00 1536	0.00 0108	0.00 458	2.69 E-05	0.00 1751	0.00 0889	5.39 E-05	0.00 0216	0.00 0135	0	0	0	0.00 0431	0.00 0108	0	0	0.00 0108	8.08 E-05	0	0	0	2.69 E-05	0.00 1239	0.00 0189	0.00 0108	0.00 1185
Chimpanzee1	omnivore	0.00 039 4	0.00 081 9	0.00 0424	0.00 0637	0.00 0167	0.00 1774	0.00 0152	0.00 0819	0.00 1	1.52 E-05	6.06 E-05	0.00 0136	0	0	0	0.00 0349	0.00 0106	0	3.03 E-05	3.03 E-05	0.00 0167	0	0	3.03 E-05	0	0.00 0485	0.00 0106	0.00 0152	0.00 0652
Chimpanzee2	omnivore	0.00 035 8	0.00 097 1	0.00 0204	0.00 0409	0	0.00 1226	0.00 0102	0.00 0358	0.00 0767	0	5.11 E-05	5.11 E-05	0	5.11 E-05	0	0.00 0511	0.00 0102	0	5.11 E-05	5.11 E-05	0.00 0153	0	0	5.11 E-05	0	0.00 0307	0.00 0204	0.00 0102	0.00 0613
Lemur	omnivore	0.00 061 4	0.00 120 9	0.00 0238	0.00 0931	0.00 0178	0.00 1902	0.00 0258	0.00 0832	0.00 0812	0	0.00 0139	0.00 0139	1.98 E-05	0	0	0.00 0416	0.00 0139	0	1.98 E-05	9.91 E-05	0.00 0159	0	0	7.93 E-05	1.98 E-05	0.00 0456	0.00 0159	0.00 0258	0.00 1209
Marmoset	omnivore	0.00 062 1	0.00 079 6	0.00 0505	0.00 0971	0.00 0155	0.00 3223	7.77 E-05	0.00 1359	0.00 0893	1.94 E-05	1.94 E-05	0.00 0252	0	0	0	0.00 0447	0.00 033	0	1.94 E-05	3.88 E-05	0.00 0291	0	0	0	0.00 1359	0.00 0136	0.00 0252	0.00 1107	

Mouse	omniv ore	0.00 039 6	0.00 071 6	0.00 0297	0.00 0642	0.00 0171	0.00 1944	0.00 0136	0.00 0533	0.00 0771	2.43 E-06	0.00 0108	5.02 E-05	8.10 E-07	3.00 E-05	3.24 E-06	0.00 0261	6.72 E-05	0	2.83 E-05	5.99 E-05	0.00 0229	0	2.43 E-06	0.00 0122	6.48 E-06	0.00 0413	0.00 0225	0.00 0354	0.00 1024	
Saki	omniv ore	0.00 050 4	0.00 097 6	0.00 0299	0.00 0456	0.00 015	0.00 1723	6.30 E-05	0.00 1125	0.00 0582	0	0.00 0228	0.00 0205	0	0	1.57 E-05	0.00 0315	0.00 0181	0	1.57 E-05	0.00 0126	0.00 011	0	0	6.30 E-05	0	0.00 0252	9.44 E-05	6.30 E-05	0.00 0921	
SpecBear	omniv ore	0.00 079 5	0.00 146 2	0.00 0333	0.00 1897	0.00 0128	0.00 3	0.00 0231	0.00 318	0.00 0744	5.13 E-05	0.00 0615	0.00 0128	0	5.13 E-05	0	7.69 E-05	2.56 E-05	5.13 E-05	5.13 E-05	5.13 E-05	0.00 0103	0	0	2.56 E-05	0	0.00 0564	0.00 0231	0.00 0564	0.00 0179	
Squirrel	omniv ore	0.00 054 9	0.00 066 3	0.00 048	0.00 1967	0.00 0252	0.00 215	9.15 E-05	0.00 167	0.00 1281	0	4.57 E-05	4.57 E-05	0	2.29 E-05	0	0.00 0435	4.57 E-05	0	0	6.86 E-05	0.00 0274	0	0	2.29 E-05	0	0.00 2562	0.00 0457	0.00 0252	0.00 0961	
CD.70.13 0117	panda	0.00 146	0.00 168 5	0.00 0708	0.00 1598	0.00 0238	0.00 3571	0.00 0523	0.00 2031	0.00 1361	0.00 0263	0.00 0242	0.00 0623	0.00 0142	0.00 0419	0.00 0602	0.00 0926	0.00 0196	0.00 0747	0.00 0412	0.00 0451	0.00 0618	0.00 0109	6.41 E-05	0.00 0823	0.00 0208	0.00 1611	0.00 1135	0.00 391	0.00 1603	
CD.73.13 0415	panda	0.00 183 5	0.00 210 5	0.00 0751	0.00 1881	0.00 036	0.00 3622	0.00 0738	0.00 2134	0.00 1535	0.00 0374	0.00 0382	0.00 0756	0.00 0201	0.00 0574	0.00 0829	0.00 0957	0.00 0282	0.00 0725	0.00 0213	0.00 0746	0.00 0732	0.00 027	9.07 E-05	0.00 0952	0.00 0187	0.00 1061	0.00 0588	0.00 1705	0.00 1736	
CX.39.13 0208	panda	0.00 067	0.00 126 6	0.00 0876	0.00 2073	0.00 0289	0.00 425	0.00 0176	0.00 3615	0.00 1883	0.00 0134	0.00 0116	0.00 0188	4.90 E-05	0.00 0139	0.00 0246	0.00 0969	8.64 E-05	0.00 0201	9.74 E-05	0.00 0218	0.00 0216	6.93 E-05	3.05 E-05	0.00 0285	6.92 E-05	0.00 4312	0.00 0306	0.00 0444	0.00 0377	
CX.6.121 213	panda	0.00 173	0.00 195 7	0.00 0599	0.00 1915	0.00 0262	0.00 3485	0.00 0563	0.00 2057	0.00 1663	0.00 0276	0.00 0334	0.00 0645	0.00 0108	0.00 0436	0.00 0393	0.00 0635	0.00 0265	0.00 035	0.00 0518	0.00 0366	0.00 0462	0.00 0122	6.18 E-05	0.00 0512	9.21 E-05	0.00 2546	0.00 0935	0.00 113	0.00 1183	
EQ.118.1 30124	panda	0.00 215 2	0.00 234 8	0.00 0731	0.00 1988	0.00 0346	0.00 3621	0.00 0813	0.00 1989	0.00 1461	0.00 0447	0.00 0304	0.00 0615	0.00 0236	0.00 0547	0.00 0808	0.00 0833	0.00 0265	0.00 0578	0.00 0343	0.00 0613	0.00 0684	0.00 0199	0.00 0111	0.00 0822	0.00 0174	0.00 1242	0.00 033	0.00 1666	0.00 1348	
EQ.128.1 30507	panda	0.00 151 5	0.00 176 8	0.00 0645	0.00 1768	0.00 0241	0.00 3662	0.00 0532	0.00 2597	0.00 1368	0.00 0238	0.00 0285	0.00 0505	0.00 0113	0.00 0361	0.00 0461	0.00 07	0.00 0246	0.00 0326	0.00 0317	0.00 041	0.00 0519	0.00 012	5.83 E-05	0.00 0454	9.44 E-05	0.00 2838	0.00 0539	0.00 1675	0.00 1102	
HH.192.0 90930	panda	0.00 139 6	0.00 164 6	0.00 0712	0.00 1793	0.00 0283	0.00 3679	0.00 0595	0.00 2643	0.00 142	0.00 0211	0.00 0328	0.00 0584	0.00 0114	0.00 0404	0.00 059	0.00 0843	0.00 0193	0.00 0564	0.00 0129	0.00 0622	0.00 0618	0.00 017	6.43 E-05	0.00 0625	0.00 0189	0.00 3226	0.00 0292	0.00 1423	0.00 1036	
HQ.47.13 0816	panda	0.00 182 3	0.00 201 9	0.00 0503	0.00 1476	0.00 0172	0.00 341	0.00 0767	0.00 2538	0.00 1253	0.00 0256	0.00 0368	0.00 0615	0.00 0117	0.00 0367	0.00 0428	0.00 039	0.00 033	0.00 0268	0.00 035	0.00 0343	0.00 0485	0.00 0111	4.92 E-05	0.00 0246	0.00 0153	0.00 2766	0.00 0349	0.00 1006	0.00 0874	
HQ.59.13 0113	panda	0.00 148 9	0.00 121 2	0.00 0761	0.00 2069	0.00 0171	0.00 3975	0.00 0325	0.00 3565	0.00 1373	0.00 0165	0.00 0237	0.00 0289	7.05 E-05	0.00 0233	0.00 0276	0.00 095	0.00 0118	0.00 0272	8.37 E-05	0.00 0269	0.00 0266	9.02 E-05	3.79 E-05	0.00 0305	0.00 0102	0.00 2494	0.00 046	0.00 043	0.00 0853	
JJ.234.13 0208	panda	0.00 197 7	0.00 212 2	0.00 088	0.00 2253	0.00 0476	0.00 3869	0.00 0661	0.00 2221	0.00 1773	0.00 0383	0.00 0401	0.00 0724	0.00 0204	0.00 0507	0.00 0966	0.00 1126	0.00 0337	0.00 0773	0.00 0352	0.00 0847	0.00 078	0.00 0326	0.00 0115	0.00 0963	0.00 0173	0.00 1017	0.00 0355	0.00 1331	0.00 1663	
JJ.257.13 0514	panda	0.00 190 2	0.00 213 4	0.00 074	0.00 1821	0.00 0362	0.00 3277	0.00 0679	0.00 2077	0.00 1552	0.00 0351	0.00 0374	0.00 0698	0.00 02	0.00 047	0.00 0836	0.00 0927	0.00 0293	0.00 0641	0.00 0166	0.00 0915	0.00 0676	0.00 0226	9.27 E-05	0.00 08	0.00 0179	0.00 1001	0.00 0376	0.00 1865	0.00 2348	
NN.149.0 91002	panda	0.00 222	0.00 216 2	0.00 0737	0.00 1793	0.00 0361	0.00 3342	0.00 0687	0.00 195	0.00 1531	0.00 0352	0.00 0337	0.00 0658	0.00 0221	0.00 0553	0.00 0853	0.00 0915	0.00 0287	0.00 0796	0.00 0239	0.00 0708	0.00 078	0.00 0261	8.73 E-05	0.00 0901	0.00 0177	0.00 091	0.00 0525	0.00 0455	0.00 1381	
QF.135.0 91001	panda	0.00 179 6	0.00 178 3	0.00 0554	0.00 1992	0.00 0223	0.00 3836	0.00 0655	0.00 2589	0.00 1482	0.00 0213	0.00 0244	0.00 0519	0.00 0107	0.00 0342	0.00 0309	0.00 0455	0.00 0236	0.00 0238	0.00 03	0.00 0358	0.00 0333	0.00 0122	4.73 E-05	0.00 0288	9.24 E-05	0.00 4479	0.00 0435	0.00 1147	0.00 0874	
QQ.102.1 30620	panda	0.00 190 3	0.00 236 3	0.00 0544	0.00 1757	0.00 027	0.00 3656	0.00 0891	0.00 2294	0.00 1648	0.00 0374	0.00 0304	0.00 0859	0.00 0158	0.00 0557	0.00 0681	0.00 0688	0.00 0433	0.00 0428	0.00 0204	0.00 0559	0.00 0598	0.00 0185	7.91 E-05	0.00 0503	0.00 0182	0.00 1779	0.00 0187	0.00 0977	0.00 1585	
QQ.98.13 0411	panda	0.00 199 8	0.00 224 9	0.00 0687	0.00 1898	0.00 0335	0.00 3628	0.00 0939	0.00 2176	0.00 1593	0.00 0391	0.00 0348	0.00 0758	0.00 0196	0.00 0603	0.00 0777	0.00 084	0.00 0301	0.00 0608	0.00 0227	0.00 0698	0.00 068	0.00 022	0.00 01	0.00 0818	0.00 0165	0.00 1381	0.00 035	0.00 2025	0.00 1399	
SY.167.0 91121	panda	0.00 164 5	0.00 162 6	0.00 0305	0.00 0759	0.00 015	0.00 047	0.00 015	0.00 208	0.00 0657	0.00 0278	4.14 E-05	0.00 0503	0.00 0122	9.40 E-06	0.00 0224	0.00 0348	0.00 0247	0.00 0985	1.84 E-05	0.00 0169	4.48 E-05	7.28 E-05	1.76 E-05	1.36 E-05	0.00 0466	0.00 0669	0.00 01	0.00 0118	8.08 E-05	
YL.173.0 90701	panda	0.00 179 9	0.00 228 7	0.00 06	0.00 1845	0.00 0374	0.00 55	0.00 0625	0.00 2007	0.00 1173	0.00 0119	0.00 0116	0.00 0171	7.08 E-05	0.00 0189	0.00 0174	0.00 0451	0.00 0265	0.00 0104	0.00 0364	0.00 0301	0.00 066	3.56 E-05	2.65 E-05	0.00 0256	3.09 E-05	0.00 2754	0.00 0361	0.00 0247	0.00 0866	
YL.178.0 91015	panda	0.00 202 1	0.00 239 2	0.00 0573	0.00 1268	0.00 0348	0.00 421	0.00 0622	0.00 2242	0.00 0977	0.00 0133	0.00 0229	0.00 0225	5.95 E-05	0.00 0191	0.00 0214	0.00 0548	0.00 0286	0.00 015	0.00 0208	0.00 0202	0.00 064	5.44 E-05	2.38 E-05	0.00 021	6.24 E-05	0.00 3856	0.00 0604	0.00 0595	0.00 1064	
ZZ.109.1 30808	panda	0.00 209 3	0.00 223 2	0.00 0779	0.00 2026	0.00 0386	0.00 3608	0.00 0879	0.00 2155	0.00 1586	0.00 0419	0.00 0463	0.00 0696	0.00 0233	0.00 0597	0.00 093	0.00 0943	0.00 0302	0.00 0653	0.00 0221	0.00 0898	0.00 0771	0.00 0256	0.00 0118	0.00 0919	0.00 0196	0.00 0322	0.00 1954	0.00 1535		
T-test (panda)	DiffPa irs	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P	NP <_P

and no-panda)	PairsP values	3.06	1.89	3.45	5.80	2.02	2.90	8.88	6.68	4.13	9.46	1.68	3.34	7.84	1.42	7.84	8.53	1.11	1.71	1.70	1.65	1.91	2.03	3.42	1.37	2.64	4.62	2.07	7.64	0.00		
		E-25	E-17	E-15	E-15	E-14	E-13	E-13	E-13	E-12	E-10	E-10	E-09	E-09	E-09	E-08	E-08	E-08	E-07	E-07	E-07	E-07	E-07	E-07	E-07	E-06	E-06	E-06	E-05	E-05	0.00	0.00
	PairsQ values	1.77	5.47	5.01	6.73	1.68	1.53	4.29	2.58	1.20	2.61	4.44	8.43	1.90	3.30	1.57	1.65	2.08	2.83	2.91	2.99	3.07	3.18	4.95	1.94	3.65	6.09	2.67	9.23	0.00		
		E-23	E-16	E-14	E-14	E-13	E-12	E-12	E-11	E-09	E-09	E-09	E-09	E-08	E-08	E-07	E-07	E-07	E-07	E-07	E-07	E-07	E-07	E-07	E-06	E-06	E-06	E-06	E-05	0.00	0.00	
		CE1	GH7	GH3	GH1	GH3	GH5	GH9	GH1	GH9	GH3	GH2	GH1	GH9	GH5	GH2	GH1	GH1	GH1	CB	CB	GH1	GH3	GH1	GH7	GH4	GH1	GH1	GH6	GH1	GH8	
		1	7	3	04	2	8	0	30	5	13	9	33	7	7	2	0	09	15	M67	23	0	M62	6	4	12	7	6	17	6		
Armadillo	carnivore	6.96 E-05	6.96 E-05	3.48 E-05	0	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0	0	6.96 E-05	0	
BelugaWhale	carnivore	4.18 E-06	0	0	0	4.18 E-06	0	0	0	0	0	4.18 E-06	4.18 E-06	0	2.30 E-05	2.51 E-05	6.26 E-06	0	0	0	0	0	0	4.18 E-06	1.04 E-05	0	2.09 E-06	0	0	0	0	
BottlenoseDolphin	carnivore	0	0	0	0	4.93 E-06	0	0	0	1.97 E-06	0	3.95 E-06	3.95 E-06	9.87 E-07	1.97 E-06	5.92 E-06	7.89 E-06	1.97 E-06	0	0	0	0	0	1.97 E-06	3.95 E-06	0	9.87 E-07	0	0	0	0	
BushDog	carnivore	7.73 E-05	0	3.09 E-05	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Coyote	carnivore	9.03 E-05	0	2.46 E-05	1.33 E-06	0.00	0.00	0	6.04 E-05	0.00	0.00	4.91 E-05	6.04 E-05	0.00	2.92 E-05	0.00	0.00	8.97 E-05	2.66 E-06	6.64 E-06	6.97 E-05	8.43 E-05	5.98 E-05	4.45 E-05	7.04 E-05	6.91 E-05	0	4.65 E-06	4.65 E-06	0		
Echidna	carnivore	0.00	0.018	0	3.06 E-05	0	0.00	0.00	0.00	0.00	0	6.13 E-05	0	1.53 E-05	0	0.00	7.66 E-05	0	1.53 E-05	3.06 E-05	0	0	0	1.53 E-05	0.00	4.60 E-05	0	1.53 E-05	1.53 E-05	0	0	
Fisher	carnivore	3.00 E-05	0	6.48 E-06	6.48 E-06	0.00	0	0	3.00 E-05	0.00	4.05 E-06	0.00	1.62 E-05	3.57 E-05	4.46 E-05	0.00	0.00	9.40 E-05	1.46 E-05	0	3.00 E-05	6.97 E-05	6.48 E-06	8.11 E-06	0.00	9.97 E-05	0	0	4.05 E-06	0		
HumpbackWhale	carnivore	0.00	0.013	0	5.41 E-05	1.18 E-05	0	0	6.59 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08 E-05	1.57 E-05	0.00	0.00	1.48 E-06	0.00	0.00	0.00	0.00	0.00	2.95 E-06	8.86 E-06	0.00	4.92 E-06
Hyena	carnivore	0.00	0.017	0	7.30 E-05	0	0.00	0	7.30 E-05	0.00	4.38 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.38 E-05	0	2.92 E-05	8.76 E-05	5.84 E-05	5.84 E-05	0.00	0.00	0.00	0.00	2.92 E-05	7.30 E-05	0	
Lion1	carnivore	0.00	0.014	7.02 E-05	0	7.02 E-05	0.00	0	7.02 E-05	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0	0.00	0	0	0.00	0.00	0.00	0.00	0	0	0	0	
Lion2	carnivore	0.00	0.00	0.00	0.00	0.00	8.00 E-05	0	8.00 E-05	0.00	8.00 E-05	0.00	8.00 E-05	0.00	0.00	0.00	0.00	8.00 E-05	1.33 E-05	0.00	0.00	4.00 E-05	4.00 E-05	1.33 E-05	4.00 E-05	0.00	8.00 E-05	1.33 E-05	0	2.67 E-05	0	
PolarBear	carnivore	0.00	0.00	0.00	7.09 E-05	0.00	1.77 E-05	0	1.77 E-05	1.77 E-05	0	0	0	0	0	0	0.00	1.77 E-05	0	0	0	0	0	0	0.00	3.55 E-05	0	0	0	0	0	
RightWhaleF11	carnivore	6.15 E-05	0	2.26 E-05	9.05 E-07	4.98 E-05	1.81 E-06	0	6.97 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.95 E-06	3.71 E-05	6.42 E-05	4.25 E-05	3.62 E-06	9.95 E-06	0.00	0.00	3.62 E-06	1.81 E-06	5.34 E-05	0	0		
RightWhaleF16	carnivore	0.00	0.014	0	5.89 E-05	5.63 E-06	5.58 E-05	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.19 E-06	3.25 E-05	0.00	0.00	7.96 E-05	1.95 E-05	1.99 E-05	0.00	0.00	0.00	0.00	0.00	3.46 E-06		
RightWhaleF9	carnivore	0.00	0.017	0	6.85 E-05	4.09 E-06	5.93 E-05	2.04 E-06	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.11 E-06	3.78 E-05	0.00	0.00	8.99 E-05	4.50 E-05	1.94 E-05	0.00	0.00	8.17 E-06	3.07 E-06	0.00	0		
Gorilla	herbivore	8.02 E-05	0	8.02 E-05	0	8.02 E-05	0	0	8.02 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.02 E-05	8.02 E-05	4.01 E-05	4.01 E-05	0	0	4.01 E-05	0.00	4.01 E-05	0	0	0	4.01 E-05	0	
AfricanElephant	herbivore	0.00	0.012	0	3.55 E-05	7.10 E-06	9.94 E-05	0	5.68 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.84 E-05	3.55 E-05	5.68 E-05	7.10 E-06	7.10 E-06	0.00	1.42 E-05	0	7.10 E-06	7.10 E-06	0	0		
BigHornsheepSD	herbivore	4.38 E-05	0	2.19 E-05	0	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.76 E-05	2.19 E-05	2.19 E-05	6.57 E-05	2.19 E-05	2.19 E-05	0.00	8.76 E-05	2.19 E-05	2.19 E-05	2.19 E-05	0	0		
BigHornsheepW3	herbivore	9.64 E-05	0	0	1.93 E-05	0.00	0.00	0	0.00	0.00	0.00	0.00	7.71 E-05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	
BlackRhino	herbivore	0.00	0.010	0	1.06 E-05	1.06 E-05	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.35 E-05	5.29 E-05	9.52 E-05	1.06 E-05	1.06 E-05	0.00	1.06 E-05	0	0	1.06 E-05	0	0		
Capybara	herbivore	0.00	0.014	0	0	0	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.79 E-05	9.31 E-06	0.00	1.86 E-05	0	0.00	1.86 E-05	9.31 E-06	0	9.31 E-06	2.79 E-05	0		
ColobusMonkey	herbivore	7.39 E-05	0	2.96 E-05	0	8.87 E-05	0	0	0.00	0.00	8.87 E-05	0.00	0.00	0.00	0.00	0.00	0.00	5.92 E-05	0.00	4.44 E-05	0.00	0	2.96 E-05	0.00	7.39 E-05	1.48 E-05	4.44 E-05	1.48 E-05	0	0		
Gazelle	herbivore	4.39 E-05	0	0	1.46 E-05	0.00	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	4.39 E-05	8.79 E-05	5.86 E-05	1.46 E-05	1.46 E-05	0.00	8.79 E-05	1.46 E-05	1.46 E-05	0	0	0		
Giraffe	herbivore	0.00	0.011	0	0	0	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.86 E-05	1.86 E-05	0.00	5.59 E-05	0	0.00	9.32 E-05	5.59 E-05	0	0	1.86 E-05	0		

Horse	herbivore	0.00 015 2	0	2.02 E-05	1.01 E-05	0.00 0111	0	0	0.00 0101	0.00 0486	0.00 0152	0.00 0951	0.00 0283	0.00 0698	0.00 0142	0.00 0881	0.00 0466	0.00 0405	0.00 0162	6.07 E-05	0.00 0142	0.00 0111	1.01 E-05	1.01 E-05	0.00 0425	2.02 E-05	1.01 E-05	2.02 E-05	6.07 E-05	2.02 E-05
Horse2	herbivore	4.11 E-05	0	8.04 E-06	0	0.00 01	0	0	6.16 E-05	0.00 0173	1.97 E-05	0.00 0398	8.31 E-05	0.00 0133	4.74 E-05	0.00 0298	0.00 0239	0.00 017	5.54 E-05	1.16 E-05	6.16 E-05	4.82 E-05	5.36 E-06	6.25 E-06	0.00 0327	2.05 E-05	4.47 E-06	8.93 E-06	5.36 E-06	5.36 E-06
HyraxSD	herbivore	0.00 011 9	0	2.37 E-05	0	9.49 E-05	0	0	0.00 0119	0.00 0166	0.00 0214	0.00 0300	9.49 E-05	0.00 0546	0.00 0119	0.00 0973	0.00 0332	0.00 0261	7.12 E-05	9.49 E-05	0	7.12 E-05	7.12 E-05	4.75 E-05	0.00 038	4.75 E-05	0	2.37 E-05	4.75 E-05	0
HyraxSTL	herbivore	0.00 021 2	0	0	0	0.00 0499	0	0	0.00 0227	0.00 0363	0.00 0166	0.00 0378	0.00 0212	0.00 1059	0.00 0151	0.00 0333	0.00 0318	6.05 E-05	0.00 0424	4.54 E-05	3.03 E-05	0.00 0151	3.03 E-05	3.03 E-05	0.00 0529	9.08 E-05	3.03 E-05	3.03 E-05	3.03 E-05	1.51 E-05
Kroo3	herbivore	0.00 027 2	0	0	0	0.00 0181	0	0	9.07 E-05	0.00 0317	0.00 0136	0.00 0272	0.00 0635	0	0.00 0544	0.00 0317	0.00 0136	0.00 0181	9.07 E-05	0.00 0181	9.07 E-05	4.54 E-05	0	0.00 0227	0	0	0	0	0	
Okapi1	herbivore	6.10 E-05	0	6.10 E-05	0	6.10 E-05	0	0	6.10 E-05	0.00 0488	0.00 0122	0.00 0335	9.15 E-05	0.00 0427	0.00 0152	0.00 0366	0.00 0549	0	0.00 0122	3.05 E-05	6.10 E-05	0.00 0122	0	6.10 E-05	0.00 0457	0.00 0122	0	0	0	0
Okapi2	herbivore	0.00 013 3	0	0	0	0.00 0177	0	0	0.00 0133	0.00 0575	0.00 0177	0.00 0354	0.00 0354	0.00 0442	0.00 0133	0.00 0619	0.00 0619	0.00 0354	8.84 E-05	4.42 E-05	4.42 E-05	8.84 E-05	0	0	0.00 0531	4.42 E-05	0	0	0	4.42 E-05
Orang1	herbivore	6.84 E-05	0	0	0	6.84 E-05	0	0	3.42 E-05	0.00 0171	0.00 0137	0.00 024	6.84 E-05	0.00 024	6.84 E-05	0.00 0171	0.00 0308	3.42 E-05	3.42 E-05	6.84 E-05	0	0.00 0103	0	3.42 E-05	0.00 0582	6.84 E-05	3.42 E-05	6.84 E-05	0	0
Pig	herbivore	0.00 020 3	0	6.76 E-05	0	0.00 0456	0	0	0.00 0203	0.00 0591	0.00 0169	0.00 0406	0.00 0152	0.00 0591	0.00 0287	0.00 0389	0.00 0439	0.00 0237	0.00 0253	5.07 E-05	6.76 E-05	0.00 022	3.38 E-05	5.07 E-05	0.00 0828	8.45 E-05	0	0	0	0
Rabbit1	herbivore	0.00 013	0	1.45 E-05	0	0.00 0275	0	0	0.00 0145	0.00 0362	0.00 0159	0.00 0232	0.00 0159	0.00 0145	7.24 E-05	0.00 0275	0.00 0434	0.00 0145	0.00 026	1.45 E-05	4.34 E-05	5.79 E-05	0	0	0.00 0724	0.00 0145	1.45 E-05	2.89 E-05	0	1.45 E-05
Rabbit2	herbivore	8.84 E-05	0	2.05 E-06	2.90 E-06	0.00 034	0	0	0.00 0104	0.00 027	0.00 0172	0.00 0217	9.28 E-05	0.00 0161	0.00 0116	0.00 0253	0.00 0238	8.55 E-05	0.00 0161	8.70 E-06	4.35 E-06	8.77 E-05	4.57 E-05	1.09 E-05	0.00 0683	9.35 E-05	1.09 E-05	1.74 E-05	2.90 E-06	4.35 E-06
Springbok	herbivore	8.17 E-05	0	0	0	0.00 0143	0	0	0.00 0143	0.00 0388	0.00 0143	0.00 045	0.00 0102	0.00 0286	0.00 0123	0.00 0572	0.00 0429	0.00 0102	0.00 0102	4.09 E-05	0	8.17 E-05	4.09 E-05	2.04 E-05	0.00 0163	6.13 E-05	0	0	0	2.04 E-05
Urial	herbivore	0.00 015 6	0	0	0	0.00 0313	0	0	9.38 E-05	0.00 0188	0.00 0125	0.00 0375	0.00 0375	0.00 0156	9.38 E-05	0.00 0281	0.00 0344	6.25 E-05	9.38 E-05	3.13 E-05	0	0.00 0125	0	0	0.00 0375	9.38 E-05	0	0	0	0
Whitetail Deer	herbivore	0.00 011 7	1.58 E-06	0.00 0185	3.96 E-06	0.00 0149	0	0	4.91 E-05	0.00 0173	8.87 E-05	0.00 0196	0.00 0112	0.00 0109	0.00 0124	0.00 0236	0.00 0183	4.59 E-05	3.17 E-05	1.66 E-05	1.82 E-05	4.99 E-05	2.22 E-05	1.74 E-05	0.00 0282	3.64 E-05	7.92 E-06	3.17 E-06	7.13 E-06	2.38 E-06
ZebraSTL1	herbivore	0.00 015 6	0	0	0	0.00 0234	0	0	0.00 0156	0.00 0701	0.00 0234	0.00 0934	0.00 0234	0.00 0311	0.00 0117	0.00 1012	0.00 0662	0.00 0311	0.00 0195	3.89 E-05	0.00 0156	7.78 E-05	0	0	0.00 035	0	0	3.89 E-05	0	0
BaboonSTL	omnivore	7.65 E-05	0	1.91 E-05	0	7.65 E-05	0	0	7.65 E-05	0.00 0268	0.00 0153	0.00 0516	0.00 0249	0.00 0459	0.00 0172	0.00 0497	0.00 0363	7.65 E-05	7.65 E-05	9.56 E-05	5.74 E-05	1.91 E-05	0	0	0.00 0516	3.82 E-05	1.91 E-05	1.91 E-05	0	1.91 E-05
BaboonW	omnivore	6.36 E-05	0	0	0	0.00 0286	0	0	0.00 0191	0.00 0159	3.18 E-05	0.00 0286	3.18 E-05	0.00 0191	0.00 0159	9.55 E-05	0.00 0127	3.18 E-05	9.55 E-05	3.18 E-05	0.00 0127	0	0	0	0.00 0605	0	3.18 E-05	6.36 E-05	0	3.18 E-05
BlackBear	omnivore	0.00 039 2	0.00 066 8	4.36 E-05	0.00 0102	0.00 1844	0	0	1.45 E-05	2.90 E-05	0	1.45 E-05	1.45 E-05	5.81 E-05	0	5.81 E-05	7.26 E-05	0	0	0	0	0	0	0	0.00 2047	0	0	1.45 E-05	0	0
BlackLemur	omnivore	0.00 021 6	0	0.00 0108	0	0.00 0647	0	0	5.39 E-05	0.00 0674	5.39 E-05	0.00 0296	0.00 0135	0.00 0566	8.08 E-05	0.00 0835	0.00 0674	5.39 E-05	0.00 0269	0	0.00 0108	0.00 0108	0	2.69 E-05	0.00 0377	0.00 0189	2.69 E-05	0	8.08 E-05	0
Chimpanzee1	omnivore	0.00 015 2	0	3.03 E-05	0	0.00 0318	0	0	0.00 0167	0.00 0349	0.00 0167	0.00 0303	0.00 0212	0.00 0197	9.10 E-05	0.00 0318	0.00 0258	0.00 0106	0.00 0152	1.52 E-05	3.03 E-05	6.06 E-05	1.52 E-05	0	0.00 047	0.00 0106	3.03 E-05	3.03 E-05	0	0
Chimpanzee2	omnivore	0	0	0.00 0102	0	0.00 0256	0	0	0.00 0102	0.00 0204	5.11 E-05	0.00 046	0	0.00 0204	0	0.00 0153	0.00 0256	5.11 E-05	0.00 0102	0	5.11 E-05	0.00 0204	0	5.11 E-05	0.00 0409	0	0	0	0	0
Lemur	omnivore	0.00 013 9	0	1.98 E-05	0	0.00 0396	0	0	9.91 E-05	0.00 0634	0.00 0119	0.00 0515	7.93 E-05	0.00 0892	9.91 E-05	0.00 0436	0.00 0694	0.00 0178	0.00 0357	0	5.94 E-05	0.00 0337	5.94 E-05	0	0.00 0773	0.00 0258	1.98 E-05	7.93 E-05	3.96 E-05	3.96 E-05
Marmoset	omnivore	0.00 023 3	0	0.00 0233	0	0.00 0602	0	0	1.94 E-05	0.00 033	9.71 E-05	0.00 0427	0.00 0214	0.00 0466	0.00 0136	0.00 0913	0.00 0583	0.00 0155	0.00 0214	0	1.94 E-05	3.88 E-05	0	0	0.00 0136	0.00 0136	0	3.88 E-05	0	0
Mouse	omnivore	0.00 013 4	0	1.38 E-05	2.43 E-06	0.00 0482	0	0	0.00 0211	0.00 0291	9.39 E-05	0.00 0263	0.00 0181	0.00 0961	0.00 0138	0.00 0313	7.12 E-05	1.46 E-05	0.00 0304	8.90 E-06	4.86 E-06	0.00 0232	2.51 E-05	4.05 E-05	0.00 0565	0.00 0242	1.62 E-06	1.21 E-05	5.67 E-06	1.62 E-06
Saki	omnivore	0.00 030 7	0	0.00 0142	7.87 E-06	0.00 0362	0	0	0.00 0244	0.00 085	0.00 026	0.00 0456	0.00 0252	0.00 1039	0.00 0291	0.00 0818	0.00 074	0.00 0189	0.00 0425	2.36 E-05	0.00 0102	0.00 0472	4.72 E-05	0	0.00 0543	7.87 E-05	3.15 E-05	7.87 E-05	0	1.57 E-05
SpecBear	omnivore	0.00 017	5.13 E-05	0	5.13 E-05	0.00 0923	0	0	0	5.13 E-05	0	0.00 041	5.13 E-05	0.00 0103	0	0.00 0462	0.00 0128	2.56 E-05	0.00 0103	2.56 E-05	0	0.00 0128	0	0	0.00 0718	0	0	0	0	0

Supplemental Table S13.The qPCR primers for *TP53* and amylase genes.

Primer code	Sequence (5'->3')	Target gene	Target species
TP53_New_BEAR_F	GAAGACCTACCCTGGCACCTA	TP53	Ursidae and giant panda
TP53_New_BEAR_R	CAGAAAAACCCAAGCGGAT		
TP53_New_CAT_F	CCCTGTCATCCTTTGTCCCT	TP53	Felidae
TP53_New_CAT_R	AAGGTCACGGGCCAAACTA		
AMY_New_BEAR_F	GCTTAGAGCTCCACAGCACA	amylase	Ursidae and giant panda
AMY_New_BEAR_R	CATTTCCATCCCCAGAAACA		
AMY_New_CAT_F	GCTTAGGGTTCTACAACACA	amylase	Felidae
AMY_New_CAT_R	CATTGCCATCCCCAGAAACA		

Supplemental Table S14. Amylase copy numbers in individuals quantified using real time PCR. Mean estimates of each individual from three replicates are reported.

Common name	Sample_ID	Copy number	Common name	Sample_ID	Copy number			
Giant panda	Yuanrui	2.11	Leopard	leopard-1	0.83			
	Eryatou	2.08		leopard-2	1.21			
	Longban	1.93	Tiger	pta03	1.05			
	Shulan	1.76		pta01	0.76			
	Yaqi	1.53		pta04	1.36			
	Qiuban	1.78		pta169	1.14			
	Wuyi	1.88		pta179	1.09			
	Yuanyuan	1.68		pta180	1.08			
	Yashuan	1.59		pta181	0.94			
	Maomao	1.79		pta199	0.98			
	Jili	1.87		pta201	1.24			
	Yuanyuany	2.12		pta202	0.99			
	Aoliao	2.08		pta203	1.24			
	Aili	1.74		pta204	1.04			
	Yingying	1.69		pta205	1.09			
	Mengmeng	1.79		pta206	1.19			
	Jinjin	2.07		pta216	1.18			
	Xiaojiao	2.01		pta217	1.15			
	Yalin	2.18		pta218	1.2			
	Qianqian	1.83		pta219	1.21			
	Dajiaozi	1.77		pta220	1.09			
	Mengmengm	1.83		pta221	1.22			
	Chengdui	2.11	pta222	1.34				
	Bingbing	2.02	pta273	1.23				
	Shuyun	1.68	Lion	lion-1	1.22			
	Yaer	1.59		lion-2	1.09			
	Menglan	1.99		lion-3	1.03			
	Hexin	2.01	Average		1.12			
	Xiaoyatou	1.93						
	Jiaozi	1.83						
Saner	1.86							
Chenggong	1.93							
Xinban	2.11							
Kelin	1.92							
Xiangbing	1.88							
Qinghe	1.89							
Nini	2.09							
Qizhen	1.8							
Bingdian	2.02							
Xingya	2.01							
Black bear	black-1	1.74						
	black-2	1.79						

Brown bear	brown-1	1.99	
	brown-2	2.07	
Average		1.89	

Supplemental Table S15. Amylase copy numbers found in whole genome data in *Carnivora* from NCBI.

Common name	Scientific name	Copy number
Amur tiger	<i>Panthera tigris altaica</i>	1
cheetah	<i>Acinonyx jubatus</i>	1
domestic cat	<i>Felis catus</i>	1
domestic ferret	<i>Mustela putorius furo</i>	1
Hawaiian monk seal	<i>Neomonachus schauinslandi</i>	1
leopard	<i>Panthera pardus</i>	1
Pacific walrus	<i>Odobenus rosmarus divergens</i>	1
Weddell seal	<i>Leptonychotes weddellii</i>	1
giant panda	<i>Ailuropoda melanoleuca</i>	2
polar bear	<i>Ursus maritimus</i>	2
dog	<i>Canis lupus familiaris</i>	6